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Article

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Mycosphere notes 449–468: saprobic and endophytic fungi in China, Thailand, and Uzbekistan

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Abstract

This is the tenth of the series Mycosphere Notes, wherein we present newly discovered saprobic and endophytic fungi isolated from various hosts in China, Thailand, and Uzbekistan. In this compilation, we introduce three new genera, *viz*., *Conicotenuis* (*Phomatosporaceae*), *Irregularispora* (*Stictidaceae*) and *Minimispora* (*Phomatosporaceae*), and 14 new species, *viz*., *Clonostachys artemisiae* (*Bionectriaceae*), *Conicotenuis fusiformis* (*Phomatosporaceae*), *Irregularispora olivacea* (*Stictidaceae*), *Melomastia loropetalicola* (*Pleurotremataceae*), *Minimispora superficialis* (*Phomatosporaceae*), *Montagnula agaves* (*Didymosphaeriaceae*), *Neodendryphiella brassaiopsidis* (*Dictyosporiaceae*), *Paramicrosphaeropsis sexualis* (*Didymellaceae*), *Pestalotiopsis camelliae-japonicae* (*Sporocadaceae*), *Pestalotiopsis pyrrosiae-linguae* (*Sporocadaceae*), *Pestalotiopsis zhaoqingensis* (*Sporocadaceae*), *Pseudocoleophoma heteropanacicola* (*Dictyosporiaceae*), *Pseudopaucispora heteropanacis* (*Lophiostomataceae*) and *Torula longan* (*Torulaceae*). In addition, two species *Melomastia phetchaburiensis* and *M. sinensis* are reviewed, and their illustrations are provided based on the holotype. A new host record of *Torula phytolaccae* is described from *Phytolacca americana*. We describe the sexual morph of *Paramicrosphaeropsis* for the first time and revise its generic concept herein.

Keywords – 17 new taxa – dematiaceous – *Dothideomycetes* – freshwater – hyaline-spored – *Lecanoromycetes* – molecular phylogeny – *Sordariomycetes* – taxonomy

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Introduction

This is a continuous series of Mycosphere Notes, following the publication by Hyde et al. (2023). In this series, a total of 17 new taxa are proposed, including three new genera and 14 new species. In addition, two interesting species in *Melomastia*, *viz.*, *M. phetchaburiensis* and *M. sinensis*, are reviewed. Each novelty is presented with a detailed morphological description, material information, photographic plate, phylogenetic tree, and a note that diagnose the new species.

Materials & Methods

The examination and interpretation of morphological characters follow the publication of Senanayake et al. (2020). The molecular tools, *viz.*, Bioedit v. 7.2.5, FigTree v. 1.4.03, Finch TV v. 1.4.0, MAFFT v. 7.409 online version (Katoh & Standley 2016), Mesquite v. 3.11, and CIPRES Science Gateway (Miller et al. 2010, 2015), utilized for phylogenetic analyses refer to the interpretation in recent papers (Manawasinghe et al. 2022, Wu & Diao 2022, Yang et al. 2023). In this study, the bootstrap support values generated from the Maximum likelihood consensus tree equal to or greater than 90% are treated as high bootstrap support. The diagnosis of novelties is guided by recently reviewed guidelines and integrative approaches (Jeewon & Hyde 2016, Chethana et al. 2021, Maharachchikumbura et al. 2021, Manawasinghe et al. 2021). Index Fungorum numbers and Facesoffungi numbers have been registered according to the instructions provided in Index Fungorum (2023) and Jayasiri et al. (2015).

Results

Taxonomy

Dothideomycetes O.E. Erikss. & Winka, Myconet 1(1): 5 (1997)
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= *Dyfrolomycetaceae* K.D. Hyde, K.L. Pang, Alias, Suetrong & E.B.G. Jones, Cryptog. Mycol. 34(3): 227 (2013)

Type genus – *Pleurotrema* Müll. Arg. 1885

Notes – *Pleurotremataceae* was established in 1929 by Watson (1929). *Dyfrolomycetaceae* was established in 2013 by Pang et al. (2013), and referred to *Dyfrolomycetales*. Subsequently, *Dyfrolomycetaceae* was treated as a synonym of *Pleurotremataceae* based on the morphological examination of *P. polysemum*, the type species of *Pleurotrema* (Maharachchikumbura et al. 2016). Therefore, *Pleurotremataceae* serves as the type and only family in *Dyfrolomycetales* (Maharachchikumbura et al. 2016). *Pleurotremataceae* comprises three genera, *viz.*, *Dyfrolomyces*, *Melomastia* and *Pleurotrema* (Wijayawardene et al. 2022).

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

= *Dyfrolomyces* K.D. Hyde, K.L. Pang, Alias, Suetrong & E.B.G. Jones, Cryptog. Mycol. 34(3): 227 (2013)

Type species – *Melomastia mastoidea* (Fr.) J. Schröt.

Notes – *Melomastia* exhibits close morphological similarities to *Dyfrolomyces*, as both possess dark, unilocular ascomata, cylindrical asci and overlapping uniseriate, fusiform, hyaline, multi-septate ascospores (Barr 1994, Pang et al. 2013). Investigations on their phylogenetic relationships from DNA sequence data became clearer upon the publication of *Melomastia italica* sequences (Norphanphoun et al. 2017). Li et al. (2022) synonymized *Dyfrolomyces* under *Melomastia* based on similar morphology and phylogenetic results. However, following a reassessment of their ascospore morphology and septation, as well as phylogenetic inference, Kularathnage et al. (2023) have reinstated *Dyfrolomyces* as a distinct genus. Meanwhile, certain species were provisionally assigned to *Melomastia sensu lato*, e.g., *M. phetchaburiens* and *M. sinensis*, considering that sparse collections and DNA sequence data may be insufficient for drawing further conclusions. In this study, we introduce a novel species *M. loropetalicola* within *Melomastia sensu stricto*, and reappraise the taxonomic issues of *M. phetchaburiensis* and *M. sinensis* regarding their ascospore morphology, ascomatal wall, and updated phylogenetic analysis.

Melomastia loropetalicola Kular., W. Dong & K.D. Hyde, sp. nov. Fig. 1

Index Fungorum number: IF900860; Facesoffungi number: FoF 14684

Etymology – referring to the host genus *Loropetalum*, from where the fungus was isolated.

Holotype – MHZU 22-0091

Saprobic on dead stem of *Loropetalum chinense*. Sexual morph: *Ascomata* 400–450 µm high, 300–320 µm diam., scattered, immersed or semi-immersed with erumpent papilla forming a black, cone-shaped structure on the host substrate, subglobose, unilocular, ostiolate, papillate, black, carbonaceous. *Peridium* 25–35 µm thick, comprising of dark brown to black, thick-walled, compressed cells of *textura angularis* and irregular cells, outer layer composed of amorphous cells fused with host substrate. *Pseudoparaphyses* 1–2 µm diam., numerous, cellular, cylindrical, aseptate, unbranched, hyaline. *Asci* 100–120 × 3–4.5 µm (av. 110 × 3.5 µm, n = 20), 8-spored, bitunicate, cylindrical, thin-walled, apically rounded, short pedicellate, with a bilobed, apical ring and an ocular chamber. *Ascospores* 13–16 × 3–4 µm (av. 15 × 3.5 µm, n = 20), uniseriate, straight or slightly curved at ends, fusiform with acute or obtuse ends, 3-septate, with one large guttulate in each cell, hyaline, thin-walled, without a sheath. Asexual morph: undetermined.

Material examined – China, Guangdong Province, Shenzhen City, Shenzhen University, on dead stem of *Loropetalum chinense* (R.Br.) Oliv. (*Hamamelidaceae*), 5 August 2020, N.D. Kularathnage NDK 32 (MHZU 22-0091, **holotype**); ex-type culture ZHKUCC 22-0174.

GenBank accession numbers – LSU: OP791870, SSU: OP739334.

Notes – *Melomastia loropetalicola* exhibits phylogenetic relationships with *M. fulvicomae* and *M. rhizophorae* within *Melomastia sensu stricto* (Fig. 2). *Melomastia loropetalicola* and *M. fulvicomae* exhibit overlapping ascospore size. However, *M. loropetalicola* is distinguished by longer asci (100–120 × 3–4.5 µm vs. 70–90 × 4–6 µm) and a greater number of septa in its ascospores (3-septate vs. mostly 2-septate) (Phukhamsakda et al. 2020). In addition, *M. fulvicomae* is characterized by the presence of a distinct mucilaginous sheath enveloping its ascospores, whereas such features are absent in the newly described species *M. loropetalicola*. The other species, *M. rhizophorae* can be easily distinguished from *M. loropetalicola* by its longer and wider asci (135–160 × 8–10 µm), larger ascospores (19–26 × 6–8 µm), and a greater number of septa (4–6-septate). In contrast, *M. loropetalicola* possesses shorter and thinner asci (100–120 × 3–4.5 µm), smaller ascospores (13–16 × 3–4 µm), and fewer septa (3-septate). With regard to DNA sequence data comparison, there is a discrepancy of 1.06% (9 out of 847) and 0.94% (9 out of 952) in nucleotide variations within the LSU and SSU genes, respectively, between *M. loropetalicola* ZHKUCC 22-0174 and *M. fulvicomae* MFLUCC 17-2083. In addition, there is a discrepancy of 4.8% (42 out of 875) in nucleotide differences within the LSU gene between *M. loropetalicola* ZHKUCC 22-0174 and *M. rhizophorae* JK5456A. Based on our phylogenetic analysis (Fig. 2) and a morphological comparison with all species compiled by Kularathnage et al. (2023), *M. loropetalicola* is proposed as a novel species within *Melomastia*.

Figure 1 – *Melomastia loropetalicola* (MHZU 22-0091, holotype). a Host. b, c Appearance of black ascomata erumpent on host. d Vertical section of an ascoma. e Peridium. f Pseudoparaphyses. g Apical apparatus. h–k Asci. l–o Ascospores. Scale bars: d = 300 µm, e = 40 µm, f, g = 5 µm, h–k = 20 µm, l–o = 15 µm.

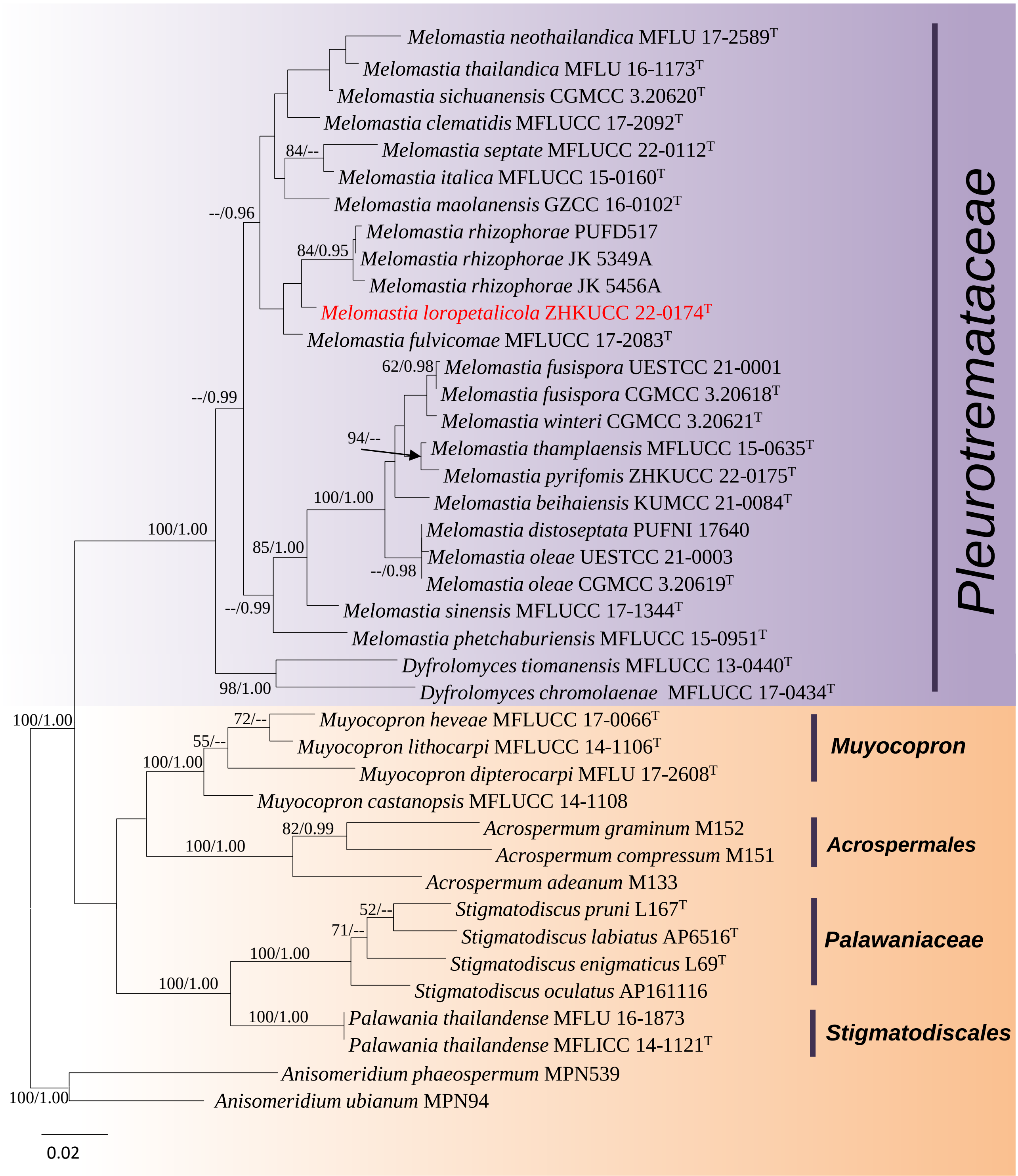

Figure 2 – Maximum likelihood consensus tree inferred from the combined LSU, SSU and *tef1-α* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 50% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.90 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Anisomeridium phaeospermum* MPN539 and *A. ubianum* MPN94. Ex-type strains are indicated with "^{T}". The new species is indicated in red.

Melomastia sinensis (Samarak., Tennakoon & K.D. Hyde) W.L. Li, Maharachch. & Jian K. Liu, Journal of Fungi 8(1, no. 76): 16 (2022) (? *Melomastia*) Fig. 3

Basionym: *Dyfrolomyces sinensis* Samarak., Tennakoon & K.D. Hyde, Mycosphere 9(2): 354 (2018)

Notes – *Dyfrolomyces sinensis* was isolated from stems of *Camellia sinensis* in Chiang Rai Province, Thailand (Hyde et al. 2018). The identification of *D. sinensis* was based on its morphological similarities with *D. phetchaburiensis* and *D. thamplaensis*, and DNA based phylogenies depicted that it belongs to *Dyfrolomyces*. Given that *Dyfrolomyces* and *Melomastia* share close morphological resemblances, their taxonomy has always been controversial in the past (Norphanphoun et al. 2017, Li et al. 2022, Kularathnage et al. 2023). Norphanphoun et al. (2017) highlighted this issue when describing *Melomastia italica*, a new species from dead branches of *Vitis vinifera* in Italy. They also discussed the problems pertaining to the differences between the two genera based on morphology and DNA sequence data. However, they did not make any taxonomic amendments. Li et al. (2022) reassessed intergeneric relationships and synonymized *Dyfrolomyces* under *Melomastia* with 11 new combinations. With further taxonomic studies, Kularathnage et al. (2023) have concluded that *M. sinensis* should not be classified under *Melomastia* or *Dyfrolomyces* considering its distinct morphology that have narrowly oblong ascospores with 6–7 septa, and instead temporarily placed in *Melomastia sensu lato*. They also reinstated the genus *Dyfrolomyces* to accommodate *M. tiomanensis* (type) and *M. chromolaenae* as the latter two taxa constituted a strongly supported subclade basal to *Melomastia*. Our updated phylogenetic analysis further confirms the conclusion of Kularathnage et al. (2023), and *M. sinensis* also clusters as a basal branch to the clade of *Melomastia sensu lato*.

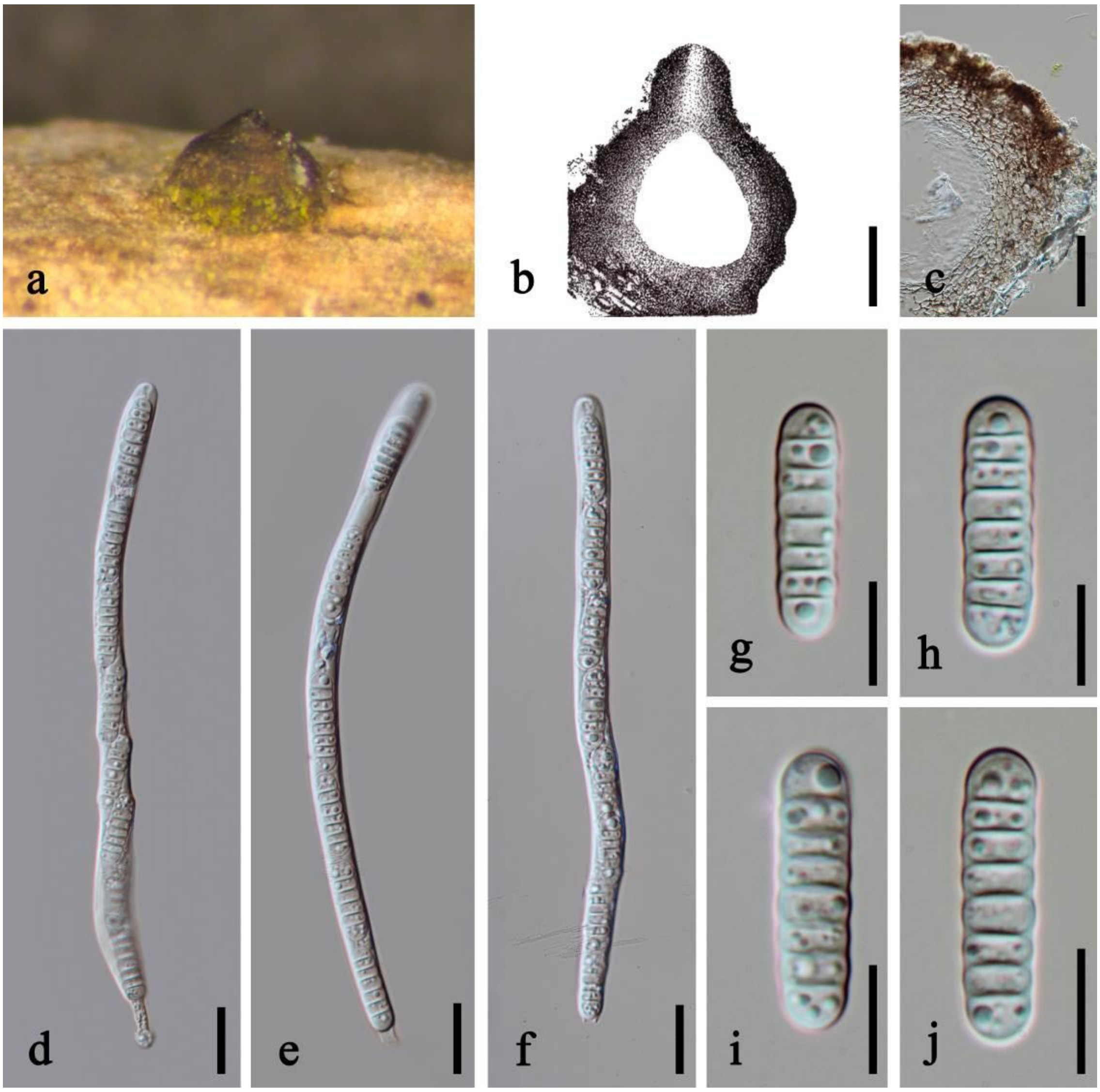

Figure 3 – *Melomastia sinensis* (Material examined – Thailand, Chiang Rai Province, Mae Fah Luang University, on stems of *Camellia sinensis* (Theaceae), 25 March 2017, Danushka S.

Tennakoon, MFLU 17-0777, holotype). a Appearance of black ascoma on the host. b Hand-drawing of a vertical section of an ascoma (Redrawn from Hyde et al. 2018). c Peridium. d–f Asci. g–j Ascospores. Scale bars: b = 200 µm, c = 50 µm, d–f = 20 µm, g–j = 10 µm.

According to the compiled information provided by Kularathnage et al. (2023), we found that the morphology of *Melomastia sinensis* is very unusual in *Pleurotremataceae*. *Melomastia sinensis* is characterized by cylindrical ascospore, which has 6–7 septa (Fig. 3). In contrast, the ascospores in *Melomastia sensu stricto* and *Melomastia sensu lato* are mostly fusiform with rounded or acute ends which have fewer septa (mostly 3). The other notable feature of *M. sinensis* is its evenly considerable thick ascomatal wall measured as 55–75 µm (Hyde et al. 2018). We doubt that if *M. sinensis* can represent a separate genus regarding its unusual morphology. However, in the phylogenetic analysis (Fig. 2), *M. neothailandica* and *M. thailandica* which share similar morphology with *M. sinensis* have distant relationships with *M. sinensis*. Although *M. neothailandica* and *M. thailandica* have weak relationships with their allies, they never group with *M. sinensis* in all previous studies (Dayarathne et al. 2020, Li et al. 2022, Kularathnage et al. 2023) and this study (Fig. 3). Therefore, we treat *M. sinensis* as uncertain species in *Melomastia* until more data are available to establish a new genus to accommodate them.

Melomastia phetchaburiensis (Dayar., E.B.G. Jones & K.D. Hyde) W.L. Li, Maharachch. & Jian K. Liu, Journal of Fungi 8(1, no. 76): 16 (2022) (? *Melomastia*) Fig. 4

Basionym: *Dyfrolomyces phetchaburiensis* Dayar., E.B.G. Jones & K.D. Hyde, Fungal Diversity 87: 33 (2017)

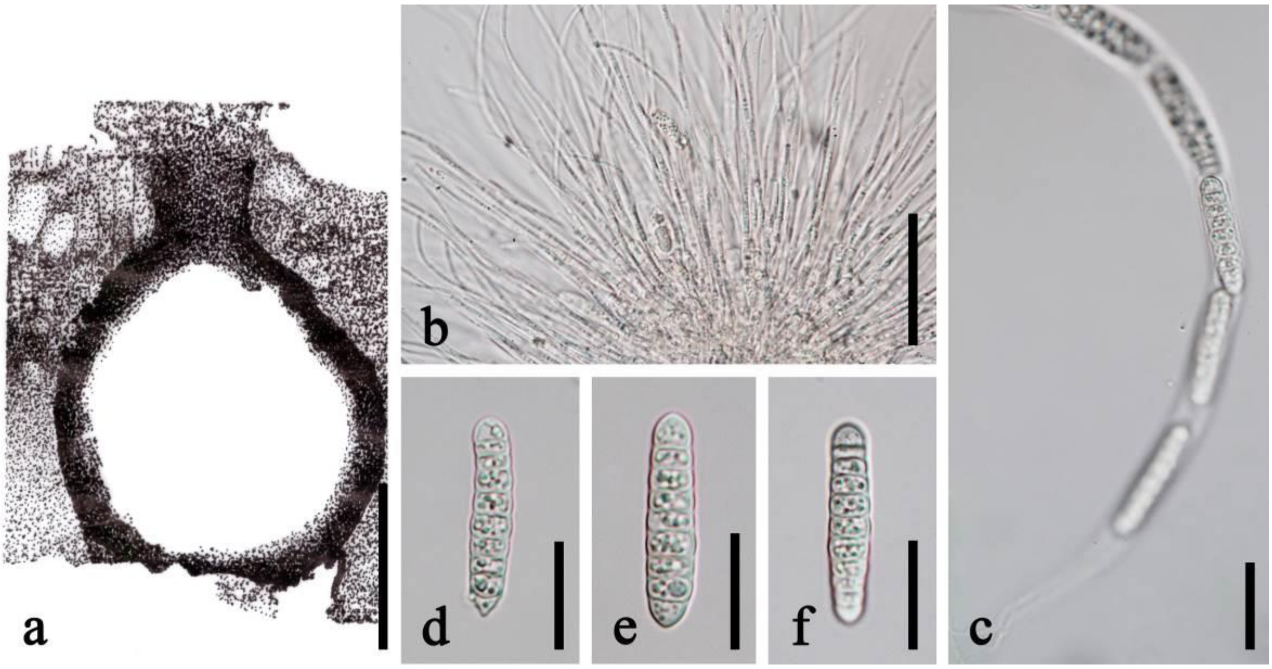

Figure 4 – *Melomastia phetchaburiensis* (Material examined – Thailand, Phetchaburi Province, Hat Chao Samran, on submerged wood of *Rhizophora apiculata*, 28 July 2015, M. Dayarathne, MFLU 16-1180, holotype). a Hand-drawing of a vertical section of an ascoma (Redrawn from Hyde et al. 2017). b Pseudoparaphyses. c Ascus. d–f Ascospores. Scale bars: a = 150 µm, b = 50 µm, c–f = 20 µm.

Notes – *Dyfrolomyces phetchaburiensis* was isolated from submerged wood of *Rhizophora apiculata* in Phetchaburi Province, Thailand, and the identification was based on limited DNA sequence data (Hyde et al. 2017). As additional DNA sequence data were acquired, Li et al. (2022) reclassified it as *M. phetchaburiensis* within *Melomastia*. However, Kularathnage et al. (2023)

disagreed with this taxonomic arrangement and provisionally placed it in *Melomastia sensu lato.* In our phylogenetic analysis, *M. phetchaburiensis* is clustered as a basal branch to *Melomastia sensu lato* and *M. sinensis* (uncertain species) but with low bootstrap support (Fig. 2). The comparison of LSU sequences reveals a discrepancy of 31 distinct nucleotides between *M. phetchaburiensis* and *M. sinensis*, implying that they are likely to represent separate genera (Jeewon & Hyde 2016). However, *M. phetchaburiensis* is quite similar to *M. sinensis*, except for the thin ascomatal wall comprising several layers of heavily pigmented, undifferentiated cells (Figs 3, 4). In addition, *M. sinensis* is still an uncertain species, so we treat *M. phetchaburiensis* as an uncertain species as well until more data are available in the future.

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

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity 80: 462 (2016)

Type genus – *Dictyosporium* Corda

Notes – *Dictyosporiaceae* (*Dothideomycetes*) was proposed to accommodate a group of saprobic asexual fungi collected from decaying wood and plant debris in terrestrial and freshwater habitats (Boonmee et al. 2016). The asexual morphs are hyphomycetous characterized by brown, multi-septate, cheirosporous conidia. The sexual morph has been determined with DNA sequence-based evidence coupled with cultural studies, and is characterized by globose to subglobose, dark ascomata and fusiform, hyaline, septate ascospores with or without a sheath (Boonmee et al. 2016). By using molecular data, the placements of some obscured species within its member *Dictyocheirospora* (e.g. *D. hyde*, *D. indica*, *D. musae* and *D. tetraploides*) have been resolved and some new genera (e.g. *Aquadictyospora*, *Jalapriya* and *Pseudocyclothyriella*) were also established (Boonmee et al. 2016, Li et al. 2017, Yang et al. 2018, Jiang et al. 2021).

Neodendryphiella Iturrieta-González, Dania García & Gené, MycoKeys 37: 25 (2018)

Type species – *Neodendryphiella tarraconensis* Iturrieta-González, Gené & Dania García

Notes – *Neodendryphiella* was recently established for three species isolated from soil, herbivore dung and plant leaf (Iturrieta-González et al. 2018). The genus is featured as differentiated conidiophores and polytretic integrated conidiogenous cells that produce acropetal branched chains of conidia. In this study, we introduce a novel species *N. brassaiopsidis* isolated from dead stems of *Brassaiopsis hainla*.

Neodendryphiella brassaiopsidis Doilom, K.D. Hyde & C.F. Liao, sp. nov. Fig. 5

Index Fungorum number: IF900861; Facesoffungi number: FoF 14685

Etymology – referring to the host *Brassaiopsis hainla*, from where it was isolated.

