

ARTICLE

Morphological and phylogenetic studies of Ascomycota from gymnosperms in Sichuan Province, China

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Abstract

Gymnosperms constitute more than 39% of forest species worldwide, playing a crucial role in terrestrial ecosystems and supplying significant quantities of wood, resin, medicinal plants and other resources key to human economic development. The fungi associated with gymnosperms serve as valuable resources exhibiting diverse biological activities. This study explored the diversity of Ascomycota associated with gymnosperms belonging to Cupressaceae, Cycadaceae, Ginkgoaceae, Pinaceae and Podocarpaceae in Sichuan Province, which harbors the second-largest number of gymnosperm species in China. Through multi-locus phylogenetic analysis and morphological examination, we introduce a new family Neodictyocheiroporaceae (Helotiales), two new genera: *Neodictyocheiropora* (Neodictyocheiroporaceae) and *Neogregarithecium* (Dictyosporiaceae), as well as 21 new species and 12 new host or country records. The new species include *Aposphaeria sichuanensis*, *Camposporium pini*, *Circinotrichum podocarpi*, *Conlarium metasequoiae*, *Dictyosporium cycadicola*, *Ellisemia cryptomeriae*, *Gregarithecium bambusae*, *Kiflimonium cryptomeriae*, *Kylindria cryptomeriae*, *Memnoniella cunninghamiae*, *Neodictyocheiropora appendiculate*, *Neodictyocheiropora sichuanensis*, *Neogregarithecium sichuanense*, *Niesslia cryptomeriae*, *Niesslia podocarpi*, *Nigrocephalum cycadicola*, *Parasympodiella cryptomeriae*, *Phragmocamarosporium ginkgonis*, *Thyridaria pini*, *Triposporium cryptomeriae*, *Vibrissea catenata*. New host or country records are documented for *Codinaea dwaya*, *Conidiocarpus caucasicu*, *Distoseptispora tectonae*, *Fulvoflamma eucalypti*, *Gyrothrix encephalarti*, *Harzia sphaerospora*, *Musicillium elettariae*, *Nigrograna locuta-pollinis*, *Phragmocephala atra*, *Pseudochaetosphaeronema magnoliae*, *Velutinus sichuanensis*, *Xenorousoella triseptata*. Furthermore, we propose the transfer of *Fulvoflamma* (Helotiales genera *incertae sedis*) to Mniaceaceae (Leotiales) based on morphological characteristics and phylogenetic analysis. Our findings highlight the discovery of unique and uncommon fungi within less speciose genera such as *Gregarithecium*, *Kiflimonium*, *Kylindria*, *Nigrocephalum*, *Parasympodiella*, *Phragmocamarosporium*, *Fulvoflamma*, *Harzia*, *Musicillium* and *Xenorousoella*, emphasizing the distinctive mycota associated with gymnosperms.

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INTRODUCTION

Fungi, as a remarkably diverse group of organisms, play crucial roles in ecosystems and exhibit substantial economic importance, serving as pathogens, biocontrol agents, biofuels, food and food additives, industrial enzymes, and pharmaceuticals (El-Tarabily & Sivasithamparam 2006, Gawai 2018, Singh et al. 2018, Copetti 2019, Hyde et al. 2020b, Pour et al. 2021, Bhunjun et al. 2022, Shahryari & Niknezhad 2023). The number of fungal species based on host association was estimated to be 1.5 to 12 million, while the number using high-throughput sequencing was estimated to be 11.7 to 13.2 million (Wu et al. 2019, Tedersoo et al. 2021, Hyde 2022). However, only about 150,000 fungal species have been discovered and reported to date, leaving a vast number of undescribed fungal resources in nature (Hyde 2022). Researchers actively investigate the mycological diversity thriving on various hosts and within diverse ecological environments, elucidating their distinct functionalities. Filamentous fungi possess complex biosynthetic pathways that produce a wide variety of often biologically active metabolites (Cox 2024). For example, white-rot fungi can produce some compounds with antibacterial and anticancer properties during their secondary metabolism (Pinar & Rodríguez-Couto 2024). The metabolites of Xylariales are very diverse, some exhibiting antibacterial and antiviral effects; however, many functions remain unexplored (Helaly et al. 2018). Furthermore, applied research reveals the role and potential of fungi in environmental services such as bioremediation and pollution mitigation and as a resource for developing drugs to combat various human diseases (Hyde et al. 2019b, Niego et al. 2023). Therefore, investigating fungal resources across diverse hosts and ecological settings can yield ecological and environmental services for human well-being, including health and nutritional benefits crucial to various industries (Niego et al. 2023). Their diverse applications and potential for further discovery make fungi a vital area of immense value in global sustainable development.

Gymnosperms, a group of evolutionary ancient plants, have long intrigued scientists due to their unique characteristics and ecological significance (De La Torre et al. 2020). Gymnosperms comprise 13 families, 86 genera, and more than 1000 species (Shen et al. 2022). Gymnosperms account for more than 39% of forest species worldwide, play a vital role in terrestrial ecosystems, and hold significant economic value (Ran et al. 2018). They are a primary source of wood, resin and medicinal plants, highlighting their importance in various industries (De La Torre et al. 2020). Beyond these products, gymnosperms also offer nutritional value, with edible seeds such as pine nuts and certain tree fruits, providing food resources for humans and wildlife (De La Torre et al. 2020). The leaves and seeds of many gymnosperms, including Ginkgoaceae, Pinaceae, Cupressaceae, and Podocarpaceae species, have significant medicinal value (Ye et al. 2021). They are used to produce commercially available drugs and dietary supplements (Shen et al. 2022). The most important and promising role of gymnosperms is as a source of effective cancer drugs (Shen et al. 2022). Various natural compounds from gymnosperms are considered potential candidates for cancer treatment. For example, the natural compounds leelamine, α -pinene, and β -myrcene, obtained from gymnosperms (Li et al. 2009, Kuzu et al. 2014, Chen et al. 2015); paclitaxel, extracted from *Taxus brevifolia* (Taxaceae) (Zhu & Chen 2019); pinostrobin and pinocembrin, extracted from pine heartwood; and pycnogenol and enzologenes, extracted from pine bark, all exhibit anticancer activity (Rasul et al. 2013, Li et al. 2015).

Studies have found that many fungi associated with medicinal gymnosperms have developed the same or similar pharmacologically active substances as their hosts during their long-term co-evolution (Chakravarthi et al. 2008, Jia et al. 2016, Singh 2021, Wu et al. 2022). However, fungi inhabiting gymnosperms have received limited attention in the past despite their potential importance and uniqueness. Most studies on fungi associated with gymnosperms include rhizosphere soil fungi, pathogenic fungi, endophytic fungi, and some macrofungi, while there are relatively few studies on the saprobes (Zhou & Dai 2012, Kandhasamy et al. 2015, Bradshaw et al. 2016, Tirza et al. 2022). Gymnosperm-associated fungi may represent highly unique species or

important fungal resources with various biological activities. For example, *Alternaria* species isolated from the Cupressaceae species exhibit antiproliferative, antifungal, and antimicrobial activities (Soltani & Hosseini Moghaddam 2014); some endophytic fungi isolated from the *Ginkgo biloba* can produce compounds with diverse new functions, including antibacterial, antioxidant, anti-cardiovascular, anti-cancer, and some novel functions (Yuan et al. 2019). Cycadaceae roots harbor highly diverse endophytic fungi (Zheng et al. 2018); *Chaetomium*, *Aspergillus*, *Alternaria*, *Penicillium* and *Charobacter* have been isolated from the roots, stems, leaves, seeds and bark of *Ginkgo biloba* (Yuan et al. 2019); three fungal species with often highly specialized substrate ecologies (*Chaenothecopsis matai*, *C. nodosa*, and *C. novae-zelandiae*) are found on exudates of endemic New Zealand conifers of the Podocarpaceae species (Beimforde et al. 2023). Therefore, exploring the diversity of gymnosperms-associated fungi can provide a basis for understanding their potential functions and economic value.

China has a rich flora of gymnosperms, and gymnosperm species co-dominate more than half of China's forest area (Li et al. 2021). There are ten gymnosperm families in China, among which the Ginkgoaceae is endemic (Yang 2015). Sichuan Province harbors six families of gymnosperms, with Pinaceae and Cupressaceae constituting the primary groups (Yang 2015). Sichuan boasts 81 gymnosperm species, accounting for 31.2% of the total in China, making it as the province with the second-highest diversity of gymnosperm species, after Yunnan Province (Yang 2015). The unique and diverse climate of Sichuan Province may provide favorable conditions for the development of gymnosperms. In this study, we surveyed specimens belonging to Cupressaceae, Cycadaceae, Ginkgoaceae, Pinaceae and Podocarpaceae in the gymnosperms from terrestrial ecosystems and a total of 127 isolates were obtained from June 2022 to October 2023. Based on the multi-locus phylogenetic analysis and morphological examination, we introduce a new family, two new genera, 21 new species, and 12 new host/country records. Species descriptions, illustrations, and updated phylogenetic trees indicating the placement of taxa are provided. This study broadens our understanding of the diversity of gymnosperms-associated fungi.

MATERIALS AND METHODS

Sample collection, morphological examination and isolation

Ascomycota fungal diversity within Cupressaceae, Cycadaceae, Ginkgoaceae, Pinaceae, and Podocarpaceae (Fig. 1) in Sichuan Province, China, was investigated over four seasons, from June 2022 to October 2023. While investigating the diversity of gymnosperm fungi, we also collected several bamboo and grass specimens. Living plant tissue and dead branches, leaves, bark, and wood were collected from 10 sites (University of Electronic Science and Technology of China; Xiyuan Avenue; Jiudaoguai; Pujiang County, Chengdu City; Songlin Village, Neijiang City; Zhongba Forest Park, Pengzhou City; Zhougong Mountain, Ya'an City; Longcanggou National Forest Park, Ya'an City; Luding County, Ganzi Prefecture; Daolingou, Luzhou City) in Sichuan Province. The specimens were taken into the laboratory in paper envelopes for examination. Microscopic characters were observed and recorded using a Nikon SMZ800N stereo microscope equipped with a Nikon DS-Fi3 camera and a Nikon ECLIPSE Ni-U microscope fitted with a Nikon DS-Ri2 microscope camera (Nikon Corporation, Japan). Measurements were conducted using the Nikon NIS-Elements Documentation Imaging Version 5.21.00 (Nikon Corporation, Japan). All photographs were processed using Adobe Photoshop version 22.0 (Adobe Inc., USA). Single spore isolation was made following the method described by Senanayake et al. (2020). Germinated ascospore/conidia were individually transferred to potato dextrose agar (PDA) media plates and incubated in the dark at 25 °C. Culture characteristics were examined and recorded at regular intervals after 1–3 weeks. For some specimens, obtaining a culture was not feasible, necessitating the direct extraction of DNA from fruiting structures instead (Wanasinghe et al. 2018).

The holotypes are deposited in the Herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (HKAS), Kunming, China, and all specimens are deposited in the Herbarium of the University of Electronic Science and Technology (HUEST), Chengdu, China. The ex-type

cultures are deposited in the China General Microbiological Culture Collection Center (CGMCC) in Beijing, China, and all living cultures are deposited in the University of Electronic Science and Technology Culture Collection (UESTCC), Chengdu, China. The taxonomic descriptions of the new taxa are deposited in Facesoffungi and MycoBank.

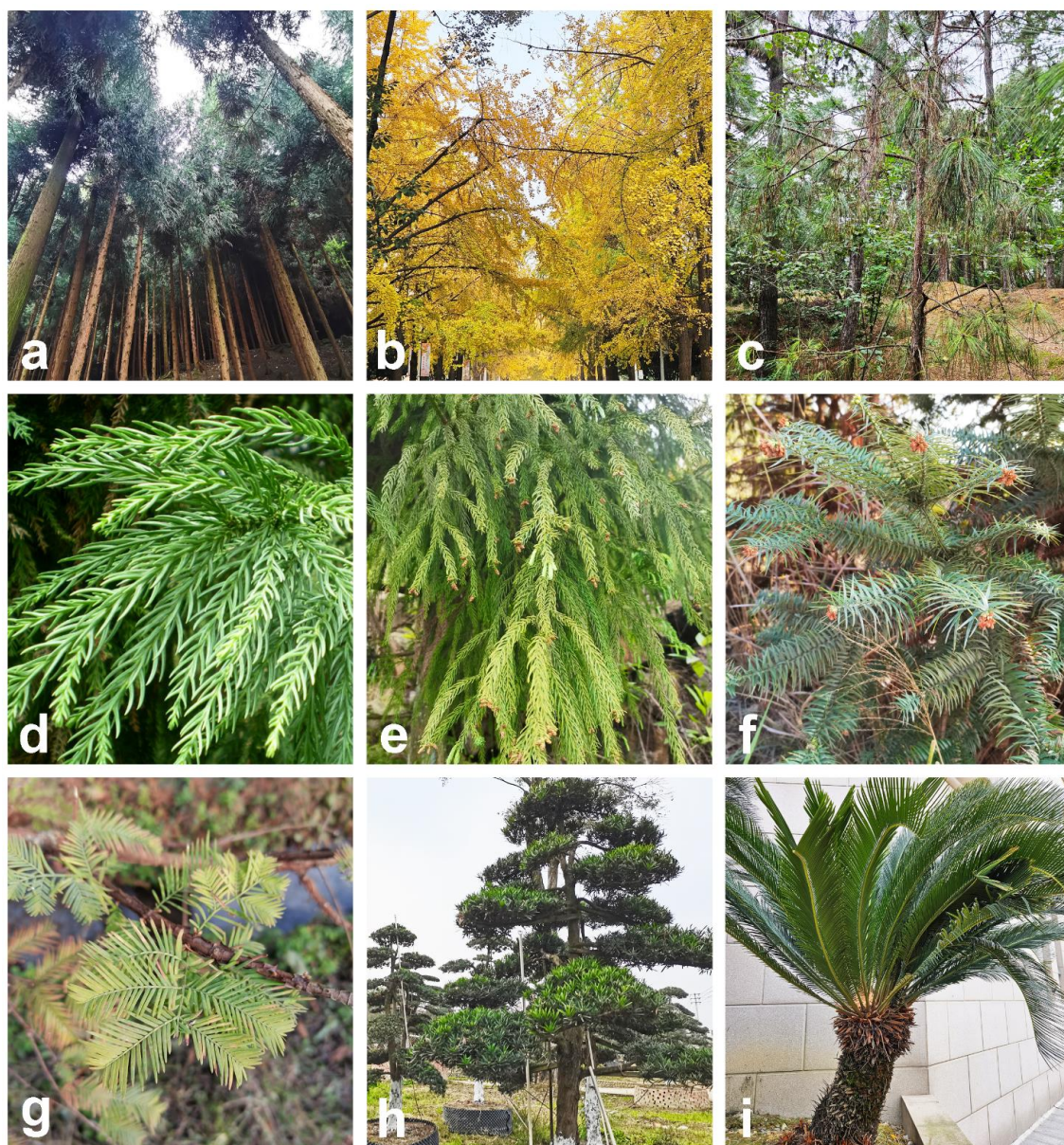


Figure 1 – Gymnosperms in Sichuan Province. a Dense *Cunninghamia lanceolata* forest (Cupressaceae). b *Ginkgo biloba* forest (Ginkgoaceae). c Pine forest (Pinaceae). d *Cryptomeria fortune* (Cupressaceae). e *Cryptomeria japonica*. f *Cunninghamia lanceolata*. g *Metasequoia glyptostroboides* (Cupressaceae). h *Podocarpus macrophyllus* (Podocarpaceae). i *Cycas revoluta* (Cycadaceae).

DNA extraction, PCR amplification, and sequencing

Fungal genomic DNA was extracted from mycelia using the Trelief™ Plant Genomic DNA Kit (TSINGKE Biotech, Shanghai, China) according to the manufacturer's protocol. Eight different loci: the nuclear ribosomal internal transcribed spacer (ITS: ITS1–5.8S–ITS2), the nuclear ribosomal small subunit rRNA (SSU), the nuclear ribosomal large subunit rRNA (LSU), the partial translation elongation factor 1-alpha (*tef1-α*), the partial second largest subunit of RNA polymerase II (*rpb2*), the partial beta-tubulin (*tub2*), the partial calmodulin (*cmdA*) and the partial actin (*act*)

were selected for study and amplified by polymerase chain reaction (PCR). The corresponding primer pairs and PCR conditions are listed in Table 1. The final reaction volume of the PCR reagent was 25 μ L, containing 2 μ L of DNA template, 1 μ L each of the forward and reverse primer, 8.5 μ L of double-distilled water (ddH₂O), and 12.5 μ L of 2 $\times$ Flash PCR MasterMix (mixture of DNA Polymerase, dNTPs, Mg²⁺ and optimized buffer; CoWin Biosciences, Jiangsu, China). The PCR products were visualized by 1% agarose gel electrophoresis. Sanger sequencing was conducted by Tsingke Biological Technology (Beijing, China).

Table 1 Loci used in this study and the corresponding PCR primers and conditions.

Locus	PCR primers	PCR: thermal cycles	References
ITS	ITS9mun or ITS5/ITS4_KYO1 or ITS4	(94 °C: 30 s, 54 °C: 30 s, 72 °C: 30 s) $\times$ 35 cycles	White et al. (1990), Toju et al. (2012)
LSU	LR0R/LR5	(94 °C: 30 s, 56 °C: 30 s, 72 °C: 1 min) $\times$ 35 cycles	Vilgalys & Hester (1990), Cubeta et al. (1991)
SSU	PNS1/NS41	(94 °C: 30 s, 56 °C: 30 s, 72 °C: 1 min) $\times$ 35 cycles	Hibbett (1996)
<i>tef1-α</i>	EF1-983F or EF1-728F/EF1-2218R	(94 °C: 30 s, 58 °C: 30 s, 72 °C: 1 min) $\times$ 35 cycles	Carbone & Kohn (1999), Jaklitsch et al. (2005), Rehner & Buckley (2005)
<i>rpb2</i>	fRPB2-5F or dRPB2-5f/fRPB2-7cR or dRPB2-7r	(94 °C: 30 s, 58 °C: 30 s, 72 °C: 1 min) $\times$ 35 cycles	Liu et al. (1999), Sung et al. (2007), Voglmayr et al. (2016)
<i>tub2</i>	Bt-2a/Bt-2b	(94 °C: 30 s, 56 °C: 30 s, 72 °C: 1 min) $\times$ 35 cycles	Glass & Donaldson (1995)
<i>cmdA</i>	CAL-228F/CAL2Rd	(94 °C: 30 s, 56 °C: 30 s, 72 °C: 1 min) $\times$ 35 cycles	Carbone & Kohn (1999), Groenewald et al. (2013)
<i>act</i>	ACT-512F/ACT-783R	(94 °C: 30 s, 56 °C: 30 s, 72 °C: 1 min) $\times$ 35 cycles	Carbone & Kohn (1999)

Phylogenetic analyses

According to the corresponding Sanger sequencing chromatograms, unstable sequencing data at the ends of the fragments were manually trimmed and assembled into consensus sequences using SeqMan Pro version 7.1.0 (DNASTAR, Inc. Madison, Wisconsin, USA). Barcode sequences of all species were downloaded from the NCBI nucleotide database using the R package Analysis of Phylogenetics and Evolution (APE) (Paradis & Schliep 2019).

The multiple sequence alignments were conducted using MAFFT version 7.310 (Katoh et al. 2002) with options “--adjustdirectionaccurately --auto,” and the alignment files were further trimmed using trimAl version 1.4 (Capella-Gutiérrez et al. 2009) with the option “-gapthreshold 0.5”, which only allows 50% of taxa with a gap in each site. The best-fit nucleotide substitution models for each locus were selected using PartitionFinder version 2.1.1 (Lanfear et al. 2016) under the Corrected Akaike Information Criterion (AICC). All sequence alignments were concatenated using an in-house Python script.

Maximum Likelihood (ML) and Bayesian analysis (BI) were conducted based on individual and combined datasets. ML phylogenetic trees were obtained using the IQ-TREE version 2.0.3 (Nguyen et al. 2014), and the topology was evaluated using 1000 ultrafast bootstrap replicates. The BI was conducted using parallel MrBayes version 3.2.7a (Huelsenbeck & Ronquist 2001). The ML trees were visualized using ggtree (Yu 2020) and further edited in Adobe Illustrator version 16.0.0.

RESULTS

The taxonomic status of the species is identified according to Wijayawardene et al. (2022a) and combined with morphology and phylogeny. Species descriptions are listed alphabetically by class, order, family, genus and species.

Ascomycota Caval. -Sm., Biol. Rev. 73: 247 (1998)

Ascomycota is the largest and most varied group of fungi and one of the most diverse and ubiquitous phyla of eukaryotes, with over 98,334 species (Wijayawardene et al. 2022a, Bánki et al. 2024). Its species exist in numerous ecological niches in both terrestrial and aquatic habitats. They fulfill many vital roles in all ecosystems and act as mutualists, parasites, and pathogens of animals, plants, and other fungi (Maharachchikumbura et al. 2021). More than 40% of all named Ascomycota are lichenized (Schoch et al. 2009), while several classes of Ascomycota produce mycorrhizal associations (Brodo et al. 2002, Maharachchikumbura et al. 2021).

Dothideomycetes O.E. Erikss. & Winka, Myconet 1(1): 5 (1997)

MycoBank number: MB501481; Facesoffungi number: FoF14145

Notes – Dothideomycetes represent the largest and most diverse class of ascomycete fungi (Schoch et al. 2009, Hyde et al. 2013, Haridas et al. 2020, Pem et al. 2021). Dothideomycetes typically produce flask-like structures called pseudothecia, but other morphologies also exist (Pem et al. 2021). Currently, Dothideomycetes is divided into two subclasses, Pleosporomycetidae and Dothideomycetidae, and some *incertae sedis* lineages, which represent 25 orders, 110 families and over 19,000 species (Wijayawardene et al. 2022a). Dothideomycetes have an incredibly diverse lifestyle and can be associated with various hosts/substrates (Haridas et al. 2020).

Capnodiales Woron., Annls mycol. 23(1/2): 177 (1925)

MycoBank number: MB90464; Facesoffungi number: FoF07632

Notes – Capnodiales, initially established with Capnodiaceae, is the second largest family within the Dothideomycetes. This order comprises leaf epiphytes associated with insect honeydew, often observed as black growths on leaf surfaces, fruit, and twigs (Crous et al. 2007a, Crous et al. 2009, Ruibal et al. 2009, Hyde et al. 2013, Chomnunti et al. 2014, Hongsanan et al. 2017b, Lücking et al. 2017, Videira et al. 2017, Abdollahzadeh et al. 2020, Wijayawardene et al. 2022a). The order encompasses fungi with highly diverse ecological niches, lifestyles and modes of nutrition, including saprobes, endophytes, epiphytes, plant pathogens, lichens, rock-inhabiting fungi and colonizers or hair shafts of mammals (Flegler 1976, Aptroot 2006, Crous et al. 2009, Crous 2010, De Hoog 2000).

Capnodiaceae (Sacc.) Höhn. ex Theiss., Verh. Kaiserl. -Königl. zool. -bot. Ges. Wien 66: 363 (1916)

MycoBank number: MB82008; Facesoffungi number: FoF06943

Notes – Members of Capnodiaceae have superficial ascomata with ovoid asci in fascicles and hyaline to dark, one to multiseptate ascospores. Anamorphs are dematiaceous, and include mycelial (phragmo- to dictyoconidia), spermatial and pycnidial synanamorphs (Flegler 1976, Cheewangkoon et al. 2009, Crous et al. 2009, Lu et al. 2022). Species of this family are widely distributed, especially prevalent in tropical and subtropical regions and temperate rainforests (Cannon & Kirk 2007).

Conidiocarpus Woron. Key to fungi (fungi imperfecti) 2: 743 (1917)

MycoBank number: MB7751; Facesoffungi number: FoF06946

Notes – *Conidiocarpus* was introduced by Woronichin in Jaczewski (1917), with *C. caucasicus* as the type species. *Conidiocarpus* is characterized by a dark, thin thallus consisting of radiating, septate hyphae, easily detached from the host surfaces (Jaczewski 1917, Chomnunti et al. 2011, Tennakoon et al. 2021). Hughes (1976) and Batista & Ciferri (1963) considered

C. penzigii as the type species and then considered *Conidiocarpus* as an asexual morph of *Phragmocapnias*. Bose et al. (2014) followed Hughes (1976) and transferred species of *Phragmocapnias* to *Conidiocarpus* based on the rules of nomenclature. In the study by Abdollahzadeh et al. (2020), based on phylogenetic analysis and comparison of morphological characters, *Phragmocapnias* was resurrected for species with conidiocarpus-like pycnidia that lack necks.

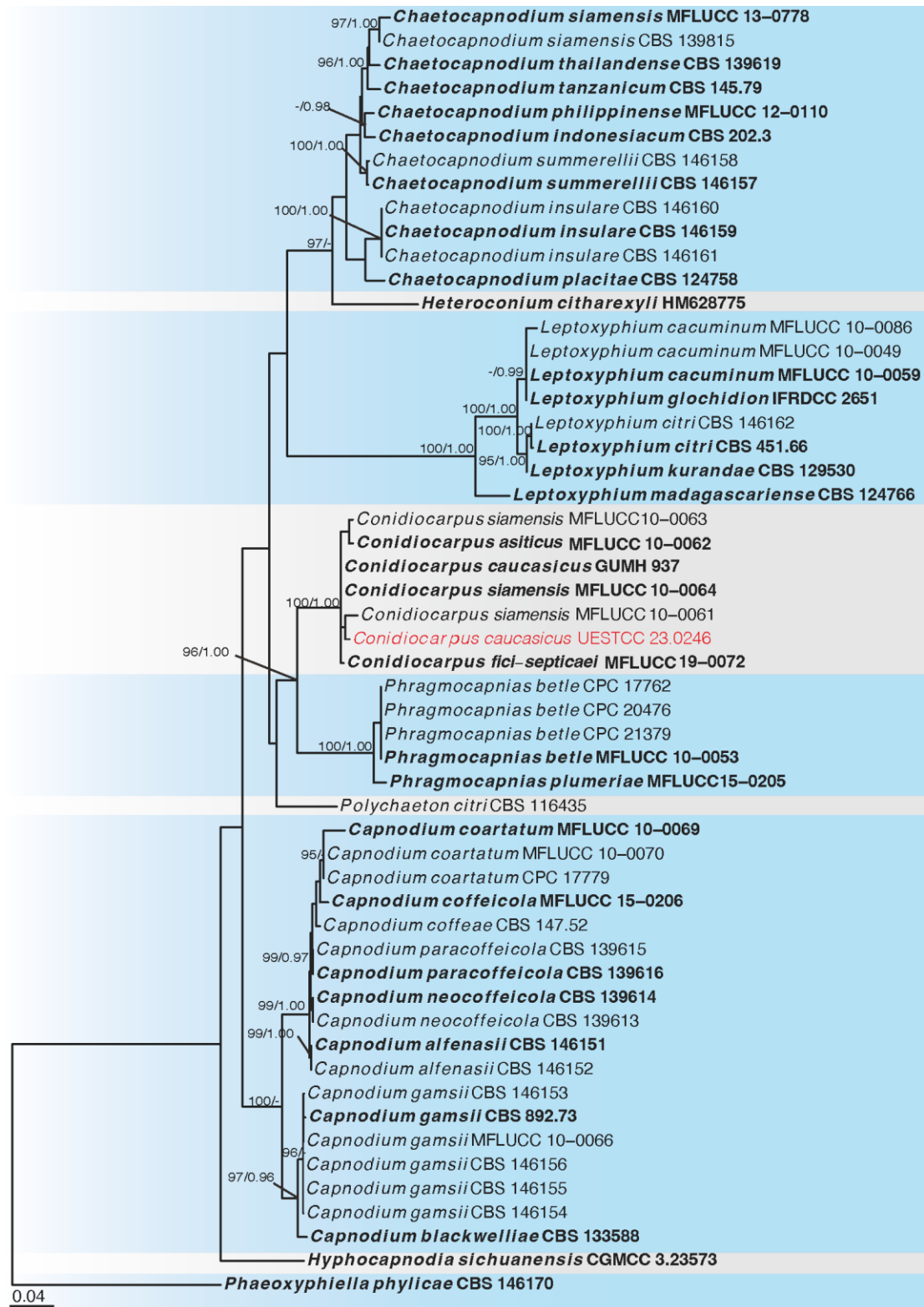


Figure 2 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, *rpb2* and *tef1-α*) of Capnodiaceae. The scale bar indicates 0.04 changes. The tree is rooted with *Phaeoxyphiella*

phylicae (CBS 146170) (Readeriellipsidaceae, Capnariales). The best ML tree with a final likelihood value of -14951.582 is presented. The alignment dataset comprises 54 taxa with 3289 sites, including 897 distinct patterns, 206 singleton sites and 2395 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Conidiocarpus caucasicus Woron. Key to fungi (fungi imperfecti) 2: 743 (1917).

Fig. 3

Mycobank number: MB803878

Saprobic on the surface of the needle-like leaves of *Cryptomeria japonica*. Asexual morph: *Thallus* superficial, consisting of a network of cylindrical and septate, 2.5–5.3 μm ($\bar{x}$ = 3.7 μm , n = 20), constricted at the septum, brown, dark towards the edge. *Pycnidia* 104–385 $\times$ 8–25 μm ($\bar{x}$ = 225 $\times$ 16 μm , n = 15), arising from capnodiaceous type hyphae, black at the base and stalk, 19–40 μm ($\bar{x}$ = 30 μm , n = 10) wide, *Pycnidium* 60–112 $\times$ 19–57 μm ($\bar{x}$ = 84 $\times$ 37 μm , n = 15), conspicuous oval swelling, brown, comprising of cylindrical septate cells. *Ostiole* 12–20 μm ($\bar{x}$ = 16 μm , n = 10) wide, surrounded by hyaline hyphae. *Conidiogenous cells* form in the inner cells of the oval part. *Conidia* 3.5–5.2 $\times$ 1.9–2.8 μm ($\bar{x}$ = 4.3 $\times$ 2 μm , n = 30), oblong to ellipsoid, 1-celled, hyaline, thick-walled, rounded ends. Sexual morph: Undetermined.

Known distribution – China, Iran, Thailand

Culture characteristics – Colonies on PDA reaching 46 mm diam. after 45 days at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, dark brown at the margin, brown in the centre; reverse: divergent at the margin, black in the centre.

Material examined – China, Sichuan Province, Pengzhou City, Zhongba Forest Park, N 30°59'46", E 104°09'1", elevation 1150 m, 29 September 2022, on dead leaves of *Cryptomeria japonica*, W.H. Tian ZB18 (HKAS 13128), living culture CGMCC 3.25643 = UESTCC 23.0246.

GenBank numbers – ITS: OR887382, LSU: OR887093, *rpb2*: PP076815, *tef1- α* : PP076823

Notes – Multi-locus analyses of combined ITS, LSU, *rpb2* and *tef1- α* sequence data showed that *Conidiocarpus* isolates clustered in five subclades (Fig. 2). Various species are grouped closely in a single subclade, making it challenging to distinguish each species clearly. Moreover, the species exhibits the following noteworthy consistent morphological characteristics: the superficial thallus is characterized by a network of cylindrical and septate structures; pycnidia, which emerge from capnodiaceous-type hyphae, demonstrate a conspicuous oval swelling, with the brown pycnidium being composed of cylindrical septate cells; the ostiole is notably surrounded by hyaline hyphae; conidiogenous cells form within the inner cells of the oval structure; the species produces ellipsoid, 1-celled, hyaline conidia (Jaczewski 1917, Chomnunti et al. 2011, Tennakoon et al. 2021). Differences were only observed in the size of pycnidia, pycnidium and conidia, a phenomenon most likely attributed to environmental conditions such as season. (Table 2). Only LSU sequence data are accessible for the ex-type strains of *C. caucasicus* (GUMH937) and *C. siamensis* (MFLUCC10-0064), and LSU/ITS sequences for other species. These species are similar based on the BLASTn NCBI GenBank database search of ITS and LSU sequences. Combining the consistent morphological characteristics and similar molecular sequences among these species in the genus *Conidiocarpus*, *C. asiaticus*, *C. caucasicus*, and *C. siamensis* might be synonyms of *Conidiocarpus caucasicus*, which is the older name. Still, more collection and further evidence are required to substantiate this. We introduce the first record of *C. caucasicus* UESTCC 23.0246 from China and provide sequence data of ITS, LSU, *rpb2* and *tef1- α* .

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

Mycobank number: MB90563; Facesoffungi number: FoF08715

Notes – Pleosporales is the largest order in the Dothideomycetes, and a group characterized by flask-shaped pseudothecia in most instances (Wijayawardene et al. 2022a). The diversity of species in Pleosporales is high, and most species are saprobes on decaying plant material in freshwater, marine, or terrestrial environments (Câmara et al. 2002, Kodsueb et al. 2006, Zhang et

al. 2008, Zhang et al. 2009a). The members of Pleosporales also can be epiphytes, endophytes or parasites on living leaves or stems, as hyperparasites on fungi or insects (Ramesh et al. 2003, Kruijs et al. 2006, Zhang et al. 2012).

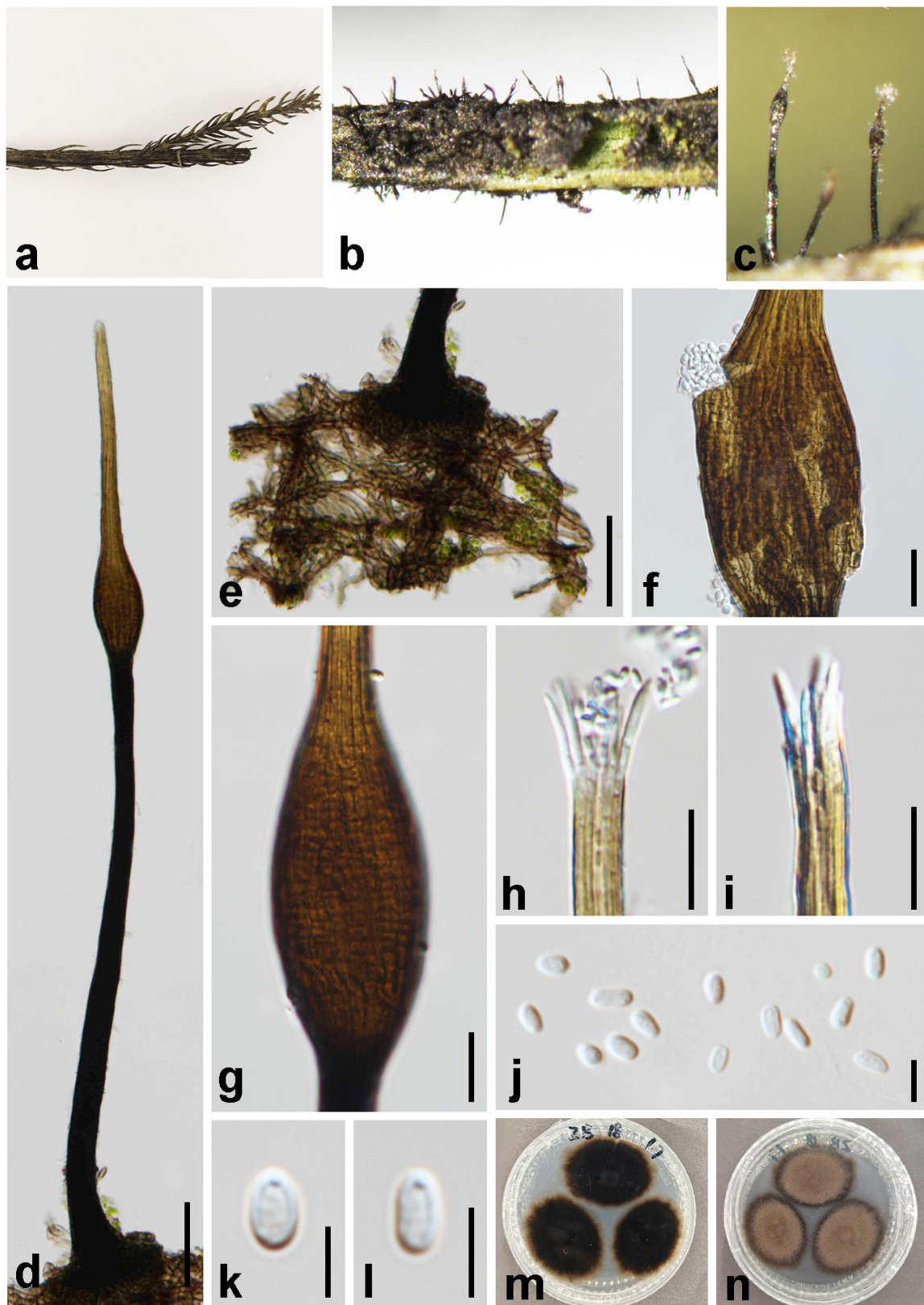


Figure 3 – *Conidiocarpus caucasicus* (HKAS 131287). a Specimen. b, c Black mycelium on the host surface. d Pycnidia. e Mycelial network. f, g Conical pycnidium and pycnidium wall. Conidia in the swollen part in f. h, i Ostiole. j–l Conidia. Scale bars: d, e = 50 μ m, f–i = 20 μ m, j–l = 5 μ m.

Table 2 Morphological comparison of the *Conidiocarpus* taxa (length unit: μm), and unavailable information is represented by “-”.

Species name	Pycnidia (High)	Pycnidia (width)	Pycnidium (width)	Conidia (length)	Conidia (width)	References
<i>Conidiocarpus asiaticus</i>	302–387	17–25	18–24	2.5–3.7	1–1.4	Chomnunti et al. (2011)
<i>Conidiocarpus caucasicus</i>	70–95	-	-	4.1–5.5	2.1–2.8	Jaczewski (1917)
<i>Conidiocarpus fici-septicae</i>	240–280	25–30	25–30	4–5	1–2	Tennakoon et al. (2021)
<i>Conidiocarpus siamensis</i>	378–458	22–31	36–41	4.5–5.2	1.9–2.4	Chomnunti et al. (2011)
<i>Conidiocarpus caucasicus</i>	104–385	8–25	19–57	3.5–5.2	1.9–2.8	This study

Dictyosporiaceae Boonmee & K.D. Hyde, Fungal Diversity 80: 457–482 (2016)

Mycobank number: MB551574; Facesoffungi number: FoF01256

Notes – The family Dictyosporiaceae was established by Boonmee et al. (2016). Dictyosporiaceae are distributed worldwide, and most taxa are saprobes on plant litter, especially dead or decaying wood in freshwater and terrestrial habitats (Boonmee et al. 2016, Li et al. 2017, Yang et al. 2018, Tian et al. 2022). Most of the asexual morphic members of the Dictyosporiaceae are hyphomycetes and characterized by the production of cheiroid, digitate, palmate and/or dictyosporous, and pale brown to brown conidia (Abdel-Aziz 2016, Boonmee et al. 2016, Wang et al. 2016).

Dictyosporium Corda, Weitenweber’s Beitr. Nat. 1: 87 (1837)

Mycobank number: MB8001; Facesoffungi number: FoF08210

Notes – *Dictyosporium* was established by Corda (1836), with *D. elegans* as the type species. Members of the *Dictyosporium* are mostly saprobes found on dead wood and plant litter in terrestrial and aquatic habitats (Ho et al. 2002, Hyde & Goh 1998, Pinnoi et al. 2006, Pinruan et al. 2007, Shu et al. 2024, Yang et al. 2018). There are 88 epithets listed in Index Fungorum (2024), some of which have been transferred to similar genus *Dictyocheiropsora* based on phylogeny or morphology (Boonmee et al. 2016, Yang et al. 2018).

Dictyosporium cycadicola W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 5

Mycobank number: MB854679; Facesoffungi number: FoF16269

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

Holotype – HKAS 134909

Saprobic on dead stems of *Cycas revoluta*. Asexual morph: Hyphomycetous. Colonies on a natural substrate were punctiform, sporodochial, scattered, dark and dark brown, and flaky. Mycelium comprised partly immersed, partly superficial, brown, septate and branched hyphae. Conidiophores micronematous, reduced to conidiogenous cell. Conidiogenous cells $10\text{--}22 \times 1.6\text{--}4 \mu\text{m}$ ($\bar{x} = 14.5 \times 3 \mu\text{m}$, $n = 20$), holoblastic, cylindrical, sometimes flat at base. Conidia $18.5\text{--}33 \times 12.5\text{--}21 \mu\text{m}$ ($\bar{x} = 26.5 \times 16 \mu\text{m}$, $n = 35$), solitary, oval to ellipsoid, brown to dark brown, cheiroid, not complanate, composed of 4–5 rows, inflated, rows not separating, each row consisting of 4–10 cell, guttulate, without appendages. Sexual morph: Undetermined.

Material examined – China, Sichuan Province, Chengdu city, University of Electronic Science and Technology of China, N $30^{\circ}45'24''$, E $103^{\circ}55'54''$, elevation 480 m, 12 June 2022, on dead stems of *Cycas revoluta*, W.H. Tian U08_1 (HKAS 134909, holotype).

GenBank numbers – ITS: PP740382, LSU: PP740388, SSU: PP740394, *tef1- α* : PP776570

Notes – Phylogenetic analyses of combined ITS, LSU, SSU and *tef1- α* sequence data showed that our collection (HKAS 134909) sister to the type strain of *Dictyosporium krabiense* (MFLU 16-

1890) (Fig. 4). Morphologically, our collection (HKAS 134909) differs from *D. krabiense* by larger conidiogenous cells ($10\text{--}22 \times 1.6\text{--}4 \mu\text{m}$ vs. $2\text{--}3.5 \times 2\text{--}3 \mu\text{m}$), longer conidia ($18.5\text{--}33 \times 12.5\text{--}21 \mu\text{m}$ vs. $14\text{--}17 \times 15\text{--}20 \mu\text{m}$), without appendages vs. 1–2 appendages and more cells in the conidia row (4–10 cell vs. 4–6 cell) (Tibpromma et al. 2018). The type strain of *Dictyosporium krabiense* lacks an ITS sequence (Tibpromma et al. 2018). Based on other pairwise nucleotide comparisons, our collection (HKAS 134909) differs from the type strain of *D. krabiense* (MFLU 16-1890) by 1/809 bp (no gaps) in LSU, 6/981 bp (gaps: 6/981 bp) in SSU, and 18/926 bp (gaps: 3/926 bp) in *tef1- α* . Based on their morphological differences, we introduce *D. cycadicola* as a new species of *Dictyosporium*.

