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# Mycosphere notes 387–412 – novel species of fungal taxa from around the world

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**Abstract**

This is the eighth of the series Mycosphere notes wherein we provide descriptions and notes on various fungal genera. In this compilation, we introduce *Neophaeosphaeriopsis* (Phaeosphaeriaceae) as a new genus, and 25 new species. The new species are *Acrodictys bambusae* (Acrodictyaceae), *Acrogenospora guizhouensis* (Acrogenosporaceae), *Aureobasidium xishuangbannaensis* (Saccotheciaceae), *Conlarium guizhouense* (Conlariaceae), *Dactylellina dulongensis* (Orbiliaceae), *Diaporthe araliae-chinensis* (Diaporthaceae), *Dibaeis jingdongensis* (Icmadophilaceae), *Dictyosporella yunnanensis* (Annulatascaceae), *Distoseptispora phragmiticola* (Distoseptisporaceae), *Fusarium camelliae* (Nectriaceae), *Helminthosporium lignicolum*, *Helminthosporium shangrilaense* (Massarinaceae), *Kirschsteiniothelia puerensis* (Kirschsteiniotheliaceae), *Melomastia septata* (Pleurotremataceae), *Montagnula aquilariae* (Didymosphaeriaceae), *Neophaeosphaeriopsis triseptatispora* (Phaeosphaeriaceae), *Neoroussoella chiangmaiensis* (Roussoellaceae), *Nigrograna heveae* (Nigrograniaceae), *Pestalotiopsis ficicrescens* (Sporocadaceae), *Pleurothecium hainanense* (Pleurotheciaceae), *Rhodoveronaea hainanensis* (Sordariomycetidae), *Roussoella chinensis* (Roussoellaceae), *Torula calceiformis* (Torulaceae), *Trichoglossum ailaoense* (Geoglossaceae) and *Zeloasperisporium spartii* (Zeloasperisporiaceae). We provide new sequence data for 25 species and updated phylogenetic trees for 24 genera (*Acrodictys*, *Acrogenospora*, *Aureobasidium*, *Conlarium*, *Dactylellina*, *Diaporthe*, *Dibaeis*, *Dictyosporella*, *Distoseptispora*, *Fusarium*, *Helminthosporium*, *Kirschsteiniothelia*, *Melomastia*, *Montagnula*, *Neophaeosphaeriopsis*, *Neoroussoella*, *Nigrograna*, *Pestalotiopsis*, *Pleurothecium*, *Rhodoveronaea*, *Roussoella*, *Torula*, *Trichoglossum*, *Zeloasperisporium*).

**Keywords** – 26 new taxa – Ascomycota – Molecular phylogeny – New genus – New species – Phylogenetic – Taxonomy

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**Introduction**

This is a continuation of the series of Mycosphere notes (Manawasinghe et al. 2022) wherein we introduce 26 new taxa, including one new genus *Neophaeosphaeriopsis* and 25 new species. For each taxon, we provide a description, photographic plates and justify the new species in the notes. Since this is a multi-authored paper with new taxa introduced from a wide range of fungi, it cannot

be assumed that all authors agree with the new species introduced and the novelty is considered as the authors' decision in writing each entry.

## Materials & Methods

The materials and methods follow the previous Mycosphere notes series (Hyde et al. 2021, Manawasinghe et al. 2022). Entries from the Greater Mekong Subregion will be deposited in the GMS database (Chaiwan et al. 2021) and entries will be extracted, modified, and added to Fungalpedia (Hyde et al. 2023). Index Fungorum numbers, Mycobank numbers, and Facesoffungi numbers were registered as instructed in Index Fungorum (2023), MycoBank (2023), and Jayasiri et al. (2015).

## Results

### Taxonomic treatment

Genera are treated in alphabetical order and followed the classification in the outline of fungi and fungus-like organisms (Wijayawardene et al. 2022). In general, the guidelines in the following papers are used to decide whether a species is novel, Ascomycetes (Chethana et al. 2021); Dothideomycetes (Pem et al. 2021) and are based on multigene phylogeny and morphology.

***Acrodictys*** M.B. Ellis, Mycol. Pap. 79: 5 (1961)

*Acrodictys* was established by M.B. Ellis and is typified by *A. bambusicola* (Ellis 1961) and belongs to Acrodictyaceae (Wijayawardene et al. 2022). *Acrodictys* species are usually associated with taxa that degrade wood (Xia et al. 2017). They are found worldwide, but particularly in tropical areas. In previous studies, the circumscription of *Acrodictys* was provided by Ellis (1961). However, Baker et al. (2002a) later provided a more precise description and circumscription of the type species, *A. bambusicola* as well as two other related taxa, *A. atroapicula*, and *A. elaeidicola*, focusing on their specific morphological features and other aspects of the genus. They also introduced a new genus, *Junewangia*, to accommodate *A. globulosa*, *A. lamma*, *A. martini*, and *A. obliqua*. Baker et al. (2002b) introduced *Rhexoacrodictys*, to accommodate *A. erecta, A. fimicola*, *A. fuliginosa*, and *A. queenslandica*. Subsequently, Baker et al. (2003) established *Pseudoacrodictys* to accommodate *A. appendiculata*, *A. breviconuta*, *A. corniculata*, *A. deightonii*, *A. dennisii*, *A. eickeri*, and *A. viridescens*. Gams et al. (2009) established the genus *Bhatia* to accommodate *A. malabarica*. At the same time, Zhao et al. (2009) established *Ramoacrodictys* to accommodate *A. malabarica*, the same species. However, Seifert et al. (2011) followed Gams et al. (2009) and accepted *Bhatia* as the valid genus.

*Acrodictys sensu stricto* is mainly characterized by percurrently proliferating, cylindrical, unbranched or infrequently branched, macronematous, mononematous conidiophores, and muriform conidia (Zhao et al. 2011, Xia et al. 2017). *Acrodictys* was accommodated in the family Acrodictyaceae J.W. Xia and X.G. Zhang, based on morphological and phylogenetic analyses (Xia et al. 2017). To date, there are 34 species in *Acrodictys sensu stricto*, one undetermined species of which 19 species and one undetermined species, have molecular data (Index Fungorum 2023, Wang et al. 2022b, this study).

***Acrodictys bambusae*** X. Tang, Jayaward., K.D. Hyde, J.C. Kang, sp. nov. Fig. 2

MycoBank number: MB900045; Facesoffungi number: FoF13348

Etymology – The epithet refers to the genus of the host plant, *Bambusa*.

Holotype – GZAAS 22-2036

*Saprobic* on decaying twigs of bamboo. Sexual morph: Undetermined. Asexual morph: *Colonies* on superficial substratum, effuse, scattered, hairy and brown to dark brown. *Mycelium* partly superficial and partly immersed, composed of branched, septate, brown to dark brown and with smooth hyphae. *Conidiophores* 48–141 × 3–6 µm ($\bar{x}$ = 94 × 5 µm, n = 30), macronematous, mononematous, brown to dark brown simple, cylindrical, septate, erect, straight or slightly

flexuous, and smooth-walled. *Conidiogenous cells* holoblastic, monoblastic, integrated, terminal, cylindrical and truncate, sometimes swollen at the middle, brown, smooth. *Conidia* 21–30 × 12–19 µm ($\bar{x}$ = 25 × 15 µm, n = 30) at the broadest part, solitary, dry, acrogenous, muriform, subglobose, obovoid to pyriform, truncated at base, rounded at apex, pale brown to brown sometimes to subhyaline at the basal cell, brown to greyish brown at other parts, with 3–4- transverse septa and 0–3- longitudinal septa, slightly constricted at the septa, with conspicuous pores in the septa and smooth.

Culture characteristics – Colonies incubate at 25 °C, circular, cottony, flat, slightly yellow with a lobate margin. In the middle, a solid colony formed by dense hyphae, rounded, gradually outward forming a feather-like sparse colony, and then a ring formed by dense hyphae, finally spreading out to form a sparse feather-like colony. The reverse side is a brown in the center that gradually extends outwards while the color changes to pale yellow with creamy white, lobate margin.

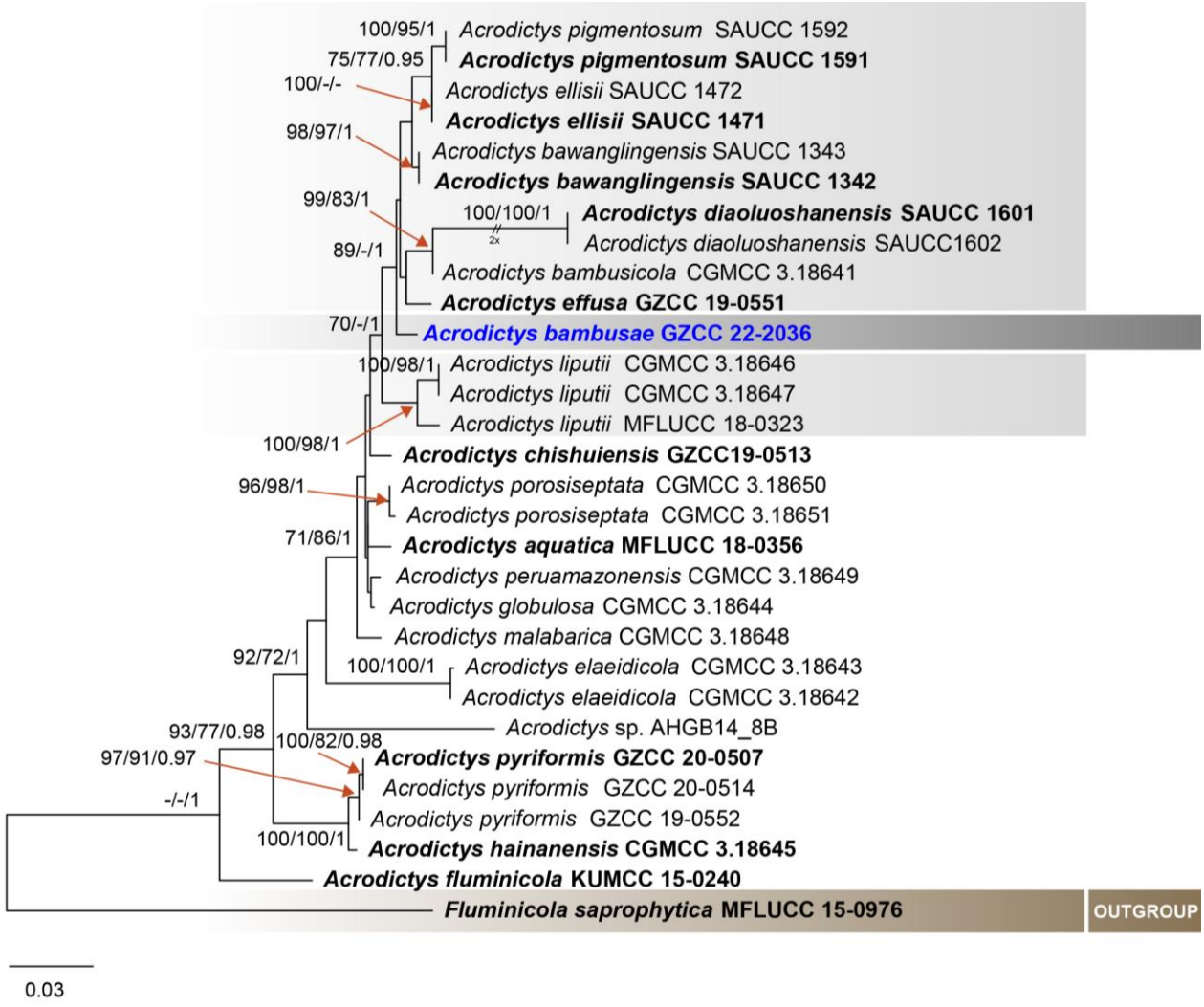


**Figure 1** – Phylogenetic tree obtained from maximum likelihood analyses of a combined ITS and LSU sequence dataset representing the species of *Acrodictys*. Thirty strains were included in the combined analyses, which comprised 1282 characters (I ITS: 1–488, LSU: 489–1282) after alignment. Bootstrap support values for maximum likelihood (ML), and maximum parsimony bootstrap (MP) equal to or greater than 60% and Bayesian Posterior Probabilities (PP) equal to greater than 0.95 are indicated at the nodes as ML/MP/PP. The tree is rooted to *Fluminicola saprophytica* (MFLUCC 15-0976). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.03 which represent the estimated number of nucleotide substitutions of site per branch.


**Figure 2** – *Acrodictys bambusae* (holotype GZAAS 22-2036). a Specimen. b, c Colonies on substrate. d–f Conidiophores bearing conidia. g, h Conidiogenous cells bearing conidia. i–l, n–p Conidia. q Germinated conidium. m Colonies on PDA (from front). r Colonies on PDA (from reverse). Scale bars: d–f = 50 μm, g, h = 20 μm, i–l, n–p = 10 μm.

Material examined – China, Guizhou Province, Sandu City, on decaying twigs of bamboo (Poaceae), 9 April 2022, X. Tang, SD26 (holotype GZAAS 22-2036, ex-type living culture GZCC 22-2036).

GenBank numbers – LSU: OP752220, ITS: OP747603

Notes – *Acrodictys bambusae* is similar to *A. bambusicola*, *A. diaoluoshanensis*, and *A. effusa*. *Acrodictys bambusae* differs from *A. bambusicola* by having short conidiophores (48–141 × 3–6 μm *vs* 280 × 5–8 μm) without proliferations. *Acrodictys bambusae* differs from *A. diaoluoshanensis* by having longer conidiophores (48–141 × 3–6 μm *vs* 34–65 × 1.8–5.6 μm); the conidiogenous cells of *A. bambusae* are sometimes swollen at the center; and larger conidia (21–30 × 12–19 μm *vs* 18–22 × 10–13 μm), and contain more transverse and longitudinal septa (3–4 transverse septa *vs* 3 transverse septa; 0–3 longitudinal septa *vs* 1–2 longitudinal septa). *Acrodictys bambusae* differs from *A. effusa* by having longer conidiophores (48–141 × 3–6 μm *vs* 60–130 × 3.5–7 μm) and larger conidia (21–30 × 12–19 μm *vs* 18–25 × 12–16 μm) with a very different culture. Phylogenetically, *Acrodictys bambusae* formed a well-resolved subclade (ML = 89%, PP = 1.00, Fig. 1), independently within *Acrodictys*, and has a close relationship with *A. bambusicola*, *A. diaoluoshanensis*, and *A. effusa*. Based on pairwise nucleotide comparisons, *A. bambusae* is different from *A. bambusicola* in 14/429 bp (3.2%) in ITS, different from *A. diaoluoshanensis* in 15/558 bp (2.7%) in ITS, 91/820 (11%) in LSU, and different from *A. effusa* in 14/517 bp (2.7%) in ITS. Therefore, we introduce *A. bambusae* as a new species based on morphology and phylogenetic evidence (Chethana et al. 2021).

***Acrogenospora*** M.B. Ellis, Dematiaceous Hyphomycetes (Kew): 114 (1971)

*Acrogenospora* was introduced by Ellis (1971) with two species, *A. sphaerocephala* and *A. carmichaeliana* (asexual morphs). Subsequently, Goh (1998) reviewed the genus and added two new species, *A. ovalia* and *A. subprolata*. A better taxonomic understanding was provided by Bao et al. (2020), who accepted nine species, including seven new species and two known species of *Acrogenospora*, with descriptions and illustrations. In previous studies and combined with this study, 21 species including 15 freshwater species and six terrestrial species have been accepted in *Acrogenospora* (Hughes 1978, Goh et al. 1998, Bao et al. 2020). *Acrogenospora* species are characterized by macronematous, mononematous, brown, sometimes percurrently proliferating conidiophores; monoblastic, terminal or intercalary conidiogenous cells; and globose, ellipsoid or obovoid, olivaceous to brown conidia (Hughes 1978, Goh et al. 1998, Bao et al. 2020). Bao et al. (2020) found that the morphological characteristics of conidia (including differences in their shape, size, color, guttules and basal cells), and the degree of pigmentation of the conidiophores are very important for the identification of *Acrogenospora* species.

***Acrogenospora guizhouensis*** J. Ma, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 4

MycoBank number: MB900046; Facesoffungi number: FoF13256

Etymology – Name refers to "Guizhou Province" where the holotype was collected.

Holotype – GZAAS 22-2022

*Saprobic* on submerged decaying wood. Sexual morph: Undetermined. Asexual morph: *Colonies* on the natural substratum effuse, dark black, glistening, hairy. *Mycelium* superficial and partially immersed, composed of septate, brown to dark brown, branched, smooth hyphae. *Conidiophores* macronematous, mononematous, single, unbranched, erect, straight or slightly flexuous, septate, smooth, 145–320 μm long, 7.5–14 μm thick ($\bar{x}$ = 236 × 11 μm, n = 20), brown to dark brown, paler towards the apex. *Conidiogenous cells* monoblastic, integrated, terminal, cylindrical, smooth, pale brown, proliferating percurrently. *Conidia* solitary, acrogenous, dry, subspherical, smooth-walled, 19–27.5 × 19.5–28.5 μm ($\bar{x}$ = 23 × 23 μm, n = 25), brown, aseptate.

Culture characteristics – Conidia germinating on WA within 12 h; Colonies growing on PDA, reaching 45 mm in 4 weeks at 25 ℃, circular, with a flat surface, edge undulate, and brown to dark brown in PDA medium; Mycelium superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.

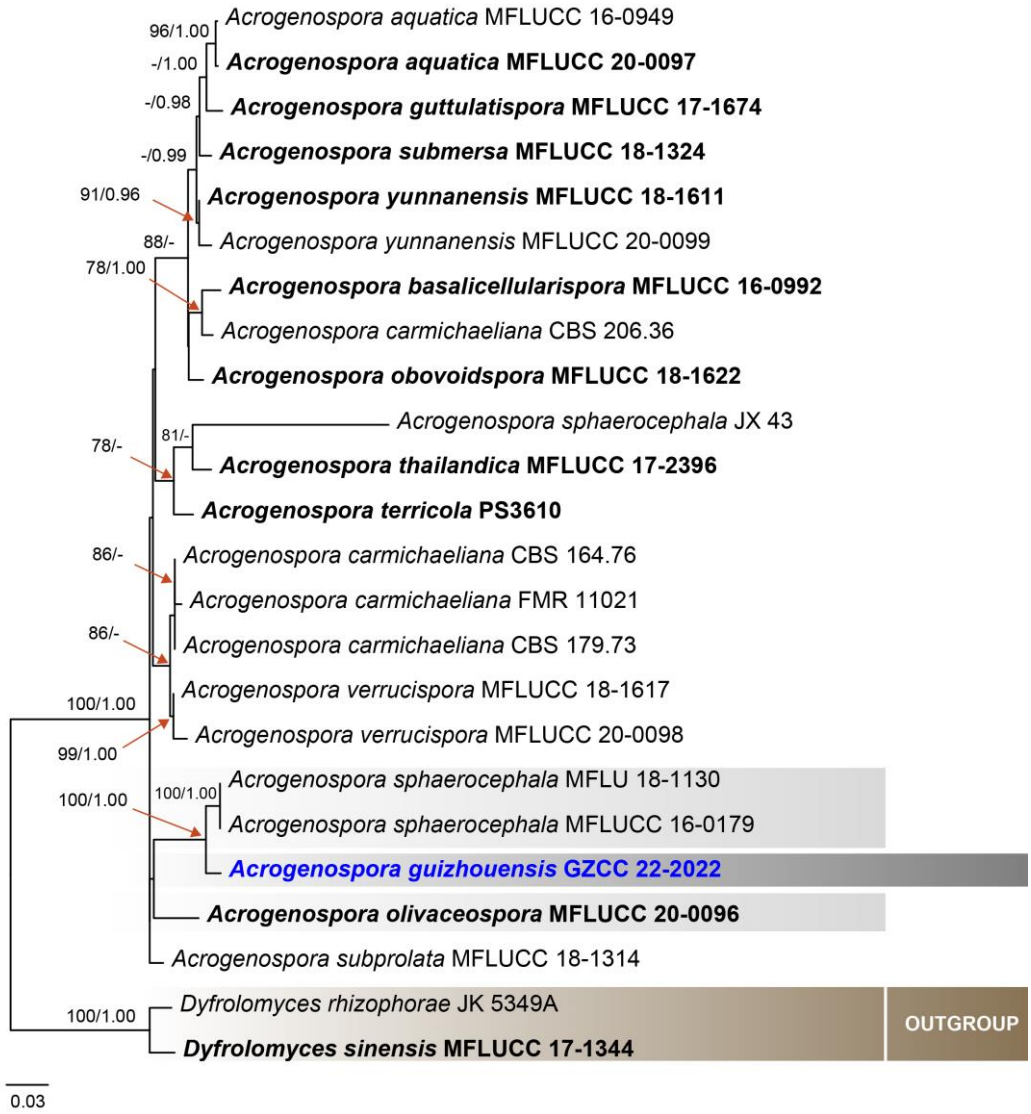


**Figure 3** – Phylogenetic tree obtained from maximum likelihood analyses of a combined LSU, SSU, *ef1α* and *rpb2* sequence data representing species of *Acrogenospora*. Twenty-four strains were included in the combined analyses, which comprised 3961 characters (LSU: 1–959, SSU: 960–1966, *ef1α*: 1967–2920, *rpb2*: 2921–3961) after alignment. Bootstrap support values for ML equal to or greater than 75% and PP equal to greater than 0.95 are indicated at the nodes as ML/PP. The tree is rooted to *Dyfrolomyces rhizophorae* (JK 5349A) and *D. sinensis* (MFLUCC 17-1344) were used as the outgroup taxa. The ex-type strains are in bold, and the new isolates of this study are in blue. Bar = 0.03 which represent the estimated number of nucleotide substitutions of site per branch.

Material examined – China, Guizhou Province, Qiannan Buyi and Miao Autonomous Prefecture, Libo County, on decaying wood from terrestrial habitat, 17 January 2021, J. Ma, XQK12 (holotype GZAAS 22-2022, ex-type living culture GZCC 22-2022).

GenBank numbers – LSU: OP748933, *ef1α*: OP750332, *rpb2*: OP750333

Notes – The morphology of *Acrogenospora guizhouensis* corresponds well with the generic concept of *Acrogenospora* (Bao et al. 2020). In the phylogenetic tree (Fig. 3), *A. guizhouensis* is a phylogenetically distinct species that is most closely related to *A. sphaerocephala* and forms a sister clade to *A. sphaerocephala* with 100 ML/ 1.00 PP support. Morphologically, *A. guizhouensis* has shorter conidiophores (145–320 μm *vs* up to 730 μm) than *A. sphaerocephala* (Bao et al. 2020). According to phylogenetic and morphological evidence, we introduce *A. guizhouensis* as a new species in *Acrogenospora*.

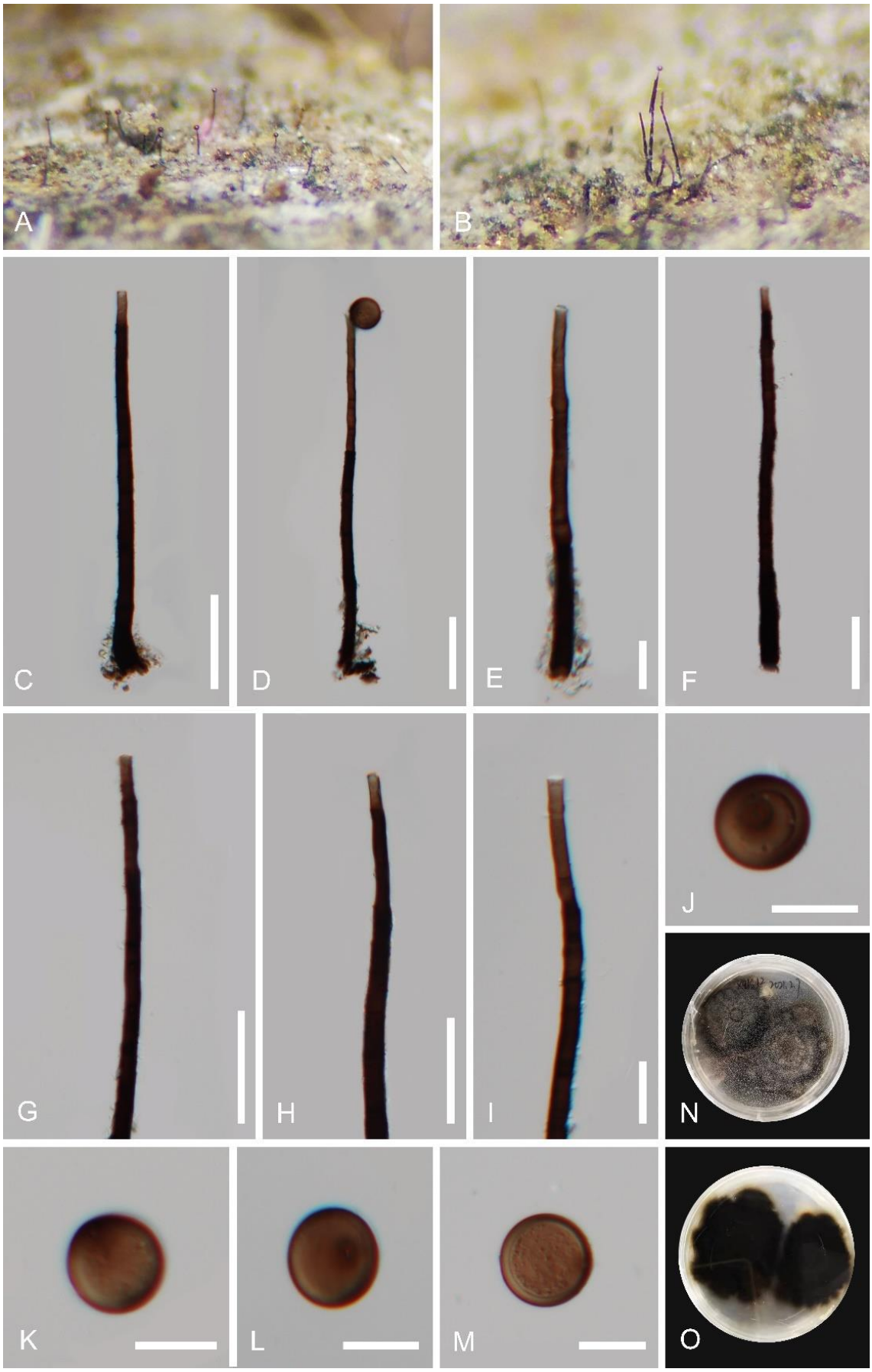


**Figure 4** – *Acrogenospora guizhouensis* (holotype GZAAS 22-2022). a, b Colonies on wood. c–f Conidiophores and conidia. g–i Conidiogenous cells. j–m Conidia. n, o Colonies on PDA from above and reverse. Scale bars: c, d, f–h = 50 μm, e, i–m = 20 μm.

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

*Aureobasidium* introduced by Viala & Boyer (1891) is typified by *A. vitis*. New species have recently been accepted based on morphology and multi-locus phylogenetic analyses of LSU and ITS data (Wang et al. 2022a, Wijayawardene et al. 2022). This is a cosmopolitan genus consisting of 59 epithets and 47 legitimate species accepted in Index Fungorum (2023), many of which are parasitic or saprobic, and are widely distributed in plants, fruits, human skin, soil, water and air (Crous et al. 2011, Arfi et al. 2012, Arzanlou & Khodaei 2012, Thambugala et al. 2014, Nieuwenhuijzen et al. 2016, Jiang et al. 2019b, Hongsanan et al. 2020). This genus is characterized by acervular to sporodochial conidiomata, reniform to sickle-shaped aseptate, and straight conidia (asexual morph), while the sexual morph is unknown (Hongsanan et al. 2020). In this study, we introduce *A. xishuangbannaensis* which was isolated from bats (Fig. 6).

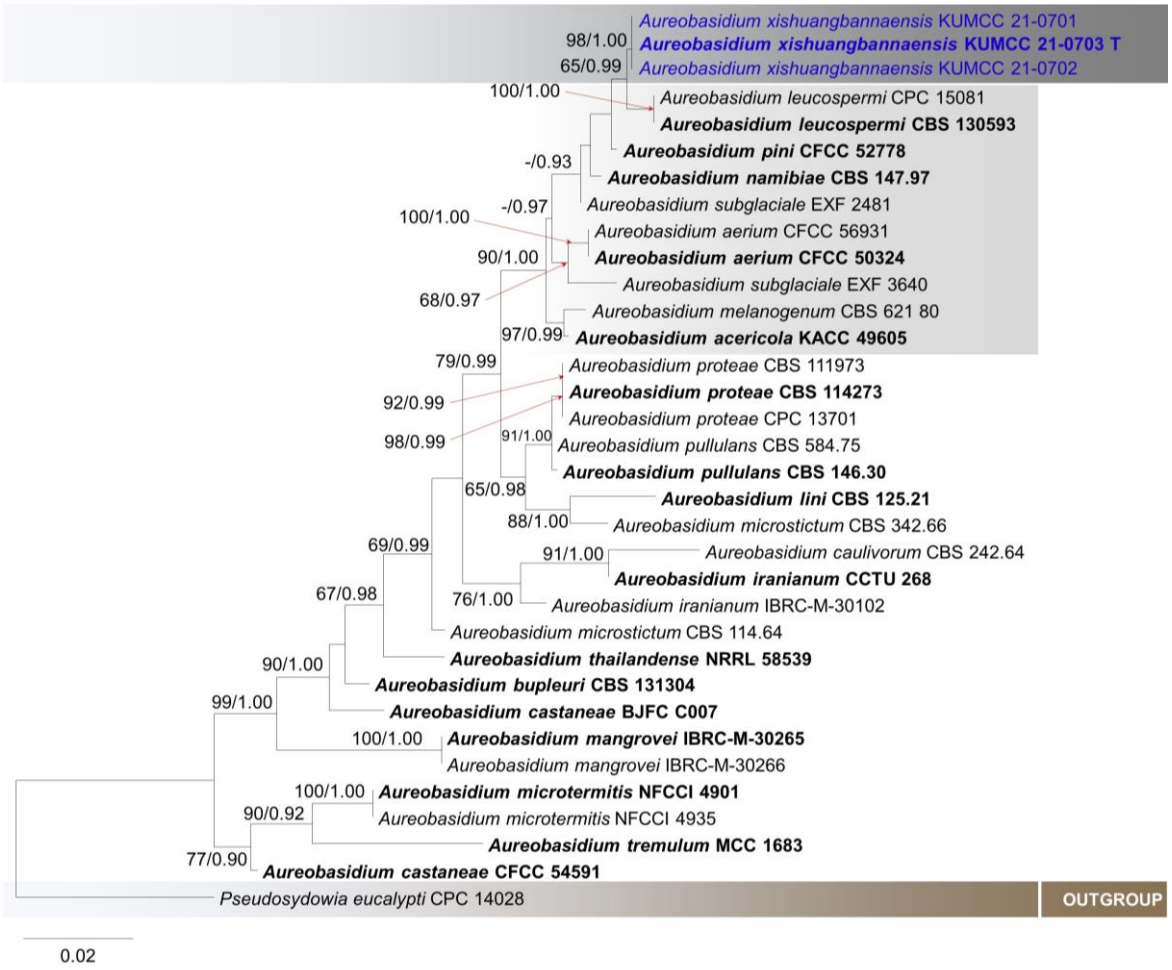


**Figure 5** – Phylogenetic tree generated from maximum likelihood analyses based on a combined LSU and ITS sequence dataset representing the species of *Aureobasidium*. Thirty-four strains are included in the combined analyses, 1167 characters with gaps (LSU: 1–600, ITS: 601–1167). Bootstrap support values for ML equal to or greater than 60% and PP equal to greater than 0.90 are indicated at the nodes as ML/PP. The ex-type strains are in bold, and the new isolates of this study are in blue. *Pseudosydowia eucalypti* (CPC 14028) was used as the outgroup taxon. Bar = 0.02 which represent the estimated number of nucleotide substitutions of site per branch.

***Aureobasidium xishuangbannaensis*** Liu, Karun, & Tibpromma, sp. nov. Fig. 6

MycoBank number: MB846321; Facesoffungi number: FoF12768

Etymology – Named after the location Xishuangbanna, where the fungus was first discovered.

Holotype – HKAS122836

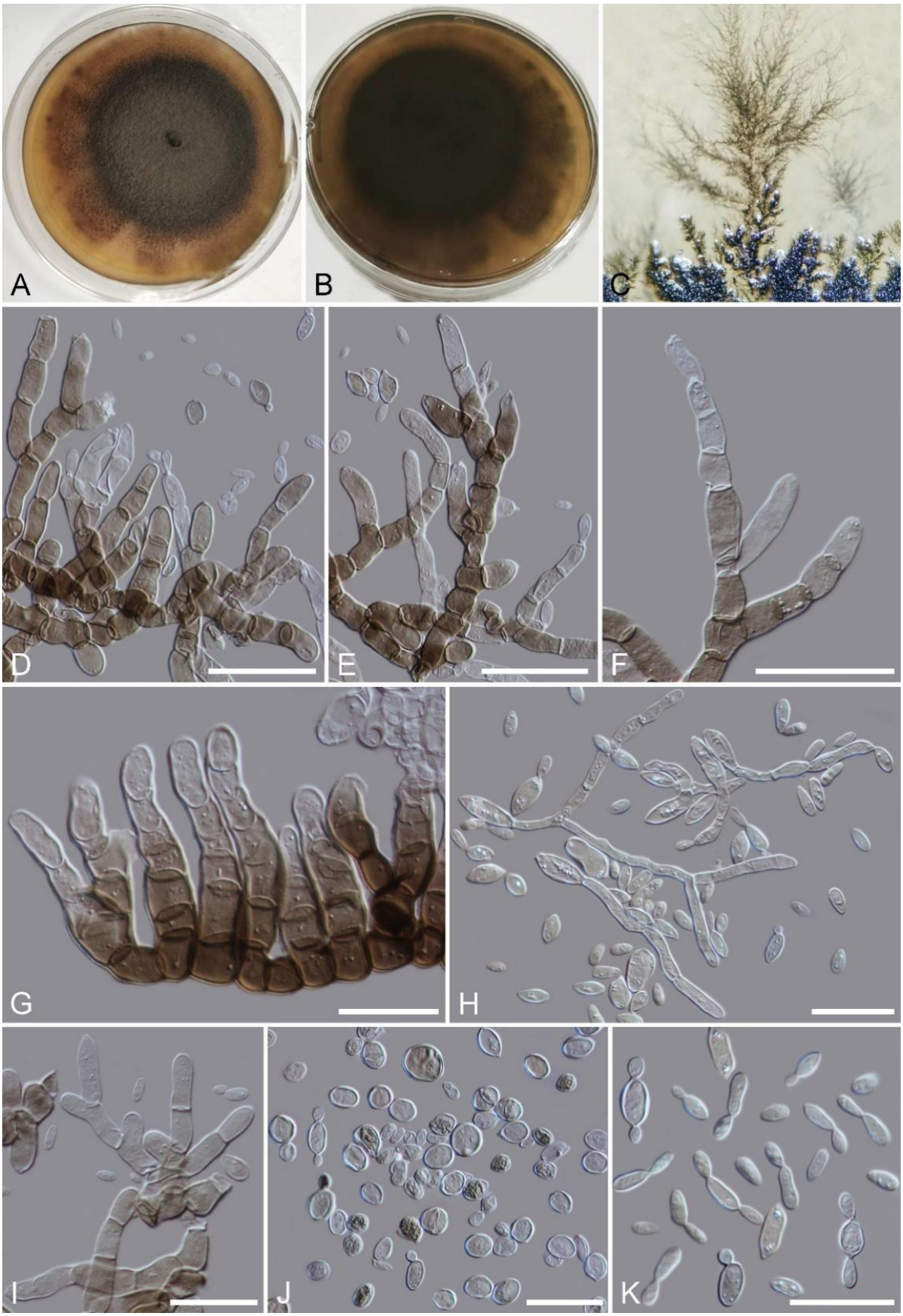


**Figure 6** – *Aureobasidium xishuangbannaensis* (ex-type living culture KUMCC 21-0703). a, b Colony characteristics on PDA (above and below). c Mycelium on PDA (60 days old culture). d–i Conidiogenous cells and conidia. j Conidia. k Secondary conidia produced from primary conidia. Scale bars: d–f = 10 μm, g–k = 20 μm.

Associated on *Myotis laniger* (bat) wing surface. Sexual morph: Undetermined. Asexual morph on PDA: *Colonies* circular, spreading, flat, dark brown to black, with irregular margins. *Mycelium* immersed, compact, without aerial mycelium. *Hyphae* 3–12 µm wide, smooth, thin- to thick-walled, arborescence, septate, branched, hyaline to yellow-brown or brown, gradually darkens from the end to the base, constricted at septa. *Conidiophores* indistinguishable from basal hyphae. *Conidiogenous cells* 5–17 × 5–8 µm, undifferentiated, holoblastic, hyaline to brown, intercalary or terminal, sometimes with papillate apex, arising from conidiophores or directly from vegetative hyphae. *Conidia* (4.2–)4.3–10.6 (–11.6) × (2.2–)2.3–10.3(–10.5) µm ($\bar{x}$ = 7.36 × 5.44 µm, n = 60), hyaline or brown, ellipsoidal, straight, rarely slightly curved, with rounded to subtruncate base and a flat basal hilum, thin-walled, with two or more guttules. *Secondary conidia* produced by terminal or sub-terminal, mono- or bipolar budding of primary conidia. *Budding* occurs frequently. *Chlamydospores* not observed.

Culture characteristics – Colonies on PDA attaining after 40 days at room temperature (20–25 ℃). Sporulation occurred on PDA after 30 days of incubation. Yeast-like growth occurred on PDA after 30 days.

Material examined – China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, Limestone Forest in Xishuangbanna Tropical Botanical Garden, 101.282404 E, 21.907599 N, on *Myotis laniger* wing surface, 15 July 2020, A.C. Hughes, 60-E (holotype HKAS122836, ex-type living culture KUMCC 21-0703). China, Yunnan Province, Xishuangbanna Dai Autonomous Prefecture, Mengla County, Menglun Town, *Rhinolophus malayanus*, 15 July 2020, A.C. Hughes, 60-D (living culture KUMCC 21-0702); *ibid*. *Rhinolophus malayanus*, 15 July 2020, A.C. Hughes, 28-A (living culture, KUMCC 21-0701).