Holotype – MHZU 23-0113

Saprobic on dead stems of *Brassaiopsis hainla*. Sexual morph: undetermined. Asexual morph: *Colonies* effuse, dense, velvety, brown on the host. *Mycelium* superficial and immersed, composed of septate, branched, smooth to verruculose, hyaline to pale brown hyphae. *Conidiophores* up to 460 µm long, 7.5–14 µm wide at the base, 4.5–6 µm wide in the middle portion, 2.5–5 µm wide near the apex, macronematous, mononematous, erect, flexuous, branched, septate, cylindrical, robust and darker at the base, brown to dark brown, black at maturity, tapering towards the apex, sometimes with a percurrent proliferation or generates a new proliferation after the break offs, which forms the subhyaline cells, smooth to verruculose. *Conidiogenous cells* 13.5–30 × 3.2–5.5 µm (av. 23.5 × 4 µm, n = 10), enteroblastic, polytretic, integrated, percurrent proliferation, terminal and intercalary, subcylindrical, brown or subhyaline, with several pores surrounded by a thickened and darkened wall. *Ramoconidia* 8–15 × 3–4.7 µm (av. 11.5 × 4.2 µm, n = 10), subcylindrical, with up to 2 terminal and lateral pores, and conidial scars often thickened and darkened, pale brown, 0–1-septate, not constricted at the septum, smooth to verruculose. *Conidia* 7.3–9.7 × 3.5–4.8 µm (av. 8.5 × 4.2 µm, n = 15), catenate, subcylindrical, with rounded or truncate ends, pale brown, (0–)1-septate, not constricted at the septum, smooth to verruculose.

Culture characteristics – colonies on PDA reaching 30 mm diam. at 25 °C after two months, flat, dry, rough, felty, margin undulate and irregular; from above, gray at the margin, brown in the middle; from below, brown at the margin, black in the middle; not producing pigmentation in the culture.

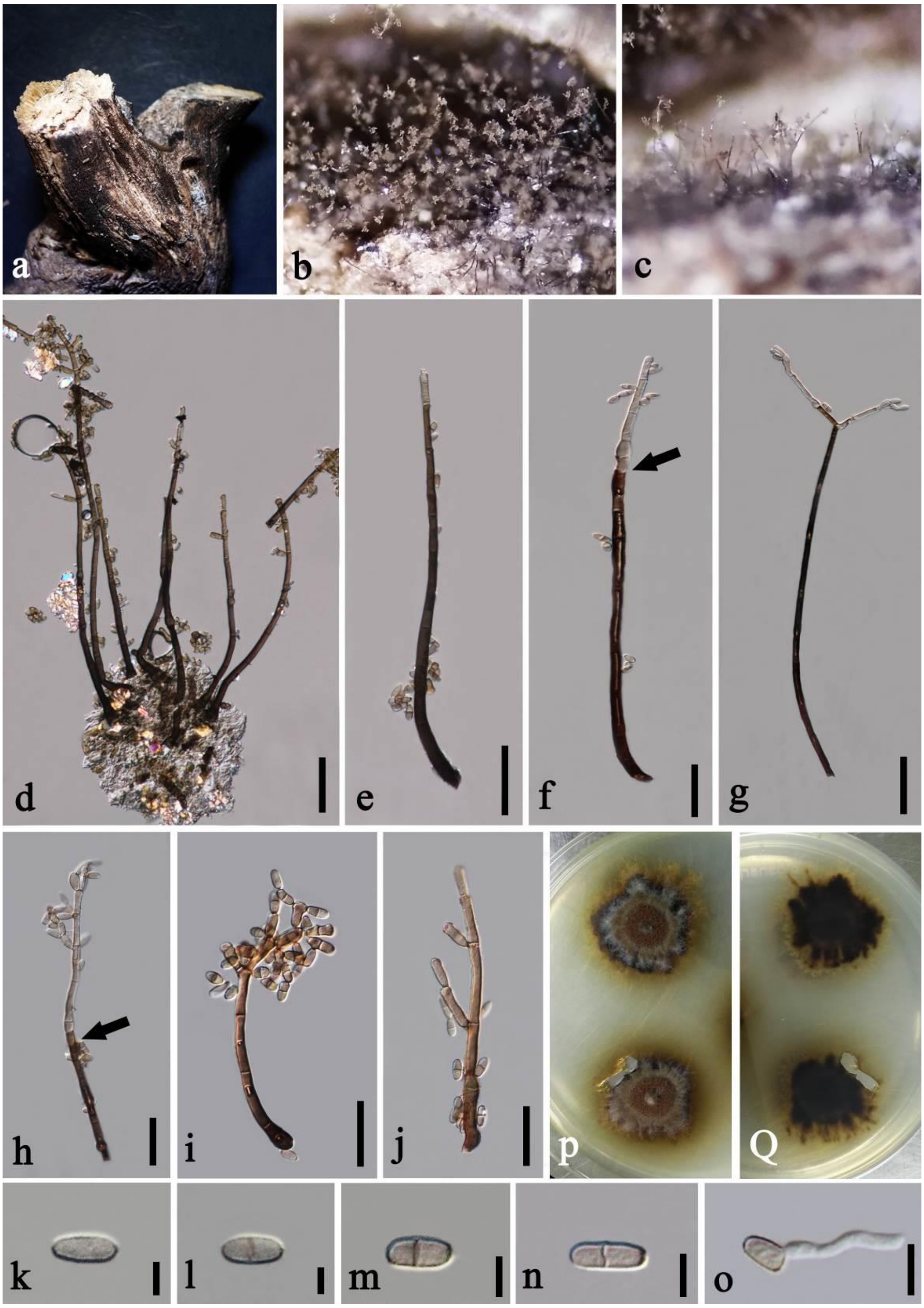

Figure 5 – *Neodendryphiella brassaiopsidis* (MHZU 23-0113, holotype). a Decaying branch of host. b, c Colonies on natural substrate. d–j Conidiophores, conidiogenous cells and conidia (arrows indicate enteroblastic conidiogenous cells). k–n Conidia. o Germinated conidium. p, q Colony on PDA (front and below). Scale bars: d, e, g = 50 µm, f = 20 µm, h–j = 30 µm, k–n = 5 µm, o = 10 µm.

Material examined – China, Yunnan Province, Kunming City, on dead stems of *Brassaiopsis hainla* (Buch.-Ham.) Seem. (*Araliaceae*), 17 August 2019, M. Doilom & C.F. Liao EH02 (MHZU 23-0113, **holotype**); ex-type culture ZHKUCC 23-0879.

GenBank accession numbers – ITS: OR365455, LSU: OR365485, SSU: OR365491.

Notes – *Neodendryphiella brassaiopsidis* is nested in the clade of *Neodendryphiella* and is basal to *N. mali* (type) and *N. michoacanensis* (Fig. 7). *Neodendryphiella brassaiopsidis* fits well with the generic concept of *Neodendryphiella* in some key morphological features such as polytretic conidiogenous cells producing the subcylindrical ramoconidia and catenate conidia. Except for *N. tarraconensis* which has 2-septate conidia, *N. mali* and *N. michoacanensis* have (0–)1-septate conidia which are similar to *N. brassaiopsidis*. However, *N. brassaiopsidis* has shorter conidia (7.3–9.7 × 3.5–4.8 µm) as compared to *N. mali* (4–15 × 3–5 µm) and *N. michoacanensis* (5–18 × 3–6 µm) (Iturrieta-González et al. 2018). In addition, *N. brassaiopsidis* is unique in the genus as its conidiogenous cells are subhyaline, have percurrent proliferation and formed enteroblastically from the conidiophores. With regard to DNA sequence data comparison, there is a discrepancy of 5.59% (24 out of 429) and 0.68% (4 out of 592) in nucleotide variations within the ITS and LSU genes, respectively, between *N. brassaiopsidis* ZHKUCC 23-0879 and *N. mali* CBS 139.95. In addition, there is a discrepancy of 3.50% (15 out of 429) and 1.01% (6 out of 592) in nucleotide variations within the ITS and LSU genes, respectively, between *N. brassaiopsidis* ZHKUCC 23-0879 and *N. michoacanensis* FMR 16098. Therefore, *N. brassaiopsidis* is introduced as a novel species within the genus based on morphology and phylogeny.

Pseudocoleophoma Kaz. Tanaka & K. Hiray., Stud. Mycol. 82: 89 (2015)

Type species – *Pseudocoleophoma calamagrostidis* Kaz. Tanaka & K. Hiray.

Notes – *Pseudocoleophoma* was introduced to accommodate the species having immersed to erumpent ascomata with central ostiolar neck, cylindrical to clavate asci, and fusiform, 1-septate ascospores with a conspicuous sheath, and coleophoma-like conidia (Tanaka et al. 2015). Despite an increase in taxon sampling in phylogenies, the relationships among *Pseudocoleophoma* species have remained obscure, with poor phylogenetic support and increased polytomies (Phukhamsakda et al. 2020, Jiang et al. 2021). Based on morphology and phylogeny, Jiang et al. (2021) transferred *Pseudocoleophoma clematidis* to a new genus *Pseudocyclothyriella*. In this study, a new species, *Pseudoco. heteropanoxicola*, is added in the genus *Pseudocoleophoma*. Our multigene phylogeny reveals that *Pseudoco. puerensis* and *Pseudoco. typhicola* are not closely related to the type species *Pseudoco. calamagrostidis* but formed two distinct branches with *Pseudoconiothyrium* with low bootstrap support (Fig. 7). This highlights that *Pseudoco. puerensis* and *Pseudoco. typhicola* are obscure species that require further taxonomic review.

Pseudocoleophoma heteropanacicola Doilom, K.D. Hyde & C.F. Liao, sp. nov. Fig. 6

Index Fungorum number: IF900862; Facesoffungi number: FoF 14686

Etymology – referring to the host *Heteropanax fragrans*, from where it was isolated.

Holotype – MHZU 23-0114

Saprobic on dead stems of *Heteropanax fragrans*. Sexual morph: *Ascomata* 230–260 µm high, 300–335 µm diam., clustered, immersed to erumpent, with a wide opening on the surface of substrate, showing the white inclusion, conical with truncate apex or depressed globose, black, unilocular, with an ostiolate, central papilla. *Ostioles* 105–115 µm wide, large, periphysate. *Peridium* 25–35 µm thick, composed of several layers of hyaline, thin-walled, compressed cells of *textura angularis*, while black and thick-walled cells surrounding the ostiole. *Pseudoparaphyses* 2–2.5 µm wide, numerous, cellular, sparsely septate, unbranched, hyaline. *Asci* 75–90 × 9–11 µm (av. 78 × 9.6 µm, n = 10), 8-spored, bitunicate, clavate, apically rounded, with a shallow ocular chamber, short pedicellate. *Ascospores* 15–19 × 3.2–4.2 µm (av. 16.8 × 3.6 µm, n = 15), bi- to overlapping tri-seriate, uniseriate towards the pedicel of asci, fusiform, straight or slightly curved, 3-septate, constricted at the mid-septum, slightly or not constricted at the septa near the ends, hyaline, smooth- and thin-walled, with an entire, conspicuous sheath. *Sheath* sharply delimited, with narrow, tapering ends, 2–4 µm thick. Asexual morph: undetermined.

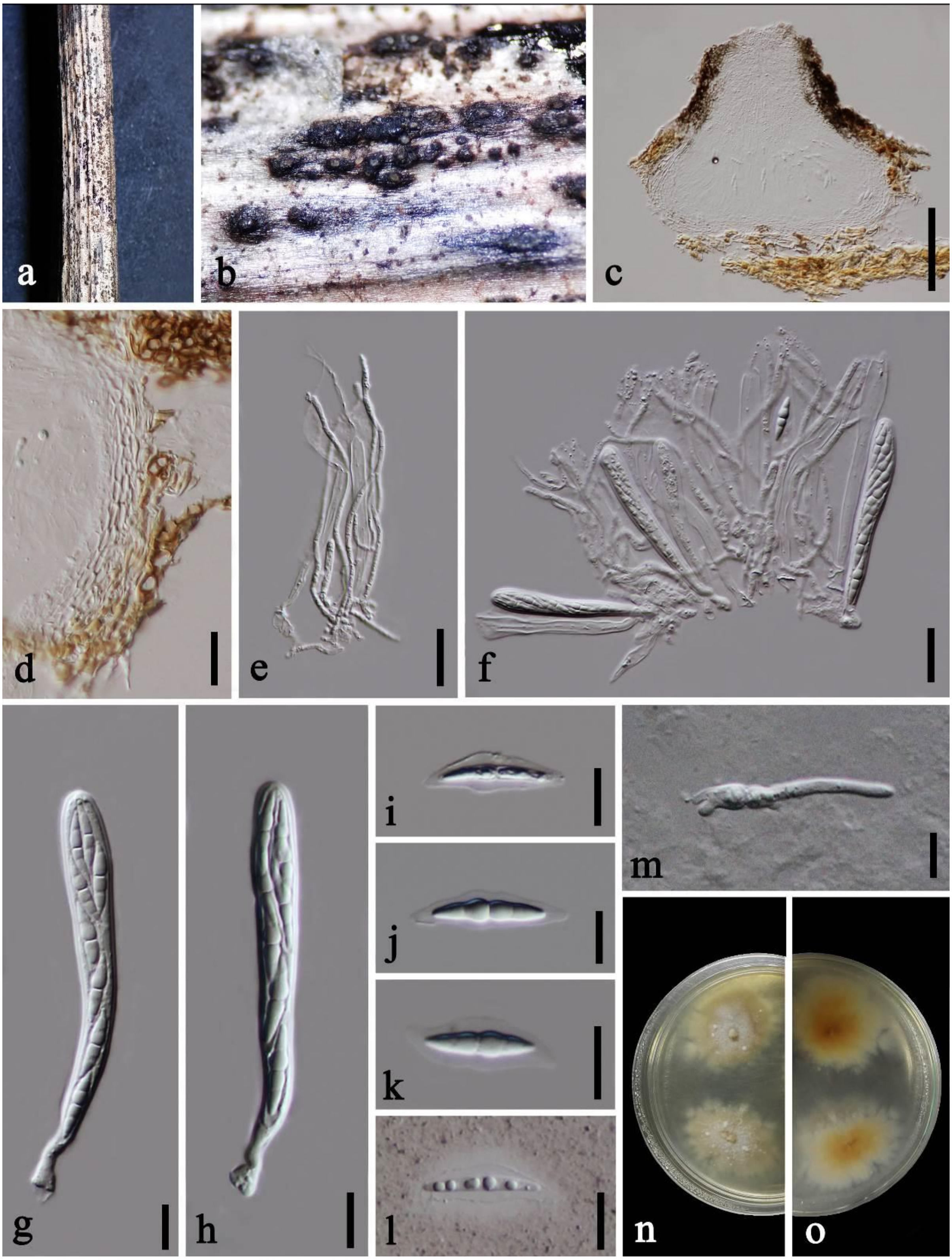

Figure 6 – *Pseudocoleophoma heteropanacicola* (MHZU 23-0114, holotype). a Decaying branch of host. b Ascomata on the host surface. c Longitudinal section of an ascoma. d Peridium. e Pseudoparaphyses. f Asci with pseudoparaphyses. g, h Asci. i–l Ascospores (l ascospore mounted in Indian Ink). m Germinated ascospore. n, o Colony on PDA (front and below). Scale bars: c = 100 µm, d–f = 20 µm, g–m = 10 µm.

Culture characteristics – colonies on PDA reaching 40 mm diam. at 25 °C after 45 days, irregular, umbonate, dry, mycelium mostly immersed in the culture, margin undulate and irregular; from above, white; from below, white at the margin, reddish brown in the middle; not producing pigmentation in the culture.

Material examined – China, Yunnan Province, Kunming City, on dead stems of *Heteropanax fragrans* (Roxb.) Seem. (*Araliaceae*), 17 August 2019, M. Doilom & C.F. Liao HF05 (MHZU 23-0114, **holotype)**; ex-type culture ZHKUCC 23-0880.

GenBank accession numbers – ITS: OR365456, LSU: OR365486, *tef1-α*: OR700204.

Notes – *Pseudocoleophoma heteropanacicola* is closely related to *P. rusci* in our phylogenetic analysis (Fig. 7). The morphology of the two species cannot be compared as *P. rusci* has a coelomycete morph, while *P. heteropanacicola* has an ascomycete morph (Li et al. 2020). The conidia are not observed in the culture of *P. heteropanacicola* but it fits well with the sexual characteristics of *Pseudocoleophoma*. *Pseudocoleophoma heteropanacicola* is similar to *P. calamagrostidis* and *P. polygonicola* in ascospore morphology but differs from *P. calamagrostidis* by the thicker peridium (25–35 μm vs. 5–10 μm) and differs from *P. polygonicola* by smaller ascospores (15–19 × 3.2–4.2 μm vs. 19–23 × 4–6 μm) (Tanaka et al. 2015). Multi-gene phylogeny indicates that the three species have weak phylogenetic relationships (Fig. 7). With regard to DNA sequence data comparison, there is a discrepancy of 2.19% (12 out of 548) and 0.84% (7 out of 832) in nucleotide variations within the ITS and LSU genes, respectively, between *P. heteropanacicola* ZHKUCC 23-0880 and its closely related species *P. rusci* MFLUCC 16-1444. Therefore, *P. heteropanacicola* is introduced as a novel species within the genus based on morphology and phylogeny.

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

Type genus – *Didymella* Sacc.

Notes – *Didymellaceae* was proposed to encompass *Phoma* sections and related phoma-like anamorphic genera (de Gruyter et al. 2009). Subsequently, Zhang et al. (2009) assigned *Didymellaceae* in suborder Pleosporineae within *Pleosporales* based on multi-locus phylogenetic analysis and morphological comparisons. In the checklist of anamorphic fungi, Wijayawardene et al. (2012) listed 11 asexual morphs within the family. Several revisions have been conducted on the members of *Didymellaceae* to establish taxonomic relationships within the *Ascochyta-Didymella-Phoma* complex (Woudenberg et al. 2013, Chen et al. 2015, Wanasinghe et al. 2018, Hongsanan et al. 2020). *Didymellaceae* encompasses 44 genera according to Wijayawardene et al. (2022).

Paramicrosphaeropsis L.W. Hou, L. Cai & Crous, Stud. Mycol. 96: 376 (2020)

Type species – *Paramicrosphaeropsis ellipsoidea* L.W. Hou, L. Cai & Crous

Notes – *Paramicrosphaeropsis* was established to accommodate a coelomycete *P. ellipsoidea*, which is characterized by pycnidial conidiomata, phialidic conidiogenous cells, and broadly ellipsoidal, oblong or ovoid, hyaline conidia (Hou et al. 2020). The genus is distinguished from its phylogenetically related genera *Neomicrosphaeropsis* and *Microsphaeropsis* by the formation of an exceptionally thin and hyaline pycnidial wall. Recently, an increasing number of species have been identified within the genus (Ahmadpour et al. 2022, Artand et al. 2022). In this study, we have identified an additional ascomycete based on multi-locus phylogenetic analysis. This is the first reported sexual morph species in the genus.

The revised generic concept of *Paramicrosphaeropsis* is presented as follows: Sexual morph: *Ascomata* tiny, solitary or gregarious, or scattered, immersed to erumpent, appear as black dots on the host, black. *Peridium* is composed of several layers of dark brown, thick-walled, large cells of *textura angularis*. *Hamathecium* comprising of aseptate, trabeculate pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, sessile. *Ascospores* bi- to tri-seriate, subcylindrica, septate, hyaline (this study). Asexual morph: coelomycetous. *Conidiomata* pycnidial, mostly semi-immersed, abundant, mostly solitary, globose to subglobose, pale brown. *Pycnidial wall* pseudoparenchymatous, thin, multi-layered, hyaline at first, dark brown with age.

Conidiogenous cells phialidic, subglobose, ampulliform to lageniform, hyaline, smooth. *Conidia* variable in shape, broad ellipsoidal, oblong or ovoid, aseptate, hyaline when young, brown with age, thin-walled, smooth (Hou et al. 2020).

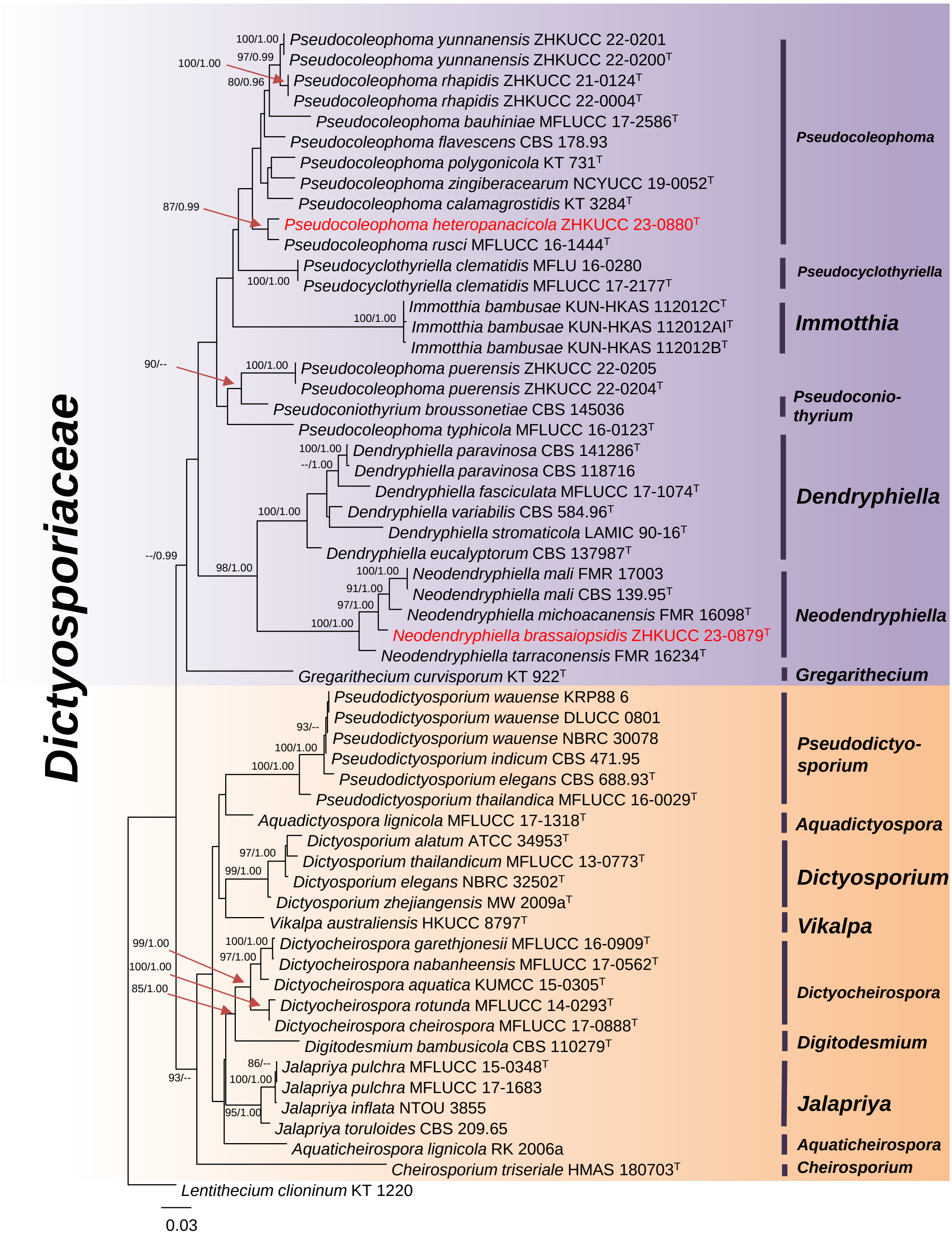

Figure 7 – Maximum likelihood consensus tree inferred from the combined ITS, LSU and *tef1-α* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates

expected changes per site. The tree is rooted to *Lentithecium clioninum* KT 1220. Ex-type strains are indicated with “^{T}”. The new species are indicated in red.

Paramicrosphaeropsis sexualis D. Pem, Gafforov & K.D. Hyde, sp. nov. Fig. 8

Index Fungorum number: IF900637; Facesoffungi number: FoF 14687

Etymology – referring to the first sexual morph within the genus.

Holotype – TASM 6168

Saprobic on dead stem. Sexual morph: *Ascomata* 90–120 µm high, 115–145 µm diam., tiny, solitary or gregarious, or scattered, immersed to erumpent, appear as black dots on the host, black. *Peridium* 20–30 µm thick, composed of 3–4 layers of dark brown, thick-walled, large cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide, comprising of aseptate, trabeculate pseudoparaphyses. *Asci* 45–85 × 12–15 µm (av. 60 × 14 µm, n = 10), 8-spored, bitunicate, fissitunicate, cylindric-clavate to clavate, sessile, with an ocular chamber. *Ascospores* 15–20 × 4.3–5.0 µm (av. 16.8 × 4.8 µm, n = 15), bi- to tri-seriate, subcylindrical with narrow ends, 1-septate, slightly constricted at the septum, upper cell slightly wider than the lower cell, hyaline, smooth-walled. Asexual morph: production of chlamydospores.

Culture characteristics – colonies on MEA reaching 30 mm diam. at 25 °C after a week, flat, dry, sparse aerial mycelium, with white, pale orange concentric rings, felty, margin well-defined; from above, pale white at the margin, dense whitish mycelium in the middle; from reverse, white at the margin, pale orange in the middle; not producing pigmentation in the culture.

Material examined – Uzbekistan, Tashkent Province, Oqtosh sanatorium, Ugam-Chatkal National Park, Western Tien-Shan mountain, on dead stems of *Alcea* sp., 4 October 2016, Y. Gafforov YG-Oq-77-1 (TASM 6168, **holotype**); ex-type culture MFLUCC 22-0087.

GenBank accession numbers – ITS: OR211371, LSU: OR211372, tub2: OR234582.

Notes – *Paramicrosphaeropsis sexualis* nests in the clade of *Paramicrosphaeropsis* and forms a distinct branch with *P. ellipsoidea* (type) and *P. zagrosensis* (Fig. 10). The morphological comparison cannot be conducted between these taxa due to the absence of any reported sexual morph within *Paramicrosphaeropsis*, and *P. sexualis* represents the first sexual morph within this genus. *Paramicrosphaeropsis sexualis* can produce subglobose to ellipsoidal, smooth, brown chlamydospores that are solitary or in chains after being cultured on MEA. These chlamydospores are similar to those produced by *P. iranica* (Ahmadpour et al. 2022), which belongs to a different phylogenetic branch. With regard to DNA sequence data comparison, there is a discrepancy of 0.35% (2 out of 571) and 3.08% (10 out of 324) in nucleotide variations within the ITS and tub2 genes, respectively, between *P. sexualis* MFLUCC 22-0087 and *P. ellipsoidea* CBS 194.97. In addition, there is a discrepancy of 0.17% (1 out of 571) and 2.16% (7 out of 324) in nucleotide variations within the ITS and tub2 genes, respectively, between *P. sexualis* MFLUCC 22-0087 and *P. zagrosensis* IRAN 4448C. Within *Paramicrosphaeropsis*, the tub2 is the most informative marker for distinguishing between the two species, while ITS exhibit comparatively lower of informativeness (Ahmadpour et al. 2022, Artand et al. 2022), which is also shown in this study. Based on phylogeny and morphology, *P. sexualis* is, therefore, introduced as a novel species within the genus.

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

Type genus – *Didymosphaeria* Fuckel, Jb. nassau. Ver. Naturk. 23-24: 140 (1870) [1869–70]

Notes – *Didymosphaeriaceae* was established by Munk (1953) and characterized by 1-septate ascospores and trabeculate pseudoparaphyses mainly anastomosing above the asci. Species in the family are saprobes, endophytes and pathogens associated with a diverse range of host plants (Hyde et al. 2013, Ariyawansa et al. 2014, Tennakoon et al. 2016, Wanasinghe et al. 2016, Mapook et al. 2020). Since *Didymosphaeriaceae* was reappraised to clarify the phylogenetic relationships of all genera (Ariyawansa et al. 2014), this family has been widely used and now comprises 33 genera according to the latest outline of fungi by Wijayawardene et al. (2022).