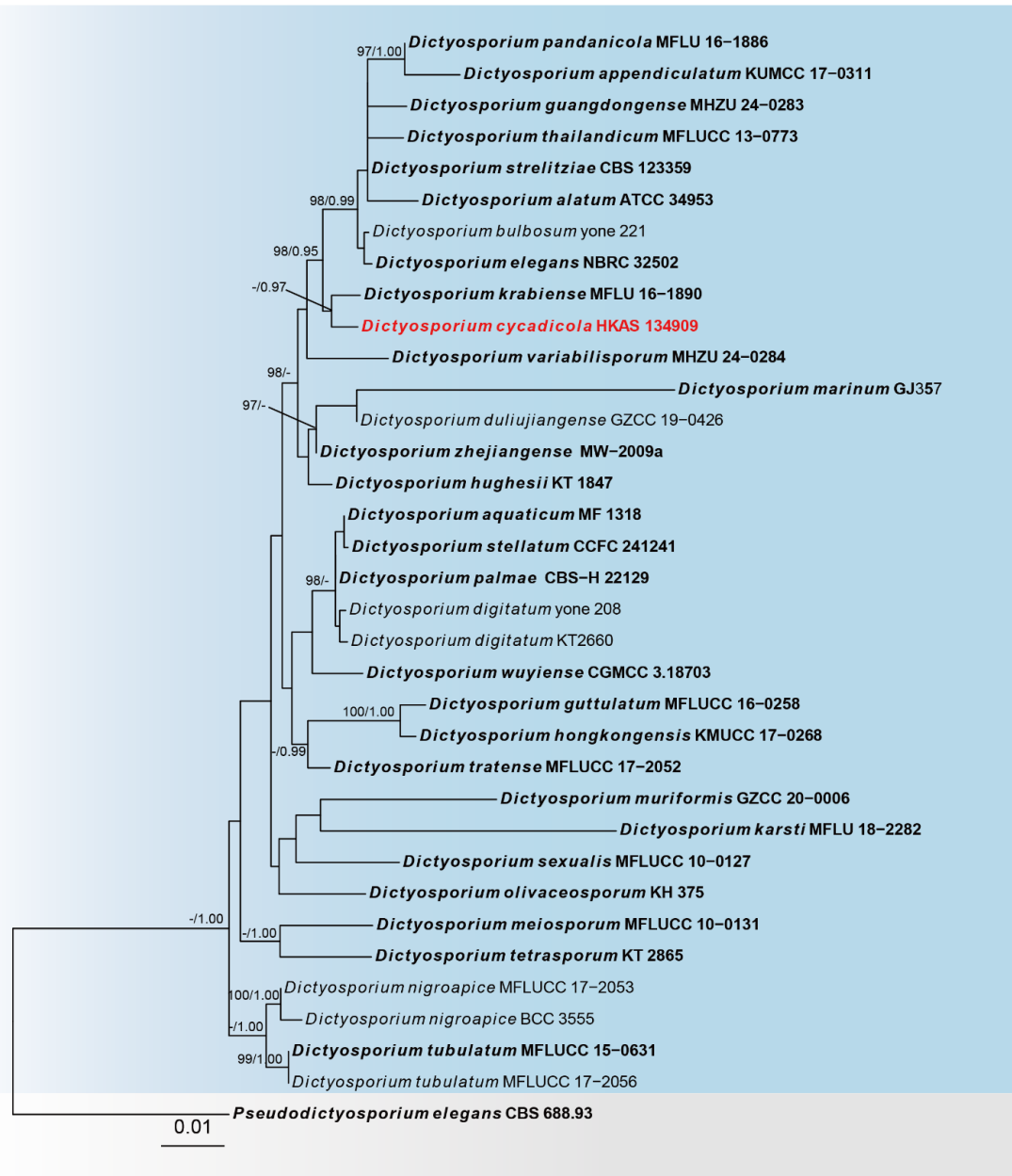


Figure 4 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU and *tef1- α*) of *Dictyosporium*. The scale bar indicates 0.01 changes. The tree is rooted with *Pseudodictyosporium elegans* (CBS 688.93) (Dictyosporiaceae, Pleosporales). The best ML tree with a final likelihood value of -9273.453 is presented. The alignment dataset comprises 35 taxa with 3334 sites, including 577 distinct patterns, 263 singleton sites and 2849 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and

posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

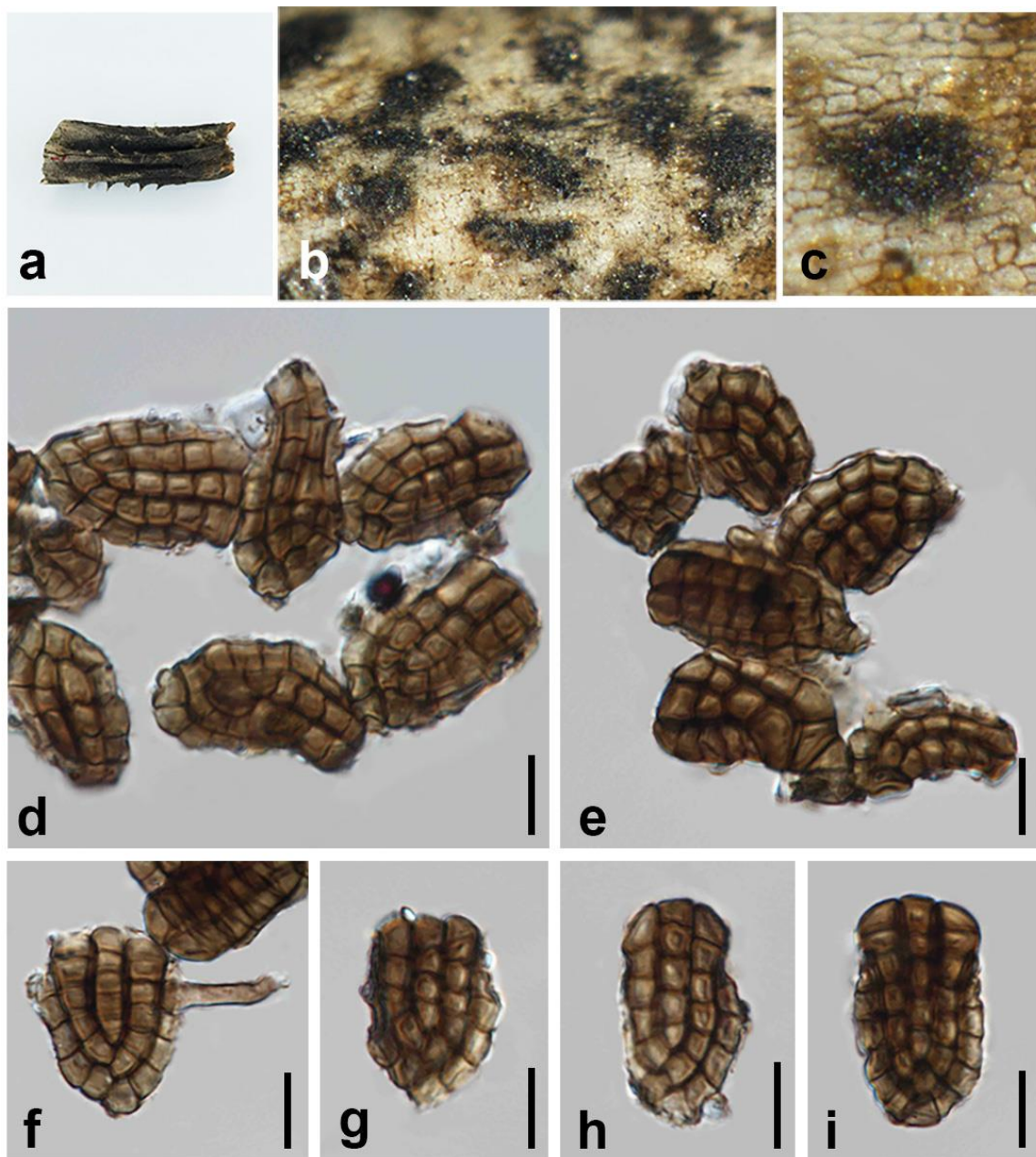


Figure 5 – *Dictyosporium cycadicola* (HKAS 134909, holotype). a Specimen. b, c Colonies on dead stems of *Cycas revoluta*. d–f Conidiogenous cells and conidia. g–i Conidia. Scale bars: d–i = 10 µm.

Gregarithecium Kaz. Tanaka & K. Hiray., Stud. Mycol. 82: 88 (2015)

Mycobank number: MB811298; Facesoffungi number: FoF08213

Notes – *Gregarithecium* was proposed by Tanaka et al. (2015) to accommodate the *G. curvisporum*. Currently, *G. curvisporum* remains the only species in the genus and is only known from its sexual morph (Tanaka et al. 2015). *Gregarithecium* is characterized by immersed to erumpent, depressed globose to hemispherical ascomata with flattened base, fissitunicate, 8-spored asci and hyaline broadly fusiform ascospores with a median septum, surrounded by an entire sheath (Tanaka et al. 2015).

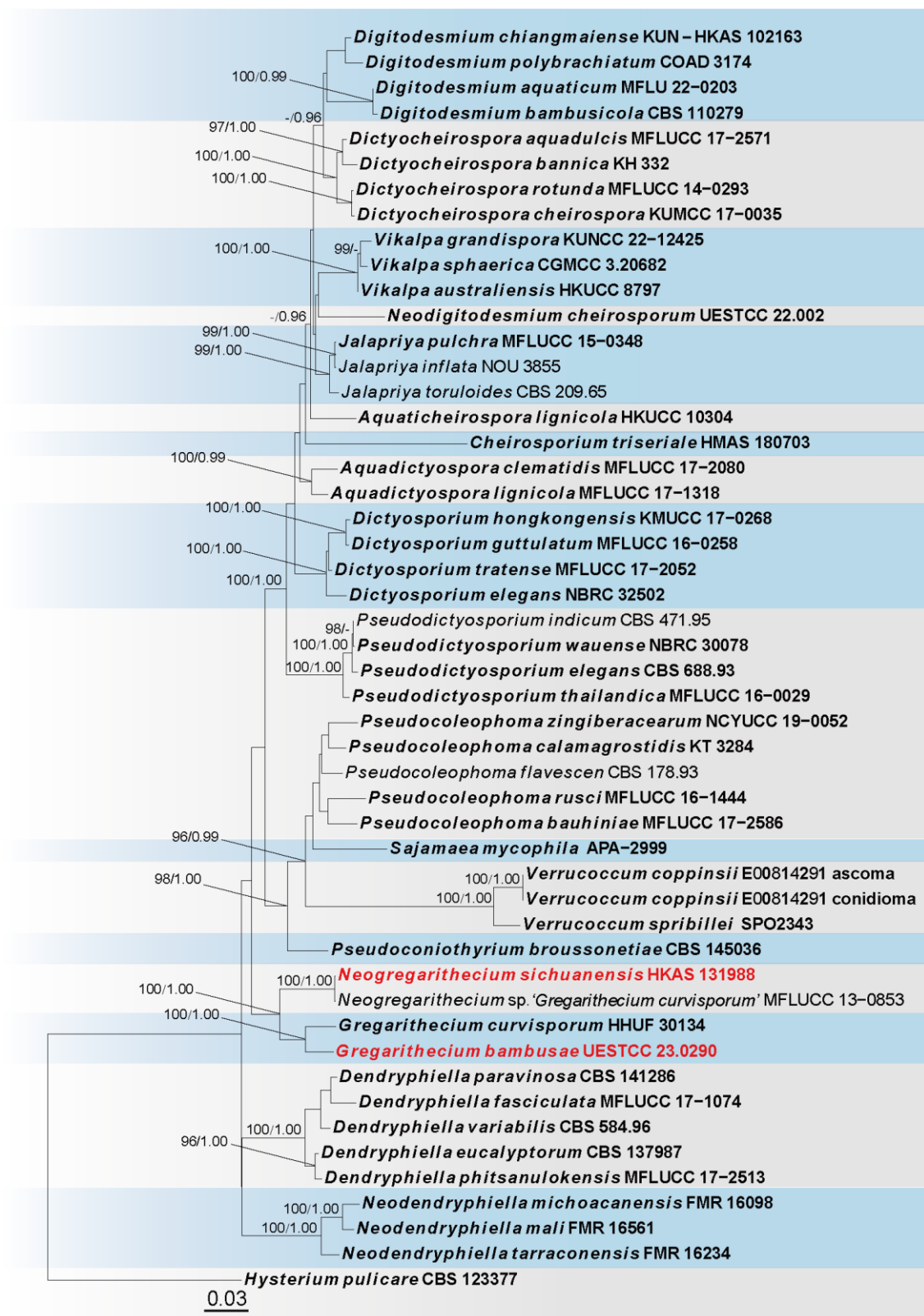


Figure 6 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU and *tef1-α*) of Dictyosporiaceae. The scale bar indicates 0.03 changes. The tree is rooted with *Hysterium pulicare* (CBS 123377) (Hysteriaceae, Hysteriales). The best ML tree with a final likelihood value of -17249.789 is presented. The alignment dataset comprises 50 taxa with 3313 sites, including 1063 distinct patterns, 303 singleton sites and 2408 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Gregarithecium bambusae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 7

Mycobank number: MB851874; Facesoffungi number: FoF02295

Etymology – Named after the host genus from which the holotype was collected, Bamboo.

Holotype – HKAS 131989

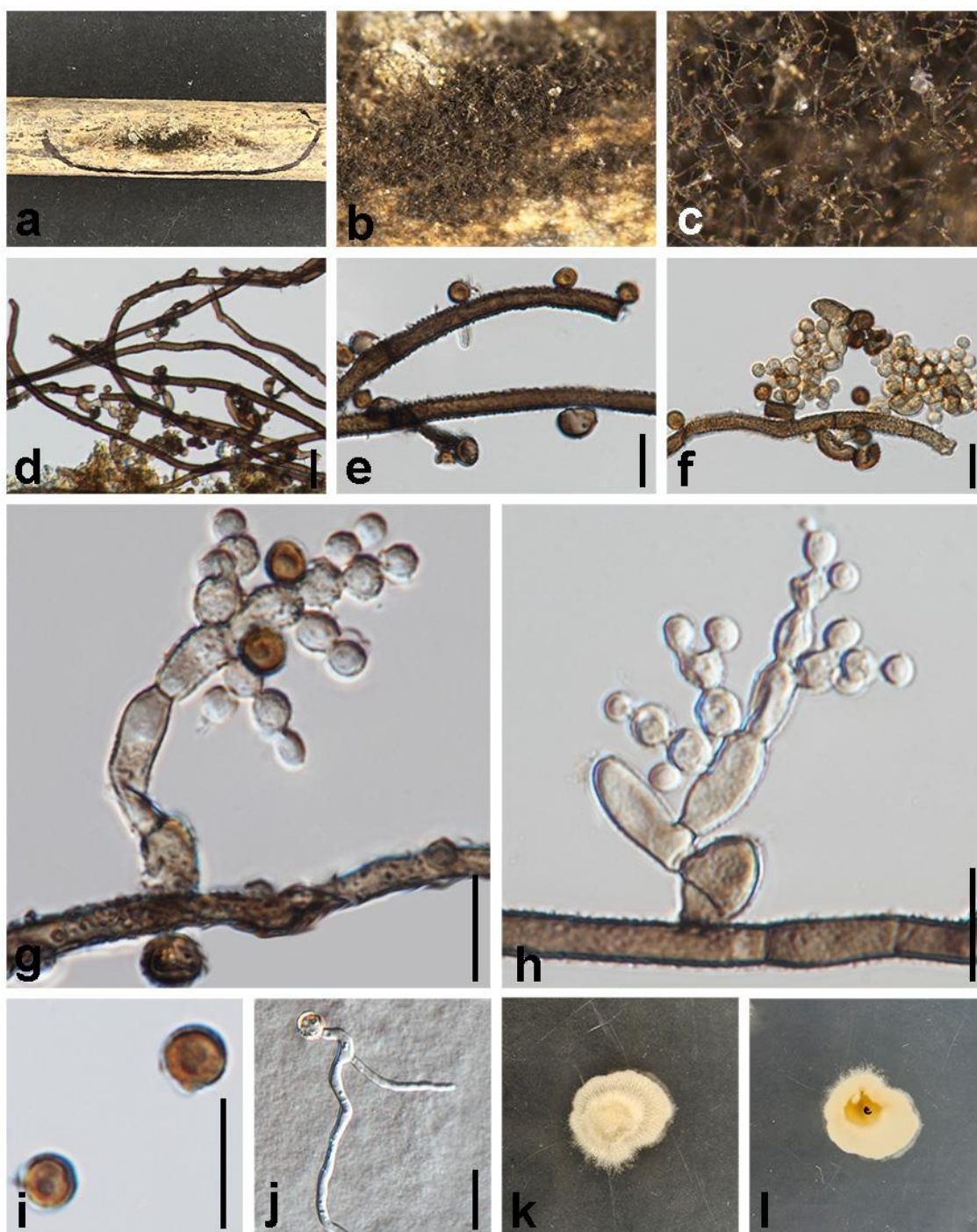


Figure 7 – *Gregarithecium bambusae* (HKAS 131989, holotype). a Specimen. b, c Mycelium on the host surface. d–f Conidiophores with lateral conidia. g, h Developing conidia in short acropetal chains. i Conidia. j Germinating conidium. k, l Culture characteristics. Scale bars: d = 20 μ m, e–j = 10 μ m.

Saprobic on the dead branch of bamboo. Asexual morph: Hyphomycetous. *Colonies* on natural substratum velvety, superficial, brown to dark brown. *Aerial hyphae* septate, pale to dark brown, verrucose. *Conidiophores* micronematosa to semi- macronematous, mononematous, arising

laterally from superficial hyphae, branched, 1–4-septate, hyaline to pale brown, becoming paler or subhyaline towards the apex, verrucose, cylindrical to ampulliform, flexuous, $10\text{--}48 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 25 \times 4 \mu\text{m}$, $n = 25$). *Conidiogenous cells* holoblastic, sympodial, discrete, retrogressive, branched, straight or slightly flexuous, hyaline to pale brown, verrucose, inflated, $6\text{--}14 \times 3\text{--}6 \mu\text{m}$ ($\bar{x} = 9 \times 4 \mu\text{m}$, $n = 25$). *Conidia* holoblastic, acropleurogenous, catenate, short, 1–4 acropetal chains, golden-brown to dark brown, verrucose, aseptate, globose, $3\text{--}5 \mu\text{m}$ ($\bar{x} = 4 \mu\text{m}$, $n = 30$) diam., with single germ pore ca $0.7\text{--}2 \mu\text{m}$ ($\bar{x} = 1.5 \mu\text{m}$, $n = 20$) diam.; conidial secession schizolytic. Sexual morph: Undetermined.

Culture characteristics – Colony on PDA reaching 12 mm diam. in 10 days at 25 °C in the dark, colonies from above: irregular circular, white, uneven entire, raised in centre, with denser mycelium at the center; from below: white, pale brown in the centre, margin undulated.

Material examined – China, Sichuan Province, Chengdu City, Yunkiao Wetland, N $30^{\circ}52'32''$, E $103^{\circ}53'23''$, elevation 570 m, 10 July 2022, on dead branch of bamboo, W.H. Tian YQ0710021 (HKAS 131989, holotype), ex-type CGMCC 3.25698 = UESTCC 23.0290.

GenBank numbers – ITS: PP294644, LSU: PP213251, SSU: PP213255, *tef1- α* : PP213050

Notes – *Gregarithecium curvisporum* was described by Tanaka et al. (2015) based on its sexual morphology and phylogenetic analyses. Multi-locus analyses of combined ITS, LSU, SSU and *tef1- α* sequence data showed that our collection (UESTCC 23.0290) is sister to the type strain of *G. curvisporum* (HHUF 30134) (Fig. 6). A comparison of sequence data of the ITS, LSU and SSU between *G. curvisporum* (HHUF 30134) and our strains (UESTCC 23.0290) show 93.26% sequence identity (318/341 bp, gaps: 10/341 bp) in ITS, 98.74% sequence identity (786/796 bp, no gaps) in LSU, and 99.03% sequence identity (1019/1029 bp, gaps: 3/1029 bp) in SSU. Consequently, we have identified our collection as a new species in *Gregarithecium*, marking it as the first known asexual morphic species within the genus.

Neogregarithecium W.H. Tian, K.D. Hyde & Maharachch., gen. nov.

Mycobank number: MB851875; Facesoffungi number: FoF16267

Etymology – Named after its morphological similarity to *Gregarithecium*.

Saprobic on the dead twigs of grass. Asexual morph: Hyphomycetous. *Colonies* on natural substrate velvety, superficial, brown to dark brown. *Aerial hyphae* septate, pale to dark brown, verrucose. *Conidiophores* micronematous, mononematous, arising laterally from superficial hyphae, simple or occasionally branched, aseptate, hyaline to pale brown, becoming paler or subhyaline towards the apex, verrucose, cylindrical to ampulliform, straight to slightly flexuous. *Conidiogenous cells* holoblastic, discrete, unbranched, straight, hyaline to pale brown, verrucose, inflated. *Conidia* holoblastic, acrogenous, catenate, in short acropetal chains, golden-brown to dark brown, verrucose, aseptate, globose. Conidial secession schizolytic. Sexual morph: Undetermined.

Type species – *Neogregarithecium sichuanense* W.H. Tian, K.D. Hyde & Maharachch.

Notes – *Gregarithecium curvisporum* HHUF 30134 was introduced as the type of *Gregarithecium* by Tanaka et al. (2015). However, *G. curvisporum* (MFLUCC 13-0853) is mistakenly regarded as the type strain (Boonmee et al. 2016, Shen et al. 2022). *Gregarithecium curvisporum* (MFLUCC 13-0853) is a strain with only sequence data in NCBI but no morphological description. Based on pairwise nucleotide comparisons, *G. curvisporum* (MFLUCC 13-0853) differs from *G. curvisporum* (HHUF 30134) by 61/472 bp (gaps: 28/472 bp) in ITS; 19/825 bp (gaps: 5/825 bp) in LSU; 20/978 bp in SSU. However, comparisons of the ITS, LSU and SSU sequences of *G. curvisporum* (MFLUCC 13-0853) and *Neogregarithecium sichuanense* (HKAS 131988) revealed 99.03% sequence identity (508/513 bp, gaps: 3/513 bp) in ITS, 100% sequence identity (771/771 bp, no gaps) in LSU and 100% sequence identity (978/978 bp) in SSU. Therefore, the isolate MFLUCC 13-0853 probably belongs to *Neogregarithecium*.

According to the multi-locus phylogeny, *Neogregarithecium* sp. (MFLUCC 13-0853) and *Neogregarithecium sichuanense* (HKAS 131988) constitute a distinct clade sister to the *Gregarithecium curvisporum* (HHUF 30134) and *Gregarithecium bambusae* (UESTCC 23.0290) (Fig. 6). The asexual morphology of *Gregarithecium* has only been observed in *G. bambusae*

(UESTCC 23.0290) (this study). *Neogregarithecium* is distinct from *Gregarithecium* in the characteristics of conidiophores. *Neogregarithecium* has micronematous, simple or occasionally branched, aseptate, straight to slightly flexuous conidiophores. *Gregarithecium* has micronematous to semi-macronematous, branched, 1–4-septate, flexuous conidiophores. Moreover, based on pairwise nucleotide comparisons, *N. sichuanense* differs from the type species *G. curvisporum* (HHUF 30134) by 58/469 bp (gaps: 25/469 bp) in ITS; 19/772 bp (gaps: 5/772 bp) in LSU; 21/1025 bp (gaps: 1/1025 bp) in SSU. Thus, we introduce the new genus *Neogregarithecium* based on the morphology and multi-locus phylogeny.

Neogregarithecium sichuanense W.H. Tian, K.D. Hyde & Maharachch., sp. nov. Fig. 8

MycoBank number: MB851876; Facesoffungi number: FoF16270

Etymology – Named after the Sichuan province, China, where the holotype was collected.

Holotype – HKAS 131988

Saprobic on the dead twigs of grass. Asexual morph: Hyphomycetous. *Colonies* on natural substratum velvety, superficial, black. *Aerial hyphae* septate, dark brown, verrucose. *Conidiophores* micronematosa, mononematous, arising laterally from superficial hyphae, simple or occasionally branched, aseptate, hyaline to pale brown, becoming paler or subhyaline towards the apex, verrucose, cylindrical to ampulliform, straight to slightly flexuous, $5\text{--}10 \times 3\text{--}4\ \mu\text{m}$ ($\bar{x} = 6 \times 3.5\ \mu\text{m}$, $n = 25$). *Conidiogenous cells* polyblastic, discrete, unbranched, straight, hyaline to pale brown, verrucose, inflated, $5\text{--}9 \times 3\text{--}4\ \mu\text{m}$ ($\bar{x} = 6 \times 3.5\ \mu\text{m}$, $n = 25$). *Conidia* holoblastic, acrogenous, catenate, 1–4 short acropetal chains, golden-brown to dark brown, verrucose, aseptate, globose, $3.5\text{--}4.5\ \mu\text{m}$ ($\bar{x} = 4\ \mu\text{m}$, $n = 30$) diam., with single germ pore $1\text{--}2\ \mu\text{m}$ ($\bar{x} = 1.7\ \mu\text{m}$, $n = 20$) diam.; conidial secession schizolytic. Sexual morph: Undetermined.

Material examined – China, Sichuan Province, Chongzhou city, Baiyungou, N $30^{\circ}47'56''$, E $103^{\circ}24'15''$, elevation 990 m, 27 September 2022, on dead twigs of grass, W.H. Tian lu59_2 (HKAS 131988, holotype).

GenBank numbers – ITS: PP294645, LSU: PP213252, SSU: PP213256, *tef1- α* : PP213051

Notes – *Neogregarithecium sichuanense* and *Gregarithecium bambusae* have different morphologies (see notes under *Neogregarithecium*), and differ in the size of conidiophores ($5\text{--}10 \times 3\text{--}4\ \mu\text{m}$ vs. $10\text{--}48 \times 3\text{--}5\ \mu\text{m}$). We could not obtain a culture from *Neogregarithecium sichuanense*, and DNA was extracted directly. Based on pairwise nucleotide comparisons, *N. sichuanense* differs from *G. bambusae* by 45/450 bp (gaps: 15/450 bp) in ITS; 18/769 bp (gaps: 7/769 bp) in LSU; 10/1024 bp (no gaps) in SSU; 35/404 bp in *tef1- α* . Thus, our collection HKAS 131988 was identified as a new genus based on morphological observation and phylogenetic evidence.

Lentitheciaceae Y. Zhang et al., C.L. Schoch, J. Fourn., Crous & K.D. Hyde, Stud. Mycol. 64: 93 (2009)

MycoBank number: MB515470; Facesoffungi number: FoF08256

Notes – Lentitheciaceae was established by Zhang et al. (2009b) with *Lentithecium* as the type genus. Lentitheciaceae forms a well-supported clade in Pleosporales, which is characterized by narrow peridia, fusiform to broadly cylindrical pseudoparaphyses, hyaline ascospores with 1–3-transverse septa and containing refractive globules, surrounded by a mucilaginous sheath or extended appendage-like sheaths and asexual morphs producing stagonospora-like or dendrophoma-like asexual morphs (Zhang et al. 2012, Hyde et al. 2013, Dhanushka et al. 2014). Members of Lentitheciaceae are mostly saprobes found on herbaceous plants and submerged wood in freshwater environments (Zhang et al. 2012).

Phragmocamarosporium Wijayaw., Yong Wang et al. & K.D. Hyde, Cryptog. Mycol. 36(2): 217 (2015)

MycoBank number: MB555365; Facesoffungi number: FoF08850

Notes – *Phragmocamarosporium* was established by Wijayawardene et al. (2015) to accommodate two species, *P. hederæ* (from *Hedera helix*, Germany) and *P. platani* (type species,

from *Platanus* sp., Guizhou, China). Currently, there are only five epithets are listed in Index Fungorum (2024). *Phragmocamarosporium* is characterized by pycnidial, subepidermal, black conidiomata, conidiomata wall comprising thin-walled cells of *textura angularis*, enteroblastic, phialidic conidiogenous cells, and medium brown, clavate or ellipsoid to subcylindrical conidia (Wijayawardene et al. 2015).

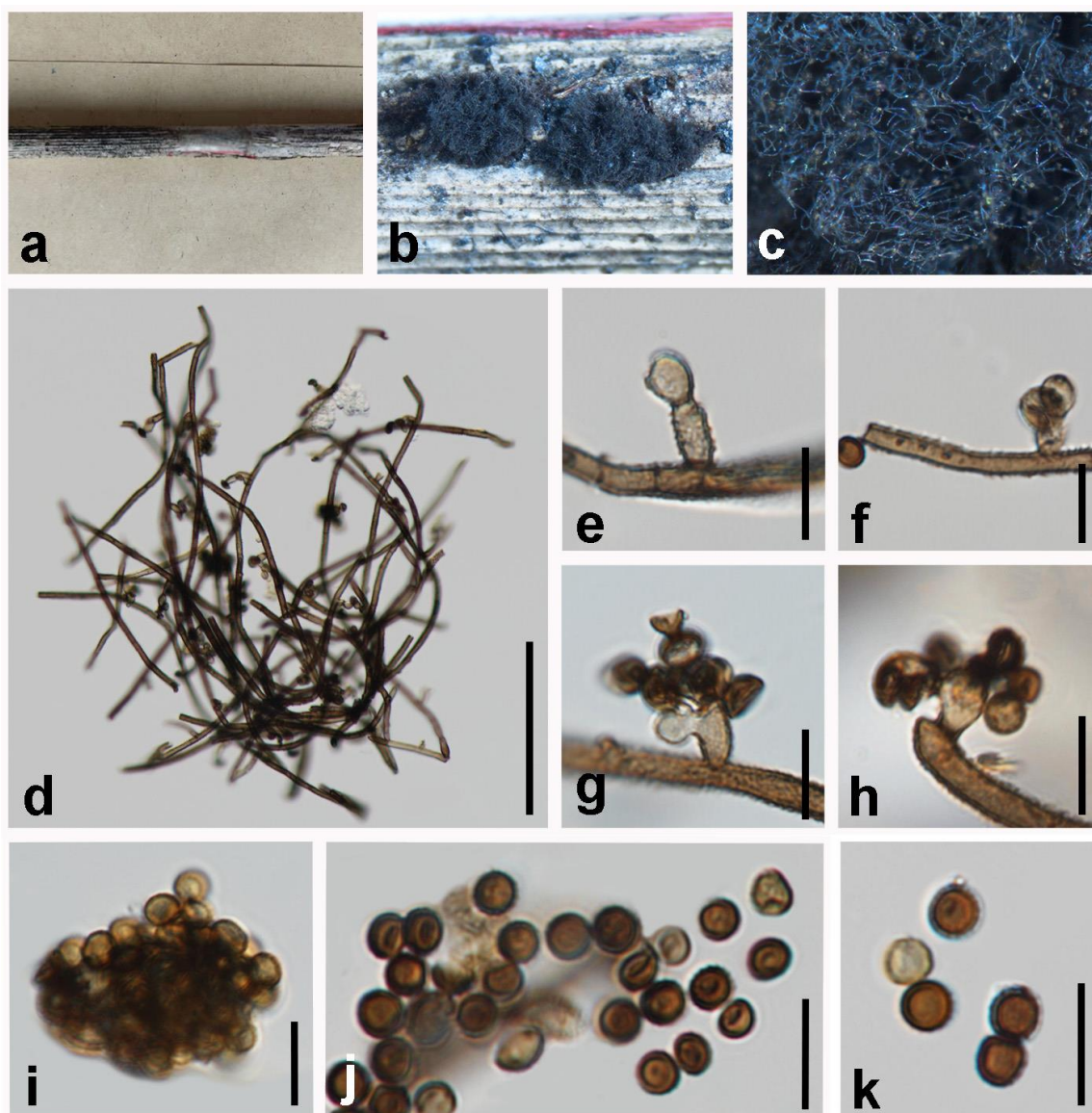


Figure 8 – *Neogregarithecium sichuanense* (HKAS 131988, holotype). a Specimen. b, c Mycelium on the host surface. d–f Conidiophores with lateral conidia. g, h Developing conidia in short acropetal chains. i–k Conidia. Scale bars: d = 100 µm, e–k = 10 µm.

Phragmocamarosporium ginkgonis W.H. Tian, K.D. Hyde & Maharachch., sp. nov. Fig. 10

Mycobank number: MB851877; Facesoffungi number: FoF16271

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

Holotype – HKAS 131284

Saprobic on dead stems of *Ginkgo biloba*. Asexual morph: *Conidiomata* 110–210 µm high × 140–165 µm diam ($\bar{x}$ = 150 × 155 µm, n = 10), pycnidial, sub-epidermal, visible as black spots, raised, unilocular, globose to sub-globose, with a centrally located papillate ostiole. *Ostioles* 50 × 55 µm, central, shiny black, conspicuous, papillate. *Conidiomatal wall* 13–35 µm wide, comprises thin inner layers of hyaline cells of *textura angularis*, with outer 3–4 layers of dark brown cells of

textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4.5–8 × 3–4.5 µm diam ($\bar{x}$ = 6 × 4 µm, n = 30), simple, short, phialidic, unbranched, hyaline, smooth-walled. *Conidia* 5.5–11 × 3.5–5 µm diam ($\bar{x}$ = 9 × 4 µm, n = 30), solitary, hyaline to dark brown, the color gradually deepens with age, smooth, clavate or ellipsoid to sub-cylindrical, with obtuse apex and truncate base, straight to curved, 3–4-septate, constricted at the septa. Sexual morph: Undetermined.

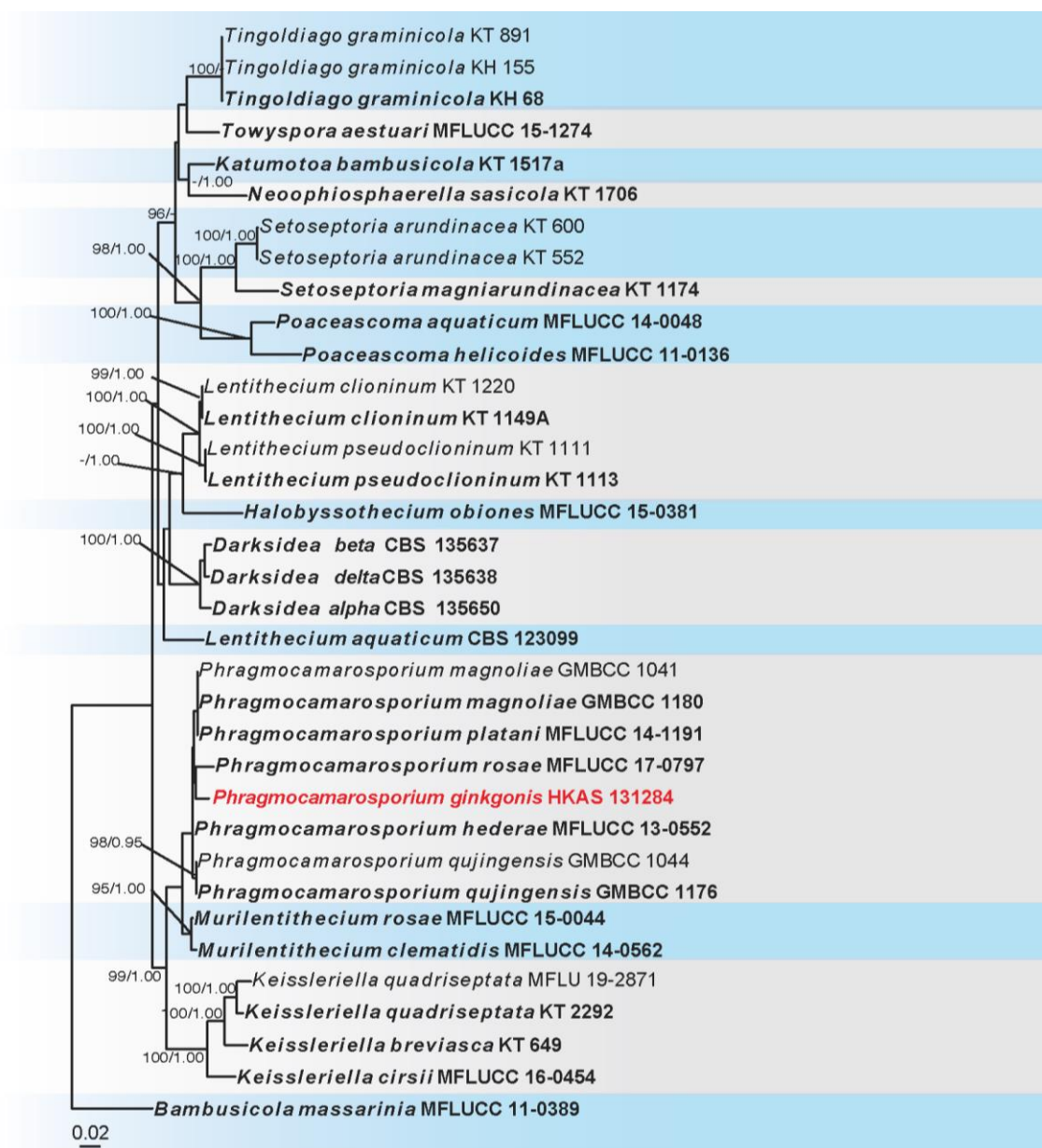


Figure 9 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *rpb2* and *tef1-α*) of Lentitheciaceae. The scale bar indicates 0.02 changes. The tree is rooted with *Bambusicola massarinia* (MFLUCC 11-0389) (Bambusicolaceae, Pleosporales). The best ML tree with a final likelihood value of -16913.107 is presented. The alignment dataset comprises 35 taxa with 4373 sites, including 1169 distinct patterns, 385 singleton sites and 3318 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Material examined – China, Sichuan Province, Chengdu city, Xiyuan Avenue, N 30°52'51", E 103°43'51", elevation 595 m, 8 December 2022, on dead stems of *Ginkgo biloba*, W.H. Tian XY20_2 (HKAS 131284, holotype).

GenBank numbers – ITS: OR887384, LSU: OR887095, SSU: OR933716, *rpb2*: PP076812; *tef1-α*: PP076824

Notes – Multi-locus phylogenetic analyses indicate that our collection (HKAS 131284) clustered with the type strain of *Phragmocamarosporium rosae* (MFLUCC 17-0797) (Fig. 9). Our collection fits well with *Phragmocamarosporium* by having conspicuous phragmospores, but differs from other species in the size of conidiogenous cells and conidia (Table 3). There is a close morphological relationship between our collection and *P. rosae* (MFLUCC 17-0797), but our collection differs in having comparatively larger conidiomata (110–210 µm) and larger conidiogenous cells ($4.5\text{--}8 \times 3\text{--}4.5$ µm), whereas *P. rosae* (MFLUCC 17-0797) has smaller conidiomata (60–100 µm), and smaller conidiogenous cells ($1\text{--}3 \times 1\text{--}2.5$ µm) (Wanasinghe et al. 2018). Based on the morphological characteristics and the multi-locus phylogeny, we introduce *P. ginkgonis* as a new species.

However, Multi-locus analyses of combined ITS, LSU, *rpb2* and *tef1-α* sequence data showed that various species of the genus *Phragmocamarosporium* are grouped closely in a single subclade (Fig. 9). A search of sequences for *Phragmocamarosporium* species in the BLASTn NCBI GenBank database revealed an extremely high degree of sequence identity, with all species lacking *rpb2* sequences (Wanasinghe et al. 2018, Wijayawardene et al. 2015, 2022b). Moreover, *P. rosae* (MFLUCC 17-0797) does not have an ITS sequence (Wanasinghe et al. 2018). Combining the consistent morphological characteristics and similar molecular sequences between these species may make them the same species, but more collections and sequences are needed to prove it.

Table 3 Morphological comparison of the *Phragmocamarosporium* species (length in µm).

Species name	Conidiomata	Conidiogenous cells	Conidia	Host	Reference
<i>Phragmocamarosporium hederæ</i>	80–110 high 100–140 diam	8–10 × 1.5–2.5	9–11 × 3–4.5 2–4-septate	<i>Hedera helix</i>	Wijayawardene et al. (2015)
<i>P. platani</i>	100–320 high 150–300 diam	1.5–3 × 1.5–2.5	12–13 × 5–7.5 3–4-septate	<i>Platanus</i> sp.	Wijayawardene et al. (2015)
<i>P. rosae</i>	60–100 high 120–200 diam	1–3 × 1–2.5	8–10 × 3.5–4.5 3-septate	<i>Rosa</i> sp.	Wanasinghe et al. (2018)
<i>P. qujingensis</i>	100–300 high 100–150 diam	6–11 × 2–5	10–14 × 3–6	<i>Magnolia grandiflora</i>	Wijayawardene et al. (2022b)
<i>P. magnoliae</i>	100–145 high 80–105 diam	12–17 × 3–6	13–17 × 4–6	<i>Magnolia grandiflora</i>	Wijayawardene et al. (2022b)
<i>P. ginkgonis</i>	110–210 high 140–165 diam	4.5–8 × 3–4.5	5.5–11 × 3.5–5 1–4-septate	<i>Ginkgo biloba</i>	This study

Macrodiplodiopsidaceae Voglmayr, Jaklitsch & Crous, IMA Fungus 6(1): 178 (2015)

Mycobank number: MB812794; Facesoffungi number: FoF08291

Notes – Macrodiplodiopsidaceae was introduced by Crous et al. (2015b) to accommodate *Macrodiplodopsis* and *Pseudochaetosphaeronema*. Species of Macrodiplodiopsidaceae have a cosmopolitan distribution on a wide range of plant hosts, encompassing endophytes, saprobes and plant pathogens (Zhang et al. 2016, Hyde et al. 2020b). Additionally, some species can even cause infections in humans (Ahmed et al. 2014).