GenBank numbers – KUMCC 21-0701 = LSU: OP363256, ITS: ON426834; KUMCC 21-0702 = LSU: OP363257, ITS: ON426836; KUMCC 21-0703 = LSU: OP363258, ITS: ON426835

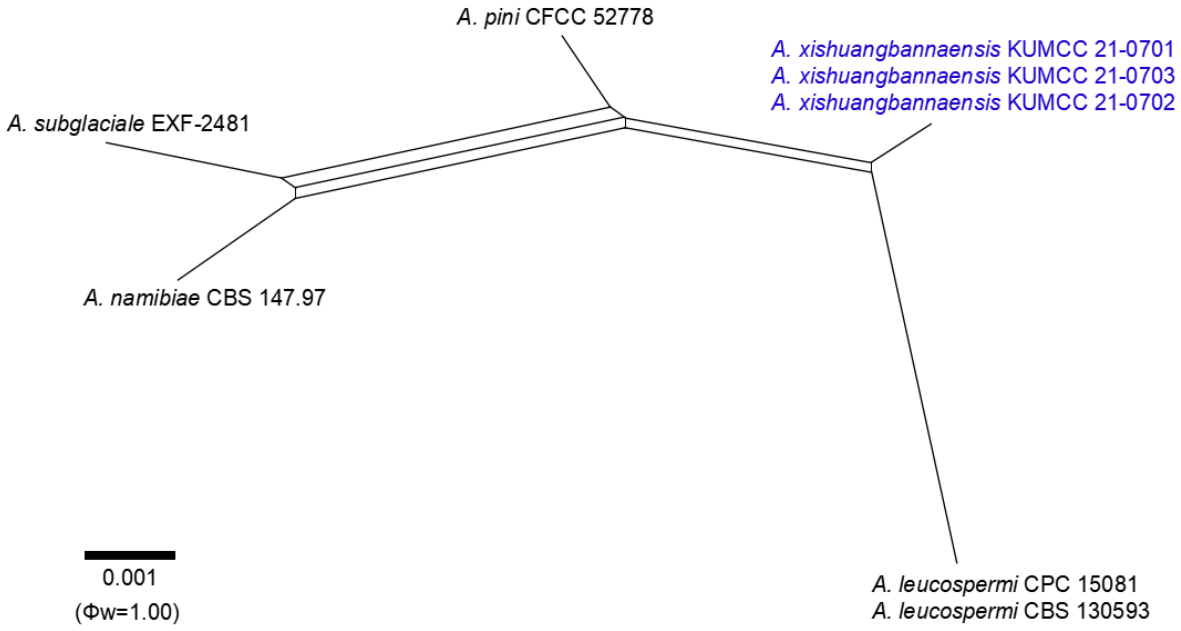


**Figure 7** – Split graphs showing the results of PHI test of *Aureobasidium xishuangbannaensis* and closely related taxa using LogDet transformation and splits decomposition. PHI test results Φw ≤ 0.05 indicate that there is significant recombination within the dataset. The new taxon is shown in blue.

Notes – *Aureobasidium xishuangbannaensis* is phylogenetically closely related to *A. leucospermi* and *A. pini* (Fig. 5). The base pair differences of *A. xishuangbannaensis* and *A. leucospermi* (CBS 130593, type) are seen as 1.00% differences in LSU (9/898 bp), and 1.95%

differences in ITS (12/615 bp) while the base pair differences of our new species and *A. pini* (CFCC 52778, type) are seen as 0.51% differences in LSU (3/587 bp); and 0.62% differences in ITS (3/486 bp). Morphologically, *A. xishuangbannaensis* differs from *A. leucospermi* by smaller conidia (4.3–10.6 × 2.3–10.3 μm *vs* 8–11 × 4–5(–8) μm) and smaller conidiogenous cells (5–17 × 5–8 μm *vs* 15–30 × 4–11 μm) (Crous et al. 2011). *Aureobasidium xishuangbannaensis* differs from *A. pini* by the latter having smaller conidia (4.3–10.6 × 2.3–10.3 μm *vs* 6.2–8.5 × 3.6–4.2 μm) and 1- to 2-celled dark chlamydospores (Jiang et al. 2019b). Based on the megablast search in the GenBank, the closest hits of the LSU and ITS sequences had the highest similarity to *A. namibiae* (LSU GenBank, MT322623.1, similarity = 886/886 (100%), Gaps = 0/886 (0%); ITS GenBank, MT325792.1, similarity = 593/599 (99%), Gaps = 3/599 (0%)), and *A. pullulans* (LSU GenBank, MH869192.1, similarity = 886/888 (99%), Gaps = 2/888 (0%); ITS GenBank, JF439462.1, similarity = 593/599 (99%), Gaps = 3/599 (0%)). Morphologically, *A. xishuangbannaensis* differs from *A. namibiae* by the latter having larger conidia (4.3–10.6 × 2.3–10.3 μm *vs* 7–17 × 3.5–7 μm) (Zalar et al. 2008, Gostinčar et al. 2014, Wang et al. 2022a). *Aureobasidium xishuangbannaensis* differs from *A. pullulans* by the latter having 1-celled elliptical smaller conidia (4.3–10.6 × 2.3–10.3 μm *vs* 7.5–16 × 3.5–7 μm) and thick-walled chlamydospores (Arnaud 1918, Wang et al. 2022a). The PHI analysis further confirms that *A. xishuangbannaensis* has no significant genetic recombination with closely related species (Φw > 0.05, Fig. 7). Thus, we introduce *A. xishuangbannaensis* as a new species.

***Conlarium*** F. Liu & L. Cai, Mycologia 104(5): 1180 (2012)

*Conlarium* was introduced by Liu et al. (2012) and is typified by *C. duplumascosporum*, which was discovered from submerged wood collected from freshwater in China. Species of *Conlarium* have been reported from both terrestrial and freshwater habitats (Liu et al. 2012, Zhang et al. 2017, Xie et al. 2019, Dubey & Manikpuri 2021, Zhang et al. 2021), and can be endophytes (Xie et al. 2019). Nine species have been accepted in this genus (Zhang et al. 2021). In this study, morphological characteristics and multi-gene phylogenetic analysis of a combined LSU, ITS and SSU sequence data reveal a new species of *C. guizhouense* from dead wood of an unidentified plant collected in China.

***Conlarium guizhouense*** J.Y. Zhang, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 9

MycoBank number: MB900039; Facesoffungi number: FoF13252

Etymology – Refers to the location “Guizhou Province, China” where the fungus was collected.

Holotype – GZAAS 22-2028

*Saprobic* on terrestrial dead wood of undetermined host. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, effuse, gregarious, sporodochial, punctiform, brown. *Mycelium* is composed of partly immersed, partly superficial, septate, brown, branched hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* up to 5.5 μm wide, monoblastic, integrated, hyaline, cylindrical, brown. *Conidia* 32–50(–67) × 20–33(–44.5) μm ($\bar{x}$ = 38 × 29 μm, n = 20), acrogenous, solitary, ellipsoidal or cylindric-clavate, or irregular in shape, muriform, fuscous, 5–14-transversely septate, 3–7-longitudinal septa, slightly constricted at septa, median brown, smooth, thin-walled.

Culture characteristics – Conidia germinating on PDA within 15 h and hyaline germ tube produced from conidia. Colonies growing on PDA at 25 °C reach 18 mm in two weeks, flat, velvety, circular margin with a smooth surface, hoar from above; claybank spread irregularly in the center, brown at the edge from reverse, and producing a ring of brown pigment around the colony in the culture.

Material examined – China, Guizhou Province, Tongren City, Jiangkou County, 27°52'44”N 108°47'36”E, on dead wood in the land, 21 May 2022, J.Y. Zhang, B1 (holotype GZAAS 22-2028, ex-type living culture GZCC 22-2028).

GenBank numbers – LSU: OP79869, ITS: OP749882

Notes – *Conlarium guizhouense* fits well with the generic concept of *Conlarium* and is morphologically similar to *C. aquaticum* in having monoblastic, integrated conidiogenous cells and muriform, ellipsoidal or irregular conidia (Zhang et al. 2017). However, *Conlarium guizhouense* can be distinguished from *C. aquaticum* by its fuscous and smaller conidia (32–50 × 20–33 µm *vs* 45–70 × 20–57 µm). In addition, we compared the nucleotides of ITS and LSU region between *C. guizhouense* and *C. aquaticum*, there are 31 bp (4%) and 5 bp (0.5%) differences, which strongly supports our species to be new following the guidelines of Pem et al. (2021). Phylogenetically, *C. guizhouense* formed a distinct clade basal to the clade including *C. aquaticum*, *C. baiseense*, *C. dupliciascosporum*, *C. muriforme*, *C. nanningense*, *C. thailandense* and *C. sichuanense* (Fig. 8).

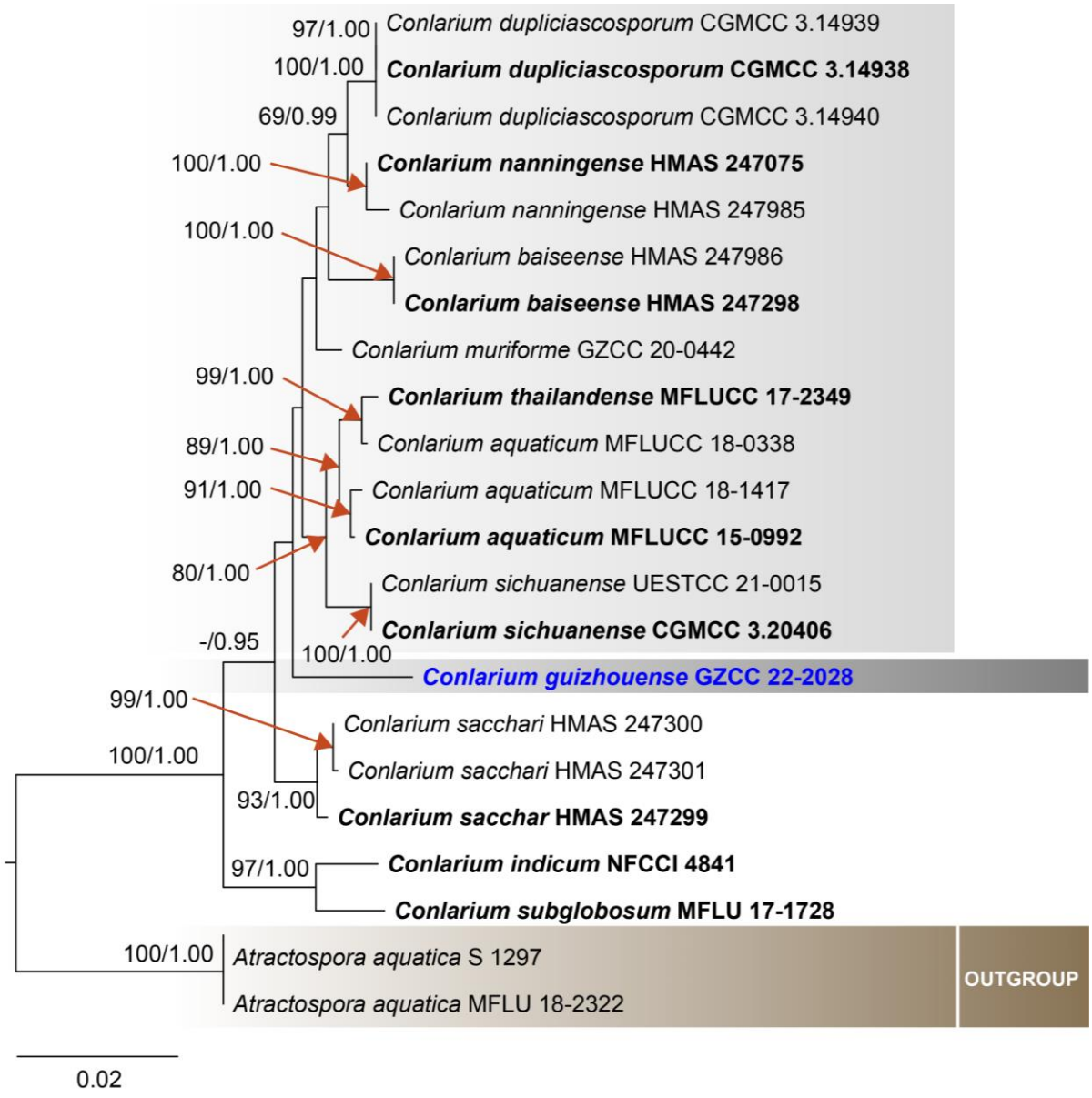


**Figure 8** – Phylogenetic tree obtained from maximum likelihood analyses of a combined LSU, ITS and SSU sequence dataset representing the species of *Conlarium*. Twenty-two strains were included in the combined analyses, which comprised 2311 characters (LSU: 1–816, ITS: 817–1325, SSU: 1326–2311) after alignment. Bootstrap support values for ML equal to or greater than 75% and PP equal to or greater than 0.95 are given above the nodes as ML/PP. The tree is rooted with *Atractospora aquatica* (MFLU 18-2322) and *A. aquatica* (S 1297). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.02 estimates the number of nucleotide substitutions of site per branch.

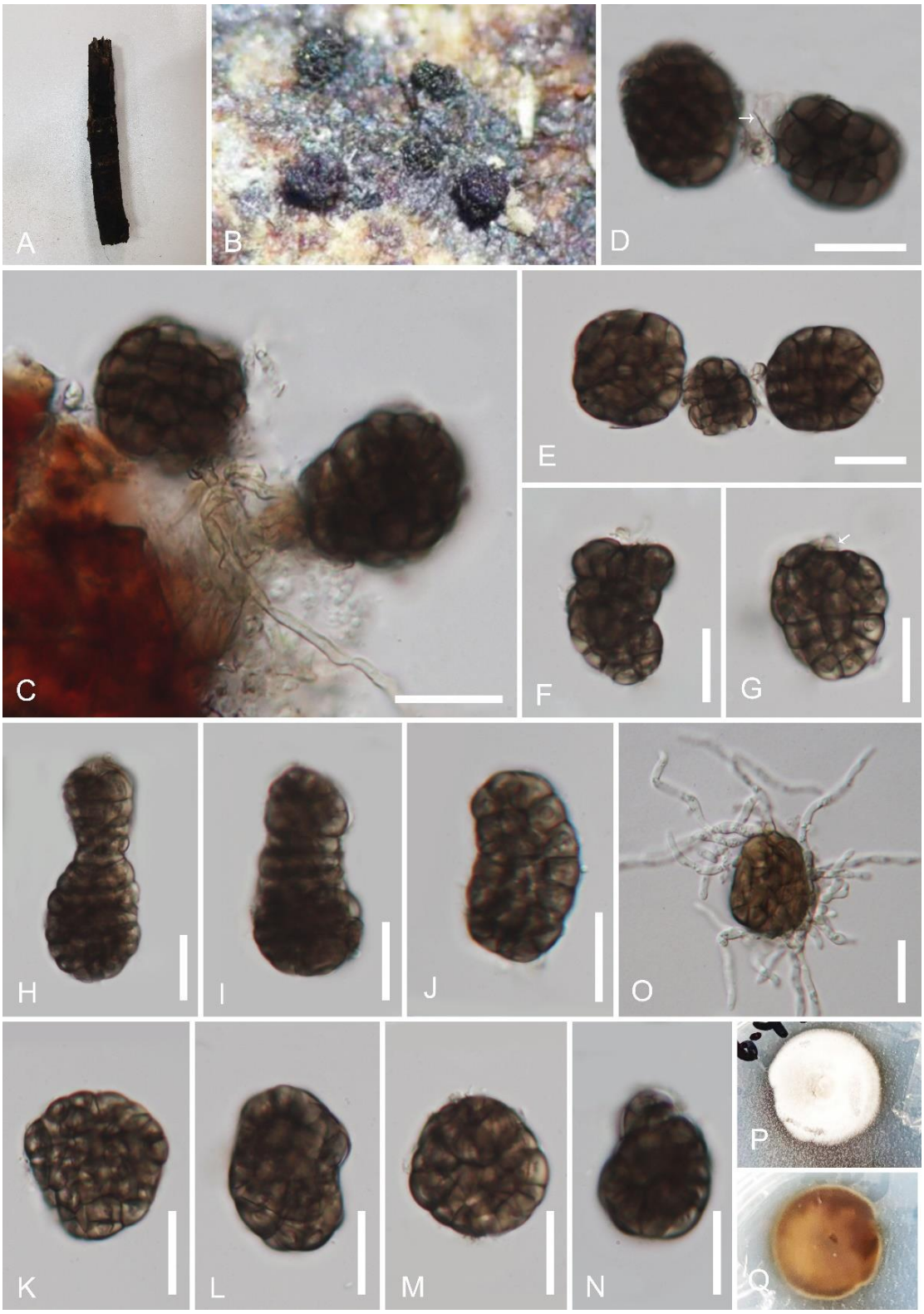


**Figure 9** – *Conlarium guizhouense* (holotype GZAAS 22-2028). a Host. b Colonies on dead wood. c–n Conidiogenous cells and conidia. o Germinating conidium. p–q Colony on PDA from above and below. Scale bars: c = 50 μm, d–o = 20 μm.

***Dactylellina*** M. Morelet, Bull. Soc. Sci. nat. Arch. Toulon et du Var 178: 6 (1968)

*Dactylellina* is an asexual nematode-trapping genus in Orbiliomycetes with high nematode-catching ability (Ji et al. 2020) and is typified by *Dactylellina leptospora* (= *Dactylella leptospora*). Morelet (1968) provided the original generic diagnosis as elongate, fusoid conidia, with microconidia rarely formed. Subsequently, according to phylogenetic analysis, Scholler et al.

(1999) revised the characteristics of this genus to catch nematodes with stalked adhesive knobs or non-constricting rings. Further, with molecular research, the attributes of *Dactylellina* were revised again to capture nematodes by means of adhesive knobs, adhesive branches and non-constricting rings (Li et al. 2005, Yang et al. 2007). There are 35 *Dactylellina* species reported (Yu et al. 2014, Index Fungorum 2023). During the survey of carnivorous fungi in Yunnan Province, China, a strain capturing nematodes by adhesive knobs was discovered from the soil sample collected in a burned forest. Phylogenetic analysis based on the combined ITS, *ef1α*, and *rpb2* dataset indicates that the isolate is distinct from existing species in *Dactylellina*.

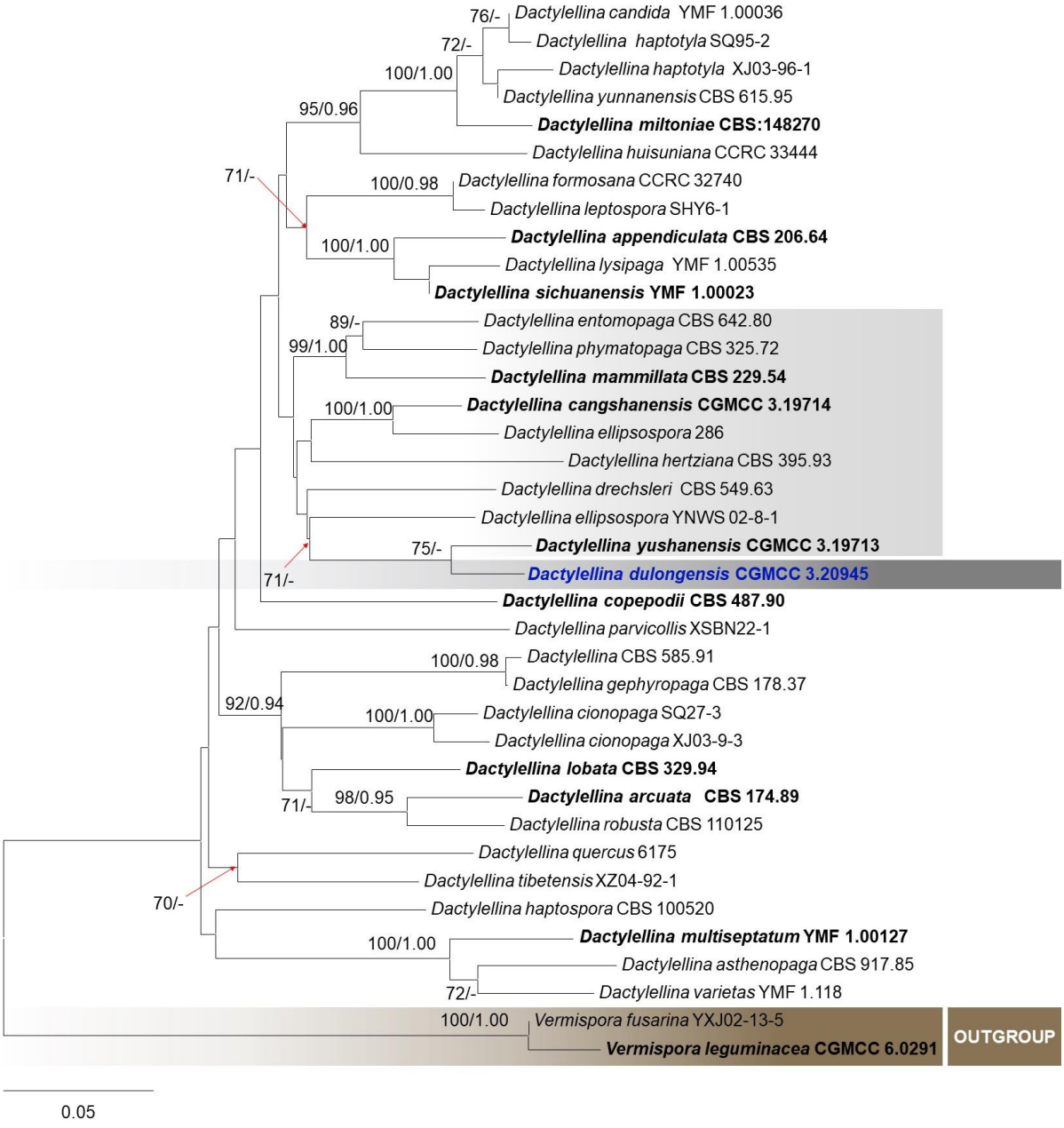


**Figure 10** – Phylogenetic tree obtained from maximum likelihood analyses based on a combined ITS, *rpb2*, and *ef1α* sequence from all *Dactylellina* species with valid sequence data. Thirty-eight strains were included in the combined analyses, which comprised 1974 characters (ITS: 1–585, *rpb2*: 586–1370, *ef1α*: 1371–1974) after alignment. Bootstrap support values for ML equal to or greater than 70% and PP equal to greater than 0.90 are indicated at the nodes as ML/PP. The tree is rooted to *Vermispora fusarium* (YXJ02-13-5) and *V. leguminacea* (CGMCC6.0291). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.05 which represent the estimated number of nucleotide substitutions of site per branch.

***Dactylellina dulongensis*** F. Zhang, X.Y. Yang, S. Boonmee & K.D. Hyde, sp. nov. Fig. 11

MycoBank number: MB846351; Facesoffungi number: FoF12885

Etymology – The species name "*dulongensis*" refers to the name of the sample collection site: Dulong, Gongshan, Nujiang, Yunnan Province, China.

Holotype – CGMCC 3.20945

*Saprobic* on soil. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on potato dextrose agar (PDA) white, cottony, growing slowly, reaching 50 mm diam. after 15 days at 26 °C. *Mycelium* partly superficial, partly immersed, septate, branched, and smooth. *Conidiophores* 120–225 × 2–4.5 µm ($\bar{x}$ = 168.4 × 3.3 µm, n = 50), erect, septate, unbranched, hyaline, usually producing two short denticles near the apex, bearing 1–2 conidia at apex. *Conidia* 31–48 × 5–14 µm ($\bar{x}$ = 42 ×9.4 µm, n = 50), clavate to fusiform, widest at the median cell, gradually tapering to both ends, 1–4-septate, mostly 4-septate, smooth-walled. *Chlamydospores* 5–12 × 5–12 µm ($\bar{x}$ = 17.4 × 14.5 µm, n = 50), globose to subglobose, ellipsoidal, growing in chains, hyaline. Capturing nematodes with adhesive knobs which can be formed spontaneously by hyphae specialization or directly produced spontaneously by conidia germination (conidial traps).

Material examined – China, Yunnan Province, Nujiang, Gongshan, Dulong, from the soil collected in burned forest, 23 April 2020, F. Zhang, BF104-1 (holotype CGMCC 3.20945, ex-type living culture DLUCC31).

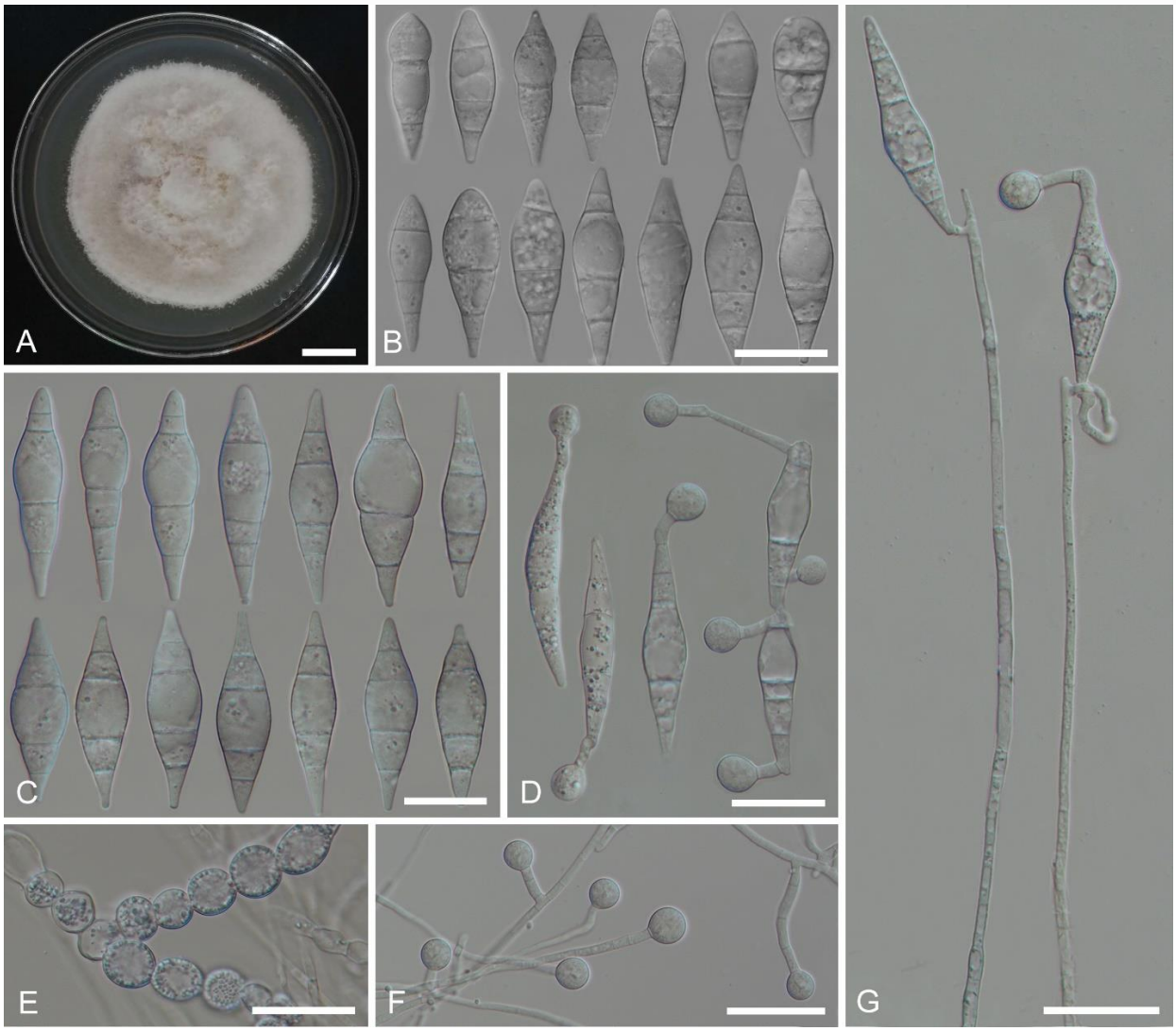


**Figure 11** – *Dactylellina dulongensis* (holotype CGMCC 3.20945). a Colony on corn meal agar (CMA). b, c Conidia. d Conidial traps. e Chlamydospore chains. f Trapping structures of adhesive knobs. g Conidiophores. Scale bars: a = 1 cm, c–g = 20 µm.

GenBank numbers – ITS: OM956085, *ef1α*: OP477093, *rpb2*: OP477094

Notes – Phylogenetic analysis placed *Dactylellina dulongensis* as a new taxon in *Dactylellina*, which is closest to *D. yushanensis* with 72% ML support (Fig. 10). There are 11% differences (57/516 bp) in ITS, 13% (108/831 bp) in *ef1α* and 6.7% (26/386 bp) in *rpb2* between *D. dulongensis* and *D. yushanensis*. Morphologically, *D. dulongensis* is similar to *D. ellipsospora*, *D. parvicolla* and *D. yushanensis* in having clavate to fusiform conidia. However, *D. dulongensis* differs from *D. yushanensis* in having globose to ellipsoidal chlamydospores (Zhang et al. 2020). Furthermore, *D. dulongensis* can be easily distinguished from *D. ellipsospora* and *D. parvicolla* by its two conidia bearing conidiophores and globose to ellipsoidal chlamydospores, while *D. ellipsospora* and *D. parvicolla* produce simple conidiophores and lack chlamydospores. In addition, the spontaneous formation of conidial traps, which has never been reported in *D. ellipsospora*, *D. parvicolla* and *D. yushanensis* (Cooke & Dickinson 1965, Tarjan 1961, Yu et al. 2014), is common in *D. dulongensis*.

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

*Diaporthe* is a large genus in *Diaporthaceae*, with 1,168 epithets listed in Index Fungorum (2023), but only one-fifth of these taxa have been studied with molecular data (Guo et al. 2020, Yang et al. 2020, Zapata et al. 2020, Norphanphoun et al. 2022). The sexual morph of *Diaporthe* is characterized by immersed perithecial ascomata and an erumpent pseudostroma with more or less elongated perithecial necks; unitunicate clavate to cylindrical asci; and fusoid, ellipsoid to cylindrical, septate or aseptate, hyaline ascospores, biseriately to uniseriately arranged in the ascus, sometimes having appendages (Udayanga et al. 2011, Senanayake et al. 2017, 2018). The asexual morph is characterized by ostiolate conidiomata, with cylindrical phialides producing three types of hyaline, aseptate conidia (Udayanga et al. 2011, Gomes et al. 2013): type I α-conidia are hyaline, fusiform, straight, guttulate or eguttulate, aseptate, and smooth-walled; type II β-conidia are hyaline, filiform, straight or hamate, aseptate, smooth-walled, and eguttulate; while type III γ-conidia are rarely produced, and are hyaline, multiguttulate, fusiform to subcylindrical with an acute or rounded apex, while the base is sometimes truncate. Currently, *Diaporthe* has 13 species complexes (Norphanphoun et al. 2022). In this study we introduce a new species *D. araliae-chinensis* found on leaves of *Aralia chinensi* in China from the *D. arecae* species complex.

***Diaporthe araliae-chinensis*** S.Y. Wang, Yong Wang bis & Y. Li, sp. nov. Fig. 13

MycoBank number: MB845964; Facesoffungi number: FoF13364

Etymology – In reference to the host plant, *Aralia chinensis*, from which this fungus was collected.

Holotype – HGUP 412

*Associated* with leaves of *Aralia chinensis*. *Asexual morph*: *Conidiomata* pycnidial, separated or aggregated, immersed or superficial, globose or subglobose, deep green to black, up to 1 mm diam., 5–8 wall layers of olive-green *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* densely aggregated, smooth, cylindrical, subulate, mostly straight, phialidic, simple, cylindrical, hyaline, 12–20 × 1.5–2.5 µm ($\bar{x}$ = 16.5 × 2 µm; n = 20), slightly tapering towards the apex, apex with inconspicuous periclinal thickening. *Alpha conidia* hyaline, fusoid to ellipsoidal, asymmetrical, smooth-walled, aseptate, tapering towards both ends, mostly straight, 5.5–9.5 × 2–3 µm ($\bar{x}$ = 7.5 × 2.4 µm; n = 30). *Beta conidia* and *gamma conidia* not observed. *Sexual morph*: Undetermined.

Culture characteristics – *Colonies* covering 9 cm diam. Petri dish after 2 weeks at 25 °C and a 12 h light/dark regime. On PDA, surface with thick aerial mycelium, initially appearing white and light yellow becoming chartreuse or olive from the centre with age; reverse white to pale yellow to light olive. On OA, surface with white or pale white thin aerial mycelium, exuding dark green to black conidial masses; reverse white or beige. On pine needles, irregular black conidial masses surrounded by sparse white mycelium.

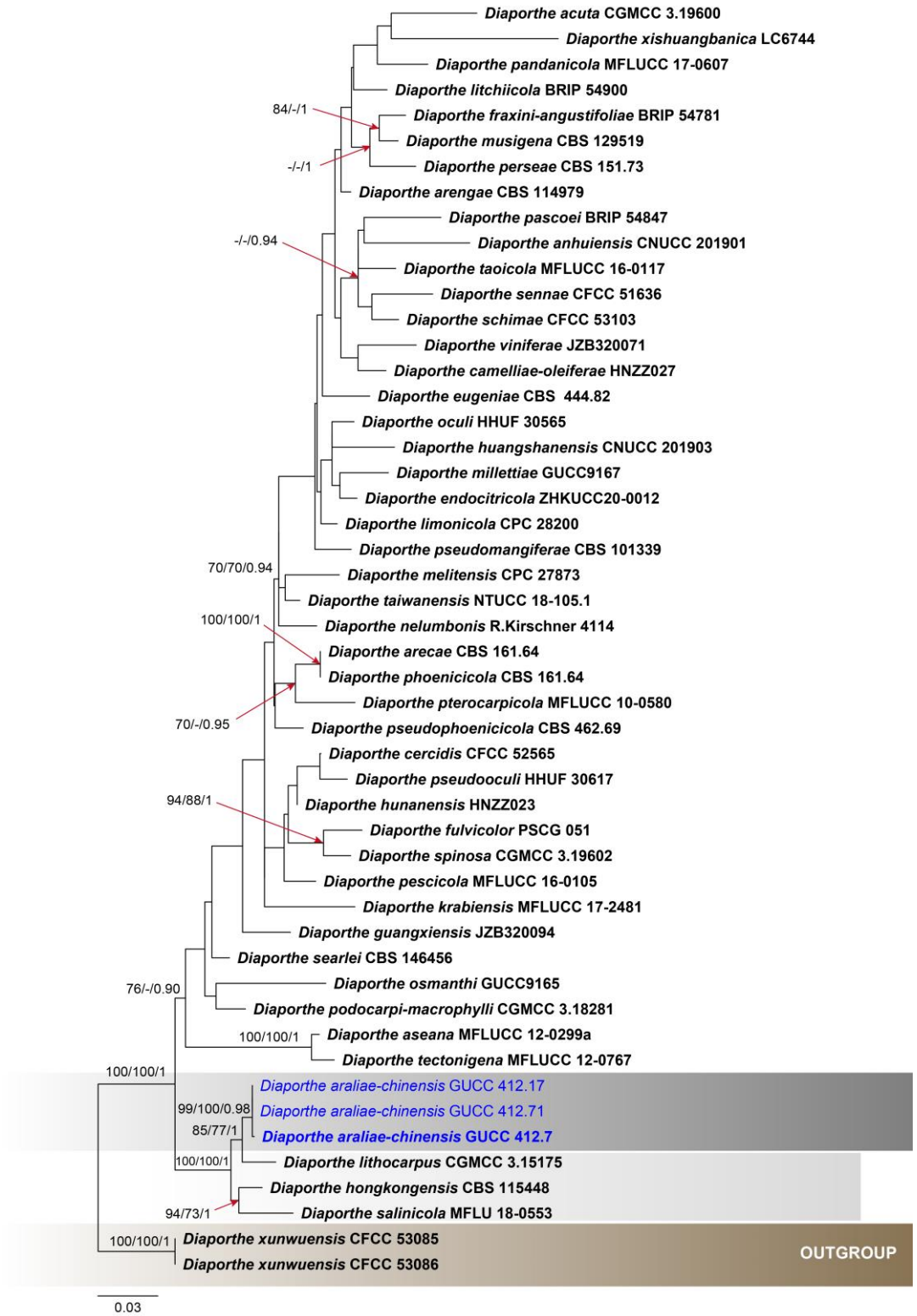


**Figure 12** – Phylogenetic tree obtained from maximum likelihood analyses of a combined ITS, *ef1α* and *β-tubulin* sequence dataset to represent the phylogenetic relationships of taxa in *Diaporthe arecae* species complex. 50 strains were included in the combined analyses, which comprised 1513 characters (ITS: 1–599, *ef1α*: 600–983, *β-tubulin*: 984–1513). The tree was rooted with *Diaporthe xunwuensis* (CFCC 53085 and CFCC 53086). Bootstrap support values for ML and MP equal to or greater than 70% and PP equal to greater than 0.95 are indicated above the nodes as ML/MP/PP. The newly generated sequences are indicated in blue. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.03 which represents the estimated number of nucleotide substitutions of site per branch.

Material examined – China, Guizhou Province, Longli County, on leaves of *Aralia chinensis* (Araliaceae), 15 June 2021, S.Y. Wang (holotype HGUP 412; ex-type living culture GUCC 412.7); *ibid*. on leaves of *A. chinensis*, 15 June 2021, S.Y. Wang, (living culture, GUCC 412.17, GUCC 412.71).

GenBank numbers – GUCC 412.7: ITS: OP581218, *ef1α*: OP688523, *β-tubulin*: OP688548; GUCC 412.17: ITS: OP581220, *ef1α*: OP688525, *β-tubulin*: OP688550; GUCC 412.71: ITS: OP581219, *ef1α*: OP688524, *β-tubulin*: OP688549

Notes – Based on phylogenetic analysis, our new species *Diaporthe araliae-chinensis* grouped within the *D. arecae* species complex with 85% ML, 77% MP, 0.98 PP support (Fig. 12), while also close to *D. lithocarpius* in this complex (Norphanphoun et al. 2022). However, conidiomata of *D. araliae-chinensis* (1 mm diam.) are larger than those of *D. lithocarpius* (120–270 µm diam., Gao et al. 2014), while its conidiogenous cells and alpha conidia are longer than those of *D. lithocarpius* (*D. araliae-chinensis*, 12–20 × 1.5–2.5 µm, 5.5–9.5 × 2–3 µm *vs* 12–15.4 × 1.9–2.6 µm, 5.7–8.1 × 2.1–3.2 µm, *D. lithocarpius*), and *D. araliae-chinensis* did not form beta conidia, while *D. lithocarpius* produced 17.6–28.1 × 0.92–1.81 µm beta conidia, Gao et al. 2014). *Diaporthe araliae-chinensis* has some nucleotide differences from *D. lithocarpius*, with seven base pair differences in ITS, 15 base pair differences in *ef1α*, and 11 base pair differences in *β-tubulin*. Hence, based on its morphological characteristics, phylogenetic analysis, nucleotide polymorphism comparison and pairwise homoplasy index (P-value = 1.0) test results, *D. araliae-chinensis* is described here as a new species and placed in the *D. arecae* species complex.