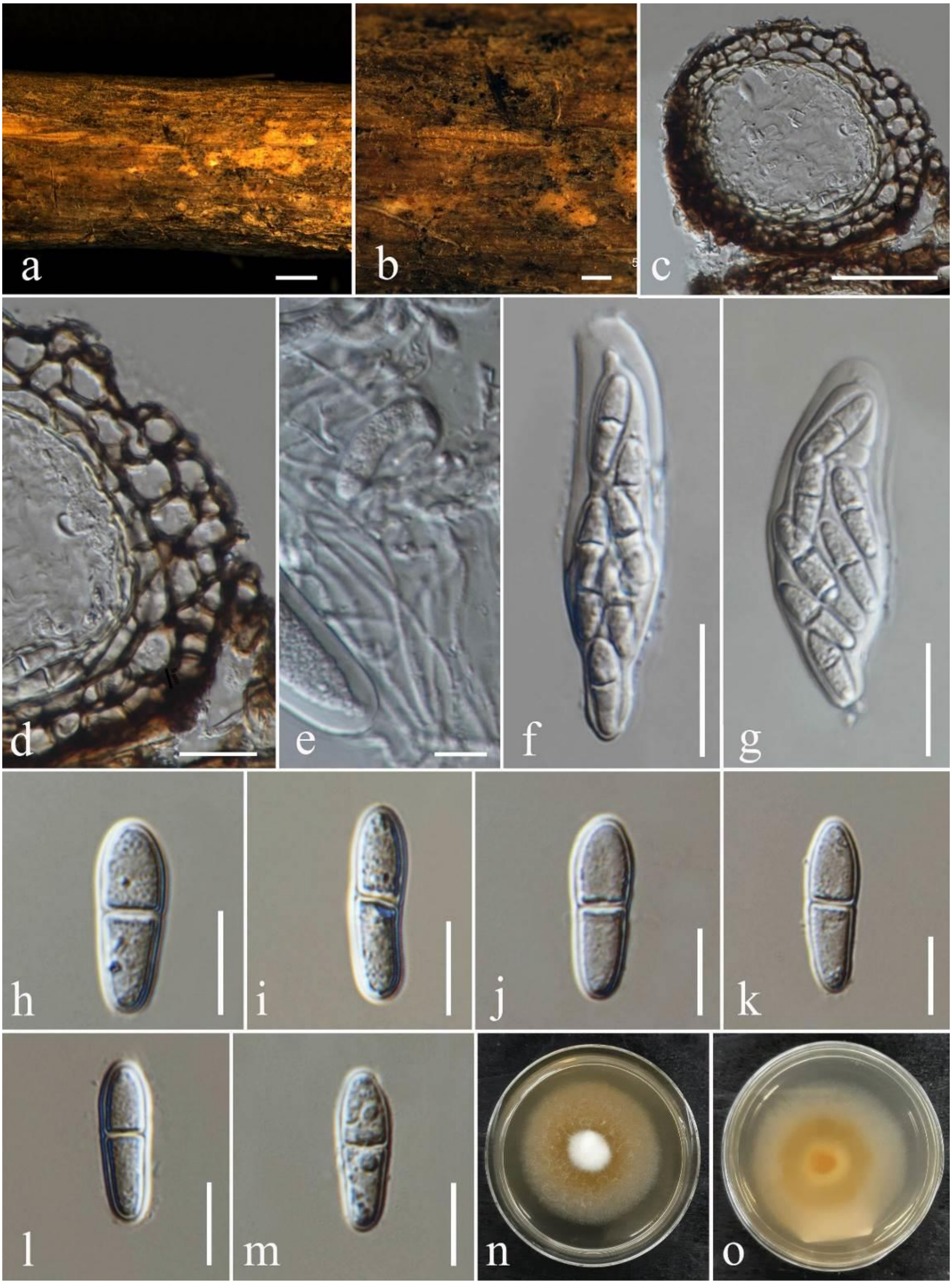

Figure 8 – *Paramicrosphaeropsis sexualis* (TASM 6168, holotype). a, b Appearance of ascomata on host substrate. c Section through ascoma. d Peridium. e Trabeculate pseudoparaphyses. f, g Asci. h–m Ascospores. n, o Colony on MEA (front and below). Scale bars: a = 2 mm, b = 500 µm, c = 50 µm, d, f, g = 20 µm, e, h–m = 10 µm.

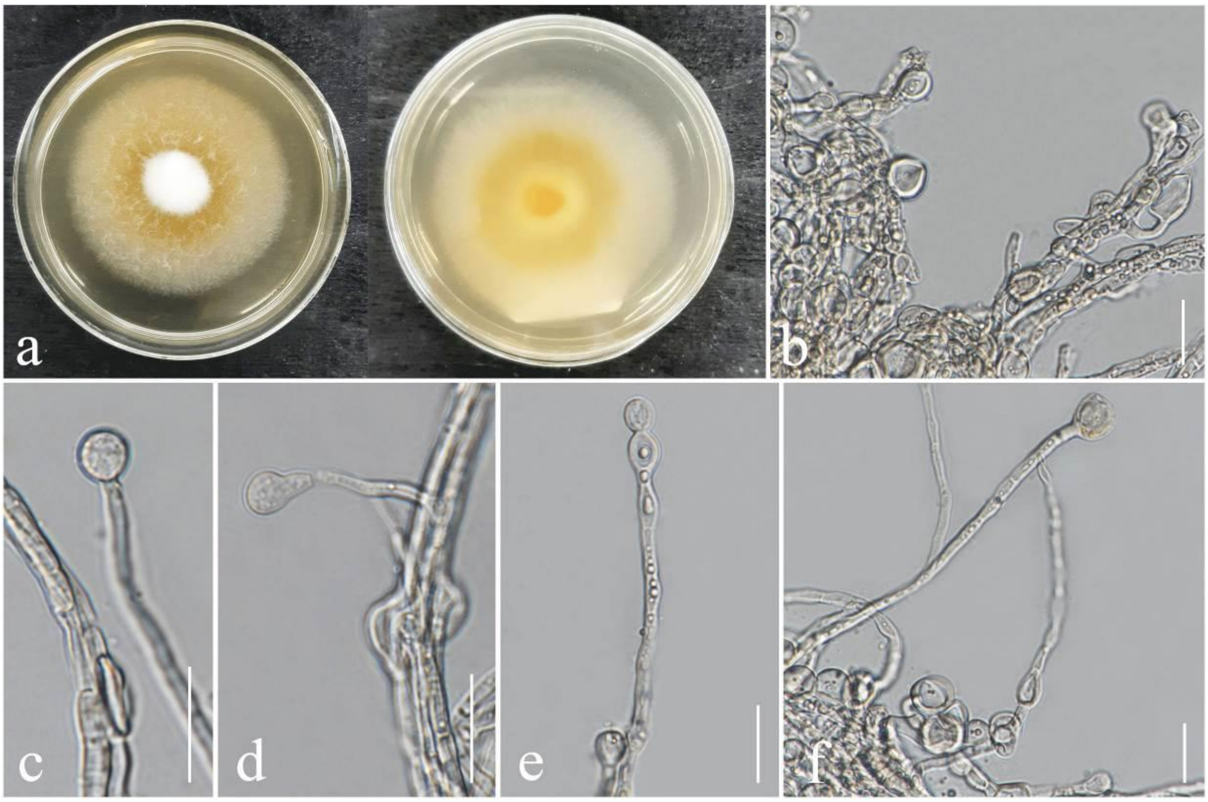

Figure 9 – Asexual morph of *Paramicrosphaeropsis sexualis* (MFLUCC 22-0087, ex-type). a Culture characters on MEA. b–f Chlamydospores produced in culture. Scale bars: b–f = 20 µm.

Montagnula Berl., Icon. Fung. (Abellini) 2(2-3): 68 (1896)

Type species – *Montagnula infernalis* (Niessl) Berl.

Notes – *Montagnula* was established for two dictyosporous species *M. gigantean* and *M. infernalis* (type), and characterized by immersed ascomata under a clypeus, long pedicellate asci and fusiform, brown ascospores (Berlese 1896). *Montagnula* was initially placed in *Montagnulaceae* based on morphology (Barr 2001), and later *Montagnulaceae* was synonymized under *Didymosphaeriaceae* based on DNA sequence data (Ariyawansa et al. 2014). Although Wanasinghe et al. (2016) and Doilom et al. (2018) resolved the phylogenetic relationships of *Montagnula* and its close ally *Munkovalsaria*, the asexual morph of *Montagnula* is still poorly understood. According to the treatment of *Montagnula* by Du et al. (2021) and Sun et al. (2023), only an asexual species which was isolated from a human skin sample has been linked to *Montagnula* based on phylogenetic analysis (Crous et al. 2020). In this study, we introduce an additional asexual species, *Montagnula agaves*, which was isolated from a dead leaf of *Agave sisalana*.

Montagnula agaves C.F. Liao, K.D. Hyde & Doilom, sp. nov. Fig. 11

Index Fungorum number: IF900633; Facesoffungi number: FoF 14688

Etymology – referring to the host *Agave sisalana*, from where it was isolated.

Holotype – MHZU 22-0067

Saprobic on dead leaf of *Agave sisalana*. Sexual morph: undetermined. Asexual morph: *Conidiomata* 215–360 µm high, 190–360 µm diam., pycnidial or cupulate, superficial, scattered on the host surface, surrounding by a mass of subhyaline to brown mycelium. *Conidiomatal wall* composed of one layer of brown, thick-walled, large cells of *textura angularis*. *Conidiophores* up to 115 µm long, 2–7 µm wide, cylindrical, branched, 3–12-septate, slightly constricted at the septa, pale brown to brown, smooth-walled. *Conidiogenous cells* 8–13 × 4–6 µm (av. 10 × 5 µm, n = 10), holoblastic, monoblastic, integrated, determinate, terminal, cylindrical, pale brown to brown, smooth-walled. *Conidia* 8–15 µm diam. (av. 10 µm, n = 20), catenate, with 2–(–5) conidia in the terminal unbranched part, obovoid, with rounded apex and slightly truncate base, didymosporous, 1-septate, deeply constricted at the septum, asymmetric, apical cell larger than the basal cell, yellowish brown to reddish brown, rough- and thick-walled, slightly verrucose when young, becoming chapped from the surface view with age, sometimes split into two cells at the septum when old.

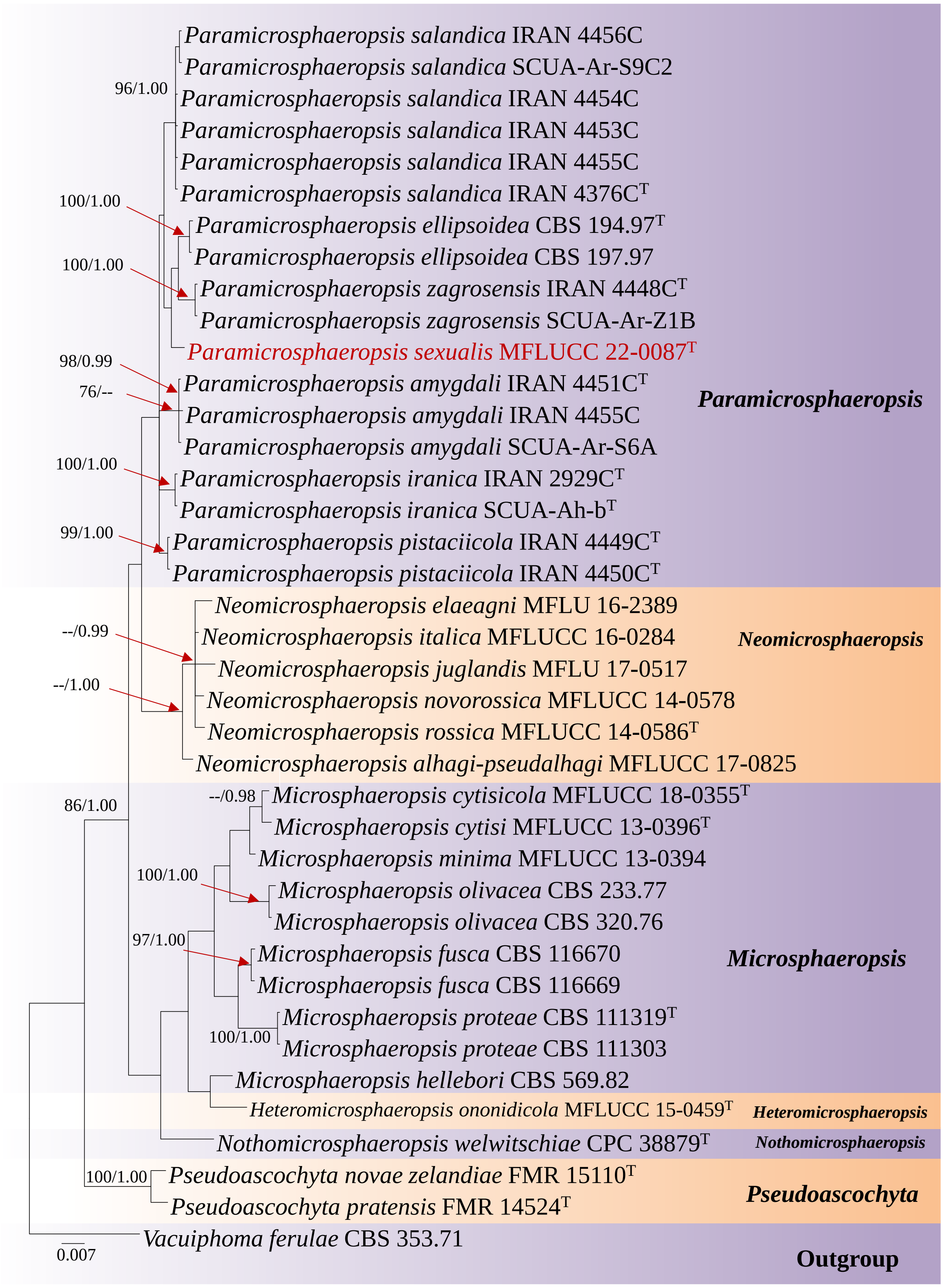

Figure 10 – Maximum likelihood consensus tree inferred from the combined LSU, ITS, tub2 and *rpb2* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first

value) equal to or greater than 70% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Vacuiphoma ferulae* CBS 353.71. Ex-type strains are indicated with “^{T}”. The new species are indicated in red.

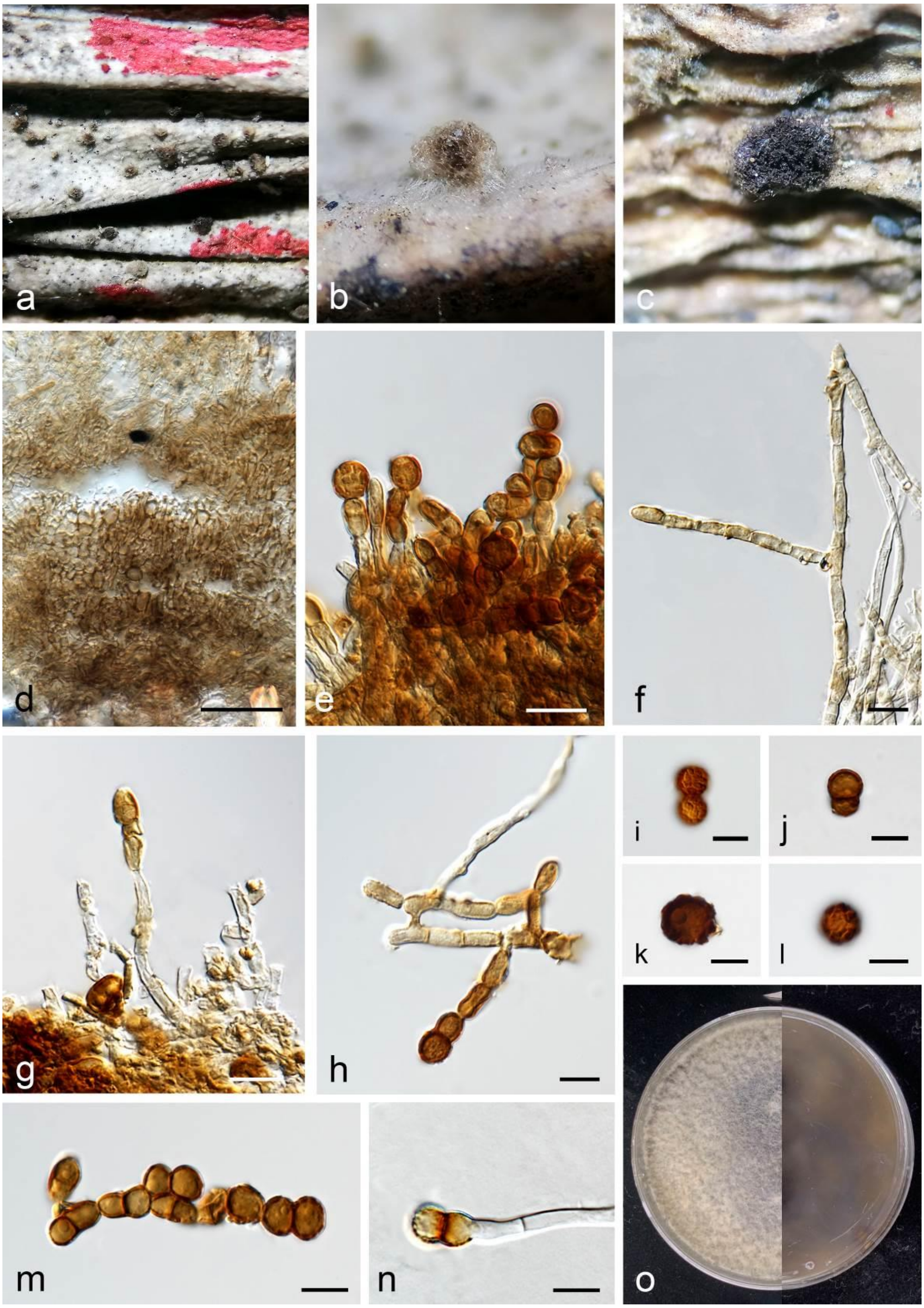

Figure 11 – *Montagnula agaves* (ZHKU 22-0067, holotype). a–c Conidiomata on leaf substate. d Conidiomatal wall. e–h Conidiophores, conidiogenous cells and conidia. i–l Conidia (k, l A

divided cell). m Catenate conidia. n Germinated conidium. o Colony on PDA (front and below). Scale bars: d = 50 µm, f = 10 µm, e, g–n = 5 µm.

Culture characteristics – colonies on PDA reaching 15 mm diam. at 25 °C after two weeks, irregular, flat, dry, margin entire; from above and below, pale brown to brown; not producing pigmentation in the culture.

Material examined – China, Guangdong Province, Guangzhou City, Zhongkai University of Agriculture and Engineering, on dead leaf of *Agave sisalana* Perr. ex Engelm. (*Agavaceae*), 17 November 2021, Y.H. Yang (MHZU 22-0067, **holotype**); ex-type culture ZHKUCC 22-0123.

GenBank accession numbers – ITS: OR198819, LSU: OR198820, SSU OR198729, *tef1-α*: OR195064.

Notes – *Montagnula agaves* forms a distinct branch with other species within *Montagnula*, supported by high bootstrap values (Fig. 12). *Montagnula agaves* is a didymosporous conidia-producing asexual morph species, which is infrequently reported within the genus. *Montagnula cylindrospora* is reported as the first coelomycetous asexual morph species within the genus, and is similar to *M. agaves* in terms of conidiomata being enveloped by mycelium or setae. *Montagnula cylindrospora* can be distinguished from *M. agaves* in all morphological aspects. *Montagnula cylindrospora* exhibits phialidic conidiogenous cells and cylindrical, aseptate, hyaline, smooth-walled conidia, and was isolated from a human skin sample. In contrast, *M. agaves* has monoblastic conidiogenous cells and calabash-shaped, didymosporous, yellowish brown to reddish brown, verrucose conidia, and it was obtained from dead leaves of a plant (Crous et al. 2020). With regard to DNA sequence data comparison, there is a discrepancy of 4.47% (24 out of 537), 1.62% (14 out of 862) and 3.55% (32 out of 901) in nucleotide variations within the ITS, LSU and *tef1-α* genes, respectively, between *M. agaves* ZHKUCC 22-0123 and *M. cylindrospora* UTHSC-DI16-208. Therefore, *M. agaves* is introduced as a novel species within the genus based on morphology and phylogeny.

Lophiostomataceae Sacc. Syll. fung. (Abellini) 2: 672 (1883)

Type genus – *Lophiostoma* Ces. & De Not.

Notes – *Lophiostomataceae* has been established for over a century, but its members have long been the subject of controversy due to different classification schemes. Through the utilization of a multi-locus phylogeny, Thambugala et al. (2015) segregated *Lophiostoma sensu lato* into 16 distinct genera, while Hashimoto et al. (2018) established eight genera to resolve the *Lophiostoma bipolare* complex. The generic classification of *Lophiostomataceae* was re-evaluated and Hashimoto et al. (2018) determined that the presence of a clypeus, brown hyphae surrounding the peridium, and one or two zones in the peridium structure were consistently reliable for distinguishing between different genera. Andreasen et al (2021) took a clumping approach to *Lophiostoma* and synonymized 14 genera. However, we do not agree with their approach as it is not supported by molecular data. Recent outline of fungi suggests 30 genera within the family, however, many of these lack sequence data and appropriate support and require further clarification in the future (Hongsanan et al. 2020, Wijayawardene et al. 2022).

Pseudopaucispora A. Hashim., K. Hiray. & Kaz. Tanaka, Stud. Mycol. 90: 175 (2018)

Type species – *Pseudopaucispora brunneospora* A. Hashim., K. Hiray. & Kaz. Tanaka

Notes – *Pseudopaucispora* was proposed to accommodate *P. brunneospora*, which is characterized by small brown ascospores and pseudopycnidial conidiomata (Hashimoto et al. 2018). The other species, *P. hyalinospora*, can be distinguished from the former by its hyaline ascospores and the different size of ascomata, peridium and asci (Brahmanage et al. 2020). In this study, we describe a new species named *P. heteropanacis* with brown ascospores.

Pseudopaucispora heteropanacis Doilom & C.F. Liao, sp. nov. Fig. 13

Index Fungorum number: IF900863; Facesoffungi number: FoF 14689

Etymology – referring to the host *Heteropanax fragrans*, from where it was isolated.
Holotype – MHZU 23-0115

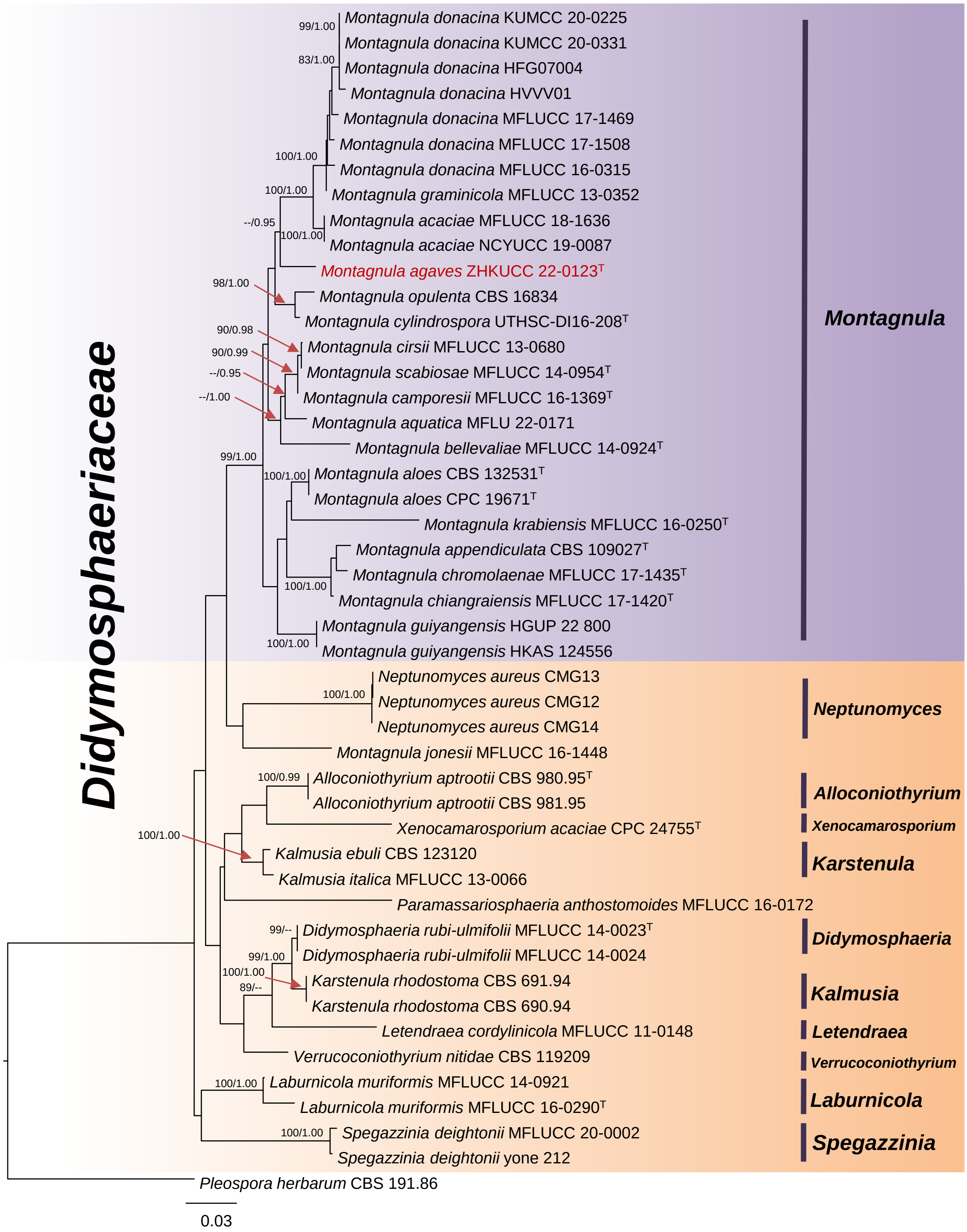

Figure 12 – Maximum likelihood consensus tree inferred from the combined LSU, ITS, SSU and *tef1-α* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Pleospora herbarum* CBS 191.86. Ex-type strains are indicated with “T”. The new species is indicated in red.

Saprobic on dead stems of *Heteropanox fregans*. Sexual morph: *Ascomata* 270–320 µm high, 320–360 µm diam., scattered, entirely immersed with black dots on the host surface, or erumpent with a slightly compressed, elongated papilla, depressed subglobose, black, unilocular, periphysate. *Peridium* uniform, 25–35 µm thick at sides and base, 2-layered, outer layer composed of brown to dark brown, thick-walled, large cells of *textura angularis*, inner layer composed of hyaline, thin-walled, compressed cells of *textura angularis*. *Pseudoparaphyses* ca. 1.3 µm wide, numerous, trabeculate, aseptate, branched, hyaline. *Asci* 65–80(–100) × 8–10.5 µm (av. 75 × 9 µm, n = 10), 8-spored, bitunicate, clavate, apically rounded with an ocular chamber, short pedicellate. *Ascospores* 12.5–15.5 × 3.5–4.5 µm (av. 14 × 4 µm, n = 20), mostly biseriate, overlapping uniseriate, fusiform with obtuse ends, slightly curved, 1-septate, slightly constricted at the septum, asymmetrical, upper cell mostly slightly wider and shorter, hyaline when young, becoming brown to dark brown, or reddish brown when mature, guttulate, smooth- and thin-walled, with bipolar internal chambers and a narrow sheath. Sheath drawn out 6.5–11.5 µm long at both ends. Asexual morph: undetermined.

Culture characteristics – colonies on PDA reaching 7 mm diam. at 25 °C after 20 days, circular, umbonate, dry, mycelium mostly immersed in the culture, margin entire and regular; from above, brown at the margin, orange brown in the middle; from below, brown at the margin, reddish brown in the middle; not producing pigmentation in the culture.

Material examined – China, Yunnan Province, Kunming City, on dead stems of *Heteropanax fragrans* (Roxburgh ex Candolle) Seemann (*Araliaceae*), 17 August 2019, M. Doilom & C.F. Liao HF04A (MHZU 23-0115, **holotype**); ex-type culture ZHKUCC 23-0881.

GenBank accession numbers – ITS: OR365457, LSU: OR365487, SSU: OR365492.