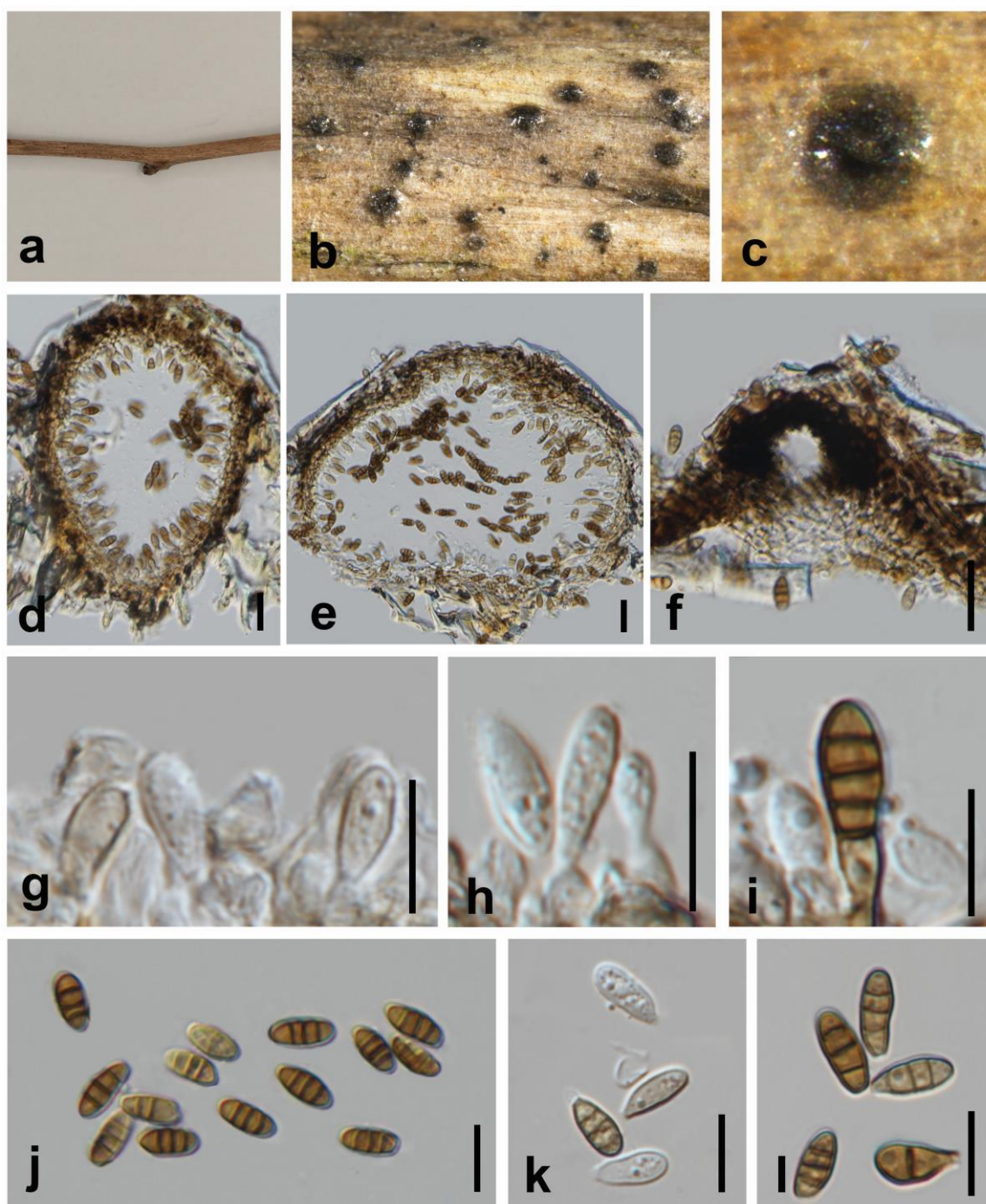


Figure 10 – *Phragmocamarosporium ginkgonis* (HKAS 131284, holotype). a Specimen. b, c Conidiomata on the host surface. d, e Sections of conidiomata. f Ostiole. g–i Conidiogenous cells with conidia. j–l Conidia. Scale bars: d–f = 20 μ m, g–l = 10 μ m.

Pseudochaetosphaeronema Punith., Nova Hedwigia 31(1–3): 126 (1979)

Mycobank number: MB9562; Facesoffungi number: FoF08294

Notes – *Pseudochaetosphaeronema* was established by Punithalingam (1979), with *P. larense* as the type species. *Pseudochaetosphaeronema* is characterized by black obpyriform pycnidia with a long neck, hyaline and phialidic conidiophores, and unicellular subspherical to ellipsoidal conidia (Ahmed et al. 2014). Members of *Pseudochaetosphaeronema* have wide distribution on various substrates as saprobes, human pathogens or endophytes (Ahmed et al. 2014, Zhang et al. 2016, Li et al. 2023).



Figure 11 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, and *tef1-α*) of *Pseudochaetosphaeronema*. The scale bar indicates 0.01 changes. The tree is rooted with *Splanchnonema platani* (CBS 222.37) (Pleomassariaceae, Pleosporales). The best ML tree with a final likelihood value of -8470.656 is presented. The alignment dataset comprises 14 taxa with 3296 sites, including 492 distinct patterns, 160 singleton sites and 2815 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Pseudochaetosphaeronema magnoliae N.I. de Silva, Lumyong & K.D. Hyde, Mycosphere 13(1): 985 (2022) Fig. 12

Mycobank number: MB559518; Facesoffungi number: FoF10716

Saprobic on dead *Cycas revoluta*. Asexual morph: *Conidiomata* 115–135 µm high × 130–145 µm diam ($\bar{x}$ = 124 × 137 µm, n = 10), solitary, raised, globose to subglobose, flat at the base, dark brown to black, conspicuous on the host surface, unilocular, ostiolate. *Conidiomatal wall* 20–45 µm wide, composed of several layers of small, flattened, brown to dark brown pseudoparenchymatous cells, cells towards the inside lightly pigmented, arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cell* 7–11.5 × 2–4 µm diam ($\bar{x}$ = 9 × 3 µm, n = 30), produced from inner stromatic tissue, monophialidic, enteroblastic, cylindrical or ampulliform, integrated, hyaline, smooth-walled. *Conidia* 10–20 × 3–4 µm ($\bar{x}$ = 15 × 3.5 µm, n = 30), hyaline, cylindrical to fusoid, guttulate, solitary, smooth, thin-walled, straight to slightly curved, 2–4-septate, apex obtuse. Sexual morph: Undetermined.

Known distribution – China, Thailand

Culture characteristics – Colonies on PDA reaching 23 mm diam after 2 weeks at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, grey; reverse: cream at the margin, black in the center.

Material examined – China, Sichuan Province, Chengdu city, University of Electronic Science and Technology of China, N 30°45'24", E 103°55'54", elevation 480 m, 12 June 2022, on living *Cycas revoluta*, W.H. Tian U07 (HUEST 23.0237), living culture UESTCC 23.0237.

GenBank numbers – ITS: OR887385, LSU: OR887096, SSU: OR933717, *tef1-α*: PP076820

Notes – *Pseudochaetosphaeronema magnoliae* was introduced by de Silva et al. (2022) from dead twigs of *Magnolia candolli* in China and Thailand. The present phylogenetic analyses indicate that our collection (UESTCC 23.0237) clustered with other isolates of *P. magnoliae* including type strain (MFLUCC 18-0707) (Fig. 11). The morphological characteristics of our isolate (UESTCC

23.0237) overlap with the type strain of *P. magnoliae* (MFLUCC 18-0707) in having monophialidic, enteroblastic, cylindrical or ampulliform, conidiogenous cells and hyaline, cylindrical to fusoid, guttulate, unicellular conidia (de Silva et al. 2022). Our isolate (UESTCC 23.0237) also resembles *P. magnoliae* (CGMCC 3.24436) in the morphology of conidiomata, conidiogenous cells and conidia (Li et al. 2023). In the NCBI BLASTn search, the ITS, LSU, SSU and *tef1-α* sequences of our isolate (UESTCC 23.0237) matched with the type strain of *P. magnoliae* (MFLUCC18-0707) with 100% sequence identity (567/567 bp,) in ITS; 99% sequence identity (838/839 bp, gap: 1/839 bp) in LSU; 99% sequence identity (947/953 bp, gaps: 5/953 bp) in SSU, and 100% sequence identity (879/879 bp, no gaps) in *tef1-α*. Therefore, we report our isolate as a new host record of *P. magnoliae* from *Cycas revoluta* in China.

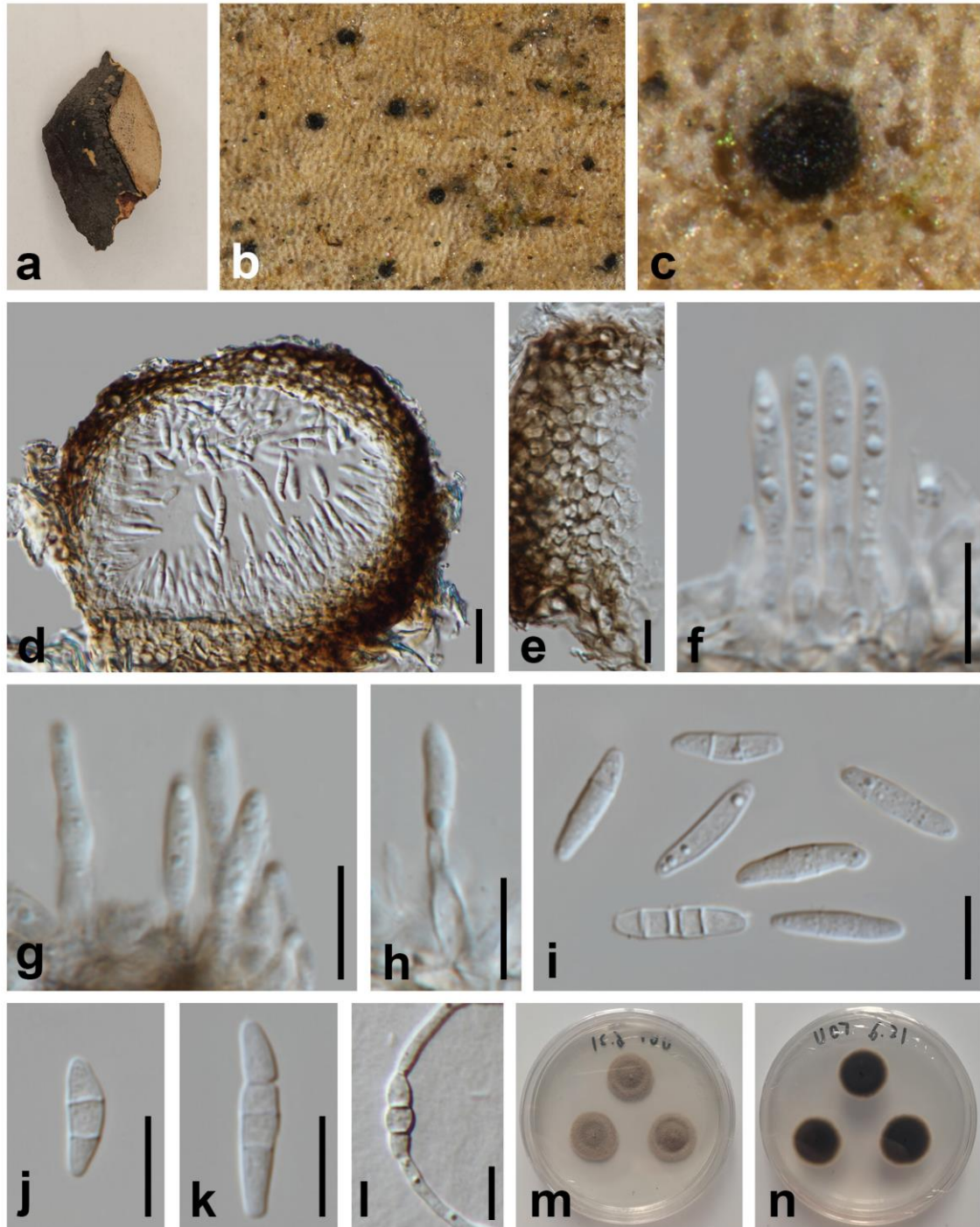


Figure 12 – *Pseudochaetosphaeronema magnoliae* (HUEST 23.0237). a Specimen. b, c Conidiomata on the host surface. d Section of conidioma. e Conidioma wall.

f–h Conidiogenous cells with conidia. i–k Conidia. l Germinating conidium. m, n Culture characteristics. Scale bars: d = 20 µm, e–l = 10 µm.

Melanommataceae G. Winter, Rabenh. Krypt. -Fl., Edn 2 (Leipzig) 1.2: 220 (1885)

Mycobank number: MB80990; Facesoffungi number: FoF01023

Notes – Melanommataceae was established by Winter (1885) with the type genus *Melanomma* and is characterized by globose or depressed perithecial ascomata, bitunicate and fissitunicate asci, pigmented and phragmosporous ascospores (Barr 1990a, Zhang et al. 2012, Hyde et al. 2013). Members of this family are mostly saprobic and hyperparasitoid found on the twigs or bark of woody plants in both aquatic and terrestrial habitats. They are widespread in temperate and subtropical regions (Zhang et al. 2012, Hyde et al. 2013).

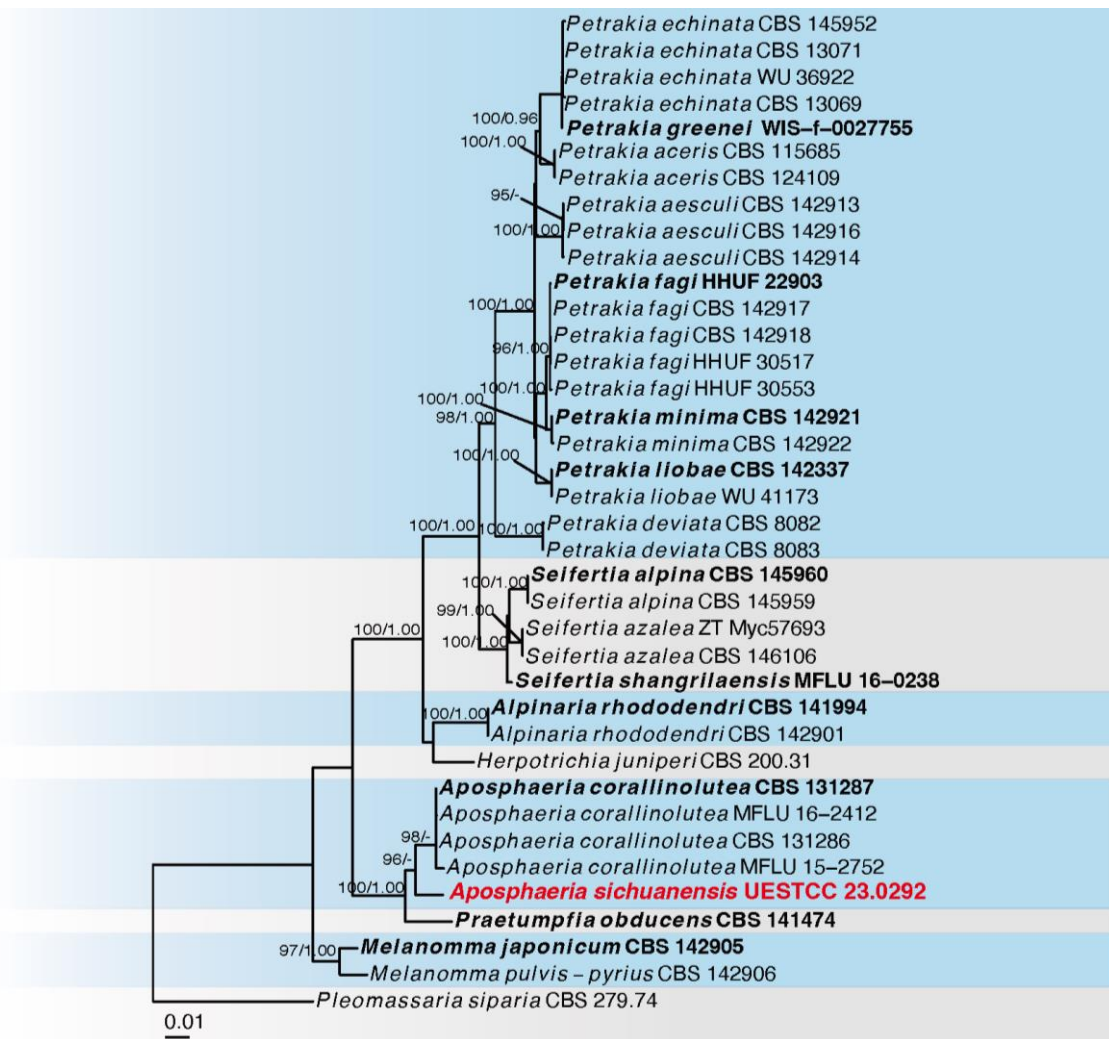


Figure 13 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *rpb2* and *tef1-α*) of Melanommataceae. The scale bar indicates 0.01 changes. The tree is rooted with *Pleomassaria siparia* (CBS 279.74) (Pleomassariaceae, Pleosporales). The best ML tree with a final likelihood value of -14150.352 is presented. The alignment dataset comprises 38 taxa with 4793 sites, including 922 distinct patterns, 176 singleton sites and 4044 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Aposphaeria Sacc., Michelia 2 (no. 6): 4 (1880)

Mycobank number: MB7198; Facesoffungi number: FoF00756

Notes – *Aposphaeria* was circumscribed by Saccardo (1880), with *A. pulviscula* selected as the type species. The genus contains more than 200 taxa, but most have no molecular sequences and have not been re-studied (Sutton 1980). Based on phylogenetic analysis, de Gruyter et al. (2013) proposed that *Aposphaeria* is related to Melanommataceae, and Tian et al. (2015) accepted *Aposphaeria* as an independent genus in this family. Tibpromma et al. (2017) described the sexual morph of *A. corallinolutea* and suggested that *Aposphaeria* s. str. may not belong to Melanommataceae. In this study, *Aposphaeria* was confirmed to be a unique genus in the Melanommataceae based on morphological and phylogenetic analysis. Still, more sequence data collection is needed to confirm this taxonomic position.

Aposphaeria sichuanensis W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 14

MycoBank number: MB851878; Facesoffungi number: FoF16272

Etymology – Named after the Sichuan Province, China, where the holotype was collected.

Holotype – HKAS 131990

Saprobic on dead branch of unidentified wood. Sexual morph: *Ascomata* 220–350 μm high $\times$ 220–395 μm diam ($\bar{x}$ = 290 $\times$ 315 μm , n = 10), scattered or clustered in small to large groups, initially immersed, becoming erumpent to superficial, globose, black, subcarbonaceous. *Peridium* 35–95 μm ($\bar{x}$ = 65 μm , n = 10), thick, composed of 11–13 layers of *textura globulosa* and *textura angularis*, outer region heavily pigment cells, black to dark-brown, inner layer consisting of hyaline gelatinous cells, thin, merging with pseudoparaphyses. *Hamathecium* comprising numerous, long, 1–2.5 μm ($\bar{x}$ = 1.6 μm , n = 30) wide, broad, transversely septate, branched, trabeculate pseudoparaphyses. *Asci* 100–150 $\times$ 12–15 μm ($\bar{x}$ = 125 $\times$ 13 μm , n = 20), (4)–8-spored, bitunicate, cylindrical, with club-shaped pedicel, apically rounded, with an ocular chamber up to 2.7–4 μm wide. *Ascospores* 14–22 $\times$ 6–8.5 μm ($\bar{x}$ = 18 $\times$ 8 μm , n = 30), overlapping uniseriate, hyaline, broadly fusiform, conical at the apex, 1-transversely septate, strongly constricted at the septa, with appendages wrapped around, wall smooth or rough, not uniform, indentations present when mature. Asexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 19 mm diam after 10 days at 25 °C, colonies from above: irregular circular, margin entire, flat, dense, spreading, cottony, raised in centre, white; reverse: cream at the margin, black in the center.

Material examined – China, Sichuan Province, Dujiangyan City, Longchi National Forest Park, N 36°6'58", E 103°33'33", elevation 1168 m, 19 September 2022, on dead branch of unknown wood, W.H. Tian sarah70_4 (HKAS 131990, holotype), ex-type CGMCC 3.25699 = UESTCC 23.0292.

GenBank numbers – ITS: PP294646, LSU: PP213253, SSU: PP213257, *rpb2*: PP213053, *tef1- α* : PP213052

Notes – Our collection (UESTCC 23.0292) formed a distinct clade in the phylogenetic tree as a sister to the *Aposphaeria corallinolutea* (Fig. 13). *Aposphaeria corallinolutea* (MFLU 15-2752) shares similar morphological characteristics with our collection (UESTCC 23.0292) in having (4)–8-spored, bitunicate, cylindrical, apically rounded asci with an ocular chamber and long, broad, transversely septate, branched, trabeculate pseudoparaphyses in the hamathecium (Tibpromma et al. 2017). However, *A. sichuanensis* (UESTCC 23.0292) exhibits distinct differences from *A. corallinolutea* (MFLU 15-2752), primarily in its peridium, which is composed of *textura globulosa* and *textura angularis* and lacks ostioles. Furthermore, *A. sichuanensis* has comparatively thinner ascospores (6–8.5 μm). In contrast, *A. corallinolutea* (MFLU 15-2752) features a peridium composed solely of *textura angularis*, includes a central ostiole, and possesses wider ascospores (7–11 μm) (Tibpromma et al. 2017). Comparisons of the ITS, LSU, SSU, *rpb2* and *tef1- α* sequences data between *A. corallinolutea* (MFLU 15-2752) and *A. sichuanensis* (UESTCC 23.0292) show 98.71% sequence identity (458/464 bp, gaps: 1/464 bp) in ITS, 98.95% sequence identity (752/760 bp, no gaps) in LSU, 99.18% sequence identity (963/971 bp, gaps: 6/971bp) in SSU, 94.15% sequence identity (708/752 bp, no gaps) in *rpb2*, and 99.10% sequence identity

(663/669 bp, no gaps) in *tef1-α*. Based on its morphological characteristics and phylogenetic analysis results, we identified *A. sichuanensis* as a new species.

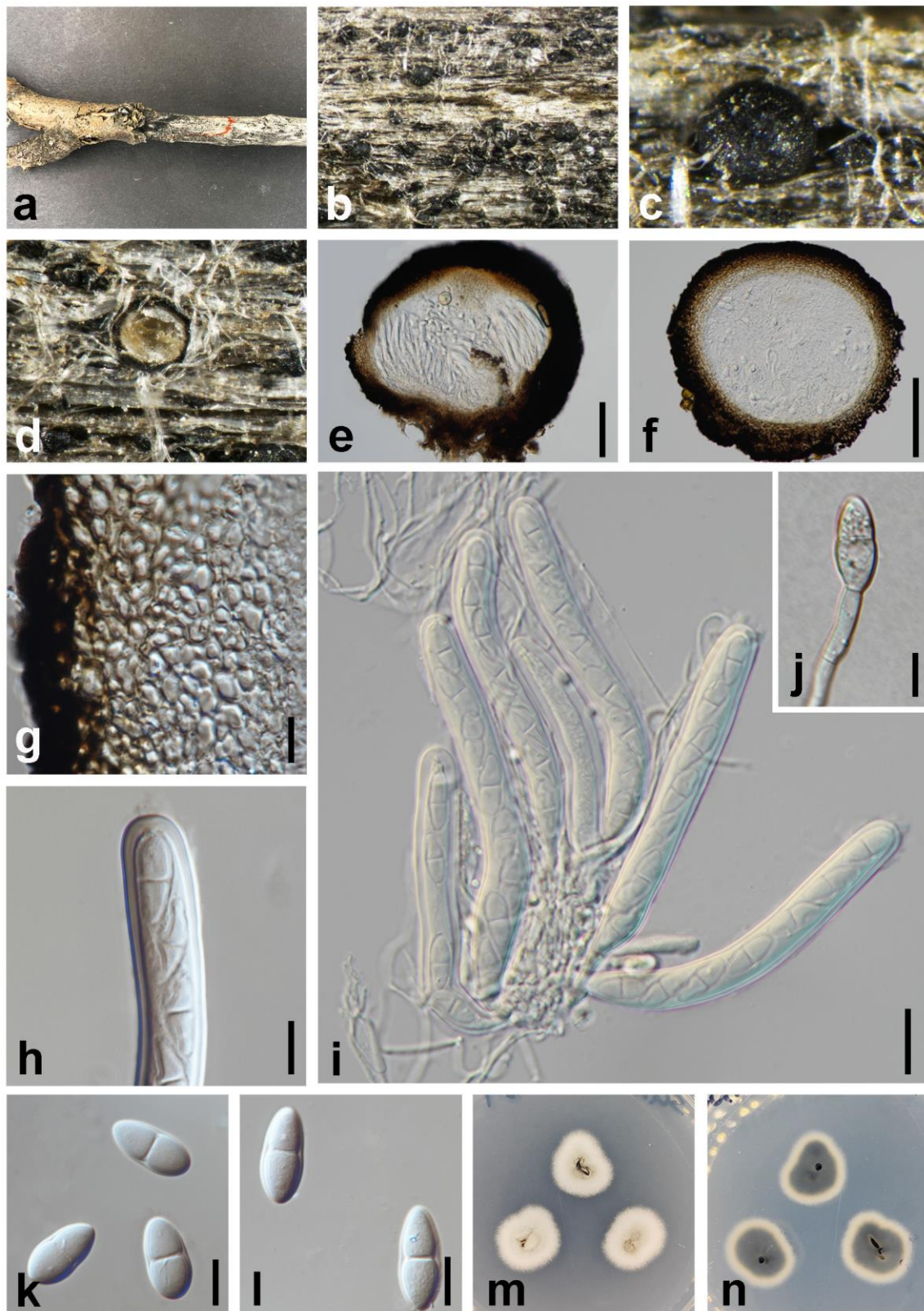


Figure 14 – *Aposphaeria sichuanensis* (HKAS 131990, holotype). a Specimen. b, c Ascomata on natural substrates. d, f Horizontal section of an ascomata on natural substrates. e Vertical section of ascomata. g Ascomata wall. h Apex of an ascus. i Asci and paraphyses. j Germinating ascospore. k, l Ascospores. m, n Culture characteristics. Scale bars: e, f = 100 μ m, g, i–l = 10 μ m, h = 20 μ m.

Camposporium Harkn., Bull. Calif. Acad. Sci. 1(no. 1): 37 (1884)

MycoBank number: MB7479; Facesoffungi number: FoF08296

Notes – *Camposporium* was introduced by Harkness (1884) and characterized by effuse, cottony, greyish brown, velvety colonies, mononematous conidiophores, monoblastic, terminal conidiogenous cells and holoblastic, solitary, dry, aerogenous conidia. *Camposporium* had a close relationship with *Fusiconidium*. Hyde et al. (2020a) reported that *Camposporium* and *Fusiconidium* grouped within Melanommataceae based on LSU, SSU, ITS, and *tef1-α* sequence data. Based on the morphological and phylogenetic evidence, Koukol & Delgado (2021) proposed that *Fusiconidium* was synonymous with *Camposporium*.

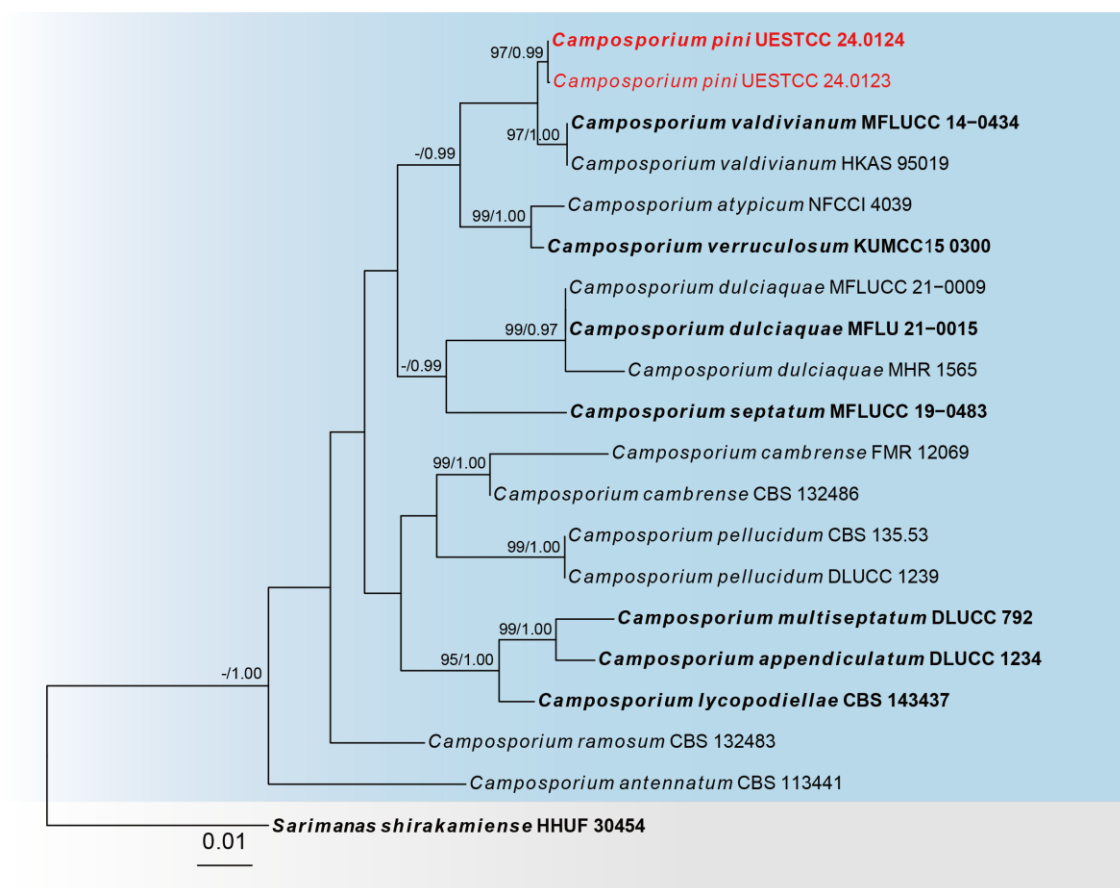


Figure 15 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *rpb2* and *tef1-α*) of *Camposporium*. The scale bar indicates 0.01 changes. The tree is rooted with *Sarimanas shirakamiense* (HHUF 30454) (Melanommataceae, Pleosporales). The best ML tree with a final likelihood value of -8942.457 is presented. The alignment dataset comprises 20 taxa with 4359 sites including 416 distinct patterns, 263 singleton sites and 3939 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Camposporium pini W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

MycoBank number: MB854680; Facesoffungi number: FoF16273

Etymology – The epithet refers to *Pinus* sp., the host plant of the fungi.

Holotype – HKAS 134910

Saprobic on dead branches of *pinus* sp. Asexual morph: Hyphomycetes. Colonies on the natural substratum effuse, minute, black. Mycelium superficial, composed of septate, unbranched, smooth, brown to dark brown hyphae. Conidiophores 95–180 µm long × 7–11 µm width ($\bar{x}$ = 130 × 9 µm, n = 20), mononematous, mononematous, unbranched, erect, straight or flexuous, dark brown,

Fig. 16

septate, thick-walled, smooth, paler towards the apex, cylindrical, with 4–12-septate. *Conidiogenous cells* enteroblastic, percurrently proliferating, cylindrical, pale brown to dark brown, thin-walled, smooth. *Conidia* 27–50 µm long × 10–14 µm wide ($\bar{x}$ = 43 × 13 µm, n = 35), acrogenous, straight or slightly curved, fusiform to ellipsoidal with round at the apex and truncate base, with 4–8-septate, pale brown to dark brown, light colored and obtuse at the apex, with broadly truncate at the base. *Conidial secession* rhexolytic. Sexual morph: Undetermined.

Culture characters – Colonies on PDA reaching 19 mm diam after 27 days at 25 °C, colonies from above: white, circular, dense, fluffy appearance, with denser mycelium at the center, slightly raised in centre; colonies from the below: black in the centre, dark brown in the margin, and producing a ring of brown pigment around the colony in the culture.

Material examined – China, Sichuan Province, Neijiang City, Songlin Village, N 29°32'19", E 105°9'28", elevation 373 m, 1 April 2023, decaying branches of *Pinus* sp., W.H. Tian SLC46_1 (HKAS 134910, holotype), ex-type CGMCC 3.27521 = UESTCC 24.0124; *ibid.*, Chengdu City, Swan Forest Farm, N 31°16'19", E 103°56'59", elevation 1352 m, 26 May 2023, decaying branches of *Cryptomeria japonica*, W.H. Tian TELC17 (UESTCC 24.0123).

GenBank numbers – HKAS 134910 = ITS: PP740383, LSU: PP740389, SSU: PP740395, *rpb2*: PP830728, *tef1-α*: PP776571; HUEST 24.0141 = ITS: PP740384, LSU: PP740390, SSU: PP740396, *rpb2*: PP830729, *tef1-α*: PP776572.

Notes – According to the multi-locus phylogeny, our collections (UESTCC 24.0124 and UESTCC 24.0123) constitute an independent clade sister to *Camposporium valdivianum* (Fig. 15). Morphologically, our collections differ from *C. valdivianum* by the longer conidiophores (95–180 µm vs. 91–114 µm) and more septate conidiophores (4–12-septate vs. 7–9-septate) (Li et al. 2017). Moreover, there are differences in their conidia morphology; the conidia of *C. valdivianum* have obvious contraction at the transverse septate, while the conidia walls of our collections are smooth (Li et al. 2017). Since the species of *C. valdivianum* lacked ITS sequence data, we compared base pair differences of the LSU, SSU, *tef1-α*, and *rpb2* gene between our collection (UESTCC 24.0124) and the type strain of *C. valdivianum* (MFLUCC 14-0434). The results showed 100% sequence identity in LSU, 3/989 bp differences (1%, 2/989 bp) in SSU, 7/839 bp differences (1%, no gaps) in *tef1-α*, and 10/784 bp differences (2%, no gaps) in *rpb2*. Based on their different morphological characteristics, we propose *Camposporium pini* as a novel species from *Pinus* sp. and *Cryptomeria japonica* in China.

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

MycoBank number: MB817780; Facesoffungi number: FoF08317

Notes – Nigrogranaceae was established by Jaklitsch & Voglmayr (2016) to accommodate the type genus *Nigrograna*. Members of Nigrogranaceae are saprobic, endophytic or pathogenic, commonly found on plant tissues and occasionally infecting humans (de Gruyter 2012, Tibpromma et al. 2017, Kolařík 2018, Zhao et al. 2018). Species of this family are widely distributed, especially prevalent in aquatic, terrestrial and marine habitats (Hyde et al. 2017, Tibpromma et al. 2017, Dayaratne et al. 2020).

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

MycoBank number: MB564794; Facesoffungi number: FoF08318

Notes – *Nigrograna* is the only genus in the family Nigrogranaceae and was first introduced by de Gruyter in 2012 to describe the human pathogen, *N. mackinnonii* (de Gruyter 2012, Zhang et al. 2020). Members of *Nigrograna* are characterized by black ascomata, clavate, short pedicellate asci and pale to chocolate brown, asymmetric, fusoid to narrowly ellipsoid, septate ascospores. This genus is reported as endophytes, saprobes, or pathogens and widely distributed around the world (Jaklitsch & Voglmayr 2016, Tibpromma et al. 2017, Kolařík 2018, Zhao et al. 2018, Dong et al. 2020, Zhang et al. 2020).

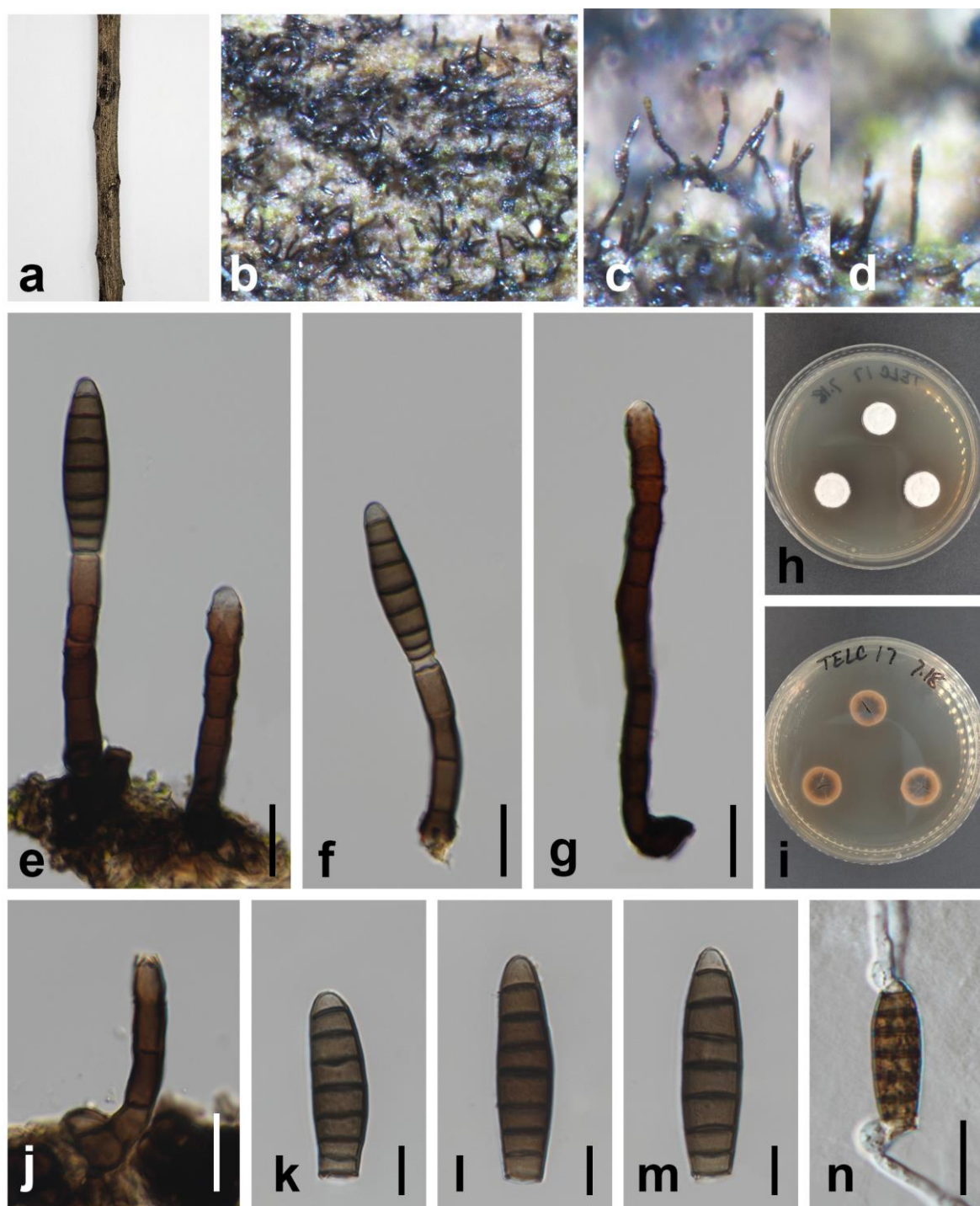


Figure 16 – *Camposporium pini* (HKAS 134910, holotype). a Specimen. b–d Colonies on dead branch of *pinus* sp. e–g, j Conidiophores and conidiophore bearing conidia. h, i Culture characteristics. k–m Conidia. n Germinating conidia. Scale bars: e–g, j, n = 20 μ m, k–m = 10 μ m.

Nigrograna locuta-pollinis F. Liu & L. Cai, Mycosphere 9(6): 1097 (2018)

Fig. 18

MycoBank number: MB824507; Facesoffungi number: FoF05223

Saprobic on dead stems of *Cycas revoluta*. Asexual morph: *Conidiomata* 180–190 μ m high $\times$ 180–280 μ m diam ($\bar{x}$ = 185 $\times$ 233 μ m, n = 10), immersed, only ostioles visible at the surface of the host, solitary, raised, globose to subglobose, dark brown to black, multilocular, ostiolate. *Conidiomatal* wall 15 $\times$ 40 μ m ($\bar{x}$ = 25 μ m, n = 20) wide, composed of several layers of dark brown, compressed pseudoparenchymatous cells arranged in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5.5–13 $\times$ 2–4.5 μ m ($\bar{x}$ = 8.5 $\times$ 3.3 μ m, n = 30),

enteroblastic, annellidic, integrated, hyaline, ampulliform to subcylindrical, or obclavate, smooth-walled. *Conidia* 3–5 × 2–3 µm ($\bar{x}$ = 4 × 2.6 µm, n = 30), hyaline, solitary, smooth, aseptate, guttulate, broadly ellipsoidal, verruculose with age, with rounded to obtuse apex, thick-walled. Sexual morph: Undetermined.

Known distribution – China, South Korea

Culture characteristics – Colonies on PDA reaching 21 mm diam after 10 days at 25 °C, colonies from above: grey at the centre, creamy white until margin, hyaline mycelia at the entire edge, dense, fluffy, and circular, colonies from below: black at the centre, becoming dark-olivaceous brown, and creamy white towards the edge.