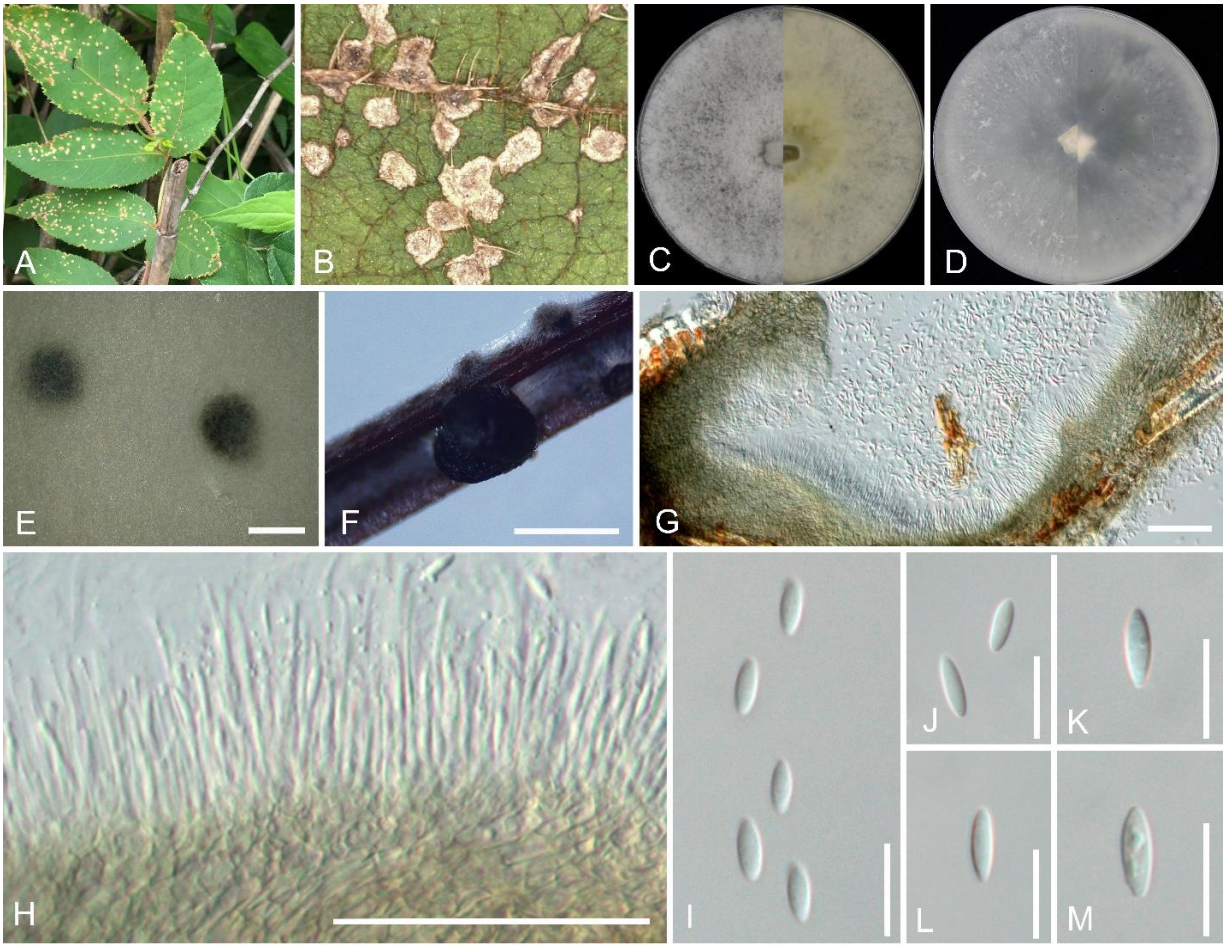


**Figure 13** – *Diaporthe araliae-chinensis* (ex-type living culture GUCC 412.7). a–b Host: *Aralia chinensis*. c Colony on PDA after 2 weeks at 25 °C (left: above, right: reverse). d Colony on OA after 2 wk at 25 °C (left: above, right: reverse). e–f Mass of conidia on OA and pine needle. g Conidioma. h Conidiogenous cells. i–m Alpha conidia. Scale bars: e = 1000 µm, f = 5000 µm, g–h = 50 µm, i–m = 10 µm.

***Dibaeis*** Clem., Gen. fung. (Minneapolis): 78 (1909)

*Dibaeis* was introduced to accommodate rose-colored hymenia species in *Baeomyces* by Clements (1909). Since then, it was placed in Icmadophilaceae based on the phylogenetic evidence of SSU rDNA data (Stenroos & DePriest 1998, Stenroos et al. 2002). *Dibaeis baeomyces* (= *Dibaeis rosea*) is the type species, and 19 epithets are listed in Index Fungorum (2023). *Dibaeis* is mainly distributed in tropical regions, characterized by a lichenized and dimorphic thallus, scattered or clustered apothecia with a stipe, 8-spored asci with an amyloid pore, and 1-septate or aseptate ascospores. *Dibaeis jingdongensis* is described here based on morphology and phylogenetic evidence.

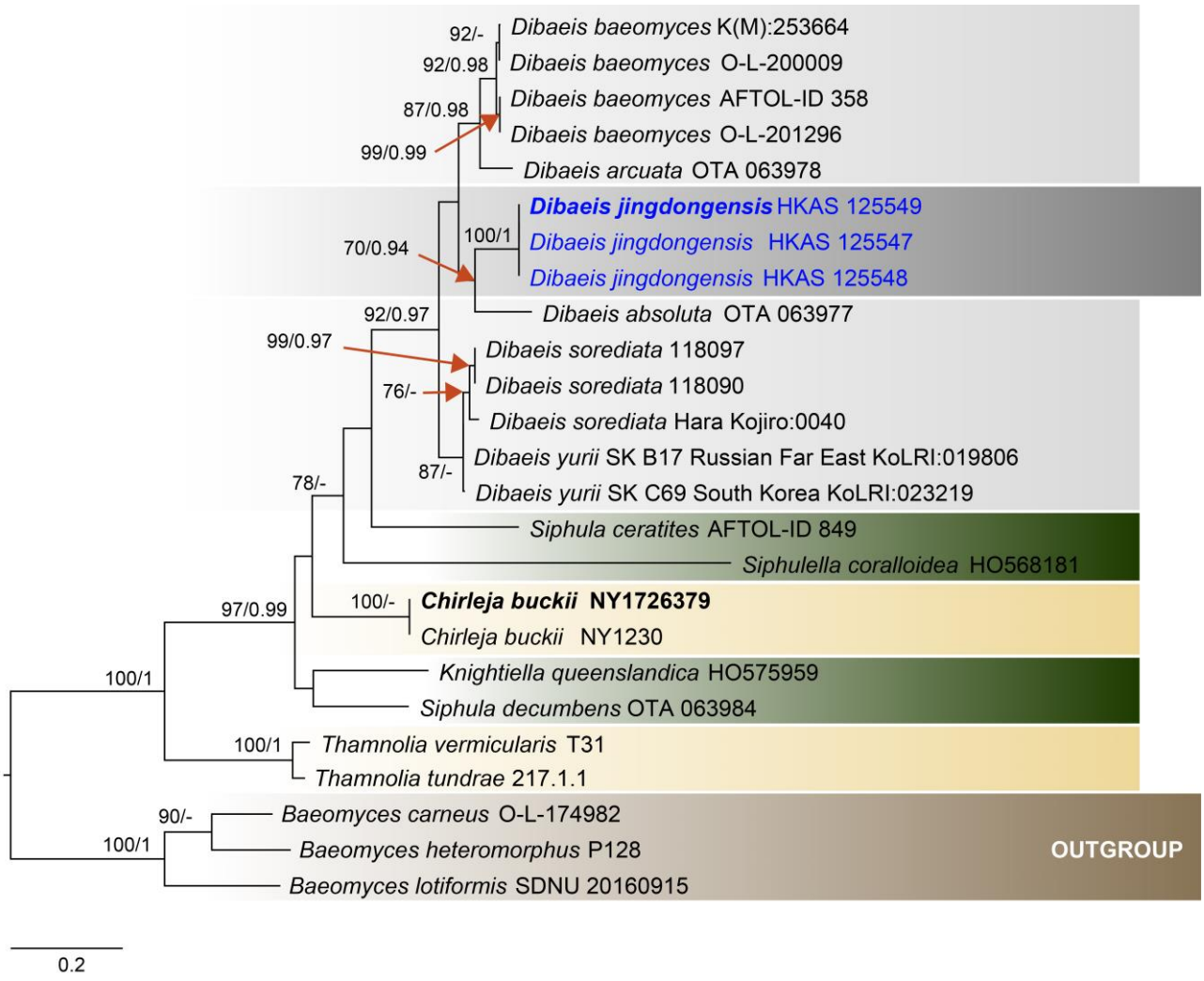


**Figure 14** – Phylogenetic tree obtained from maximum likelihood analyses based on ITS sequence data of the genus in Icmadophilaceae. Twenty-five strains were included in the analyses, which comprised 577 characters after alignment. Bootstrap support values for ML greater than 70% and Bayesian posterior probabilities greater than 0.90 are given near nodes as ML/PP, respectively. The tree was rooted with *Baeomyces carneus* (O-L-174982), *Baeomyces heteromorphus* (P128) and *B. lotiformis* (SDNU 20160915). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.2 which represents the estimated number of nucleotide substitutions of site per branch.

***Dibaeis jingdongensis*** C.J.Y. Li & K.D. Hyde, sp. nov. Fig. 15

MycoBank number: MB846931; Facesoffungi number: FoF12928

Etymology – The specific epithet refers to the locality “Jingdong County” from where the holotype specimen was collected.

Holotype – HKAS 125549

*Thallus* crustose, green, unevenly lumpy, mostly wrinkled when fresh and dry, photobiont a unicellular green alga, ellipsoid cells with one narrow rounded end, 10–15 × 8–14 μm ($\bar{x}$ = 13 × 11 mm, n = 20). Sexual morph: *Apothecia* cup-shaped when fresh and dry, 1–1.5 mm wide × 0.7–1.5 mm high ($\bar{x}$ = 1.3 × 1 mm, n = 20), scattered, superficial. *Disc* flat and circular, pink when fresh, pink to whitish pink, wrinkled with yellow refraction particles on surface when dry. *Receptacle* 0.3–0.7 mm high, smooth and flat when fresh, wrinkled and rough when dry, concolorous to the disc. *Stipe* 0.1–0.3 mm wide × 0.8–1 mm high ($\bar{x}$ = 0.2 × 0.9 mm, n = 20), smooth, whitish pink, covered with unicellular green alga. *Excipulum* 35–55 μm, thin, comprised of irregular brown refraction particles. *Hypothecium* 160–260 μm, thick, comprising densely hyaline cells of *textura intricata*, hyphae 3–5 μm, thin-walled, septate, branched and non-gelatinous. *Hymenium* 140–160 μm, hyaline, covering the same materials to the ectal excipulum on the outer layer, turning greenish blue in Melzer's reagent. *Paraphyses* 3.5–4.7 μm ($\bar{x}$ = 4.2 μm, n = 25) wide at tips, numerous, filiform, hyaline, obtuse and swollen at the apex, branched, aseptate, rough, guttulate, exceeding the asci in length. *Asci* 92–127 × 9–13 μm ($\bar{x}$ = 108 × 11 μm, n = 50), 8-spored, icmadophila-type, narrowly cylindric, apex rounded, slightly thicken with amyloid on the outmost part, tapering to subtruncate base. *Ascospores* (15.2–)15.8–20.1(–22.2) × (5.6–)5.8–7.3(–7.5) μm ($\bar{x}$ = 18 × 6.4 μm, n = 100), Q = 2.2–3.4(–3.8) μm, Qm = 2.8 ± 0.1 μm, uniseriate, sometimes overlapping, ellipsoidal, tapering to narrowly rounded at one end, hyaline, thick-walled, smooth, aseptate with a large guttule. *Pycnidia* not found. Asexual morph: Undetermined.

Material examined – China, Yunnan Province, Puer City, Jingdong County, altitude 2520m, on moist rocks and soil near by a lake, 9 June 2022, C.J.Y. Li, LCJY-777 (holotype HKAS 125549). Yunnan Province, Puer City, Jingdong County, 22 August 2022, on moist rocks near by a lake, LCJY-770 (paratype HKAS 125548); *ibid*., 22 August 2022, on moist rocks near by a lake, LCJY-758 (paratype HKAS 12554).

GenBank numbers – HKAS 125549 = ITS: OP745052; HKAS 125548 = ITS: OP745050; HKAS 125547 = OP745051

Notes – The phylogenetic analysis of ITS data and typical morphological characteristics indicates that our collections belong to *Dibaeis*. The ITS region of *D. jingdongensis* (HKAS 125549) is similar to that of *D. baeomyces* (strain O-L-200009) (483/541 with 12 gaps) and *D. absoluta* (strain OTA 063977) (475/535 with 12 gaps). *Dibaeis jingdongensis* formed an independent clade sister to *D. absoluta* with 70% ML bootstrap and 0.94 Bayesian probability (Fig. 14).

*Dibaeis jingdongensis* is mainly characterised by typically small, pink, cup-shaped apothecia, narrow stipes, wide hyphae of the hypothecium, and long, broad asci with large ellipsoidal ascospores. *Dibaeis jingdongensis* resembles *D. absoluta* by having a similar habitat, pink cup-shaped apothecia when dry, loose paraphyses with swollen tips and icmadophila-type asci. Our species differs from *D. absoluta* by having longer stipes, larger asci (92–127 × 9–13 μm *vs* 65–80 × 8 μm) and larger ascospores (15.8–20.1 ×5.8–7.3 μm *vs* 8–11 × 2–3.5 μm) (Yadav 2020).

***Dictyosporella*** Abdel-Aziz, Fungal Diversity 75: 143 (2015)

*Dictyosporella* was introduced as an aquatic hyphomycetous species with *D. aquatica* as the type species. *Dictyosporella* is characterized by dictyoseptate conidia which are helicoid when young and become masses of cells at maturity (Ariyawansa et al. 2015). While the three asexual species *viz*; *D. ellipsoidea, D. guizhouensis* and *D. hydei* have dictyoseptate conidia, they are not helicoid when young (Song et al. 2018, Yuan et al. 2020). *Dictyosporella ellipsoidea* and *D. guizhouensis* have separating cells at the conidial base, while the other two species *D. aquatica* and *D. hydei* lack this structure (Dong et al. 2021).

Junewangiaceae was recently revised by Dong et al. (2021) and Goh et al. (2020) providing an updated multi-gene phylogenetic tree with four genera, *Dictyosporella*, *Jennwenomyces*, *Junewangia*, and *Sporidesmiella*. *Dictyosporella* comprises six epithets in Index Fungorum (2023) and its polyphyletic nature has been shown in previous studies (Dong et al. 2021).

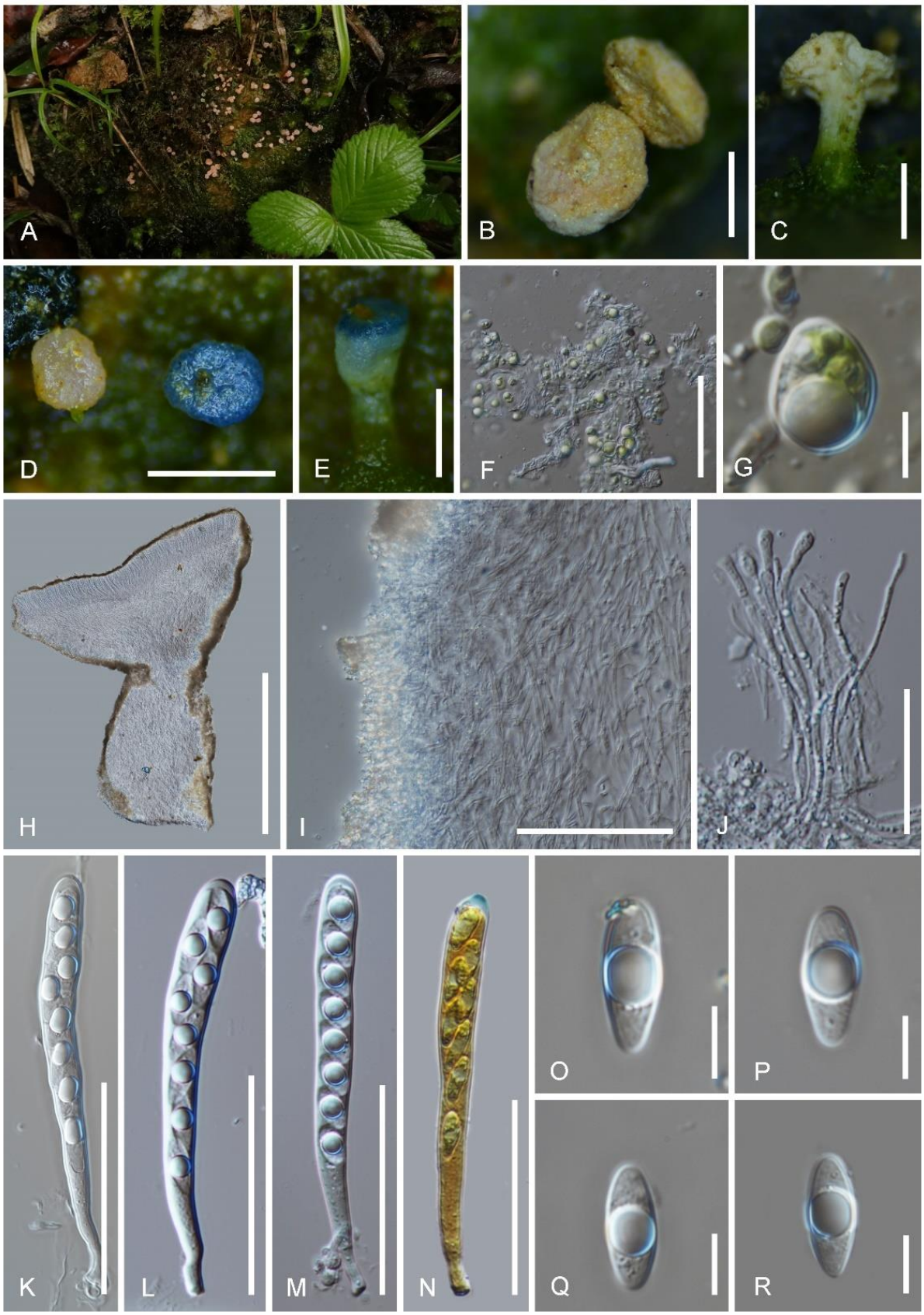


**Figure 15** – *Dibaeis jingdongensis* (holotype HKAS 125549). a Fresh ascomata on the natural habitat. b, c Dried ascomata on substrate. d–e Rehydrated ascomata and pigmented in Meltzer's reagent. f–g Cells of photobiont. h Vertical section of ascoma. i Excipulum. j Paraphyses. k–n Asci (Asci in Meltzer's reagent). o–p Ascospores. Scale bars: b, h = 1000 μm, c = 1200 μm, d = 2000 μm, e = 800 μm, f = 70 μm, g = 6 μm, i = 100 μm, j = 40 μm, k–n = 60 μm, O–R = 8 μm.

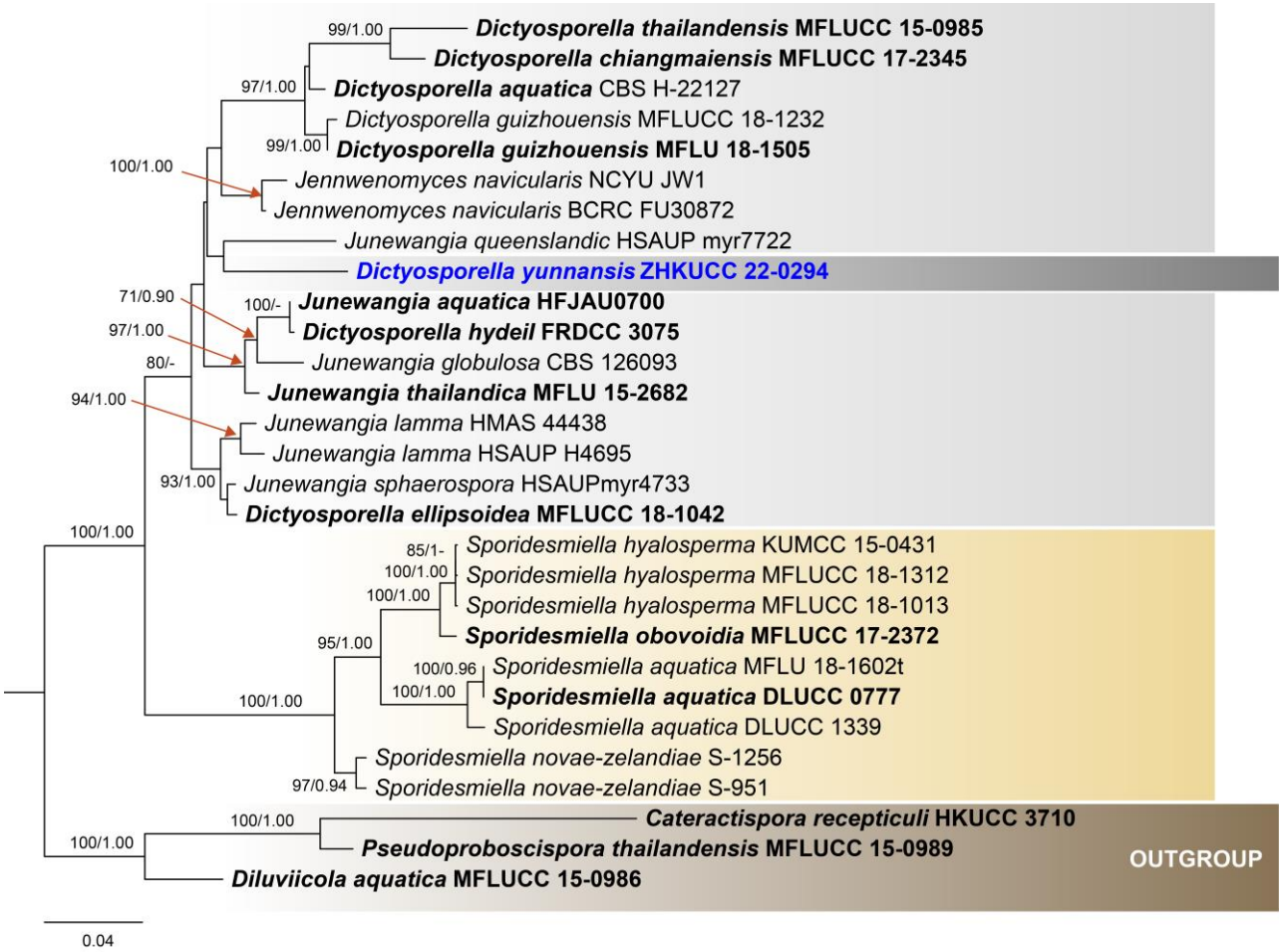


**Figure 16** – Phylogenetic tree obtained from maximum likelihood analyses of a combined ITS, LSU, SSU, and *ef1α* sequence data, representing the species in Junewangiaceae. Related sequences were obtained from Dong et al. (2021). Twenty-nine strains were included in the combined analyses, which comprised 3862 characters (ITS: 1–574, LSU: 575–1501, SSU: 1502–2952, *ef1α*: 2953–3862) after alignment. Bootstrap support values for ML equal to or greater than 70% and PP equal to or greater than 0.90 are given above the nodes as ML/PP. *Cateractispora recepticuli* (HKUCC 3710), *Pseudoproboscispora thailandensis* (MFLUCC 15-0989), and *Diluviicola aquatica* (MFLUCC 15-0986) were used as the outgroup taxa. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.04 which represents the estimated number of nucleotide substitutions of site per branch.

***Dictyosporella yunnanensis*** X.G. Tian & Tibpromma, sp. nov. Fig. 17

MycoBank number: MB846357; Facesoffungi number: FoF10600

Etymology – The specific epithet refers to the location "Yunnan Province, China", where the species was first collected.

Holotype – ZHKU 22-0165

*Saprobic* on submerged wood in freshwater. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate sporodochial, punctiform, raised, gregarious or scattered, black. *Mycelium* partly immersed, partly superficial on substance, consisting of hyaline, thin-walled hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–15 × 2–4 µm ($\bar{x}$ = 11.5 × 2.5 µm, n = 10), holoblastic, monoblastic, integrated, determinate, terminal, subcylindrical, hyaline, smooth-walled. *Separating cells* 5–9 × 6–10 µm ($\bar{x}$ = 7.5 × 7.5 µm, n = 10), inflated, globose to subglobose or cup-shaped, hyaline, smooth and thin-walled. *Conidia* 18–20 × 12–13 µm ($\bar{x}$ = 19 × 12.5 µm, n = 55), acrogenous, solitary, ellipsoidal or subglobose, dictyoseptate, yellow-brown to brown, slightly constricted at septa, with a truncate base, thin and smooth-walled.

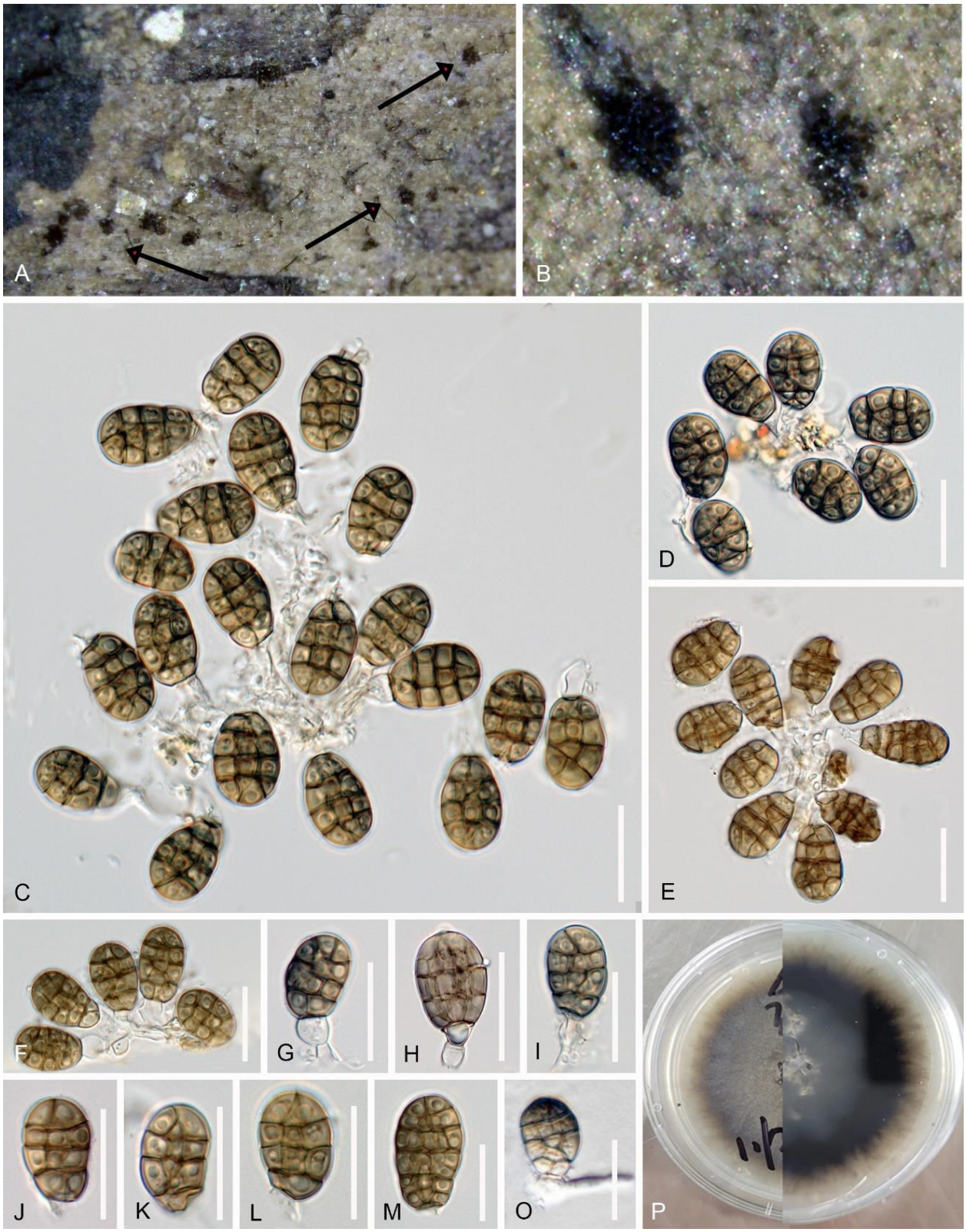


**Figure 17** – *Dictyosporella yunnansis* (holotype ZHKU 22-0165). a, b Colonies on a submerged piece of wood (arrows indicate fungi on substrate). c–i Conidiogenous cells with conidia. j–m Conidia. o Germinated conidium. p Upper and reverse views of the culture on PDA. Scale bars: c–o = 20 μm.

Culture characteristics – On PDA, colony regular, reaching 20 mm in 15 days at 25 °C, dark grey from above, black from below, surface smooth, dry, with dense mycelium, undulate at the edge.

Material examined – China, Yunnan Province, Xishuangbanna District, on a submerged piece of wood in a stream, 17 September 2021, X.G. Tian, wb20 (holotype ZHKU 22-0165, ex-type living culture ZHKUCC 22-0294).

GenBank numbers – LSU: OL753700, ITS: OL606180, *ef1α*: OL606193

Notes – NCBI Blast results of the LSU sequence of *Dictyosporella yunnanensis* (wb20) showed similarities to *D. guizhouensis* MFLU 18-1505 (98.06%), *D. thailandensis* MFLUCC 15-0985 (97.82%), and *Junewangia globulosa* CBS 126093 (97.58), while Blast results of the ITS sequence showed similarities to *Jennwenomyces navicularis* NCYU-H1-1-1 (88.83%), *J. sphaerospora* (89.39%), *J. globulosa* CBS 126093 (85.29%) and Blast results of the *ef1α* sequence showed similarities to *Sporidesmiella lignicola* JAUCC 3436 (92.09%), *Sporidesmiella aquatica* MFLU18-1602 (91.93%), *Cancellidium cinereum* MFLUCC 18-0424 (91.28%) and *D. thailandensis* MFLUCC 15-0985 (91.09%). In the phylogenetic analyses of combined ITS, LSU, SSU, and *ef1α* sequence data, our collection (wb20) clusters with *Junewangia* (Fig. 16). However, our strain (wb20) morphologically belongs in *Dictyosporella* due to the sporodochial, punctiform colonies, dictyoseptate conidia with a separating cell and the absence of macronematous conidiophores (Song et al. 2018, Yuan et al. 2020). However, *Junewangia* is different from *Dictyosporella* by having effuse, hairy colonies, macronematous, long conidiophores with percurrent proliferations, and oval to subspherical conidia (Baker et al. 2002a). Since the morphology of our collection is in agreement with the genus *Dictyosporella* and the phylogenetic placement of *Junewangia* and *Dictyosporella* unclear, we identify our collection as a new species in *Dictyosporella*, namely *D. yunnanensis*.

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

*Distoseptispora* was established by Su et al. (2016) based on evidence from morphology and phylogeny. The asexual morph of this genus is characterized by darker conidia with slightly paler, but not hyaline rounded apices, basal cells truncate base, and relatively short conidiophores (Su et al. 2016). The sexual morph which resembles *Sporidesmium thailandense* was first found on decaying wood submerged in a freshwater stream by Yang et al. (2021). In this study, a new species *D. phragmiticola* is introduced based on evidence of morphology and phylogenetic placement (Figs 18, 19).

***Distoseptispora phragmiticola*** Qian Zhang, Yong Wang bis & K.D. Hyde, sp. nov. Fig. 19

MycoBank number: MB846989; Facesoffungi number: FoF13260

Etymology – Named after the host genus *Phragmites*.

Holotype – HGUP 220100

*Saprobic* on *Phragmites australis*. Sexual morph: Undetermined. Asexual morph: Colonies on *Phragmites australis* effuse, hairy, dark brown, scattered or in small groups, glistening. *Mycelium* partly immersed, partly superficial, composed of septate, smooth-walled, pale brown to hyaline hyphae. *Conidiophores* macronematous, mononematous, erect, straight or slightly flexuous, cylindrical, truncate at the apex, smooth-walled, septate, unbranched, dark brown, 50–145 × 5–8 µm ($\bar{x}$ = 100.8 × 6.2 µm, n = 30). *Conidiogenous* cells monoblastic, integrated, terminal, determinate, cylindrical, pale brown, rounded and pale brown at the apex, sometimes elongating percurrently. *Conidia* acrogenous, obclavate, rostrate, pale brown, greyish brown or mid brown, paler towards the apex, 4–25-septate, 34–155 × 10.5–17.5 µm ($\bar{x}$ = 83.5 × 14.5 µm, n = 30), smooth walled, truncate at the base.

Culture characteristics – Conidia germinating on PDA within 24 h and germ tubes produced from both ends. Colonies growing on PDA slow growing, reaching 10–15 mm in two weeks at 25 °C, circular, with dense, gray mycelium in the middle, darker of the inner ring, with sparser, white mycelium of the outer ring on the surface, in reverse dark brown to black with smooth margin.

Material examined – China, Guizhou Province, Libo County, 25°17′24″ N, 108°4′0″ E, on *Phragmites australis* (Poaceae), 12 March 2022, Q. Zhang (holotype HGUP 220100, ex-type living culture GUCC 220201 = GUCC 220202).

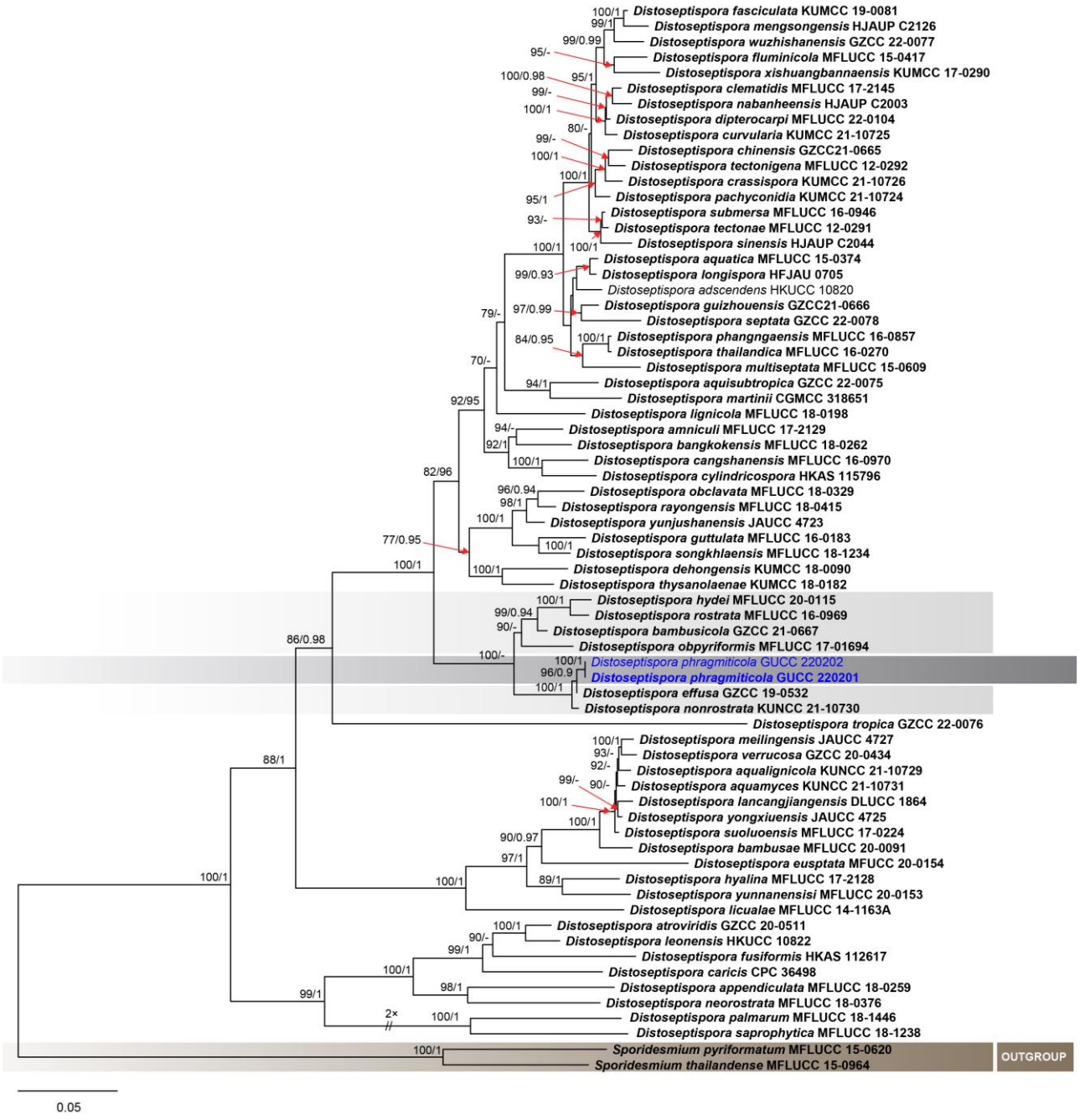


**Figure 18** – Phylogenetic tree obtained from maximum likelihood analyses of a combined LSU, ITS, *ef1α* and *rpb2* sequence dataset representing the species of *Distoseptispora*. Sixty-nine strains were included in the combined analyses, which comprised 3,393 characters (LSU: 1–854, ITS: 855–1473, *ef1α*: 1474–2362, *rpb2*: 2363–3393) after alignment. Bootstrap support values for ML equal to or greater than 70% and PP equal to greater than 0.95 are indicated at the nodes as ML/MP/PP. The tree is rooted to *Sporidesmium pyriformatum* (MFLUCC 15-0620) and *Sporidesmium thailandense* (MFLUCC 15-0964). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.05 which represent the estimated number of nucleotide substitutions of site per branch.

GenBank numbers – GUCC 220201 = LSU: OP749880, ITS: OP749887, *ef1α*: OP749891, *rpb2*: OP752699; GUCC 220202 = LSU: OP749881, ITS: OP749888, *ef1α*: OP749892, *rpb2*: OP752700

Notes – *Distoseptispora phragmiticola* is nested within the clade containing *D. rostrata*, *D. hydei*, *D. obpyriformis*, *D. bambusicola* (unpublished) and *D. effusa* and is phylogenetically

related to *D. effusa* (Fig. 18). Morphologically, *D. phragmiticola* is similar to *D. effusa* (Yang et al. 2021) with percurrently elongate conidiophores and obclavate, distoseptate conidia, but differs by the shape of the apex of conidiophores (truncate *vs* rounded), having a larger number of septa (4–25 *vs* 4–9) and larger conidia (34–155 × 10.5–17.5 µm *vs* 35.5–113 × 7–12.5 µm). Morphological differences and phylogenetic distinction from other related species showed that *D. phragmiticola* is a new species.


**Figure 19** – *Distoseptispora phragmiticola* (holotype HGUP 220100). a–c Colonies on *Phragmites australis*. d–g Conidiophores. h–k Conidia. l Germinated conidium. m, n Colony on PDA, M from above, N from below. Scale bars: d–l = 50 µm.