Notes – *Pseudopaucispora heteropanacis* clusters with *P. brunneospora* with high bootstrap support (Fig. 14). They share similarities in the morphology of their asci and ascospores, but can be distinguished by the characteristics of their ascomata and peridium. The ascomata of *P. brunneospora* possess a crest-like, elongated, laterally compressed neck on the host surface, whereas those of *P. heteropanacis* are often entirely immersed with black dots on the host surface or sometimes erumpent with a slightly compressed, elongated papilla (Hashimoto et al. 2018). Furthermore, *P. heteropanacis* exhibits a thicker peridium compared to *P. brunneospora* (25–35 µm vs. 15–18 µm). With regard to DNA sequence data comparison, there is a discrepancy of 1.95% (13 out of 665), 1.62% (13 out of 801) and 0.20% (2 out of 967) in nucleotide variations within the ITS, LSU and SSU genes, respectively, between *P. heteropanacis* ZHKUCC 23-0881 and *P. brunneospora* CBS 143661. Therefore, *P. heteropanacis* is introduced as a novel species within the genus based on morphology and phylogeny.

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

Type genus – *Torula* Pers.

Notes – *Torulaceae* was established in 1829 and widely used since Crous et al. (2015) confirmed its familial placement within *Pleosporales* through sequencing a neotype of the type species *Torula herbarum*. Subsequently, new genera have been continuously introduced into this family based on multi-locus phylogeny and morphology (Li et al. 2016, Su et al. 2016, 2018, Boonmee et al. 2021). Until now, seven genera have been accepted according to Wijayawardene et al. (2022).

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

Type species – *Torula herbarum* (Pers.) Link

Notes – *Torula* is a hyphomycete characterized by phragmosporous conidia in branched chains that arise from cupulate conidiogenous cells (Crous et al. 2015). *Torula* species have a cosmopolitan distribution and are capable of colonizing a diverse range of hosts (Wijayawardene et al. 2017). There is a lack of DNA sequence data for most *Torula* species, and their phylogenetic relationships can be inferred since the studies of Crous et al. (2015) and Su et al. (2016). Subsequently, new species have been incorporated into the genus through the integration of phylogenetic analyses and morphology (Li et al. 2017, 2020, Su et al. 2018, Hyde et al. 2019, Li et al. 2023). In this study, we present a newly discovered species, *Torula longan*, which was collected from Baiyun Mountain in Guangdong Province, China.

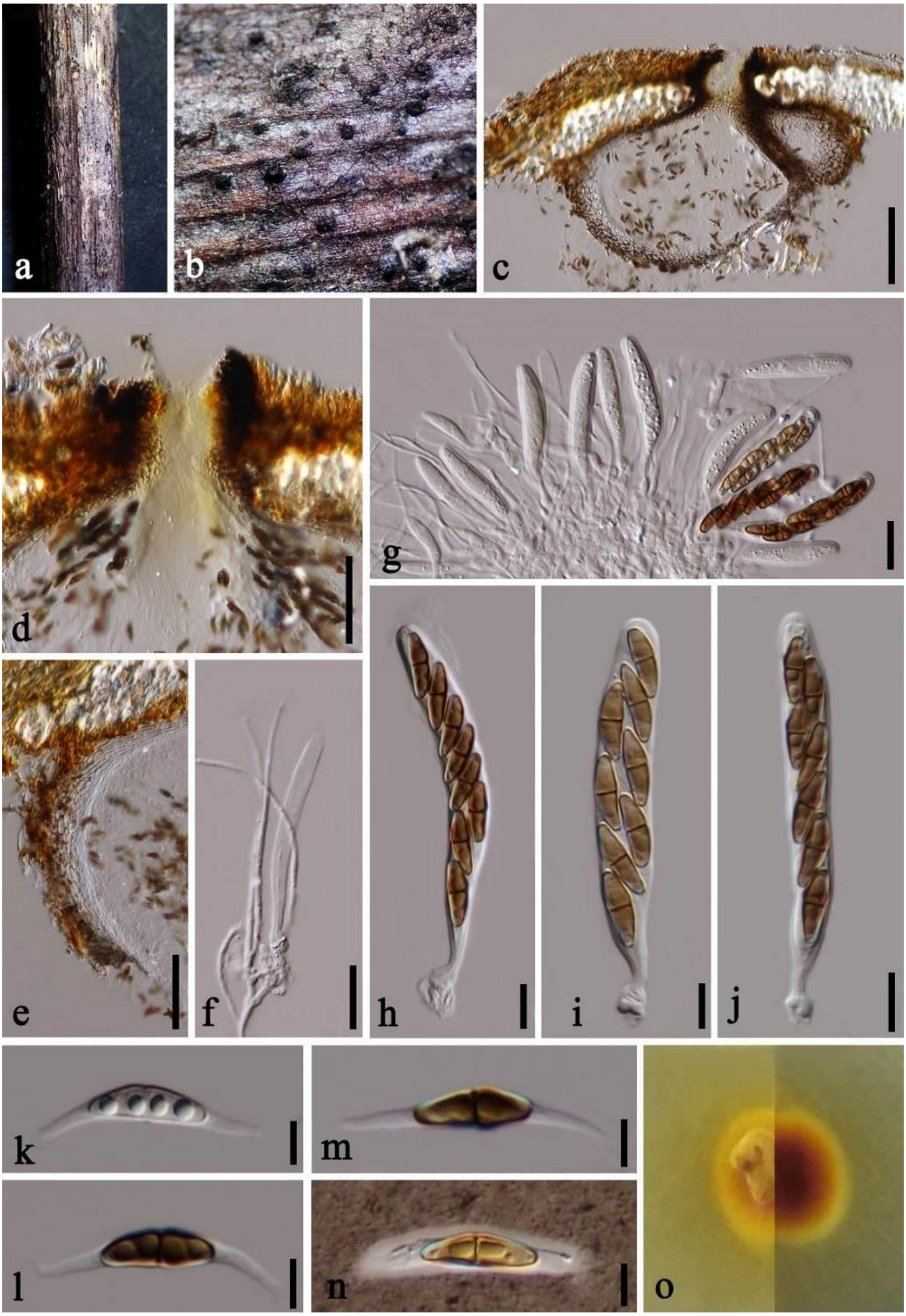

Figure 13 – *Pseudopaucispora heteropanacis* (MHZU 23-0115, holotype). a Decaying branch of host. b Appearance of necks erumpent through host. c Vertical section of ascoma. d Vertical section of neck. e Vertical section of peridium. f Pseudoparaphyses. g Asci with pseudoparaphyses.

h–j Bitunicate asci. k–n Ascospores (n ascospore mounted in Indian Ink). o Colony on PDA (front and below). Scale bars: c = 100 µm, d, e = 50 µm, f, h–j = 10 µm, g = 20 µm, k–n = 5 µm.

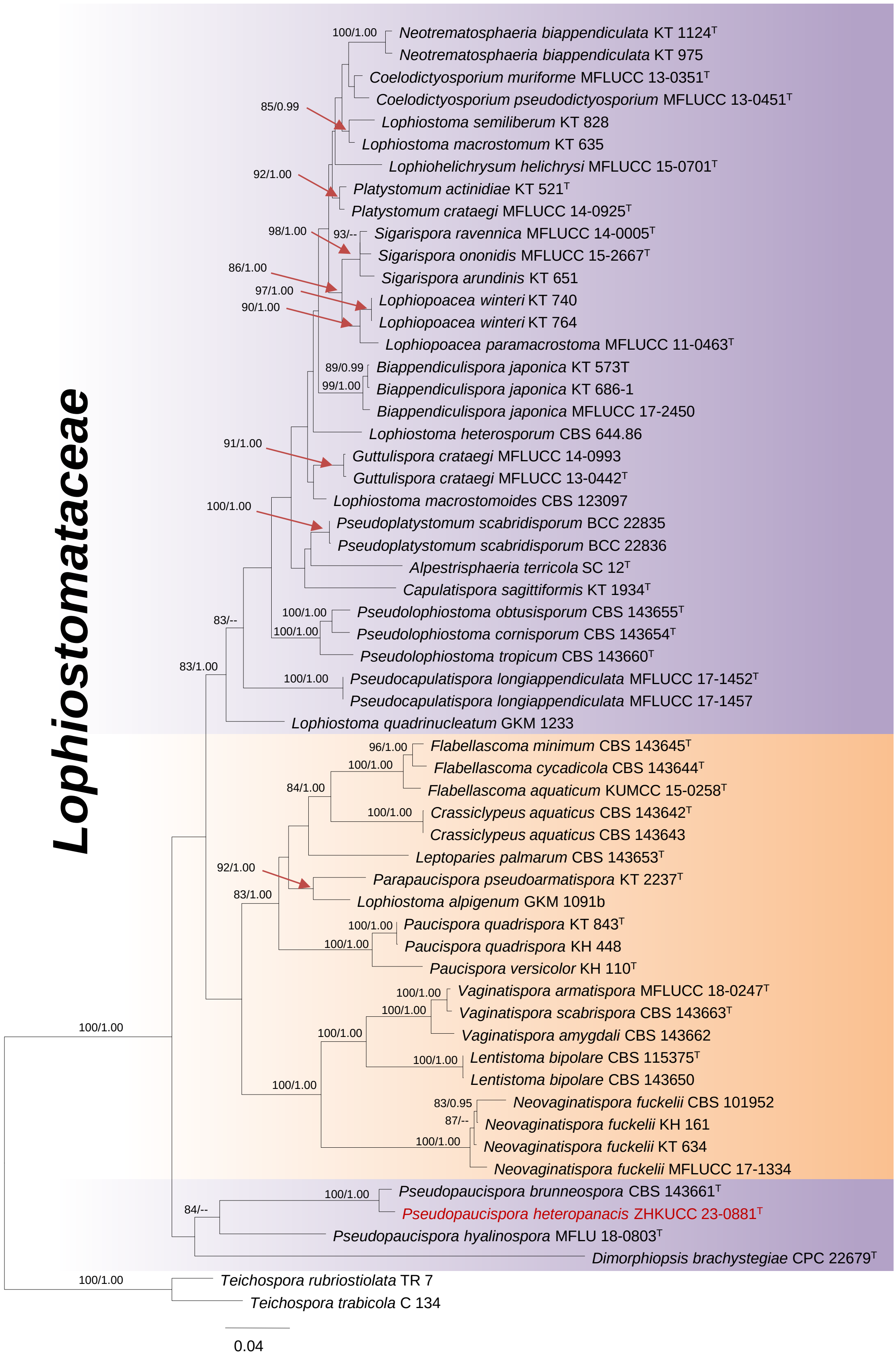

Figure 14 – Maximum likelihood consensus tree inferred from the combined LSU, SSU, ITS, *tef-1α* and *rpb2* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML,

first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Teichospora rubriostiolata* TR 7 and *T. trabicola* C 134. Ex-type strains are indicated with “^{T}”. The new species are indicated in red.

Torula longan Y.H. Yang & Manawasinghe, sp. nov. Fig. 15

Index Fungorum number: IF900698; Facesoffungi number: FoF 14690

Etymology – referring to the host *Dimocarpus longan,* from where it was isolated.

Holotype – MHZU 22-0066

Saprobic on dead branches of *Dimocarpus longan*. Sexual morph: undetermined. Asexual morph: *Colonies* effuse, dense, velvety, dark grey to black on the host. *Mycelium* 2–6 µm wide, immersed or superficial on the substrate, consists of smooth, branched, septate, light brown hyphae. *Conidiophores* 5–10 × 2–6 µm (av. 7 × 4 µm, n = 10), macronematous, mononematous, simple, flexuous, unbranched, smooth, thick-walled, subcylindrical, septate, brown. *Conidiogenous cells* 4–8 × 4–6 µm (av. 6 × 5 µm, n = 10), monoblastic, intercalary or terminal, cupulate, pale brown to brown, smooth to minutely verruculose, thick-walled. *Conidia* 5–33 × 4–8 µm (av. 18 × 7 µm, n = 20), phragmosporous, catenate, in branched chains, acrogenous, moniliform, 1–5-septate, consisting of dark brown, subglobose cells, uneven in colour, sometimes apical cell smaller and paler than the other cells, straight or slightly curved, verruculose, thick-walled. *Conidial secession* schizolytic.

Culture characteristics – colonies on PDA reaching 35 mm diam. at 28 °C after one month, raised, dry, rough, velvety, with dense hyphae in the middle and sparse hyphae at the edge, margin entire and nearly circular; from above, yellowish brown in the middle, pale brown at the margin; from below, dark brown to black in the middle, pale brown at the margin; not producing pigmentation in the culture.

Material examined – China, Guangdong Province, Guangzhou City, Baiyun Mountain (113°17′ E, 23°11′ N), on dead branches of *Dimocarpus longan* Lour. (*Sapindaceae*), 16 August 2021, Y.H. Yang BLY013 (MHZU 22-0066, **holotype**); ex-type culture ZHKUCC 22-0121; *ibid*., living culture ZHKUCC 22-0122.

GenBank accession numbers – ZHKUCC 22-0121 = ITS: OR194035, LSU: OR194027, SSU: OR194032, *tef1-α*: OR228537, *rpb*2: OR228535; ZHKUCC 22-0122 = ITS: OR194036, LSU: OR194028, SSU: OR194033, *tef1-α*: OR228538, *rpb*2: OR228536.

Notes – in our phylogenetic analysis, *T. longan* shows close relationships with *T. breviconidiophora* and *T. chromolaenae* with high bootstrap support; however, it forms a distinct branch (Fig. 17). *Torula longan* is similar to *T. breviconidiophora* in terms of having dark brown conidia, but differs by possessing shorter conidiophores (5–10 µm vs. 3.5–28 µm) and longer conidia (5–33 µm vs. 8–21 µm) (Hyde et al. 2019). *Torula longan* can be distinguished from *T. chromolaenae* based on differences in conidial colour (dark brown vs. pale brown), length (5–33 µm vs. 12–16.5 µm), and septation (1–5-septate vs. 2–3-septate) (Li et al. 2017). With regard to DNA sequence data comparison, there is a discrepancy of 2.30% (11 out of 478), 0.12% (1 out of 835), 0.24% (2 out of 847) and 0.47% (3 out of 635) in nucleotide variations within the ITS, LSU, SSU and *tef1-a* genes, respectively, between *T. longan* ZHKUCC 22-0121 and *T. breviconidiophora* KUMCC 18-0130. In addition, there is a discrepancy of 1.45% (7 out of 482), 0.12% (1 out of 845), 0, 0.58% (5 out of 861) and 1.71% (14 out of 817) in nucleotide variations within the ITS, LSU, SSU, *tef1-a* and *rpb2* genes, respectively, between *T. longan* ZHKUCC 22-0121 and *T. chromolaenae* KUMCC 16-0036. Therefore, *T. longan* is introduced as a novel species within the genus based on morphology and phylogeny.

Torula phytolaccae Y.X. Li, C.F. Liao & Doilom, Phytotaxa 584(1): 9 (2023) Fig. 16

Index Fungorum number: IF559683; Facesoffungi number: FoF 11438

Saprobic on dead stems of *Phytolacca americana*. Sexual morph: undetermined. Asexual morph: *Colonies* effuse, dense, velvety, black on the host. *Mycelium* 2–4 µm thick, immersed to superficial on the substrate, septate, branched, smooth, brown. *Conidiophores* 9–17 µm long, 3–6 µm wide (av. 11.5 × 4.5 µm, n = 10), macronematous to semi-macronematous, mononematous, simple, flexuous, unbranched, smooth to minutely verruculose, thick-walled, subcylindrical, consisting of 1–2 cells or reduced to conidiogenous cells, pale brown, arising from lateral and terminal of hyphae. *Conidiogenous cells* 3.5–7.5 µm long, 4–7.7 µm diam. (av. 5.7 × 6 µm, n = 10), polyblastic, intercalary or terminal, cupulate, brown to black, smooth to minutely verruculose, thick-walled. *Conidia* (8–)26–33(−64) × 4.5–9 (av. 30 × 6 µm, n = 20), phragmosporous, solitary or catenate in branched chains, acrogenous, mostly subcylindrical, rounded at both ends, straight or slightly curved, pale brown to black, mostly pale brown in the apical cupulate cell, verruculose, 2–18-septate, predominantly 4–5-septate, composed of subglobose cells, constricted at the septa, thick-walled.

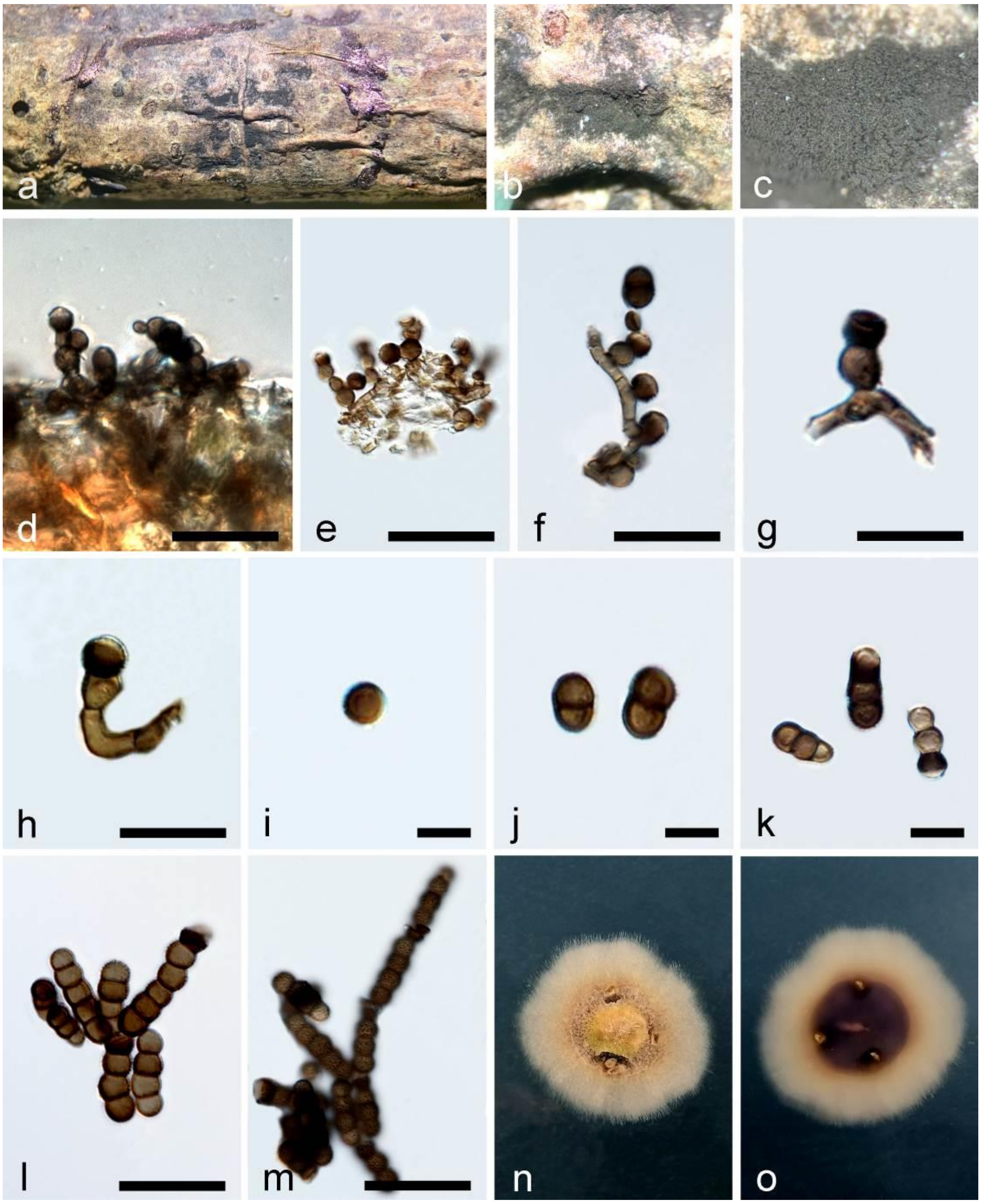

Figure 15 – *Torula longan* (MHZU 22-0066, holotype). a–c Colonies on dead branch. d–h Conidiogenous cells with conidia. i–k Solitary conidia. l, m Catenate conidia in branched chains. n, o Colony on PDA (front and below). Scale bars: d–h, l, m = 20 µm, i–k = 10 µm.

Figure 16 – *Torula phytolaccae* (MHZU 23-0118). a Dead stem of *Phytolacca americana*. b Appearance of colonies on natural substrate. c, g–n Conidia. d–f Conidiogenous cells with conidia. o Germinated conidium. p, q Colony on PDA after 14 days (front and below). Scale bars: c = 30 µm, d, n = 20 µm, e–m, o = 10 µm.

Culture characteristics – colonies on PDA reaching 15 mm diam. at 25 °C after 2 w, raised, dry, rough, margin entire and circular; from above and below, yellowish brown at the margin, orange brown in the middle; producing yellow pigmentation in the culture.

Material examined – China, Yunnan Province, Kunming City, on dead stems of *Phytolacca americana* L. (*Phytolaccaceae*), 28 June 2019, C.F. Liao PHY04 (MHZU 23-0118); living culture ZHKUCC 23-0884.

GenBank accession numbers – ITS: OR365458, LSU: OR365488, SSU: OR365493, *tef1-a*: OR700205.

Notes – The new collection MHZU 23-0118 clusters with *T. phytolaccae* with high bootstrap support (Fig. 17). They possess very similar morphological characteristics and have overlapping conidial size, but the new collection often exhibits branched chains of conidia which were not found in the holotype (Li et al. 2022). With regard to DNA sequence data comparison, there is a discrepancy of 0.80% (4 out of 501), 0, 0.54% (5 out of 928) and 0 in nucleotide variations within the ITS, LSU, SSU and *tef1-a* genes, respectively, between MHZU 23-0118 and *T. phytolaccae* ZHKUCC 22-0107. The phylogenetic analysis and morphological comparison identify the new collection as *T. phytolaccae*. This is a new host record of *T. phytolaccae* from *Phytolacca americana* in China.

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

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

Notes – Members of *Sporocadaceae* are mostly acervular coelomycete with appendages, and they function as endophytes, plant pathogens or saprobes in a diverse range of host plants (Jaklitsch et al. 2016, Liu et al. 2019). Liu et al. (2019) demonstrated that *Sporocadaceae* is a well-defined family within *Xylariales* and identified 30 genera through phylogenetic analyses and morphological comparisons. Wijayawardene et al. (2022) recognized 36 genera in the family.

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

Type species – *Pestalotiopsis maculans* (Corda) Nag Raj

Notes – *Pestalotiopsis* is an appendage-bearing conidial genus, which was established by Steyaert (1949) with *P. maculans* as the type species. *Pestalotiopsis* species are widely distributed in tropical and temperate ecosystems, primarily as pathogens and endophytes, but also occurring as saprobes (Jeewon et al. 2003, 2004, Maharachchikumbura et al. 2011, 2014, Liu et al. 2017). The species within *Pestalotiopsis* exhibit highly similar morphological characteristics, and the conventional approach of relying on host associations and median cell colour intensities has resulted in misidentifications (Maharachchikumbura et al. 2014). Species identification has been facilitated by the research conducted by Maharachchikumbura et al. (2011, 2012, 2014). The genetic markers ITS, *tef1-α* and tub2 are commonly employed for multi-locus phylogenetic analyses. In this study, we describe three new species, including two endophytes isolated from leaves of *Pyrrosia lingua* and *Camellia japonica*, respectively, and a saprobe isolated from dead leaves of an unknown host. According to the analysis of newly generated data in this study, *tef1-α* emerges as the most informative marker for distinguishing between the two species, while ITS and tub2 exhibit comparatively lower of informativeness (see notes of *Pestalotiopsis pyrrosiae-linguae* and *P. zhaoqingensis*).

Pestalotiopsis camelliae-japonicae Y.X. Shu & W. Dong, sp. nov. Fig. 18

Index Fungorum number: IF900751; Facesoffungi number: FoF 14692

Etymology – referring to the host *Camellia japonica*, from where it was isolated.

Holotype – MHZU 23-0110

Endophytic on *Camellia japonica*. Sexual morph: undetermined. Asexual morph: *Conidiomata* acervular, saucer-shaped, black, scattered, immersed, semi-immersed, superficial, shining, releasing black conidial masses on the surface. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous* cells 5–17 × 1.6–2.6 µm (av. 10.7 × 2 µm, n = 10), holoblastic, monoblastic, determinate, subcylindrical, hyaline, smooth. *Conidia* 13–23 × 5–7 µm (av. 20 × 6 µm, n = 25), fusiform, straight to slightly curved, (2–)–4 septate, slightly constricted and heavily pigmented at septa, mostly with three brown median cells and two subhyaline end cells, smooth- and thin-walled; basal cell 4–7 µm long, funnel-shaped, hyaline to subhyaline, sometimes with 1–2 filiform, unbranched basal appendages, 2–7 µm long; apical cell 3–5 µm long, conical or sometimes subcylindrical, hyaline to subhyaline, with (1–)–3 filiform, unbranched apical appendages, 9–22 µm long.

Culture characteristics – colonies on PDA reaching 40 mm diam. at 28 °C after nine days, circular, rough, dry, margin entire; from above, white and milky with several conidiomata on the surface; from below, yellowish brown; not producing pigmentation in the culture. Conidiomata produced in PDA at 28 °C after 24 days, subglobose or irregular-shaped, scattered, semi-immersed to erumpent, dark brown to black; exuding globose, dark brown to black conidial masses.

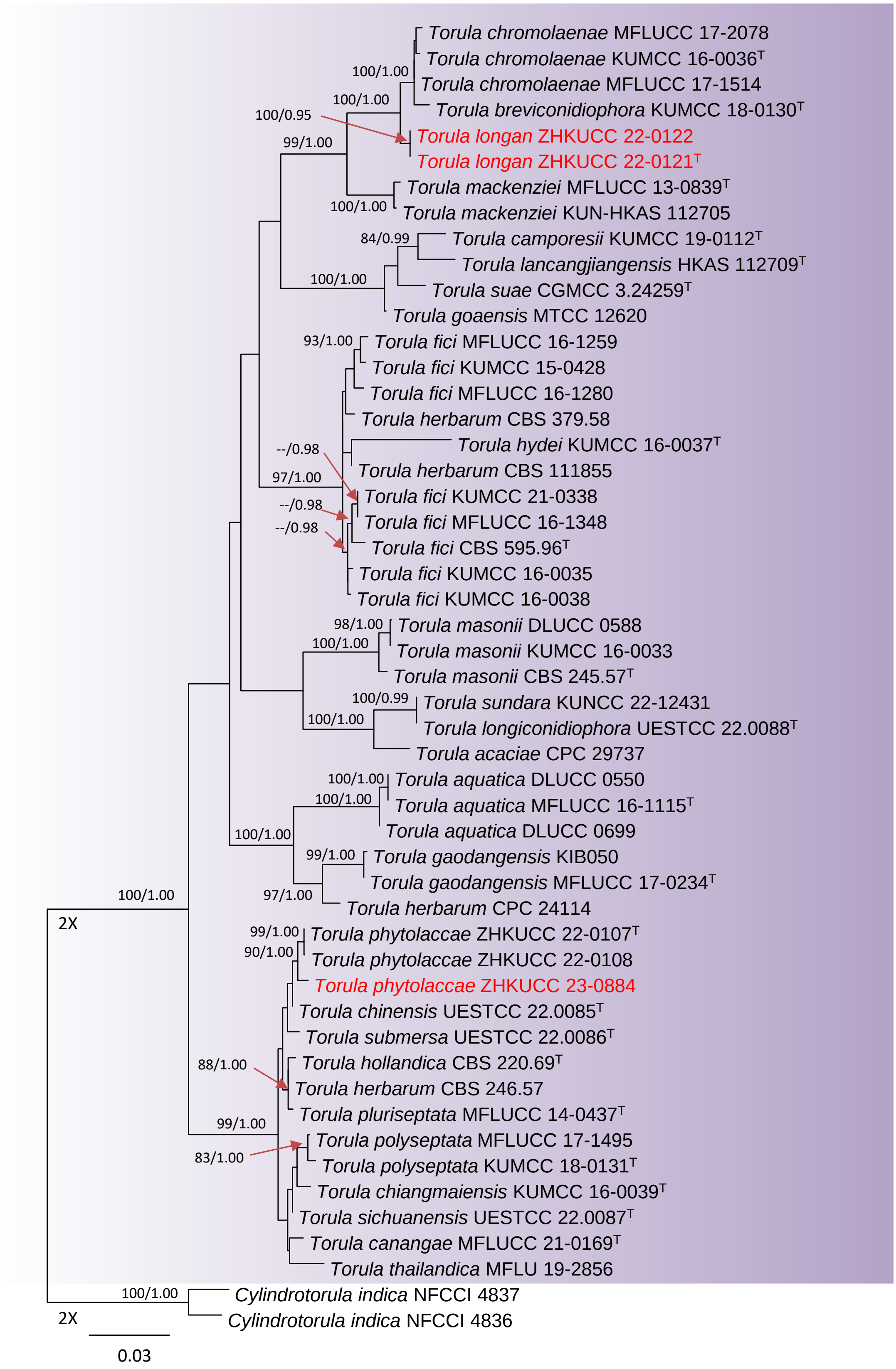

Figure 17 – Maximum likelihood consensus tree inferred from the combined LSU, SSU ITS, *tef1-a* and *rpb2* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses

(BYPP, second value) equal or higher than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Cylindrotorula indica* (NFCCI 4836 and NFCCI 4837). Ex-type strains are indicated with "^{T}". The new species and new record are indicated in red.