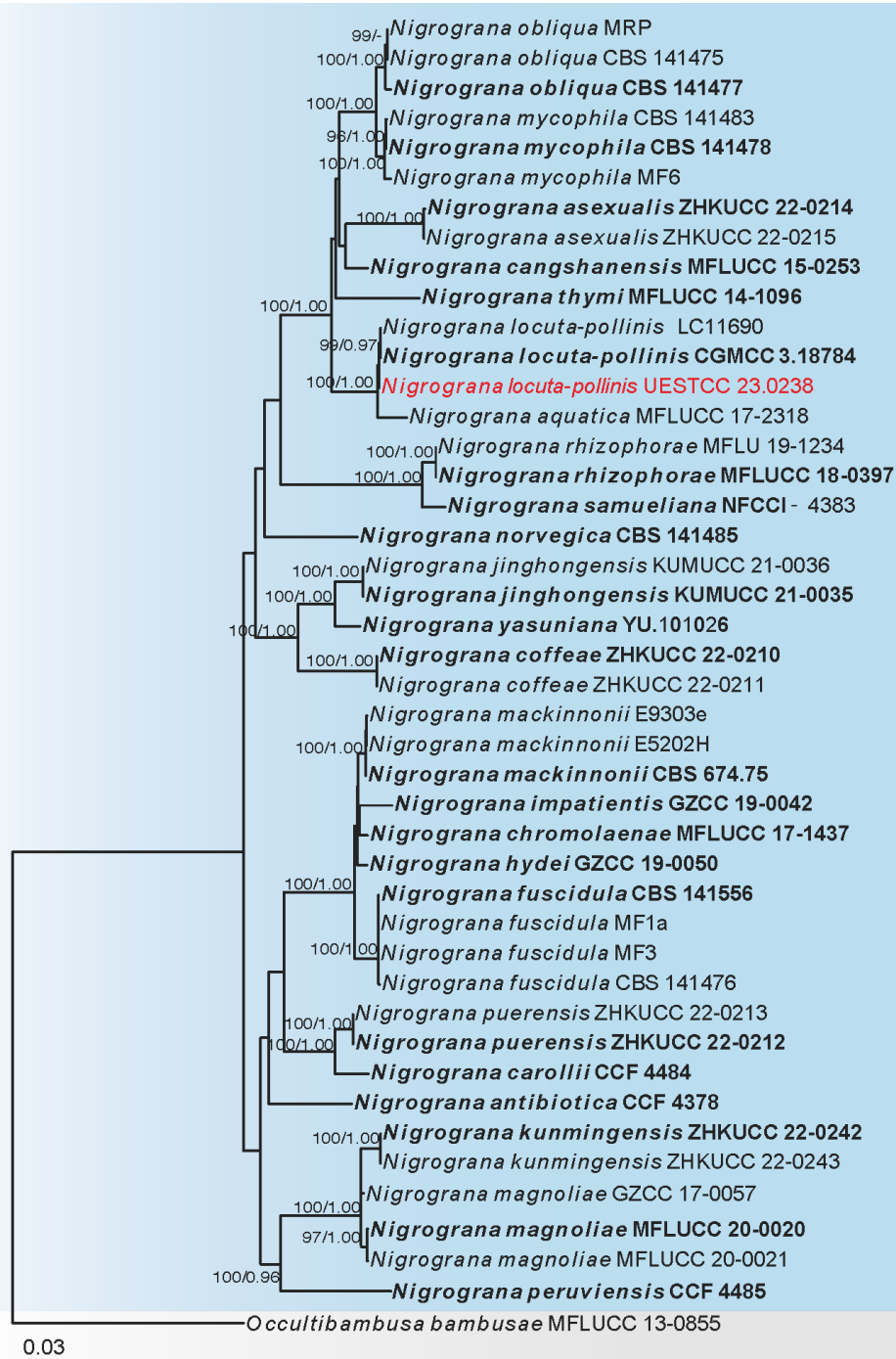


Figure 17 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *rpb2* and *tef1-α*) of *Nigrograna*. The scale bar indicates 0.03 changes. The tree is rooted with *Occultibambusa bambusae* (MFLUCC 13-0855) (Occultibambusaceae, Pleosporales). The best ML

tree with a final likelihood value of -17075.862 is presented. The alignment dataset comprises 44 taxa with 4374 sites, including 1165 distinct patterns, 253 singleton sites and 3421 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Material examined – China, Sichuan Province, Chengdu City, University of Electronic Science and Technology of China, N 30°45'24", E 103°55'54", elevation 480 m, 12 June 2022, on dead stems of *Cycas revoluta*, W.H. Tian U08_2 (HUEST 23.0238), living culture UESTCC 23.0238.

GenBank numbers – ITS: OR887383, LSU: OR887094, *tef1-α*: PP076821

Notes – Zhao et al. (2018) first isolated the *Nigrograna locuta-pollinis* from hive-stored pollen but it proved sterile in culture. Therefore, based on molecular and phylogenetic analyses, Zhao et al. (2018) introduced the isolate CGMCC 3.18784 as the type strain of *N. locuta-pollinis*. Multi-locus analyses of combined ITS, LSU, SSU, *rpb2* and *tef1-α* sequence data showed that our strain (UESTCC 23.0238) clusters with the type strain of *N. locuta-pollinis* (CGMCC 3.18784) and *N. locuta-pollinis* (LC 11690) (Fig. 17). Sequence comparison for the ITS, LSU and *tef1-α* region between *N. locuta-pollinis* (CGMCC 3.18784) and our isolate (UESTCC 23.0238) showed 99.59% sequence identity (481/483 bp, no gaps) in ITS, 99.76% sequence identity (832/834 bp, 1bp gap) in LSU, and 99.9% sequence identity (976/977 bp, 1bp gap) in *tef1-α*. Sequence comparison for the ITS and LSU region between *N. aquatica* (MFLUCC 17-2318) and our isolate (UESTCC 23.0238) showed 98.74% (470/476 bp, 1bp gap) and 99.39% (817/822 bp, no gaps) base pair sequence identity (Dong et al. 2020). Hence, we document our isolate as a novel host record of *N. locuta-pollinis* from *Cycas revoluta* in China, and this is the first asexual morphological description and illustrations of this species.

Roussoellaceae Jian K. Liu, Phook., D.Q. Dai & K.D. Hyde, Phytotaxa 181(1): 7 (2014)

Mycobank number: MB804651; Facesoffungi number: FoF08360

Notes – The family Roussoellaceae was established by Liu et al. (2014) to accommodate three genera, *Neoroussoella*, *Roussoellopsis* and the type genus *Roussoella*. It is a well-resolved family in the Pleosporales. Roussoellaceae species are saprophytic in a variety of hosts from terrestrial plants, including bamboo, palms and mangrove trees (Dai et al. 2017, Devadatha et al. 2018, Jiang et al. 2019).

Xenoroussoella Mapook & K.D. Hyde, Fungal Diversity 101: 93 (2020)

Mycobank number: MB557367; Facesoffungi number: FoF07822

Notes – Mapook et al. (2020) introduced the genus *Xenoroussoella* and described the sexual morph of the type strain *X. triseptata* (MFLUCC 17-1438) found in dead stems of *Chromolaena odorata* in Thailand. The genus is characterized by immersed, solitary, globose to subglobose ascomata, with protruding ostiolar neck, cylindric-clavate to clavate asci, and brown to dark brown, ellipsoid to obovoid, 3-septate ascospores (Mapook et al. 2020). Phylogenetic analysis based on the combined dataset of ITS, LSU, *tef1-α* and *rpb2* genes revealed that *Xenoroussoella* forms a separate branch and groups with *Pseudoroussoella* species.

Xenoroussoella triseptata Mapook & K.D. Hyde, Fungal Diversity 101: 95 (2020)

Fig. 20

Mycobank number: MB557368; Facesoffungi number: FoF07823

Saprobic on dead stems of *Cycas revoluta*. Asexual morph: Coelomycetes. *Conidiomata* 100–155 µm high × 110–290 µm diam ($\bar{x}$ = 130 × 215 µm, n = 10), pycnidial, solitary to gregarious, multi-locular, dark brown to black, immersed under a clypeus, slightly raised, becoming erumpent at maturity, ostiolate. *Ostioles* 20 µm high, 18 µm wide, central, black. *Conidiomatal wall* 18–40 µm ($\bar{x}$ = 27, n = 20) wide, composed of thick-walled, dark brown cells of *textura angularis*; inner layer thin, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.3–7

$\times 2.7\text{--}4.7\ \mu\text{m}$ ($\bar{x} = 5 \times 3.7\ \mu\text{m}$, $n = 30$), phialidic, ampulliform to cylindrical, hyaline, smooth-walled. *Conidia* $2.5\text{--}4.5 \times 2\text{--}2.7\ \mu\text{m}$ ($\bar{x} = 3.7 \times 2.3\ \mu\text{m}$, $n = 30$), initially hyaline, becoming pale brown when mature, ellipsoidal, straight, both ends broadly rounded, aseptate, smooth-walled. Sexual morph: Undetermined.

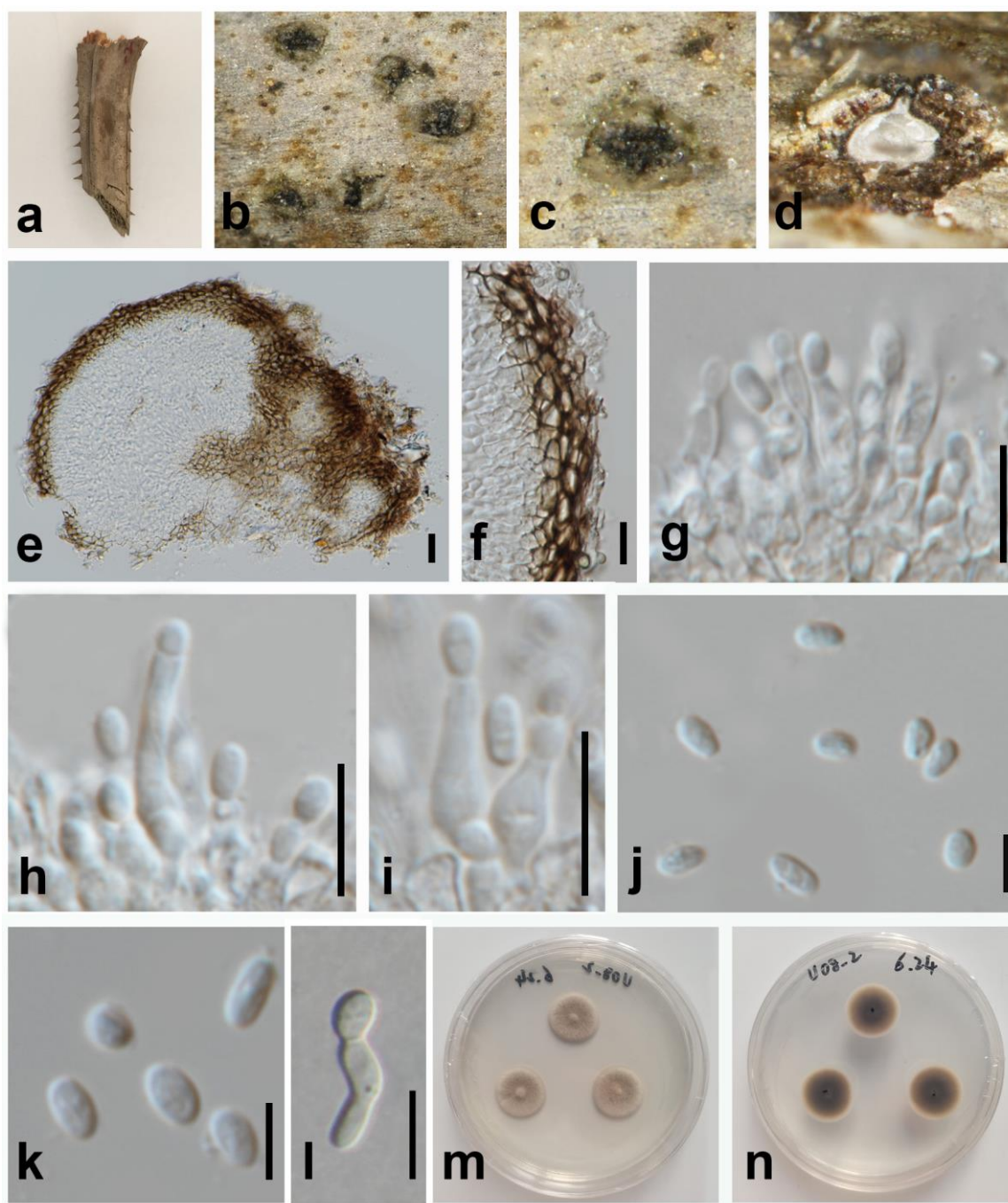


Figure 18 – *Nigrograna locuta-pollinis* (HUEST 23.0238). a Specimen. b, c Conidiomata on the host surface. d, e Vertical sections of conidiomata. f Conidioma wall, g–i Conidiogenous cells with conidia. j, k Conidia. l Germinating conidium. m, n Culture characteristics. Scale bars: e = 20 μm , f–i, l = 10 μm , j, k = 5 μm .

Known distribution – China (this study), South Korea, Thailand

Culture characteristics – Colonies on PDA reaching 44 mm diam after 10 days at 25 °C, colonies from above: white, circular, dense, fluffy appearance, slightly raised at the centre; colonies from the reverse: black at the centre, becoming dark-olivaceous brown, cream at the margin.

Material examined – China, Sichuan Province, Chengdu City, Xiyuan Avenue, N 30°52'51", E 103°43'51", elevation 595 m, 8 December 2022, on dead stems of *Cycas revoluta*, W.H. Tian XY24_2 (HUEST 23.0244), living culture UESTCC 23.0244; *ibid.*, University of Electronic Science and Technology of China, N 30°45'24", E 103°55'54", elevation 480 m, 12 June 2022, on dead stems of *Cycas revoluta*, W.H. Tian U08_3 (HUEST 23.0239), living culture UESTCC 23.0239.

GenBank numbers – UESTCC 23.0244 = ITS: OR887388, LSU: OR887099, *rpb2*: PP076813, *tef1-α*: PP076825; UESTCC 23.0239 = ITS: OR887386, LSU: OR887097

Notes – Based on the multi-locus phylogeny, de Silva et al. (2022) introduced an asexual morph of *X. triseptata* (MFLUCC 21-0197) from dead twigs of *Anomianthus dulcis* and *Desmos chinensis* in Thailand. Multi-locus phylogeny indicates that our collections nest with *X. triseptata* group with 100% ML, 1.00 PP statistical support (Fig. 19). The BLASTn searches of the ITS, LSU, *rpb2* and *tef1-α* sequence of our strain (UESTCC 23.0244) and the type strain of *X. triseptata* (MFLUCC 17-1438) showed 99.21% sequence identity (503/507 bp, no gaps) in ITS, 100% sequence identity in LSU, 99.83% sequence identity (578/579 bp, no gaps) in *rpb2*, and 99.2% sequence identity (873/880 bp, 3 bp gaps) in *tef1-α* (Mapook et al. 2020). In addition, as morphological characteristics examined largely overlapped with *X. triseptata* (MFLUCC 21-0197) (de Silva et al. 2022), we report our collections as a new host record of *X. triseptata* from *Cycas revoluta*. This is the first time *X. triseptata* has been reported from China.

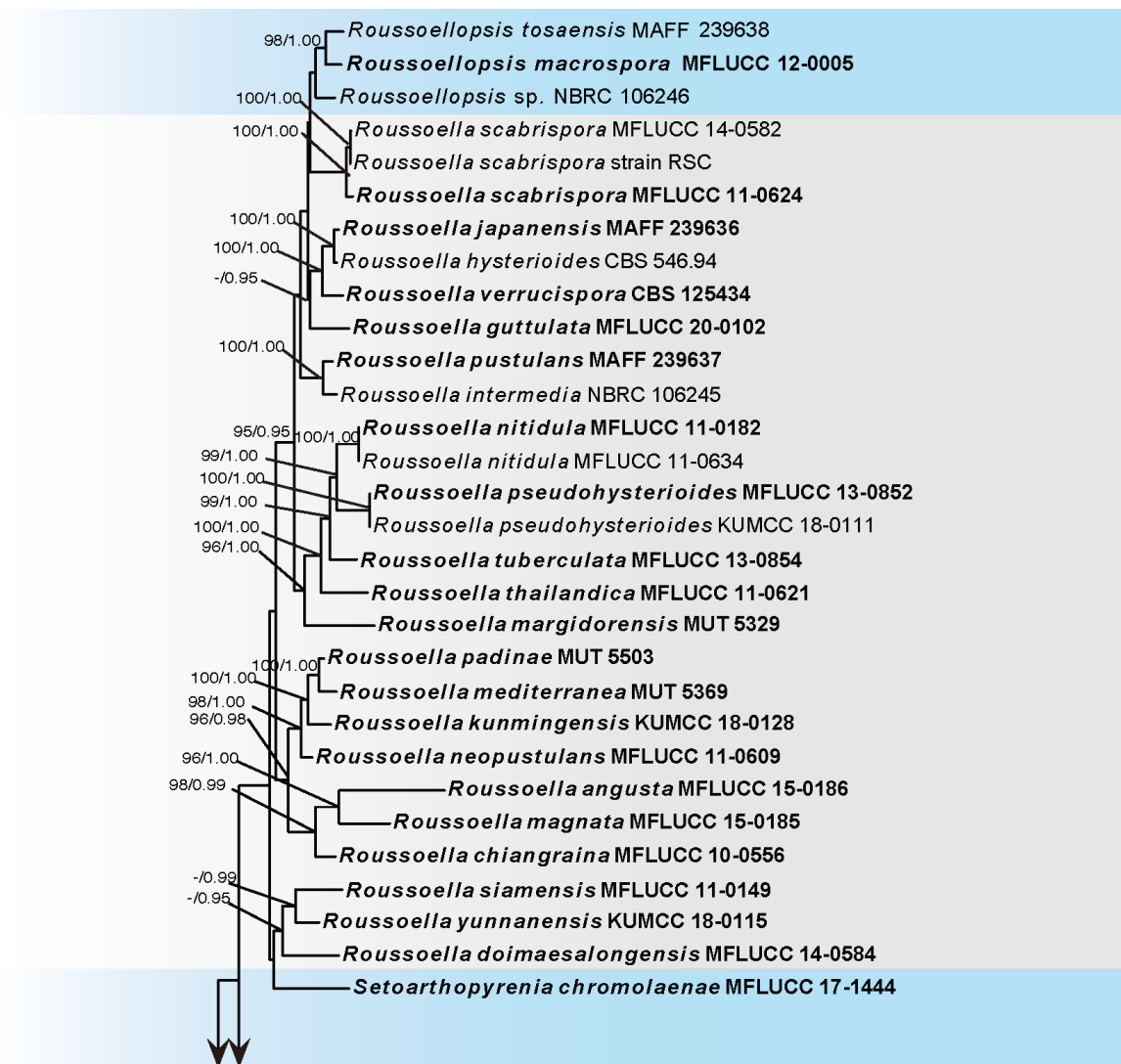


Figure 19 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, *rpb2* and *tef1-α*) of Roussoellaceae. The scale bar indicates 0.01 changes. The tree is rooted with *Torula*

hollandica (CBS 220.69) (Torulaceae, Pleosporales). The best ML tree with a final likelihood value of -22830.517 is presented. The alignment dataset comprises 54 taxa with 3302 sites, including 1331 distinct patterns, 286 singleton sites and 2164 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

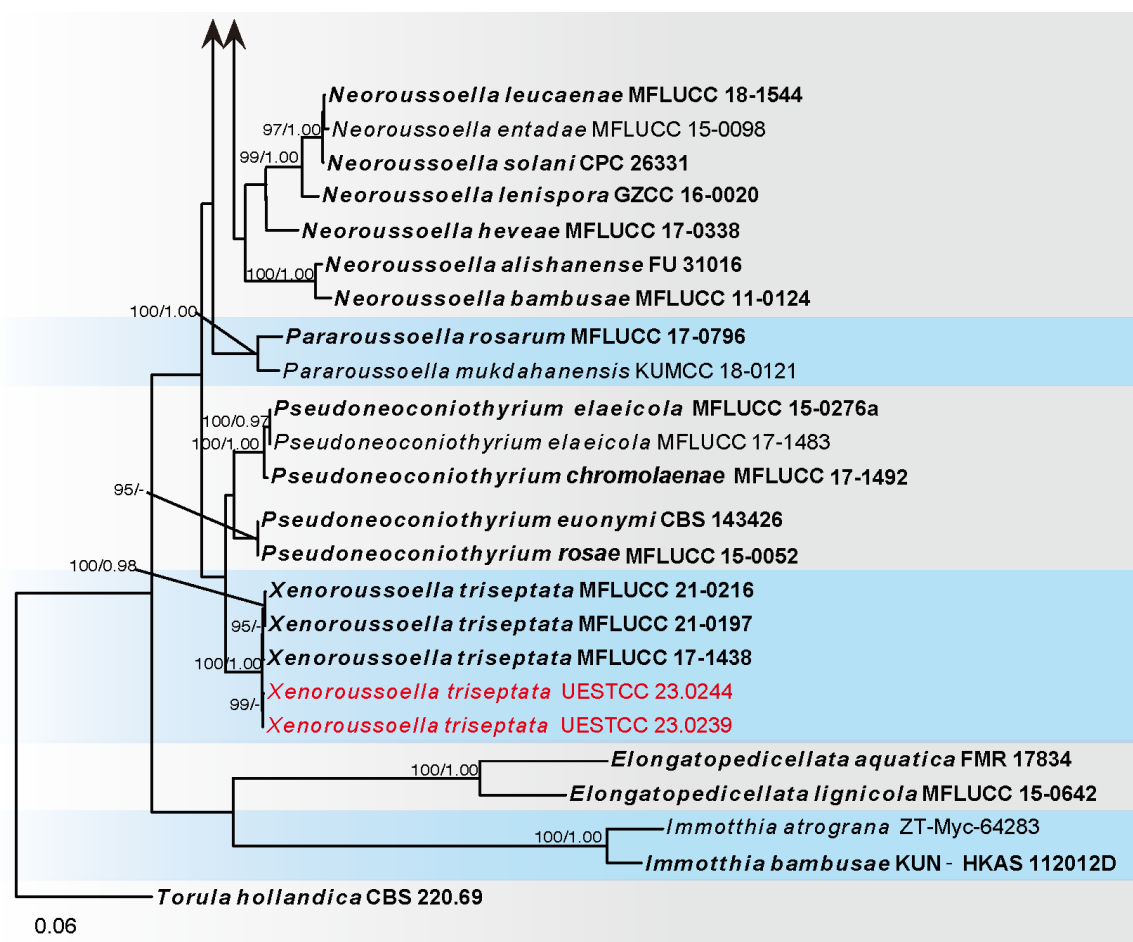


Figure 19 – Continued.

Thyridariaceae Q. Tian & K.D. Hyde, in Hyde et al., Fungal Diversity 63: 254 (2013)

MycoBank number: MB805172; Facesoffungi number: FoF08374

Notes – Thyridariaceae was proposed by Hyde et al. (2013) to accommodate the genus *Thyridaria*. There are eight genera accommodated in Thyridariaceae: *Chromolaenomyces*, *Cycasicola*, *Liua*, *Parathyridaria*, *Parathyridariella*, *Pseudothyridariella*, *Thyridaria* and *Thyridariella* (Wijayawardene et al. 2022a).

Thyridaria Sacc., Grevillea 4(no. 29): 21 (1875)

MycoBank number: MB805172; Facesoffungi number: FoF08375

Notes – *Thyridaria* was introduced by Saccardo (1875) and typified by *T. broussonetiae*. *Thyridaria* was characterized by aggregated perithecia and orvalsoid stromata (Jaklitsch & Voglmayr 2016). The members of this genus are mostly saprobes on a diverse range of plant substrates (Hongsan et al. 2020, Hyde et al. 2013, Jaklitsch & Voglmayr 2016). Only five species have sequence data in GenBank.

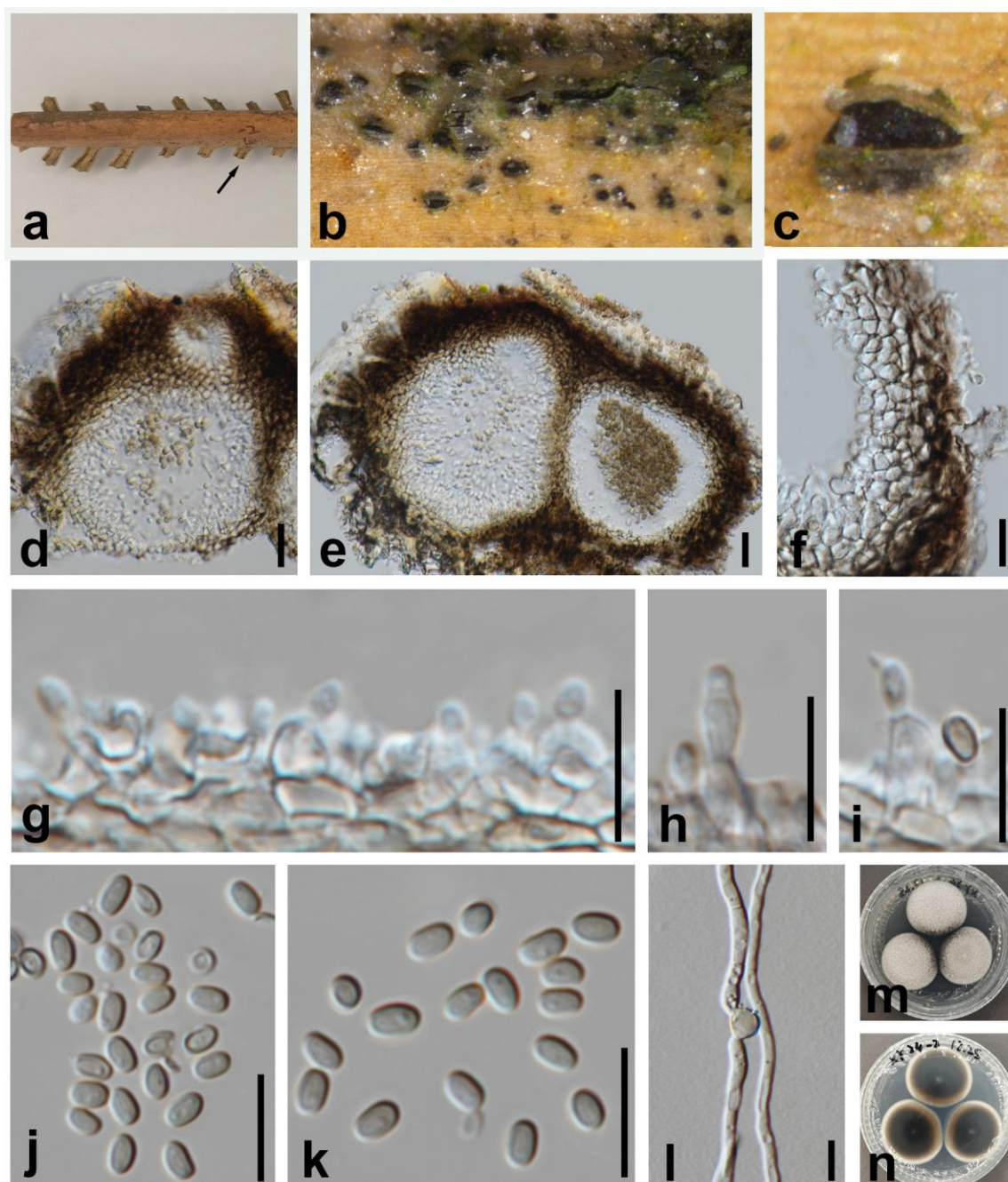


Figure 20 – *Xenorousoella triseptata* (HUEST 23.0244). a Specimen. b, c Conidiomata on the host surface. d, e Sections of conidiomata. f Conidioma wall. g–i Conidiogenous cells with conidia. j, k Conidia. l Germinating conidium. m, n Culture characteristics. Scale bars: d, e = 20 μ m, f–l = 10 μ m.

Thyridaria pini W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 22

Mycobank number: MB854681; Facesoffungi number: FoF16274

Etymology – The epithet refers to *Pinus* sp., the host plant of the fungi.

Holotype – HKAS 134911

Saprobic on dead branch of *pinus* sp. Asexual morph: *Conidiomata* 128–285 μ m diam $\times$ 85–275 μ m high ($\bar{x}$ = 200 $\times$ 185 μ m, n = 15), black, scattered to aggregated, depressed globose to subglobose, variable in size and appearance depending on the specimen, immersed in bark and wood. *Ostiole* 67–86 μ m diam $\times$ 28–97 μ m high ($\bar{x}$ = 78 $\times$ 67 μ m, n = 15) central papillate, black, short. *Conidiomatal* wall 7–54 μ m wide, composed of two layers, with outer stratum comprising pale brown to brown, compressed, thick-walled cells of *textura angularis*, fused with the host

tissues, and inner stratum multi-layered and composed of lightly pigmented to hyaline cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–16 × 1.6–4.6 µm ($\bar{x}$ = 9.5 × 3 µm, n = 30) enteroblastic, integrated, determinate, clavate or ampulliform to lageniform, hyaline, smooth-walled. *Conidia* 3.5–5.5 × 2.5–4.5 µm ($\bar{x}$ = 4 × 3.5 µm, n = 35), ellipsoidal to globose, aseptate, straight or curved, rounded at both ends, first hyaline, turning to brown, thick and smooth-walled, verruculose. Sexual morph: Undetermined.

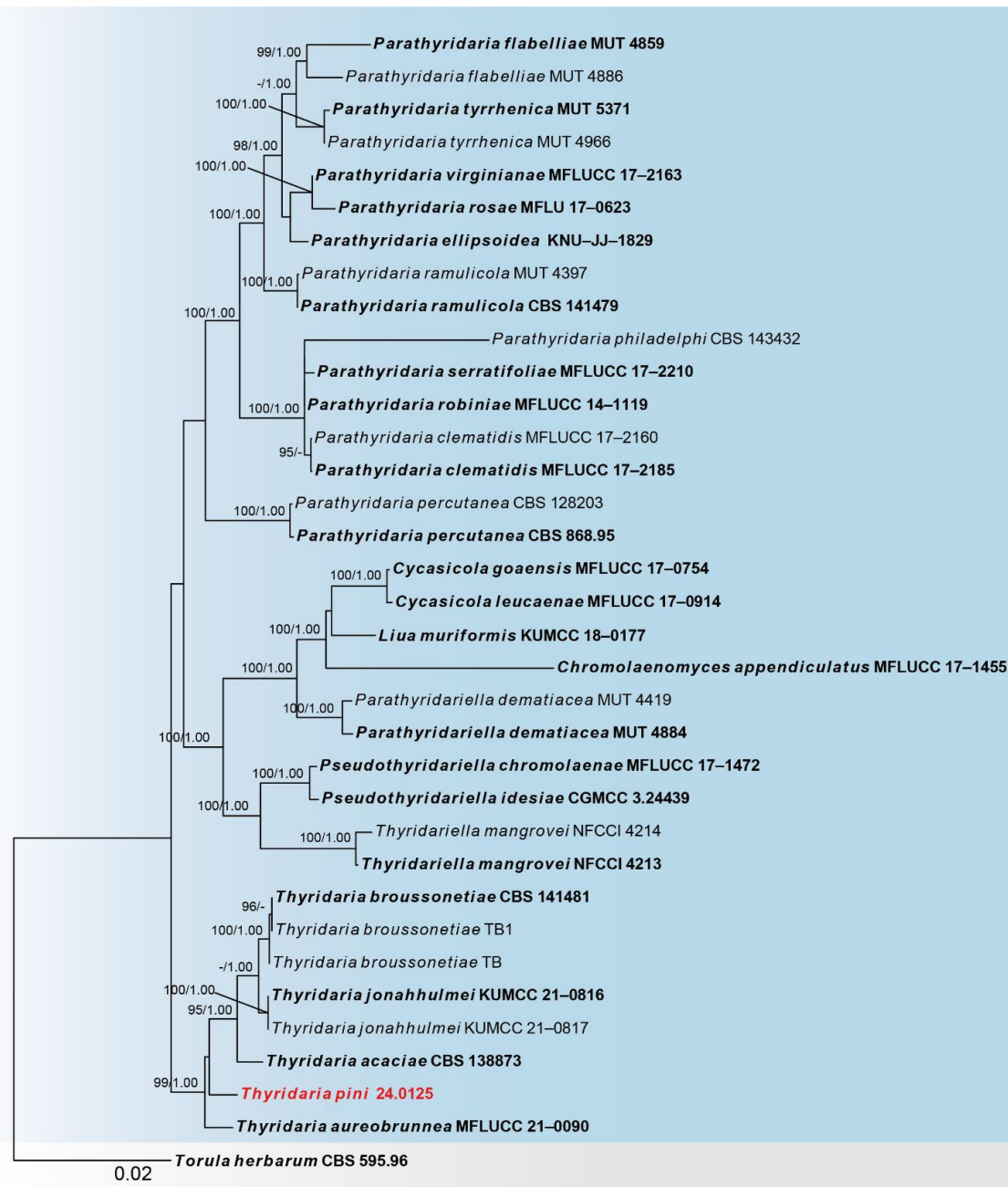


Figure 21 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *tef1-α* and *rpb2*) of Thyridariaceae. The scale bar indicates 0.02 changes. The tree is rooted with *Torula herbarum* (CBS 595.96) (Torulaceae, Pleosporales). The best ML tree with a final likelihood value of -20495.552 is presented. The alignment dataset comprises 35 taxa with 4321 sites, including 1409 distinct patterns, 494 singleton sites and 3020 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Culture characteristics – Colonies on PDA reaching 36 mm diam. after two weeks at 25 °C, colonies from above: circular, margin entire, dense, slightly raised, white at the margin, yellow in the centre; reverse: divergent at the margin, grey in the centre.

Material examined – China, Sichuan Province, Neijiang City, Songlin Village, N 29°32'19", E 105°9'28", elevation 373 m, 1 April 2023, decaying branches of *Pinus* sp., W.H. Tian SLC35 (HKAS 134911, holotype), ex-type UESTCC 24.0125.

GenBank numbers – ITS: PP740385, LSU: PP740391, SSU: PP740397, *rpb2*: PP779424, *tef1-α*: PP776573

Notes – Phylogenetic analysis based on the combined dataset of ITS, LSU, SSU, *tef1-α* and *rpb2* loci revealed that our strain (UESTCC 24.0125) forms a separate branch sister to *Thyridaria acaciae* and *T. aureobrunnea* (Fig. 21). *Thyridaria acacia* is characterized by ampulliform to doliiform, 3–7 × 5–7 μm conidiogenous cells and subcylindrical, straight to slightly curved, apex obtuse, base truncate, 5–10 × 2–3 μm conidia (Crous et al. 2014b). However, our collection is characterized by phialidic, clavate or ampulliform to lageniform 5–16 × 1.6–4.6 μm conidiogenous cells and ellipsoidal to globose, verruculose, 3.5–5.5 × 2.5–4.5 μm conidia. *Thyridaria aureobrunnea* is known only as sexual morph (Boonmee et al. 2021); thus, we cannot compare the morphology. Based on pairwise nucleotide comparisons, our strain (UESTCC 24.0125) differs from *T. aureobrunnea* (MFLUCC 21-0090) by 24/482 bp (gaps: 10/482 bp) in ITS; 8/779 bp (no gaps) in LSU. Thus, we introduce the new species *Thyridaria pini* based on the morphology and multi-locus phylogeny.

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

MycoBank number: MB501487; Facesoffungi number: FoF14248

Notes – Eriksson & Winka (1997) proposed Leotiomyces to accommodate inoperculate discomycetes. Leotiomyces is one of the most diverse groups within Ascomycota, and most are saprobes of a wide variety of substrates, such as Helotiaceae, Lachnaceae and Hyaloscyphaceae on dead plant material and Thelebolales on dung or as endophytes (Berbee 2001, Wang et al. 2006a). Species of this class comprised endophytes, mycorrhizae, fungal parasites, root symbionts, and wood rot fungi, most of which are described from the temperate Northern Hemisphere. Still, some members in Helotiales and Rhytismatales show a broader geographic distribution (Wang et al. 2006a, 2006b, Ekanayaka et al. 2017).

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

MycoBank number: MB90476; Facesoffungi number: FoF13859

Notes – Helotiales is the largest order in Leotiomyces of non-stromatic discomycetes that usually, but not always, have brightly colored apothecia (Wang et al. 2006a). Members of this class are mostly saprobic, living on fallen leaves and decaying wood, but some are parasitic to pathogenic or symbiotic with other organisms (Ye et al. 2009). The Helotiales is the most diverse group in the Leotiomyces and has already been subject to several nomenclatural reinterpretations (Carpenter 1988, Korf & Lizon 2000, 2001).

Fulvoflamma Crous, Stud. Mycol. 55: 56 (2006)

MycoBank number: MB500801

Notes – *Fulvoflamma* was introduced by Crous (2006) to accommodate *F. eucalypti* found in *Eucalyptus* sp. in Spain. This genus is placed within Helotiales as genera *incertae sedis* (Wijayawardene et al. 2022b). Currently, *F. eucalypti* remains the only species in this genus, and in our study, we provide a new geographical record and morphology.

Fulvoflamma eucalypti Crous, Stud. Mycol. 55: 56 (2006)

MycoBank number: MB500802

Saprobic on dead bark of *Cryptomeria japonica*. Asexual morph: *Mycelium* immersed, consisting of smooth, hyaline, branched, septate hyphae, aggregating in the epidermis to form a

Fig. 24

dark brown to black stroma, 75–130 μm ($\bar{x}$ = 100 μm , n = 10) wide, which gives rise to a conidiomata. *Conidiomata* sporodochial, appearing as erect, transparent orange, fusoid structures on the bark surface (like the flame of a candle), 120–235 μm ($\bar{x}$ = 175 μm , n = 15) high; basal region consisting of pale brown cells of *textura oblita* to *textura epidermoidea*; giving rise to thick-walled,

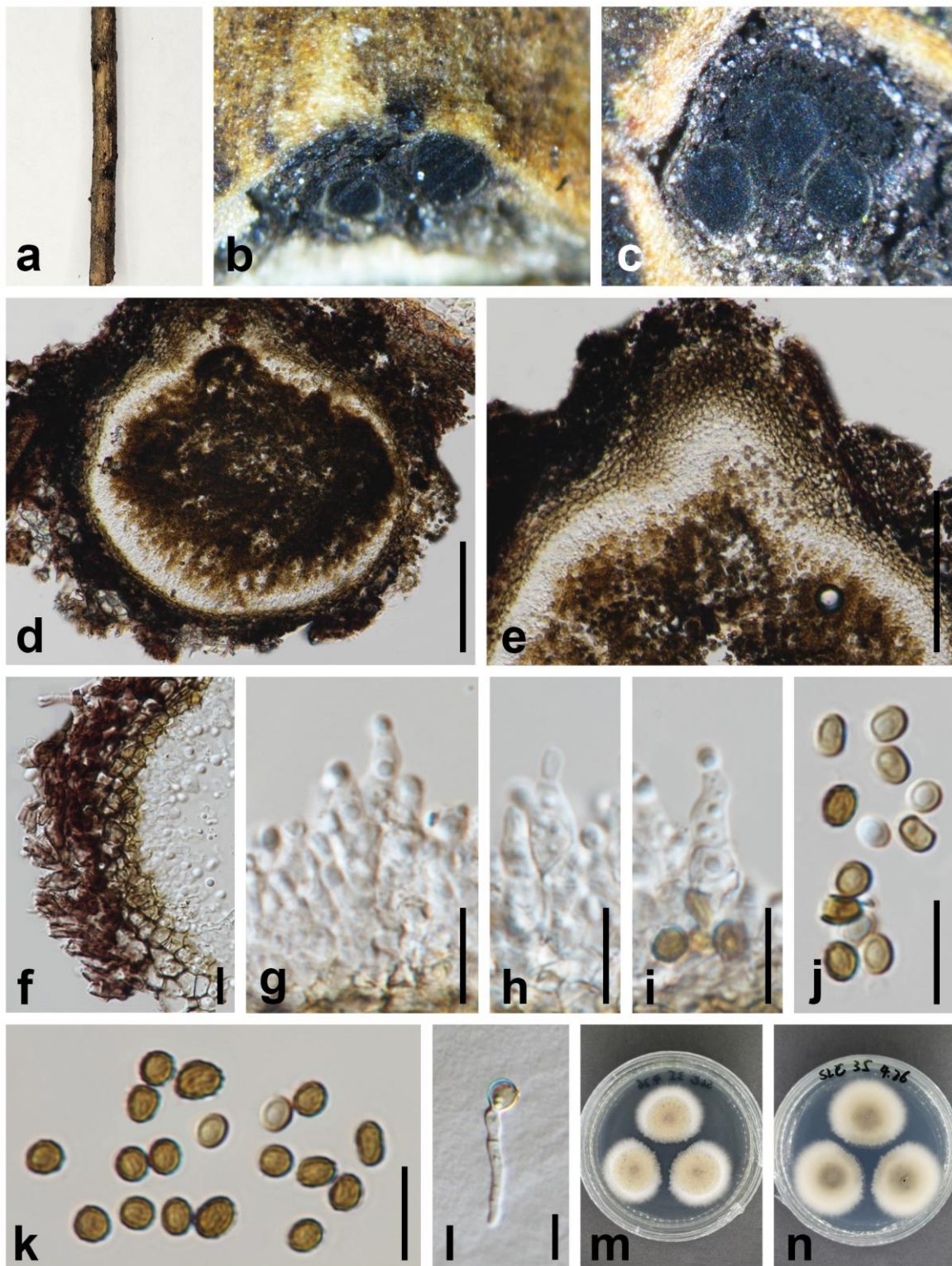


Figure 22 – *Thyridaria pini* (HKAS 134911, holotype). a Specimen. b horizontal section of conidiomata c cross section of conidiomata. d Vertical section of conidiomata. e Ostiole. f Conidiomatal wall. g–i Conidiogenous cells with conidia. j, k Conidia. l Germinating conidium. m, n Culture characteristics. Scale bars: d, e = 100 μm , f–l = 10 μm .