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

*Fusarium* (Hypocreales, Nectriaceae) with a worldwide distribution, is widely recognized as the most important group of mycotoxigenic plant pathogens. There are over 450 phylospecies distributed among 23 monophyletic species complexes (Geiser et al. 2021, Geiser et al. 2013, O'Donnell et al. 2013). Among them, *F. buharicum* species complex (FBSC) comprised three species: *F. buharicum* (Gerlach & Scharif 1970, Jaczewski 1929), *F. convolutans* (Sandoval-Denis et al. 2018) and *F. sublunatum* (Reinking 1934). O'Donnell et al. (2022) represent the most detailed assessment of evolutionary relationships and species diversity within the FBSC to date and I follow

this system. The present study describes a novel taxon based on morphological description and phylogenetic analysis.

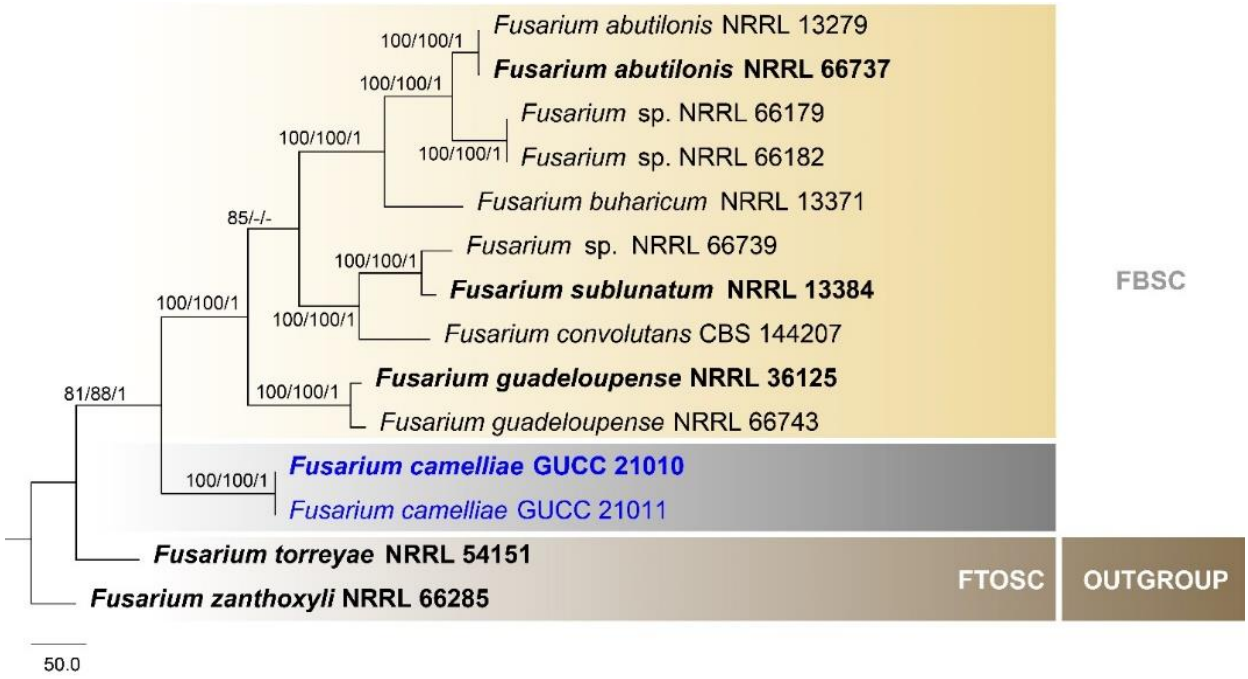


**Figure 20** – The most parsimonious trees obtained from a heuristic search of a combined *rpb2* and *ef1α* sequence dataset representing the species of *Fusarium*. Fourteen strains were included in the combined analyses, which comprised 2531 characters (*rpb2*: 1–1844, *ef1α*: 1845–2531) after alignment. Bootstrap support values for ML and MP equal to or greater than 80% and PP equal to greater than 0.90 are indicated at the nodes as MP/ML/PP. *Fusarium torreyae* (NRRL 54151T) and *F. zanthoxyli* (NRRL 66285T) are used as the outgroup taxa. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 50 which represent the estimated number of nucleotide substitutions of site per branch. FBSC: *F. buharicum* species complex, FTOSC: *F. torreyae* species complex.

***Fusarium camelliae*** Y.K. He & Yong Wang bis, sp. nov. Figs 21, 22

MycoBank number: MB846322; Facesoffungi number: FoF14241

Etymology – '*camelliae*', in reference to the host genus *Camellia* from which the new species was isolated.

Holotype – HGUP 10010

Sexual morph: Undetermined. Asexual morph: Colony margins regular. *Conidiophores* unbranched or sparingly branched, aerial phialides subulate to subcylindrical, straight, thin- and smooth- walled. *Microconidia* hyaline, ellipsoidal to falcate, smooth- and thin-walled, 0–1 septate; 0-septate, 5–12 × 3–4 µm or 1-septate, 12–18 × 3–6 µm. *Macroconidia* formed on aerial mycelium, falcate, curved dorsiventrally with almost parallel sides tapering slightly towards both ends, with a blunt to papillate, curved apical cell and a blunt to foot-like basal cell, hyaline, smooth- and thin-walled. *Sporodochial conidia* mostly 7–9-septate, 50–65 × 4–6 µm (n = 56), sometimes 6-septate (55–60 × 3–4 µm, n = 3) or 10-septate (62–70 × 4.5–5 µm, n = 2). *Conidia* absent or sparsely produced in aerial mycelium on PDA in ambient light. *Aerial conidia* 45–55 × 2.5–4 µm, produced from lateral solitary phialides on hyphae of aerial mycelium, or fascicles of hyphae. *Chlamydospores* sparse, single or in chains of up to 6, intercalary or terminal, hyaline, globose, 4–8 µm diam.

Culture characteristics – Colonies on PDA media with an average radial growth rate of 1.5-2.1 mm/d at 24 ℃. The colony was yellow with abundant and flocculent aerial hyphae, but later turned orange, odour absent.

Material examined – China, Guangxi Province: Guang Xi Medicinal Botanical Garden, on a leaf of *Camellia* (Theaceae), November 2017, Q. Zhang (holotype HGUP 10010, ex-type living culture GUCC 21010).

GenBank numbers – GUCC21010: *ef1α*: OP757314, *rpb2*: OP800100; GUCC21011: *ef1α*: OP800102, *rpb2*: OP820349

Notes – *Fusarium camelliae* form a genealogically exclusive lineage within the *F. buharicum* species complex, but its precise phylogenetic relationship with seven other species within this complex is unresolved by molecular phylogenetic analyses of a 2-gene data set (Fig. 20). Morphologically, the two strains, *F. camelliae* (GUCC 21010, GUCC 21011), have some similar characteristics to other FBSC members, including slow growth rates, a relative sparseness of microconidia and chlamydospores. However, *F. camelliae* can easily be distinguished from the other species by having shorter conidia, with more septate (Table 1).

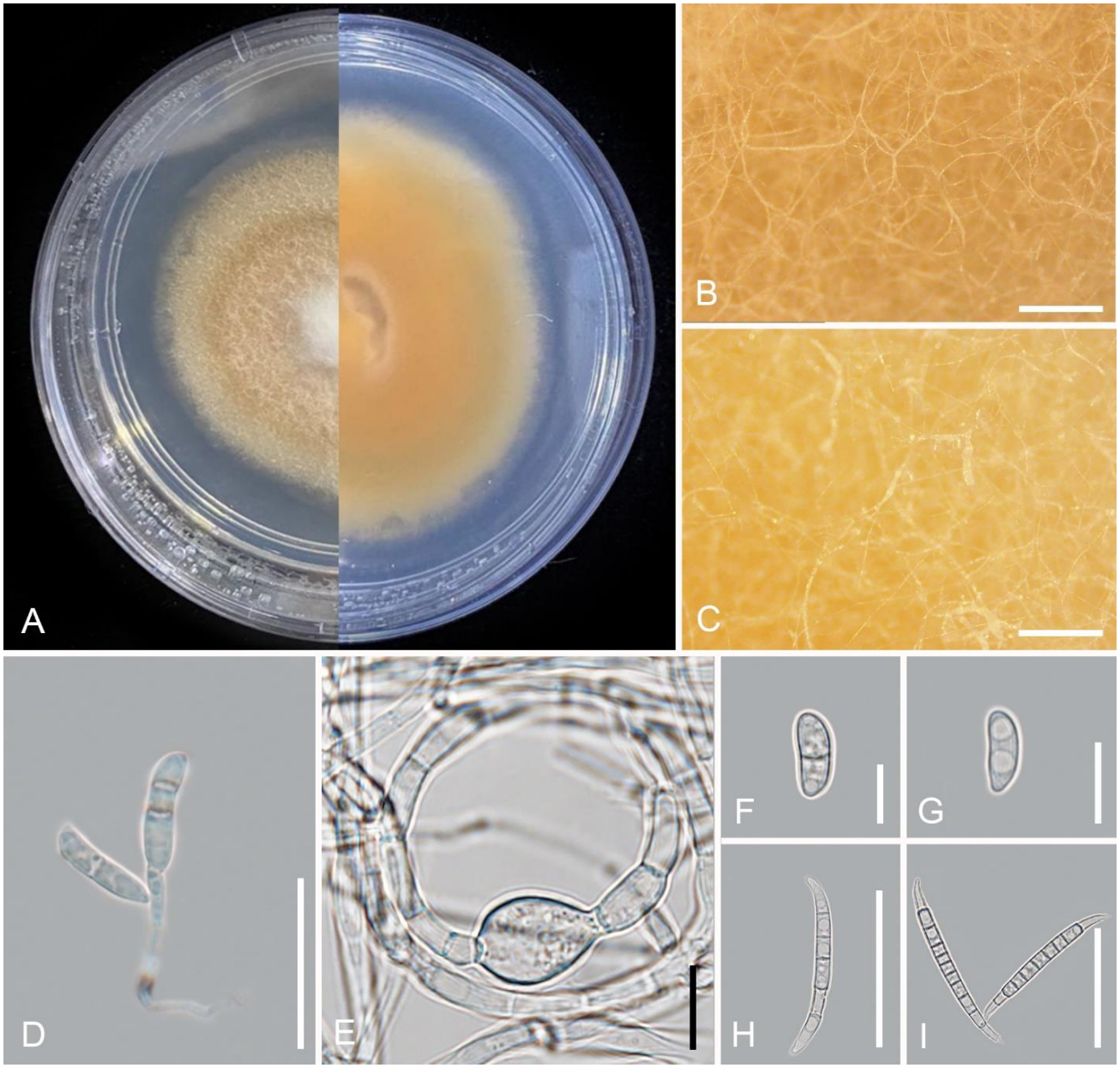


**Figure 21** – *Fusarium camelliae* (holotype HGUP 10010). a surface of colony on PDA after 21 d at 24 °C under continuous white light and reverse of colony on PDA. b, c Mycelium on PDA. d conidiophores and phialides on aerial mycelium. e Chlamydospores. f–g Aerial conidia (microconidia). h–i Sporodochial conidia (macroconidia). Scale bars: b–c = 1 mm, d, e, h, i = 50 µm, f, g = 10 µm.

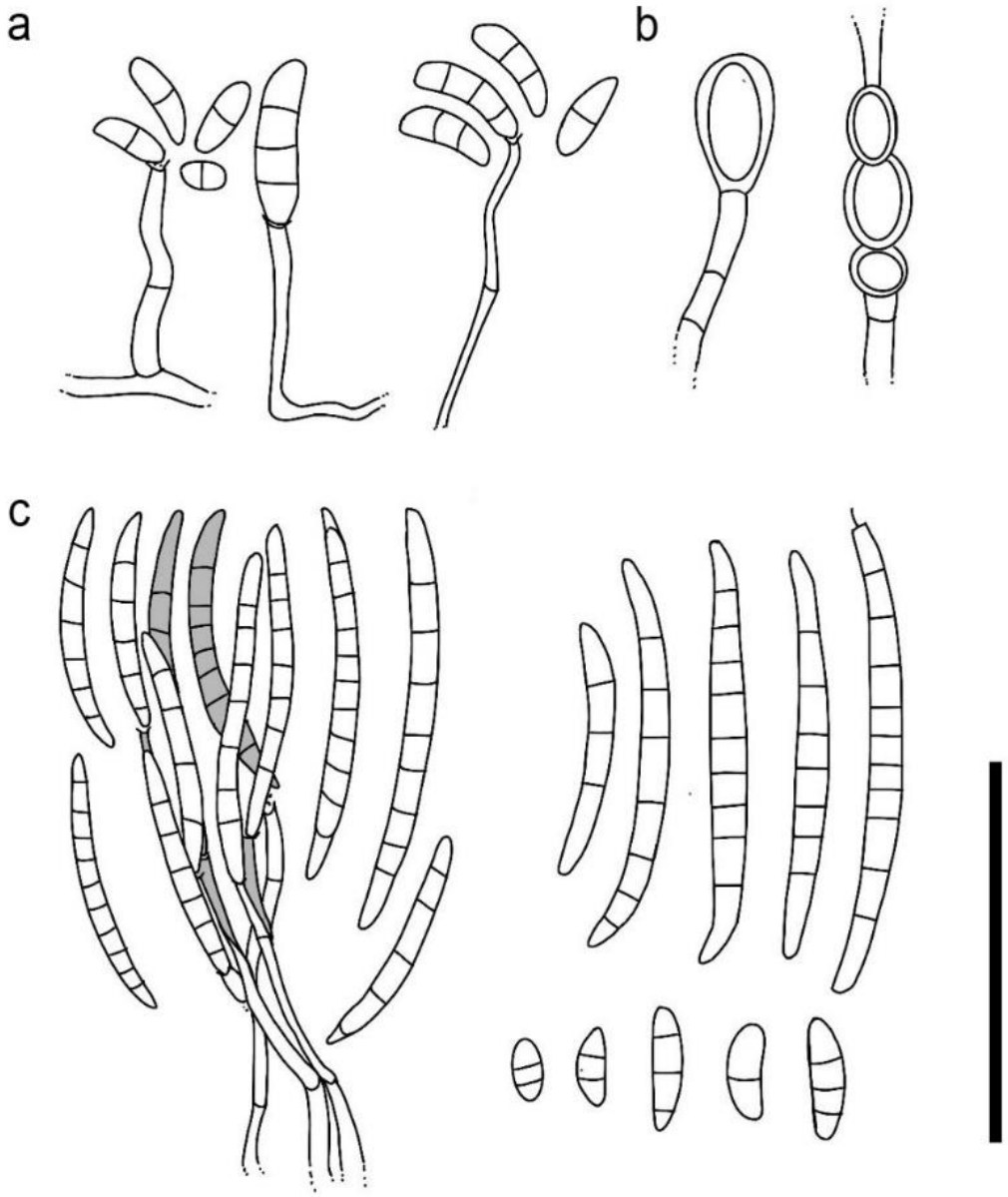


**Figure 22** – *Fusarium camelliae* (holotype HGUP 10010). a Conidiophores. b Chlamydospores. c Macroconidia. d Microconidia. Scale bars: 50 μm.

**Table 1** Comparison of conidia of *Fusarium* species related to this study.

| Species | Strain | Macroconidia | | Reference |
|---|---|---|---|---|
| | | Size (μm) | Septate | |
| *F. abutilonis* | NRRL 13279 | 64–85 × 7–9 | mostly 5-septate, sometimes 4-or 6-septate | O'Donnell et al. (2022) |
| *F .buharicum* | NRRL 66737 | typically, 45–65 × 5.3–6.5 | 0–8 | Gerlach et al. (1982) |
| *F .convolutans* | CBS 144207 | 25.5–38.5 × 4–7.5 | 1–3 | Sandoval-Denis et al. (2018) |
| *F .guadeloupense* | NRRL 36125 | 41.5–63 × 5–6 | mostly 5-septate, rarely 6-septate | O'Donnell et al. (2022) |
| *F .sublunatum* | NRRL 13384 | 48–66 long | – | Wollenweber & Reinking (1935) |
| *F .camelliae* | GUCC 21010 | typically, 50–65 × 4–6 | mostly 7–9-septate, rarely 6-septate, or 10-septate | This study |

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

*Helminthosporium* is a polyphyletic genus in Massarinaceae (Pleosporales). It is a species-rich genus with a worldwide distribution. *Helminthosporium* was introduced by Link (1809) with *H. velutinum* as the type species. *Helminthosporium* is characterized by macronematous, cylindrical, rather straight, septate, erect conidiophores with tretic conidiogenous cells and clavate or obclavate, distoseptate conidia (Luttrell 1964, Voglmayr et al. 2017). Konta et al. (2021) sated there were 216 *Helminthosporium* names, however many species are identified only based on morphological studies, and only 25 species have sequence data. In addition, there are 771 epithets of *Helminthosporium* (Index Fungorum 2023), whereas many of them are not congeneric with the generic type and were reclassified into other groups in subsequent studies. Chen et al. (2022) provided a recent account of *Helminthosporium* with several new isolates. In this study, two new species of *Helminthosporium*, *H. lignicolum* and *H. shangrilaense*, are introduced and described. *Helminthosporium lignicolum* was collected from decaying wood in a damp environment in northern Thailand, while *H. shangrilaense* was collected from the dead stem of an unidentified plant in southwestern China. *Helminthosporium lignicolum* and *H. shangrilaense*, is described herein as two new species based morphological characteristics and phylogenetic evidence (Fig. 20).

***Helminthosporium lignicolum*** R.J Xu, S. Boonmee, Q. Zhao & K.D. Hyde, sp. nov. Fig. 24

MycoBank number: MB847559; Facesoffungi number: FoF13250

Etymology – Referring to the wood dwelling nature of the new species.

Holotype – MFLU 22-0155

*Saprobic* on decaying wood in a damp environment. Sexual morph: Undetermined. Asexual morph: Colony on natural substrate superficial, effuse, dark brown, hairy. *Mycelium* mostly immersed, towards the surface forming stroma-like aggregations of light to dark brown pseudoparenchymatous cells. *Conidiophores* 287–502 × 9–14 µm ($\bar{x}$ = 421 × 11, n = 20). macronematous, mononematous, unbranched, arising solitarily or in small groups from the stroma cells, erect, straight or flexuous, thick-walled, subcylindrical, smooth, pale to dark brown, paler near the apex, multiple-septa. *Conidiogenous cells* mono- to polytretic, integrated, terminal and intercalary, cylindrical, cicatrized, with dark scars, with distinct pores. *Conidia* 74–84 × 12–17 µm ($\bar{x}$ = 79 × 14, n = 30)., solitary, obclavate, lunate, straight to slightly curved, fuscous truncate at the base, smooth, grey-white to pale brown, 8–11-distoseptate, sometimes Y-shaped branches at the apex (Fig. 24n).

*Culture characters*: Conidium germinating on PDA within 24 h and germ tubes produced from both ends or middle. Colonies on PDA reaching 10 mm diam., in a week at room temperature, efuse, hairy, mycelium radiating outwards, fimbriate edge, dense, pale. Mycelium superficial and partly immersed, light brown.

Material examined – Thailand, Chiang Rai Province, Mueang, Nang Lae, saprobic on submerged decaying wood in a freshwater stream, 560 msl, 99°52′52.93″E, 20°3′2.52″N, 14 August 2020, R.J Xu, MD-82 (holotype MFLU 22-0155, ex-type living culture MFLUCC 22-0118).

GenBank numbers – LSU: OP740252, ITS: ON329811, SSU: OP740253, *rpb2*: OP757656, *ef1α*: OP757657

Notes – Multigene analyses of combined of SSU, LSU, *rpb2*, *ef1α* and ITS sequence data showed that our strain (MFLUCC 22-0118) clusters with the ex-type strain *Helminthosporium aquaticum* (MFLUCC 15-0357) with low support (Fig. 23). Sequence comparison for the ITS region between *H. lignicolum* (MFLUCC 22-0118) and *H. aquaticum* (MFLUCC 15-0357) showed a 13.64% (70/513 bp, excluding gap) base pair difference (Jeewon & Hyde 2016). Species of *Helminthosporium* are complex and share common features such as terminal and intercalary conidiogenous cells as well as solitary conidia with distosepta. *Helminthosporium lignicolum* is distinct from *H. aquaticum* in sometimes Y-shaped branches at the apex conidia, culture characteristics and molecular data (Zhu et al. 2016). Therefore, we introduce *H. lignicolum* as a new species.

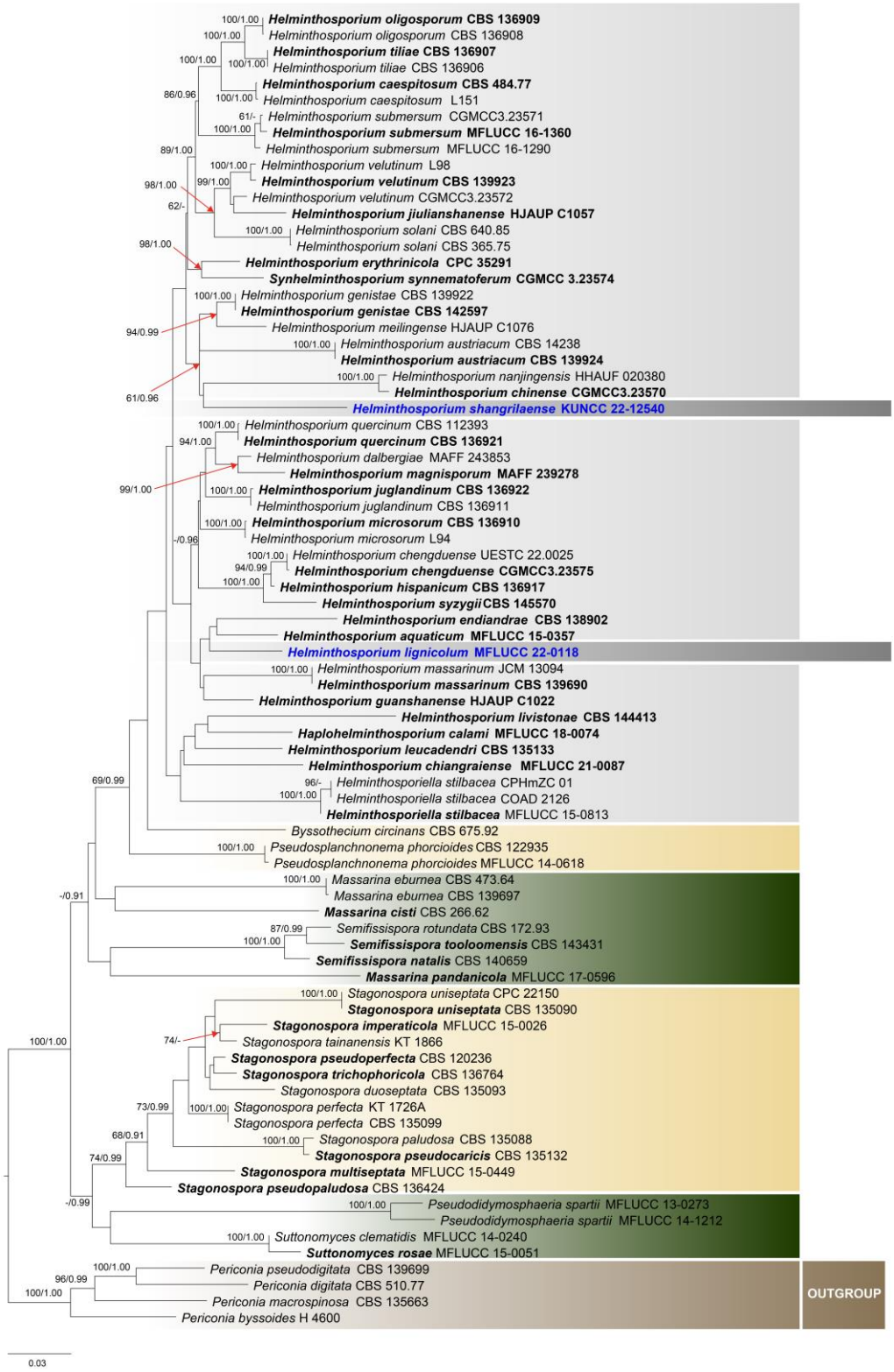


**Figure 23** – Phylogenetic tree obtained from Bayesian inference analyses of a combined ITS, LSU, SSU, *rpb2*, and *ef1α* sequence dataset representing the species of *Helminthosporium*. Eighty-one strains were included in the combined analyses, which comprised 5072 characters (LSU: 1–855, SSU:856–1888, ITS: 1889–2446, *ef1α*: 2447–3775, *rpb2*: 3776–4888) after alignment. Bootstrap support values for ML equal to or greater than 60% and PP equal to greater than 0.95 are indicated at the nodes as ML/PP. The tree is rooted in *Periconia digitata* (CBS 510.77), *P. pseudodigitata* (CBS 139699), *P. macrospinoa* (CBS 135663), and *P. byssoides* (H 4600). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.03 which represent the estimated number of nucleotide substitutions of site per branch.


**Figure 24** – *Helminthosporium lignicolum* (holotype MFLU 22-0155). a, b Colonies on nature substrate. c–f Conidiophores with conidiogenous cells and conidia. g Conidiogenous cells with developmental conidia. h–l Conidiogenous cells with immature conidia. m–q Conidia. r Germinated conidium. s Culture on PDA. Scale bars: c–f = 100 µm, h–r = 20 µm.

***Helminthosporium shangrilaense*** Y.Y. Yang & K.D. Hyde, sp. nov. Fig. 25

MycoBank number: MB847560; Facesoffungi number: FoF13251

Etymology – Referring to the collecting site "Shangri-La City, Yunnan Province" where the holotype was collected.

Holotype – HKAS 125896

*Saprobic* on the dead stem of an unidentified plant. Sexual morph: Undetermined. Asexual morph: Colonies on the substratum superficial, effuse, dark brown to black, hairy. Mycelium mostly immersed and composed of dark brown hyphae. *Conidiophores* 661–898 × 15–25 µm ($\bar{x}$ = 730 × 21, n = 10), mononematous, erect, straight or flexuous, multiseptate, unbranched, subcylindrical, smooth, thick-walled, light brown to dark brown, gradually paler from the base to the apex, arising solitarily or in fascicles from the stroma cells. *Conidiogenous cell* monotretic, terminal, cylindrical, septa, brown, hyaline when immature, rhexolytic, percurrent, giving rise to conspicuous scars on conidiophores. *Conidia* 52–96 × 15–23 µm ($\bar{x}$ = 78 × 19, n = 30), solitary, obclavate with oval base and with ellipsoidal lumina, flexuous, smooth, light brown to brown, 8–12-distoseptate, guttulate, with a blackish-brown, 4–6 µm wide ($\bar{x}$ = 5, n = 30), scar at the base and a hyaline distal end.

*Culture characters*: Culture was established from germinating conidium. Germ tubes were produced from both ends or middle of the conidium. The colony was slowly grown on PDA media, reaching 2.5 cm after incubation for 23 days at room temperature (±23 ℃), light yellow at center, ashen at periphery, nearly circular, plicate, velvety, with growth rings and radially striated, reverse dark gray, with a yellow margin.

**Table 2** Morphological synopsis of *Helminthosporium shangrilaense* with other similar species in this study.

| **Taxa** | **Strain no.** | **Conidiophore** | | **Conidiogenous cells** | **Conidia** | | **References** |
|---|---|---|---|---|---|---|---|
| | | **Shape** | **Size (µm)** | **Shape** | **Shape** | **Size (µm)** | |
| *H. chinense* | CGMCC 3.23570 | solitarily or in fascicles, with well-defined small pores at the apex, no scars | 214–461 × 8–16 | mono- to poly-tretic, terminal and intercalary, secession schizo-lytic. | non-guttulate, obclavate with subcylindrical base, angular lumina, 4–10-distoseptate | 42–109 × 5–11 | Chen et al. (2022) |
| *H. nanjingense* | HHAUF 020380 | solitary or in fascicles, with well-defined small pores at the apex and laterally beneath the upper 1–4 septa, no scar | 250–470 × 8.6–11 | unknown record | non-guttulate, subulate or nearly whip-like, 6–17-distoseptate | 65–170 × 7–10 | Wang et al. (2014) |
| *H. shangrilaense* | HKAS 125896 | mononematous, scars | 661–898 × 15–25 | monotretic, terminal, hyaline when young, rhexolytic, percurrent | guttulate, obclavate with oval base and with ellipsoidal lumina, 8–12-distoseptate | 52–96 × 15–23 | In this study |


**Figure 25** – *Helminthosporium shangrilaense* (holotype HKAS 125896). a Natural substrate. b, c Colonies on the substrate. d, e Conidiophores with conidiogenous cells and conidia. f, i Conidiophores with conidiogenous cells. g, h Conidiogenous cells with developmental conidia with scars at red arrow pointed. j–m Conidia. n Germinated conidium. o, p Culture on PDA after 23 days. Scale bars: d–f = 200 μm, h–i, n = 50 μm, g, j–m =20 μm.

Material examined – China, Yunnan Province, Shangri-La City, Gezan Village, on a dead stem of an unidentified plant, altitude: 3271.67m, 19 June 2022, Y.Y. Yang, YYY274 (holotype HKAS 125896, ex-type living culture KUNCC22-12540).

GenBank numbers – LSU: OP767126, ITS: OP767128, SSU: OP767127, *ef1α*: OQ186449

Notes – Phylogenetic analyses of combined SSU, LSU, *rpb2*, *ef1α* and ITS sequence data showed that the species *Helminthosporium shangrilaense* (HKAS 125896) formed a sister clade with *H. chinense* (CGMCC3.23570) and *H. nanjingense* (HHAUF 020380) although lack of well support (Fig. 23). Morphologically (Table 2), *H. shangrilaense* differs from *H. chinense* in having longer conidiophores (661–898 × 15–25 μm) with conspicuous scars, rhexolytic, percurrent conidiogenous cells and guttulate conidia (52–96 × 15–23 μm), obclavate and oval at the lower part and 8–12-distoseptate. However, *H. chinense* has shorter conidiophores (214–461 × 8–16 μm) without scars, schizolytic conidiogenous cells, producing aguttulate conidia (42–109 × 5–11 μm) with a subcylindrical base, with angular lumina and 4–10 distosepta (Chen et al. 2022). *H. nanjingense* can be distinguished from *H. shangrilaense* by having larger conidiophores (661–898 × 15–25 μm *vs* 250–470 × 8.6–11 μm) without scars, lateral to terminal, schizolytic, polytretic conidiogenous cells, with subulate or nearly whip-like conidia (64.5–170.5 × 7.3–10.3 μm) and 6–17 distosepta (Wang et al. 2014). Therefore, we introduce our isolate as a new species of *Helminthosporium* based on morphological observation and phylogenetic evidence.

***Kirschsteiniothelia*** D. Hawksw., Botanical Journal of the Linnean Society 91: 182 (1985)

*Kirschsteiniothelia* (*Kir.*) introduced by Hawksworth (1985) was typified by *Kir. aethiops*. Thirty-three *Kirschsteiniothelia* epithets are listed in Index Fungorum (2023). *Kirschsteiniothelia* is widespread in tropical regions and commonly occurs on dead wood (Mehrabi et al. 2017). The sexual morph of *Kirschsleiniothelia* is characterized by brown or black, globose to subglobose ascomata with or without central papilla, a thick-walled peridium, filiform and hyaline pseudoparaphyses, cylindrical-clavate with 8-spored asci and ellipsoidal, brown to dark brown ascospores (Hawksworth 1985, Boonmee et al. 2012, Hyde et al. 2013, Mehrabi et al. 2017). Boonmee et al. (2012) found that the type species of *Kirschsteiniothelia* (*Kir. aethiops*) grouped with the type species of *Dendryphiopsis* (*D. atra*) in their phylogenetic analyses, and this shows that *Dendryphiopsis* represents the asexual morph of *Kirschsteiniothelia*. The connection was confirmed by Hawksworth (1985), and accepted by Boonmee et al. (2012), Hyde et al. (2013) and Wijayawardene et al. (2014). In this study, we introduced one new species of *Kirschsteiniothelia*, and this is the first report of *Kirschsteiniothelia* from coffee.

***Kirschsteiniothelia puerensis*** L. Lu & Tibpromma, sp. nov. Fig. 27

MycoBank number: MB559884; Facesoffungi number: FoF12893

Etymology – Refering to the host location, "Pu'er" City, where the holotype was collected.

Holotype – ZHKU 22-0142

*Saprobic* on decaying coffee wood. Sexual morph: Undetermined. Asexual morph: *Colonies* scattered on coffee wood, hairy, solitary or clustered, black, conspicuous on surface. *Mycelium* exposed on the surface of the substrate except for the roots. *Conidiophores* 100–250 × 5–12 μm, ($\overline{x}$ = 148.5 × 9 μm, n = 20), macronematous, mononematous, solitary or caespitose, cylindrical, straight or slightly flexuous, smooth, dark brown, unbranched, slightly swollen at the base, 7–15 septate. *Conidiogenous cells* 15–25 × 5–10 μm, ($\overline{x}$ = 19 × 8 μm, n = 20) monoblastic, dark brown to black, terminal and smooth. *Conidia* 60–140 × 5–20 μm ($\overline{x}$ = 98 × 14 μm, n = 20), acrogenous, solitary, obclavate, 5–12 septate, invagination in the septate, hyaline when immature and become pale-brown to brown, straight or curved, pale-brown at the apex, truncate at base, tapering towards apex, sometimes has long stipes up to 73 μm, some with a hyaline sheath around the tip (some two globose sheaths).

Culture characteristics – Conidia germinated within 12 hours on PDA. Colonies on PDA reaching 40 mm diam, after two months at room temperature (22 ℃). Circular, dark green, with aerial mycelium, dense and fluffy on the surface, sparse on the edge, black in reverse.

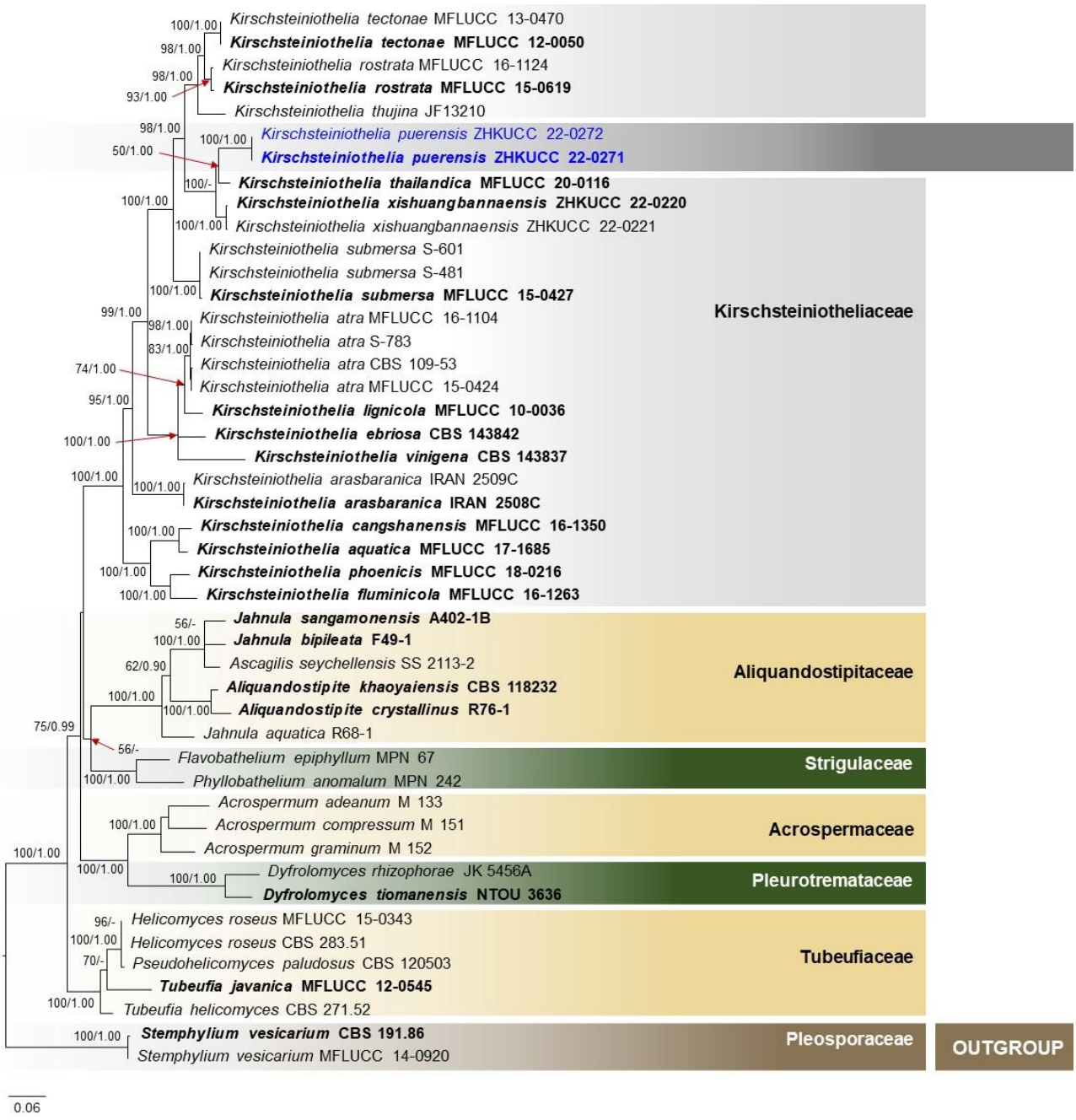


**Figure 26** – Phylogenetic tree obtained from maximum likelihood analyses of a combined ITS, LSU and SSU sequence dataset, representing the species of *Kirschsteiniothelia*. Related sequences were obtained from Bao et al. (2018). Fourty-six strains were included in the combined analyses, which comprised 2406 characters (SSU: 1–1055, LSU: 1056–1954, ITS: 1955–2406) after alignment. Bootstrap support values for ML equal to or greater than 50% and PP equal to greater than 0.90 are indicated at the nodes as ML/PP. *Stemphylium vesicarium* (CBS191.86, MFLUCC 14-0920) were used as the outgroup taxa. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.06 which represent the estimated number of nucleotide substitutions of site per branch.

Material examined – China, Pu'er, Yunnan Province, on a dead wood of *Coffea* sp. (Rubiaceae), 23 December 2020, L. Lu, MJ-C3 (holotype ZHKU 22-0142, ex-type living culture ZHKUCC 22-0271 = ZHKUCC 21-0272).