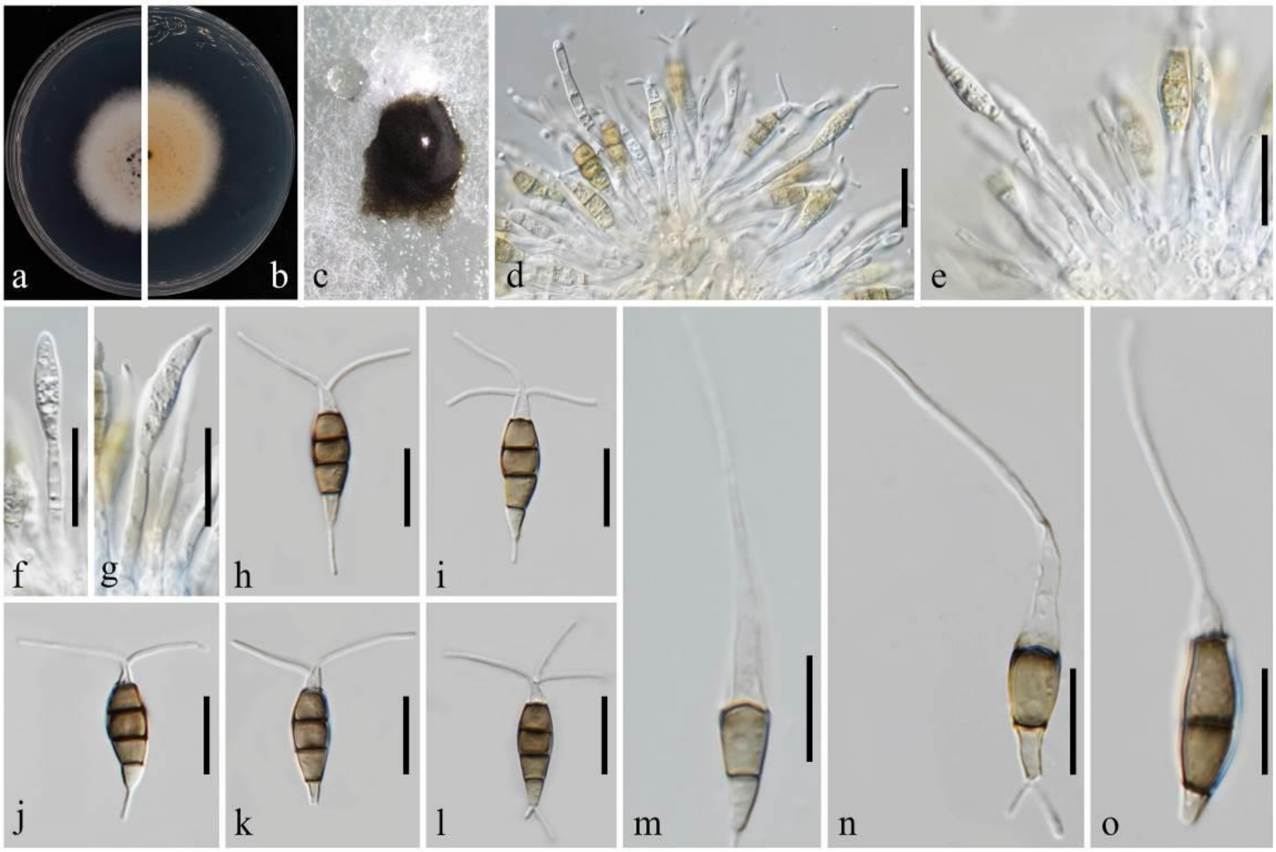

Figure 18 – *Pestalotiopsis camelliae-japonicae* (MHZU 23-0110, holotype). a, b Front and below view of a nine-day-old colony on PDA. c Conidial mass. d–g Conidiogenous cells bearing conidia. h–o Conidia. Scale bars: d–o = 10 µm.

Material examined – China, Guangdong Province, Guangzhou City, associated with leaf spot of *Camellia japonica* L. (*Theaceae*), 14 March 2022, Y.X. Shu HNZWY21 (MHZU 23-0110, **holotype**); ex-type culture ZHKUCC 23-0826; *ibid*., MHZU 23-0111, isotype; living culture ZHKUCC 23-0827; *ibid*., MHZU 23-0112; living culture ZHKUCC 23-0828.

GenBank accession numbers – ZHKUCC 23-0826 = ITS: OR258040, *tef1-α*: OR251480, tub2: OR251483; ZHKUCC 23-0827 = ITS: OR258041, *tef1-α*: OR251481, tub2: OR251484; ZHKUCC 23-0828 = ITS: OR258042, *tef1-α*: OR251482, tub2: OR251485.

Notes – *Pestalotiopsis camelliae-japonicae* forms a distinct branch within *Pestalotiopsis* in the phylogenetic analysis (Fig. 21). *Pestalotiopsis camelliae-japonicae* is similar to its phylogenetically related species, *viz*., *P. dracontomelonis*, *P. lithocarpi*, *P. sabal* and *P. smilacicola*, exhibiting only slight variations in conidial size and appendages which are commonly observed within the genus (Liu et al. 2015, Jiang et al. 2022, Xiong et al. 2022, Sun et al. 2023). *Pestalotiopsis camelliae-japonicae* is most similar to *P. sabal* in terms of their overlapping conidial size (13–23 × 5–7 µm vs. 17.5–23 × 5.5–7 µm), the same number of appendages ((1–)–3) and similar length of appendages (9–22 µm vs. 7–20 µm). With regard to DNA sequence data comparison, there is a discrepancy of 0, 4.94% (12 out of 243) and 0.52% (4 out of 764) in nucleotide variations within the ITS, *tef1-a* and tub2 genes, respectively, between *P. camelliae-japonicae* ZHKUCC 23-0826 and *P. sabal* ZHKUCC 22-0035. Therefore, *P. camelliae-japonicae* is introduced as a novel species within the genus based on morphology and phylogeny.

Pestalotiopsis pyrrosiae-linguae H. Li, sp. nov. Fig. 19

Index Fungorum number: IF900638; Facesoffungi number: FoF 14691

Etymology – referring to the host *Pyrrosia lingua*, from where it was isolated.

Holotype – MHZU 23-0109

Endophytic on leaves of *Pyrrosia lingua*. Sexual morph: undetermined. Asexual morph: *Conidiomata* acervular, saucer-shaped, black, solitary or aggregated in clusters, semi-immersed, superficial, shining, releasing black conidial masses on the surface. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–12.5 × 2–3.5 µm (av. 9.4 × 2.4 µm, n = 10), holoblastic, monoblastic, determinate, subcylindrical, hyaline, smooth. *Conidia* 19–24 × 4–6 µm (av. 21.5 × 5.2 µm, n = 30), fusiform to clavate, straight or slightly curved, 4-septate, slightly or not constricted, darker at the septa, with three brown median cells but not often uniform in colour, and with a hyaline apical cell and a pale brown basal cell, smooth- and thin-walled; basal cell 3.5–6 µm long, funnel-shaped, pale brown, often with a single, filiform, unbranched appendage, 4.5–10(–13) µm long; apical cell 3–5 µm long, conical or sometimes subcylindrical, hyaline, with 2–3 filiform, unbranched apical appendages, 9–25 µm long.

Culture characteristics – colonies on PDA reaching 65 mm diam. at 25 °C after five days. Colonies filamentous to circular, moderately dense, flat, white, reverse pale yellow. Sparse conidiomata produced in PDA at 25 °C after 42 days, irregular-shaped, scattered, semi-immersed to erumpent, dark brown to black; exuding globose, dark brown to black conidial masses.

Material examined – China, Guangdong Province, Guangzhou City, on leaves of *Pyrrosia lingua* (Thunb.) Farwell (*Polypodiaceae*), 16 August 2021, H. Li LH35-C4028 (MHZU 23-0109, **holotype**); ex-type culture ZHKUCC 23-0807; *ibid*., living culture ZHKUCC 23-0808.

GenBank numbers – ZHKUCC 23-0807 = ITS: OR199902, *tef1-α*: OR259260, tub2: OR259258; ZHKUCC 23-0808 = ITS: OR199903, *tef1-α*: OR259261, tub2: OR259259.

Notes – *Pestalotiopsis pyrrosiae-linguae* is positioned as a distinct branch within *Pestalotiopsis*, as illustrated in Fig. 21. A comparative analysis of morphological characteristics indicates that *P. pyrrosiae-linguae* bears close resemblance to *P. diploclisiae*, but can be distinguished by its shorter basal appendage (4.5–10(–13) µm vs. 14–16 µm) (Maharachchikumbura et al. 2014). With regard to DNA sequence data comparison, there is a discrepancy of 0.19% (1 out of 539), 2.55% (12 out of 470) and 0 in nucleotide variations within the ITS, *tef1-a* and tub2 genes, respectively, between *P. pyrrosiae-linguae* ZHKUCC 23-0807 and *P. diploclisiae* CBS 115587. Supported by phylogenetic and morphological evidences, we propose the recognition of *P. pyrrosiae-linguae* as a novel species.

Pestalotiopsis zhaoqingensis H.J. Zhao & W. Dong, sp. nov. Fig. 20

Index Fungorum number: IF900715; Facesoffungi number: FoF 14693

Etymology – referring to the Zhaoqing City, from where the fungus was collected.

Holotype – MHZU 23-0109

Saprobic on dead leaves of unknown host. Sexual morph: undetermined. Asexual morph: *Conidiomata* acervular, saucer-shaped, black, scattered or aggregated, semi-immersed, shining, releasing black conidial masses on the surface. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–12 × 2–7 µm, holoblastic, monoblastic, determinate, hyaline, smooth. *Conidia* 17–24 × 4–8 µm (av. 21 × 6 µm, n = 30), fusiform, straight to slightly curved, 4-septate, slightly constricted and darker at septa, with three brown median cells (not often concolorous) and two subhyaline end cells, smooth- and thin-walled; basal cell 2–5 µm long, obconic, hyaline to subhyaline, with 1–2(–3) filiform, branched basal appendages, 4–17 µm long, basal appendage sometimes with a knot; apical cell 2–5 µm long, conical, hyaline to subhyaline, with 2–4 filiform, unbranched apical appendages, occasionally branched, 8–20 µm long.

Culture characteristics – colonies on PDA reaching 60 mm diam. at 28 °C after 7 days. Surface margin undulate, with grey aerial mycelium, grey at the margin, dark grey at the middle, raised, dry, margin irregular. Reverse pale grey at the margin, orange brown at the middle, irregular. Several conidiomata produced in PDA at 28 °C after 30 days, irregular-shaped, scattered, semi-immersed to erumpent, dark brown to black; exuding globose, dark brown to black conidial masses.

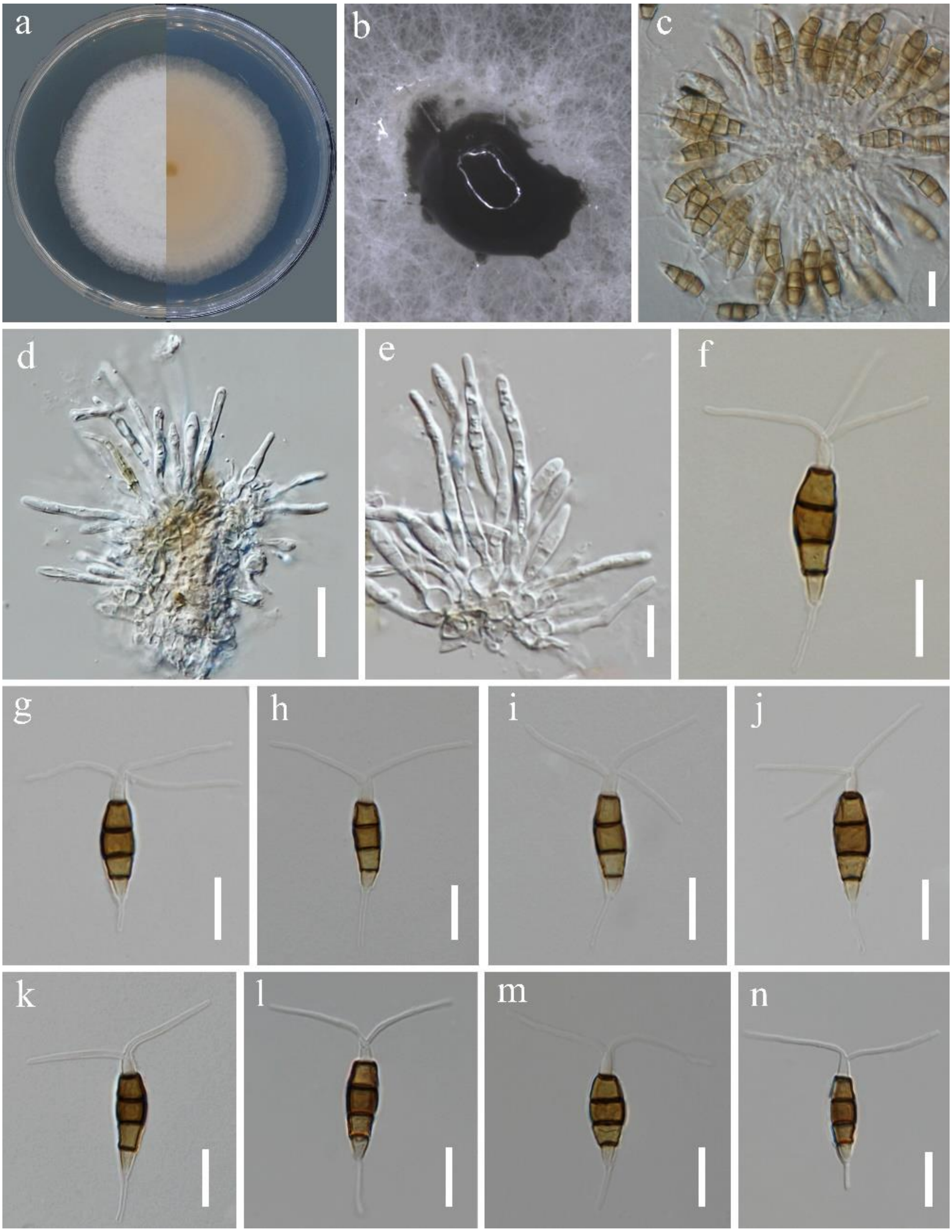

Figure 19 – *Pestalotiopsis pyrrosiae-linguae* (MHZU 23-0109, holotype). a Front and below view of a five-day-old colony on PDA. b Conidial mass. c–e Conidiophores, conidiogenous cells and conidia. f–n Conidia. Scale bars: c, e–n = 10 µm, d = 20 µm.

Material examined – China, Guangdong Province, Zhaoqing City, Dinghu Mountain, on dead leaves of unknown host, 8 November 2021, H.J. Zhao FS1 (MHZU 23-0109, **holotype**); ex-type culture ZHKUCC 23-0825.

GenBank accession numbers – ITS: OR233336, *tef1-α*: OR239061, tub2: OR239062.

Notes – *Pestalotiopsis zhaoqingensis* is related to *P. jinchanghensis* with high bootstrap support (Fig. 21). The two species can be easily differentiated by the morphology and dimensions of their conidia. In comparison to *P. jinchanghensis*, *P. zhaoqingensis* possesses broad fusiform conidia, while those of *P. jinchanghensis* are long and narrow. *Pestalotiopsis zhaoqingensis* possesses shorter conidia (17–24 × 4–8 µm) and shorter apical appendages (8–20 µm) compared to those of *P. jinchanghensis*, which measure 22–32 × 5.5–8.5 µm and 15–33.5 µm, respectively. In addition, *P. jinchanghensis* is devoid of apical branched appendages, whereas they are occasionally discernible in *P. zhaoqingensis* (Liu et al. 2017). With regard to DNA sequence data comparison, there is a discrepancy of 1.20% (6 out of 500), 1.07% (5 out of 463) and 0 in nucleotide variations within the ITS, *tef1-α* and tub2 genes, respectively, between *P. zhaoqingensis* ZHKUCC 23-0825 and *P. jinchanghensis* LC6636. Therefore, *P. zhaoqingensis* is introduced as a novel species within the genus based on morphology and phylogeny.

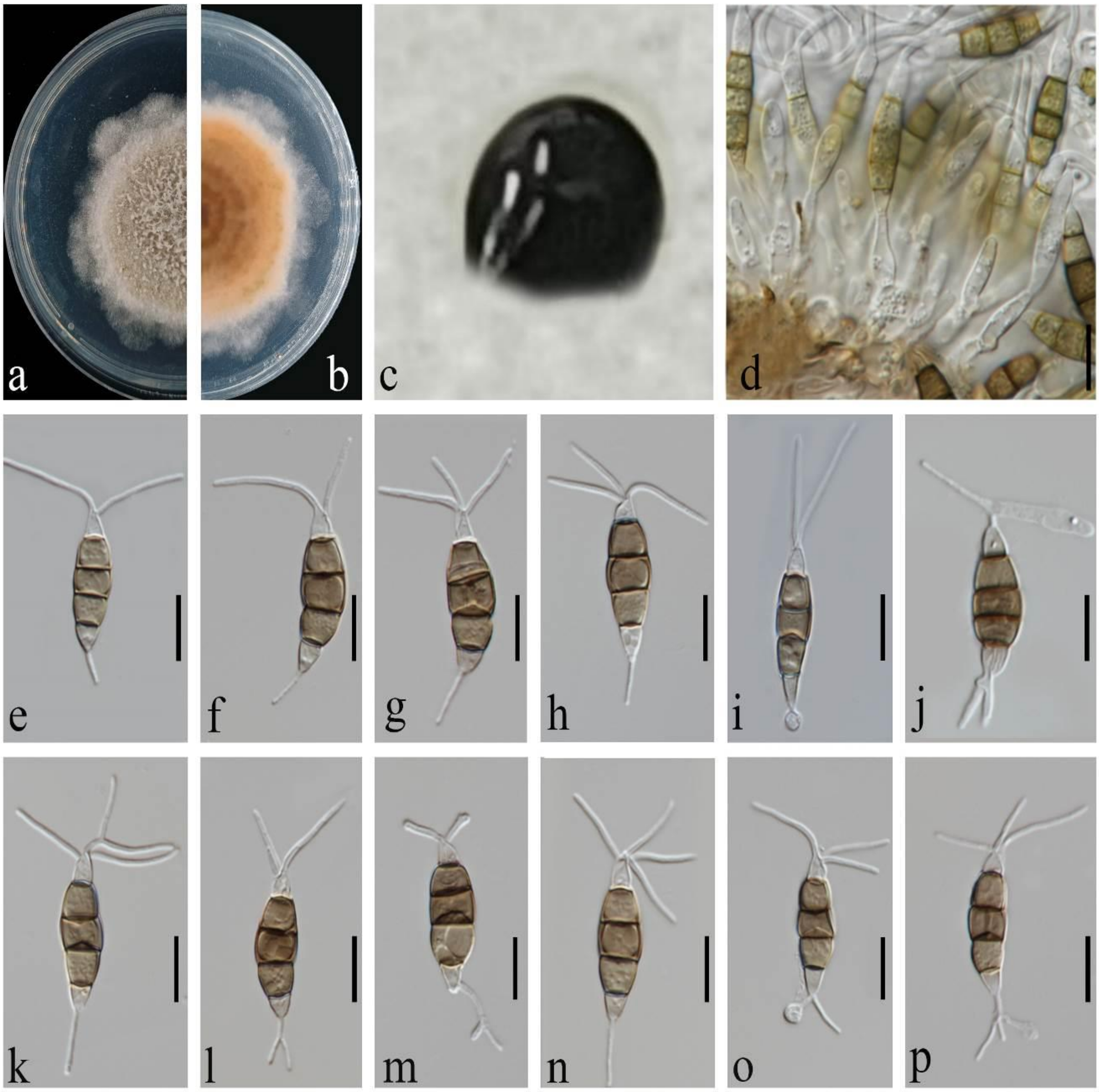

Figure 20 – *Pestalotiopsis zhaoqingensis* (MHZU 23-0109, holotype). a Colony on PDA (front view). b Colony on PDA (below view). c Conidial mass. d Conidiogenous cells giving rise to conidia. e–p Conidia. Scale bars: d = 10 µm, e–p = 15 µm.

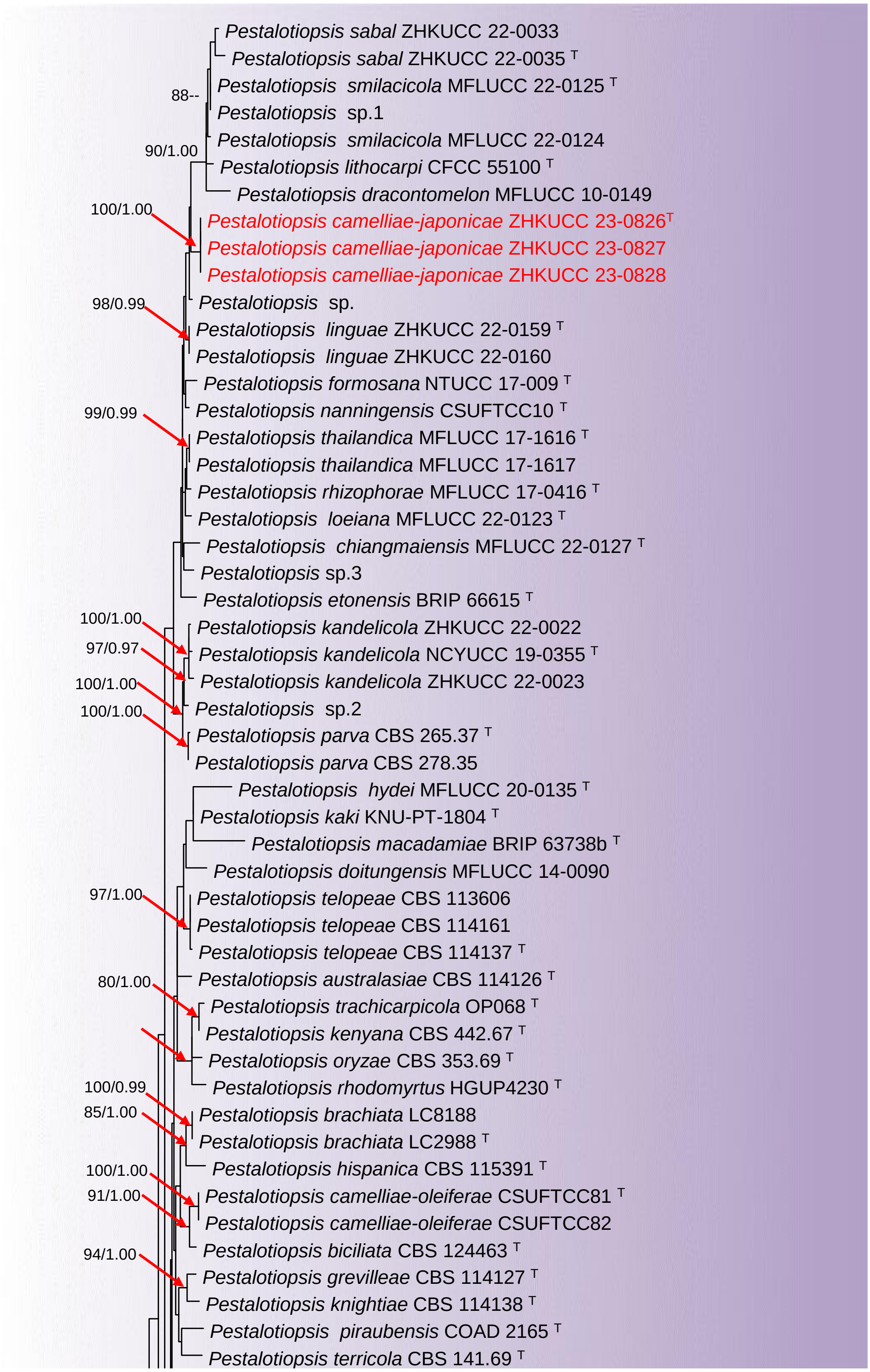

Figure 21 – Maximum likelihood consensus tree inferred from the combined ITS, *tef1-α* and tub2 multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates

expected changes per site. The tree is rooted to *Neopestalotiopsis magna* MFLUCC 12-0652. Ex-type strains are indicated with "T". The new species is indicated with red.

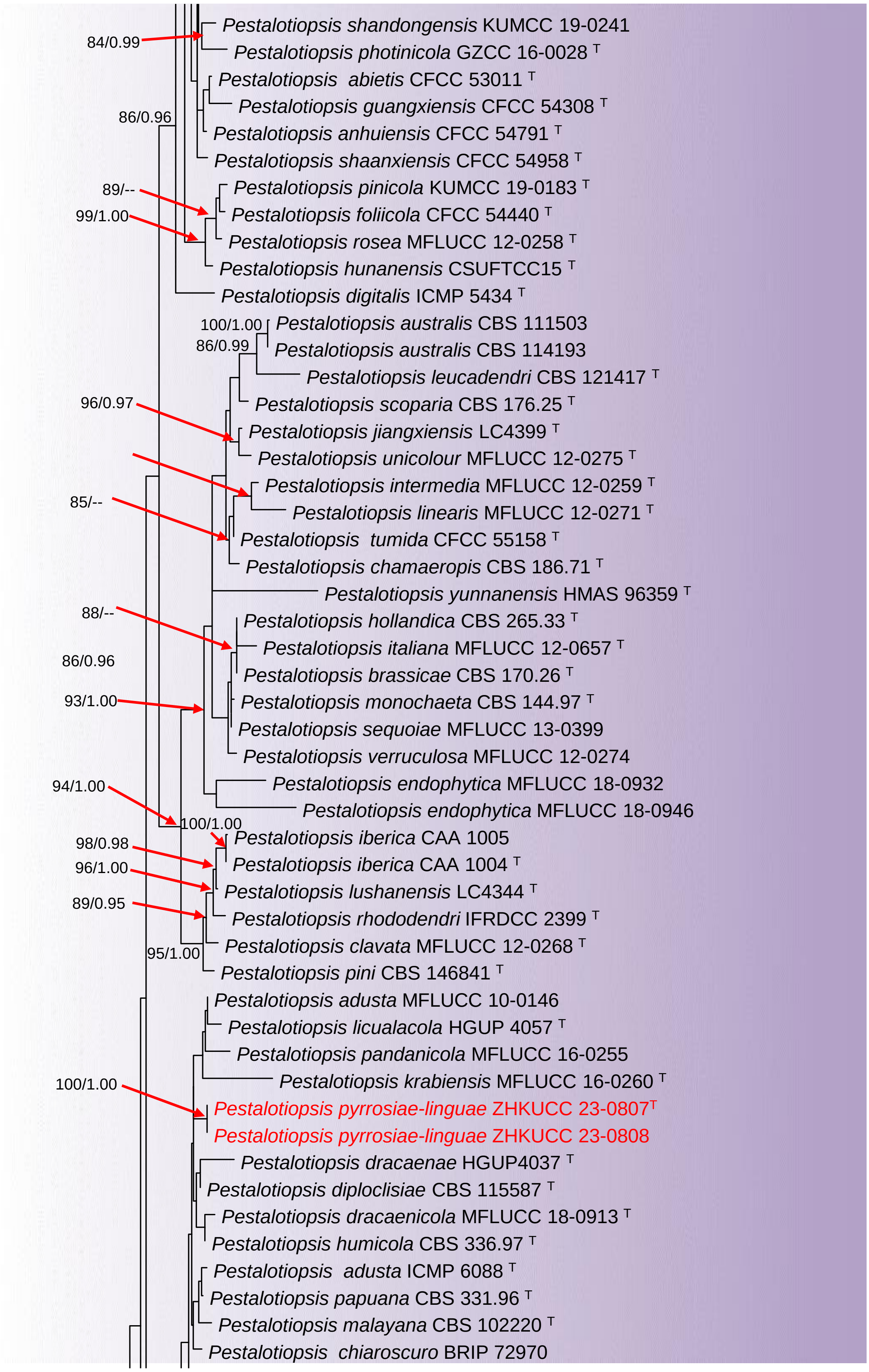

Figure 21 – Continued.