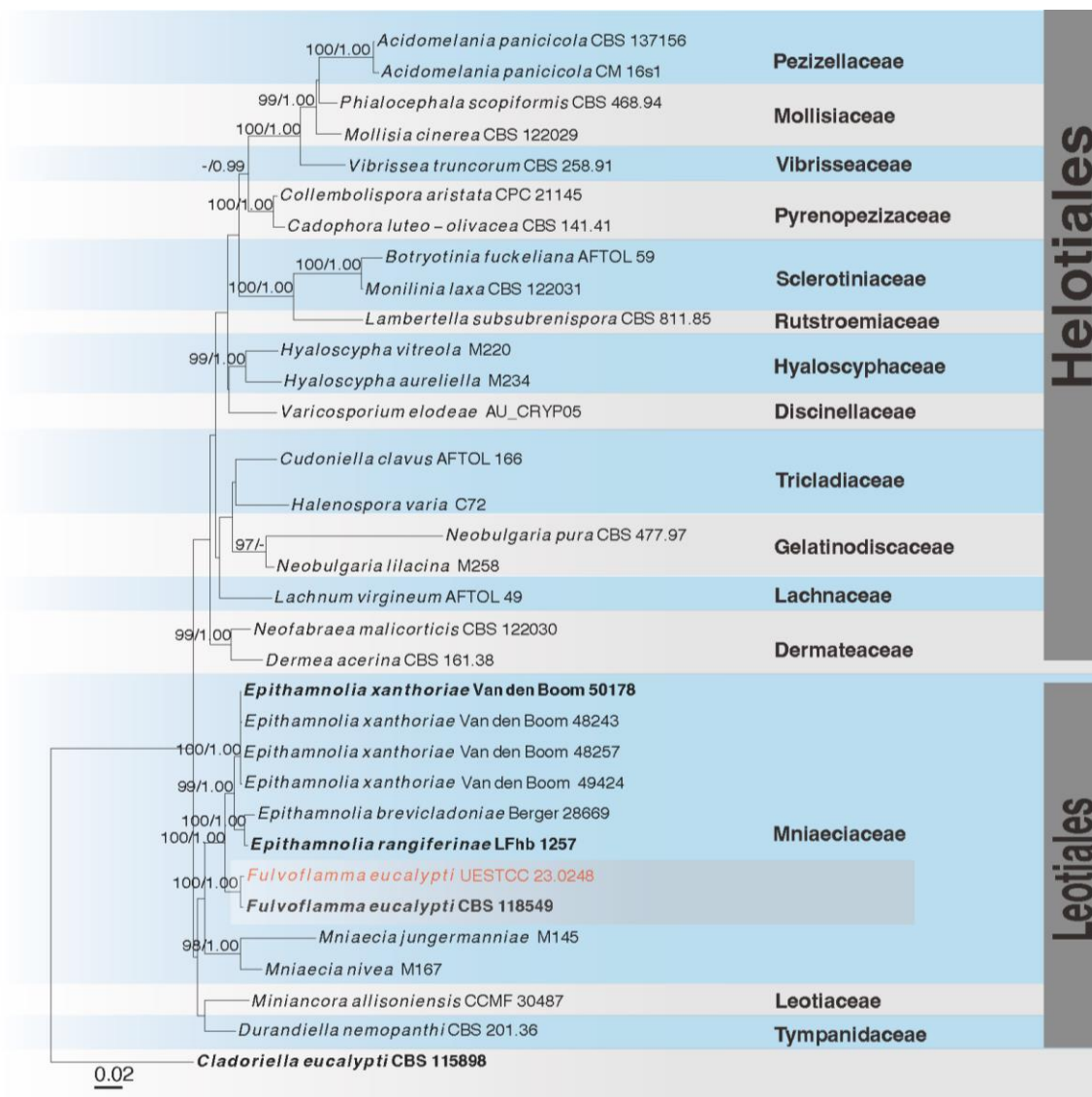


Figure 23 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU and SSU) of Lichinodiales and Helotiales. The scale bar indicates 0.02 changes. The tree is rooted with *Cladoriella eucalypti* (CBS 115898) (Cladoriellaceae, Cladoriellales). The best ML tree with a final likelihood value of -12371.477 is presented. The alignment dataset comprises 43 taxa with 2546 sites, including 776 distinct patterns, 234 singleton sites and 1883 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

pale brown cells of *textura porrecta*, becoming thin-walled, hyaline, and radiating outwards from the narrower, semi-cylindrical sporodochial base, branching sympodially to give rise to hyaline, smooth, thin-walled setae that terminate in bluntly rounded, obtuse ends, and give the conidiomatal margin a feathery appearance; the inner layer of the conidioma gives rise to a mixture of setae and conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical, 12–30 × 1–2 µm ($\bar{x}$ = 20 × 1.7 µm, n = 30) proliferating sympodially, giving rise to additional conidiogenous cells, or conidia. *Conidia* subcylindrical, straight or curved, aseptate, hyaline, smooth, guttulate, filiform, with thin and obtusely rounded ends, 40–70 × 1–2 µm ($\bar{x}$ = 55 × 1.7 µm, n = 30). Sexual morph: Undetermined.

Known distribution – China (this study), Spain

Culture characteristics – Colonies on PDA reaching 38 mm diam after 45 days at 25 °C, colonies from above: circular, spreading, erumpent, folded, with sparse aerial mycelium, surface pale luteous, with ring-like circular texture, slightly raised at the centre; colonies from reverse: luteous, cream at the margin.

Material examined – China, Sichuan Province, Ya'an City, Zhougong Mountain, N 29°58'1", E 103°2'8", elevation 1196 m, 16 November 2022, within dead bark of *Cryptomeria japonica*, W.H. Tian ZGS42_2 (HUEST 23.0248), living culture UESTCC 23.0248.

GenBank numbers – ITS: OR887389, LSU: OR887100, SSU: OR933719

Notes – According to the multi-locus phylogeny, our collection is nested with *Fulvoflamma eucalypti* (CBS 118549) with 100% ML and 1.00 BYPP support (Fig. 23). Through a BLASTn search of the SSU, LSU and ITS sequences on NCBI GenBank, our collection (UESTCC 23.0248) shows 99.11% sequence identity (1000/1009 bp, no gaps) to *F. eucalypti* (CBS 118549) in SSU, 100% sequence identity (849/849 bp, no gaps) in LSU, and 98.32% sequence identity (469/477 bp, no gaps) in ITS. Our collection morphologically fits into the generic concept of *Fulvoflamma* and shares similar characteristics with *F. eucalypti* (CBS 118549) in having immersed, consisting of smooth, hyaline, branched, septate hyphae, forming brown stromata that give rise to conidiomata mycelium; sporodochial, appearing as erect, orange, fusoid structures conidiomata and subcylindrical, straight or slightly curved with obtuse ends, hyaline, guttulate conidia (Crous et al. 2006). Therefore, based on phylogeny and morphology evidence, we present our collection as a new host record of *F. eucalypti* from *Cryptomeria japonica*, and this is the first time *F. eucalypti* has been reported from China.

Our multi-locus phylogeny (ITS, LSU and SSU) indicates that the *Fulvoflamma* species is sister to the *Epithamnolia* with 100% ML and 1.00 BYPP statistical support. They are also clustered with the *Mniaecia* species, which belong to Mniaeciaceae (Leotiales) (Fig. 17). *Epithamnolia* and *Mniaecia* are treated in Mniaeciaceae (Leotiales). At the same time, the *Fulvoflamma* is placed in Helotiales, genera *incertae sedis* (Wijayawardene et al. 2022a). Mniaeciaceae was introduced by Johnston (2019), with *Mniaecia* designated as its type genus, exclusively found as a sexual morph (Johnston et al. 2019). We examined and provided illustrations of *F. eucalypti* (UESTCC 23.0248). Notably, it shares similar morphological characteristics with *Epithamnolia* of Mniaeciaceae. Their conidiomata and conidia have the following similar characteristics: conidiomata when young pycnidoid, sub-immersed, later opening to form a broadly cupuliform structure, revealing a pale brown interior, arise singularly and disperse. The exciple appears dark to medium brown in cross-section, while it resembles a *textura angularis/globulosa* or *textura porrecta* in surface view. The conidia are filiform, straight or occasionally curved, with rounded apices and distinct tapering towards both ends (Suija et al. 2018). Hence, based on the morphological characteristics and phylogenetic analysis, we transfer *Fulvoflamma* (Helotiales genera *incertae sedis*) to the family Mniaeciaceae (Leotiales).

Neodictyocheiropsoraceae W.H. Tian, K.D. Hyde & Maharachch., fam. nov.

MycoBank number: MB851879; Facesoffungi number: FoF16266

Asexual morph: Hyphomycetous. Colonies sporodochia, punctiform, superficial, scattered. Conidiophore present or reduced to conidiogenous cell, micronematous, semi-macronematous to macronematous, mononematous or synnematous, simple or branched, pale brown to dark brown, smooth-walled. Conidiogenous cells holoblastic, integrated, terminal, sometimes flat at base, smooth, brown. Conidia acrogenous, holoblastic, solitary, cheiroid, oval to ellipsoid or irregular-shaped, complanate, pale brown to dark brown, conidial rows unicellular to multiseptated, rows not separating, euseptate or distoseptate, smooth-walled, smooth, with or without appendages; appendages when present subglobose, hyaline, gelatinous, guttulate. Sexual morph: Undetermined.

Type genus – *Neodictyocheiropsora* W.H. Tian, K.D. Hyde & Maharachch.

Notes – According to phylogenetic analysis, our two collections (HKAS 131277 and HKAS 131278) constitute a distinct clade, positioned as a sister group to Drepanopezizaceae and

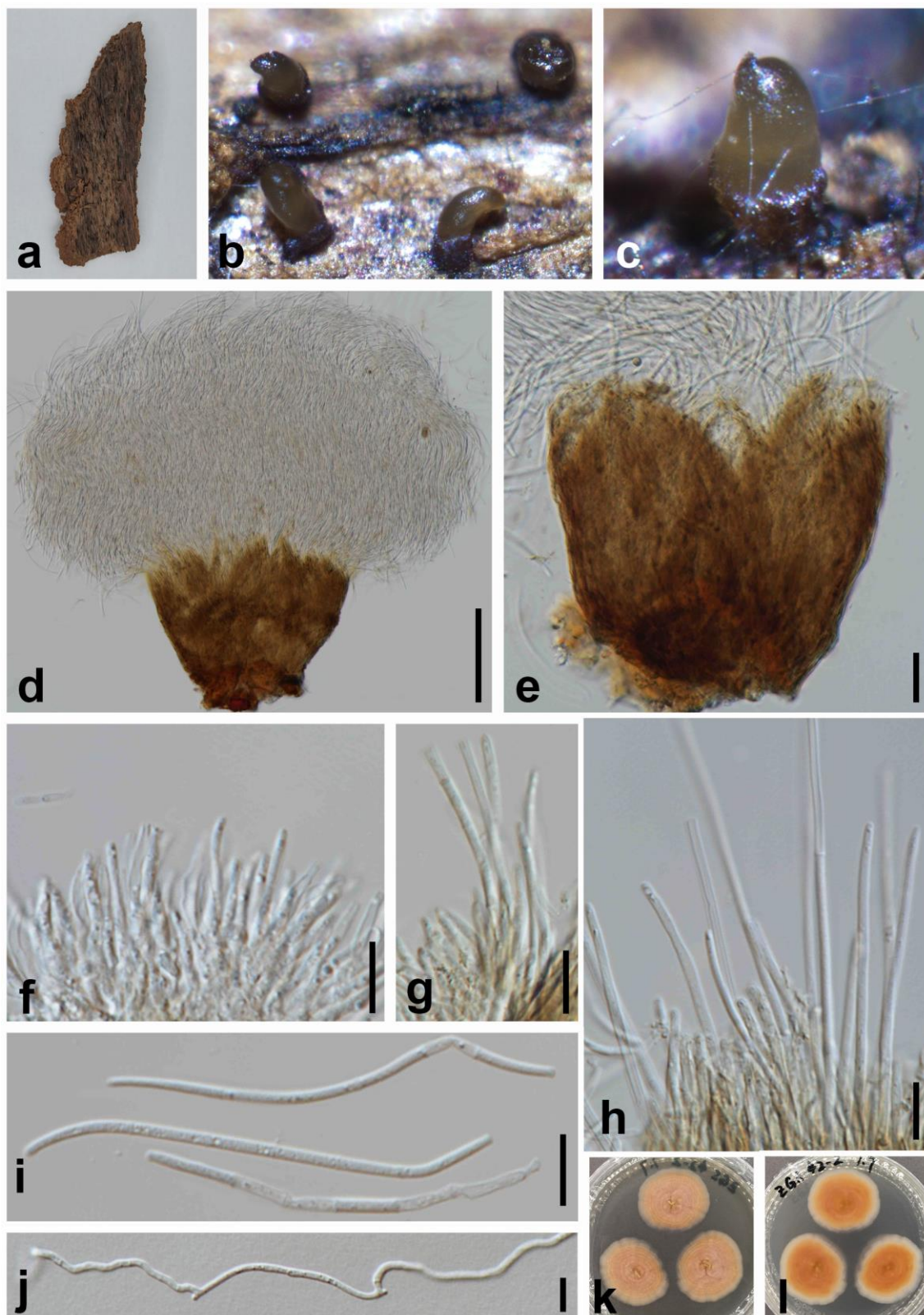


Figure 24 – *Fulvoflamma eucalypti* (HUEST 23.0248). a Specimen. b, c Conidiomata on the host surface. d, e Conidiomata and conidia. f–h Conidiogenous cells with conidia. i Conidia. j Germinating conidium. k, l Culture characteristics. Scale bars: d = 100 μ m, e = 20 μ m, f–j = 10 μ m.

Heterosphaeriaceae (Fig. 19). However, they differ significantly in their morphologically. The conidia of the Drepanopezizaceae are 0–1-septate, variously-shaped, and rarely staurosporous

(Johnston et al. 2019), and Heterosphaeriaceae are hyaline, long-fusiform to filiform or lunate and 2–3-septate (Phutthacharoen et al. 2021). Neodictyocheiroporaceae (Leotiomycetes) shares similarities with the family Dictyosporiaceae in Dothideomycetes in having superficial, sporodochial, punctiform colonies; acrogenous, holoblastic, cheiroid, oval to ellipsoid or irregular-shaped, brown, and rows of unicellular to multiseptate conidia (Boonmee et al. 2016). Despite these resemblances, it is crucial to note that they belong to different classes. Therefore, considering both morphology and phylogeny, we propose introducing a new family, Neodictyocheiroporaceae, within the order Helotiales (Leotiomycetes).

Neodictyocheiropora W.H. Tian, K.D. Hyde & Maharachch., gen. nov.

Mycobank number: MB851880; Facesoffungi number: FoF16268

Etymology – Named after its morphological similarity to *Dictyocheiropora*.

Asexual morph: Hyphomycetous. *Colonies* sporodochia, punctiform, superficial, scattered. *Conidiophores* present or reduced to conidiogenous cells, micronematous, simple or branched, pale brown, smooth, thin-walled. *Conidiogenous cells* holoblastic, integrated, terminal, sometimes flat at the base, smooth, brown. *Conidia* acrogenous, holoblastic, solitary, cheiroid, oval to ellipsoid or irregular-shaped, complanate, brown, euseptate or distoseptate, smooth-walled, with 5–15 vertical rows of subglobose cells, each row with 5–20 cells, rows not separating, smooth, with or without appendages. Sexual morph: Undetermined.

Type species – *Neodictyocheiropora appendiculate* W.H. Tian, K.D. Hyde & Maharachch.

Notes – The new genus contains two species: *Neodictyocheiropora appendiculate* and *Neodictyocheiropora sichuanensis*, forming a distinct subclade in Helotiales in the phylogenetic analyses (Fig. 19). The sexual morph of *Neodictyocheiropora* is undetermined, and the asexual morph has a unique morphology compared to those phylogenetically related species in Helotiales. *Neodictyocheiropora* is characterized by its acrogenous, solitary, brown, oval to ellipsoid or irregular-shaped, palmate or dictyosporous conidia.

Neodictyocheiropora appendiculate W.H. Tian, K.D. Hyde & Maharachch., sp. nov. Fig. 26

Mycobank number: MB851881; Facesoffungi number: FoF16275

Etymology – The name refers to its subglobose appendages.

Holotype – HKAS 131277

Saprobic on the dead twigs of *Cryptomeria fortunei*. Asexual morph: Hyphomycetous. *Colonies* sporodochia, punctiform, velvety, superficial, pulvinate, and dark brown to black. *Conidiophores* micronematous, simple or branched, hyaline or pale brown, smooth, and thin-walled. *Conidiogenous cells* 1.3–2 μm ($\bar{x}$ = 1.6 μm , n = 20) wide, holoblastic, hyaline or pale brown, terminal, determinate, and smooth-walled. *Conidia* 25–45 $\times$ 15–28 μm ($\bar{x}$ = 38 $\times$ 20 μm , n = 40), acrogenous, holoblastic, solitary, cheiroid, oval to ellipsoid, greyish orange to dark brown, consisting of 5–9 vertical rows of cells, each row of 7–13 cells with an apical hyaline, inflated, gelatinous, subglobose, guttulate, cap-like appendage 3.5–7 $\times$ 3–4.5 μm ($\bar{x}$ = 4.9 $\times$ 3.8 μm , n = 40); rows not separating, constricted at the septa, smooth. Sexual morph: Undetermined.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, within dead twigs of *Cryptomeria fortunei*, W.H. Tian LCGS08_2 (HKAS 131277, holotype).

GenBank numbers – ITS: OR887391, LSU: OR887102

Notes – The phylogenetic analyses showed that *Neodictyocheiropora appendiculate* clustered as sister to *Neodictyocheiropora sichuanensis* with 98% ML, 1.00 BYPP statistical support (Fig. 25). However, they differ in morphology, i.e., conidia of *N. appendiculate* and *N. sichuanensis* vary in size (25–45 $\times$ 15–28 μm vs. 25–120 $\times$ 17–77 μm), shapes (cheiroid and oval to ellipsoid vs. irregular-shaped), cell composition (5–9 vertical rows of cells and each row of 7–13 cells vs. 6–12 vertical rows of subglobose cells and each row with 8–12 cells) and appendages (subglobose and cap-like appendage vs. without appendages). In addition, the colonies of *N. appendiculate* are velvety, pulvinate, and dark brown to black, while the colonies of

N. sichuanensis are scattered, solitary, pale brown. Based on pairwise nucleotide comparisons, *N. appendiculata* differs from *N. sichuanensis* by 33/488 bp (gaps: 11/488 bp) in ITS; 20/794 bp (gaps: 3/794 bp) in LSU.

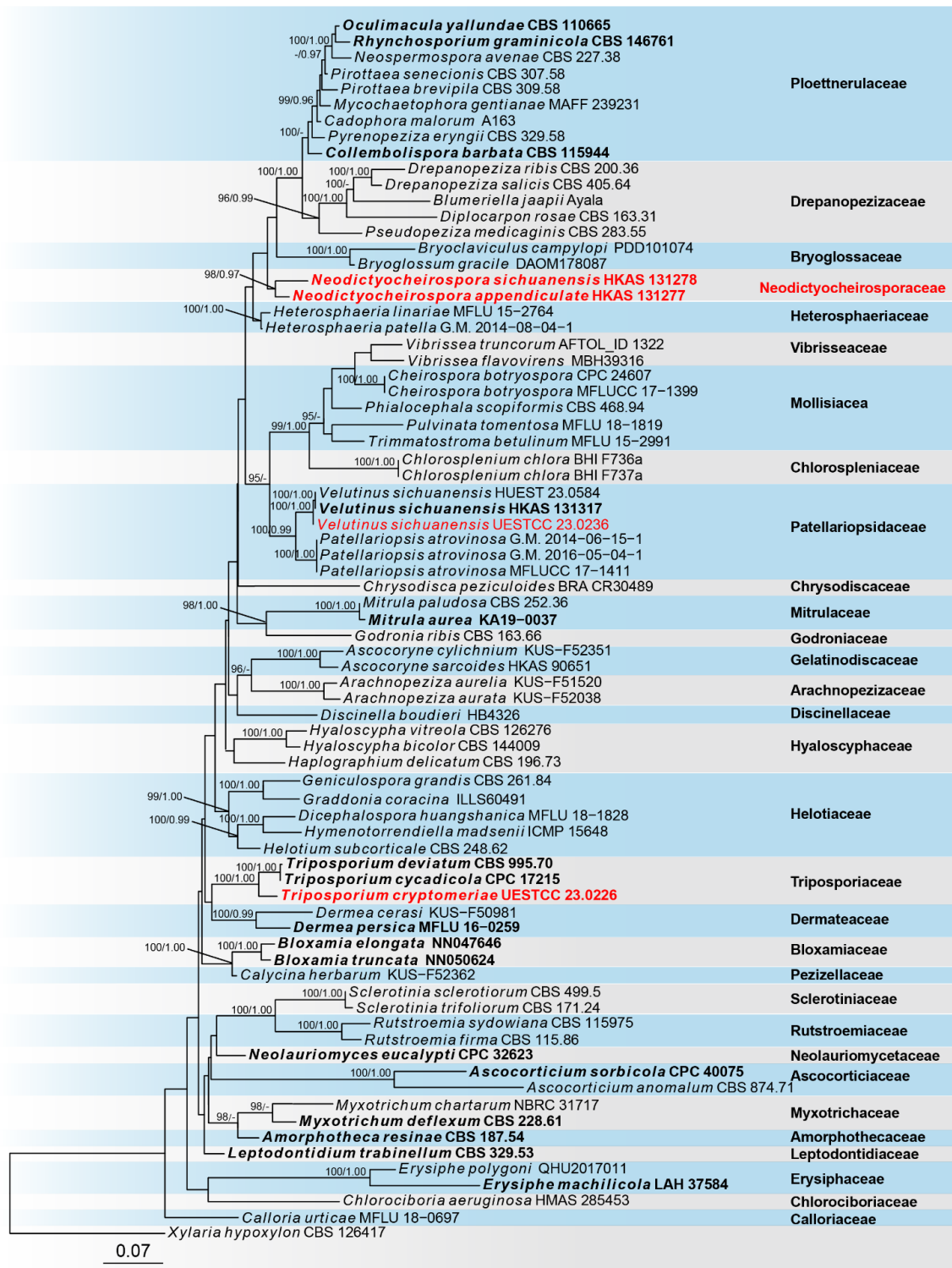


Figure 25 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU) of Helotiales. The scale bar indicates 0.07 changes. The tree is rooted with *Xylaria hypoxylon* (CBS 126417) (Xylariaceae, Xylariales). The best ML tree with a final likelihood value of -21822.139 is presented. The alignment dataset comprises 76 taxa with 1430 sites, including 853 distinct patterns, 172 singleton sites and 682 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or

greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

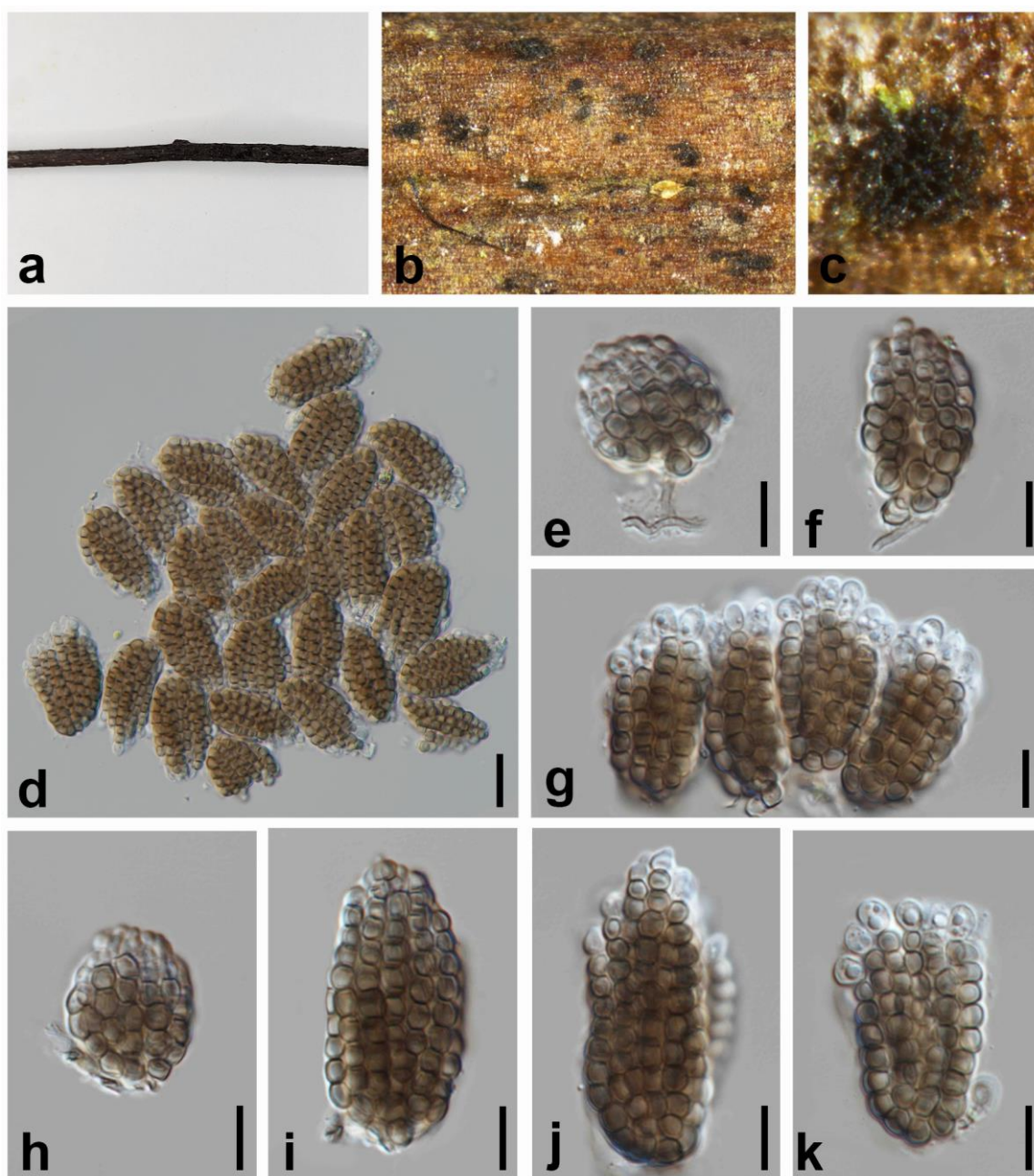


Figure 26 – *Neodictyocheiropora appendiculata* (HKAS 131277, holotype). a Specimen. b, c Colonies on dead twigs of *Cryptomeria fortunei*. d Squash mount of a colony. e, f Conidiogenous cells and conidia. g–k Conidia. Scale bars: d = 20 µm, e–k = 10 µm.

Neodictyocheiropora sichuanensis W.H. Tian, K.D. Hyde & Maharachch., sp. nov. Fig. 27
 MycoBank number: MB851882; Facesoffungi number: FoF16276
 Etymology – Named after the Sichuan Province, China, where the holotype was collected.
 Holotype – HKAS 131278.

Saprobic on the dead twigs of *Cryptomeria fortunei*. Asexual morph: Hyphomycetous. Colonies punctiform, superficial, scattered, solitary, pale brown. Conidiophores micronematous, synnematus, reduced to conidiogenous cells. Conidiogenous cells holoblastic, integrated, terminal, sometimes flat at base, smooth, pale brown to brown. Conidia 25–120 × 17–77 µm ($\bar{x}$ = 46 × 27 µm, n = 40), solitary, irregular-shaped, mostly oval to ellipsoid, complanate, with inconspicuous

consisting of 6–12 vertical rows of subglobose cells, each row with 8–12 cells, rows not separating, smooth, with a basal connecting cell, pale brown, without appendages or mucilaginous sheath. Sexual morph: Undetermined.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, within dead twigs of *Cryptomeria fortunei*, W.H. Tian LCGS08_3 (HKAS 131278, holotype).

GenBank numbers – ITS: OR887392, LSU: OR887103

Notes – See notes under *N. appendiculate*.

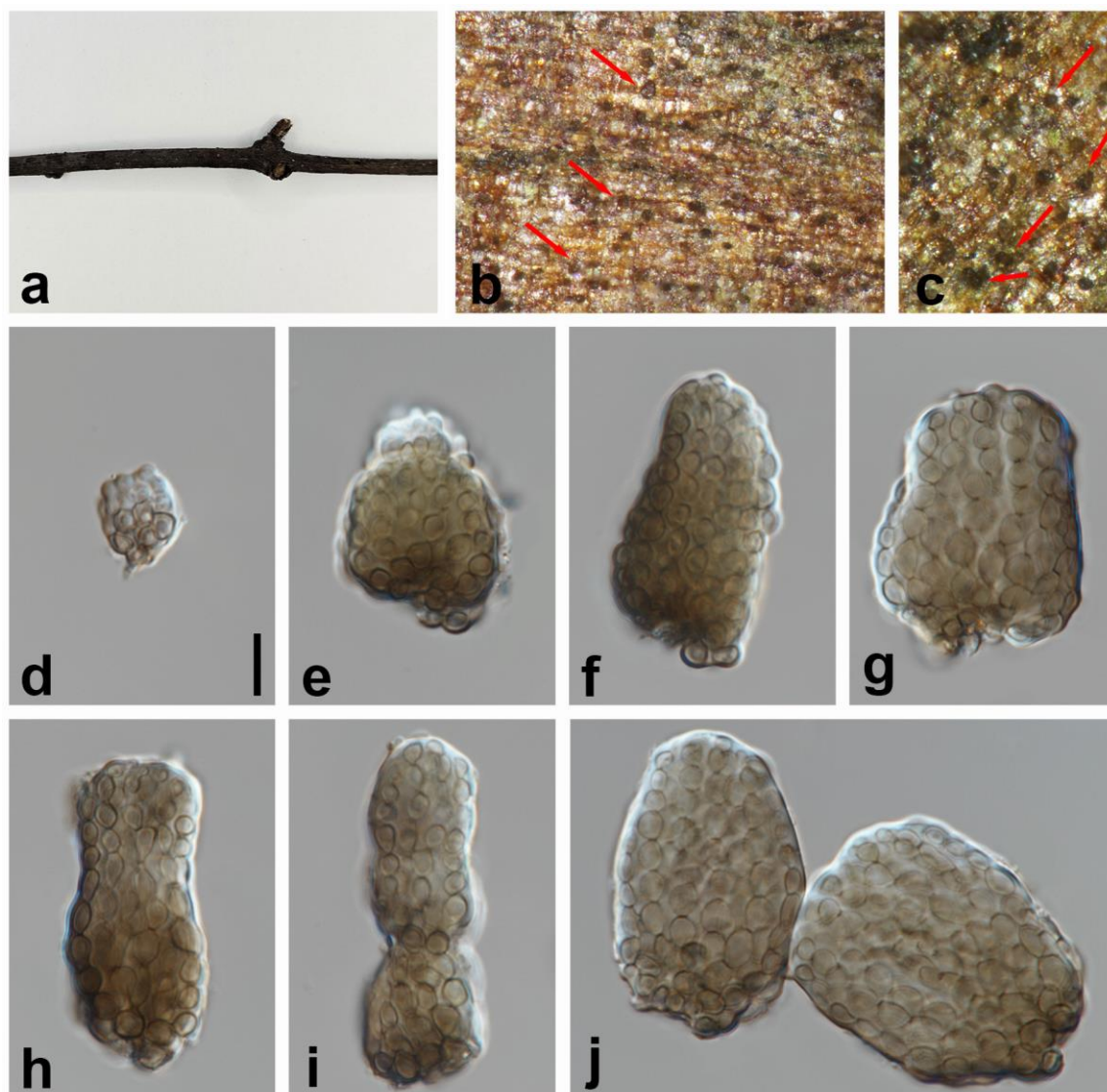


Figure 27 – *Neodictyocheiropora sichuanensis* (HKAS 131278, holotype). a Specimen. b, c Solitary conidia on dead twigs of *Cryptomeria fortunei*. d–e Immature conidia. f–j Mature conidia. Scale bars: d–j = 10 μ m. The scale bar of d applies to d–j.

Patellariopsidaceae Karun., Camporesi & K.D. Hyde, *Frontiers in Microbiology* 11(no. 906): 3 (2020)

Mycobank number: MB556719; Facesoffungi number: FoF06573

Notes – Patellariopsidaceae was introduced by Karunarathna et al. (2020) to accommodate the genus *Patellariopsis*. The asexual morphology of the family Patellariopsidaceae is characterized by having sporodichium with cheiroid conidium complex, while the sexual morphology is characterized by having a sessile discoid apothecium, paraphyses with filiform, branched and

pigmented apices, cylindric-clavate, amyloid asci and ellipsoid to hyaline septate ascospores (Karunarathna et al. 2020).

Velutinus N. Wu & Jian K. Liu, Phytotaxa 638(2): 165–174 (2024)

Mycobank number: MB901518, Facesoffungi number: FoF15233

Notes – *Velutinus* was circumscribed by Wu et al. (2024), with *V. sichuanensis* as the type species found in the medicinal plant *Loropetalum chinense* in China. Based on strong phylogenetic and morphological support, this genus represents the second genus in Patellariopsidaceae.

Velutinus sichuanensis N. Wu & Jian K. Liu, Phytotaxa 638(2): 165–174 (2024)

Fig. 28

Mycobank number: MB901519; Facesoffungi number: FoF15234

Saprobic on decaying branches of *Pinus* sp. Asexual morph: Hyphomycetous. Colonies on natural substrate sporodochial, superficial, hyaline to olive black, scattered, gregarious, punctiform. Mycelium immersed in the substratum, composed of septate, hyaline hyphae. Conidiophores 45–80 × 2.3–6.5 µm ($\bar{x}$ = 60 × 4 µm, n = 30), mononematous, cylindrical, straight or slightly curved, septate, slightly constricted at septa, hyaline, expanding toward the apices, smooth, guttulate, smooth-walled, thick-walled. Conidiogenous cells monoblastic, terminal, integrated, hyaline. Conidia 25–50 × 17–28 µm ($\bar{x}$ = 37 × 22 µm, n = 40), acrogenous, solitary, muriform, constricted at septa, oval to ellipsoidal, smooth-walled, pale brown when immature, broadly obtuse at apex and dark brown, truncate at base, dark brown when mature, sometimes with a hyaline, elliptical to globose basal cell, 8–12 × 5–15 µm ($\bar{x}$ = 11 × 9 µm, n = 20). Sexual morph: Undetermined.

Culture characteristics – Colony on PDA reaching 30 mm diam after 28 days at 25 °C, colonies from above: circular, even entire, white, with thinner mycelium at the center and becoming denser at the edge, zonate; from below: zonate, pale yellow.

Material examined – China, Sichuan Province, Neijiang City, Songlin Village, N 29°32'19", E 105°9'28", elevation 373 m, 1 April 2023, decaying branches of *Pinus* sp., W.H. Tian SLC22_1 (HKAS 131282), living culture CGMCC 3.25639 = UESTCC 23.0236.

GenBank numbers – ITS: OR887393, LSU: OR887104

Notes – Wu et al. (2024) introduced *Velutinus* and described it based on the asexual morph of the type *V. sichuanensis* found in dead branches of *Loropetalum chinense* in China (Fig. 25). Multi-locus phylogeny indicates that our collection is sister to the *V. sichuanensis* group with 100% ML, 1.00 PP statistical support (Fig. 25). The BLASTn searches of the ITS and LSU sequence of our strain (UESTCC 23.0236) and the type strain of *V. sichuanensis* (HKAS 131317) showed 99.43% sequence identity (523/526 bp, no gaps) in ITS, 100% sequence identity in LSU. In addition, the morphological characteristics examined largely overlapped with *V. sichuanensis* (Wu et al. 2024). Thus, based on both morphological comparison and phylogenetic analyses, we report our collections as a new host record of *V. sichuanensis* from *Pinus* sp.

Tripasporiaceae Nann., Repert. mic. uomo: 507 (1934)

Mycobank number: MB81499

Notes – Tripasporiaceae was introduced by Nannizzi (1934) to accommodate the type genus *Tripasporium*, which is characterized by having stauriform conidia composited of a short basal cylindrical stalk, and 3–4-septate arms (Crous et al. 2014a). This family contains only one genus, *Tripasporium*, which was reported hundreds of years ago, and only two species have sequence data (Hernández-Restrepo et al. 2017).

Tripasporium Corda, Icon. fung. (Prague) 1: 16 (1837)

Mycobank number: MB10318, Facesoffungi number: FoF08051

Notes – *Tripasporium* was erected by Corda (1837) with *T. elegans* as the type species and placed in the Tripasporiaceae. However, since *T. elegans* has never been sequenced, the placement of the genus in Helotiales is provisional (Hernández-Restrepo et al. 2017).

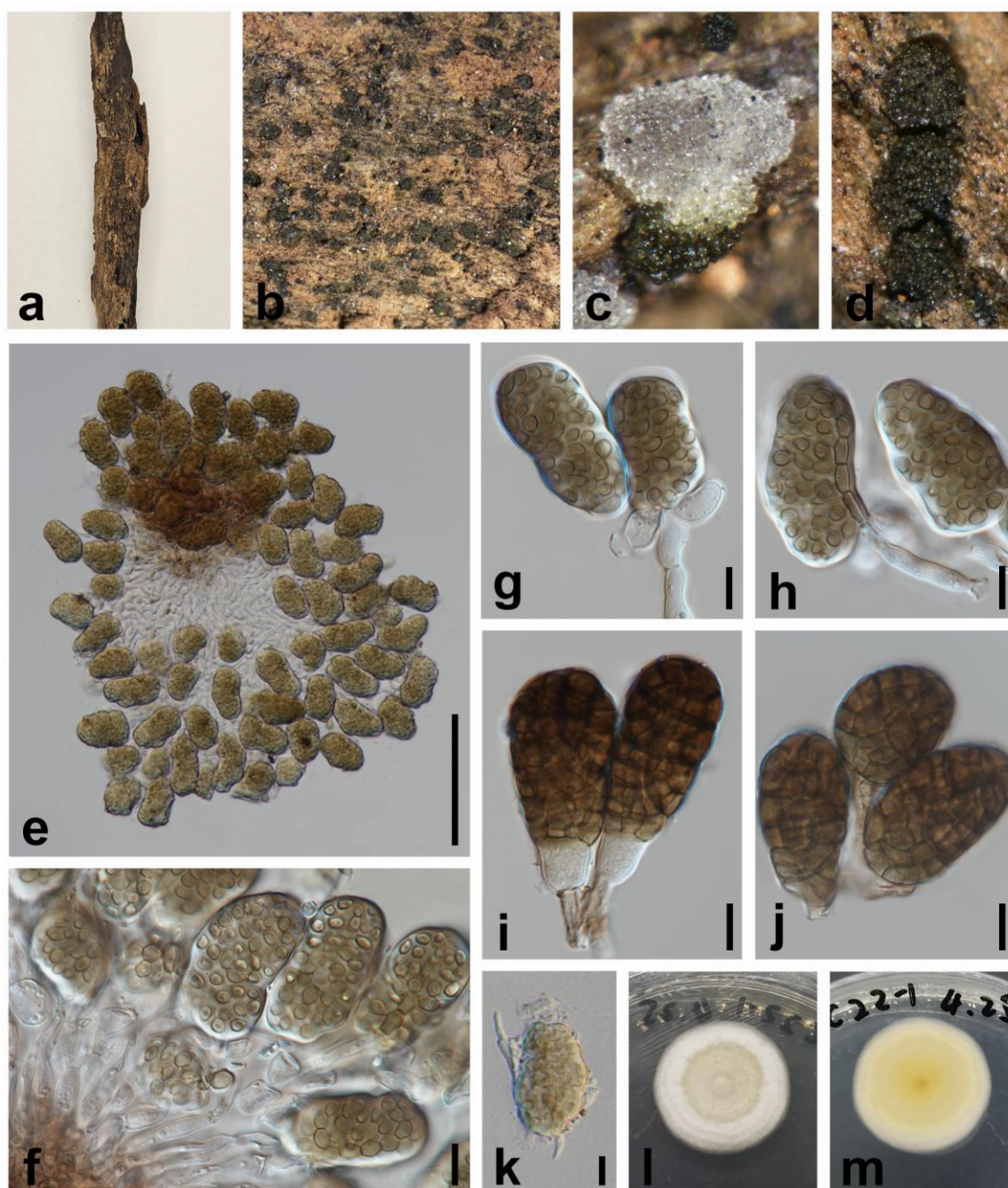


Figure 28 – *Velutinus sichuanensis* (HKAS 131282). a Specimen. b–d Colonies on decaying branches of *Pinus* sp. e, f Conidiophore attached to the host. g, h Conidiophores and immature conidia. i, f Mature conidia. k Germinating conidium. l, m Culture characteristics. Scale bars: e = 100 μ m, f–k = 10 μ m.

Triposporium cryptomeriae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 29

Mycobank number: MB851885; Facesoffungi number: FoF16277

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

Holotype – HKAS 131275.

Saprobic on dead bark of *Cryptomeria japonica*. Asexual morph: *Mycelium* consisting of branched, septate, black, 3–7 μ m diam hyphae. *Conidiophores* erect, subcylindrical, vertical or slightly flexuous, unbranched, constricted at the septum at the apex, 65–155 $\times$ 3–6.5 μ m ($\bar{x}$ = 110 $\times$ 5 μ m, n = 20). *Conidiogenous cells* holoblastic, terminal, dolium informibus, brown, smooth, 1–6 dolium informibus emerging at the apex, 6–12 $\times$ 3–5 μ m ($\bar{x}$ = 8.5 $\times$ 4 μ m, n = 20). *Conidia* solitary,

dark brown to black, thick-walled, guttulate, basal cell with truncate hilum, bearing 2–3 lateral arms, extending outwards; arms subcylindrical, tapering towards obtuse ends, 3–7-septate, $20\text{--}45 \times 8\text{--}15 \mu\text{m}$ ($\bar{x} = 27 \times 11 \mu\text{m}$, $n = 30$) (including basal cell). Sexual morph: Undetermined.

Culture characteristics – Colony on PDA reaching 34 mm diam after 38 days at 25 °C, colony from above: circular, spreading, white, with sparse aerial mycelium, smooth margins; colony from the reverse: white, folded.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, within dead bark of *Cryptomeria japonica*, W.H. Tian LCGS03_1 (HKAS 131275, holotype), ex-type CGMCC 3.25637 = UESTCC 23.0226.