GenBank numbers – ZHKUCC 22-0271 = ITS: OP450977, LSU: OP451017, SSU: OP451020; ZHKUCC 22-0272 = ITS: OP450978, LSU: OP451018, SSU: OP451021

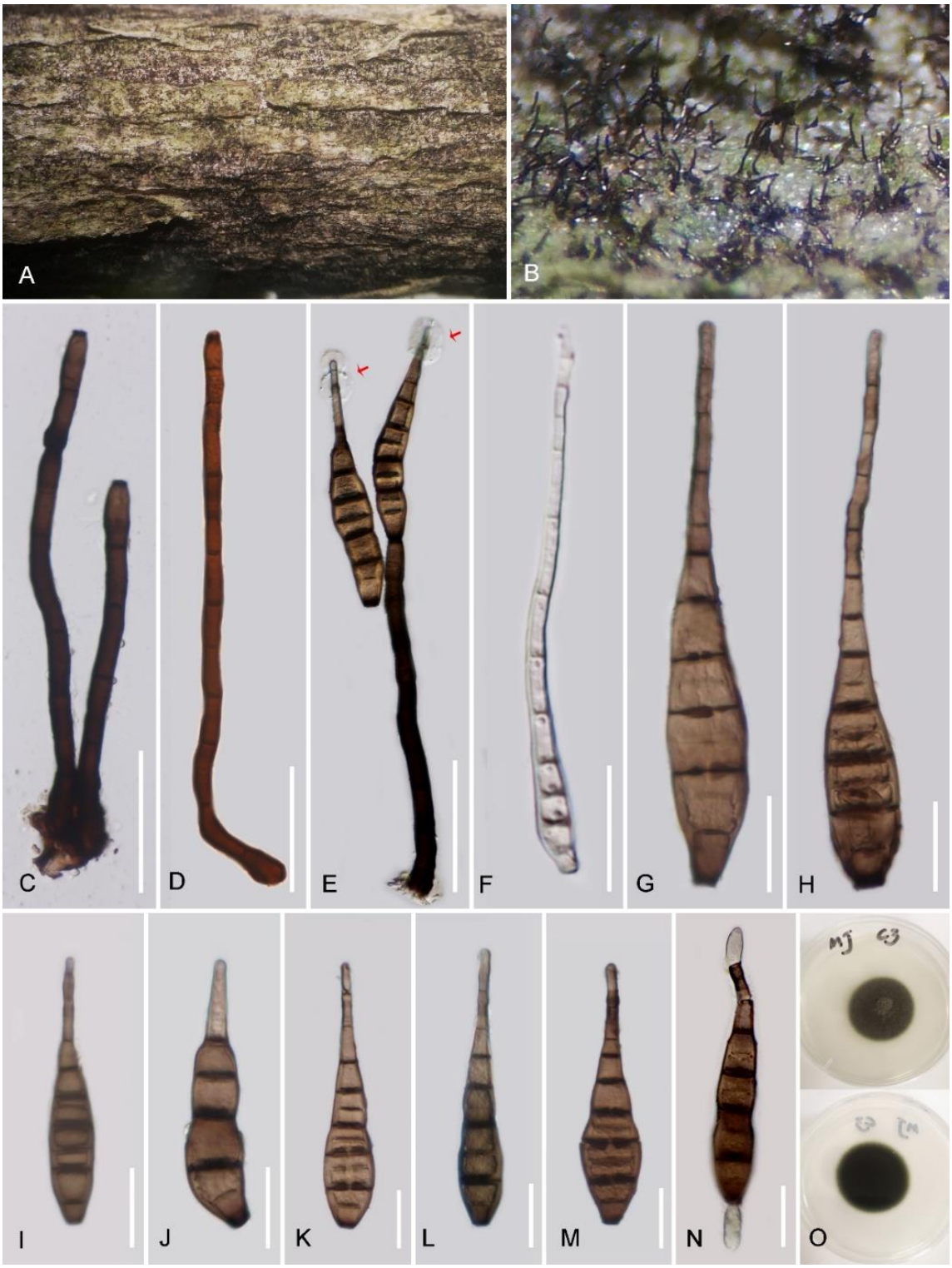


**Figure 27** – *Kirschsteiniothelia puerensis* (holotype ZHKU 22-0142). a, b Colonies on the host. c, d Conidiophore. e Conidiophore with conidia and sheaths (red arrows indicate mucilaginous sheaths). f–m Conidia. n Germinated conidium. o Culture on PDA from above and reverse. Scale bars: c–e = 50 μm, f–n = 20 μm.

Notes – In the phylogenetic tree, *Kirschsteiniothelia puerensis* formed a well-separated clade sister to *Kir. thailandica* (MFLUCC 20-0116) with 50% ML/1.00 PP support (Fig. 26), while both taxa are sister to *Kir. xishuangbannaensis* (ZHKUCC 22-0220) with 100% ML bootstrap support. Based on the blast results, ITS and SSU gene sequences showed 90% and 98% similarities to *Kir. thailandica* (MT985633) and (MT984280) respectively. The LSU sequence showed 93.5%

similarity to *Kir. rostrata* (NG 059790). In morphology, *Kir. puerensis* also has similar morphological features to *Kir. rostrata*, *Kir. thailandica* and *Kir. xishuangbannaensis* (Hyde et al. 2017, Sun et al. 2021, Xu et al. 2023). However, *Kir. puerensis* conidiophores (100–250 × 5–12 μm, 7–12 septate) are longer than *Kir. thailandica* (55–93 × 7–10 μm), but shorter than *Kir. rostrata* (190–450 × 9–15 μm, 7–24 septate). In addition, conidia of *Kir. puerensis* are 5–12 septate, while in *Kir. thailandica* they are 6–8-septate, 8–13-septate in *Kir. rostrata*, and 3–8-septate in *Kir. xishuangbanaensis* (Hyde et al. 2017, Sun et al. 2021, Xu et al. 2023). Hence, based on both morphology and phylogeny, we introduce *Kir. puerensis* as a new species.

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

*Melomastia* was established by Saccardo (1875) to accommodate the type species *Melomastia mastoidea* (= *Melomastia friesii*) collected from *Viburnum opulus* (Adoxaceae) in Germany. The taxonomic placement of *Melomastia* has been widely debated (Lumbsch & Huhndorf 2010, Maharachchikumbura et al. 2015, 2016), and was finally verified in Pleurotremataceae by Norphanphoun et al. (2017). According to the latest treatment of Li et al. (2022) with 20 accepted species of *Melomastia*, we describe a novel species of *M. septata* that is assigned to Pleurotremataceae based on the evidence of phylogenetic analysis and morphological features.

***Melomastia septata*** J.Y. Zhang, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 29

MycoBank number: MB900040; Facesoffungi number: FoF13253

Etymology – Refers to the septate ascospores.

Holotype – MFLU 22-0233

*Saprobic* on terrestrial dead branch of an undetermined host. Sexual morph: *Ascomata* 166–344 μm high × 198–434 diameter ($\bar{x}$ = 269 × 281 μm, n = 9), immersed, only ostioles visible at the surface of host, solitary, scattered, globose to subglobose, dark brown. *Ostioles* central, black, papillate. *Hamathecium* composed of long, 3–3.5 μm wide, cellular pseudoparaphyses, septate, unbranched, not anastomosing, dense, filiform, hyaline. *Peridium* comprising 2–3 layers, 8–16 μm wide, thin-walled, composed of dark brown cells of *textura angularis*, mixed with host tissues. *Asci* 85–96 × 5–7.5 μm ($\bar{x}$ = 90 × 6.3 μm, n = 18), 8-spored, bitunicate, cylindrical, sessile to subsessile, thin-walled, apically round. *Ascospores* 12–16 × 3.5–4.5 μm ($\bar{x}$ = 14.5 × 4 μm, n = 25), uniseriate or biseriate, partly overlapping, oblong or narrowly fusiform, hyaline, 3-celled, 2-septate, slightly constricted at the septa, smooth-walled, guttulate, thick-walled with a mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on WA within 12 hours at room temperature (25–28 °C). The hyaline germ tube germinates from the ends of the ascospores. Colonies growing on PDA, slowly growth, reaching 11 mm diam. after 20 days at 25 °C, flat, velvety, circular margin with a smooth surface, yellowish white from above; blond to creamy-yellow mycelium in reverse from enter to margin, and not producing pigmentation in culture.

Material examined – Thailand, Chiang Rai Province, Mae Fah Luang University, on a dead branch on the land, 14 June 2019, J.Y. Zhang, Y50 (holotype MFLU 22-0233, ex-type living culture MFLUCC 22-0112).

GenBank numbers – LSU: OP749870, ITS: OP749883, *ef1α*: OP760198

Notes – In a BLASTn search of NCBI GenBank, the closest match of the LSU sequence of *Melomastia septata* was *M. italica* (MFLUCC 15-0160) with 99.02% similarity, while the closest match of the *ef1α* sequence with 93.23% similarity was *M. clematidis* (MFLUCC 17-2092, MT394663). In our multigene phylogenetic tree, *M. septata* formed a distinct clade, which shares a sister relationship to *M. italica* with a 94% ML/1.00 PP support (Fig. 28). Morphologically, *M. septata* is most similar to *M. sichuanensis* (HKAS 121313) in the shapes of asci and ascospores with a thin sheath (Li et al. 2022). However, *M. septata* differs from *M. sichuanensis* by its smaller ascomata (166–344 × 198–434 μm *vs* 419.5–506 × 335–577 μm), shorter asci (85–96 μm *vs* 101–112.5 μm), and smaller ascospores (12–16 × 3.5–4.5 μm *vs* 15–17.5 × 4.7–5.1 μm).

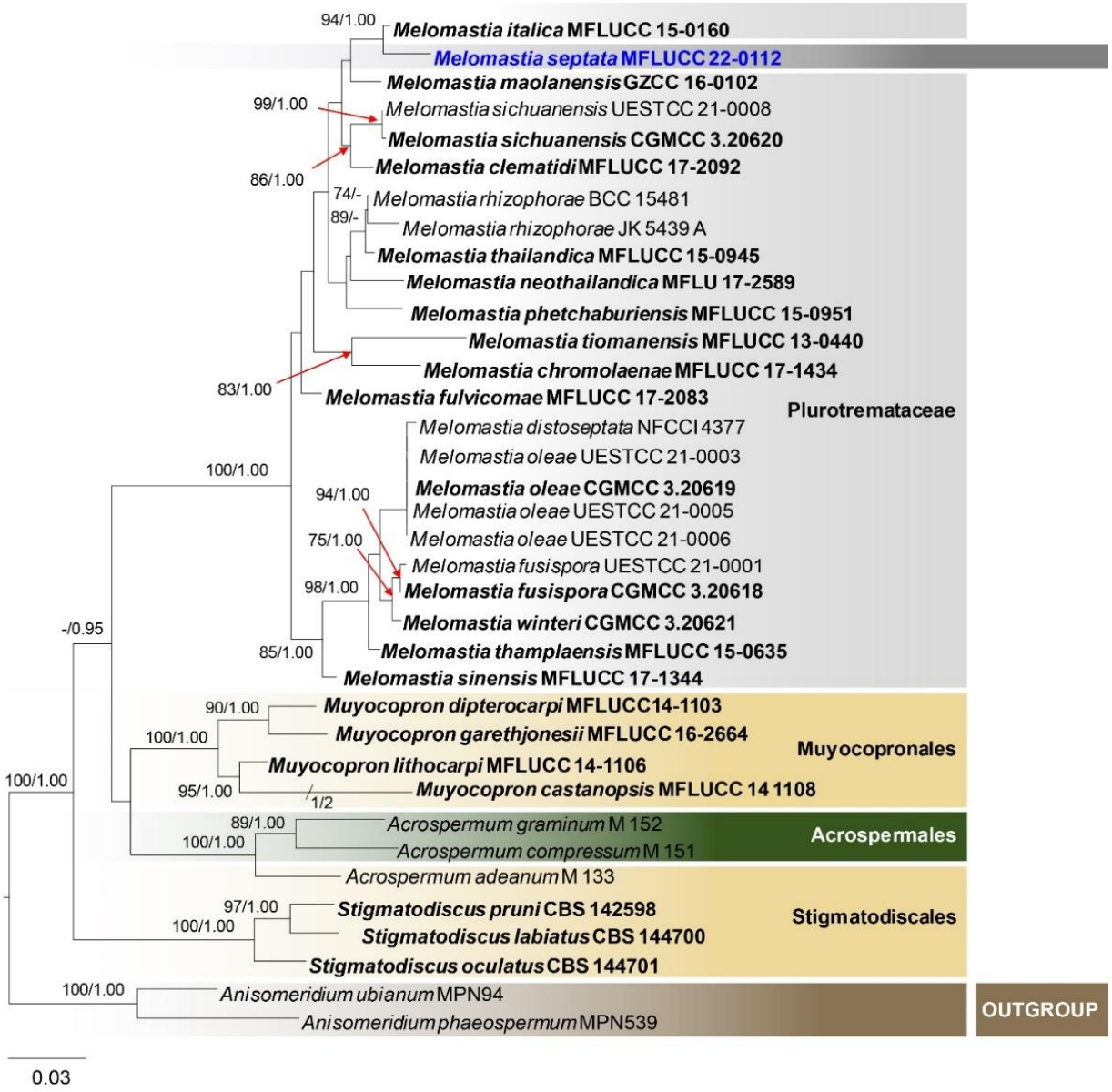


**Figure 28** – Phylogenetic tree obtained from maximum likelihood analyses of a combined LSU, ITS and *ef1α* sequence dataset representing the species in Pleurotremataceae. Thirty-six strains were included in the combined analyses, which comprised 2726 characters (LSU: 1–874, SSU: 875–1891, *ef1α*: 1892–2726) after alignment. Bootstrap support values for ML equal to or greater than 70% and PP equal to greater than 0.95 are indicated at the nodes as ML/PP. The tree is rooted with *Anisomeridium phaeospermum* MPN539 and *A. ubianum* MPN94. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.03 which represent the estimated number of nucleotide substitutions of site per branch.

***Montagnula*** Berl., Icon. fung. (Abellini) 2(2–3): 68 (1896)

*Montagnula* was introduced by Berlese (1896), with *Mo. infernalis* as the type species. According to Barr (2001), *Montagnula* was placed in Montagnulaceae based on morphological characteristics. Later, *Montagnula* was transferred from Montagnulaceae to Didymosphaeriaceae by Ariyawansa et al. (2014). Subsequently, Wanasinghe et al. (2016) transferred two species of *Munkovalsaria* (*Mo. appendiculata* and *Mo. donacina*) to *Montagnula* based on phylogenetic analyses. Recently, two new species *Mo. aquatica* and *Mo. guiyangensis* have been introduced into *Montagnula*, and four species *viz. Mo. chromolaenicola*, *Mo. puerensis*, *Mo. saikhuensis*, and *Mo. thailandica* have been synonymized under *Mo. donacina* based on morphological examination and molecular data (Sun et al. 2023). *Montagnula* has 47 records in Species Fungorum (2023).

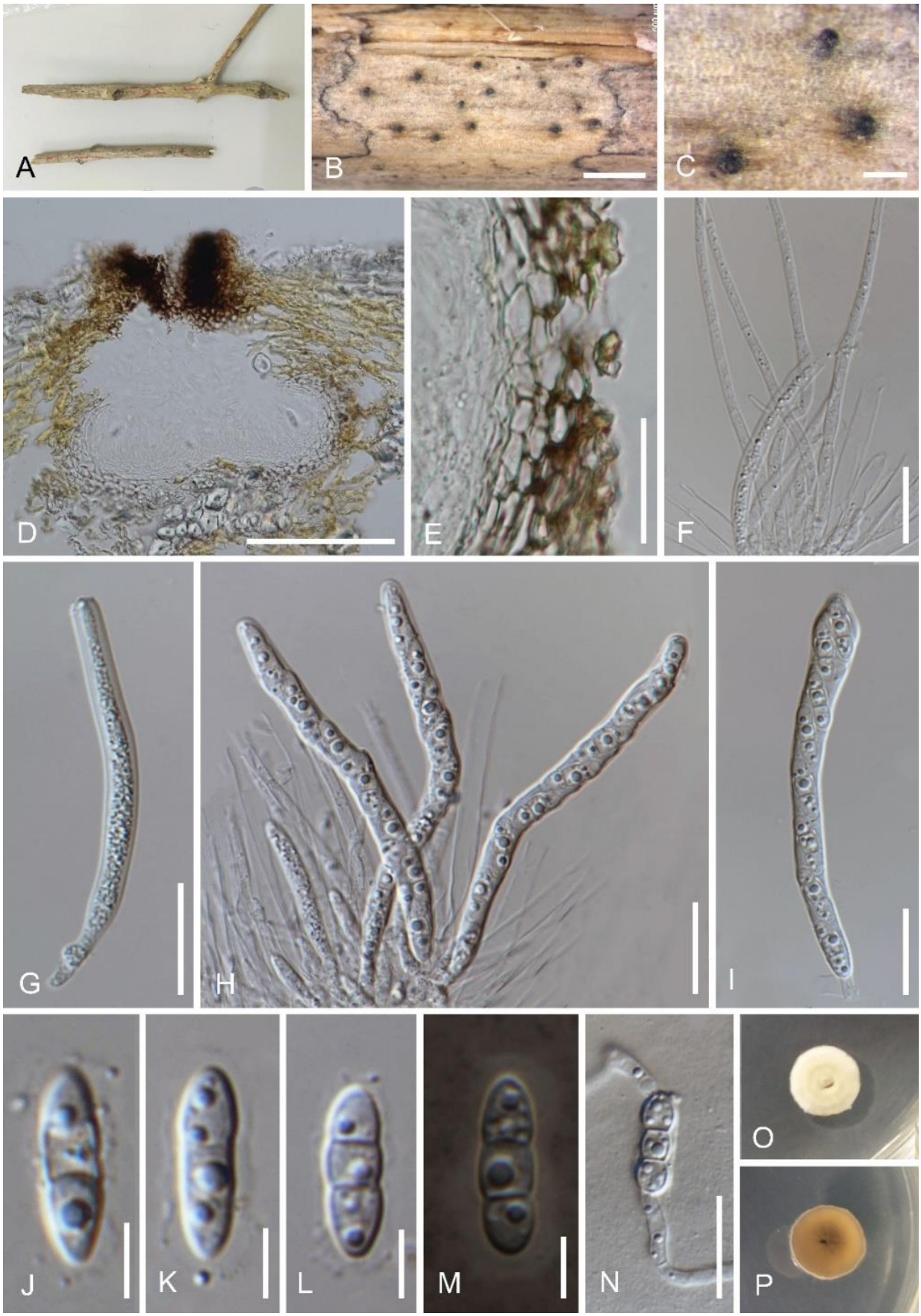


**Figure 29** – *Melomastia septata* (holotype MFLU MFLU 22-0233). a–c Immersed ascomata on host. d Section through an ascoma. e Peridium. f Hamathecium. g–i Asci. j–m Ascospores. n Germinating ascospore. o–p Colony on PDA from above and below. Scale bars: b = 1000 µm, c = 200 µm, d = 100 µm, e–i, n = 20 µm, j–m = 5 µm.

Species of genus *Montagnula* (*Mo.*) are characterized by immersed to erumpent, gregarious or grouped, globose or spherical, black ascomata, mostly cylindric-clavate to clavate asci with long pedicels, and straight or slightly curved, and fusoid or ellipsoid ascospores (Barr 1990, Ariyawansa et al. 2014, Tennakoon et al. 2016, Tibpromma et al. 2018, Hongsanan et al. 2020). *Montagnula* plays a vital role as saprobes on a wide range of hosts in various countries (Ariyawansa et al. 2014, Du et al. 2021). In this study, a new *Montagnula* species is introduced, based on morphology and molecular data.

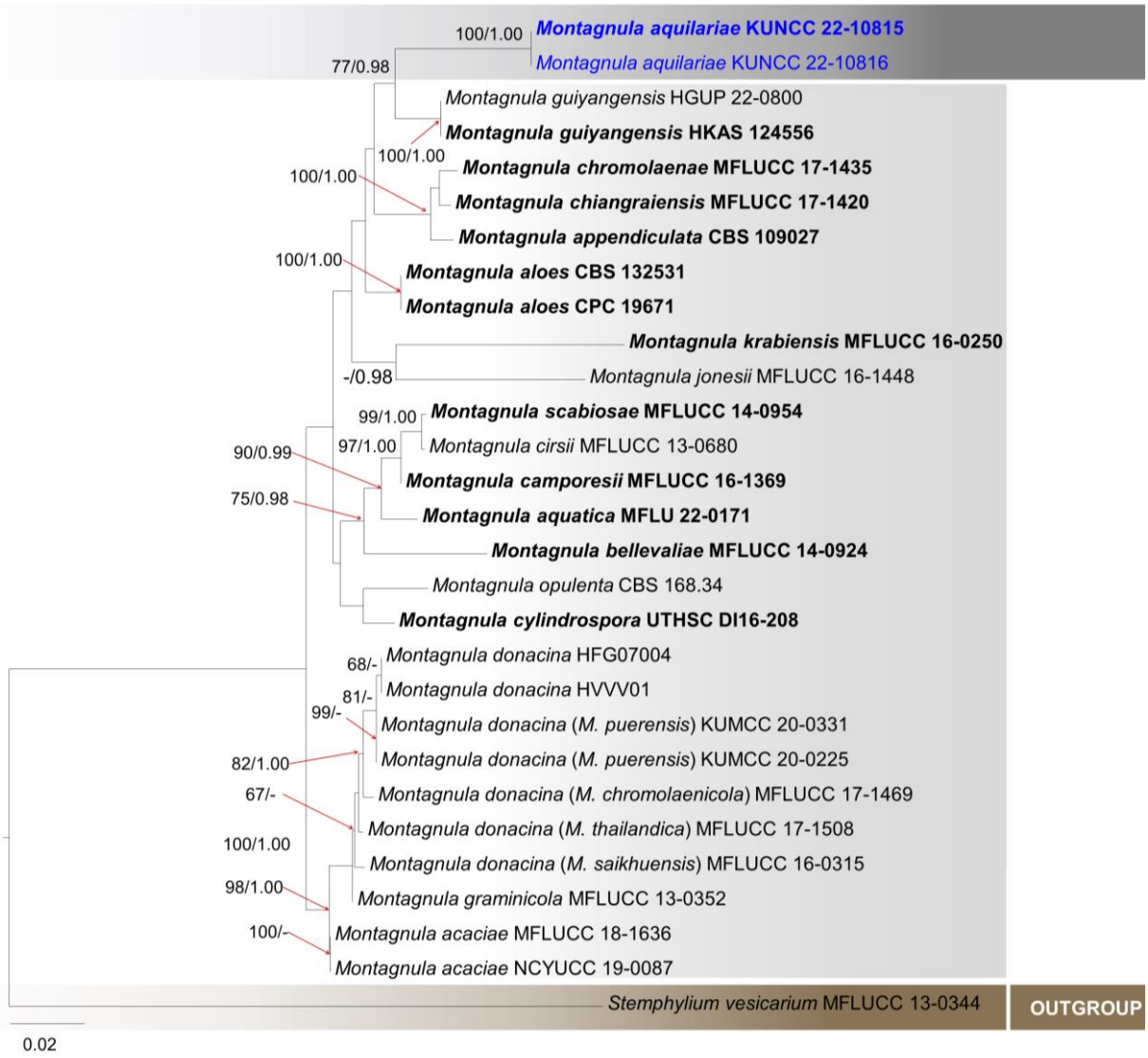


**Figure 30** – Phylogenetic tree generated from maximum likelihood analyses of a combined ITS, LSU, SSU, and *ef1α* sequence dataset representing the species of *Montagnula*. Twenty-nine strains were included in the combined analyses, which comprised 3471 characters (ITS: 1–570, LSU: 571–1490, SSU: 1491–2544, *ef1α*: 2545–3471) after alignment. Bootstrap support values for ML equal to or greater than 60% and PP equal to greater than 0.95 are indicated at the nodes as ML/PP. *Stemphylium vesicarium* (MFLUCC 13-0344) was used as the outgroup taxon. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.02 which represent the estimated number of nucleotide substitutions of site per branch.

***Montagnula aquilariae*** T.Y. Du & Tibpromma, sp. nov. Fig. 31

MycoBank number: MB846332; Facesoffungi number: FoF12850

Etymology – Named after the host genus *Aquilaria* from which the holotype was collected.

Holotype – HKAS 124186


**Figure 31** – *Montagnula aquilariae* (holotype HKAS 124186). a, b Appearance of ascomata on the host. c Section of an ostiole. d Section of an ascoma. e–g Asci. h Ascus stained by Melzer's reagent. i–n Ascospores. o Pseudoparaphyses. p Peridium. q Ascospore stained by Indian ink. r A germinating ascospore. s, t Colonies on PDA medium (after one week in culture). Scale bars: c = 100 μm, d = 200 μm, e–h = 50 μm, i–o = 10 μm, p = 20 μm, q = 10 μm, r = 20 μm.

*Saprobic* on dead twigs of *Aquilaria sinensis*. Sexual morph *Ascomata* 300–450 × 300–420 μm ($\bar{x}$ = 380 × 361 μm, n = 5), immersed, solitary to gregarious, mostly gregarious, subglobose to globose, black, with a long ostiole. *Ostiole* 100–180 × 60–160 μm ($\bar{x}$ = 147 × 117 μm, n = 5), central, straight, dark brown to black, without periphysate. *Peridium* 20–60 μm wide, fused with host tissues, thick-walled, pale brown to dark brown cells of *textura angularis*. *Hamathecium* comprising 1.5–2 μm wide, numerous filamentous, branched, septate, guttulate, trabeculate pseudoparaphyses. *Asci* 45–75(–88) × (13–)15–20 μm ($\bar{x}$ = 60 × 18 μm, n = 30) (spore-bearing part), bitunicate, 8-spored, elongate-clavate, slightly curved, with a furcate, 45–70 μm long pedicel. *Ascospores* 17–20 × 7–10 μm ($\bar{x}$ = 19 × 8 μm, n = 30), uni-to bi-seriate, fusoid or ellipsoid, straight or slightly curved, 1-septate, slightly or strongly constricted at the septum, widest at the centre, tapering towards ends, hyaline to yellow when immature, become brown to dark brown when mature, turns reddish-brown in Melzer's reagent, guttulate, with a thin mucilaginous sheath. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 h at 28 ℃, germ tubes produced from both upper and lower cells. Colonies on PDA reaching 6 cm diam., after one week at 28 ℃, mycelium white, flossy, circular with the entire edge, with filiform margin; white in reverse.

Material examined – China, Yunnan Province, Xishuangbanna, on dead twigs of *Aquilaria sinensis* (Thymelaeaceae), 13 September 2021, T.Y. Du, YNA25 (holotype HKAS 124186, ex-type living cultures KUNCC 22-10815 = KUNCC 22-10816).

GenBank numbers – KUNCC 22-10815 = LSU: OP482265, ITS: OP554219, SSU: OP482268, *ef1α*: OP426318; KUNCC 22-10816 = LSU: OP482266, ITS: OP452927, SSU: OP482269, *ef1α*: OP426319

Notes – In the NCBI BLASTn search, the ITS sequences of *Montagnula aquilariae* matched with *Mo. opulenta* (MW187736) in 98.39% similarity; the LSU sequences of *Mo. aquilariae* matched with *Mo. aloes* (NG_042676) in 97.55% similarity; the SSU sequences of *Mo. aquilariae* matched with *Mo. thailandica* (OL780525) in 96.61% similarity; and the *ef1α* sequences of *Mo. aquilariae* matched with *Mo. thailandica* (MT235774) in 96.94% similarity.

In the phylogenetic analyses, *Mo. aquilariae* forms a sister branch with *Mo. guiyangensis* (HGUP 22-0800, HKAS 124556) with moderate statistical support (Fig. 30). However, they differ in morphological characteristics i.e., ascospores of *Mo. aquilariae* with a thin mucilaginous sheath, not form polar appendages; while ascospores of *Mo. guiyangensis* with sheath drawn out to form polar appendages, from both ends of the ascospores. In morphology, *Mo. aquilariae* resembles *Mo. opulenta* in having immersed ascomata, branched and septate pseudoparaphyses, and ascospores with a mucilaginous sheath. However, they are different because *Mo. aquilariae* has trabeculate pseudoparaphyses (sensu Liew et al. 2000), and ascospores uni or bi-seriate, slightly or strongly constricted at the septum, while *Mo. opulenta* has cellular pseudoparaphyses, ascospores bi-seriate, and strongly constricted at the septum (Aptroot 1995b, Wang 2000). In addition, the ascomata in *Mo. aquilariae* are smaller than those of *Mo. opulenta* (300–450 μm *vs* 400–1200 μm) (Aptroot 1995b). Therefore, based on phylogenetic analyses and morphological characteristics, *Mo. aquilariae* is introduced as a new species from China.

***Neophaeosphaeriopsis*** H.D. Yang & K.D. Hyde, gen. nov.

MycoBank number: MB846367; Facesoffungi number: FoF13380

Etymology – Morphologically resembling the genus *Phaeosphaeriopsis*.

*Ascomata* scattered, solitary, semi-immersed, globose to subglobose, psedoparenchymatous, ostiole penetrates through the host surface. *Asci* bitunicate, fissitunicate, cylindrical to cylindric-clavate, with a well-developed ocular chamber. *Ascospores* septate, guttulate. *Conidiomata*, pycnidial. *Conidiophores* septate, branched, flexuous, torulose, smooth-walled. *Conidiogenous cells* are inflated, smooth-walled, ampulliform, subcylindrical, producing conidium at the apex. *Conidia are* cylindrical to oblong, guttulate, aseptate, smooth-walled. *Mycelium* on medium smooth walled, branched, guttulate.

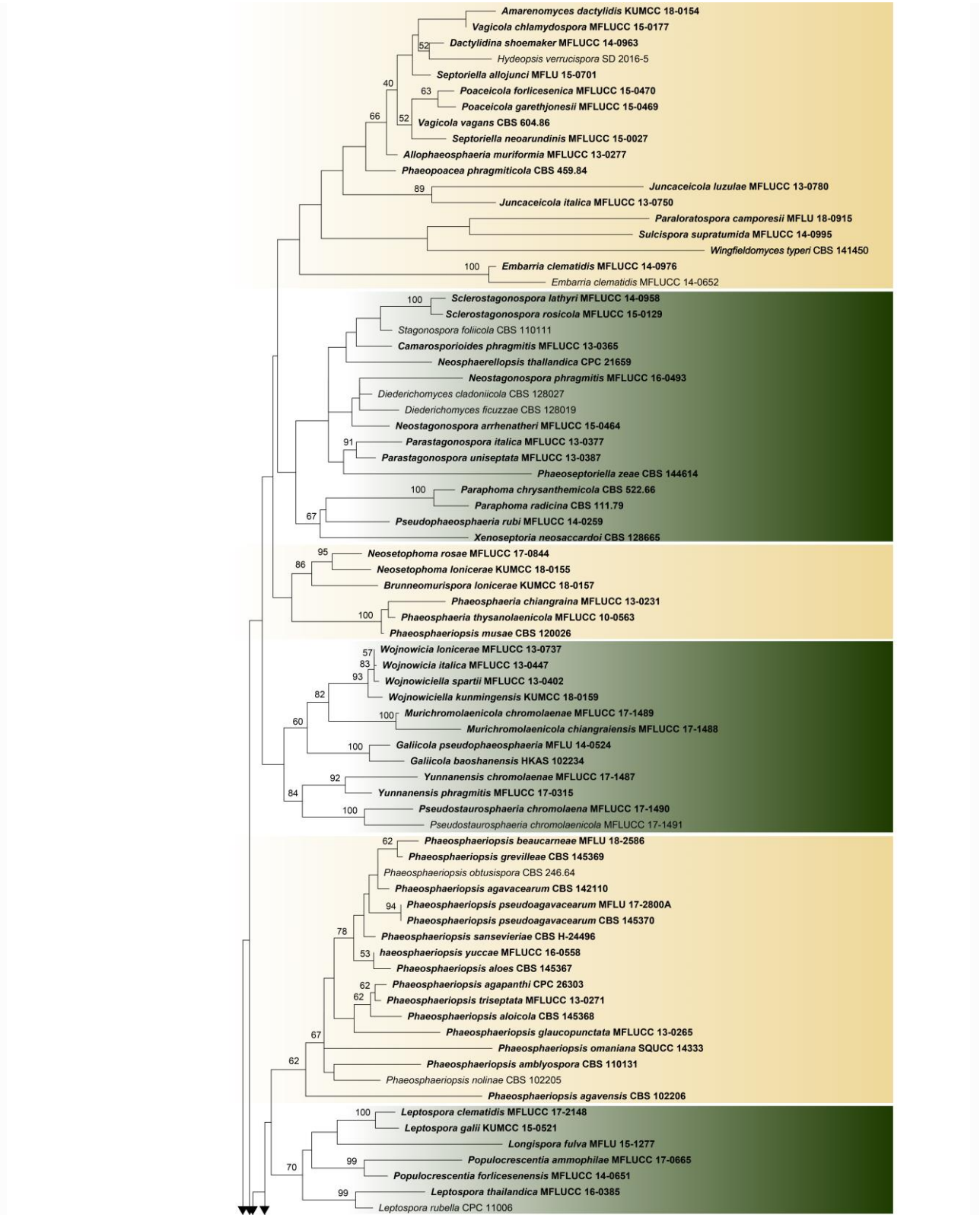


**Figure 32** – Phylogenetic tree inferred from maximum likelihood analyses of a combined *EF1-α*, LSU, ITS and SSU sequence dataset representing the species in Phaeosphaeriaceae. 125 strains were included in the combined analyses, which comprised 3050 characters (ITS: 1–401, SSU: 402–1343, LSU: 1344–2181, *ef1α*: 2182–3050) after alignment. Bootstrap support values for ML equal to or greater than 50% are indicated at the nodes. The tree is rooted to *Pyrenophora bromi*, *Pyrenophora triticilinerepentis*, *Stemphylium botryosum*, *Stemphylium vesicarium* and *Edenia gomezpompae*. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.01 estimated number of nucleotide substitutions per site per branch.

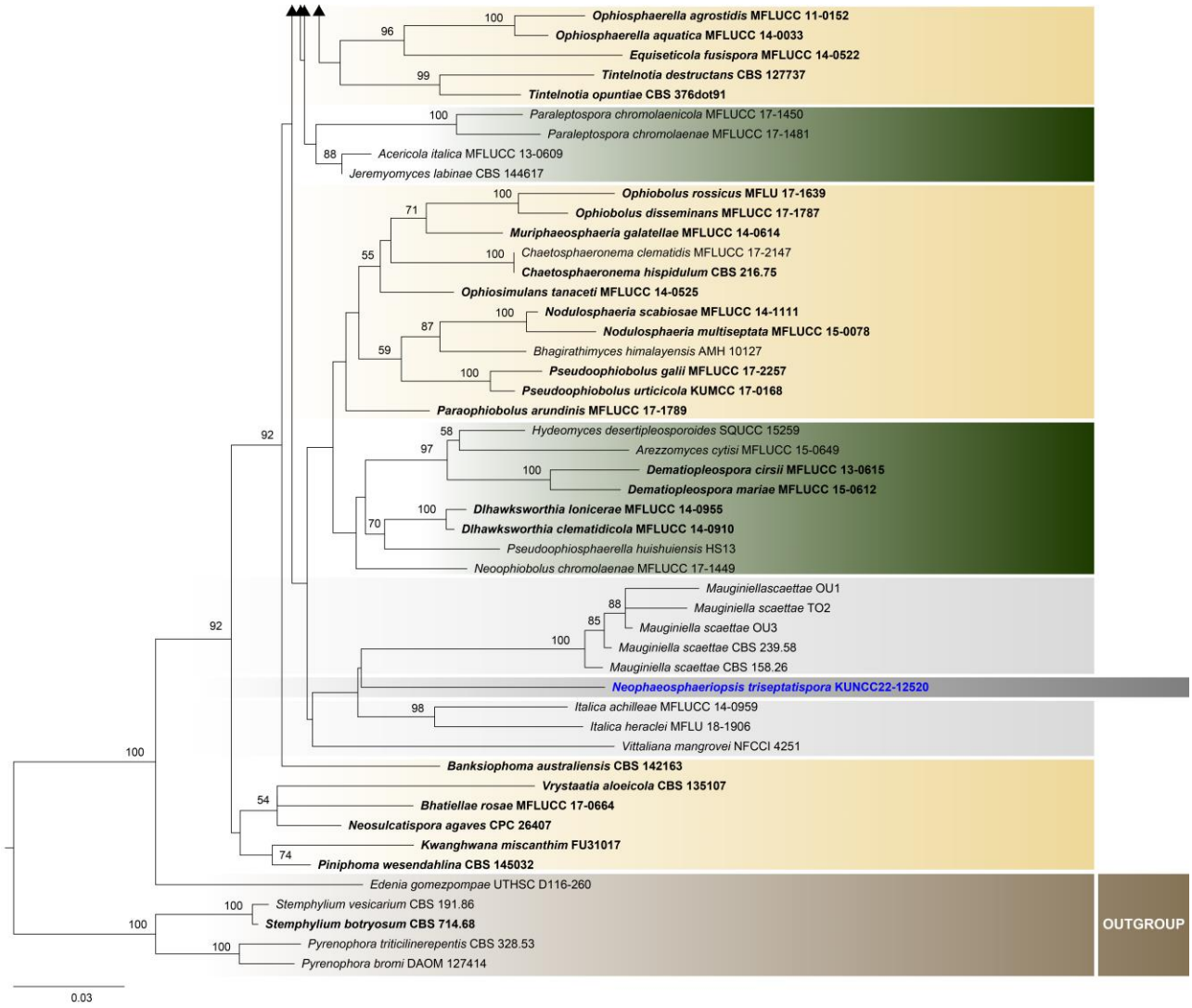


**Figure 32** – continued.

Type species – *Neophaeosphaeriopsis triseptatispora* H.D. Yang & K.D. Hyde

Notes – *Neophaeosphaeriopsis* is typified by *Neo. triseptatispora* which was described with both sexual- and asexual morphs. It morphologically resembles *Phaeosphaeriopsis* (Al-jaradi et al. 2020, Tennakoon et al. 2020). However, phylogenetic analysis shows it separated from the *Phaeosphaeriopsis* lineage, and is close to *Mauginiella* (Fig. 32). *Mauginiella* is a monotypic genus containing only *M. scaettae* which is introduced solely with the asexual morph that produces arthroconidia by segmentation of the aerial hyphae and is different from *Neophaeosphaeriopsis* (Abdullah et al. 2005).

***Neophaeosphaeriopsis triseptatispora*** H.D. Yang & K.D. Hyde, sp. nov. Figs 33, 34

MycoBank number: MB846368, Facesoffungi number: FoF13381

Etymology – The epithet 'triseptatispora' refers to the 3-septate ascospores.

Holotype – HKAS 128404

*Saprobic* on dead twigs. Sexual morph: *Ascomata* 169–285 µm diam, 110–192 µm high, scattered, solitary, semi-immersed, slightly raised, dark brown to black, visible as black spots on host surface, uniloculate, globose to subglobose, pseudoparenchymatous, ostiole central, penetrating through the host surface. *Peridium* comprising 12.5–18.5 µm wide, composed of 2–4 layers of pseudoparenchymatous cells, arranged in *textura angularis*, the outer layers comprising 1–2 layers of brown to dark brown, thick-walled cells, the inner layer comprising 1–22 layers of hyaline to light brown, thin-walled cells. *Hamathecium* 2–4 µm wide, numerous, cellular, hyaline,-


**Figure 33 –** *Neophaeosphaeriopsis triseptatispora* (holotype, HKAS 128404). a–c Ascomata on host surface. d–e Section through ascomata. f–g Section through peridium. h–i Asci. j Asci with ocular chamber. k–m Asci with long pedicellate in Congo red. n–q Ascospores. r Germinating ascospores. Scale bars: d–e = 100 µm, f–g = 30 µm, h–i = 20 µm, j =10 µm, k–l = 50 µm, m = 20 µm, n–q = 10 µm, r = 20 µm.