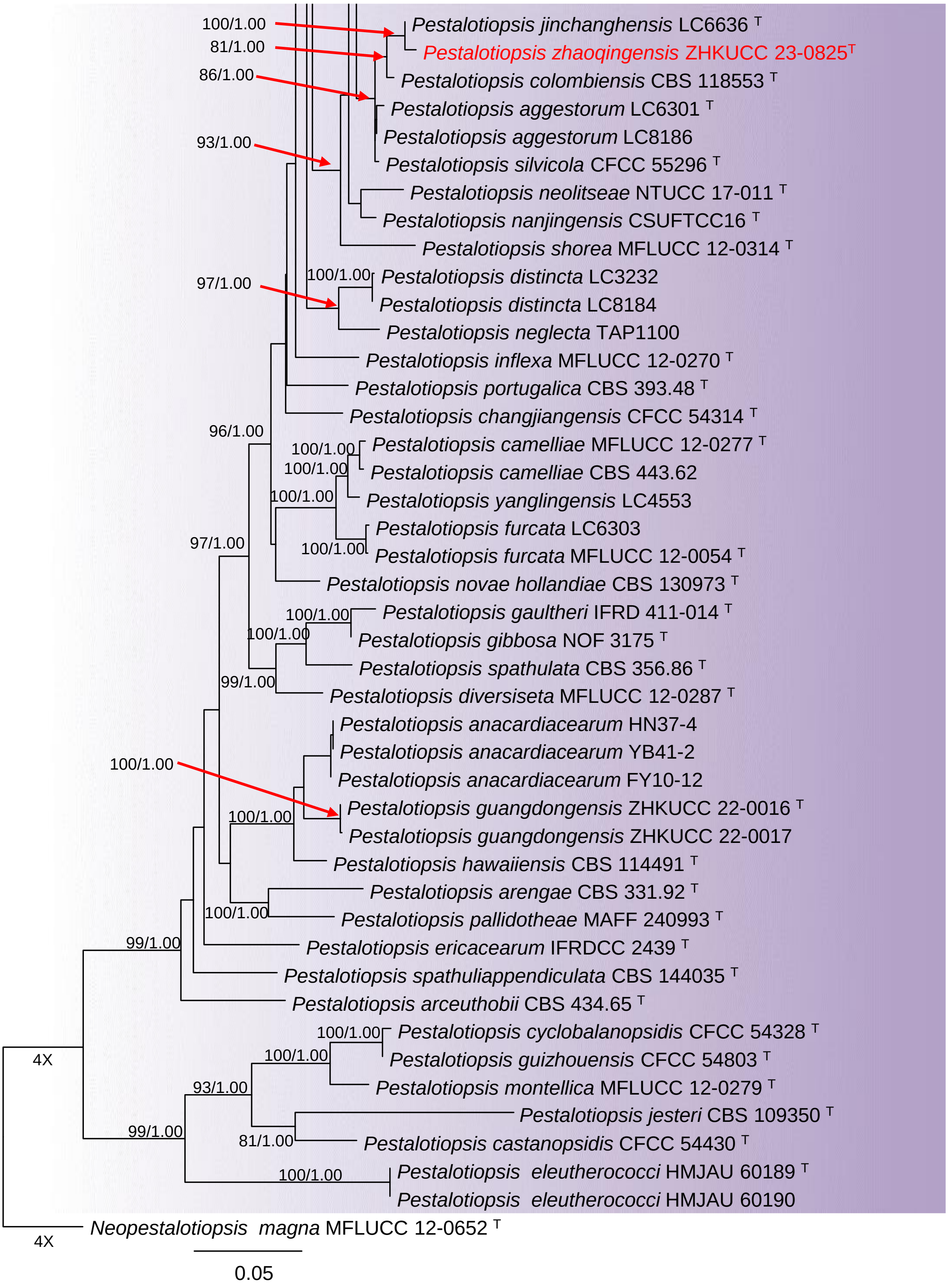

Figure 21 – Continued.

Bionectriaceae Samuels & Rossman, Stud. Mycol. 42: 15 (1999)

Type genus – *Clonostachys* Corda

Notes – *Bionectriaceae* was initially established with 26 genera in the monograph of Rossman (1999). A modified description of *Bionectriaceae* was subsequently provided by Hyde et al. (2020) and updated by Perera et al. (2023). This family is known as its large size and morphological diversity, with the recent outline of fungi listing a total of 47 genera

(Wijayawardene et al. 2022). However, due to only LSU sequence data is available for most genera, our understanding of their evolutionary relationships remains incomplete (Rossman et al. 2001). Hyde et al. (2020) emphasized that many genera need to be recollected and reappraised to confirm their phylogenetic placements.

Clonostachys Corda, Pracht-Fl. Eur. Schimmelbild.: 31 (1839)

Type species – *Clonostachys rosea* (Link) Schroers, Samuels, Seifert & W. Gams

Notes – *Clonostachys*, the asexual morph of *Bionectria*, was thoroughly reviewed in Schroers's monograph (Schroers 2001). Subsequently, *Bionectria* was synonymized with *Clonostachys*, thus rendering *Clonostachys* a holomorphic genus (Rossman et al. 2013). *Clonostachys* is distinguished by well-developed stromata, narrowly clavate to clavate asci, typically with an apical, horizontal ring, and ellipsoidal, 1-septate ascospores that are spinulose to warted or striate. The asexual morph exhibits dimorphic or monomorphic conidiophores, phialidic conidiogenous cells, and ellipsoidal to sub-fusiform, 0–1-septate, hyaline or greenish hyaline, smooth-walled conidia (Schroers 2001, Perera et al. 2023). The type species *C. rosea* is a saprobic filamentous species with strong biological control ability against various fungal plant pathogens, nematodes, and insects (Kosawang et al. 2014, Samsudin et al. 2017). In this study, we introduce a new species isolated from dead plant stems; however, its potential for biological control remains to be determined in future investigations.

Clonostachys artemisiae Doilom, K.D. Hyde & C.F. Liao, sp. nov. Fig. 22

Index Fungorum number: IF900864; Facesoffungi number: FoF 14694

Etymology – referring to the host *Artemisia argyi*, from where it was isolated.

Holotype – MHZU 23-0116

Saprobic on dead stems of *Artemisia argyi*. Sexual morph: undetermined. Asexual morph: *Colonies* effuse, dense, velvety, white to pale yellow on the host. *Mycelium* immersed, composed of septate, branched, smooth, hyaline to pale brown hyphae. *Conidiophores* up to 50 µm long, 6–8 µm wide, monomorphic, micronematous, mononematous, erect, sparsely branched, cylindrical, distantly septate, hyaline, smooth, bearing three terminal conidiogenous cells. *Conidiogenous cells* 19–25 × 7.5–9 µm (av. 22 × 8 µm, n = 10), enteroblastic, phialidic, integrated, determinate, terminal, subulate, with a conspicuous collarette. *Conidia* 13–19 × 7–9 µm (av. 15.5 × 8.5 µm, n = 20), solitary, ellipsoidal, attenuated at the apex, with a protruding hilum at the base, hyaline, aseptate, smooth-walled.

Culture characteristics – colonies on PDA reaching 45 mm diam. at 25 °C after 30 days, flat, dry, rough, margin filiform and irregular; from above, yellowish brown and white; from below, pale brown with several dark brown blobs in the middle; not producing pigmentation in the culture.

Material examined – China, Yunnan Province, Kunming City, on dead stems of *Artemisia argyi* H. Lév. & Vaniot (*Asteraceae*), 14 September 2019, C.F. Liao LC011 (MHZU 23-0116, **holotype**); ex-type culture ZHKUCC 23-0882.

GenBank accession numbers – ITS: OR365451, tub2: OR700206.

Notes – *Clonostachys artemisiae* bears a close relationship with *C. apocyni* in our phylogenetic analysis (Fig. 23). *Clonostachys artemisiae* and *C. apocyni* exhibit key features of asexual *Clonostachys*, including penicillate conidiophores and phialidic conidiogenous cells that produce hyaline conidia (Schroers 2001). However, *C. artemisiae* can be distinguished from *C. apocyni* by its subulate, shorter conidiogenous cells (19–25 µm long) with a conspicuous collarette, whereas the latter has cylindrical, longer conidiogenous cells (up to 40 µm long) without a visible collarette. In addition, *C. artemisiae* is frequently characterized by a protruding hilum at the conidial base, whereas this feature remains concealed in *C. apocyni*. With regard to DNA sequence data comparison, there is a discrepancy of 2.28% (11 out of 482) and 4.06% (24 out of 591) in nucleotide variations within the ITS and tub2 genes, respectively, between *C. artemisiae* ZHKUCC 23-0882 and *C. apocynin* CBS 130.87. Based on phylogenetic analyses and morphological characteristics, *C. artemisiae* is identified as a novel species within *Clonostachys*.

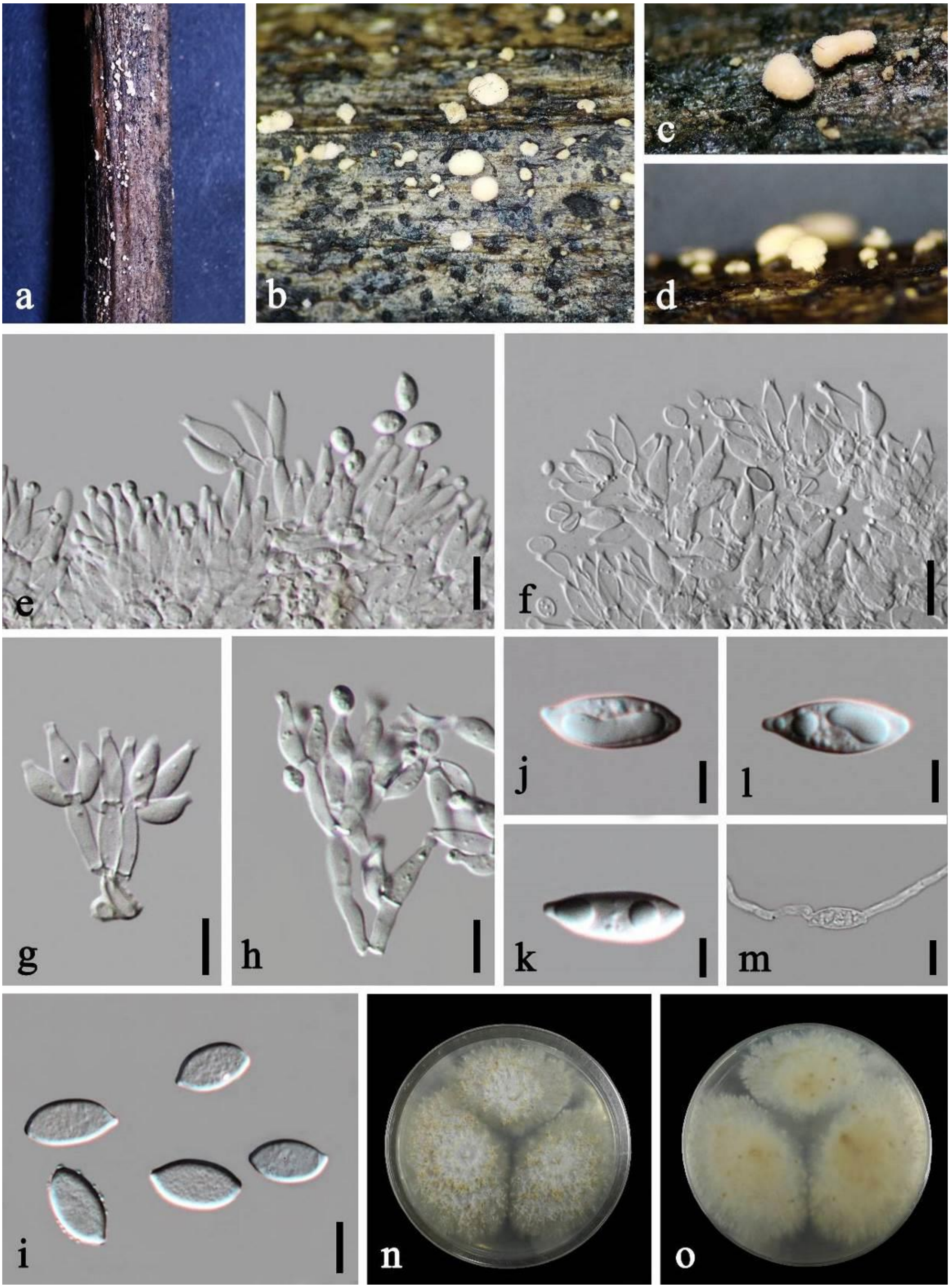

Figure 22 – *Clonostachys artemisiae* (MHZU 23-0116, holotype). a Decaying branch of host. b–d Colonies on natural substrate. e–h Conidiophores, conidiogenous cells and conidia. i–l Conidia. m Germinated conidium. n Colony on PDA (front view). o Colony on PDA (below view). Scale bars: e–i, m = 10 µm, j–l = 5 µm.

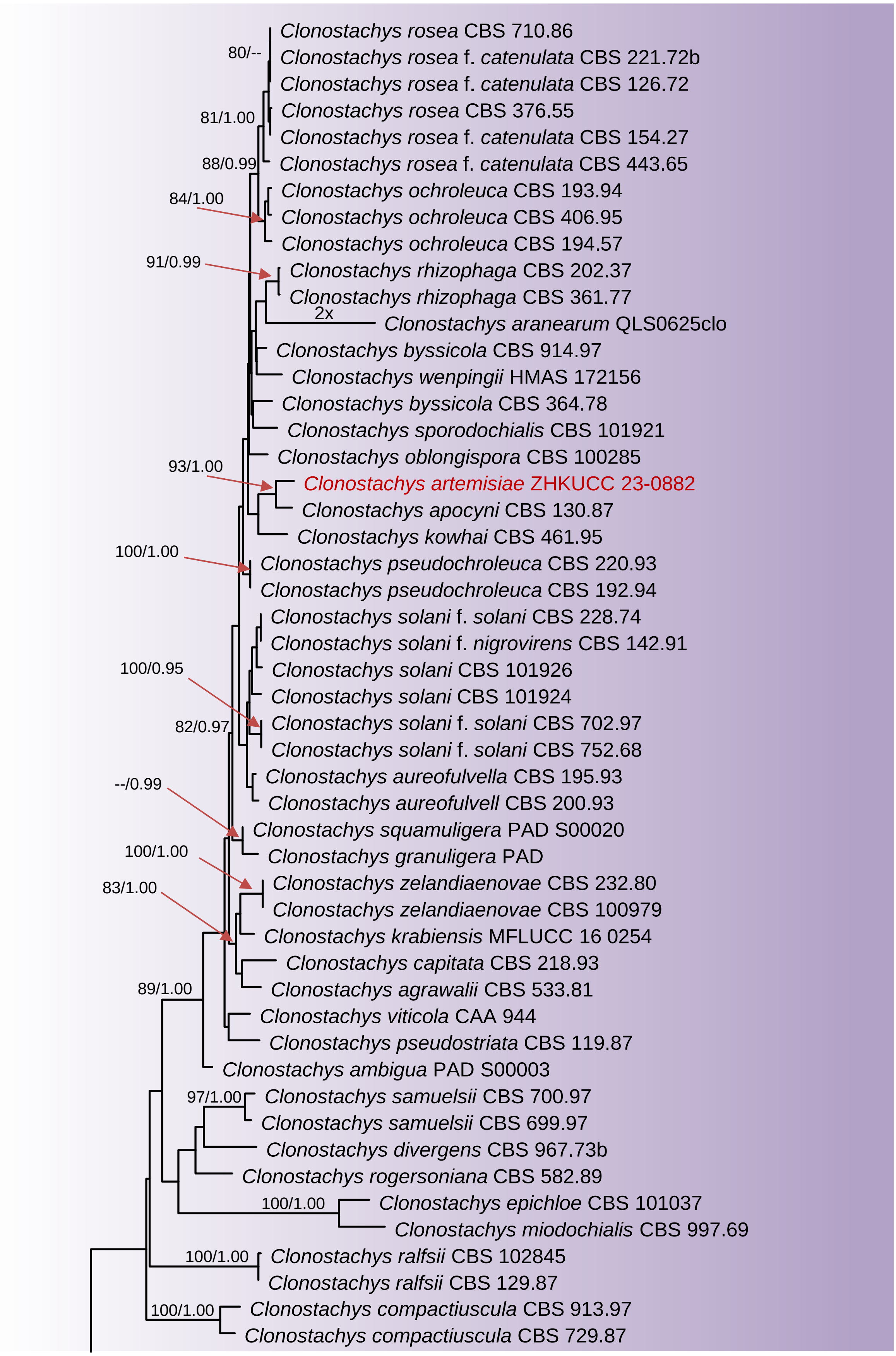

Figure 23 – Maximum likelihood consensus tree inferred from the combined ITS and tub2 multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected

changes per site. The tree is rooted to *Fusarium acutatum* CBS 402.97 and *Nectria cinnabarina* CBS 125165. Ex-type strains are indicated with “^{T}”. The new species is indicated with red.

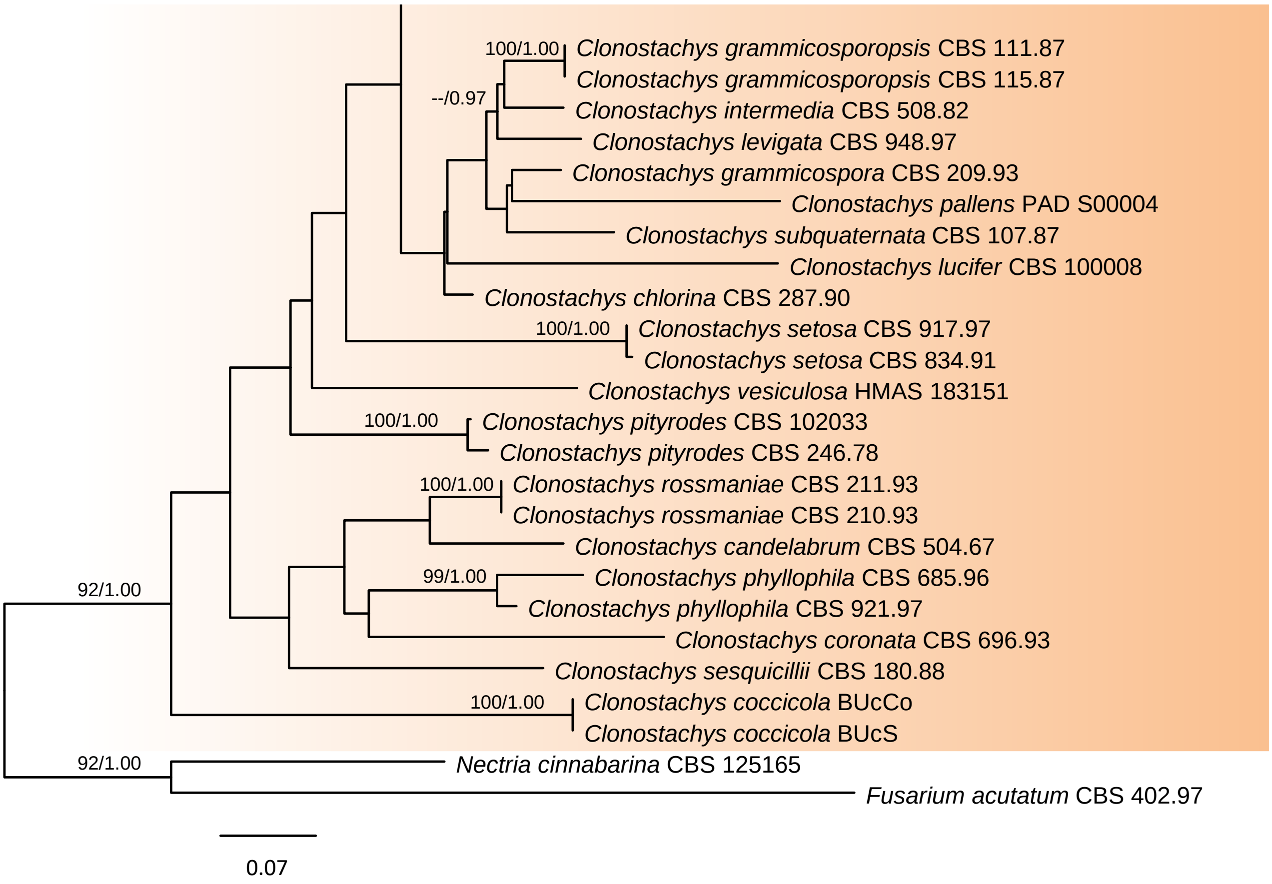

Figure 23 – Continued.

Phomatosporales Senan., Maharachch. & K.D. Hyde, Mycosphere 7(5): 631 (2016)
Phomatosporaceae Senan., Maharachch & K.D. Hyde, Mycosphere 7(5): 633 (2016)

Type genus – *Phomatospora* Sacc.

Notes – *Phomatosporaceae* was initially proposed invalidly by von Arx (1951), but later reinstated to accommodate three genera, *viz*., *Phomatospora* (type), *Lanspora* and *Tenuimurus* (Senanayake et al. 2016). Due to limitations in sampling and insufficient DNA sequence data, the family remains poorly studied, resulting in several taxonomic issues arising with the addition of more taxa to the phylogenetic tree. In our updated phylogenetic tree, *Lanspora* is found to be polyphyletic. The type species *L. coronata* clustered with the genus *Minimispora*, while *L. cylindrospora* formed another clade with *Conicotenuis* and *Paramicrodochium* (Fig. 26). Furthermore, *Phomatospora* species did not consistently form a monophyletic clade or cluster with significant statistical support upon incorporation of the new data. Thus, a reevaluation of the classification of these taxa is currently pending. The following two novel genera, *viz*., *Conicotenuis* and *Minimispora*, are proposed. A key to sexual genera within the family is provided as well.

Key to sexual genera within *Phomatosporaceae*

1. Ascomata entirely superficial and tiny (< 70 µm diam.), lacking a clypeus…………***Minimispora***
1. Ascomata immersed or becoming erumpent, developing under a small/large blackened clypeus………………………………………………………………………………………….2
2. Asci and ascospores are quite small, asci < 80 µm in height, and ascospores < 10 µm in length……………………………………………………………………………….***Tenuimurus***
2. Asci and ascospores are not as mentioned above……………………………………………3

3. Ascomata conical, ascospores distinct fusiform, verrucose, longitudinally striate, and with bipolar apiculis at both ends………………………………………………………….***Conicotenuis***
3. Ascomata globose or subglobose, ascospores narrowly ellipsoidal with round ends……………..4
4. Ascospores with crown-like, sheet-like, irregular and radiating, delicate and sub-gelatinous appendages at both ends, longitudinally striate…………………………………………….***Lanspora***
4. Ascospores lacking crown-like, sheet-like appendages, sometimes with filamentous appendages at both ends, sometimes longitudinally striate………………………………………..***Phomatospora***

Conicotenuis W. Dong & K.D. Hyde, gen. nov.

Index Fungorum number: IF900865; Facesoffungi number: FoF 14695

Etymology – referring to conical shape of ascomata and delicate, thin peridium.

Type species – *Conicotenuis fusiformis* W. Dong & K.D. Hyde

Sexual morph: *Ascomata* scattered, immersed or becoming erumpent, conical, black, unilocular, glabrous, with an ostiolate papilla, developing under a small, blackened clypeus. *Peridium* comprises a few layers of brown, thin-walled, compressed cells of *textura angularis*. *Paraphyses* sparse, hypha-like, septate, hyaline. *Asci* 8-spored, unitunicate, cylindrical, pedicellate, with a refractive, apical ring. *Ascospores* uniseriate and overlapping biseriate near the centre, fusiform, aseptate, hyaline, thin-walled, verrucose, longitudinally striate, with bipolar apiculis. Asexual morph: undetermined.

Notes – BLASTn searches conducted on our new collection MFLUCC 18-1009 using LSU, SSU and ITS loci consistently reveal DNA sequence similarities with members of *Phomatosporaceae*, *viz.*, *Lanspora*, *Phomatospora* and *Tenuimurus*, as well as three other species *Paramicrodochium gracile*, *Paramicrothyrium chinensis* and *Microdochium sclerotiorum*. In our phylogenetic analysis inferred from a combined dataset of LSU, SSU and ITS loci, MFLUCC 18-1009 is classified within *Phomatosporaceae* but is distant from all known members. It forms a sister branch with *Paramicrodochium* (Fig. 26).

Paramicrodochium, typified by *P. gracile*, is characterized as a hyphomycete with acicular and falcate, hyaline spores, but its sexual morph remains unknown (Hernández-Restrepo et al. 2016). Therefore, a morphological comparison between *P. gracile* and the new collection MFLUCC 18-1009 could not be conducted. Nucleotide comparison between *P. gracile* CBS 493.70 and MFLUCC 18-1009 reveals that there are 24 nucleotide differences spanning over 822 nucleotides in the LSU locus, with a similarity of 97.08%. Both nucleotide comparison and phylogenetic analysis indicate that MFLUCC 18-1009 represents a distinct genus. It can be distinguished from other genera within the family by its possession of conical ascomata and distinct fusiform ascospores with verrucose, longitudinally striate ornamentation, and bipolar apiculis at both ends. Hence, a novel genus *Conicotenuis* is proposed to accommodate the newly collected strain, namely *C. fusiformis*.

Conicotenuis fusiformis W. Dong & K.D. Hyde, sp. nov. Fig. 24

Index Fungorum number: IF900866; Facesoffungi number: FoF 14696

Etymology – referring to the fusiform ascospores of the fungus.

Holotype – MFLU 18-1173

Saprobic on submerged wood in a lotic stream. Sexual morph: *Ascomata* 190–210 µm high, 150–180 µm diam., scattered, immersed or becoming erumpent, conical, black, unilocular, glabrous, with an ostiolate papilla, developing under a small blackened clypeus. *Peridium* 9–11 µm thick, ca. 15 µm thick around the ostiole, comprising 4–6 layers of brown, thin-walled, compressed cells of *textura angularis*. *Paraphyses* 6–6.5 µm diam., sparse, hypha-like, septate, constricted at the septa, hyaline. *Asci* 100–125 × 7.5–8.5 µm (av. 110 × 8 µm, n = 10), 8-spored, unitunicate, cylindrical, thin-walled, pedicellate, with a refractive, apical ring. *Ascospores* 15.5–17.5 × 3.5–4.3 µm (av. 16.5 × 4 µm, n = 15), uniseriate and overlapping biseriate near the centre, straight or slightly curved, fusiform, aseptate, hyaline, guttulate, thin-walled, verrucose, clearly seen in the cotton blue, longitudinally striate, with bipolar apiculis. Asexual morph: undetermined.

Culture characteristics – colonies on PDA reaching 30 mm diam. at 25 °C after 25 days, flat, dry, felty, wavily veined, margin undulate and irregular; from above and below, white and milky at the margin, pale yellow in the middle; not producing pigmentation in the culture.