GenBank numbers – ITS: OR887390, LSU: OR887101, *tef1-α*: PP076817

Notes – Phylogenetic analyses of combined ITS, LSU and *tef1-α* sequence data showed that our collection (UESTCC 23.0226) forms a sister group to *Triposporium cycadicola* (CPC 17215) and *T. deviatum* (CBS 995.70) with 100% ML and 1.00 BYPP support (Fig. 25). Based on pairwise nucleotide comparisons, *T. cryptomeriae* differs from *T. cycadicola* by 47/569 bp (gaps: 5/569 bp) in ITS, differs from *T. deviatum* by 47/510 bp (gaps: 5/510 bp) in ITS. Morphologically, *T. cryptomeriae* differs from *T. cycadicola* in the shape of conidiogenous cells (barrel shape vs. subcylindrical) and in having smaller conidiogenous cells ($16\text{--}12 \times 3\text{--}5 \mu\text{m}$ vs. $15\text{--}25 \times 4\text{--}5 \mu\text{m}$), as well as shorter and wider conidial arms ($20\text{--}45 \times 8\text{--}15 \mu\text{m}$ vs. $30\text{--}70 \times 7\text{--}9 \mu\text{m}$) (Crous et al. 2014a). *Triposporium cryptomeriae* resembles the type species *T. elegans*, having similar morphological characteristics and size of conidiophores ($65\text{--}155 \times 3\text{--}6.5 \mu\text{m}$ vs. $50\text{--}100 \times 4\text{--}7 \mu\text{m}$), conidiogenous cells ($6\text{--}12 \times 3\text{--}5 \mu\text{m}$ vs. $6\text{--}8 \times 4\text{--}5 \mu\text{m}$) and conidia ($20\text{--}45 \times 8\text{--}15 \mu\text{m}$ vs. $30\text{--}53 \times 8\text{--}10 \mu\text{m}$) (Wu & Zhuang 2008). Therefore, based on morphology and phylogeny, we introduce and place *T. cryptomeriae* in *Triposporium* s. str. from the dead bark of *Cryptomeria japonica* in China. However, molecular data are unavailable for most species in *Triposporium*, and more collections may be needed to resolve the phylogeny of the genus.

Vibrisseaceae Korf, Mycosystema 3: 23 (1990)

MycoBank number: MB82072

Notes – Vibrisseaceae was introduced by Korf (1990) to accommodate the genera *Vibrissea*, *Chlorovibrissea* and *Leucovibrissea*. Currently, this family has six genera and 43 species (Wijayawardene et al. 2022a). In this family, genera other than *Srinivasanomyces* have been primarily identified through their sexual morphology (Sandoval-Leiva et al. 2014, Hyde et al. 2020a). Based on phylogenetic and morphological evidence, we propose and describe a second asexual morphology genus in the family.

Vibrissea Fr., Syst. mycol. (Lundae) 2(1): 4, 31 (1822)

MycoBank number: MB5737

Notes – Most collections of *Vibrissea* are from southern Chile and are typically found on fallen, waterlogged tree trunks in forests (Sandoval-Leiva et al. 2014). For example, the ascomata of one species grow on branches of *Nothofagus antarctica* (G. Forst.) Oerst., half-buried in snow in forested areas (Sandoval-Leiva et al. 2014). Earlier studies have identified *Vibrissea* as a polyphyletic genus (Wang et al. 2006, Sandoval-Leiva et al. 2014). Previously, *Vibrissea* was known solely by its sexual morphology, characterized by long, filiform ascospores (Sandoval-Leiva et al. 2014). Based on phylogenetic analysis in this study, we identified and reported the asexual morph of *Vibrissea* for the first time.

Vibrissea catenata W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 31

MycoBank number: MB852221; Facesoffungi number: FoF16278

Etymology – The epithet refers to the chained conidia, from the Latin “*catenata*” for chain.

Holotype – HKAS 131991

Saprobic on decaying branches of *Pinus* sp. Asexual morph: Hyphomycetous. Colonies on

natural substrate effuse, black, hairy, glistening. *Mycelium* immersed or superficial, composed of septate, branched, on the surface forming stroma-like aggregations of dark brown to dark

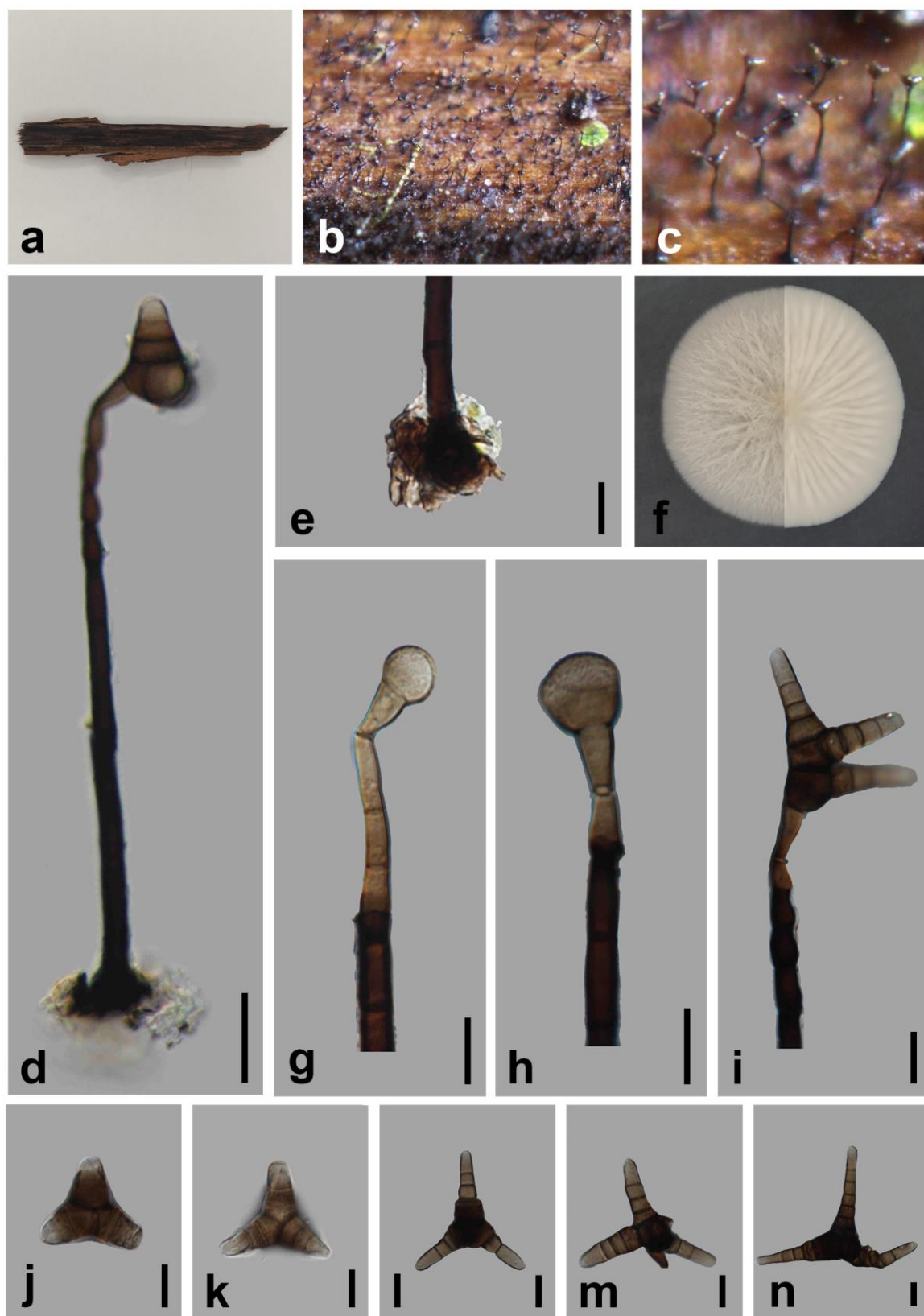


Figure 29 – *Triposporium cryptomeriae* (HKAS 131275, holotype). a Specimen. b, c Colonies on the bark of *Cryptomeria japonica*. d Conidiophore bearing conidia. e Conidiophore base. f Culture characteristics. g–i Conidiophores with apical conidia. j–m Conidia. n Germinating conidium. Scale bars: d, e = 20 μ m, g–n = 10 μ m.

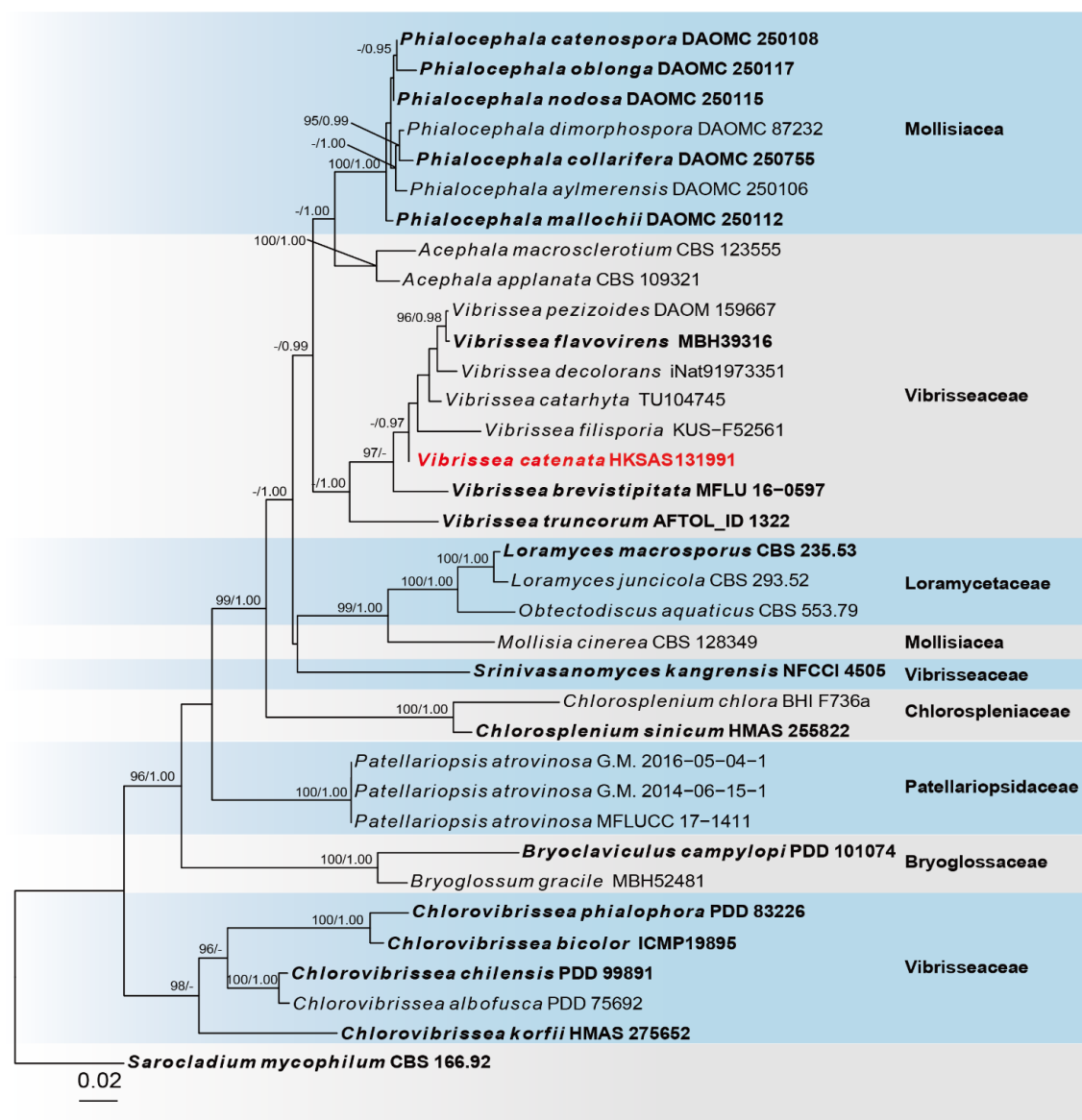


Figure 30 – Phylogram of the best ML tree based on a combined dataset (ITS and LSU) of Vibrissaceae and Mollisiaceae. The scale bar indicates 0.04 changes. The tree is rooted with *Sarocladium mycophilum* (CBS 166.92) (Sarocladiaceae, Helotiales). The best ML tree with a final likelihood value of -9089.889 is presented. The alignment dataset comprises 34 taxa with 1547 sites, including 588 distinct patterns, 203 singleton sites and 964 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

pseudoparenchymatous cells. *Conidiophores* macronematous, reduced to conidiogenous cells. *Conidiogenous cells* 20–77 × 8–11 µm ($\bar{x}$ = 53 × 9 µm, n = 40) holoblastic, integrated, retrogressive, erect, brown, smooth, cylindrical, thick-walled, unbranched to once or twice-branched, length indeterminate, occurring singly or caespitose, terminal, extensions sympodial, with 1–2 conidiogenous loci, subdenticulate, collarettes cylindrical to flaring, 2 × 6.5 µm ($\bar{x}$ = 5 µm, n = 20). *Conidia* 40–180 × 7–11 µm ($\bar{x}$ = 77 × 9 µm, n = 40), acrogenous, solitary, catenar, 2–30-septate, slightly constricted at septa, cylindrical, straight or curved, rough-walled, dark brown to black, broadly obtuse at apex, truncate at base. Sexual morph: Undetermined.

Material examined – China, Sichuan Province, Aba Prefecture, Miyaluo, N 31°42'23", E 102°47'47", elevation 2856 m, 19 October 2022, on decaying branches of *Pinus* sp., W.H. Tian MYL29_1 (HKAS 131991, holotype).

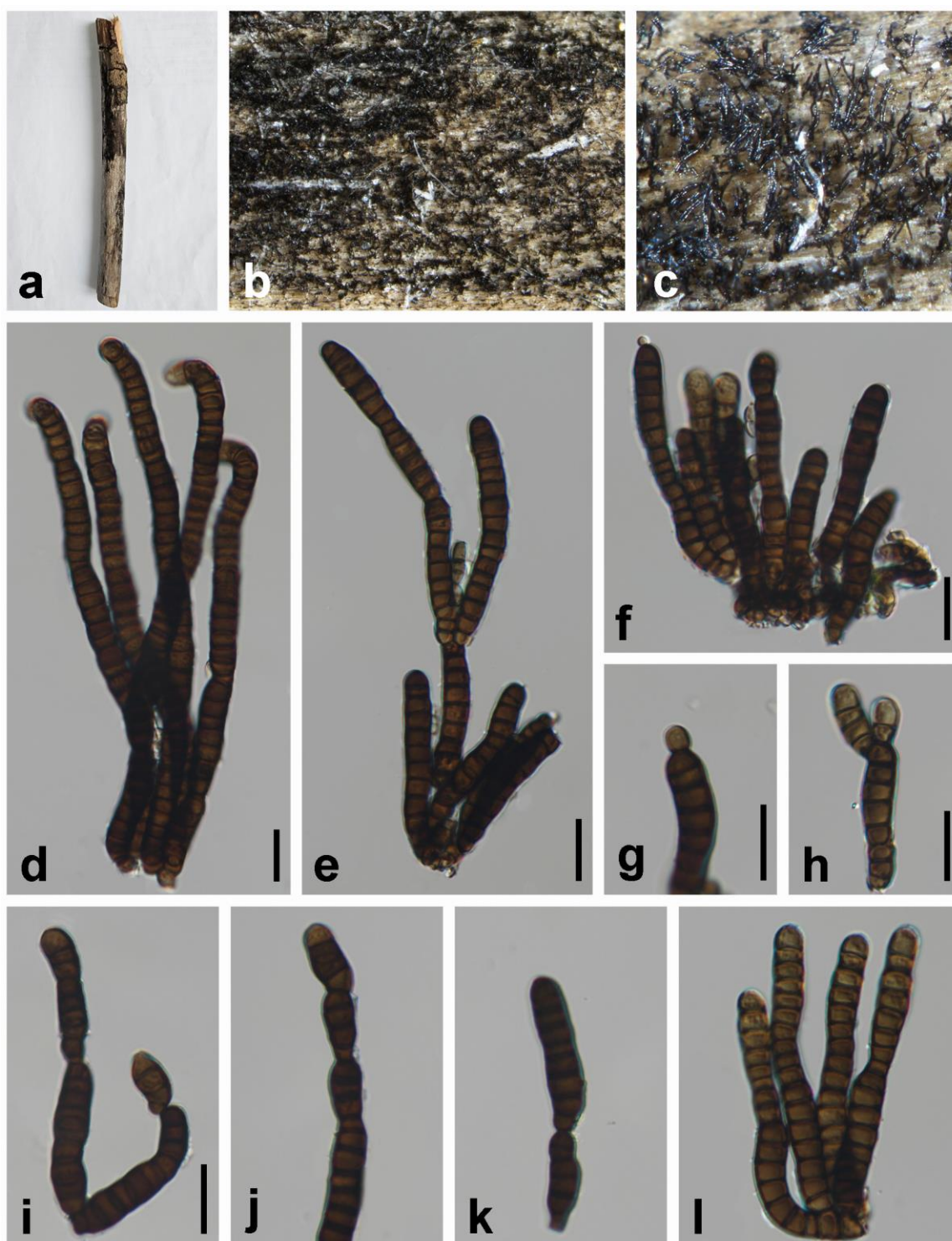


Figure 31 – *Vibrissea catenata* (HKAS 131991, holotype). a Specimen. b, c Colonies on decaying branches of *Pinus* sp. d, f, l Conidiophores and conidia. e, g–k Conidiophore bearing catenary conidia. Scale bars: d–l = 10 μ m.

GenBank numbers – ITS: PP294647, LSU: PP213254

Notes – According to the multi-locus phylogeny, our collection (HKAS 131991) is nested with the genus *Vibrissea* (Fig. 30). However, species of *Vibrissea* are known only by their sexual morphology (Sandoval-Leiva et al. 2014). In our collection HKAS 131991, only the asexual morphology was observed and the conidia failed to germinate on culture media. Our collection (HKAS 131991) resembles *Phialocephala* in the family Mollisiaceae but differs in the size and the number of septa in conidia ($40\text{--}180 \times 7\text{--}11 \mu\text{m}$, 2–30-septate vs. $10\text{--}28.5 \times 4.5\text{--}6 \mu\text{m}$, 1–5-septate)

(Tanney et al. 2016). Based on phylogenetic analysis, we introduce *Vibrissea catenata* as a new species.

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

MycoBank number: MB90350; Facesoffungi number: FoF14263

Notes – Sordariomycetes was established by Eriksson & Winka in 1997 (Eriksson & Winka 1997, Ashton 2009). According to Wijayawardene et al. (2022a) and the latest reported records, the class Sordariomycetes currently includes 7 subclasses, 51 orders, 191 families, and more than 1,700 genera (Sun et al. 2021, Sugita & Tanaka 2022, Perera et al. 2023, Yang et al. 2023). The diversity of fungal groups in Sordariomycetes is high, and most species are saprophytic fungi, which can degrade organic matter in nature and promote the material cycle of the ecosystem (Mäkelä et al. 2014, Maharachchikumbura et al. 2016, Luo et al. 2019, Chen et al. 2023).

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

MycoBank number: MB501514; Facesoffungi number: FoF09685

Notes – Chaetosphaeriales was introduced by Huhndorf et al. (2004) to accommodate a broad and morphologically diverse lineage distinct from the Sordariales. Four families are accommodated in Chaetosphaeriales: Chaetosphaeriaceae, Helminthosphaeriaceae, Leptosporaceae and Linocarpaceae (Wijayawardene et al. 2022a).

Chaetosphaeriaceae Locq., Mycol. gén. struct. (Paris): 174 (1984)

MycoBank number: MB82100; Facesoffungi number: FoF01139

Notes – The family Chaetosphaeriaceae was introduced by Locquin (1984) and placed in the Sordariales due to similar ascomal wall and sexual morphologies. Subsequently, Réblová (1999) placed the family in the Trichosphaeriales and included several additional genera. Based on LSU sequence data, Chaetosphaeriaceae was separated with high bootstrap support of 98% from other families in the order and Huhndorf et al. (2004) placed the family in Chaetosphaeriales. Members of Chaetosphaeriaceae are saprobes on decaying plant material, including leaves, stems, bark, rotten wood, and fruits, and are distributed on herbaceous to woody plants in both terrestrial and freshwater habitats (Wu & Diao 2022).

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

MycoBank number: MB7720; Facesoffungi number: FoF13053

Notes – *Codinaea* was proposed by Maire (1937) to accommodate *C. aristata*. Li et al. (2012) adopted Réblová's (2000) proposal to separate *Codinaea* and *Dictyochaeta* into independent genera based on the presence or absence of conidial setulae (Réblová et al. 2021). The *Codinaea* is a genus of phialidic dematiaceous hyphomycete that are saprobic, pathogenic or endophytic on plant tissues and are found in the tropical and temperate climatic zones (Réblová et al. 2021).

Codinaea dwaya (Subram. & J. Bhat) Réblová & Hern. -Restr. Restr., Journal of Fungi 7 (12, no. 1097): 31 (2021) Fig. 33

MycoBank number: MB842192; Facesoffungi number: FoF11037

Saprobic on dead twigs of *Cryptomeria fortunei*. Asexual morph: Hyphomycetous. Colonies on natural substrate superficial, effuse, scattered, brown, with hyaline conidia on the apex of conidiophores. Mycelium consists of unbranched, septate, smooth, brown to dark brown. Conidiophores 185–440 × 6–9 µm ($\bar{x}$ = 330 × 7 µm, n = 20), wider towards the ends, macronematous, mononematous, erect, single or in groups, unbranched, straight or slightly flexuous, cylindrical, thick- and smooth-walled, septate, dark brown, paler toward the apex. Conidiogenous cells 15–4 × 6–10 µm ($\bar{x}$ = 29 × 8 µm, n = 20), integrated, terminal, monophialidic, extending percurrently, subcylindrical with a swollen venter, becomes flared after sporulation, pale brown, guttulate, with an inconspicuous apical collarette. Conidia in succession by percurrent proliferation from a single fertile locus, acrogenous, globose or pyriform, 5–17 µm ($\bar{x}$ = 14 µm, n =

30) diam, thick- and rough-walled, aseptate, arranged in slimy round hyaline heads, with 6–13 straight or gently curved tubular appendages distributed over the surface, 9–14 μm ($\bar{x}$ = 7 μm , n = 30) long. Sexual morph: Undetermined.

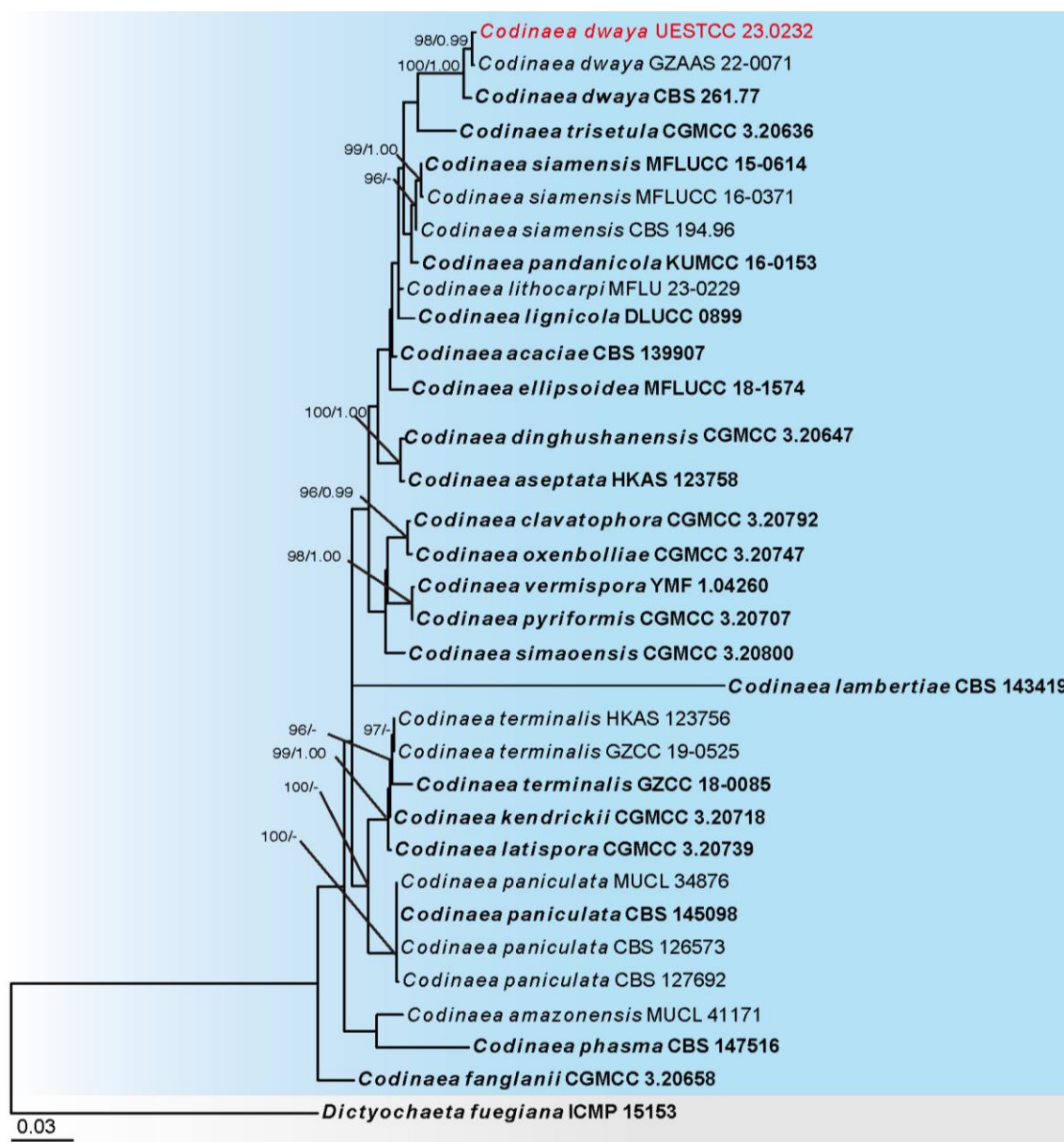


Figure 32 – Phylogram of the best ML tree based on a combined dataset (ITS and LSU) of *Codinaea*. The scale bar indicates 0.03 changes. The tree is rooted with *Dictyochaeta fuegiana* (ICMP 15153) (Chaetosphaeriaceae, Chaetosphaeriales). The best ML tree with a final likelihood value of -4356.909 is presented. The alignment dataset comprises 34 taxa with 1357 sites, including 287 distinct patterns, 101 singleton sites and 1124 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Known distribution – China and India

Culture characters – Colony on PDA reaching 25 mm diam in 2 weeks at 25 °C in the dark, colonies from above: irregular circular, white, uneven entire, with denser mycelium at the center and becoming sparser at the edge; from below: white, pale brown in the centre, margin undulated.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, within dead twigs of *Cryptomeria fortunei*, W.H. Tian LCGS10 (HUEST 23.0232), living culture UESTCC 23.0232.

GenBank numbers – ITS: OR887394, LSU: OR887105

Notes – Our collection (UESTCC 23.0232) resembles the type strain of *Codinaea dwaya* (CBS 261.77) by having terminal, subcylindrical with a swollen venter, becomes flared after sporulation, with inconspicuous apical collarete conidiogenous cells and acrogenous, globose or pyriform, with straight or gently curved tubular appendages distributed over the conidia surface (Réblová et al. 2021). In the phylogenetic analysis, our collection sister to the *C. dwaya* (GZAAS 22-0071) with 98% ML, 0.99 PP statistical support (Fig. 32). A comparison of sequence data of the ITS and LSU between *C. dwaya* (GZAAS 22-0071) and our strains (UESTCC 23.0232) show 98.97% sequence identity (481/486 bp, gaps: 4/486 bp) in ITS, 99.88% sequence identity (818/819 bp, no gaps) in LSU. We identified the new collection as *C. dwaya* based on morphology and phylogenetic analyses and reported it from *Cryptomeria fortunei* for the first time.

Conlariales K.D. Hyde & Hongsanan, Fungal Diversity 107(14): 94 (2021)

MycoBank number: MB557987; Facesoffungi number: FoF09417

Notes – Based on phylogenetic analyses and divergence time estimates, Conlariales was established by Hyde et al. (2021) to accommodate the family Conlariaceae, which was previously placed in the order Atractosporales (Zhang et al. 2017).

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

MycoBank number: MB553758; Facesoffungi number: FoF0336

Notes – Conlariaceae was introduced by Zhang et al. (2017), comprising two genera, *Conlarium* and *Riomyces*. Conlariaceae is a family of freshwater ascomycetes characterized by superficial, dark, globose to subglobose ascomata with cylindrical, mostly straight necks, cylindrical asci with a distinct, refractive, massive, barrel-shaped, apical ring and short pedicel and biseriate, fusiform, aseptate to multi-septate, guttulate ascospores with or without appendages (Zhang et al. 2017).

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

MycoBank number: MB564382; Facesoffungi number: FoF12819

Notes – *Conlarium* was introduced by Liu et al. (2012) to accommodate *C. duplumascospora* found on submerged wood in China. This genus currently contains 11 species, mostly from freshwater environments (Liu et al. 2012, Zhang et al. 2017, Phookamsak et al. 2019). *Conlarium* is characterized by gregarious, coriaceous and beaked ascomata; cylindrical, unitunicate asci with a bipartite apical ring; biseriate, fusiform, hyaline, 0–5-septate ascospores with or without appendages; and anamorph with muriform conidia (Liu et al. 2012).

Conlarium metasequoiae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 35

MycoBank number: MB851889; Facesoffungi number: FoF16279

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

Holotype – HKAS 131281

Saprobic on decaying *Metasequoia glyptostroboides* in a damp environment. Asexual morph: Hyphomycetous. Colonies sporodochial, punctiform, gregarious, raised, dark brown to black. Mycelium mostly immersed, smooth, consisting of septate, thin-walled, hyaline to pale brown hyphae. Conidiophores absent or reduced to conidiogenous cells. Conidiogenous cells 3–9 × 2–3.6 µm ($\bar{x}$ = 5.5 × 3 µm, n = 30) holoblastic, monoblastic, integrated, determinate, terminal, subcylindrical, pale brown, smooth. Conidia 13–28 × 12–22 µm ($\bar{x}$ = 21 × 18 µm, n = 30), acrogenous, solitary, dry, thin-walled, smooth-walled, irregular-shaped, mostly subglobose, 2–3-transversely septate, 1–2-longitudinal septate, clathrate, muriform, dictyoseptate, slightly

constricted at septa, brown to dark brown, with 1–2 small, sub-round, ornamentation on the surface of each cell. Sexual morph: Undetermined.

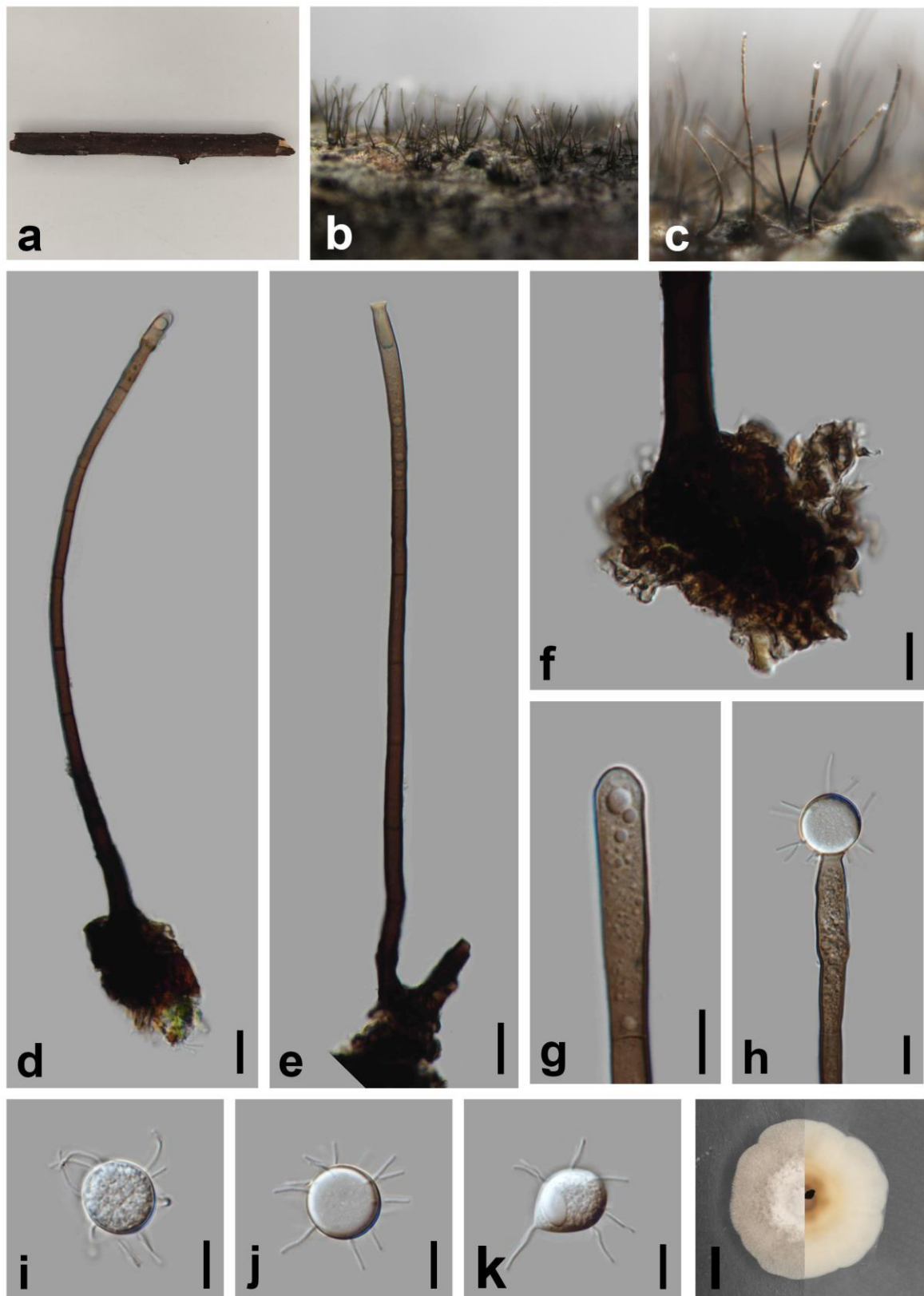


Figure 33 – *Codinaea dwaya* (HUEST 23.0232). a Specimen. b, c Colonies on dead twigs of *Cryptomeria japonica*. d, e Conidiophores and conidiogenous cells. f Conidiophores bases. g, h Conidiogenous cell with conidia. i Germinating conidiophore. j–l Conidia. m Culture characteristics. Scale bars: d–e = 20 μ m. f–l = 10 μ m.

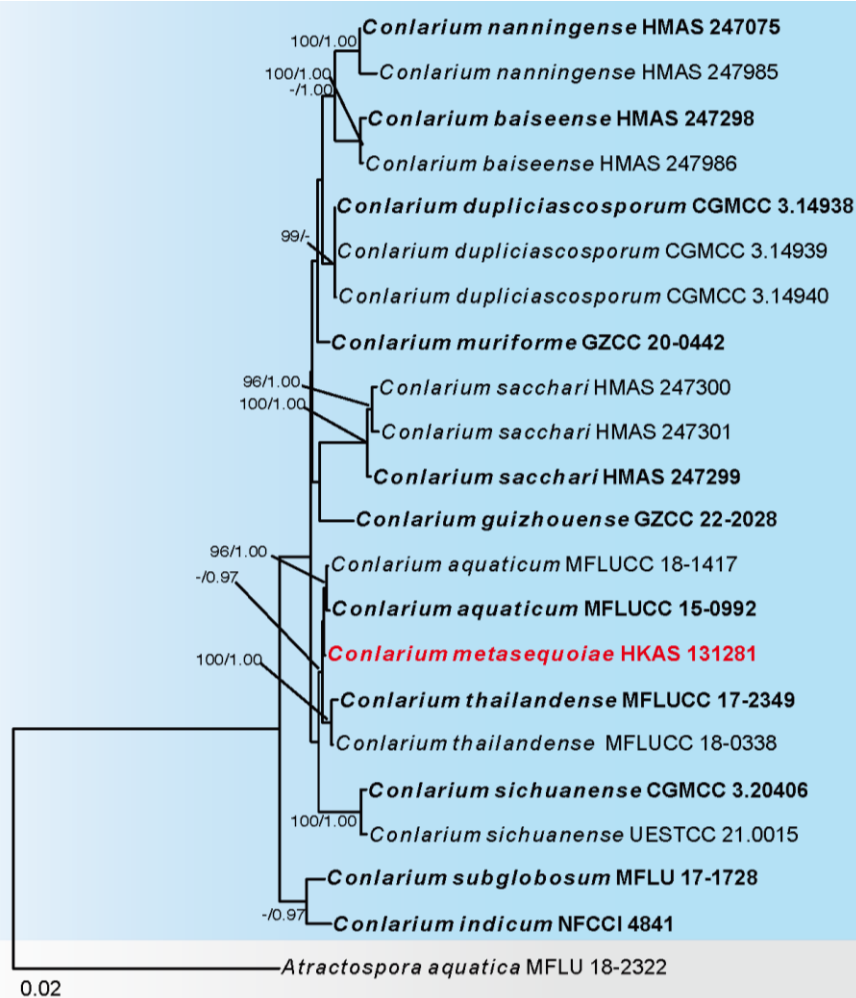


Figure 34 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *rpb2* and *tef1-α*) of *Conlarium*. The scale bar indicates 0.02 changes. The tree is rooted with *Atractospora aquatica* (MFLU 18-2322) (Atractosporaceae, Atractosporales). The best ML tree with a final likelihood value of -9305.250 is presented. The alignment dataset comprises 22 taxa with 4376 sites, including 397 distinct patterns, 254 singleton sites and 3924 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Material examined – China, Sichuan Province, Chengdu City, Pujiang County, N 30°7'59", E 103°30'0", elevation 526 m, 11 July 2022, on decaying *Metasequoia glyptostroboides*, W.H. Tian PJ16 (HKAS 131281, holotype).

GenBank numbers – ITS: OR887395, LSU: OR887106

Notes – According to the multi-locus analyses of combined ITS, LSU, SSU, *rpb2* and *tef1-α* sequence data showed that the species of *Conlarium aquaticum*, *C. thailandense* and our collection are grouped closely in a single subclade (Fig. 34). The comparison of ITS and LSU sequence data of these species were similar and all species lacked *rpb2* sequences, and only *C. aquaticum* (MFLUCC 18-1417 and MFLUCC 15-0992) have *tef1-α* sequences. Thus, it is tough to identify them by molecular sequence (Zhang et al. 2017, Phookamsak et al. 2019). However, morphologically, our collection is different from those of these species. Our collection differs from *C. aquaticum* (MFLUCC 15-0992) in the shape of conidia (subglobose vs. oblong or irregular) and the number of septa in conidia (2–3-transversely septate vs. 6–12-transversely septate; 1–2-longitudinal septate vs. 4–10-longitudinal septate) (Zhang et al. 2017). Moreover, our collection can differ from *C. aquaticum* (MFLUCC 15-0992) in having smaller conidia (13–28 × 12–22 μm

vs. $45\text{--}70 \times 20\text{--}57 \mu\text{m}$) with 1–2 small, sub-round, ornamentation on the surface of each cell (Zhang et al. 2017). Our collection differs from *C. thailandense* (MFLUCC 17-2349) by the smaller conidia ($13\text{--}28 \times 12\text{--}22 \mu\text{m}$ vs. $25\text{--}45 \times 17\text{--}33 \mu\text{m}$) (Phookamsak et al. 2019). Due to their differences in morphology, we introduced *C. metasequoiae* as a new species from China.

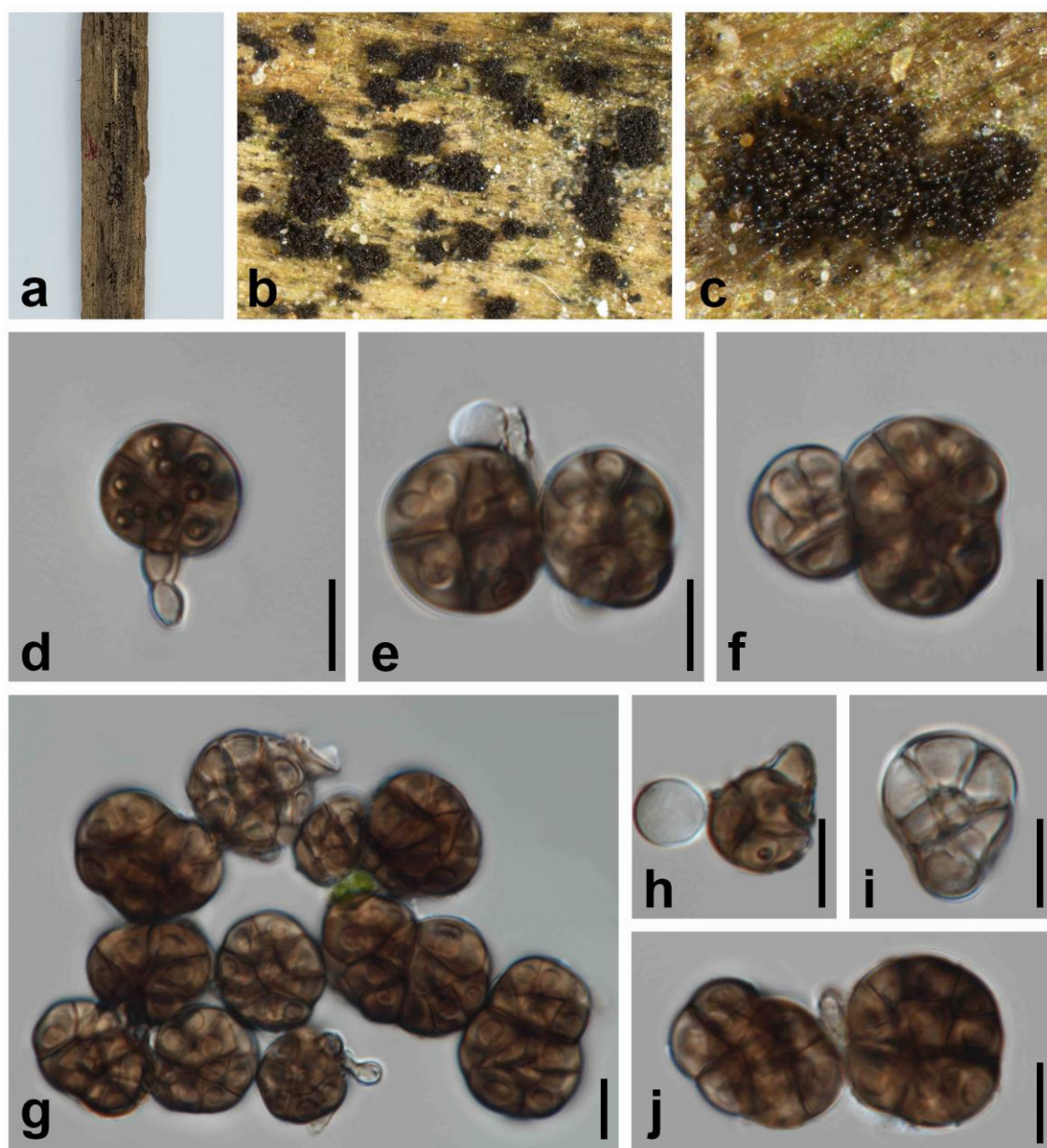


Figure 35 – *Conlarium metasequoiae* (HKAS 131281, holotype). a Specimen. b, c Colonies on decaying *Metasequoia glyptostroboides*. d Conidiogenous cells with conidia. e–g, j Conidia. h, i Immature conidium. Scale bars: d–j = $10 \mu\text{m}$.