-septate, rarely branching. *Asci* 55–80 × 12.5–16.5 µm ($\bar{x}$ = 71.2 × 14.7 µm, n = 25), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, long pedicellate, apically rounded, with a

well-developed ocular chamber. *Ascospores* 19–28.5 × 5.5–8.5 µm ($\bar{x}$ = 23.8 × 8.6 µm, n = 50), overlapping 3-seriate, phragmosporous, oblong to cylindrical, slightly curved, constricted at the septa, often enlarged at the third cell and present a diagonal septum, with basal and apical cells obtuse ends, light brown to brown, guttulate, verruculose, no observed mucilaginous sheath. Asexual morph: *Conidiomata* produced from PDA medium surface, pycnidial, globose to subglobose, solitary to gregarious, yellowish-brown to brown. *Conidiophores* up to 100 µm long, septate, branched, flexuous, torulose, hyaline. *Conidiogenous cells* up to 12 µm long, inflated, smooth-walled, ampulliform, subcylindrical, producing conidium at the apex. *Conidia* 8−13.5 × 4.5−7.5 µm ($\bar{x}$ = 11 × 6 µm, n = 25), cylindrical to oblong, guttulate, aseptate, with rounded ends, smooth, hyaline.

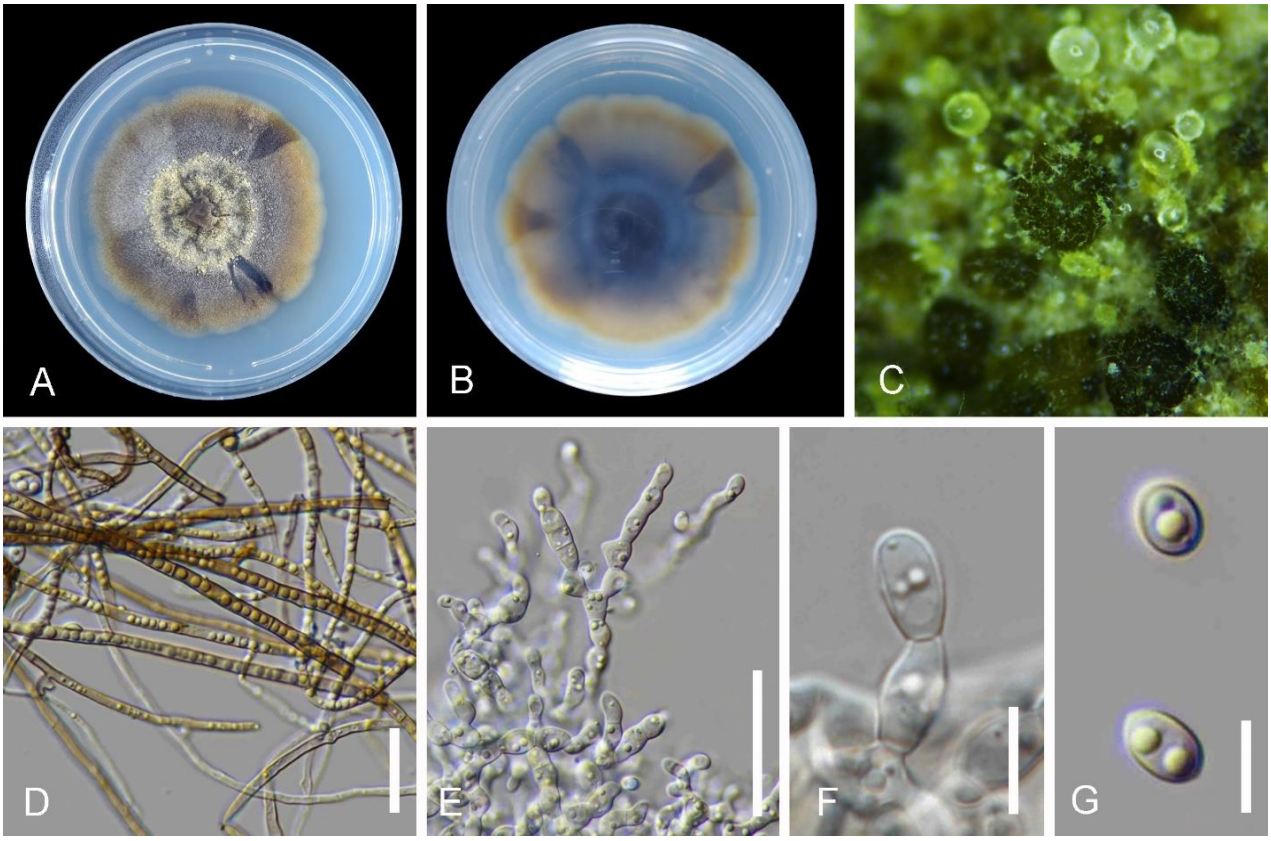


**Figure 34** – *Neophaeosphaeriopsis triseptatispora*. (Ex-type KUNCC22-12520). a–b Colony on PDA (front and reverse). c Pycnidia forming on PDA. d Mycelium. e Conidiophores. f Conidiogenous cells and conidium. g Conidia. Scale bars: d = 20 µm, e = 50 µm, f–g = 10 µm.

Culture characteristics – Colonies on PDA reaching 80–83 mm diam after two months at 25 °C, moderate aerial mycelium**,** slightly umbonate at the center, margin entire, regular, smoke grey to olivaceous grey, reverse olivaceous grey, sometimes present radially furrowed zones, mycelium hyaline to brown, smooth, slightly thicken walled, branched, guttulate.

Material examined – China, Yunnan Province, Kunming, on unidentified dead twigs, 8 December 2021, H.D. Yang (holotype YHD229, ex-type living culture KUNCC22-12520).

GenBank numbers – LSU: OP610061, ITS: OP610064, SSU: OP610063, *ef1α*: OP610595, RPB2: OP610597, HIS3: OP610596, ACT: OP610594

Notes – *Neophaeosphaeriopsis triseptatispora* is characterised by long pedicellate asci with an ocular chamber, septate, guttulate ascospores, torulose conidiophores and guttulate mycelium. In our phylogenetic analysis, *Neo. triseptatispora* is close to *Mauginiella*, although this is not well-supported (Fig. 32). However, *Mauginiella* is known as only producing arthroconidia by segmentation of the aerial hyphae and differs from *Neo. triseptatispora* which has well-developed conidiophores.

***Neoroussoella*** Jian K. Liu, Phook. & K.D. Hyde, Phytotaxa 181(1): 21 (2014)

Roussoellaceae was introduced by Liu et al. (2014) to accommodate *Neoroussoella*, *Roussoella* and *Roussoellopsis*. *Neoroussoella* was initially established to accommodate a single species, *N. bambusae* (Liu et al. 2014). Eleven species have been accepted in this genus and all were introduced by incorporating morphological and molecular data (Dai et al. 2022). These species commonly live as saprobes associated with decaying branches, stems and pods of dicotyledonous and monocotyledonous plants (Liu et al. 2014, Hyde et al. 2016, Jayasiri et al. 2019, Karunarathna et al. 2019, Phukhamsakda et al. 2020, Poli et al. 2020, Yuan et al. 2020). *Neoroussoella solani* was isolated from keratitis in human patients with keratomycosis (Mochizuki et al. 2017).

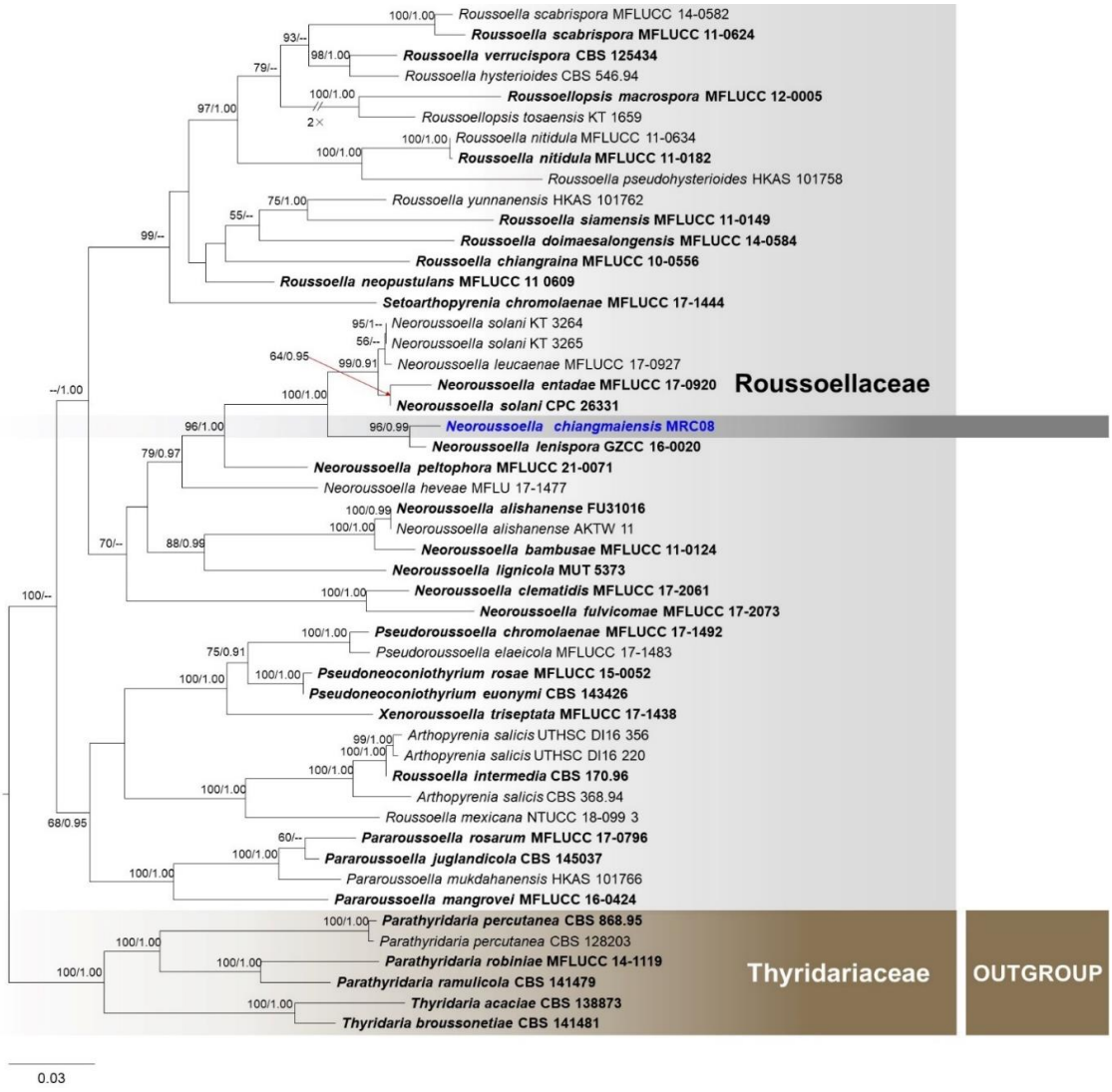


**Figure 35** – Phylogenetic tree obtained from maximum likelihood analyses of a combined LSU, ITS, SSU, *ef1α* and *rpb2* sequence dataset representing the species in Roussoellaceae. Fifty strains were included in the combined analyses, which comprised 4201 characters (LSU: 1–839, ITS: 840–1345, SSU: 1346–2343, *ef1α*: 2344–3246, *rpb2*: 3247–4201) after alignment. Bootstrap support values for ML equal to or greater than 50% and PP equal to greater than 0.90 are indicated at the nodes as ML/PP. The tree is rooted to species in Thyridariaceae. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.03 which represent the estimated number of nucleotide substitutions of site per branch.

The sexual morph of *Neoroussoella* is characterized by semi-immersed to immersed ascomata, cylindrical, uniseriate asci, and fusiform, brown, two-celled, longitudinally ribbed

ascospores. The asexual morphs have black, subglobose conidiomata, phialidic, cylindrical to ampulliform conidiogenous cells and ellipsoidal, hyaline to pale brown, aseptate conidia (Liu et al. 2014).

***Neoroussoella chiangmaiensis*** D.P. Wei & K.D. Hyde, sp. nov. Fig. 36

Index Fungorum number: IF900478; Facesoffungi number: FoF13918

Etymology – The specific epithet refers to "Chiang Mai Province, Thailand" from where the holotype was collected.

Holotype – MFLU 22-0205

*Saprobic* on dead stem of vine stem. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 104–124 ($\bar{x}$ = 116, n = 10) μm in diam., black, subglobose, pycnidial, subepidermal, unilocular, glabrous, scatter or aggregate in small group. *Conidiomatal wall* 5.7–10 ($\bar{x}$ = 7.7, n = 25) μm thick, composed of two layers of cells of *textura angularis*, with brown cells in the outer layer and hyaline cells in the inner layer. *Paraphyses* absent. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cell* 3.6–9.5 × 1.5–3.6 ($\bar{x}$ = 5.7 × 2.4, n = 25) μm, enteroblastic, phialidic, cylindrical to ampulliform, hyaline, smooth-walled, determinate, discrete, arising from the innermost later of the pycnidium. *Conidia* 3–4 × 1.6–2.2 ($\bar{x}$ = 3.4 × 1.8, n = 25) μm, hyaline when immature, becoming pale brown with age, ellipsoidal, aseptate, smooth-walled, biguttulate.

Culture characteristics – Colonies made from germinating conidia, reaching 2 cm diam. after incubation at 25–30 °C for one month, white, circular, fattened, velvety, edge entire, reverse pale white, no pigment diffusing into agar.

Material examined – Thailand, Chiang Mai, Pa Pae Mae Taeng District, Mushroom Research Center, on a decaying stem of vine, 17 February 2019, D.P. Wei, MRC08 (holotype MFLU 22-0205, ex-type living culture MFLUCC 22-0168).

GenBank numbers – LSU: OQ065735, ITS: OQ065738, SSU: OQ065736, *ef1α*: OQ186448, *rpb2*: OQ186450

Notes – Species of *Neoroussoella* cluster into a monophyletic lineage within Roussoellaceae with maximum likelihood support and Bayesian analysis. The new species *N. chiangmaiensis* is sister *N. lenispora*, forming a clade distantly related to other taxa of this genus with 0.96 ML/ 0.99 PP support (Fig. 35). *Neoroussoella lenispora* is known only from its sexual morph (Hyde et al. 2016), while *N. chiangmaiensis* is introduced based on its asexual morph, which makes it impossible to compare its morphological characteristics. In addition, only LSU sequences are available in NCBI for *N. lenispora* and hence other DNA regions cannot be compared. *Neoroussoella lenispora* was found on decaying branches in Guizhou Province, China (Hyde et al. 2016), while *N. chiangmaiensis* occurs on a dead stem of a vine in Chiang Mai province in Thailand. Herein, we treat *N. chiangmaiensis* and *N. lenispora* as different species. The sexual-asexual connection between these two species needs establishing with fresh collections and molecular data.

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

*Nigrograna* (*Ni.*) was introduced by de Gruyter et al. (2012) with *Ni. mackinnonii* as the type species. The genus represents 20 epithets in Index Fungorum (2023). Most of these records aremfrom marine and terrestrial habitats (Hyde et al. 2017, Tibpromma et al. 2017, Dayarathne et al. 2020, Boonmee et al. 2021). Most of the taxa in the genus *Nigrograna* exhibit saprobic lifestyles and were recorded as human pathogens and endophytes with a cosmopolitan distribution (Kolařík 2018, Zhao et al. 2018). The sexual morph of *Nigrograna* is characterized by black ascomata with clavate, short pedicellate asci and pale to chocolate brown, septate ascospores (Jaklitsch et al. 2016, Boonme et al. 2021). The pycnidia of asexual morph are similar to ascomata, peridium brown, pseudoparenchymatous, conidiophores filiform, simple to sparsely branched, with pegs along one or two sides and solitary terminal phialides, phialides ampulliform, lageniform or subcylindrical, conidia forming on pegs and phialides, oblong, cylindrical or allantoid, sometimes ellipsoid, hyaline or subhyaline, one-celled, and smooth-walled (Jaklitsch et al. 2016).

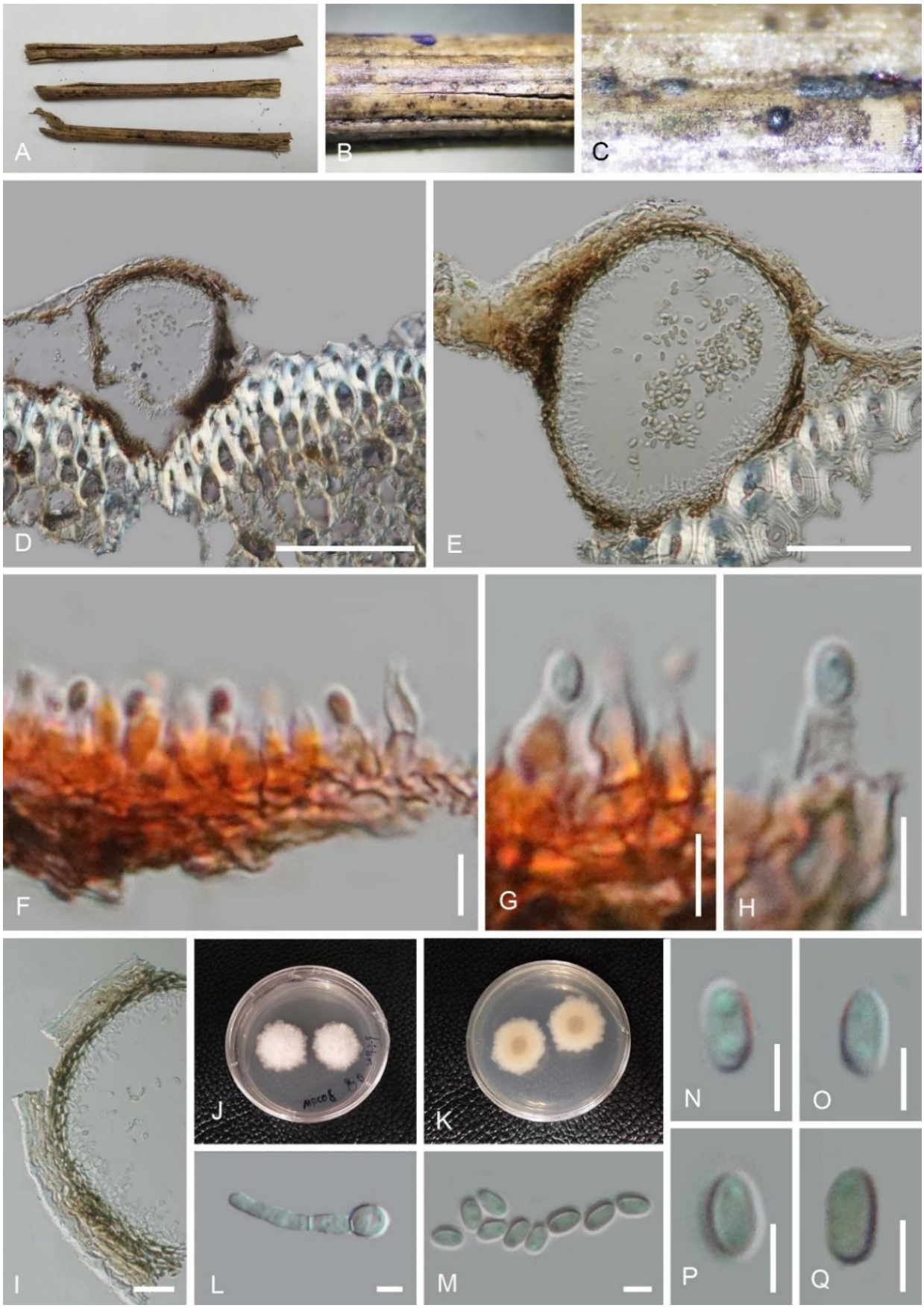


**Figure 36** – *Neoroussoella chiangmaiensis* (holotype MFLU 22-0205). a Host. b, c Conidiomata on host. d, e Vertical section through conidiomata. f–h Conidiogeneous cell bearing conidia. i Peridium. j, k Upper and lower view of culture on PDA. l Germinating conidium. m–q Conidia. Scale bars: d = 100 µm, e = 50 µm, i = 10 µm, f–h =5µm, l–q = 3µm.

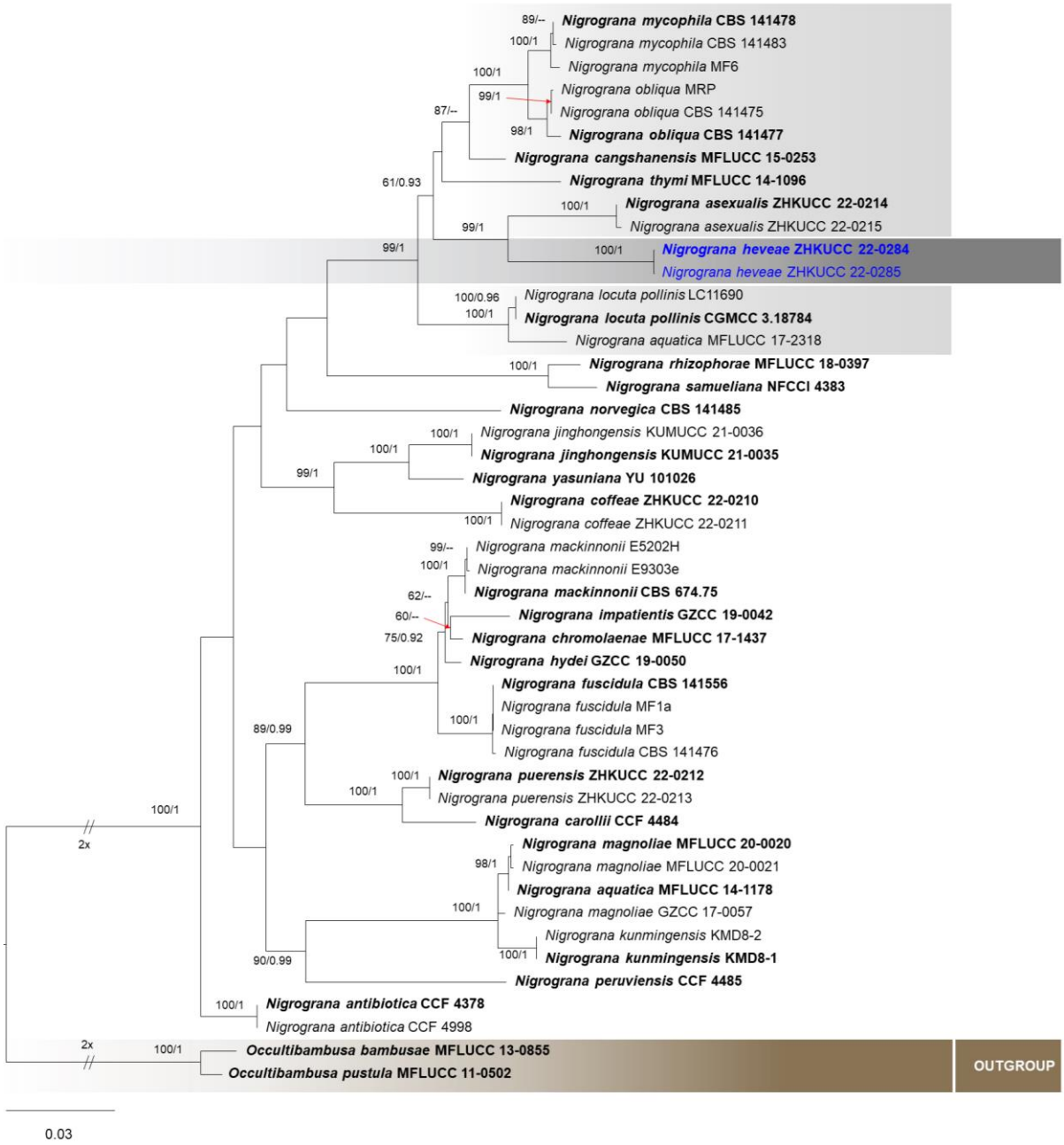


**Figure 37** – Phylogenetic tree generated from maximum likelihood analyses of a combined ITS, LSU, SSU, *rpb2* and *ef1α* sequence dataset representing the species of *Nigrograna*. Related sequences were obtained from Boonmee et al. (2021) and Lu et al. (2022). Forty-seven strains were included in the combined analyses, which comprised 4444 characters (ITS: 1–531, LSU: 532–1434, SSU: 1435–2465, *rpb2*: 2466–3486, *ef1α*: 3487–4444) after alignment. Bootstrap support values for ML equal to or greater than 60% and PP equal to greater than 0.90 are indicated at the nodes as ML/PP. *Occultibambusa pustula* (MFLUCC 11-0502) and *Occultibambusa bambusae* (MFLUCC 13-0855) were used as the outgroup taxon. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.03 which represent the estimated number of nucleotide substitutions of site per branch.

***Nigrograna heveae*** R.F. Xu & Tibpromma, sp. nov. Fig. 38

MycoBank number: MB559985; Facesoffungi number: FoF12908

Etymology – The specific epithet 'heveae' to the host genus *Hevea* from which the holotype was collected.

Holotype – ZHKU 22-0152

*Saprobic* on *Hevea brasiliensis* (rubber tree). Sexual morph: *Ascomata* 200–460 × 150–200 µm ($\bar{x}$ = 369 × 166µm, n = 5), immersed, under to clypeus, some inconspicuous on host surface, some can see small bumps, solitary, uniloculate, dark brown, globose or ellipsoid, neck. *Neck* 192–206 µm high, consists of two parts, first a small subglobose with 75–85 µm wide, second a large globose with 100–105 µm wide, brown to dark brown. *Peridium* 25–65 µm wide, comprising dark-brown to dark of *textura angularis*. *Hamathecium* 2–3 µm wide, branched, hyaline, pseudoparaphyses. *Asci* 45–70 × 7–10 µm ($\bar{x}$ = 57 × 8µm, n = 10), 1–8-spored, bitunicate, cylindrical to clavate, club shape or furcated, apically rounded, thick-walled. *Ascospores* 10–20 × 3–5µm ($\bar{x}$ = 14 × 4 µm, n= 30), inequilateral, 0-3-septate, slightly rounded or pointed at both ends, constricted at the central septum, yellow-brown to brown with age, guttulate, thick-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 hours, circular, entire edge, raised, floppy, grey to taupe, dark brown reverse.

Material examined – China, Yunnan Province, Pu'er, on stem of *Hevea brasiliensis* (Euphorbiaceae), 16 September 2021, R.F. Xu, XPER-18 (holotype ZHKU 22-0152, ex-type living culture ZHKUCC 22-0284 = ZHKUCC 22-0285).

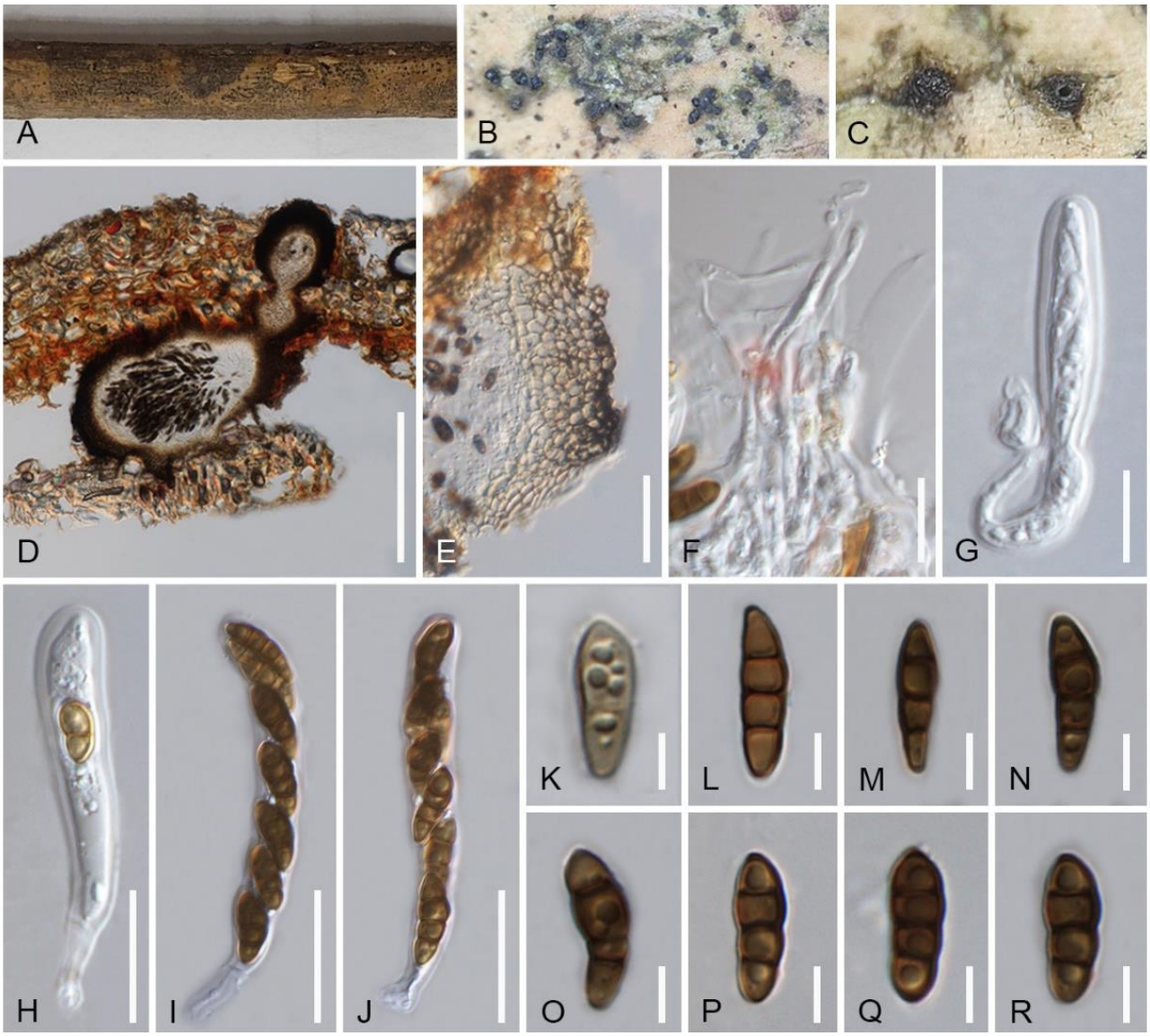


**Figure 38** – *Nigrograna heveae* (holotype ZHKU 22-0152). a–c Appearance of ascostromata on the host substrate. d Section of an ascoma. e Peridium. f Hamathecium. g–j Asci. k–r Ascospores. Scale bars: d = 200 µm, e = 30 µm, f, h, i = 20 µm, g = 10 µm, k–L = 5 µm.

GenBank numbers – ZHKUCC 22-0284 = ITS: OP584492, LSU: OP584488, SSU: OP584490, *rpb2*: OP750374, *ef1α*: OP750372; ZHKUCC 22-0285 = ITS: OP584493, LSU: OP584489, SSU: OP584491, *rpb2*: OP750375, *ef1α*: OP750373

Notes – NCBI BLASTn searches of *Nigrograna heveae* (ZHKUCC 22-0284) showed 94.06% similarity to *Ni. cangshanensis* (MFLUCC 15-0253) in ITS sequence; LSU and *ef1α* sequence showed 99.30% and 96.65% similarities to *Ni. locuta-pollinis* (LC11690); and SSU and *rpb2* sequence showed 92.93% and 87.79% similarities to *Ni. obliqua* (CBS141475). *Nigrograna heveae* is phylogenetically closely related to *Ni. asexualis*, with 100% ML/ 1.00 PP statistical support (Fig. 37). The sequence comparisons between our strain and *Ni. asexualis* (ZHKUCC 22-0214) show 17 bp (3.65%) differences in 465 bp fragment of ITS, 115 bp (11.28%) differences in 1019 bp fragment of *rpb2* and 48 bp (5%) differences in 960 bp fragment of *ef1α* (Lu et al. 2022). According to Chethana et al. (2021), a minimum of >1.5% nucleotide differences in the ITS regions is indicative of a new species. *Nigrograna asexualis* was documented as a saprobic asexual morph on coffee from Yunnan Province and our taxon was also found in the same location. Unfortunately, the sexual morph was not available for *Ni. asexualis* to compare with our novel taxon. Based on morphology and phylogenetic analyses, we introduce *Ni. heveae* as a new species.

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

*Pestalotiopsis* produces 5-celled conidia with appendages and was introduced by Steyaert et al. (1949). Maharachchikumbura et al. (2015) revisited *Pestalotiopsis* spp. and proposed a new family, Pestalotiopsidaceae on the basis of morphological observation and multi-gene (ITS, *β-tubulin*, *ef1α*), which was further divided into three lineages to accommodate taxa. When taking into account the different median cells of conidia, three genera including two novels (*Neopestalotiopsis* and *Pseudopestalotiopsis*) were established. Although their family name is synonymized under Sporocadaceae (Jaklitsch et al. 2016), the three generic names were accepted by many mycologists and plant pathologists (Index Fungorum 2023). In this paper, a novel taxon *P. ficicrescens* is introduced based on evidence of morphology and phylogenetic analysis (Fig. 39).

***Pestalotiopsis ficicrescens*** Qi Yang & Yong Wang bis, sp. nov. Fig. 40

MycoBank number: MB846988; Facesoffungi number: FoF13371

Etymology – Refers to the host plant (*Ficus tikoua*) from which the fungus was isolated.

Holotype – HGUP 861

*Associated* with leaf spots of *Camellia japonica*. Leaf spots shape irregular, brown, slightly sunken on leaves surface. Small yellow spots appeared initially and then gradually enlarged, changing to brown spots. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 400 to 1200 µm in diam., pycnidial, globose, solitary, black, semi-immersed on PDA, exuding brown to dark brown conidia. *Conidiophores* branched or unbranched, hyaline, thin walled. *Conidiogenous cell* discrete to lageniform, obclavate, hyaline or rarely light brown, smooth-walled. *Conidia* (18–)23 × 3(–5.5) µm ($\bar{x}$ = 20.4 × 4.6 µm, n = 30), fusiform to clavate, straight to slightly curved, 4-septate; basal cell cylindrical to obconic, hyaline, thin-walled, smooth, 2–5 µm ($\bar{x}$ = 3.4 µm, n = 30); the three median cells 11–15 µm ($\bar{x}$ = 12.8 µm, n = 30), concolorous, dark brown with septa darker than the rest of the cells, the second cell from base 3–5 µm ($\bar{x}$ = 4.2 µm, n = 30); the third cell 2.5–4.5 µm ($\bar{x}$ = 3.4 µm, n = 30); the fourth cell 3–5 µm ($\bar{x}$ = 3.8 µm, n = 30); apical cell 2.5–5 µm ($\bar{x}$ = 3.5 µm, n = 30), cylindrical, hyaline; 2–3 tubular apical appendages, arising from the apex of the apical cell each at different points, flexuous, 10.5–18 µm ($\bar{x}$ = 14.3 µm, n = 30); basal appendage present, single, tubular, unbranched, 3.5–7 µm ($\bar{x}$ = 5.1 µm, n = 30).

Culture characteristics – Colonies on PDA reaching 4–4.5 cm in diam. after 7 d at room temperature (28 ℃), under light 12 hr/dark. Colonies filamentous to circular, whitish, with clustered black fruiting bodies and filiform and fluffy margin, white from above and reverse.

Material examined – China, Guizhou Province, Guiyang City, leaf spots of *Ficus tikoua* (Moraceae), 17 July 2019, J. Yuan, HGUP 861 (holotype HGUP 861, ex-type living culture GUCC 21556).

GenBank numbers – ITS: MZ477311, *β-tubulin*: MZ868301, *ef1α*: MZ868328

Notes – Based on phylogenetic analysis of combined genes (Fig. 39), *Pestalotiopsis ficicrescens* is sister to *P. biciliata* (CBS 124463) with 97/73/0.97, ML/MP/PP support (Fig. 39). There were two nucleotide differences in the ITS regions and 11 nucleotides differences in β-tubulin (Table 2). Morphologically, *P. ficicrescens* differs from *P. biciliata* by having smaller conidia (*P. ficicrescens*: (18–)23 × 3(–5.5) µm *vs* (21–)22–28.5(–30) × (5.5–)6–7.5(–8) µm: *P. biciliate*); shorter three median cells (*P. ficicrescens*: 11–15 µm *vs* (13.5–)14.5–17.5(–18.5) µm: *P. biciliate*) and on the number of basal appendages (*P. ficicrescens*: one *vs* two: *P. biciliate*) (Maharachchikumbura et al. 2014). Thus, it is introduced as a new species.

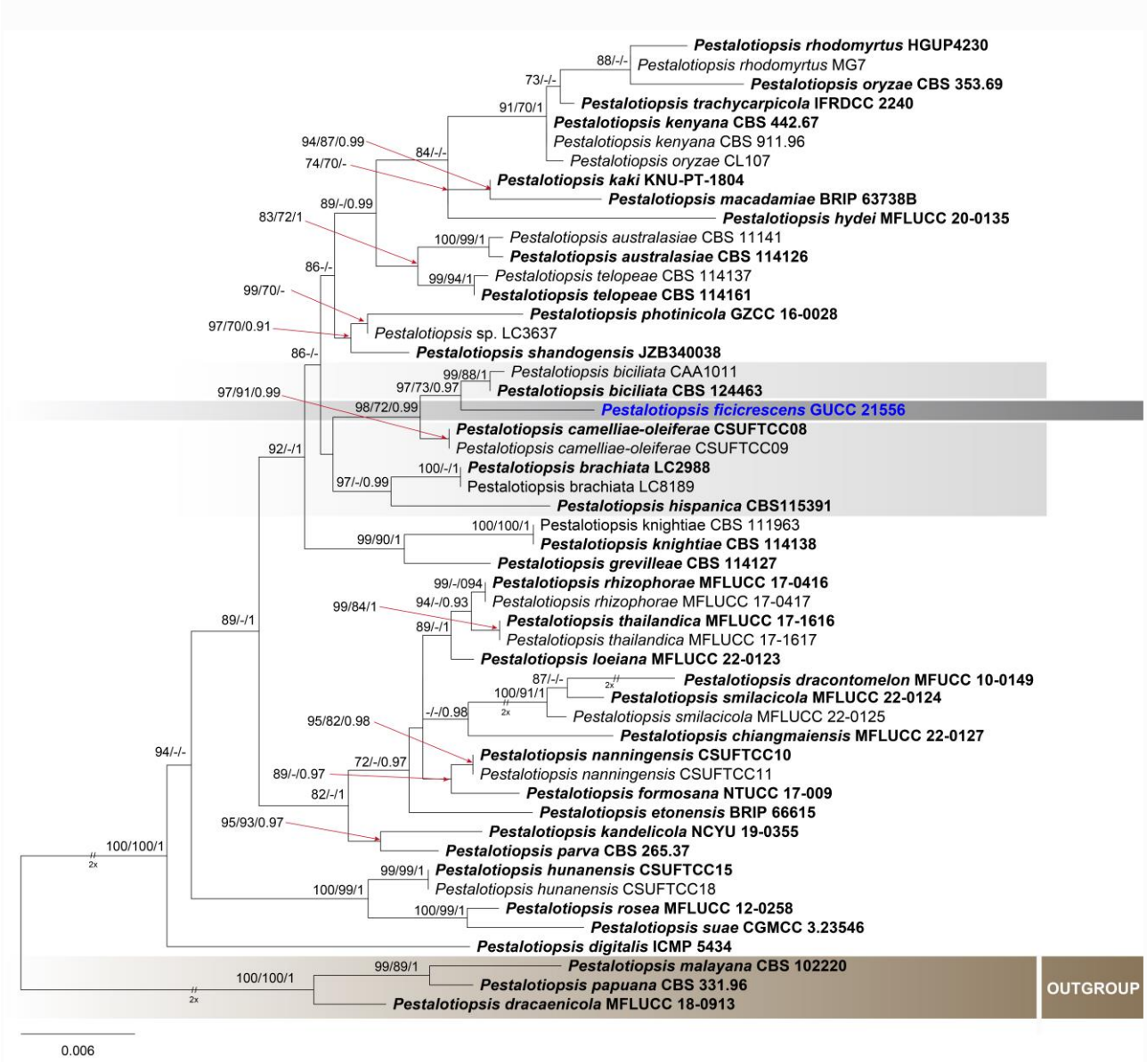


**Figure 39** – Phylogenetic tree obtained from maximum likelihood analyses of a combined ITS, *ef1α* and *β-tubulin* sequence dataset representing the species of *Pestalotiopsis*. Fifty-one strains were included in the combined analyses, which comprised 1455 characters (ITS: 1–541, *tef1α*: 542–1024, *tub2*: 1025–1455) after alignment. Bootstrap support values for ML and MP equal to or greater than 70% and PP equal to greater than 0.95 are indicated at the nodes as ML/MP/PP. The tree is rooted to *Pestalotiopsis dracaenicola* (MFLUCC 18-0913), *P. malayana* (CBS 102220) and *P. papuana* (CBS 331.96). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.006 which represents the estimated number of nucleotide substitutions of site per branch.