Material examined – China, Yunnan Province, Honghe City, Pingbian County, on submerged wood in a lotic stream, 20 September 2017, W. Dong TSSK-1-1B (MFLU 18-1173, **holotype**); ex-type culture MFLUCC 18-1009; *ibid*., HKAS 101699, isotype; living culture KUMCC 18-0048.

GenBank accession numbers – ITS: OR365452, LSU: OR365482, SSU: OR365489.

Notes – *Conicotenuis fusiformis* is similar to *Phomatospora biseriata* in having immersed or erumpent ascomata developed under a small, blackened clypeus, cylindrical, thin-walled asci, and hyaline, aseptate, longitudinally striate ascospores (Senanayake et al. 2016). However, they can be distinguished based on the arrangement of ascospores in the asci (primarily uniseriate vs. biseriate) and the shape and ornamentation of ascospores (fusiform with bipolar apiculis vs. ellipsoidal without bipolar apiculis). The multi-locus phylogenetic analysis reveals that they are positioned into distinct lineages within *Phomatosporaceae* (Fig. 26). Given that a quarter of *Phomatospora* species have been established in the nineteenth century and the majority were reported during the twentieth century, obtaining authentic morphological data for those species lacking sequences is unattainable. Therefore, based on our current knowledge, *C. fusiformis* does not belong in *Phomatospora* and is proposed as a new genus/species in this study.

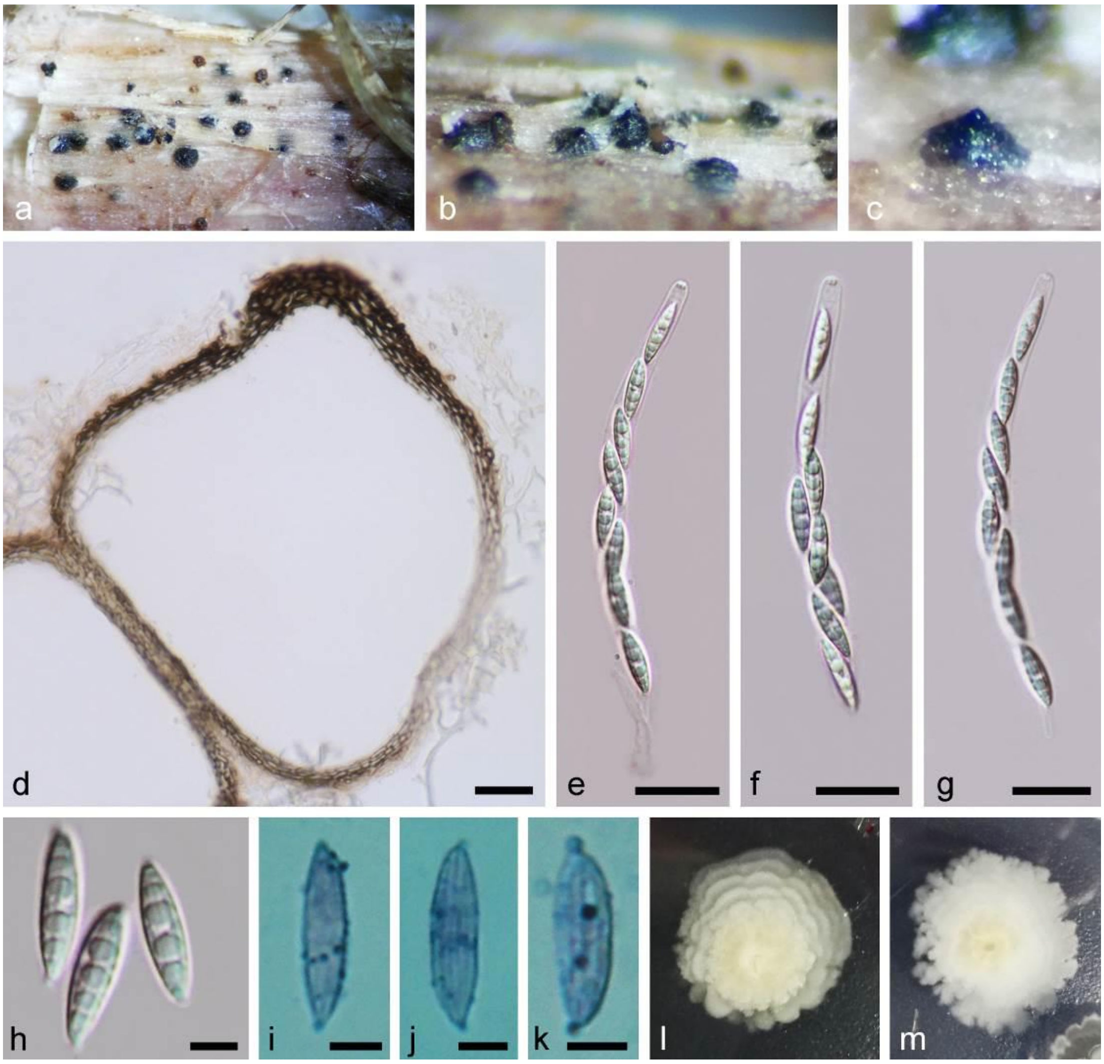

Figure 24 – *Conicotenuis fusiformis* (MFLU 18-1173, holotype). a–c Appearance of black ascomata erumpent to superficial on host. d Vertical section of ascoma. e–g Unitunicate asci. h–k Ascospores (i–k ascospores mounted in cotton blue). l Colony on PDA (front view). m Colony on PDA (below view). Scale bars: d = 30 μm, e–g = 20 μm, h–k = 5 μm.

Minimispora W. Dong & K.D. Hyde, gen. nov.

Index Fungorum number: IF900867; Facesoffungi number: FoF 14697

Etymology – referring to the tiny ascomata of the fungus.

Type species – *Minimispora superficialis* W. Dong & K.D. Hyde

Sexual morph: *Ascomata* scattered, superficial, globose, black, unilocular, thin-walled, glabrous, ostiolate, with a short beak. *Peridium* thin, composed of pale brown, thin-walled, large cells of *textura angularis*. *Paraphyses* numerous, cylindrical, hyaline, septate. *Asci* 8-spored, unitunicate, cylindrical, thin-walled, pedicellate, apically rounded, with a refractive, apical ring. *Ascospores* uniseriate, narrowly ellipsoidal, straight, hyaline, aseptate, thin- and smooth-walled. Asexual morph: undetermined.

Notes – BLASTn searches conducted on our new collection MFLUCC 18-1021 using LSU and SSU loci revealed DNA sequence similarities with *Microdochium sclerotiorum*, *Paramicrothyrium chinensis* and species of *Phomatosporaceae*. The phylogenetic analysis of the combined LSU, SSU and ITS loci further demonstrates that *Microdochium sclerotiorum*, *Paramicrothyrium chinensis* and MFLUCC 18-1021 form a well-supported clade as a sister group to *Lanspora coronata* in *Phomatosporaceae* (Fig. 26).

Microdochium sclerotiorum is a species with limited documentation, which was originally isolated from a contaminated culture of insect fungi in Ghana (Mouchacca & Samson 1973). Although the LSU and ITS sequence data of *M. sclerotiorum* CBS 106.73 (type) are available, its morphology remains unclear (Vu et al. 2019). The classification of *M. sclerotiorum* is challenging due to its clustering in *Phomatosporaceae* in our phylogenetic analysis (Fig. 26), despite the fact that the type species *M. phragmitis* belongs to *Microdochiaceae* (Hernández-Restrepo et al. 2016). Due to the lack of informative morphological characteristics, it is currently impossible to determine whether *M. sclerotiorum* has been misidentified. Therefore, we have decided to maintain its taxonomic status as "*Microdochium sclerotiorum*" within *Phomatosporaceae* until further data becomes available.

Paramicrothyrium chinensis, a microthyrium-like microfungus, is characterized by circular thyriothecia, bitunicate asci and fusiform-clavate, septate ascospores. These features are typical of the family *Microthyriaceae*, *Dothideomycetes* (Wu et al. 2011). In its protologue, *P. chinensis* was referred to as *Dothideomycetes* genera *incertae sedis* (Wu et al. 2011). However, subsequent studies have demonstrated that clusters with different groups within *Dothideomycetes* without statistical support (Hongsanan et al. 2014, Wu et al. 2014, Singtripop et al. 2016, Hyde et al. 2017, Jayasiri et al. 2018). Based on BLASTn searches using LSU and SSU loci, *P. chinensis* IFRDCC 2258 exhibits DNA sequence similarities to members of *Phomatosporaceae* in *Sordariomycetes* rather than *Dothideomycetes*, which is consistent with the phylogenetic analysis conducted by Hernández-Restrepo et al. (2016) and our study (Fig. 26). Given its microthyrium-like morphology in *Dothideomycetes* and its phylogenetic position in *Phomatosporaceae*, *Sordariomycetes*, an interesting taxonomic issue arises. Both single gene comparison and multigene phylogenetic analysis indicate that *P. chinensis* IFRDCC 2258 and the new collection MFLUCC 18-1021 are conspecific, but their morphology presents a contradiction. Thus, it is likely that the sequence data of *P. chinensis* was obtained from a different species (pers. comm. H.X. Wu). In this study, we consider "*Paramicrothyrium chinensis*" as an indetermined species. A new genus *Minimispora* is proposed for the collection MFLUCC 18-1021, namely *M. superficialis*, to differentiate it from "*Paramicrothyrium chinensis*".

Minimispora can be distinguished from the phylogenetically related genus *Lanspora* by the characteristics of ascomata (superficial vs. immersed or becoming exposed), ascus shape (cylindrical vs. cylindrical or oblong-ventricose) and ascospore shape and appendages (narrowly ellipsoidal without appendages vs. ellipsoidal with bipolar, numerous, sheet-like appendages) (Hyde & Jones 1986). *Minimispora* is similar to *Tenuimurus* in having cylindrical, thin-walled asci and uniseriate, ellipsoidal, hyaline ascospores. However, *Minimispora* possesses superficial ascomata in contrast to the immersed ascomata that develop under a small blackened clypeus in *Tenuimurus* (Senanayake et al. 2016). In contrast to other genera in *Phomatosporaceae*, *Minimispora* exhibits entirely superficial ascomata, while the former mainly possess immersed ascomata or those becoming erumpent (Senanayake et al. 2016).

Minimispora superficialis W. Dong & K.D. Hyde, sp. nov. Fig. 25

Index Fungorum number: IF900868; Facesoffungi number: FoF 14698

Etymology – referring to the superficial ascomata on natural substrate.

Holotype – MFLU 18-1211

Saprobic on submerged wood in a lotic stream. Sexual morph: *Ascomata* 50–70 µm high, 40–60 µm diam., scattered, superficial, globose, black, unilocular, thin-walled, glabrous, ostiolate, with a short beak. *Peridium* 5–10 µm thick, comprising 2–3 layers of pale brown, thin-walled, large cells of *textura angularis*. *Paraphyses* 4.5–6.5 µm diam., numerous, cylindrical, swollen, hyaline, septate, constricted at the septa. *Asci* 60–70(–90) × 3–4 µm (av. 70 × 3.5 µm, n = 10), 8-spored, unitunicate, cylindrical, thin-walled, pedicellate, with a refractive, apical ring. *Ascospores* 5.5–7 × 2–3 µm (av. 6 × 2.5 µm, n = 20), uniseriate, straight, hyaline, aseptate, narrowly ellipsoidal, thin- and smooth-walled. Asexual morph: undetermined.

Culture characteristics – colonies on PDA reaching 25 mm diam. at 25 °C after 50 days, umbonate, dry, rough, margin lobate and irregular; from above and below, white and milky at the margin, pale golden yellow in the middle; not producing pigmentation in the culture.

Material examined – China, Yunnan Province, Honghe City, Pingbian County, on submerged wood in a lotic stream, 20 September 2017, W. Dong PB28B (MFLU 18-1211, **holotype**); ex-type culture MFLUCC 18-1021; *ibid*., HKAS 101715, isotype; living culture KUMCC 18-0064.

GenBank accession numbers – ITS: OR365454, LSU: OR365484, SSU: OR365490.

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

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

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

Type genus – *Stictis* Pers.

Notes – *Stictidaceae* was proposed for the saprobic genus *Stictis*, which is characterized by apothecioid ascomata, cylindrical asci and filiform ascospores (Winka et al. 1998). The familial concept has been revised by the introduction of an atypical novel species and a new combination (Wei et al. 2021). The generic composition of *Stictidaceae* has been continuously debated and extended over time, resulting in the inclusion of both morphologically and phylogenetically related genera with diverse lifestyles (Aptroot et al. 2014; Thiyagaraja et al. 2021; Wedin et al. 2005; Baloch et al. 2013). According to the most recent outline of fungi, *Stictidaceae* comprises 30 genera (Wijayawardene et al. 2022), while 32 genera have been accepted in recent publications (Wei et al. 2021; Thiyagaraja et al. 2021). In this study, we introduce a novel genus that was discovered from the decaying stem of *Artemisia argyi* in Yunnan Province, China.

Irregularispora W. Dong, K.D. Hyde & Doilom, gen. nov.

Index Fungorum number: IF900869; Facesoffungi number: FoF 14699

Etymology – referring to the irregular-shaped conidia of the fungus.

Type species – *Irregularispora olivacea* W. Dong, K.D. Hyde, C.F. Liao & Doilom

Sexual morph: undetermined. Asexual morph: *Colonies* effuse, dense, velvety, black on the host. *Mycelium* partly immersed, composed of septate, branched, smooth, subhyaline to pale brown hyphae. *Conidiophores* often reduced. *Conidiogenous cells* obscured, subcylindrical, subhyaline to pale brown. *Conidia* solitary, irregular-shaped, olivaceous to dark olivaceous, septate, rough- and thin-walled.

Notes – the BLASTn searches on our collection using the LSU reveals *Irregularispora* with the closest relationships to *Glomerobolus* (97.34%), followed by *Ostropomyces* (95.86%), *Neohormodochis* (95.43%), *Stictis* (95.22%), *Acarosporina* (94.83%), *Robergea* (94.34%) and *Absconditella* (94.34 %). All of these taxa belong to the family *Stictidaceae*. The BLASTn searches using ITS reveals *Irregularispora* having the highest sequence similarity with *Neohormodochis* (92.95%), *Schizoxylon* (92.93%) and *Hormodochis* (92.64%). In our phylogenetic analysis based on combined LSU, ITS, SSU and *rpb2* loci, *Irregularispora* was also placed within *Stictidaceae* but exhibited distant relationships with all of its allies. *Irregularispora* was positioned in a distinct lineage sister to *Glomerobolus* (Fig. 28). *Glomerobolus* has a reproductive structure called a hyphoma, which consists of sterile hyphae embedded in a gelatinous matrix and produces a ballistic propagule (Kohlmeyer & Volkmann-Kohlmeyer 2018). The unique discharge mechanism is attributed to the absorption of water by the gelatinous matrix, which results in a forceful ejection of the propagule. It is evident that *Glomerobolus* and *Irregularispora* belong to entirely different genera. In addition, a morphological study based on the latest taxonomic account of Wei et al. (2021, 2022) reveals that none of the extant asexual genera exhibits similar morphology to *Irregularispora*. Therefore, *Irregularispora* is established as a novel genus in *Stictidaceae*.

Figure 25 – *Minimispora superficialis* (MFLU 18-1211, holotype). a Appearance of black ascomata superficial on host. b Vertical section of ascoma. c Structure of peridium. d–f Unitunicate asci. g Ascus with paraphyses. h Ascospores. i Germinated ascospore. j Colony on PDA (from front). k Colony on PDA (from below). Scale bars: b = 15 µm, c, h, i = 5 µm, d–g = 10 µm.

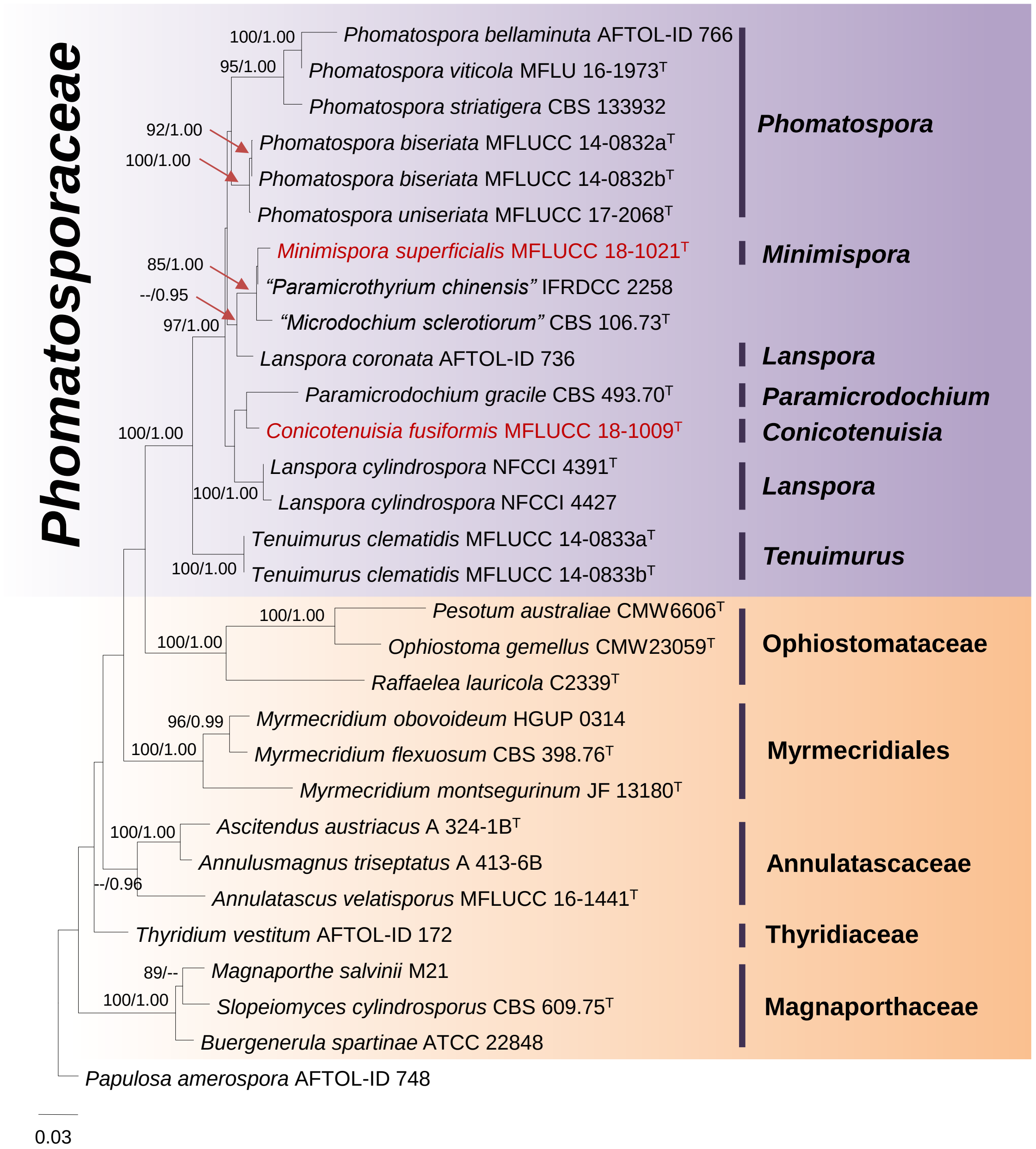

Figure 26 – Maximum likelihood consensus tree inferred from the combined LSU, SSU and ITS multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Papulosa amerospora* AFTOL-ID 748. Ex-type strains are indicated with “^{T}”. The new species are indicated with red.

Irregularispora olivacea W. Dong, K.D. Hyde, C.F. Liao & Doilom, sp. nov. Fig. 27

Index Fungorum number: IF900870; Facesoffungi number: FoF 14700

Etymology – referring to the olivaceous conidia of the fungus.

Holotype – MHZU 23-0117

Saprobic on dead stem of *Artemisia argyi*. Sexual morph: undetermined. Asexual morph: *Colonies* effuse, dense, velvety, black on the host. *Mycelium* partly immersed, composed of septate, branched, smooth, subhyaline to pale brown hyphae. *Conidiophores* micronematous, mononematous, unbranched, septate, not constricted at the septa, smooth, subhyaline, thin-walled, often reduced to conidiogenous cells. *Conidiogenous cells* 2.5–5.5 × 1.5–2.5 µm (av. 3.7 × 2 µm, n = 10), obscured, subcylindrical, subhyaline to pale brown. *Conidia* 7.5–30 µm diam. (av. 15.5 µm, n = 20), solitary, irregular in shape, subglobose, ovoid, obovoid, slightly crenate in some conidia when mounted in water, olivaceous when young, dark olivaceous to black when mature, multi-celled, rough- and thin-walled.

Culture characteristics – colonies on PDA reaching 7 mm diam. at 25 °C after 45 days, flat, dry, rough, margin entire; from above and below, white; not producing pigmentation in the culture.

Material examined – China, Yunnan Province, Qujing City, on dead stem of *Artemisia argyi* H. Lév. & Vaniot (*Asteraceae*), 1 October 2019, C.F. Liao AL01 (MHZU 23-0117, **holotype**); ex-type culture ZHKUCC 23-0883.

GenBank accession numbers – ITS: OR365453, LSU: OR365483.

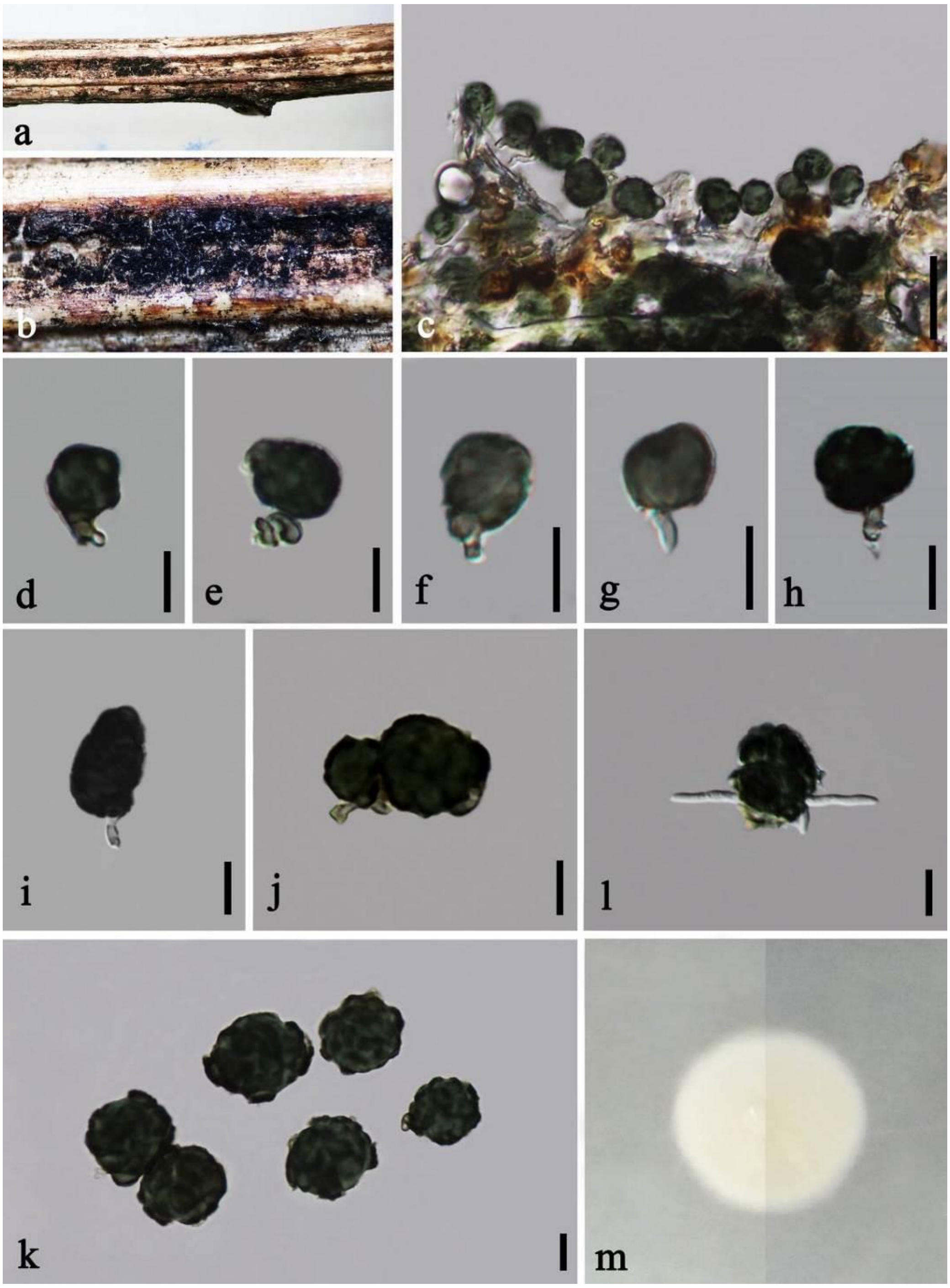

Figure 27 – *Irregularispora olivacea* (MHZU 23-0117, holotype). a, b Colonies on natural substrate. c Conidiogenous cells and conidia. d–k Conidia. l Germinated conidium. m Colony on PDA (front and below view). Scale bars: c = 20 μm, d–l = 10 μm.

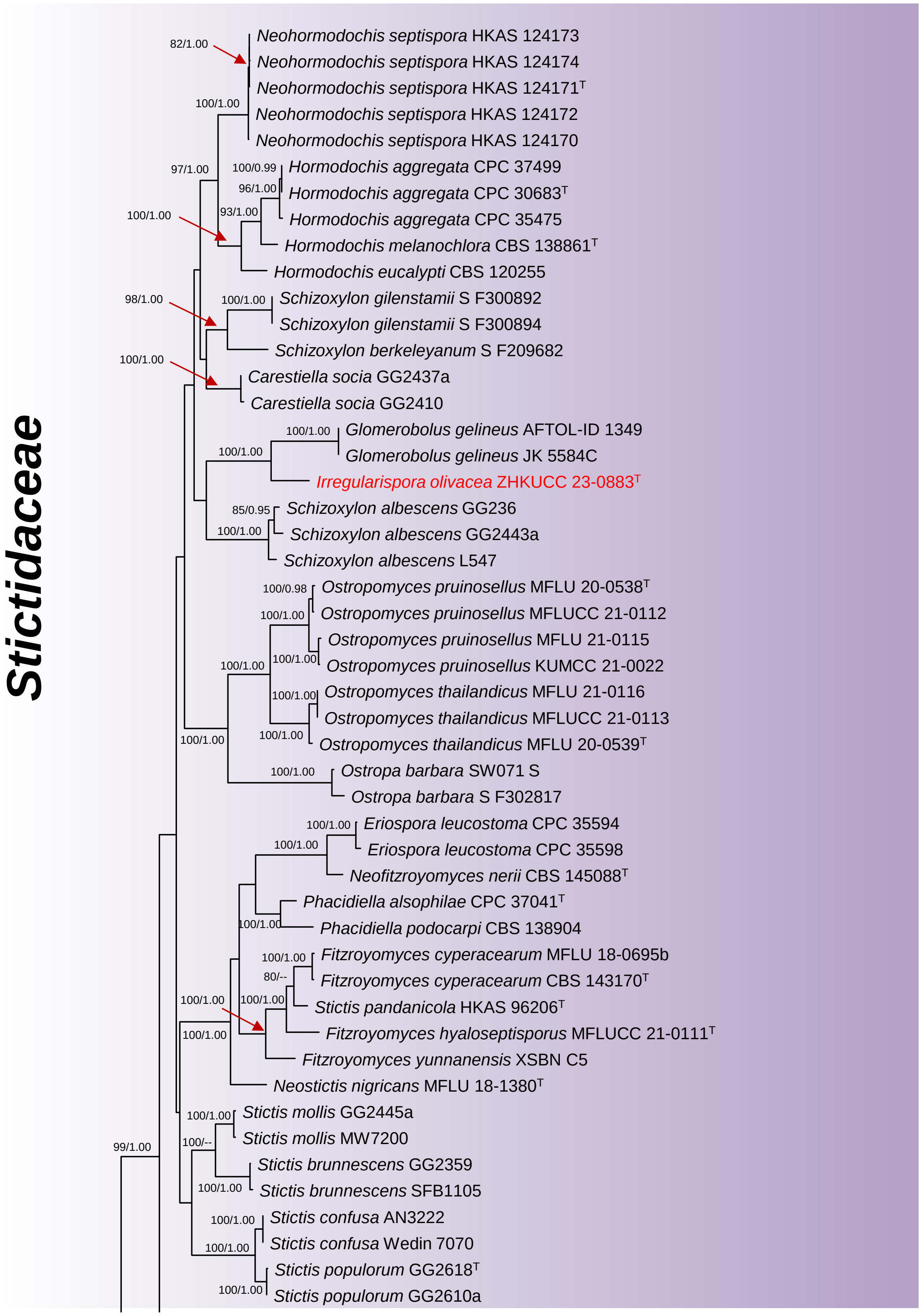

Figure 28 – Maximum likelihood consensus tree inferred from the combined LSU, ITS, SSU and *rpb2* multiple sequence alignments. Bootstrap support values for maximum likelihood (ML, first value) equal to or greater than 80% and Bayesian posterior probabilities from MCMC analyses (BYPP, second value) equal to or greater than 0.95 are given above the nodes. The scale bar indicates expected changes per site. The tree is rooted to *Placopsis perrugosa* KS132 and *Trapelia coarctata* KS22. Ex-type strains are indicated with "^{T}". The new species is indicated in red.