Coronophorales Nannf., Nova Acta R. Soc. Scient. upsal., Ser. 4 8(no. 2): 54 (1932)

MycoBank number: MB501516; Facesoffungi number: FoF06517

Notes – Coronophorales are widely distributed Sordariomycetes fungi, primarily inhabiting wood (Mugambi & Huhndorf 2010). The families included in this order are Bertiaceae, Ceratostomataceae, Chaetosphaerellaceae, Coronophoraceae, Nitschkiaceae and Scortechiniaceae (Wijayawardene et al. 2022a). Coronophorales are characterized by taxa with mostly superficial ascomata, sometimes with an extensive hyphal subiculum or well-developed basal stroma that often becomes cupulate or collapsed. Sometimes, an ostiolar opening is indistinct or lacking (Mugambi & Huhndorf 2010).

Ceratostomataceae G. Winter, Rabenh. Krypt. -Fl., Edn 2 (Leipzig) 1.2: 247 (1885)

MycoBank number: MB80575; Facesoffungi number: FoF01803

Notes – Winter (1885) proposed Ceratostomataceae. Members of this family are mostly saprobic and live on plant material. The family is widely distributed on various substrates and is closely associated with other fungi, soil, or rotting vegetation (Cannon & Kirk 2007, Maharachchikumbura et al. 2016). Some species are considered potential biocontrol agents because they can grow on other plant pathogens (Cannon & Kirk 2007, Maharachchikumbura et al. 2016).

Harzia Costantin, Mucéd. Simpl. (Paris): 42 (1888)

MycoBank number: MB8458; Facesoffungi number: FoF10517

Notes – *Harzia* was established by Costantin (1888) as dimorphic fungi with a *Proteophiala* (Aspergillus-like) synanamorphic state, with *H. acremonioides* as the type species (Gams et al. 2009). *Harzia* is a seed-borne fungus that occurs in the soil and currently includes 12 species (Grove 1944, Domsch et al. 1980). Members of this genus are composed of a hyaline mycelium, a brown thick-walled blasto conidia, and hyaline conidiophores (Domsch et al. 1980).

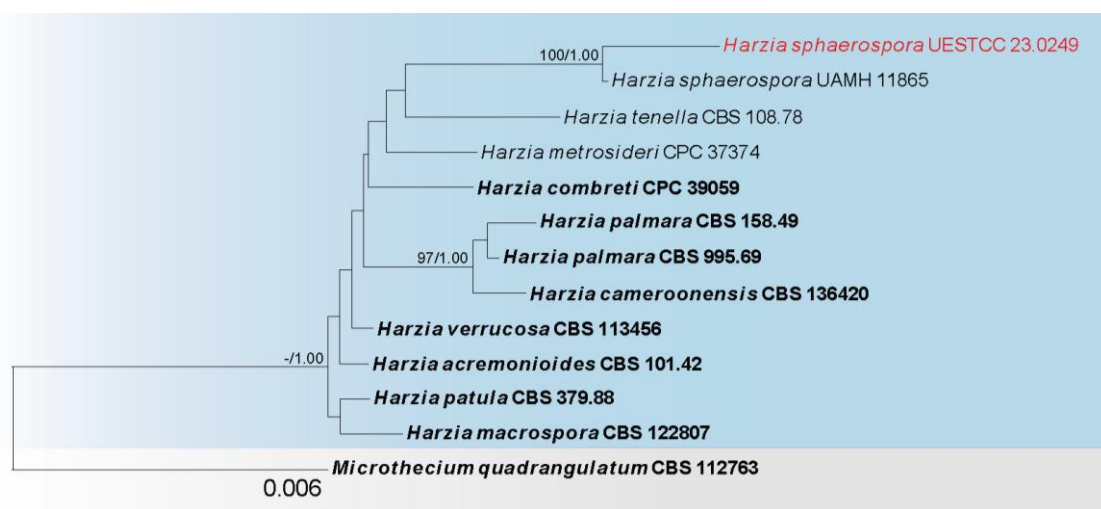


Figure 36 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU and SSU) of *Harzia*. The scale bar indicates 0.006 changes. The tree is rooted with *Microthecium quadrangulatum* (CBS 112763) (Ceratostomataceae, Coronophorales). The best ML tree with a final likelihood value of -6667.862 is presented. The alignment dataset comprises 13 taxa with 3244 sites, including 255 distinct patterns, 182 singleton sites and 2969 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Harzia sphaerospora (Matsush.) D.W. Li & N.P. Schult., in Schultes, Murtishi & Li, Fungal Biology 121(10): 897 (2017) Fig. 37

MycoBank number: MB820477

Saprobic on dead leaves of *Cryptomeria japonica*. Asexual morph: *Mycelium* consisting of hyaline, branched, septate, 4–8 μm diam hyphae. *Conidiophores* erect, simple or sparsely branched, 290–420 $\times$ 4–8 μm ($\bar{x}$ = 357 $\times$ 4 μm , n = 15) wide at the base, straight or slightly flexuous, 4–6 septate, thick-walled, smooth. The terminal fertile part of conidiophores 5–15 μm long, often extending, with 3–6 denticle conidiogenous cells. *Conidiogenous cells* denticles arranged in irregular verticils, tapering to the apex, 6.5–20 $\times$ 2.5–5 μm ($\bar{x}$ = 11 $\times$ 3.5 μm , n = 30), rarely constricted at the base, often branched and developing new denticles or extending and forming new conidiophores. *Conidia* unicellular, solitary, subhyaline to pale ochraceous, spherical or subspherical, smooth or verruculose, sometimes with a small papilla at the base, 15–25 μm ($\bar{x}$ = 20

µm, n = 30) diam, with 0.5–1 µm thick wall. *Conidial secession* rhexolytic. Sexual morph: Undetermined.

Known distribution – China (this study), USA

Culture characters – Colonies on PDA reaching 27 mm diam in a week at 25 °C in the dark, colonies from above: colonies flat, spreading, with moderate aerial mycelium and feathery, lobate margin, cottony, uneven entire, white to pale luteous; from below: luteous.

Material examined – China, Sichuan Province, Ya'an City, Zhougong Mountain, N 29°58'1", E 103°2'8", elevation 1196 m, 16 November 2022, on dead leaves of *Cryptomeria japonica*, W.H. Tian ZGS54_1 (HUEST 23.0249), living culture UESTCC 23.0249.

GenBank numbers – ITS: OR887396, LSU: OR887107, SSU: OR933720

Notes – In the phylogenetic analyses, our collection (UESTCC 23.0249) clustered with *Harzia sphaerospora* (UAMH 11865) with 100% ML and 100 BYPP support (Fig. 36). *Harzia sphaerospora* (= *Olpitrichum sphaerosporum*) was introduced by Matsushima in 1975. Schultes et al. (2017) transferred *Olpitrichum sphaerosporum* to the genus *Harzia* based on ITS and LSU sequence analyses and morphological comparison. *Harzia sphaerospora* (UESTCC 23.0249) is similar to *H. sphaerospora* (UAMH 11865) in terms of the morph and size of conidiophores, conidiogenous cells and conidia (Li et al. 2016). Sequence comparison for the ITS, LSU and SSU region between *H. sphaerospora* (UAMH 11865) and our isolate (UESTCC 23.0249) showed 99.47% sequence identity (567/570 bp, no gaps) in ITS, 99.77% sequence identity (851/853 bp, no gaps) in LSU, and 98.74% sequence identity (1017/1030 bp, gaps: 13bp/1030 bp) in SSU. Thus, we identify our new collection as *H. sphaerospora*, the first report on dead leaves of *Cryptomeria japonica* in China.

Distoseptisporales Z.L. Luo, K.D. Hyde & H.Y. Su, Fungal Diversity 99: 482–484 (2019b)

Mycobank number: MB555640; Facesoffungi number: FoF01754

Notes – Distoseptisporales was introduced by Luo et al. (2019) to accommodate the family Distoseptisporaceae. Distoseptisporales is a well-supported clade in Diaporthomycetidae commonly known from freshwater environments (Shen et al. 2021). There are two families in the order Distoseptisporales: Aquapteridosporaceae and Distoseptisporaceae.

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

Mycobank number: MB551850; Facesoffungi number: FoF01754

Notes – The family Distoseptisporaceae was established by Su et al. (2016) to accommodate *Sporidesmium*-like taxa based on morphology and phylogeny. Based on multigene phylogenetic analysis, Hongsanan et al. (2017) proposed that Distoseptisporaceae may belong to Magnaporthales. Hyde et al. (2017) further proposed placing Distoseptisporaceae (121 million years ago) within the Magnaporthales based on the divergence time estimation. However, the study of Luo et al. (2019) showed that Distoseptisporaceae is not related to Magnaporthales and transferred it to Distoseptisporales.

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

Mycobank number: MB551833

Notes – *Distoseptispora* was established by Su et al. (2016), with *D. fluminicola* as the type species. The genus is characterized by macronematous, mononematous, unbranched conidiophores, mono- or polyblastic, holoblastic, conidiogenous cells and acrogenous, obclavate or cylindrical, rostrate, euseptate or distoseptate, solitary conidia (Su et al. 2016). Members of *Distoseptispora* are mostly saprobic, living on terrestrial or freshwater environments (Luo et al. 2018, Zhai et al. 2022).

Distoseptispora tectonae Doilom & K.D. Hyde, Fungal Diversity 80: 221–223 (2016) Fig. 39

Mycobank number: MB552223; Facesoffungi number: FoF01877

Saprobic on dead twigs of *Metasequoia glyptostroboides*. Asexual morph: Mycelium superficial, numerous, hairy, dark brown, scattered, single or in groups. Conidiophores 45–80 × 5–

10 μm ($\bar{x}$ = 55 $\times$ 7 μm , n = 30), macronematous, mononematous, simple, erect, straight to slightly curved, septate, slightly constricted at the septa, dark brown, 2–7-septate, cylindrical. *Conidiogenous cells* 3.8–7.5 $\times$ 4.5–7 μm ($\bar{x}$ = 5.5 $\times$ 5.6 μm , n = 30), monoblastic, integrated, terminal, lageniform or cylindrical, dark brown, smooth, with lageniform or doliiform. *Conidia* 45–180 $\times$ 12–22 μm ($\bar{x}$ = 105 $\times$ 16 μm , n = 30) wide at the middle and lower part, 7–24-septate, thick septate, flexuous, cylindric-obclavate, uneven width, elongated, straight or slightly curved, verruculose, rounded at apex, obconically truncate at base, dark brown and somewhat paler towards the apex, thick-walled, smooth, secession schizolytic. Sexual morph: Undetermined.

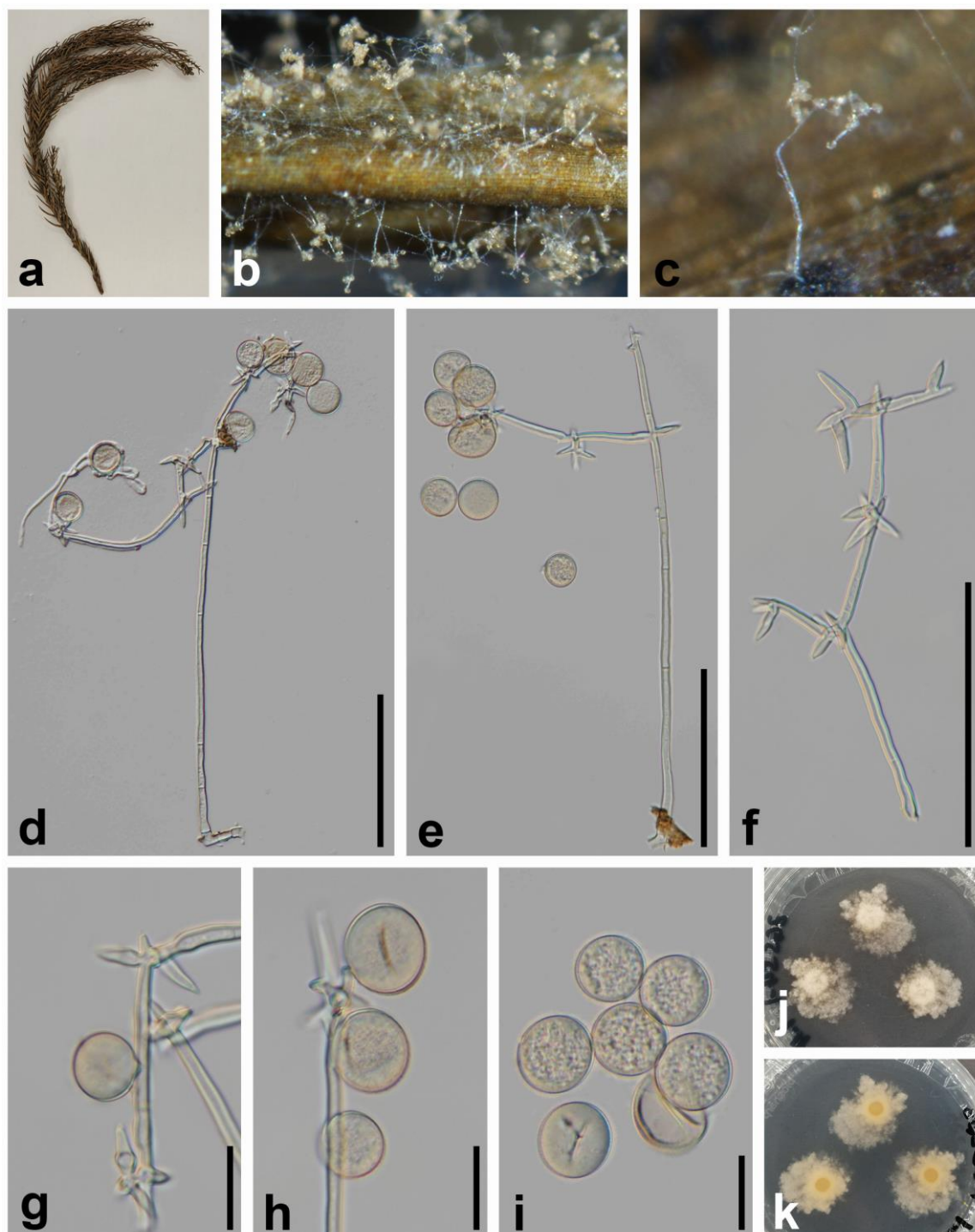


Figure 37 – *Harzia sphaerospora* (HUEST 23.0249). a Specimen. b, c Colonies on dead leaves of *Cryptomeria japonica*. d, e Conidiophores, conidiogenous cells with conidia. f Conidiogenous

cells. g, h Conidiogenous cells with conidia. i Conidia. j, k Culture characteristics. Scale bars: d–f = 100 μ m. g–i = 20 μ m.



Figure 38 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, *rpb2* and *tef1-α*) of *Distoseptispora*. The scale bar indicates 0.04 changes. The tree is rooted with *Aquapteridospora fusiformis* (MFLUCC 18-1606) (Aquapteridosporaceae). The best ML tree with a final likelihood value of -30152.053 is presented. The alignment dataset comprises 83 taxa with 3392 sites, including 1572 distinct patterns, 322 singleton sites and 2005 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Known distribution – China, Thailand

Culture characteristics – Colonies on PDA reaching 22 mm diam after 24 days at 25 °C, colonies from above: circular, margin entire, flat, dense, raised in centre, dusty at periphery, light grey; reverse: cream at the margin, black in the center.

Material examined – China, Sichuan Province, Chengdu City, Xiyuan Avenue, N 30°52'51", E 103°43'51", elevation 595 m, 8 December 2022, on dead twigs of *Metasequoia glyptostroboides*, W.H. Tian XY04_2 (HUEST 23.0240), living culture UESTCC 23.0240.

GenBank numbers – ITS: OR887397, LSU: OR887108

Notes – *Distoseptispora tectonae* was introduced by Hyde et al. (2016) from a dead twig of *Tectona grandis* in Thailand. In the phylogenetic analyses, our collection (UESTCC 23.0240) grouped with the other isolates *D. tectonae* (MFLUCC 12-0291, MFLUCC 16-0946) (Fig. 38). In the NCBI BLASTn search, the ITS and LSU sequences of *D. tectonae* (UESTCC 23.0240) matched with the type strain of *D. tectonae* (MFLUCC 12-0291) with 99% sequence identity (445/449 bp, gaps: 1/449 bp) in ITS and 99% sequence identity (849/851 bp, no gaps) in LSU. Our new collection (UESTCC 23.0240) shares overlapping morphological characters with type strain. They share dark brown conidiophores with monoblastic, lageniform or doliiform conidiogenous cells that

produce thick septate, flexuous, cylindric-obclavate conidia (Hyde et al. 2016). Therefore, we identified our collection as *D. tectonae*, which was first recorded from dead twigs of *Metasequoia glyptostroboides* in China.

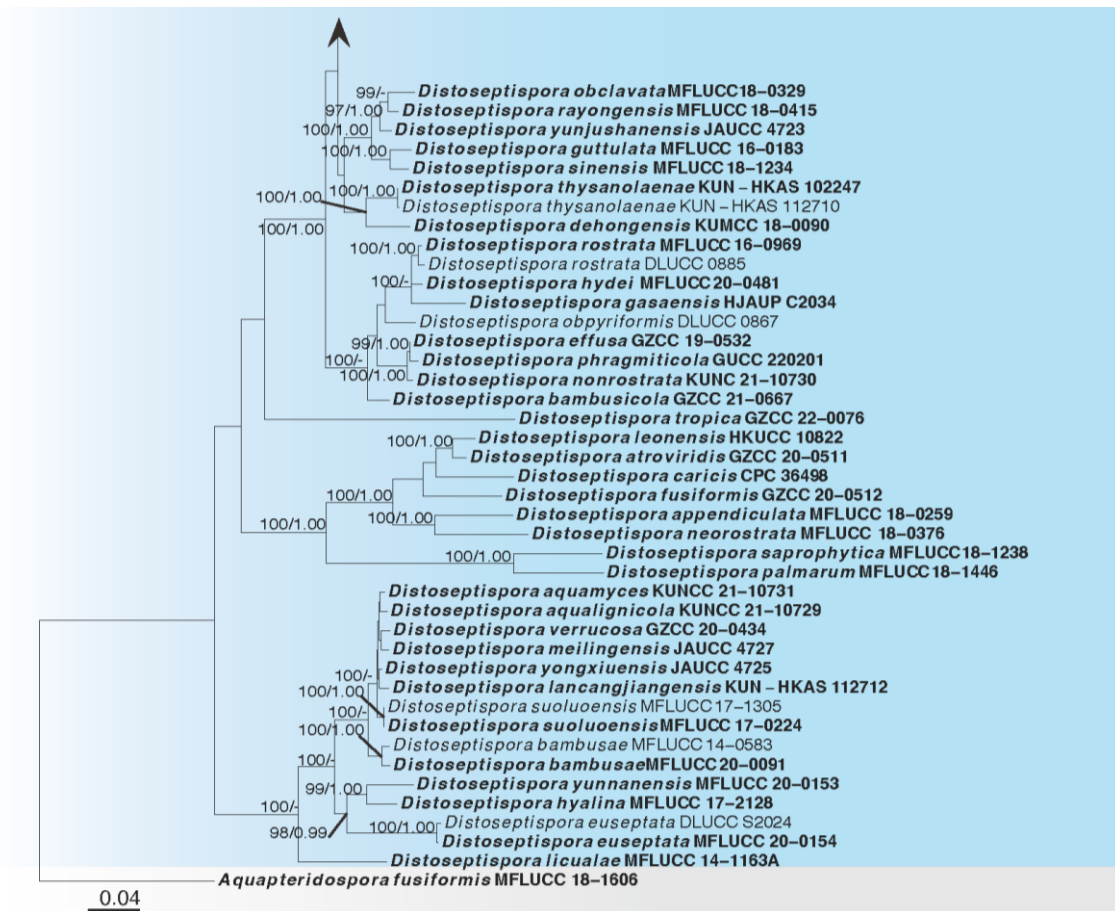


Figure 38 – Continued.

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert, Stud. Mycol. 68: 170 (2011)

MycoBank number: MB515429; Facesoffungi number: FoF09687

Notes – Glomerellales was established by Réblová et al. (2011) in the class Sordariomycetes and currently comprises five families Australiascaceae, Glomerellaceae, Malaysiascaceae, Plectosphaerellaceae and Reticulascaceae (Wijayawardene et al. 2022a). Glomerellales comprises endophytic fungi and parasites of living plants, characterized by ascomata that vary from endostromatal to apostromatal and often possess unicellular, hyaline ascospores (Réblová et al. 2011).

Plectosphaerellaceae W. Gams, Summerb. & Zare, Nova Hedwigia 85(3–4): 476 (2007)

MycoBank number: MB510694; Facesoffungi number: FoF01334

Notes – Plectosphaerellaceae was introduced by Zare et al. (2007) with *Plectosphaerella* as the type genus. The members of this family are mostly asexual, characterized by having simple or verticillate conidiophores with phialidic conidiogenous cells and mostly cylindrical or ellipsoidal conidia arranged in slimy heads (Zare et al. 2007). Plectosphaerellaceae are mainly soil-borne saprobes or weak to virulent, facultative or obligate plant pathogens. Some are causal agents of important diseases in different host plants worldwide (Cannon et al. 2012, Carlucci et al. 2012, Hyde et al. 2014, Giraldo et al. 2017).

Musicillium Zare & W. Gams, Nova Hedwigia 85(3–4): 482 (2007)

MycoBank number: MB510696; Facesoffungi number: FoF013535

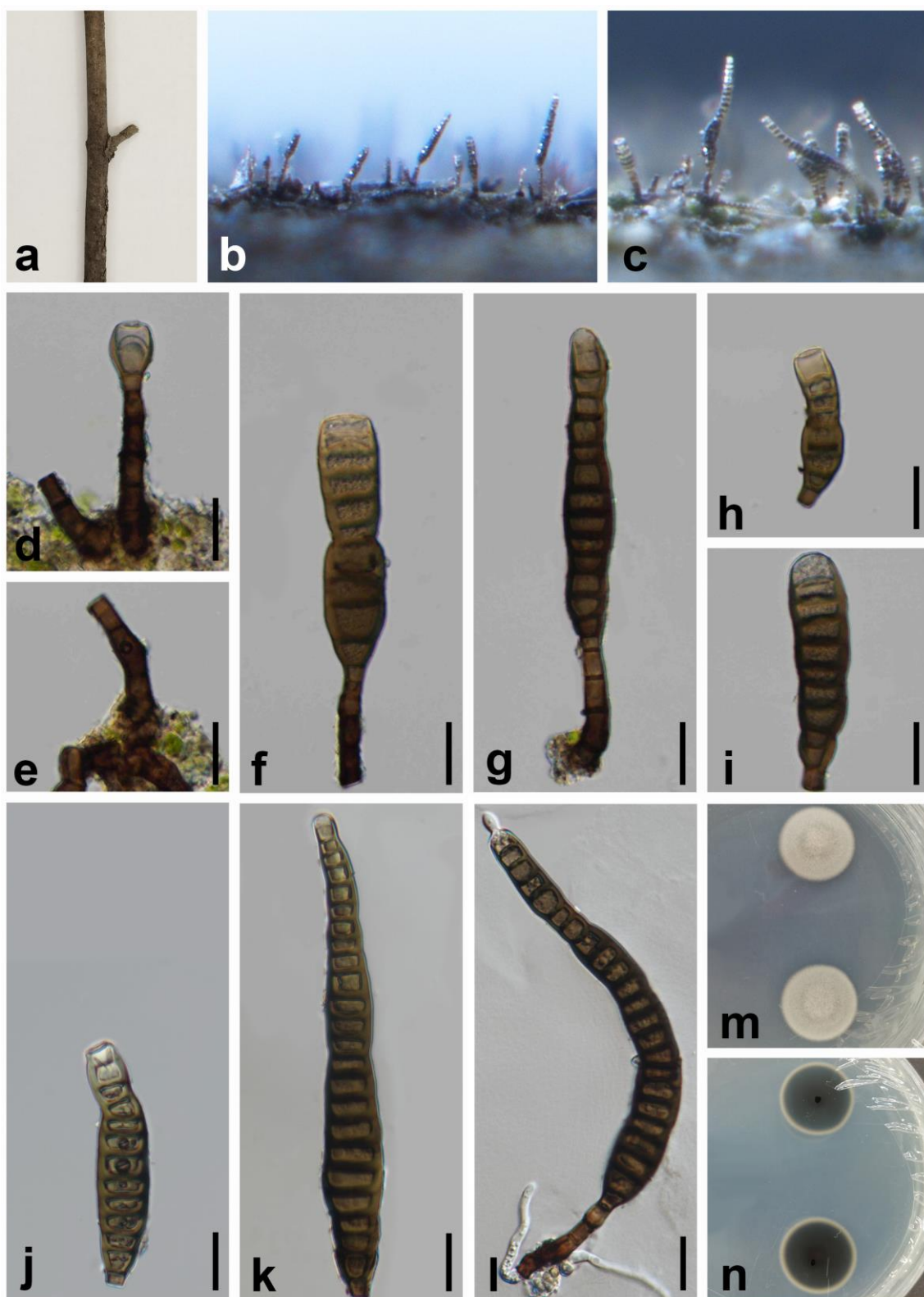


Figure 39 – *Distoseptispora tectonae* (HUEST 23.0240). a Specimen. b, c Colonies on dead twigs of *Metasequoia glyptostroboides*. d, f, g Conidia attached to conidiophores. h–k Conidia. l Germinating conidium. m, n Culture characteristics. Scale bars: d–l = 20 μ m.

Notes – Based on the morphological difference from *Verticillium* species, *Musicillium* was established by Zare et al. (2007). Currently, the genus comprises four species *M. elettariae*, *M. pandanicola*, *M. theobromae* and *M. tropicale* (Zare et al. 2007, Giraldo & Crous 2019). *Musicillium* is characterized by conidiophores that arise from submerged hyphae, and are erect,

septate, repeatedly verticillate towards the apex and distinctly brown throughout (slightly pale only near the tip). Chlamydospores are lacking, while the moniliform hyphae are initially subhyaline, but turning brown (Zare et al. 2007, Giraldo & Crous 2019).

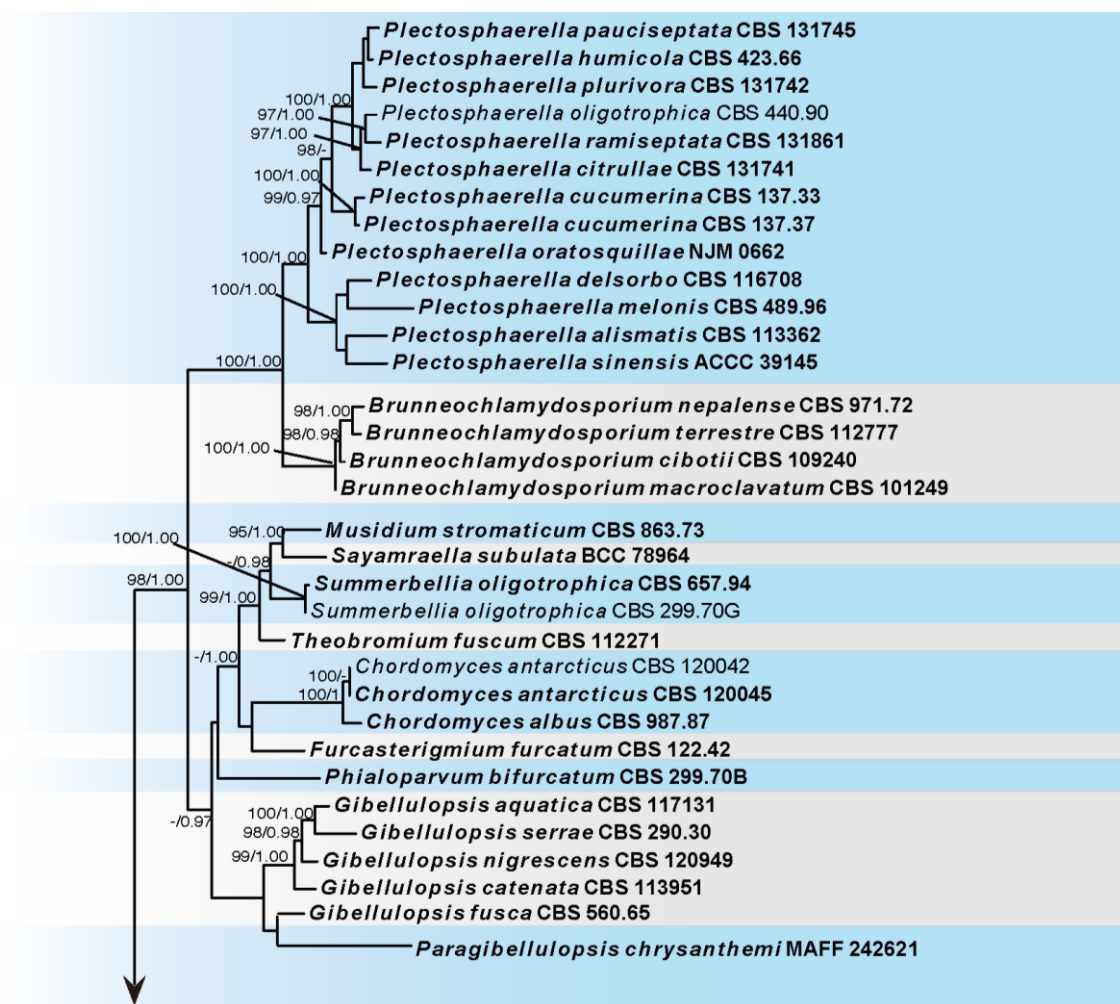


Figure 40 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *rpb2* and *tef1-α*) of Plectosphaerellaceae. The scale bar indicates 0.04 changes. The tree is rooted with *Monilochaetes infuscans* (CBS 379.77) (Australiascaceae, Glomerellales). The best ML tree with a final likelihood value of -27389.832 is presented. The alignment dataset comprises 78 taxa with 3881 sites, including 1125 distinct patterns, 200 singleton sites and 2852 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Musicillium elettariae Giraldo López & Crous, Studies in Mycology 92: 267 (2018)
MycoBank number: MB828065

Fig. 41

Saprobic on dead twigs of *Cycas revoluta*. Asexual morph: *Mycelium* consisting of branched septate, smooth, dark brown with age, thin-walled hyphae, 4–13 µm wide. *Conidiophores* 75–340 × 4–13 µm ($\bar{x}$ = 168 × 6 µm, n = 15), erect, subcylindrical, vertical or slightly flexuous, with 5–11 septa in the lower part, wider towards the end, bearing up to 4 whorls of 2–7 phialides, sometimes with lateral branches, 6–18 µm ($\bar{x}$ = 12 µm, n = 10) wide at the base, often tuberculate at base. *Phialides* usually in divergent whorls of 2–7 (rarely solitary), terminal, lateral, ampulliform to subcylindrical, hyaline, thick- and smooth-walled, 9–27 × 2–5 µm ($\bar{x}$ = 18 × 3 µm, n = 30), with inconspicuous collarette and periclinal wall thickening at the conidiogenous locus. *Conidia* cylindrical with rounded ends, smooth to slightly verrucose, aseptate, hyaline to pale brown with

age, thin- and smooth-walled, $3.2\text{--}7 \times 1.2\text{--}2.7 \mu\text{m}$ ($\bar{x} = 4.5 \times 2 \mu\text{m}$, $n = 30$), arranged in slimy round heads. Sexual morph: Undetermined.

Known distribution – China (this study), Rwanda, Thailand

Culture characteristics – Colony on PDA reaching 11 mm diam after 4 days at 25 °C, colony from above: circular, dense, divergent at the margin, white; reverse: white, divergent at the margin.

Material examined – China, Sichuan Province, Chengdu City, Pujiang County, N 30°7'59", E 103°30'0", elevation 526 m, 11 July 2022, on dead twigs of *Cycas revoluta*, W.H. Tian PJ17 (HUEST 23.0235), living culture UESTCC 23.0235.

GenBank numbers – ITS: OR887399, LSU: OR887110, SSU: OR933722, *rpb2*: PP076808

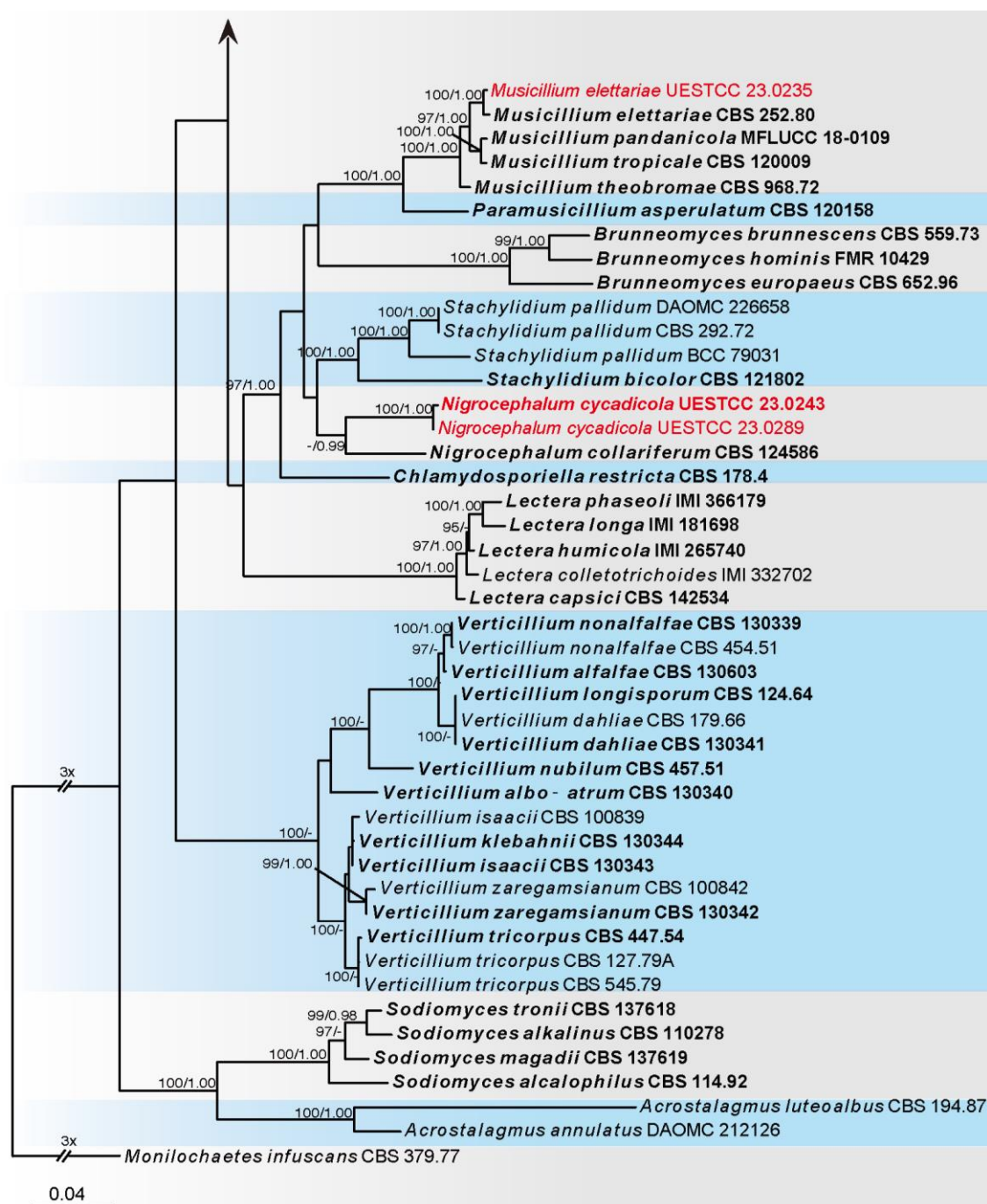


Figure 40 – Continued.

Notes – According to the multi-locus phylogeny, our collection (UESTCC 23.0235) grouped with *Musicillium elettariae* (CBS 252.80) with 100% ML and 1.00 PP support (Fig. 40). Our

collection (UESTCC 23.0235) shares morphology similarities with type collection in having terminal, lateral, subcylindrical to subulate, hyaline, with inconspicuous collarette and periclinal wall thickenings at the conidiogenous locus phialides; cylindrical with rounded ends, 1-celled, hyaline, arranged in slimy heads conidia (Giraldo & Crous 2019). Hence, we present our collection as a novel host record of *M. elettariae*, identified from deceased twigs of *Cycas revoluta*. Furthermore, this is the first documented occurrence of *M. elettariae* in China.

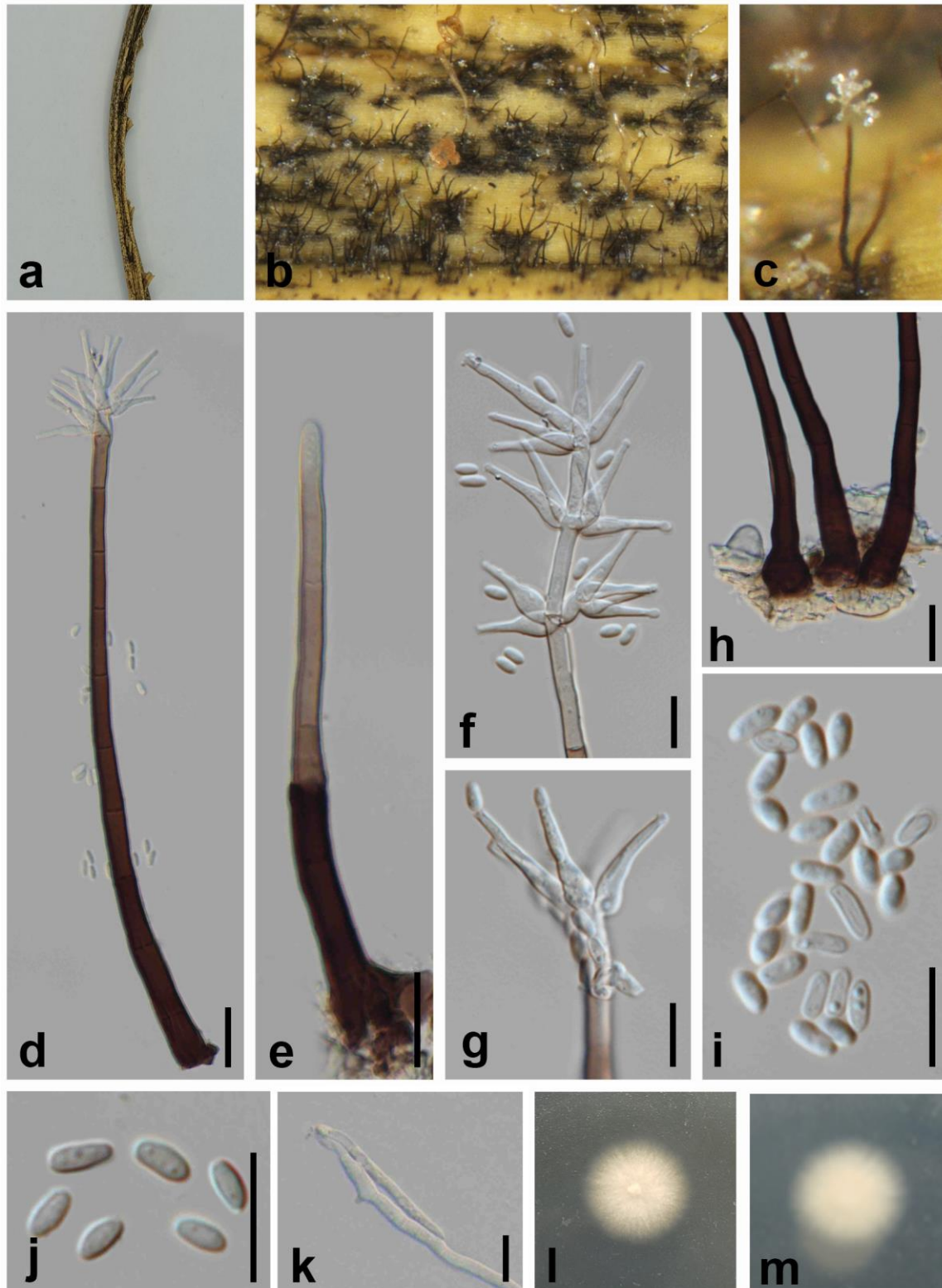


Figure 41 – *Musicillium elettariae* (HUEST 23.0235). a Specimen. b, c Colonies on dead twigs of *Cycas revoluta*. d Conidiophore, conidiogenous cells and conidia. e Initially conidiophore.

f, g Conidiogenous cells. h Conidiophore bases. i, j Conidia. k Germinating conidium. l, m Culture characteristics. Scale bars: d, e, h = 20 μm , f, g, i–k = 10 μm .

Nigrocephalum Giraldo López & Crous, Stud. Mycol. 92: 271 (2018)

MycoBank number: MB828071; Facesoffungi number: FoF013537

Notes – Giraldo & Crous (2019) established the monotypic genus *Nigrocephalum* to accommodate the species *N. collariferum*, formerly described as *Acremonium collariferum*. *Nigrocephalum collariferum* was isolated from human skin and nail lesions and showed *in vitro* abilities to grow at 33 °C and degrade keratin (Weisenborn et al. 2010). In this study, we describe and report the second species of this genus, representing the first recorded species from plants.