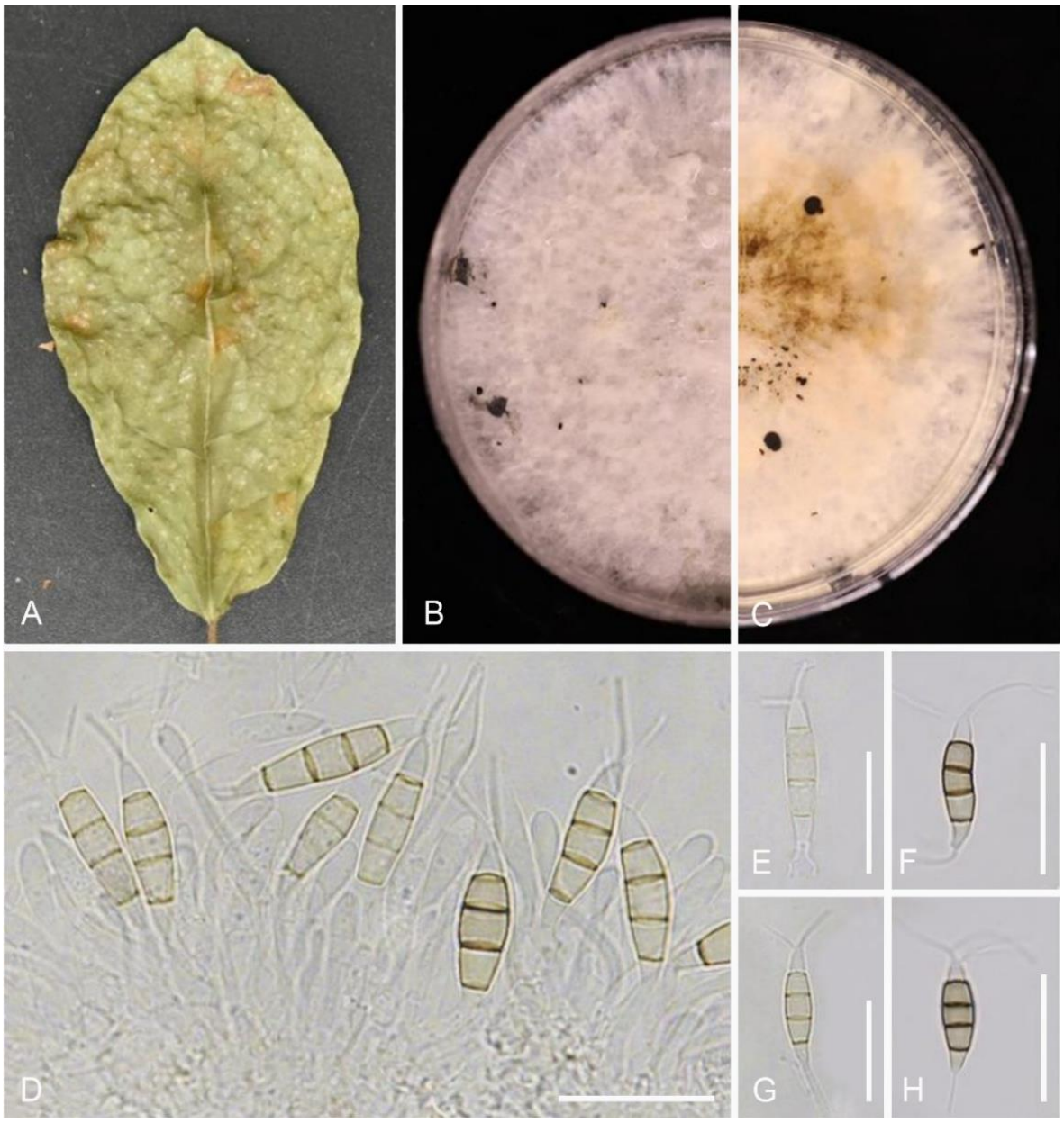


**Figure 40** – *Pestalotiopsis ficicrescens* (ex-type living culture GUCC 21556). a Leaf spots of *P. ficicrescens*. b, c Culture on PDA (b-above, c-reverse). d Conidia and conidiophores. e–h Conidia. Scale bars: d–h = 20 µm.

***Pleurothecium*** Höhn., Ber. dt. bot. Ges. 37: 154 (1919)

*Pleurothecium* (*Pl.*) was established by Höhnel (1919) with *Pl. recurvatum* (≡ *Acrothecium recurvatum*) as the type species, without a description or designation of a type specimen. Therefore, it was later formally introduced by Höhnel (1923). The first sexual species *Carpoligna pleurothecii* was regarded as a synonym of *Pl. recurvatum* based on phylogenetic analyses (Fernández et al. 1999, Réblová et al. 2016). *Pleurothecium semifecundum* is the second sexual species described by Réblová et al. (2012) from culture. *Pleurothecium* is characterized by astromatic, semi-immersed to superficial, dark brown, subglobose to conical perithecia, with a papilla or short beak, sometimes lying along the host, with or without setae. Species have sparse or abundant, septate, hyaline paraphyses, cylindrical-clavate, short-stipitate asci with a distinct, J-apical ring and hyaline, septate, ellipsoidal to fusiform ascospores. The asexual morphs have distinct brown conidiophores and polyblastic, sympodially denticulate conidiogenous cells and unicellular or septate, ellipsoidal, fusiform or clavate conidia (Wu & Zhang 2009, Réblová et al. 2012). *Pleurothecium* consists of eleven species in Species Fungorum (2023). In previous studies and combined with this study, eight

species are associated with molecular data, and only four species, including *Pl. recurvatum*, *Pl. semifecundum*, *Pl. guttulatum* and *Pl. hainanense* have sexual morphs (Luo et al. 2019, Réblová et al. 2012, Hyde et al. 2020).

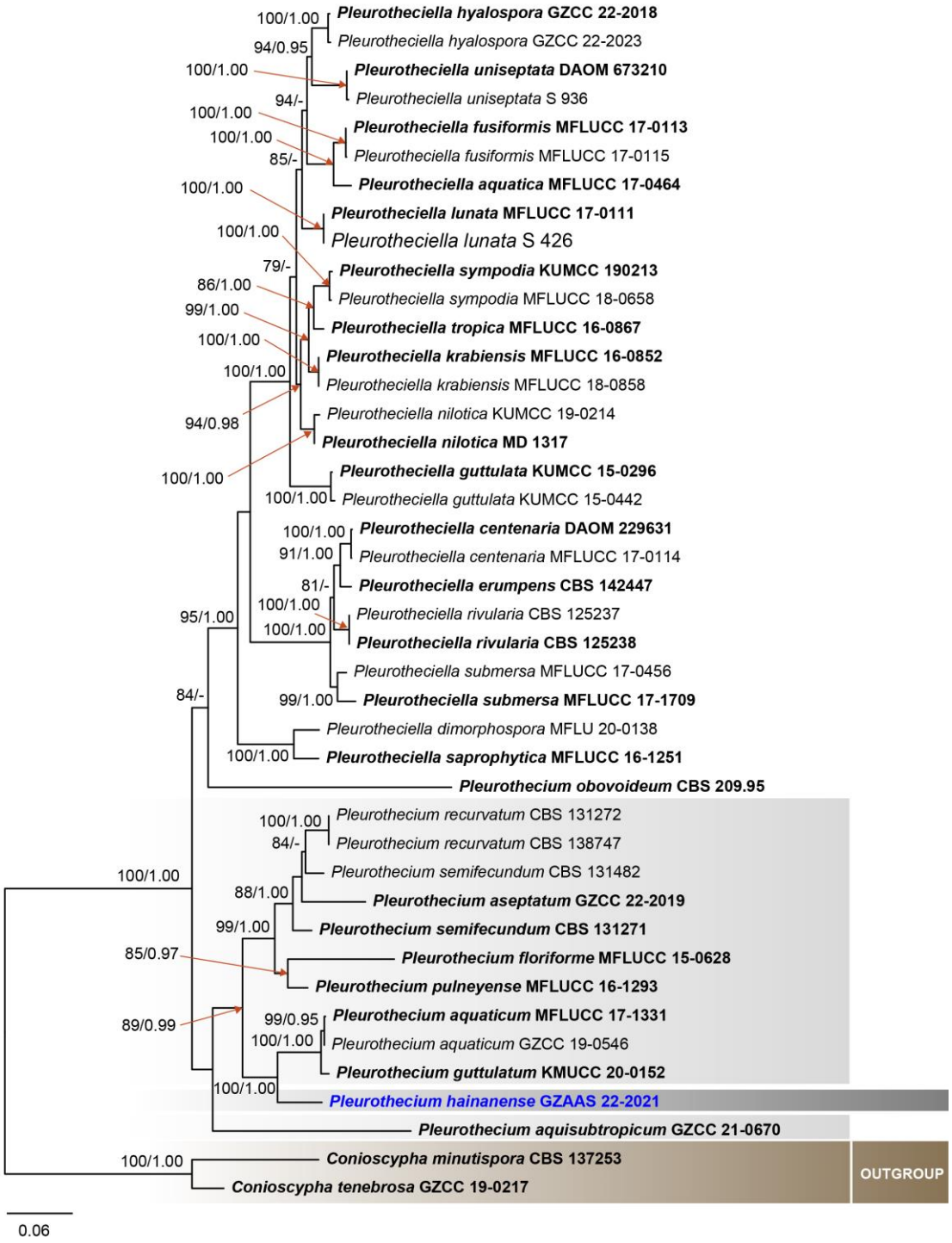


**Figure 41** – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU and *rpb2* sequence data representing the species of Pleurotheciaceae. Forty-two strains were included in the combined analyses, which comprised 3490 characters (ITS: 1–656 LSU: 657–1521, SSU: 1522–2478, *rpb2*: 2479–3490) after alignment. Bootstrap support values for ML equal to or greater than 75% and PP equal to or greater than 0.95 are given above the nodes as ML /PP. *Conioscypha minutispora* (CBS 137253) and *Conioscypha tenebrosa* (GZCC 19-0217) were used as the outgroup taxa. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.06 which represent the estimated number of nucleotide substitutions of site per branch.

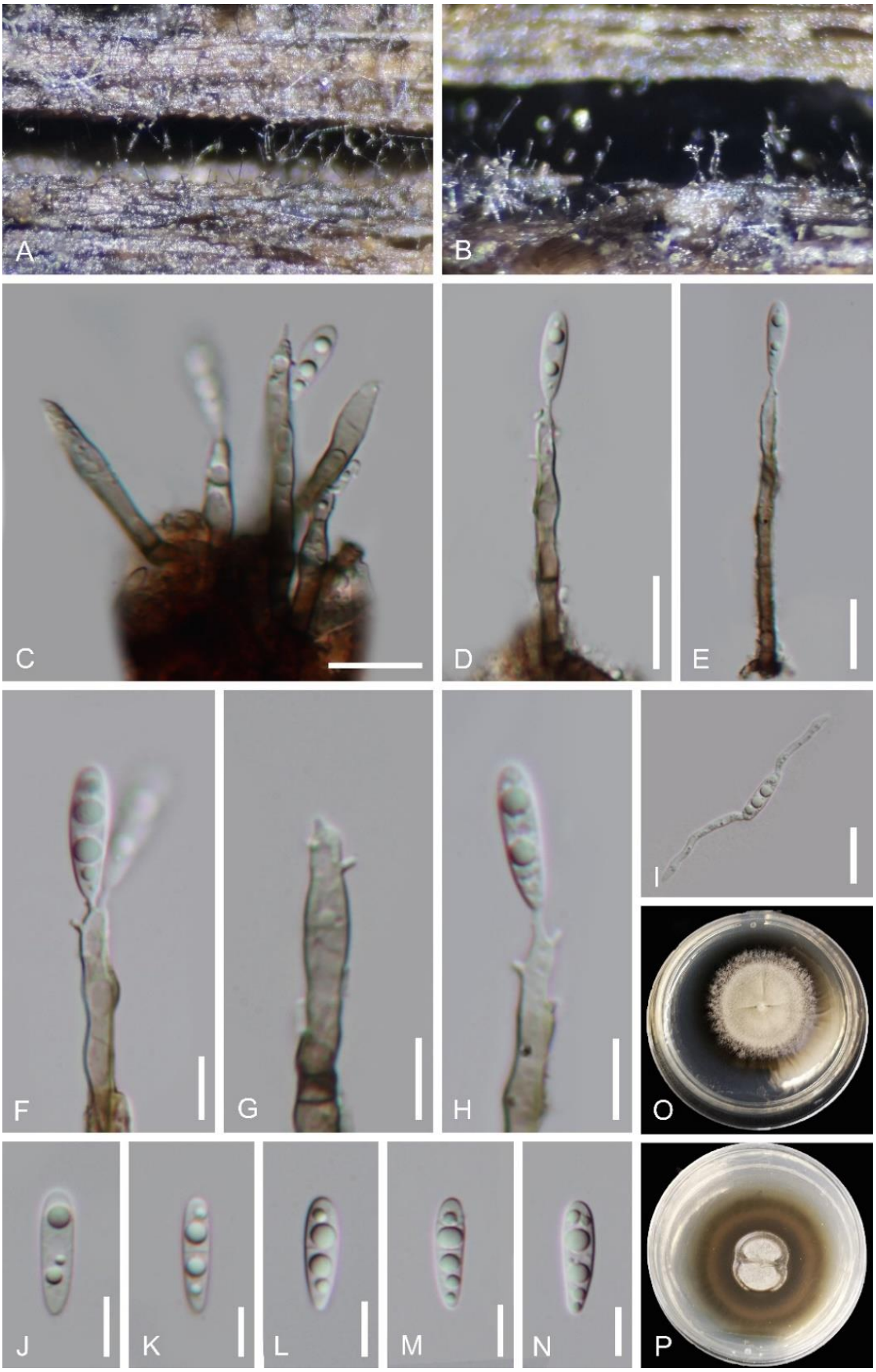


**Figure 42** – *Pleurothecium hainanense* (holotype GZAAS 22-2021). a, b Colonies on wood. c–e Conidiophores, conidiogenous cells and conidia. f–h Conidiogenous cells bearing conidia. j–n Conidia. i Germinating conidium. o, p Colony on PDA from above and reverse. Scale bars: c–e, i = 20 μm; f–h, j–n = 10 μm.

***Pleurothecium hainanense*** J. Ma, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 42

MycoBank number: MB900047; Facesoffungi number: FoF13258

Etymology – Refers to the location "Hainan Province" where the holotype was collected.

Holotype – GZAAS 22-2021

*Saprobic* on submerged decaying wood. Sexual morph: Undetermined. Asexual morph: *Colonies* effuse, superficial, solitary, hairy, grayish to dark brown with visible whitish to grayish conidia. *Mycelium* mostly immersed, partly superficial, composed of branched, septate, brown hyphae. *Conidiophores* macronematous, mononematous, straight or slightly flexuous, 1-septate, smooth, 27–75 μm ($\bar{x}$ = 50.5 μm, n = 20) long, 3.5–7 μm ($\bar{x}$ = 5.5 μm, n = 20) wide, pale brown, ecoming subhyaline towards the apex. *Conidiogenous cells* polyblastic, terminal, integrated, cylindrical to tapered, sympodial, denticulate at the apex, 15–36 × 3–5.5 μm, with 1–4 denticles, pale brown to subhyaline. *Conidia* clavate, straight or slightly curved, rounded at the apex, tapering towards the base, 1–3-septate occasionally, 14–20 × 3.5–6.5 μm ($\bar{x}$ = 17.5 × 5 μm, n = 30), hyaline, often with 2-6 large guttules in each cell, smooth-walled.

Culture characteristics – Conidia germinating on PDA within 12 h; Colonies growing on PDA, reaching 45 mm in 4 weeks at 25 ℃, circular, with a flat surface, edge undulate, grayish and pale brown in PDA medium; Mycelium superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.

Material examined – China, Hainan Province, Baihualing Tropical Rainforest Cultural Tourism area, on submerged decaying wood in a freshwater stream, 30 December 2021, J. Ma, BHL (holotype GZAAS 22-2021, ex-type living culture GZCC 22-2021).

GenBank numbers – ITS: OP748934, LSU: OP748931

Notes – *Pleurothecium hainanense* is phylogenetically closer to *Pl. guttulatum* with 100%, ML, 1.00 PP support (Fig. 41) and the phylogeny supports them as distinct species. *Pleurothecium hainanense* fits well the generic concept of *Pleurothecium* in having brown conidiophores, polyblastic, sympodially conidiogenous cells with cylindrical to tapered denticles and hyaline, clavate conidia (Réblová et al. 2012, Luo et al. 2018). *Pleurothecium hainanense* is however, different from *Pl. guttulatum* in having smaller conidia (14–20 μm *vs* 22–28 μm) and smaller conidiogenous cells (15–36 μm *vs* 30–39 μm) (Luo et al. 2018). Therefore, we introduce *Pl. hainanense* as a new species.

***Rhodoveronaea*** Arzanlou, W. Gams & Crous, Stud. Mycol. 58: 89 (2007)

The asexual genus *Rhodoveronaea* (*Rh.*) was established by Arzanlou (2007) with *Rh. varioseptata* as the type species growing on decaying wood of *Bertia moriformis* from Germany. Subsequently, Réblová (2009) illustrated the sexual morph of this species. *Rhodoveronaea aquatica* was reported from freshwater habitats, and characterized by macronematous, mononematous, cylindrical, straight or flexuose, septate, red-brown conidiophores, terminally integrated, polyblastic, sympodial, smooth conidiogenous cells, ellipsoid to obovoid, pale brown, septate conidia by Luo et al. (2019). *Rhodoveronaea everniae*, a species of *Evernia prunastri*, was reported by Crous et al. (2021) from Drenthe Province in the Netherlands. In this study, we introduce a fourth species *R. hainanensis*, which was collected from wood in freshwater from Hainan Province, China. In previous studies and combined with this study, four species (two freshwater species and two terrestrial) are accepted in *Rhodoveronaea*.

***Rhodoveronaea hainanensis*** J. Ma, K.D. Hyde & Y.Z. Lu, sp. nov. Fig. 44

MycoBank number: MB900048; Facesoffungi number: FoF13257

Etymology – Refers to the location "Hainan Province", where the holotype was collected.

Holotype – GZAAS 22-2020

*Saprobic* on submerged wood in freshwater habitats. Sexual morph: Undetermined. Asexual morph: *Colonies* effuse, brown, hairy. *Mycelium* mostly immersed, consisting of branched, septate, smooth hyphae. *Conidiophores* macronematous, mononematous, cylindrical, arising vertically from creeping hyphae, straight or flexuose, simple, 58–172 μm × 5.5–10.5 μm ($\bar{x}$ = 109 × 8 μm, n = 20),

thick-walled, septate, red-brown, paler at apex. *Conidiogenous cells* polyblastic, terminally integrated, sympodial, sometimes branched, smooth, thick-walled, pale brown at the base, paler towards the apex. *Conidia* acropleurogenous, ellipsoid to obovoid, apically rounded, with a flat basal scar, 1–3-septate, 10–15 µm × 4–5.5 µm ($\bar{x}$ = 12 × 5 µm, n = 30), pale brown, smooth-walled.

Culture characteristics – Conidia germinated on WA within 10 h with germ tubes produced from conidia. Colonies on PDA reaching 30 mm diam. in 25 days at 25 °C, circular, flat, red brown at the entire margin, white in the center, reverse-side red-brown.

Material examined – China, Hainan Province, Baoting County, Sandao Town, Yanoda Rainforest Cultural Tourism Area, on rotting wood in a freshwater stream, 23 October 2021, J. Ma, Y24 (holotype GZAAS 22-2020, ex-type living culture GZCC 22-2020).

GenBank numbers – ITS: OP748935, LSU: OP748932

Notes – *Rhodoveronaea hainanensis* shares a sister relationship to *Rh. aquatica* with 100% ML/ 1.00 PP support (Fig. 43). However, *Rh. hainanensis* differs from *Rh. aquatica* by having smaller conidiophores (58–172 × 5.5–10.5 µm *vs* 182–310 × 9–13 µm) and smaller conidia (10–15 × 4–5.5 µm *vs* 23–27 × 9–11 µm). Moreover, *Rh. hainanensis* is distinguished from *Rh. aquatica* by having distinctly branched conidiogenous cells (Luo et al. 2019). In addition, based on a pairwise comparison of ITS nucleotides, *Rh. hainanensis* differs from *Rh. aquatica* by 18/481 bp (3.7%). Following the guidelines for defining species boundaries of Chethana et al. (2021). We, therefore, introduce *Rh. hainanensis* as a new species.

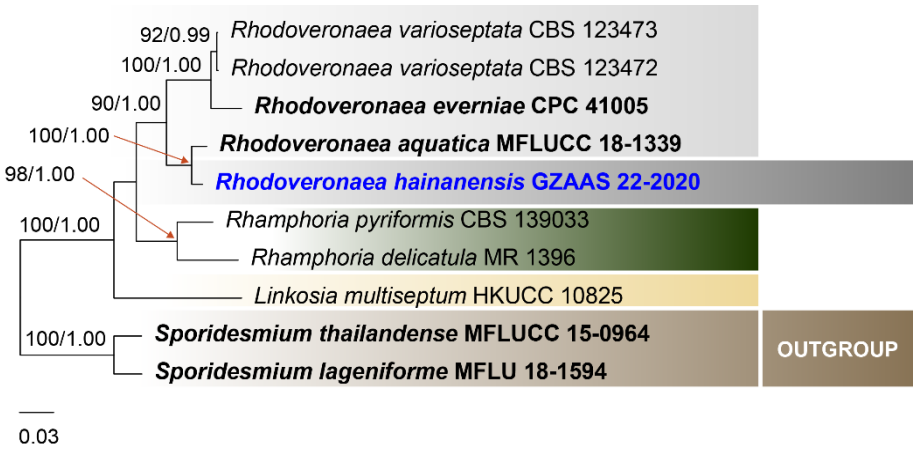


**Figure 43** – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, SSU, *ef1α* and *rpb2* sequence data representing the species of Rhamphoriaceae. Ten strains were included in the combined analyses, which comprised 4410 characters (ITS: 1–534, LSU: 535–1045, SSU = 1046–2420, *ef1α* = 2421–3319, *rpb2* = 3320–4410) after alignment. Bootstrap support values for ML equal to or greater than 75% and PP equal to or greater than 0.95 are given above the nodes. *Sporidesmium lageniforme* (MFLU 18-1594) and *Sporidesmium thailandense* (MFLUCC 15-0964) were used as the outgroup taxa. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.03 which represents the estimated number of nucleotide substitutions of site per branch.

***Roussoella*** Sacc., Atti Inst. Veneto Sci. lett., ed Arti, Sér. 6 6: 410 (1888)

*Roussoella* was introduced by Saccardo and Paoletti (1888) with *R. nitidula* as the type species. The species are saprobic on various flowering plants in terrestrial or submerged wood in freshwater habitats, mainly on bamboo and palms (Dong et al. 2020). An epitype of *R. nitidula* was designated by Liu et al. (2014). *Roussoella* accommodates species having large ascomata with multi-loculate, bitunicate asci and brown, fusiform to ellipsoidal, ornamented, didymospores (Tanaka et al. 2009, Hyde et al. 2013, Liu et al. 2014, Dai et al. 2017, Jiang et al. 2019a, Dong et al. 2020). The asexual morph of *Roussoella* was reported as *Cytoplea* and found either in culture or on the host substrates in nature (Aptroot 1995a, Hyde et al. 1996, Liu et al. 2014). The asexual morph

of *Roussoella* species can be characterized by superficial conidiomata containing ampulliform, enteroblastic conidiogenous cells and oblong-ellipsoidal, hyaline to dark brown conidia, sometimes with verrucose ornamentation (Liu et al. 2014, Dai et al. 2017). In this study, we introduce *R. chinensis* from a decaying pod of *Wisteria* sp.

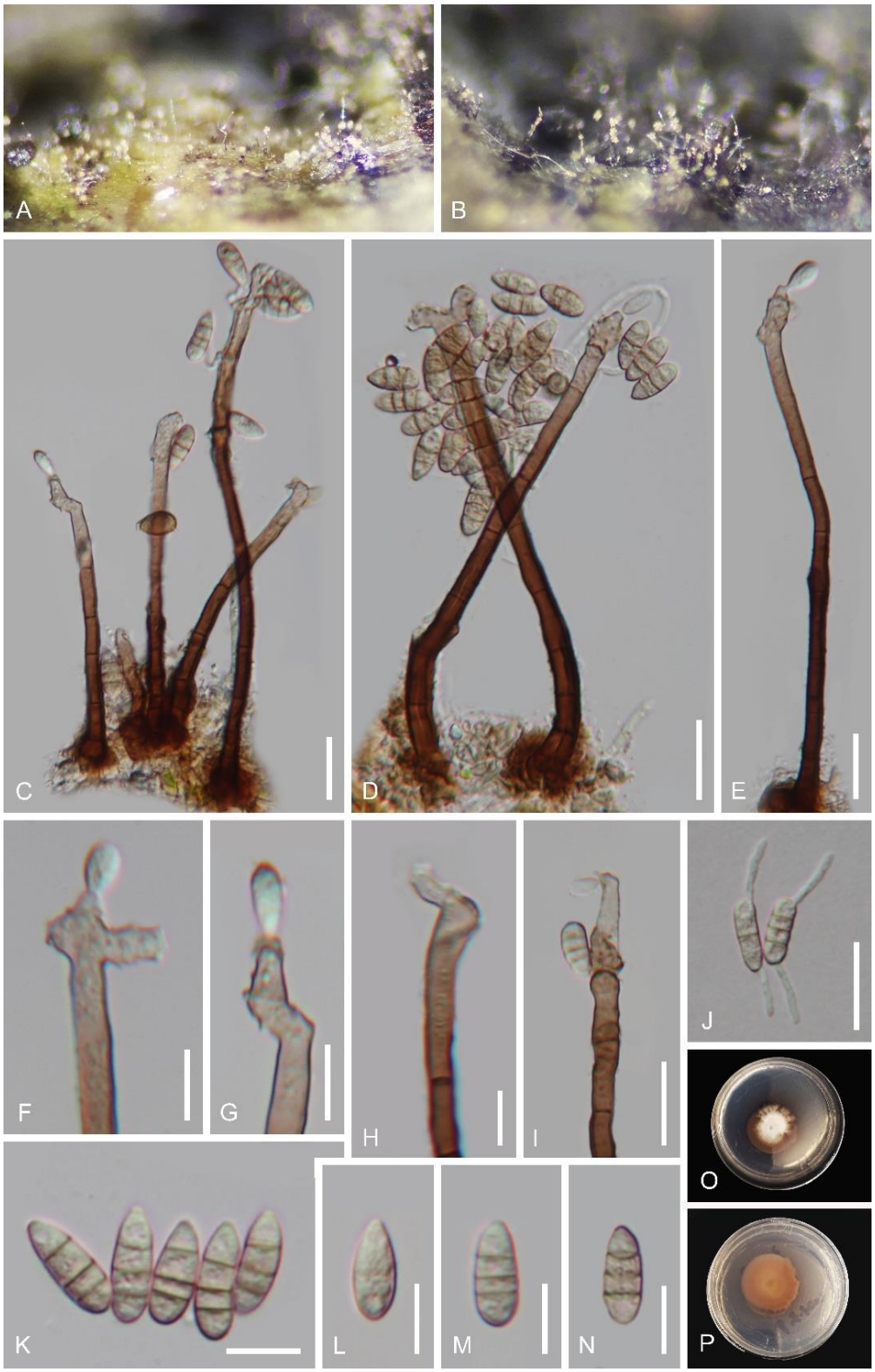


**Figure 44** – *Rhodoveronaea hainanensis* (holotype GZAAS 22-2020). a, b Colonies on submerged wood. c–e Conidiophores, conidiogenous cell bearing conidia. f–i Conidiogenous cell and conidia. k–n Conidiogenous cell and conidia. j Germinated conidia. o, p Colony on PDA from above and below. Scale bars: c–e, i–j = 20 μm, f–h, k–n = 10 μm.

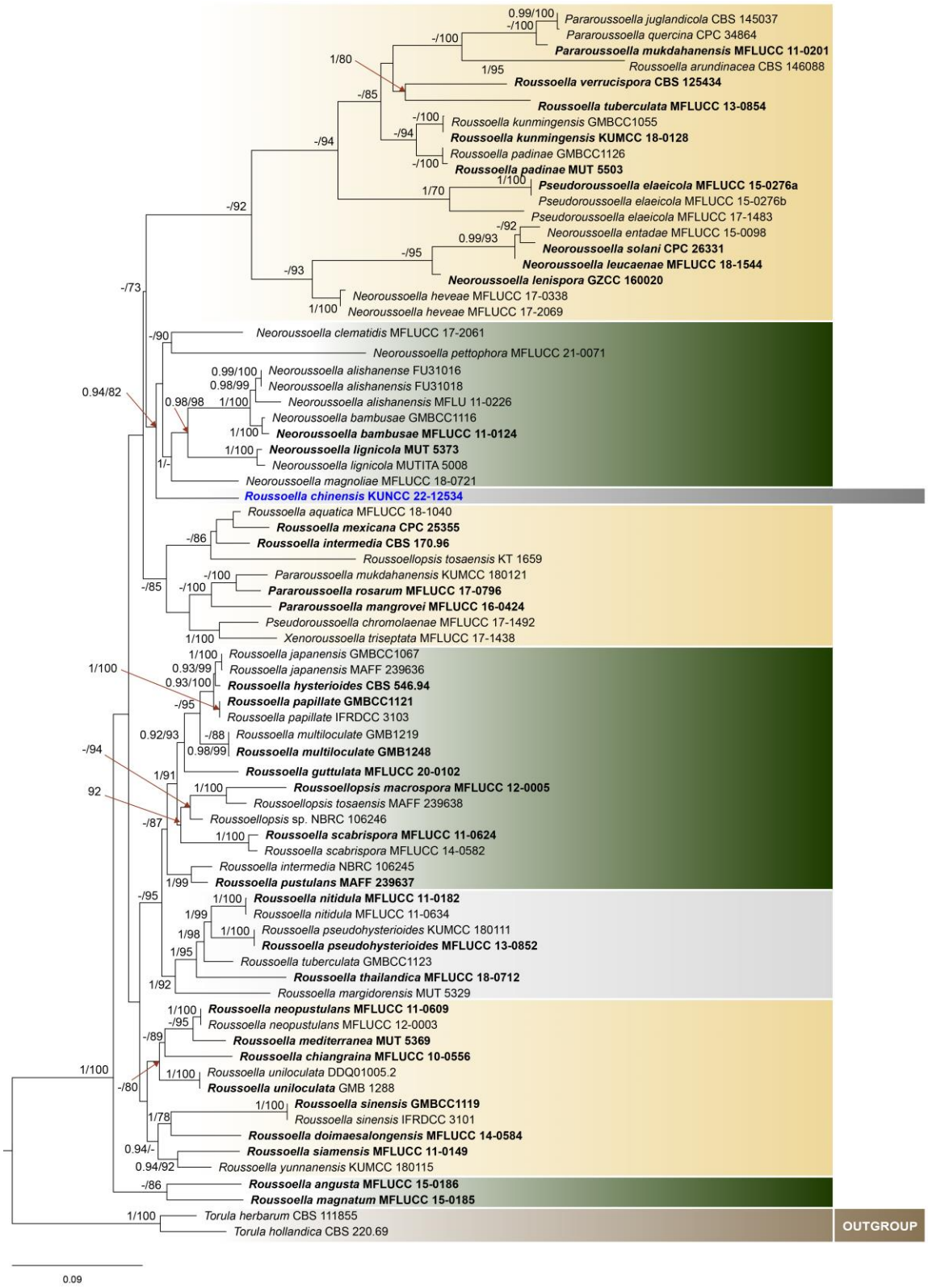


**Figure 45** – Phylogenetic tree obtained from maximum likelihood analysis based on combined ITS, LSU, SSU, *rpb2*, and *ef1α* sequence dataset representing the species of Roussoellaceae. Seventy-seven strains were included in the combined analyses, which comprised 2111 characters (ITS: 1–521, LSU: 522–1,370, SSU: 1,371–2,352, *rpb2*: 2,353–3,403, *tef1*: 3,404–4,333) after alignment. Bootstrap support values for ML equal to or greater than 70% and PP equal to greater than 0.9 are indicated at the nodes as PP/ML. The tree is rooted in *Torula herbarum* (CBS 111855) and *Torula hollandica* (CBS 220.69). The ex-type strains are in bold, and the new isolates of this study are in blue. Bar = 0.05 represents the estimated number of nucleotide substitutions site per branch.

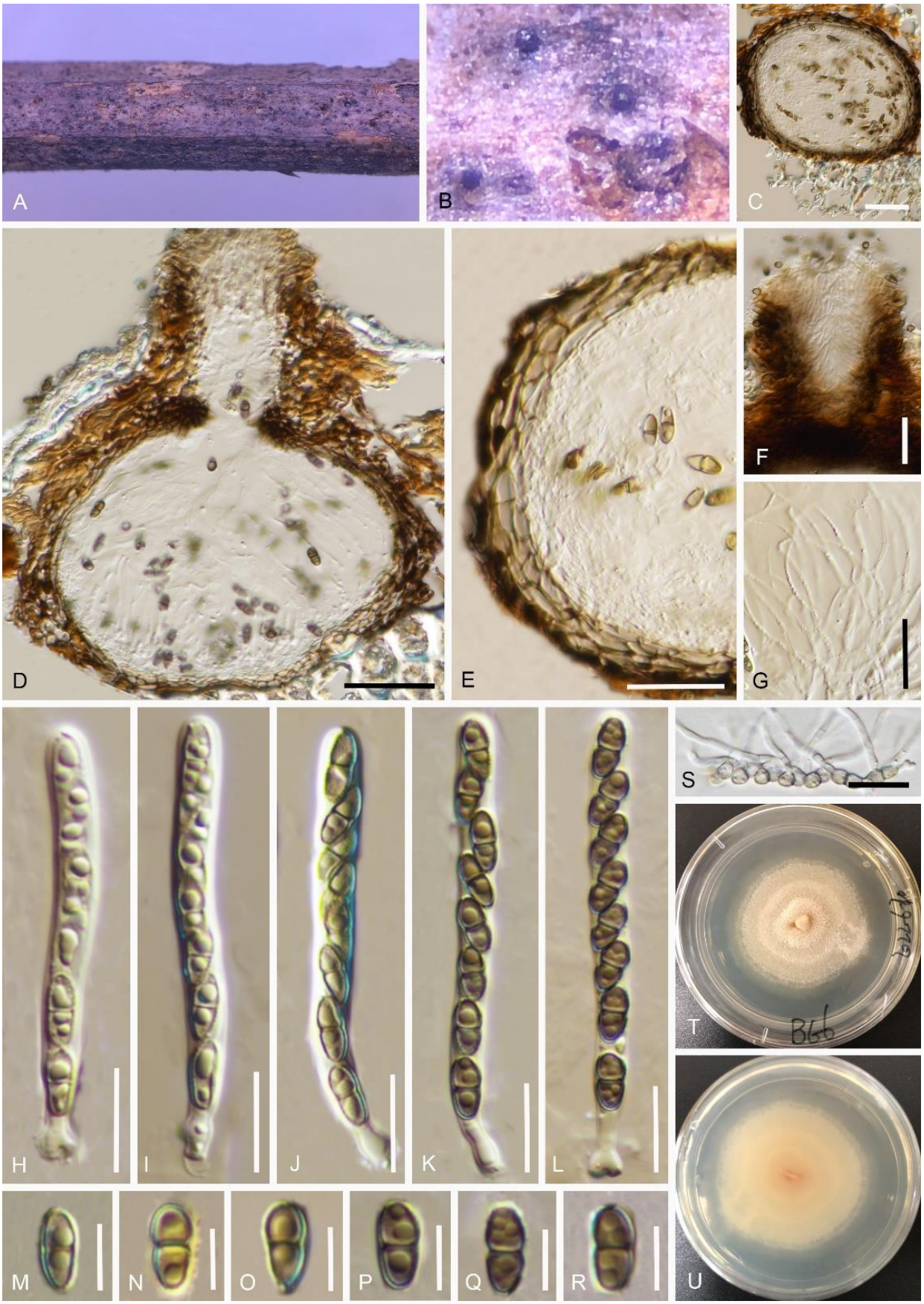


**Figure 46** – *Roussoella chinensis* (ex-type living culture HKAS 125555). a, b Ascomata on dead branches. c, d Vertical section of ascoma. e Peridium. f Ostiole. g Pseudoparaphyses. h–l Asci. m–r Ascospores. s Germinating ascospores. t Colony on PDA (from above). u Colony on PDA (from below). Scale bars: c, d = 30 µm, e–g = 20 µm, h–l = 10 µm, m–r = 5 µm, s = 20 µm.

***Roussoella chinensis*** Y. Gao, H. Gui, A.R.D. De Farias & K.D. Hyde, sp. nov. Fig. 46

MycoBank number: MB846319; Facesoffungi number: FoF12901

Etymology – The name refers to China, the country from where this fungus was collected.