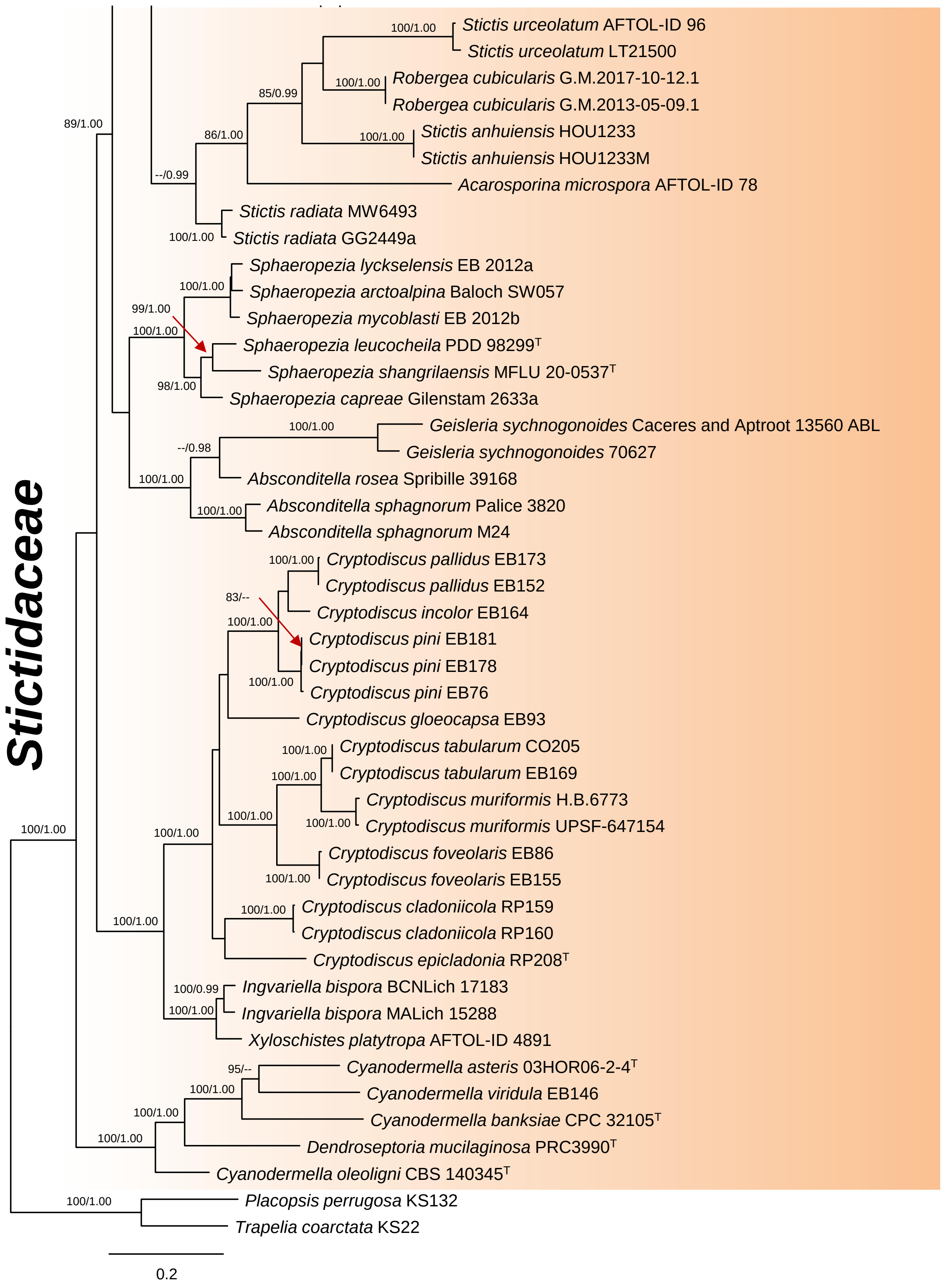

Figure 28 – Continued.

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References

Ahmadpour SA, Mehrabi-Koushki M, Farokhinejad R, Asgari B. 2022 – New species of the family *Didymellaceae* in Iran. Mycological Progress 21, 28.

Andreasen M, Skrede I, Jaklitsch W, Voglmayr H et al. 2021 – Multi-locus phylogenetic analysis of lophiostomatoid fungi motivates a broad concept of *Lophiostoma* and reveals nine new species. Persoonia 46, 240–271.

Aptroot A, Parnmen S, Luecking R, Baloch E et al. 2014 – Molecular phylogeny resolves a taxonomic misunderstanding and places *Geisleria* close to *Absconditella* s. str. (*Ostropales*: *Stictidaceae*). The Lichenologist 46, 115–128.

Ariyawansa HA, Tanaka K, Thambugala KM, Phookamsak R et al. 2014 – A molecular phylogenetic reappraisal of the *Didymosphaeriaceae* (= *Montagnulaceae*). Fungal Diversity 68, 69–104.

Artand S, Mehrabi-koushki M, Tabein S, Hyde KD et al. 2022 – Revision of the *Microsphaeropsis* complex with addition of four new *Paramicrosphaeropsis* L.W. Hou, L. Cai & Crous species from Zagrosian forest trees in Iran. Cryptogamie, Mycologie 43, 159–175.

Baloch E, Gilenstam G, Wedin M. 2013 – The relationships of *Odontotrema* (*Odontotremataceae*) and the resurrected *Sphaeropezia* (*Stictidaceae*) – new combinations and three new *Sphaeropezia* species. Mycologia 105, 384–397.

Barr ME. 1994 – Notes on the *Amphisphaeriaceae* and related families. Mycotaxon 51, 191–224.

Barr ME. 2001 – *Montagnulaceae*, a new family in the *Pleosporales* and lectotypification of *Didymosphaerella*. Mycotaxon 77, 193–200.

Berlese AN. 1896 – Icones fungorum. *Pyrenomycetes* 2, 1–216.

Boonmee S, D'souza MJ, Luo ZL, Pinruan U et al. 2016 – *Dictyosporiaceae* fam. nov. Fungal Diversity 80, 457–482.

Boonmee S, Wanasinghe DN, Calabon MS, Huanraluek N et al. 2021 – Fungal diversity notes 1387–1511: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 111, 1–335.

Brahmanage RS, Dayarathne MC, Wanasinghe DN, Thambugala KM et al. 2020 – Taxonomic novelties of saprobic *Pleosporales* from selected dicotyledons and grasses. Mycosphere 11, 2481–2541.

Chen Q, Jiang JR, Zhang GZ, Cai L et al. 2015 – Resolving the *Phoma* enigma. Studies in Mycology 82, 137–217.

Chethana KWT, Manawasinghe IS, Hurdeal VG, Bhunjun CS et al. 2021 – What are fungal species and how to delineate them? Fungal Diversity 109, 1–25.

Crous PW, Carris LM, Giraldo A, Groenewald JZ et al. 2015 – The genera of fungi-fixing the application of the type species of generic names–G 2: *Allantophomopsis*, *Latorua*, *Macrodiplodiopsis*, *Macrohilum*, *Milospium*, *Protostegia*, *Pyricularia*, *Robillarda*, *Rotula*, *Septoriella*, *Torula*, and *Wojnowicia*. IMA Fungus 6, 163–198.

Crous PW, Wingfield MJ, Chooi YH, Gilchrist CLM et al. 2020 – Fungal Planet description sheets: 1042–1111. Persoonia 44, 301–459.

de Gruyter J, Aveskamp MM, Woudenberg JH, Verkley GJ et al. 2009 – Molecular phylogeny of *Phoma* and allied anamorph genera: towards a reclassification of the *Phoma* complex. Mycological Research 113, 508–519.

Dayarathne MC, Jones EBG, Maharachchikumbura SSN, Devadatha B et al. 2020 – Morpho-molecular characterization of microfungi associated with marine based habitats. Mycosphere 11, 1–188.

Doilom M, Hyde KD, Phookamsak R, Dai DQ et al. 2018 – Mycosphere notes 225–274: types and other specimens of some genera of *Ascomycota*. Mycosphere 9, 647–754.

Du T, Hyde KD, Mapook A, Mortimer PE et al. 2021 – Morphology and phylogenetic analyses reveal *Montagnula puerensis* sp. nov. (*Didymosphaeriaceae*, *Pleosporales*) from southwest China. Phytotaxa 514, 1–25.

Hashimoto A, Hirayama K, Takahashi H, Matsumura M et al. 2018 – Resolving the *Lophiostoma bipolare* complex: generic delimitations within *Lophiostomataceae*. Studies in Mycology 90, 161–189.

Hernández-Restrepo M, Groenewald JZ, Crous PW. 2016 – Taxonomic and phylogenetic re-evaluation of *Microdochium*, *Monographella* and *Idriella*. Persoonia 36, 57–82.

Hongsanan S, Chomnunti P, Crous PW, Chukeatirote E et al. 2014 – Introducing *Chaetothyriothecium*, a new genus of *Microthyriales*. Phytotaxa 161, 157–164.

Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al. 2020 – Refined families of *Dothideomycetes*: Dothideomycetidae and Pleosporomycetidae. Mycosphere 11, 1553–2107.

Hou LW, Groenewald JZ, Pfenning LH, Yarden O et al. 2020 – The phoma-like dilemma. Studies in Mycology 96, 309–396.

Hyde KD, Chaiwan N, Norphanphoun C, Boonmee S et al. 2018 – Mycosphere notes 169–224. Mycosphere 9, 271–430.

Hyde KD, Jones EBG. 1986 – Marine fungi from Seychelles. II. *Lanspora coronata* gen. et sp. nov. from driftwood. Canadian Journal of Botany 64, 1581–1585.

Hyde KD, Jones EBG, Liu JK, Ariyawansa H et al. 2013 – Families of *Dothideomycetes*. Fungal Diversity 63, 1–313.

Hyde KD, Norphanphoun C, Abreu VP, Bazzicalupo A et al. 2017 – Fungal diversity notes 603–708: taxonomic and phylogenetic notes on genera and species. Fungal Diversity 87, 1–235.

Hyde KD, Norphanphoun C, Ma J, Yang HD et al. 2023 – Mycosphere notes 387–412 – novel species of fungal taxa from around the world. Mycosphere 14, 663–744.

Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ et al. 2020 – Refined families of *Sordariomycetes*. Mycosphere 11, 305–1059.

Hyde KD, Tennakoon DS, Jeewon R, Bhat DJ et al. 2019 – Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 96, 1–242.

Index Fungorum. 2023 – http://www.indexfungorum.org/ (Accessed on June 2023).

Iturrieta-González I, Gené J, Guarro J, Castañeda-Ruiz RF et al. 2018 – *Neodendryphiella*, a novel genus of the *Dictyosporiaceae* (*Pleosporales*). MycoKeys 37, 19–38.

Jaklitsch WM, Gardiennet A, Voglmayr H. 2016 – Resolution of morphology-based taxonomic delusions: *Acrocordiella*, *Basiseptospora*, *Blogiascospora*, *Clypeosphaeria*, *Hymenopleella*, *Lepteutypa*, *Pseudapiospora*, *Requienella*, *Seiridium* and *Strickeria*. Persoonia 37, 82–105.

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat DJ et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74, 3–18.

Jayasiri SC, Hyde KD, Jones EBG, Xu J et al. 2018 – Seed decaying *Dothideomycetes* in Thailand: *Zeloasperisporium pterocarpi* sp. nov., (*Zeloasperisporiaceae*, *Zeloasperisporiales*) on carpel of *Pterocarpus* sp. (*Fabaceae*) seed pod. Asian Journal of Mycology 1, 106–113.

Jeewon R, Hyde KD. 2016 – Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. Mycosphere 7, 1669–1677.

Jeewon R, Liew ECY, Hyde KD. 2004 – Phylogenetic evaluation of species nomenclature of *Pestalotiopsis* in relation to host association. Fungal Diversity 17, 39–55.

Jeewon R, Liew ECY, Simpson JA, Hodgkiss IJ, Hyde KD. 2003 – Phylogenetic significance of morphological characters in the taxonomy of *Pestalotiopsis* species. Molecular Phylogenetics and Evolution 27, 372–383.

Jiang HB, Jeewon R, Karunarathna SC, Phukhamsakda C et al. 2021 – Reappraisal of *Immotthia* in *Dictyosporiaceae*, *Pleosporales*: introducing *Immotthia bambusae* sp. nov. and *Pseudocyclothyriella clematidis* comb. et gen. nov. based on morphology and phylogeny. Frontiers in Microbiology 12, 656235.

Jiang N, Voglmayr H, Xue H, Piao CG et al. 2022 – Morphology and phylogeny of *Pestalotiopsis* (*Sporocadaceae*, *Amphisphaeriales*) from *Fagaceae* leaves in China. Microbiology Spectrum 10, e03272-22.

Katoh K, Standley DM. 2016 – A simple method to control over-alignment in the MAFFT multiple sequence alignment program. Bioinformatics 32, 1933–1942.

Kohlmeyer J, Volkmann-Kohlmeyer B. 2018 – Fungi on *Juncus roemerianus*. 6. *Glomerobolus* gen. nov., the first ballistic member of *Agonomycetales*. Mycologia 88, 328–337.

Kosawang C, Karlsson M, Vélëz H, Rasmussen PH et al. 2014 – Zearalenone detoxification by zearalenone hydrolase is important for the antagonistic ability of *Clonostachys rosea* against mycotoxigenic F*usarium graminearum*. Fungal Biology 118, 364–373.

Kularathnage ND, Tennakoon DS, Zhu X, Zhou J et al. 2023 – Reinstating *Dyfrolomyces* and introducing *Melomastia pyriformis* sp. nov. (*Pleurotremataceae*, *Dyfrolomycetales*) from Guangdong Province, China. Current Research in Environmental & Applied Mycology 13, 426–438.

Li JF, Bhat DJ, Phookamsak R, Mapook A et al. 2016 – *Sporidesmioides thailandica* gen. et sp. nov. (*Dothideomycetes*) from northern Thailand. Mycological Progress 15, 1169–1178.

Li JF, Jeewon R, Mortimer PE, Doilom M et al. 2020 – Multigene phylogeny and taxonomy of *Dendryphion hydei* and *Torula hydei* spp. nov. from herbaceous litter in northern Thailand. PloS one 15, e0228067.

Li JF, Phookamsak R, Jeewon R, Bhat DJ et al. 2017 – Molecular taxonomy and morphological characterization reveal new species and new host records of *Torula* species (*Torulaceae*, *Pleosporales*). Mycological Progress 16, 1–15.

Li WJ, McKenzie EHC, Liu JK, Bhat DJ et al. 2020 – Taxonomy and phylogeny of hyaline-spored *coelomycetes*. Fungal Diversity 100, 279–801.

Li WL, Luo ZL, Liu JK, Bhat DJ et al. 2017 – Lignicolous freshwater fungi from China I: *Aquadictyospora lignicola* gen. et sp. nov. and new record of *Pseudodictyosporium wauense* from northwestern Yunnan Province. Mycosphere 8, 1587–1597.

Li WL, Maharachchikumbura SSN, Cheewangkoon R, Liu JK. 2022 – Reassessment of *Dyfrolomyces* and four new species of *Melomastia* from Olive (*Olea europaea*) in Sichuan Province, China. Journal of Fungi 8, 76.

Li YX, Doilom M, Dong W, Liao CF et al. 2023 – A taxonomic and phylogenetic contribution to *Torula*: *T. phytolaccae* sp. nov. on *Phytolacca acinosa* from China. Phytotaxa 584, 1–17.

Liu F, Bonthond G, Groenewald J, Cai L et al. 2019 – *Sporocadaceae*, a family of coelomycetous fungi with appendage-bearing conidia. Studies in Mycology 92, 287–415.

Liu F, Hou L, Raza M, Cai L. 2017 – *Pestalotiopsis* and allied genera from *Camellia,* with description of 11 new species from China. Scientific Reports 7, 866.

Liu JK, Hyde KD, Jones EBG, Ariyawansa HA et al. 2015 – Fungal Diversity Notes 1–110: taxonomic and phylogenetic contributions to fungal species. Fungal Diversity 72, 1–197.

Maharachchikumbura SSN, Chen Y, Ariyawansa HA, Hyde KD et al. 2021 – Integrative approaches for species delimitation in *Ascomycota*. Fungal Diversity 109, 155–179.

Maharachchikumbura SSN, Guo LD, Cai L, Chukeatirote E et al. 2012 – A multi-locus backbone tree for *Pestalotiopsis*, with a polyphasic characterization of 14 new species. Fungal Diversity 56, 95–129.

Maharachchikumbura SSN, Guo LD, Chukeatirote E, Bahkali AH et al. 2011 – *Pestalotiopsis* – morphology, phylogeny, biochemistry and diversity. Fungal Diversity 50, 167–187.

Maharachchikumbura SSN, Hyde KD, Groenewald JZ, Xu J et al. 2014 – *Pestalotiopsis* revisited. Studies in Mycology 79, 121–186.

Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC et al. 2016 – Families of *Sordariomycetes*. Fungal Diversity 79, 1–317.

Manawasinghe IS, Calabon MS, Jones EBG, Zhang YX et al. 2022 – Mycosphere notes 345–386. Mycosphere 13, 454–557.

Manawasinghe IS, Phillips AJL, Xu J, Balasuriya A et al. 2021 – Defining a species in fungal plant pathology: beyond the species level. Fungal Diversity 109, 267–282.

Mapook A, Hyde KD, McKenzie EHC, Jones EBG et al. 2020 – Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). Fungal Diversity 101, 1–175.

Miller MA, Pfeiffer W, Schwartz T. 2010 – Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: Gateway Computing Environments Workshop (GCE), San Diego Supercomput 1–8.

Miller MA, Schwartz T, Pickett BE, He S et al. 2015 – A RESTful API for access to phylogenetic tools via the CIPRES science gateway. Evolutionary Bioinformatics 11, 43–48.

Mouchacca J, Samson RA. 1973 – Deux nouvelles espèces du genre *Microdochium* Sydow. Revue de mycologie 37, 267–275.

Munk A. 1953 – The system of the *Pyrenomycetes*. Dansk Botanisk Arkiv 15, 1–163.

Norphanphoun C, Jeewon R, McKenzie EHC, Wen TC et al. 2017 – Taxonomic position of *Melomastia italica* sp. nov. and phylogenetic reappraisal of *Dyfrolomycetales*. Cryptogamie, Mycologie 38, 507–525.

Pang KL, Hyde KD, Alias SA, Suetrong S et al. 2013 – *Dyfrolomycetaceae*, a new family in the *Dothideomycetes*, *Ascomycota*. Cryptogamie, Mycologie 34, 223–232.

Perera RH, Hyde KD, Jones EBG, Maharachchikumbura SSN et al. 2023 – Profile of *Bionectriaceae*, *Calcarisporiaceae*, *Hypocreaceae*, *Nectriaceae*, *Tilachlidiaceae*, *Ijuhyaceae* fam. nov., *Stromatonectriaceae* fam. nov. and *Xanthonectriaceae* fam. nov. Fungal Diversity 118, 95–271.

Phukhamsakda C, McKenzie EHC, Phillips AJL, Jones EBG et al. 2020 – Microfungi associated with *Clematis* (*Ranunculaceae*) with an integrated approach to delimiting species boundaries. Fungal Diversity 102, 1–203.

Rossman AY, McKemy JM, Pardo-Schultheiss RA, Schroers HJ. 2001 – Molecular studies of the *Bionectriaceae* using large subunit rDNA sequences. Mycologia 93, 100–110.

Rossman AY, Samuels GJ, Rogerson CT, Lowen R. 1999 – Genera of *Bionectriaceae*, *Hypocreaceae* and *Nectriaceae* (*Hypocreales*, *Ascomycetes*). Studies in Mycology 42, 1–248.

Rossman AY, Seifert KA, Samuels GJ, Minnis AM et al. 2013 – Genera in *Bionectriaceae*, *Hypocreaceae*, and *Nectriaceae* (*Hypocreales*) proposed for acceptance or rejection. IMA Fungus 4, 41–51.

Samsudin NIP, Rodriguez A, Medina A, Magan N. 2017 – Efficacy of fungal and bacterial antagonists for controlling growth, FUM1 gene expression and fumonisin B1 production by *Fusarium verticillioides* on maize cobs of different ripening stages. International Journal of Food Microbiology 246, 72–79.

Schroers HJ. 2001 – A monograph of *Bionectria* (*Ascomycota*, *Hypocreales*, *Bionectriaceae*) and its *Clonostachys* anamorphs. Studies in Mycology 46, 1–214.

Senanayake IC, Al-Sadi AM, Bhat DJ, Camporesi E et al. 2016 – *Phomatosporales* ord. nov. and *Phomatosporaceae* fam. nov., to accommodate *Lanspora*, *Phomatospora* and *Tenuimurus*, gen. nov. Mycosphere 7, 628–641.

Senanayake IC, Rathnayake AR, Marasinghe DS, Calabon MS et al. 2020 – Morphological approaches in studying fungi: collection, examination, isolation, sporulation and preservation. Mycosphere 11, 2678–2754.

Singtripop C, Hongsanan S, Li J, De Silva NI et al. 2016 – *Chaetothyrina mangiferae* sp. nov., a new species of *Chaetothyrina*. Phytotaxa 255, 21–33.

Steyaert RL. 1949 – Contribution à l'étude monographique de *Pestalotia* de Not. et *Monochaetia* Sacc. (*Truncatella* gen. nov. et *Pestalotiopsis* gen. nov.). Bulletin du Jardin Botanique de l'Etat a Bruxelles 19, 285–354.

Su HY, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA et al. 2016 – The families *Distoseptisporaceae* fam. nov., *Kirschsteiniotheliaceae*, *Sporormiaceae* and *Torulaceae*, with new species from freshwater in Yunnan Province, China. Fungal Diversity 80, 375–409.

Su XJ, Luo ZL, Jeewon R, Bhat DJ et al. 2018 – Morphology and multigene phylogeny reveal new genus and species of *Torulaceae* from freshwater habitats in northwestern Yunnan, China. Mycological Progress 17, 531–545.

Sun YR, Jayawardena RS, Sun JE, Wang Y. 2023 – Pestalotioid species associated with medicinal plants in southwest China and Thailand. Microbiology Spectrum 11, e03987-22.

Sun YR, Zhang JY, Hyde KD, Wang Y, Jayawardena RS. 2023 – Morphology and phylogeny reveal three *Montagnula* species from China and Thailand. Plants 12, 738.

Tanaka K, Hirayama K, Yonezawa H, Sato G et al. 2015 – Revision of the Massarineae (*Pleosporales*, *Dothideomycetes*). Studies in Mycology 82, 75–136.

Tennakoon DS, Hyde KD, Wanasinghe DN, Bahkali AH et al. 2016 – Taxonomy and phylogenetic appraisal of *Montagnula jonesii* sp. nov. (*Didymosphaeriaceae*, *Pleosporales*). Mycosphere 7, 1346–1356.

Thambugala KM, Hyde KD, Tanaka K, Tian Q et al. 2015 – Towards a natural classification and backbone tree for *Lophiostomataceae*, *Floricolaceae*, and *Amorosiaceae* fam. nov. Fungal Diversity 74, 199–266.

Thiyagaraja V, Lucking R, Ertz D, Karunarathna SC et al. 2021 – The evolution of life modes in *Stictidaceae*, with three novel taxa. Journal of Fungi 7, 105.

Von Arx JA. 1951 – Über die Gattung Laestadia und die *Gnomoniaceae*. Antonie van Leeuwenhoek 17, 259–272.

Vu D, Groenewald M, De Vries M, Gehrmann T et al. 2019 – Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom Fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92, 135–154.

Wanasinghe DN, Jones EBG, Camporesi E, Dissanayake AJ et al. 2016 – Taxonomy and phylogeny of *Laburnicola* gen. nov. and *Paramassariosphaeria* gen. nov. (*Didymosphaeriaceae*, Massarineae, *Pleosporales*). Fungal Biology 120, 1354–1373.

Wanasinghe DN, Phukhamsakda C, Hyde KD, Jeewon R et al. 2018 – Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on *Rosaceae*. Fungal Diversity 89, 1–236.

Watson W. 1929 – The classification of lichens. New Phytologist 28, 85–116.

Wedin M, Döring H, Könberg K, Gilenstam G. 2005 – Generic delimitations in the family *Stictidaceae* (*Ostropales*, *Ascomycota*): the *Stictis* – *Conotrema* problem. The Lichenologist 37, 67–75.

Wei DP, Gentekaki E, Wanasinghe DN, Hyde KD et al. 2022 – *Neohormodochis septispora* gen. et sp. nov. (*Stictidaceae*) from Yunnan Province, China. Phytotaxa 573, 247–261.

Wei DP, Wanasinghe DN, Gentekaki E, Thiyagaraja V et al. 2021 – Morphological and phylogenetic appraisal of novel and extant taxa of *Stictidaceae* from northern Thailand. Journal of Fungi 7, 880.

Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M et al. 2022 – Outline of Fungi and fungus-like taxa – 2021. Mycosphere 13, 53–453.

Wijayawardene NN, Hyde KD, Rajeshkumar KC, Hawksworth DL et al. 2017 – Notes for genera: *Ascomycota*. Fungal Diversity 86, 1–594.

Wijayawardene NN, McKenzie EHC, Hyde KD. 2012 – Towards incorporating anamorphic fungi in a natural classification checklist and notes for 2011. Mycosphere 3, 157–228.

Winka K, Ahlberg C, Eriksson OE. 1998 – Are there lichenized *Ostropales*? The Lichenologist 30, 455–462.

Woudenberg JHC, Groenewald JZ, Binder M, Crous PW. 2013 – *Alternaria* redefined. Studies in Mycology 75, 171–212.

Wu HX, Li YM, Ariyawansa HA, Li WJ et al. 2014 – A new species of *Microthyrium* from Yunnan, China. Phytotaxa 176, 213–218.

Wu HX, Schoch CL, Boonmee S, Bahkali AH et al. 2011 – A reappraisal of *Microthyriaceae*. Fungal Diversity 51, 189–248.

Wu W, Diao Y. 2022 – Anamorphic chaetosphaeriaceous fungi from China. Fungal Diversity 116, 1–546.

Xiong YR, Manawasinghe IS, Maharachchikumbura SSN, Lu L et al. 2022 – Pestalotioid species associated with palm species from Sothern China. Current Research in Environmental & Applied Mycology 12, 285–321.

Yang J, Liu JK, Hyde KD, Jones EBG et al. 2018 – New species in *Dictyosporium*, new combinations in *Dictyocheirospora* and an updated backbone tree for *Dictyosporiaceae*. Mycokeys 36, 83–105.

Yang J, Liu LL, Jones EBG, Hyde KD et al. 2023 – Freshwater fungi from karst landscapes in China and Thailand. Fungal Diversity 119, 1–212.

Zhang Y, Fournier J, Crous PW, Pointing SB et al. 2009 – Phylogenetic and morphological assessment of two new species of *Amniculicola* and their allies (*Pleosporales*). Persoonia 23, 48–54.