Holotype – HKAS 125555

*Saprobic* on a decaying pod of *Wisteria* sp. Sexual morph: *Ascomata* 110–145 μm diam, 85–105 μm high, ($\bar{x}$ = 133× 98 μm, n = 10), scattered, immersed in host tissue, visible as papillate spots on the host surface, dark brown to black, subglobose to ampulliform, with ostioles. *Ostioles* 56–77 μm diam, 50–66 μm high, ($\bar{x}$ = 69× 58 μm, n = 10), with pronounced papillae, internally lined with periphyses. *Peridium* 6–14 μm thick ($\bar{x}$ = 9.8 μm, n = 30), composed of several layers of brown to hyaline, compressed pseudoparenchymatous cells, arranged in a *textura angularis*. *Hamathecium* 1.2–2.3 μm broad ($\bar{x}$ = 1.5 μm, n = 20), composed of numerous, septate, branched, anastomosing, filiform, hyaline, pseudoparaphyses. Asci 45–60 × 3.5–5 μm ($\bar{x}$ = 53 × 4.3 μm, n = 20), 8-spored, bitunicate, cylindrical to cylindric-clavate, straight to curved, short pedicellate with slightly furcate pedicel, apically rounded. Ascospores 6–8 × 2.5–3.5 μm ($\bar{x}$ = 7× 3 μm, n = 40), 1-seriate, ellipsoidal to fusiform, light yellowish to brown, 1-septate, slightly constricted at the septum, straight, rough-walled. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinating on PDA within 24 hr. Germ tubes produced from both ends of the ascospores. Colonies coriaceous, pinkish white, circular, woolly from above, lower surface off white, reaching 25 mm diam. in 30 days at 25–27 °C. Mycelia are superficial, with regular edge.

Material examined – China, Yunnan Province, Xishuangbanna, Mengla County, Menglunzhen, on decaying branches, 23 May 2022, Y. Gao, BG6 (holotype HKAS 125555, ex-type living culture KUNCC 22-12534).

GenBank numbers – ITS: OP555451, LSU: OP555449, SSU: OP555446

Notes – Phylogenetic analyses of combined ITS, LSU, SSU, *rpb2*, and *ef1α* sequence data of taxa in Roussoellaceae indicated that our isolate, *R. chinensis* forms distinct branch with other known species in *Roussoella* (0.94 PP and 82% ML support, Fig. 45). The species is close to *Neoroussoella magnoliae* (MFLUCC 18-0721) and *Neoroussoella lignicola* (MUTITA 5008), and *Roussoella aquatica* (MFLUCC 18-1040). *Neoroussoella magnoliae* was published by its sexual morph as saprobic on Saprobic on *Magnolia* sp. (Yuan et al. 2020). The remaining three species were introduced based on only their asexual morphs; *N. lignicola* was isolated from the brown alga *Padina pavonica* and (Poli et al. 2020) and *Roussoella aquatica*, saprobic on submerged wood (Dong et al. 2020). Our isolate only produced the sexual morph with subglobose ascomata, cylindrical to cylindric-clavate asci, with 1-seriate, ellipsoidal to fusiform, light yellowish to brown, and 1-septate ascospores, which is similar to the sexual morph of *Roussoella* species. Therefore, we introduce *R. chinensis* based on phylogenetic and sexual morph as a novel taxon in Roussoellaceae.

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

*Torula* (Torulaceae) was introduced by Persoon (1795) and is typified by *T. herbarum*. Although there are more than 500 records in Index Fungorum (2023), Seifert & Gams (2011) only recognized six species. *Torula* is only found in its asexual form and is characterized by terminal or lateral, monoblastic or polyblastic conidiogenous cells which have basally thickened and heavily melanized walls, with the apex thin-walled and frequently collapsing and becoming coronate (Crous et al. 2016, Leland Crane and Miller 2016, Su et al. 2018, Li et al. 2020). Based on morphology and phylogenetic analyses, we introduce a new species of *Torula* from China.

***Torula calceiformis*** S.C. He, K.D. Hyde sp. nov. Fig. 48

Index Fungorum number: IF900369; Facesoffungi number: FoF 13350

Etymology – The specific epithet is referred to calceus conidia of this fungus.

Holotype – HKAS 125551

*Saprobic* on dried wood of an unidentified plant in the forest. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on the substrate surface, black, powdery, mycelium-

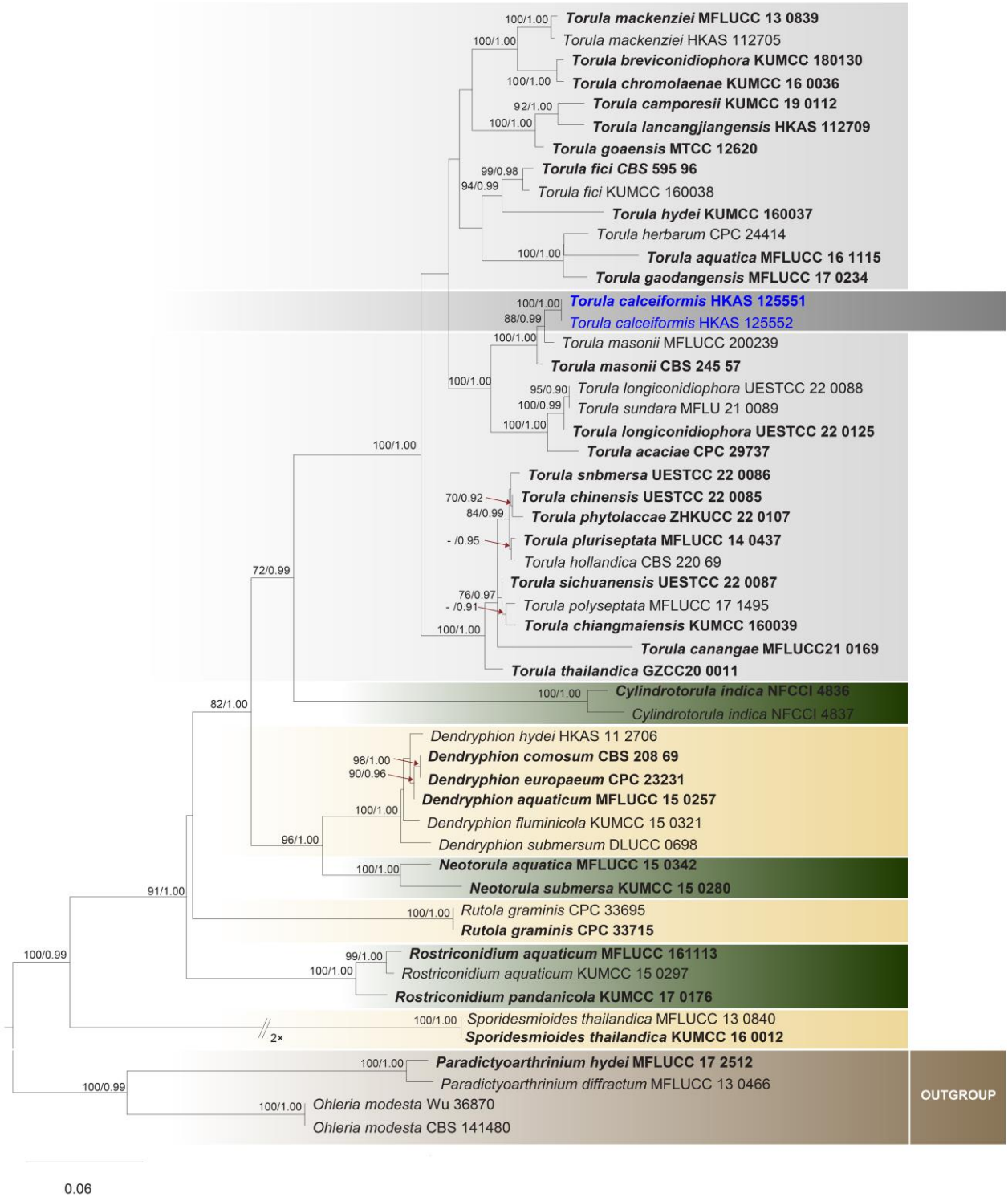


**Figure 47** – Phylogram generated form maximum likelihood analysis based on combined the multi-gene alignment of LSU, SSU, *ef1α*, *rpb2* and ITS sequence data representing Torulaceae in Pleosporales. Related sequences are taken from Torulaceae and additions according to the BLAST searches in NCBI. Fifty-five strains are included in the combined analyses which comprised 3510 characters (LSU: 1–781, SSU: 782–1531, *ef1α*: 1532–2342, *rpb2*: 2343–3008, ITS: 3009–3510) after alignment. Bootstrap support values for ML equal to or greater than 70% and PP equal to or greater than 0.90 are given at the nodes as ML/PP. *Paradictyoarthrinium hydei* (MFLUCC17-2512), *Ohleria modesta* (Wu 36870), *Ohleria modesta* (CBS 141480) and *Paradictyoarthrinium diffractum* (MFLUCC13-0466) in Pleosporales were used as the outgroup taxa. The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.06 which represent the estimated number of nucleotide substitutions of site per branch.

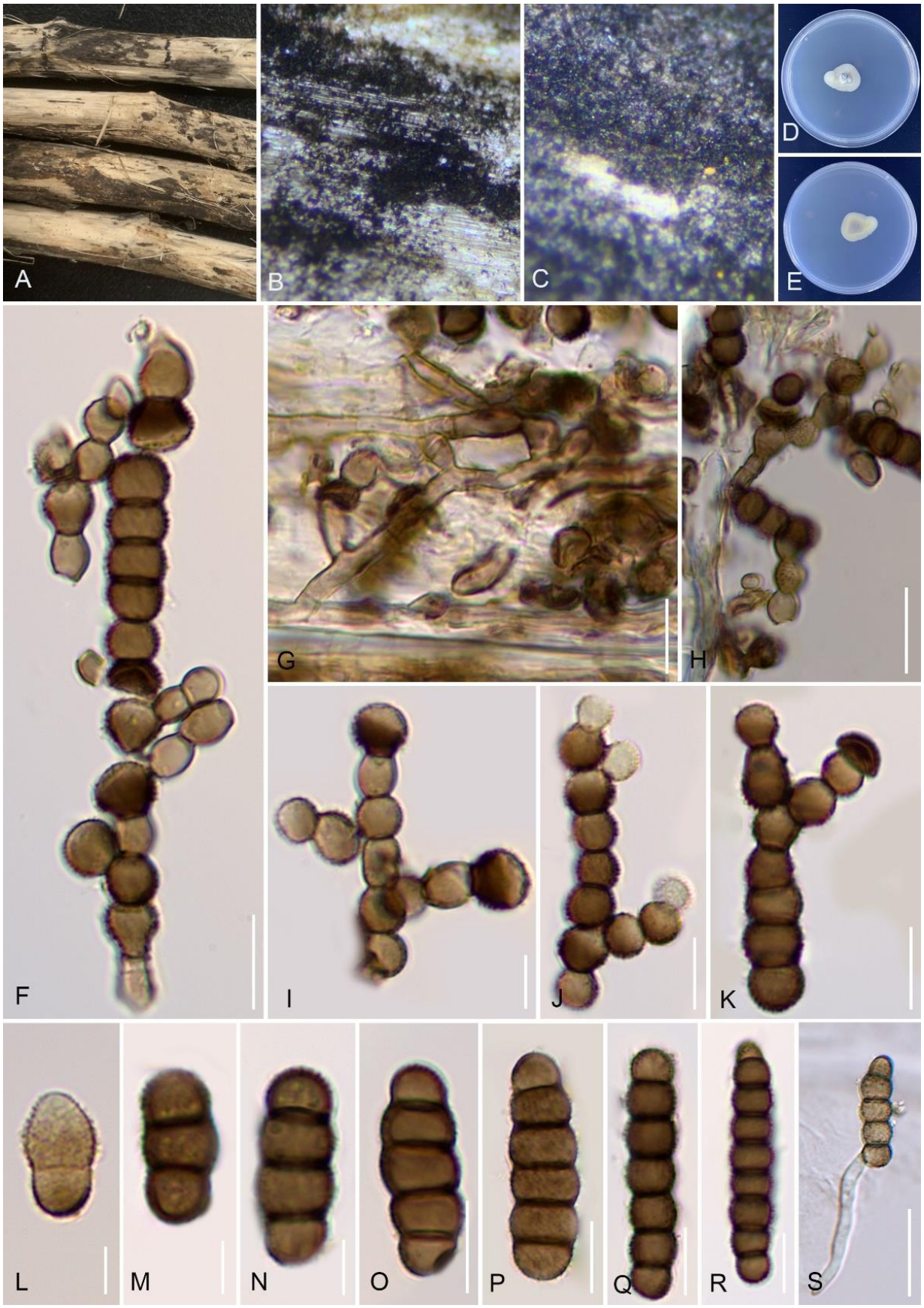


**Figure 48** – *Torula calceiformis* (holotype HKAS 125551). a–c Colonies on natural substrate. d–e Culture on PDA. f Conidiophores. g–h Conidiogenous cells giving rise to conidia. i–k Branched chains of conidia. l–r Conidia. s Germinated conidia. Scale bars: f–k, o–s = 10 μm, l–n = 5 μm.

-immersed on the substrate, branched, smooth, black brown hyphae. *Conidiophores* macronematous, mononematous, erect, simple, straight or flexuous, branched, verruculose, thick-walled, rough-walled, aseptate, dark brown at the base, hyaline at the apex, single cell 6.3–6.7 × 5.1–5.9 μm ($\bar{x}$ = 5.5 × 6.5 μm, n = 15). *Conidiogenous cells* polyblastic, terminal, smooth to verruculose, doliiform to ellipsoid, hyaline when young, dark brown to black when mature 22.6–23.8 × 5.4–6 μm ($\bar{x}$ = 23.2 × 5.7 μm, n = 20). *Conidia* catenate, acrogenous, monilioid, verruculose, thick-walled, rough-walled, 1–8-septate, pale brown when young; black brown when mature 21.9–33.3 × 7.2–11.2 μm ($\bar{x}$ = 27.6 × 9.2 μm, n = 10), single cell 6.3–6.9 × 4.3–5.2 μm ($\bar{x}$ = 6.6 × 4.8 μm, n = 20).

*Culture characters*: Conidia germinating within 12 h on PDA media at 25℃, reaching 3.1–3.3 cm after 25 days, medium sparse, entire edge, slightly raised, smooth, no pigment. On PDA surface and reverse white.

Material examined – China, Guizhou Province, Zunyi City, Renhuai City, on dried wood, 5 October 2021, S.C. He, HSC351 (holotype HKAS 125551, ex-type living culture KUNCC22-12449). China, Guizhou Province, Zunyi City, Renhuai City, on dried wood, 5 October 2021, S.C. He, HSC275 (paratype HKAS 125552, living cultures KUNCC22-12448).

GenBank numbers – LSU: OP751052, ITS: OP751054, SSU: OP751050, *rpb2:* OQ630510, *ef1α*: OQ630512

Notes – The new species was isolated from unknown wood in China. Phylogenetic analyses of a multi-gene dataset showed that our species is closely related to *Torula masonii* (CBS 245.57, type), a species collected from *Brassica* sp. in the United Kingdom (Fig. 47). The base pair differences of *T. calceiformis* and *T. masonii* (CBS 245.57, DLUCC 0588, MFLUCC 20-0239) are seen as 0.37% differences in LSU (3/801 bp); 2.25% differences in ITS (12/532 bp); 0.25% differences in SSU (2/799 bp); 2.2% differences in *rpb2* (18/817 bp); and 0.47% differences in *ef1α* (4/856 bp). Morphologically, *T. calceiformis* differs from *T. masonii* by having branched conidiophores and wider of conidia (*T. calceiformis*: 7–11 μm *vs* 6–7(–8) μm: *T. masonii*) (Crous et al. 2015). Thus, we introduce *T. calceiformis* as a novel taxon.

***Trichoglossum*** Boud., Bull. Soc. mycol. Fr. 1: 110 (1885)

*Trichoglossum* is a paraphyletic genus in *Geoglossaceae* (*Geoglossales*, *Geoglossomycetes*) reported worldwide from tropical and temperate forests (Ekanayaka et al. 2017, Lee et al. 2021, Chakraborty et al. 2022, de la Fuente et al. 2022). *Trichoglossum* is typified by *Trichoglossum hirsutum* (Boudier 1907) and characterized by club-like, dark brown to black ascomata entirely covered with setae, septate paraphyses, 4–8-spored, and filiform, septate, brown ascospores (Boudier 1885, Lee et al. 2021, Chakraborty et al. 2022, de la Fuente et al. 2022). *Trichoglossum* has 20 accepted species/varieties/forms, supported by morphology and phylogeny (Ekanayaka et al. 2017, Lee et al. 2021, Chakraborty et al. 2022, de la Fuente et al. 2022, Species Fungorum 2023 (accessed March 2023)).

***Trichoglossum ailaoense*** H.L. Su & Q. Zhao, sp. nov. Fig. 50

MycoBank number: MB845968; Facesoffungi number: FoF12891

Etymology – Referring to the type locality Ailao Mountains, Yunnan Province in China.

Holotype – HKAS 124482

*Diagnosis*: Characterized by short asci and ascospores, the mature ascospores are dark brown and 0–3 septate, paraphyses are light brown at base and apex, hyaline in the middle.

*Saprobic* on the soil. Sexual morph: *Ascomata* superficial, scattered, 3–5 cm high, black, an inflated head that tapers into a thin stipe, typically spathulate, long stipitate. *Fertile part* 0.2–0.4 × 0.5 –1 cm, flattened, usually vertically grooved, irregularly twisted, black, surface dry, densely setose. *Stipe* up to 4.5 cm tall and about 1–3 mm in diam, cylindrical, surface densely setose, rough, black. *Ascomatal core* lightly brownish, 2.5–4.5 μm ($\bar{x}$ = 3.3 μm, n = 72) in middle, thick-walled cells of *textura intricata*. *Stipitipellis* 60–90μm ($\bar{x}$ = 70 μm, n = 14) thick, light brownish, 11–23 × 6–11 μm ($\bar{x}$ = 15.5 × 8 μm, n = 34), cells of *textura porrecta*, with setae at the outmost flanks.

*Hymenial setae* 130–340 × 5.5–12 µm ($\bar{x}$ = 193 × 7.8 µm, n = 28), needle-like, mostly sharp-pointed, rarely blunt or pointed, unbranched, mostly aseptate, rarely multi-septate, thick-walled, smooth, brown to black, numerous. *Stipe setae* 130–275 × 6.5–16 µm ($\bar{x}$ = 186 × 10.5 µm, n = 25), the shape and color are similar to hymenial setae. *Paraphyses* 2–3.5 µm ($\bar{x}$ = 172 × 2.9 µm, n = 54) in middle, longer than asci, filiform, swollen and hooked at the apices, swollen part 4–7.5 µm ($\bar{x}$ = 5.1 µm, n = 54) in diam, unbranched, septate, thin-walled, slightly smooth, light brown at base and apex, colourless in the middle, numerous. *Asci* 200–250 × 14–25 µm ($\bar{x}$ = 218 × 19.4 µm, n = 36), 8-spored, unitunicate, narrowly cylindrical to broadly clavate, rounded apex, narrowed below, inoperculate, pleurorhynchous, wall apically thickened and laterally thin, hyaline, amyloid. *Ascospores* (109/2/2) (46.5–)49.5–67 (–69.5) × (4–)4.8–6.9(–7.6) µm ($\bar{x}$ = 59.7 × 5.8 µm, Q = 7.7–14.2, *Q* = 10.4 ± 1.07), clavate with rounded ends, slightly curved to straight, slightly smooth, thin-walled, 0–3-septate, with 1–4 large oil guttules, initially hyaline, eventually becoming dark brown. Asexual morph: Undetermined.

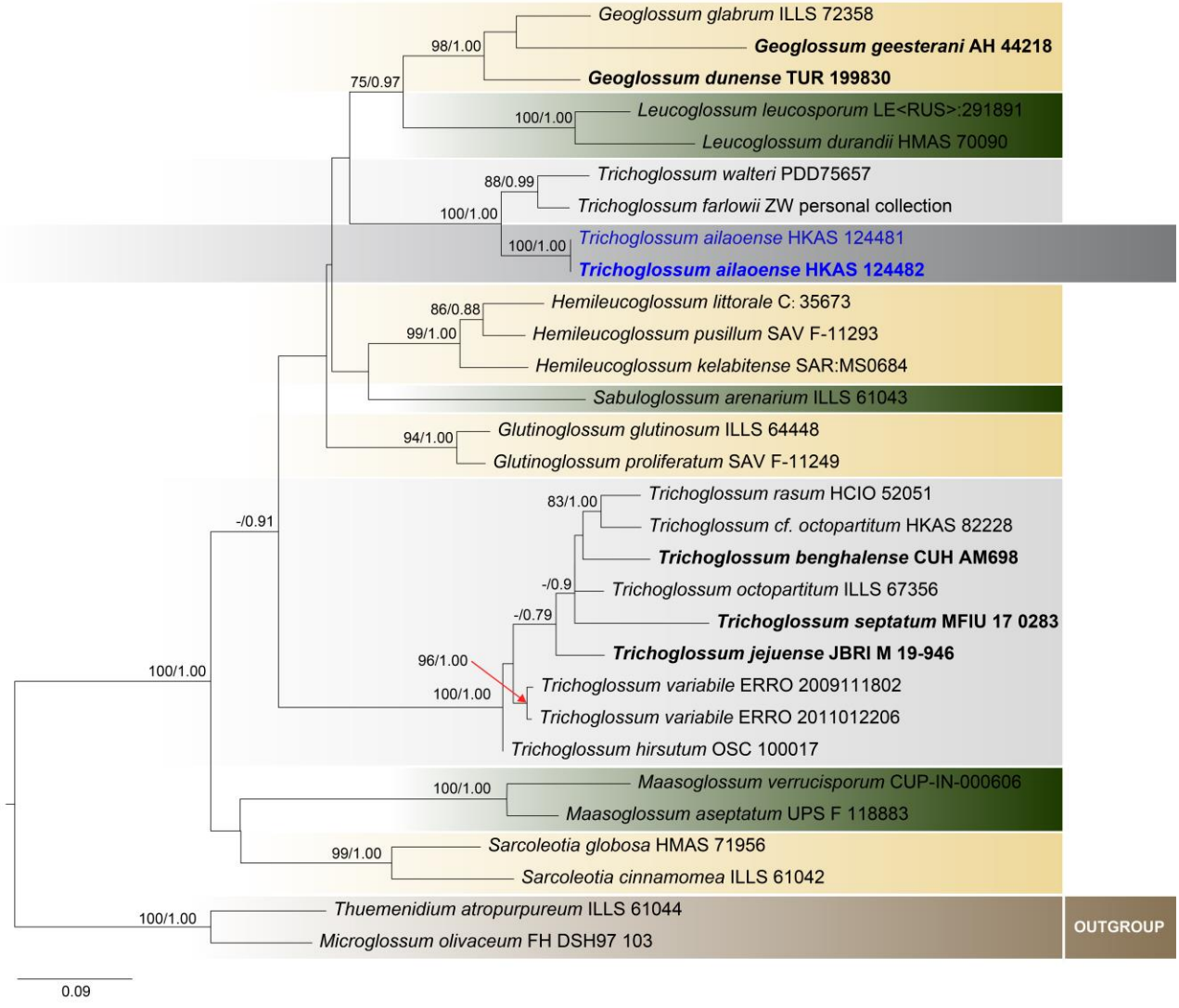


**Figure 49** – Phylogenetic tree obtained from maximum likelihood analyses of ITS sequences data representing the species of Geoglossaceae. Thirty strains were included in the analyses, which comprised 520 characters after alignment. Bootstrap support values for ML equal to or greater than 75% and PP equal to greater than 0.75 are indicated at the nodes as ML/PP. The tree is rooted to *Thuemenidium atropurpureum* (ILLS 61044) and *Microglossum olivaceum* (FH-DSH97-103). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.09 which represents the estimated number of nucleotide substitutions of site per branch.


**Figure 50** – *Trichoglossum ailaoense* (HKAS 124482, holotype). a Habitat. b–c Typical mature apothecia. d Vertical section of apothecia. e Section of ascomatal core. f–h Hymenial setae. i Transverse section of stipe. j Stipitipellis. k Paraphyses and immature asci. l–n Asci. o Ascospores. Scale bars: b–c = 1 cm, d = 200 µm, e = 50 µm, f–i = 100 µm, j = 10 µm, k–n = 50 µm, o = 20 µm.

Material examined – China, Yunnan Province, Ailao Mountains, alt. 2434 m, on soil, 1 September 2021, H.L. Su, SHL145 (holotype HKAS 124482). Yunnan, Ailao Mountains, alt. 2478 m, on soil, 29 August 2021, H.L. Su, SHL64 (paratype HKAS 124481).

GenBank numbers – HKAS 124481: ITS: OP538028; HKAS 124482: ITS: OP538029

Notes – The phylogenetic analyses show that *Trichoglossum ailaoense* is sister to the *Tri. walteri* and *Tri. farlowii* (Fig. 49). They all have clavate, black apothecia, densely covered with needle-like setae and similar paraphyses. However, *Tri. walteri* has larger asci and ascospores, and the mature ascospores are 7-septate, while the mature ascospores of *Tri. ailaoense* are 3-septate. *Trichoglossum farlowii* has mature light brown ascospores with 5 septa, while *Tri. ailaoense* has mature dark brown ascospores with 3 septa. De la Fuente (2022) introduced two species (*Tri. caespitosum* and *Tri. tropicale*) without ITS. *Trichoglossum ailaoense* is obviously different from *T. caespitosum* in macroscopical morph and ascospores, *Tri. caespitosum* has caespitose ascomata with compressed ascogenous portion, however, *Tri. ailaoense* has scattered ascomata with oblate oval ascogenous portion, besides, *Tri. ailaoense* has smaller ascospores (46.5–69.5 × 4–7.6 μm) than *Tri. caespitosum* (119–127 × 5–7 μm). *Trichoglossum ailaoense* and *Tri. tropicale* are different in paraphyses and ascospores, *Tri. ailaoense* has swollen and hooked apex, while *Tri. tropicale* has capitate to bulbous apex, besides, *Tri. ailaoense* has distinctly smaller ascospores than *Tri. tropicale* (122–132 × 5–5.5 μm).

***Zeloasperisporium*** R.F. Castañeda, Mycotaxon 60: 284 (1996)

= *Neomicrothyrium* Boonmee, H.X. Wu & K.D. Hyde, in Wu, Schoch, Boonmee, Bahkali, Chomnunti & Hyde, Fungal Diversity 51(1): 217 (2011).

*Zeloasperisporium* was introduced by Castañeda et al. (1996) to accommodate *Z. hyphopodioides* R.F. Castañeda, a species isolated from air in Cuba. The genus was placed as Ascomycota genera *incertae sedis* based on its morphology differing from other hyphomycetes. Subsequently, *Z. searsiae* was found to be a member of *Zeloasperisporiaceae* (*Zeloasperisporiales*) (Crous et al. 2015b, Hongsanan et al. 2015). Currently, the genus contains a total of eight species (Species Fungorum 2023). Sexual-asexual morphs have been described for four species, including *Z. ficicola*, *Z. hyphopodioides*, *Z. pterocarpi* and *Z. wrightiae* (Crous et al. 2007, Hongsanan et al.2015, Jayasiri et al. 2018). *Zeloasperisporium siamense* were introduced as asexual morphs (Hongsanan et al.2015). The remaining three species, including *Z. cliviae*, *Z. eucalyptorum*, *Z. searsiae were* introduced by sexual morphs (Cheewangkoon et al. 2009, Crous et al.2015b, c). In this study, we found a new asexual morph isolate of *Zeloasperisporium* from China on decaying stem of *Spartium junceum* L.

***Zeloasperisporium spartii*** Y. Gao, H. Gui, Gomes de Farias & K.D. Hyde, sp. nov. Fig. 52

MycoBank number: MB846298; Facesoffungi number: FoF12900

Etymology – Named after the host genus *Spartium* from which it was collected.

Holotype – HKAS 124663

*Saprobic* on decaying stem of *Spartium junceum* L. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 113–210 × 22–36 μm ($\bar{x}$ = 166 × 28 μm, n = 10), solitary or scattered, superficial, flattened, globose to subglobose, brown to dark brown spots, upper wall composed of ellipsoid angular cells, arranged in parallel radiating lines from the center to the outer rim covering the host, with a poorly developed basal layer and an irregular margin. Outer cell layers darker than central cell layers, ostioles lacking. *Pycnidial wall* 10–20 μm wide, composed of 1–3 layers of thin-walled, pale brown, large cells of *textura angularis*. *Conidiogenous cells* 4–6 × 4.5–6 μm. ($\bar{x}$ = 5.2 × 5.3 μm, n = 20), hyaline or light yellow, globose to subglobose, simple, smooth, *Conidia* 15–22 × 3–5 μm ($\bar{x}$ = 19 × 4 μm, n = 30), hyaline, with 2 transverse septa, thin-walled, smooth, lunate to fusiform, straight or curved, wide in the middle, tapering on both sides.

Culture characteristics – Conidia germinating on PDA within 24 hr. Germ tubes produced an end of conidia. Colonies on PDA grow slowly, reaching 1 cm after 4 weeks at 25–27 °C, irregular,

hard, irregular bulge, dark brown at the middle with white margins, mycelium superficial to immersed in media.

Material examined – China, Yunnan Province, Kunming City, Kunming Institute of Botany Garden, decaying stem of *Spartium junceum* (Fabaceae), 20 April 2021, Y. Gao, GY93 (holotype HKAS 124663, ex-type living culture CGMCC: 3.23751).

GenBank numbers – HKAS 124663 = LSU: OP555447, SSU: OP555444; CGMCC: 3.23751 = LSU: OP555448, SSU: OP555445

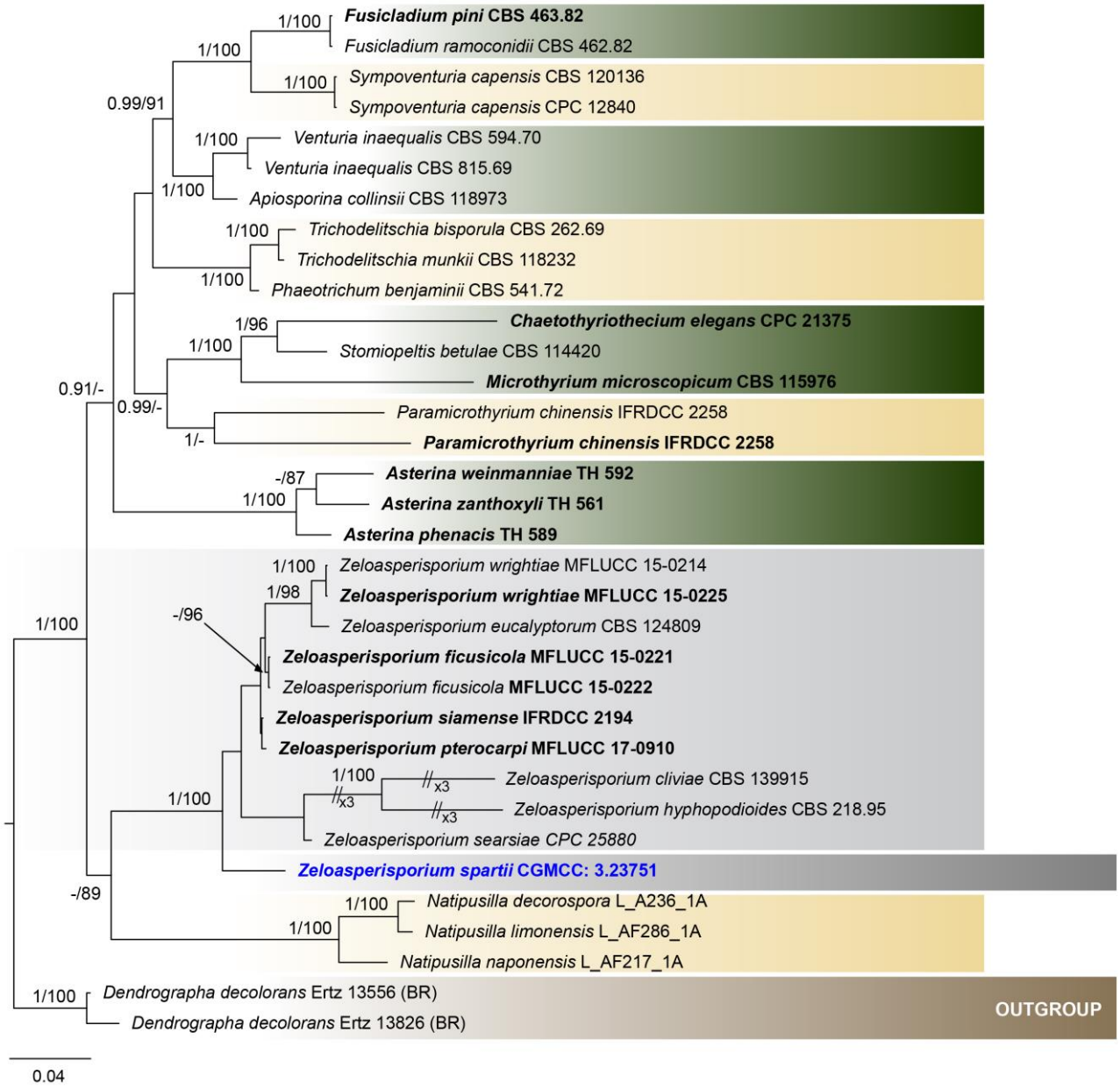


**Figure 51** – Phylogenetic tree obtained from Bayesian inference analyses of a combined LSU and SSU sequence dataset representing the species of *Zeloasperisporium*. Thirty-four taxa were included in the combined analyses, which comprised 1387 characters (LSU = 1–826, SSU = 827–1387) after alignment. Bootstrap support values for ML and MP equal to or greater than 70% and PP equal to greater than 0.9 are indicated at the nodes as PP/ML. The tree is rooted to *Dendrographa decolorans* (Ertz 13556, Ertz 13826 (BR)). The ex-type strains are in bold and the new isolates of this study are in blue. Bar = 0.04 which represent the estimated number of nucleotide substitutions of site per branch.

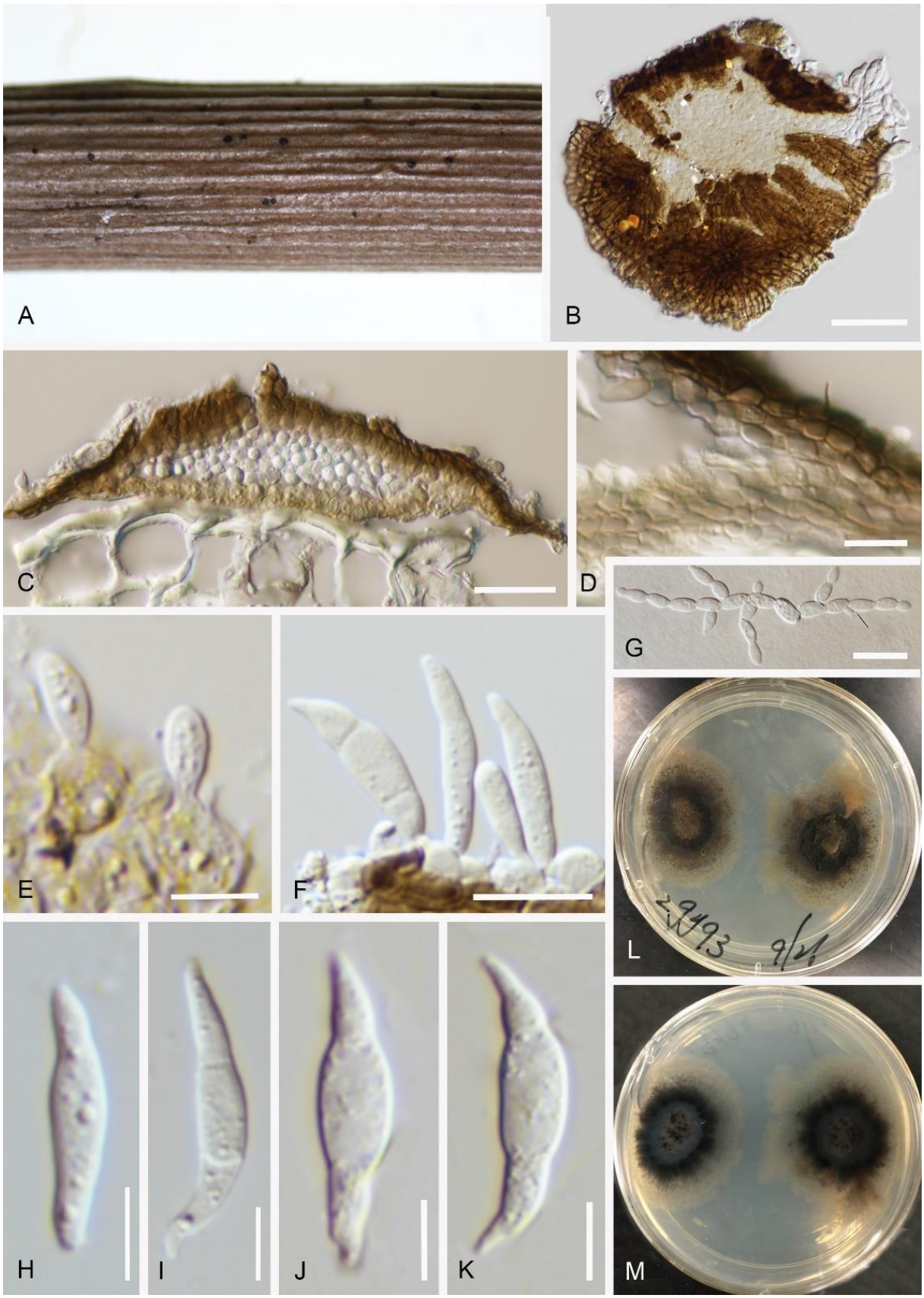


**Figure 52** – *Zeloasperisporium spartii* (ex-type living culture HKAS 124663). a Conidia on the substrate. b Reverse view of the conidioma. c Vertical section of the conidioma. e, f Conidiogenous cells and growing conidia. g Germinated conidium. h–k Conidia. l Frontal view of the culture. m Reverse view of the culture. Scale bars: b = 50 µm, c = 20 µm, d = 10 µm, e = 5 µm, f, g = 10 µm, h–k =5 µm.

Notes – Phylogenetic analyses based on a multi-gene sequence dataset showed that *Zeloasperisporium spartii* can be distinguished from all species of *Zeloasperisporium* by branch length with 100% ML/1.00 PP support (Fig. 51). Our novel species *Z. spartii* clusters with the strain of *Z. ficusicola* (MFLUCC 15-0222). There are great differences between *Z. spartii* and *Z. ficusicola* in morphology. *Zeloasperisporium spartii* differs from *Z. ficusicola* in having larger (15–22 μm diam), lunate to fusiform, 3-septate conidia *vs* 14–16 μm diam, fusiform to obclavate or cylindrical, 1-septate conidia (Hongsanan et al. 2015). Thus, we introduce *Z. spartii* as a novel taxon.

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