Nigrocephalum cycadicola W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 42

MycoBank number: MB851890; Facesoffungi number: FoF16280

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

Holotype – HKAS 131285

Saprobic on dead twigs of *Cycas revoluta*. Asexual morph: *Mycelium* consisting of branched, septate, pale brown, finely to roughly warted and thick-walled hyphae, 2–3 μm wide. *Conidiophores* erect, slightly bent, arising directly from mycelium, sometimes tuberculate at the base, simple or branched, 47–105 $\times$ 2–3 μm ($\bar{x}$ = 68 $\times$ 2 μm , n = 15), 5.5–7 μm ($\bar{x}$ = 6 μm , n = 10) wide at the base, pale brown, smooth-walled, thick-walled. *Conidiogenous cells* mostly lateral, sub-cylindrical to subulate, slightly wavy at the apex, pale brown, thick- and smooth-walled, 9–27 $\times$ 2–5 μm ($\bar{x}$ = 18 $\times$ 3 μm , n = 20), with conspicuous funnel-shaped collarete and periclinal thickening at the conidiogenous locus, commonly with a percurrent proliferation. *Conidia* broadly ellipsoidal, aseptate, hyaline to pale brown, guttulate, verruculose with age, with rounded to obtuse apex, black in masses, thick- and smooth-walled, 2.8–4.8 $\times$ 1.8–2.6 μm ($\bar{x}$ = 3.7 $\times$ 2.3 μm , n = 30), arranged in slimy blackheads. Sexual morph unknown. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 25 mm diam after 46 days at 25 °C, colonies from above: circular, margin entire, flat, dense, slightly raised in centre, dusty at the periphery, dark brown to black; reverse: cream at the margin, olive black in the center.

Material examined – China, Sichuan Province, Chengdu City, Xiyuan Avenue, N 30°52'51", E 103°43'51", elevation 595 m, 8 December 2022, on dead stems of *Cycas revoluta*, W.H. Tian XY24_1 (HKAS 131285, holotype), ex-type culture CGMCC 3.25641 = UESTCC 23.0243; *ibid.*, Chengdu City, University of Electronic Science and Technology of China, N 30°45'24", E 103°55'54", elevation 480 m, 12 June 2022, on dead stems of *Cycas revoluta*, W.H. Tian U12_1 (HUEST 23.0290), living culture UESTCC 23.0289.

GenBank numbers – CGMCC 3.25641 = ITS: OR887398, LSU: OR887109, SSU: OR933721, *rpb2*: PP076814, *tef1- α* : PP076826; UESTCC 23.0289 = ITS: OR887387, LSU: OR887098, SSU: OR933718, *rpb2*: PP076807, *tef1- α* : PP076822

Notes – According to the multi-locus phylogeny, our collections (UESTCC 23.0243 and UESTCC 23.0289) constitute an independent clade sister to *Nigrocephalum collariferum* (CBS 124586) (Fig. 40). We compared base pair differences of the ITS, LSU and *tef1- α* gene between our collection (UESTCC 23.0243) and *N. collariferum* (CBS 124586). The results showed 12% differences (65/590 bp, gaps: 45/590 bp) in ITS, 2% differences (14/810 bp, gaps: 1/810 bp) in LSU, 6% differences (44/787 bp, no gaps) in *tef1- α* . Morphologically, *N. cycadicola* (UESTCC 23.0243) differs from *N. collariferum* (CBS 124586) by the size of conidiogenous cells (9–27 $\times$ 2–5 μm vs. 17–51.5 $\times$ 1.5–2.5 μm) and the color of conidia (hyaline to pale brown vs. pale olive-brown to dark brown) (Giraldo & Crous 2019). Therefore, based on morphology and phylogenetic analyses, we introduce *N. cycadicola* as a novel species from *Cycas revoluta* in China.

Reticulascaceae Réblová & W. Gams, Stud. Mycol. 68: 180 (2011)

MycoBank number: MB515435; Facesoffungi number: FoF01311

Notes – Based on analysis of combined ITS, LSU, SSU and *rpb2* sequence data, the family Reticulascaceae was proposed by Réblová et al. (2011). Currently, the family comprises four genera *Blastophorum*, *Cylindrotrichum*, *Kylindria* and *Sporoschismopsis* (Wijayawardene et al. 2022a). Asexual members of Reticulascaceae are generally hyphomycetes and are usually found as saprobes occurring on various hosts in lentic habitats (Maharachchikumbura et al. 2018).

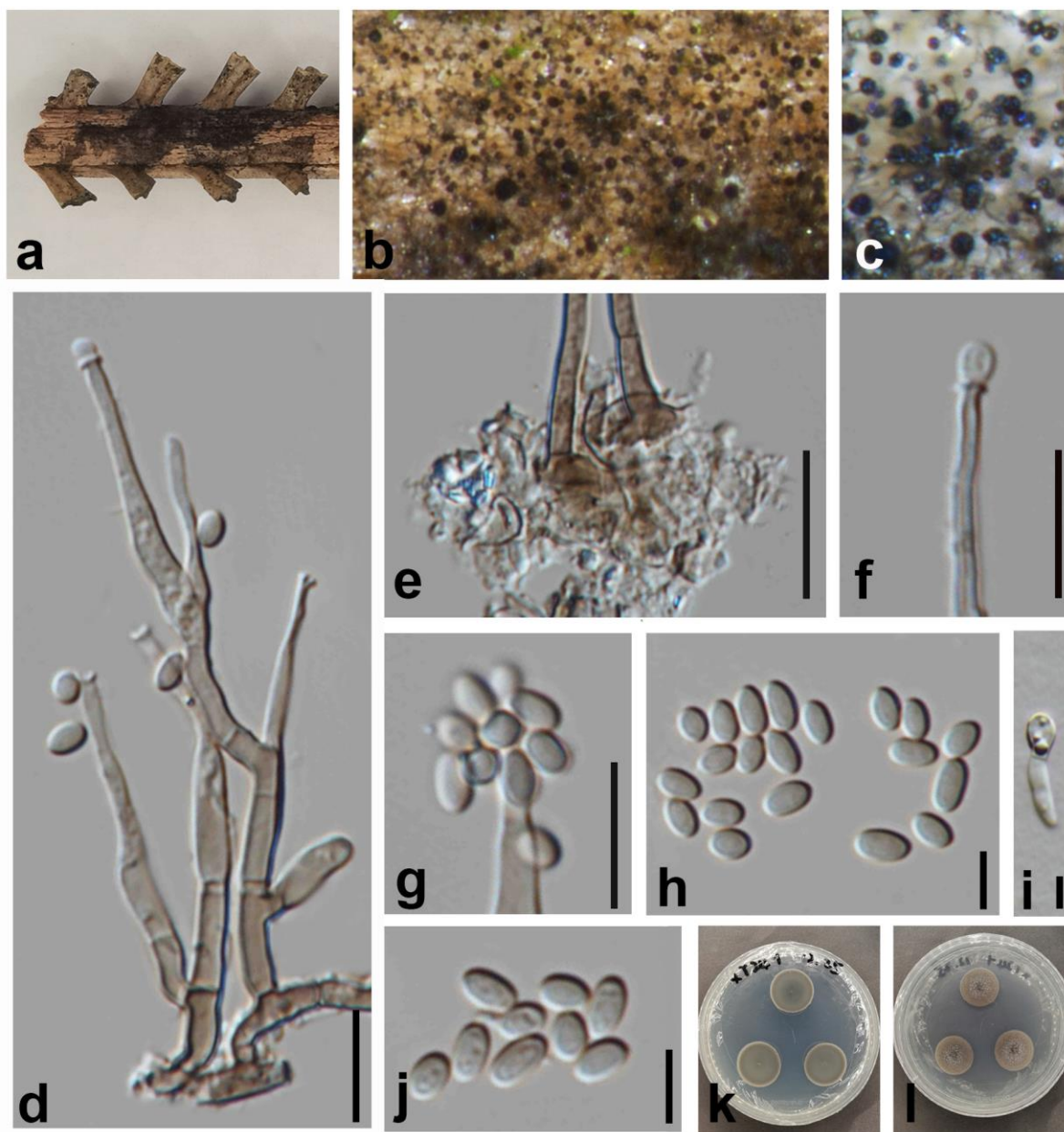


Figure 42 – *Nigrocephalum cycadicola* (HKAS 131285, holotype). a Specimen. b, c Colonies on dead stems of *Cycas revoluta*. d Conidiophore, conidiogenous cells and conidia. e Conidiophore bases. f, g Conidiogenous cells with conidia. h, j Conidia. i Germinating conidium. k, l Culture characteristics. Scale bars: d–g = 10 µm, h–j = 5 µm.

Kylindria DiCosmo, S.M. Berch & W.B. Kendr., Mycologia 75(6): 970 (1983)

Mycobank number: MB11115; Facesoffungi number: FoF013555

Notes – *Kylindria* was erected by DiCosmo et al. (1983) with the type species *K. triseptatum* ($\equiv$ *Cylindrotrichum triseptatum*) and another four *Cylindrotrichum* species. Species of this genus are characterized by unbranched, macronematous, brown conidiophores, integrated, terminal, ampulliform, monophialidic conidiogenous cells having narrow apertures at the apex, with or

without conspicuous collarette, and unicellular or euseptate, hyaline conidia usually with an excentric lateral flat scar (DiCosmo et al. 1983, Zhang et al. 2010). Members of *Kylindria* are mostly found on dead branches, decaying leaves or rotten rachides in terrestrial habitats; *K. aquatica* and *K. chinensis* are found in submerged wood of aquatic environments (Maharachchikumbura et al. 2018).

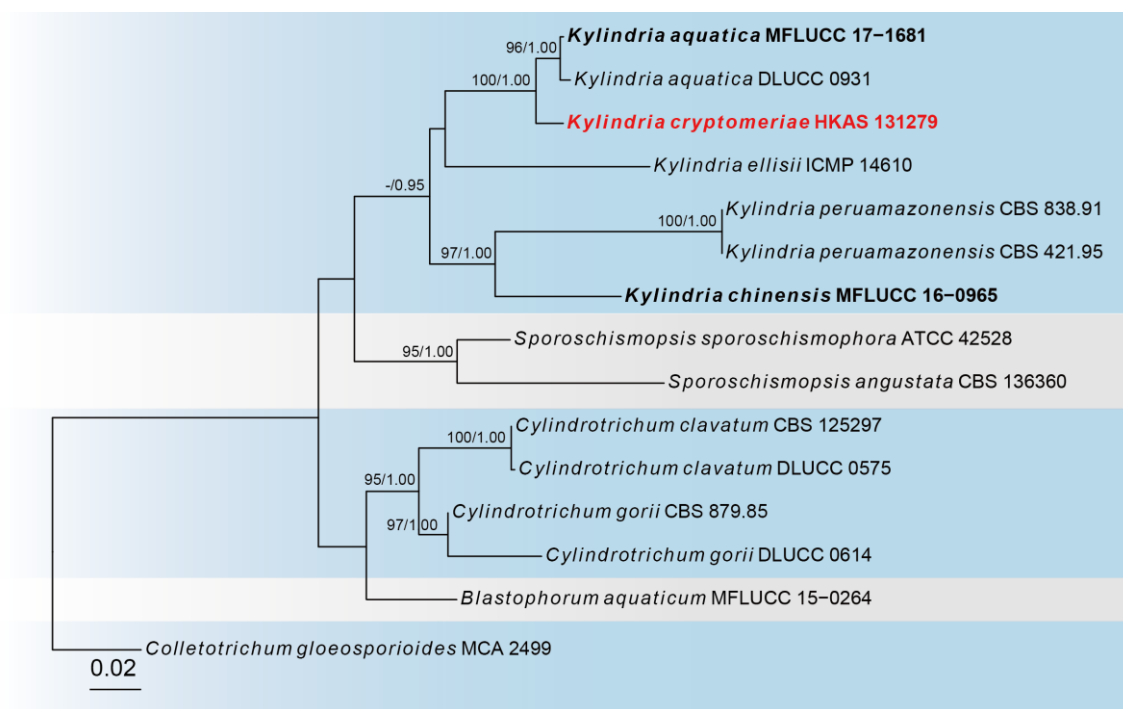


Figure 43 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU and *rpb2*) of Reticulascaceae. The scale bar indicates 0.02 changes. The tree is rooted with *Colletotrichum gloeosporioides* (MCA 2499) (Glomerellaceae, Glomerellales). The best ML tree with a final likelihood value of -7894.424 is presented. The alignment dataset comprises 15 taxa with 2534 sites, including 558 distinct patterns, 220 singleton sites and 1960 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Kylindria cryptomeriae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 44

Mycobank number: MB851891; Facesoffungi number: FoF16281

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

Holotype – HKAS 131279

Saprobic on twigs of *Cryptomeria fortunei*. Asexual morph: Hyphomycetous. Colonies on natural substrate evenly distributed, superficial, effuse, scattered, hairy, glistening. Mycelium immersed, composed of septate, unbranched, subhyaline to pale brown, smooth- and thick-walled hyphae. Conidiophores 180–310 × 6–11 μm ($\bar{x}$ = 230 × 8 μm, n = 20), mononematous, macronematous, erect, solitary, straight or slightly flexuous, unbranched, smooth, 5–10-septate, brown to dark brown, paler toward the apex, swollen at the base. Conidiogenous cells phialidic, ampuliform, terminal, integrated, smooth, 43–60 μm ($\bar{x}$ = 52 μm, n = 25) long, 11–35 μm ($\bar{x}$ = 23 μm, n = 20) wide at the base, broadest above the middle, 10–15 μm ($\bar{x}$ = 13 μm, n = 25) wide, tapering near the apex, with an inconspicuous apical collarette. Conidia 22–32 × 9–12 μm ($\bar{x}$ = 39 × 11 μm, n = 30), cylindrical, oblong with obtuse ends, 0–3-septate, slightly constricted at septa, hyaline, guttulate, with a slimy mucilaginous coating around, slightly curved to side at base, aggregated in mucilaginous masses. Sexual morph: Undetermined.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, within dead twigs of *Cryptomeria fortunei*, W.H. Tian LCGS09_3 (HKAS 131279, holotype).

GenBank numbers – ITS: OR887400, LSU: OR887111, *rpb2*: PP076809

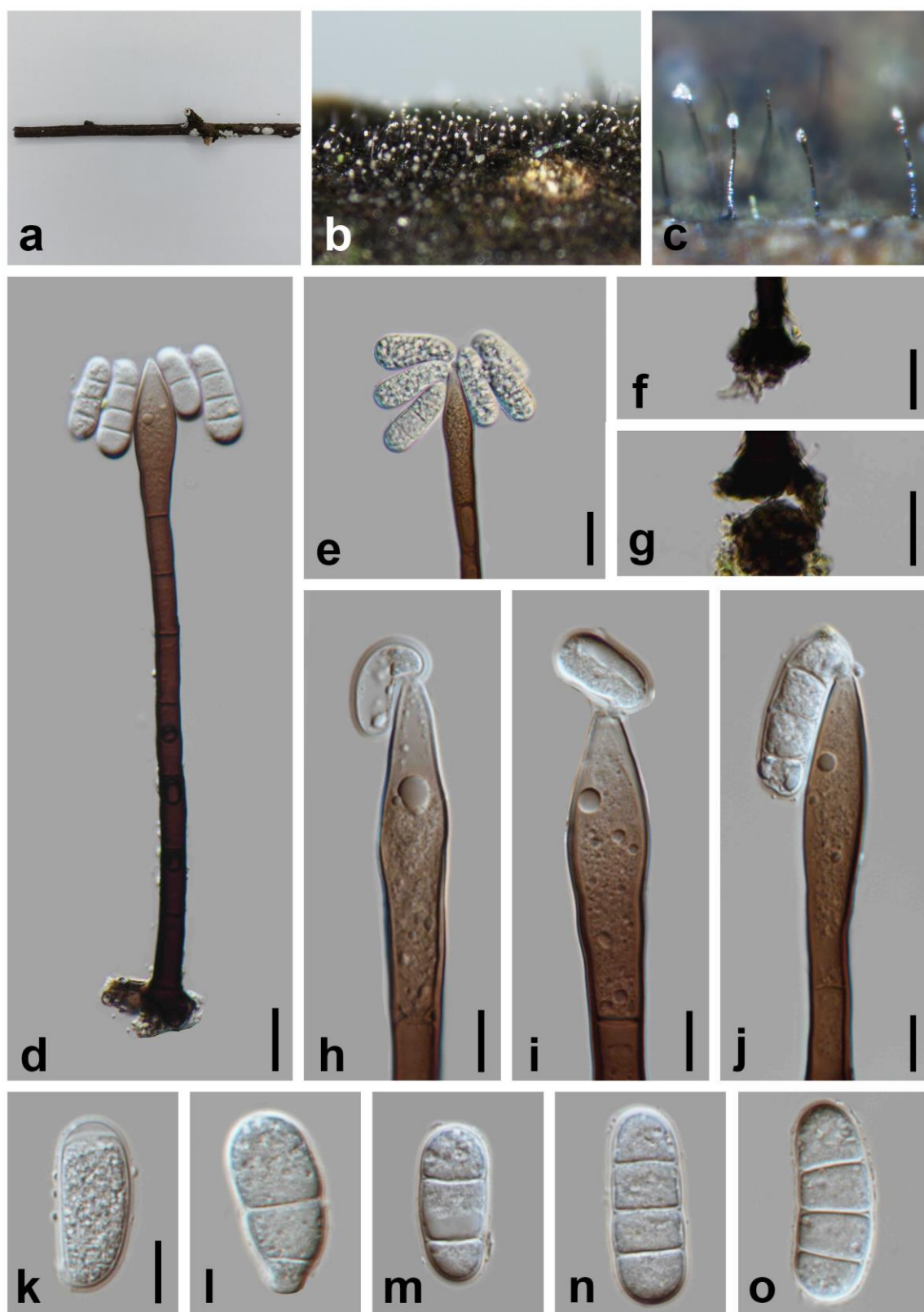


Figure 44 – *Kylandria cryptomeriae* (HKAS 131279, holotype). a Specimen. b, c Colonies on dead twigs of *Cryptomeria fortunei*. d Conidiophores, conidiogenous cells with conidia.

e, h–j Conidiogenous cell with conidia. f, g Conidiophore bases. k–o Conidia. Scale bars: d–f = 20 μm . g–o = 10 μm . The scale bar of k applies to k–o.

Notes – In the phylogenetic analysis of Reticulascaceae, *Kylindria cryptomeriae* formed a well-supported monophyletic clade sister to *K. aquatica* (Fig. 43). Comparisons of the LSU and ITS sequences between *K. cryptomeriae* (HKAS 131279) and the type strain of *K. aquatica* (MFLUCC 17–1681) revealed 99.25% sequence identity (798/804 bp, no gaps) in LSU and 96.59% sequence identity (453/469 bp, gaps: 8/469 bp) in ITS. *K. cryptomeriae* and *K. aquatica* have overlapping morphology with solitary, unbranched, septate conidiophores; phialidic, ampulliform conidiogenous cells and oblong with obtuse ends, 0–3-septate conidia (Maharachchikumbura et al. 2018). However, *K. cryptomeriae* (HKAS 131279) differs from *K. aquatica* (MFLUCC 17–1681) in having longer conidiophores ($180\text{--}310 \times 6\text{--}11 \mu\text{m}$ vs. $137\text{--}247 \times 7\text{--}9 \mu\text{m}$) with larger number of septa (5–10-septate vs. 3–5-septate) and larger conidia ($22\text{--}32 \times 9\text{--}12 \mu\text{m}$ vs. $20\text{--}24 \times 9\text{--}11 \mu\text{m}$). *Kylindria cryptomeriae* is also similar to *K. chinensis* and *K. eucalypt* in morphological characteristics but differ by the size of conidia ($22\text{--}32 \times 9\text{--}12 \mu\text{m}$ vs. $17\text{--}23 \times 5\text{--}7 \mu\text{m}$ vs. $18\text{--}24 \times 4\text{--}6 \mu\text{m}$) (Maharachchikumbura et al. 2018, Barreto & Gusmão 2022). Therefore, we introduce a new species of *Kylindria* based on morphological characteristics and phylogenetic evidence.

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

MycoBank number: MB90477; Facesoffungi number: FoF02091

Notes – Hypocreales is an order of fungi within the class Sordariomycetes that includes entomopathogenic, mycoparasitic, and mycosaprotrophic species with various ecological and biotechnological roles (Gams et al. 2004). According to the Wijayawardene et al (2022a), the order encompasses 15 families. Xiao et al. (2023) recently introduced the new family Polycephalomycetaceae to Hypocreales.

Hypocreaceae De Not., G. bot. ital. 2(1): 48 (1844)

MycoBank number: MB80892; Facesoffungi number: FoF01904

Notes – The family *Hypocreaceae* was proposed by Lindau (1897) with *Hypocrea* as the type genus. Species in this family are recognizable by their brightly colored perithecial ascomata, typically yellow, orange or red (De Notaris 1845). Currently, *Hypocreaceae* comprises 17 genera (Wijayawardene et al. 2022a).

Kiflimonium Summerb., J.A. Scott, Guarro & Crous, Microorganisms 6(3, 88): 17 (2018)

MycoBank number: MB826819; Facesoffungi number: FoF13218

Notes – *Kiflimonium* was established by Summerbell et al. (2018) with *K. curvulum* as the type species. Members of this genus are mostly isolated from soil (Summerbell et al. 2018). *Kiflimonium* is characterized by simple conidiophores arising laterally from somatic hyphae, bearing 1–4 phialidic conidiogenous cells, and 0–1 septate, lunate to falcate, hyaline conidia (Summerbell et al. 2018). Crous et al. (2021) reported and described the second species of this genus, *K. junci*, and *K. cryptomeriae* introduced in this study is the third species of this genus.

Kiflimonium cryptomeriae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 46

MycoBank number: MB851892; Facesoffungi number: FoF16282

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

Holotype – HKAS 131288

Saprobic on dead leaves of *Cryptomeria japonica*. Asexual morph: *Mycelium* consisting of hyaline, smooth, branched, septate, 1–2.5 μm diam hyphae. *Conidiophores* $35\text{--}60 \times 1\text{--}2.5 \mu\text{m}$ ($\bar{x} = 48 \times 2 \mu\text{m}$, $n = 15$), erect, hyaline, thick- and smooth-walled, subcylindrical, arising from superficial mycelium, base slightly swollen, wider towards the base, frequently branched, giving rise to 1–3 conidiogenous cells, 1–3-septate. *Conidiogenous cells* hyaline, smooth-walled, slightly

curved, subcylindrical with apical taper, monophialidic, with non-flared apical collarette, $7\text{--}13 \times 1.3\text{--}2.4 \mu\text{m}$ ($\bar{x} = 10 \times 2 \mu\text{m}$, $n = 15$). *Conidia* solitary, hyaline, arranged in slimy round hyaline heads, narrow ellipsoidal, smooth-walled, guttulate, verruculose with age, cylindrical with rounded ends, tapering to apex, $5.5\text{--}7 \times 1.3\text{--}2 \mu\text{m}$ ($\bar{x} = 6.3 \times 1.6 \mu\text{m}$, $n = 30$). Sexual morph: Undetermined.

Culture characters – Colonies on PDA reaching 57 mm diam. in 47 days at 25 °C in the dark, flatted, irregular, spreading, surface folded, submerged, pale luteous to luteous, with sparse aerial mycelium and smooth, lobate margin, colonies from above: black; from below: luteous in the centre, pale luteous at the margin.

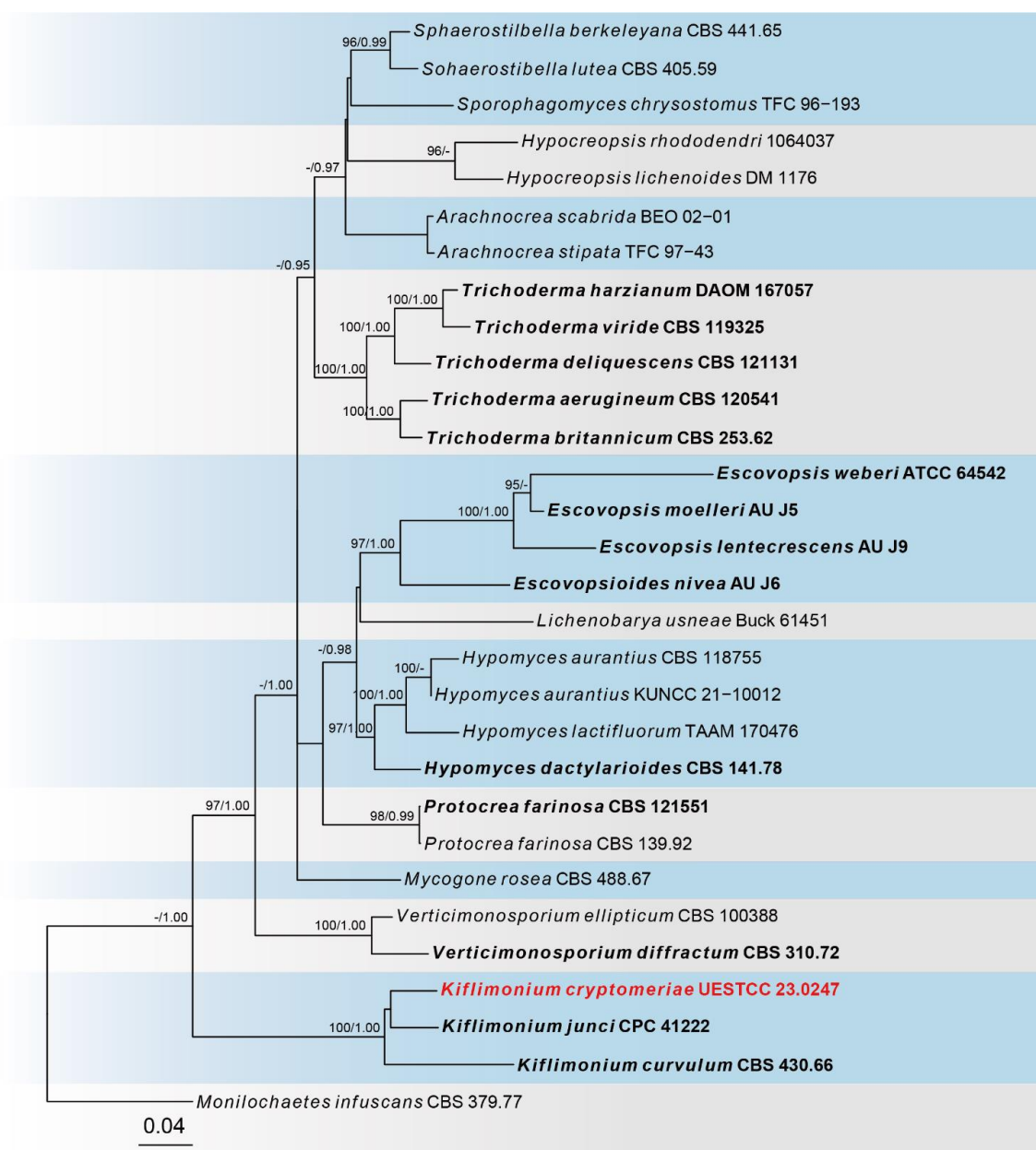


Figure 45 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU, SSU, *rpb2* and *tef1-α*) of Hypocreaceae. The scale bar indicates 0.04 changes. The tree is rooted with *Monilochaetes infuscans* (CBS 379.77) (Australiascaceae, Glomerellales). The best ML tree with a final likelihood value of -22555.523 is presented. The alignment dataset comprises 30 taxa with 4351 sites, including 1409 distinct patterns, 597 singleton sites and 2843 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

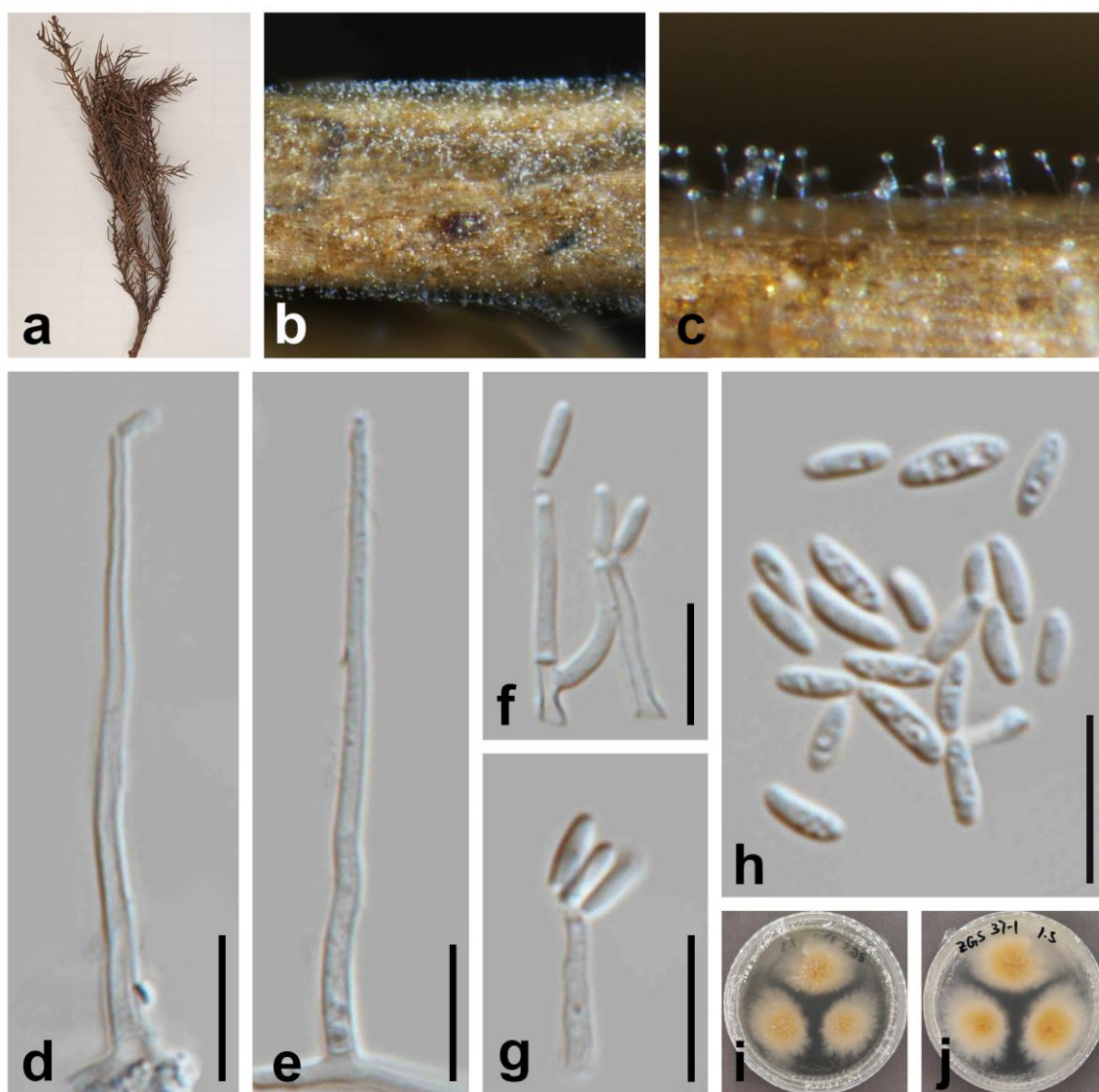


Figure 46 – *Kiflimonium cryptomeriae* (HKAS 131288, holotype). a Specimen. b, c Colonies dead leaves of *Cryptomeria japonica*. d, e Conidiophores, conidiogenous cells and conidia. f, g Conidiogenous cells with conidia. h Conidia. i, j Culture characteristics. Scale bars: d–h = 10 μ m.

Material examined – China, Sichuan Province, Ya'an City, Zhougong Mountain, N 29°58'1", E 103°2'8", elevation 1196 m, 16 November 2022, on dead leaves of *Cryptomeria japonica*, W.H. Tian ZGS37_1 (HKAS 131288, holotype), ex-type CGMCC 3.25644 = UESTCC 23.0247.

GenBank numbers – ITS: OR887401, LSU: OR887112, SSU: OR933723, *rpb2*: PP076816, *tef1- α* : PP076827

Notes – The phylogenetic analyses showed that our strain forms a sister branch to *Kiflimonium junci* (CPC 41222) (Fig. 45). We compared base pair differences of the ITS and LSU regions between our collection and *K. junci* (CPC 41222). The results showed 43/480 bp differences (9%, gaps: 10/480 bp) in ITS, 8/814 bp differences (1%, no gaps) in LSU. The morphological characteristics of *K. cryptomeriae* resemble *K. junci* in having erect, hyaline, subcylindrical, arising from superficial mycelium, base slightly swollen, frequently branched conidiophores (Crous et al. 2021). However, *K. cryptomeriae* (UESTCC 23.0247) can be distinguished from *K. junci* (CPC 41222) in having smaller conidiophores (35–60 $\times$ 1–2.5 μ m vs. 60–110 $\times$ 2.5–4 μ m), smaller conidiogenous cells (7–13 $\times$ 1.3–2.4 μ m vs. 50–100 $\times$ 2–3 μ m), narrower conidia (5.5–7 $\times$ 1.3–2 μ m vs. 3.5–7 $\times$ 2–3) and different conidial shape (narrow

ellipsoidal vs. reniform) (Crous et al. 2021). Thus, we introduce our collection as a new species, *Kiflimonium cryptomeriae*, from the dead leaves of *Cryptomeria japonica* in China.

Niessliaceae Kirschst., Annls mycol. 37(1/2): 89 (1939)

Mycobank number: MB81070; Facesoffungi number: FoF01126

Notes – The family Niessliaceae was erected by Kirschstein (1939) to accommodate a variety of taxa characterized by small, dark, superficial, saprotrophic, setose perithecioid ascomata, with *Niesslia* as the type genus. Niessliaceae are distributed worldwide and most taxa are saprophytic or parasitic on wood or lichens or other fungi (Müller & von Arx 1962, Barr 1990b, Crous et al. 2007b, Tang et al. 2007, Jaklitsch & Voglmayr 2012).

Niesslia Auersw., Myc. Europ., Abbild. Sämmtl. Pilze Eur. 5–6: 30 (1869)

Mycobank number: MB3506; Facesoffungi number: FoF01127

Notes – The genus *Niesslia* was introduced by Auerswald (1869), with *N. chaetomium* as the type species. It is a species-rich ascomycete genus characterized by tuberculate perithecia, surrounded by brown, septate setae, clavate asci and filiform ascospores (Gams et al. 2019). The members of *Niesslia* are found in decaying plant matter and are parasites of lichens, other fungi, or nematode eggs (Auerswald 1869).

Niesslia cryptomeriae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 48

Mycobank number: MB851893; Facesoffungi number: FoF16283

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

Holotype – HKAS 131286

Saprobic on dead leaves of *Cryptomeria japonica*. Asexual morph: *Mycelium* consisting of hyaline, smooth, branched, septate. *Conidiophores* reduced to conidiogenous cells, arising singly from superficial hyphae, erect, flexuous, subcylindrical to subulate, with apical taper, thick-walled in lower region, with non-flared cylindrical apical collarette, $35\text{--}65 \times 3\text{--}10\ \mu\text{m}$ ($\bar{x} = 48 \times 6\ \mu\text{m}$, $n = 20$). *Conidia* adhering to slimy heads, subcylindrical with subobtuse apices, aseptate, hyaline, smooth- and thin-walled, guttulate, verruculose, $5\text{--}20 \times 1.5\text{--}2\ \mu\text{m}$ ($\bar{x} = 8 \times 1.8\ \mu\text{m}$, $n = 30$). Sexual morph: Undetermined.

Culture characters – Colonies on PDA reaching 36 mm diam in 45 days at 25 °C in the dark, colonies from above: spreading, irregular, with medium mycelium, slightly raised, zonate, even margin, cottony, white, thinner at the margin; from below: margin undulated, brownish-yellow in the center.

Material examined – China, Sichuan Province, Pengzhou City, Zhongba Forest Park, N 30°59'46", E 104°09'1", elevation 1150 m, 29 September 2022, on dead leaves of *Cryptomeria japonica*, W.H. Tian ZB09_1 (HKAS 131286, holotype), ex-type CGMCC 3.25642 = UESTCC 23.0245.

GenBank numbers – ITS: OR887403, LSU: OR887113, *tef1- α* : PP076828, *tub2*: PP150073, *act*: PP150069

Notes – According to the multi-locus phylogeny, our collection clustered with the *Niesslia ilicifolia* (CBS 459.74) clade (Fig. 47). Based on pairwise nucleotide comparisons, *N. cryptomeriae* (UESTCC 23.0245) shows 96.31% sequence identity (391/406 bp, gaps: 3/406 bp) in ITS to *N. ilicifolia* (CBS 459.74), 93.87% sequence identity (383/408 bp, gaps: 11/408 bp) in ITS to *N. exosporioides* (CBS 390.70), 99.41% sequence identity (846/851 bp, gap: 1/851 bp) in LSU to *N. ilicifolia* (CBS 459.74), 99.53% sequence identity (847/851 bp, gap: 1/851 bp) in LSU to *N. ilicifolia* (CBS 390.70), 98.58% sequence identity (416/422 bp, no gaps) in *tef1- α* to *N. ilicifolia* (CBS 459.74), 97.39% sequence identity (411/422 bp, no gaps) in *tef1- α* to *N. exosporioides* (CBS 390.70), 95.21% sequence identity (179/188 bp, gaps: 4/188 bp) in *act* to *N. exosporioides* (CBS 390.70), 89.19% sequence identity (165/185 bp, gap: 1/185 bp) in *act* to *N. ilicifolia* (CBS 459.74), 89.52% sequence identity (205/229 bp, gaps: 4/229 bp) in *tub2* to *N. ilicifolia* (CBS 459.74),

88.23% sequence identity 195/221 bp, gaps: 2/221 bp) in *tub2* to *N. exosporioides* (CBS 390.70). Morphologically, *N. cryptomeriae* differs from *N. ilicifolia* and *N. exosporioides* in having larger conidia ($5\text{--}20 \times 1.5\text{--}2 \mu\text{m}$ vs. $3.2\text{--}6.5 \times 1.0\text{--}1.7 \mu\text{m}$ vs. $5\text{--}6 \times 1.0\text{--}1.5 \mu\text{m}$) (Gams et al. 2019). Thus, our collection was identified as a new species and described here as *N. cryptomeriae* sp. nov.

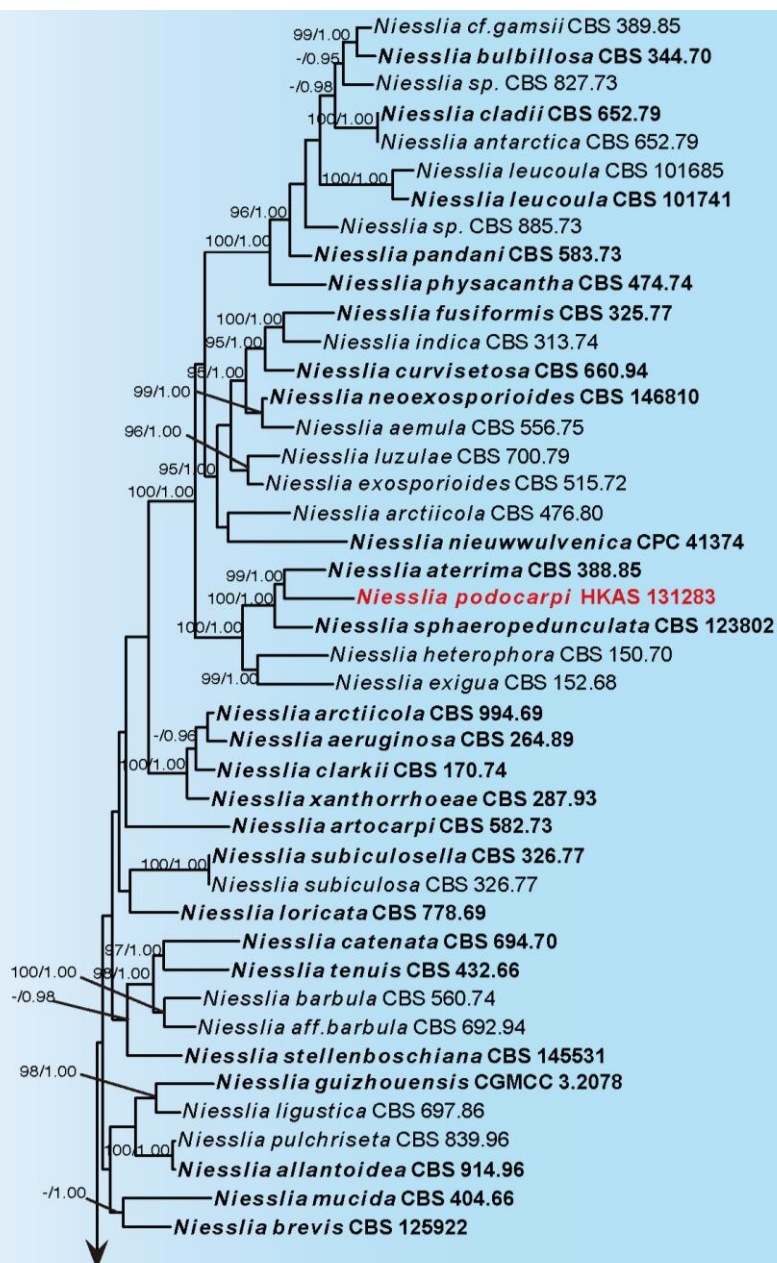


Figure 47 – Phylogram of the best ML tree based on a combined dataset (ACT, ITS, LSU, *tub2* and *tef1-α*) of *Niesslia*. The scale bar indicates 0.05 changes. The tree is rooted with *Trichoderma aggressivum f. europaeum* (CBS 100526) (Hypocreaceae, Hypocreales). The best ML tree with a final likelihood value of -37535.203 is presented. The alignment dataset comprises 68 taxa with 2649 sites, including 1411 distinct patterns, 340 singleton sites and 1345 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Niesslia podocarpi W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 49

Mycobank number: MB851894; Facesoffungi number: FoF16284

Etymology – Named after the host genus from which the holotype was collected,

Podocarpus.
Holotype – HKAS 131283.

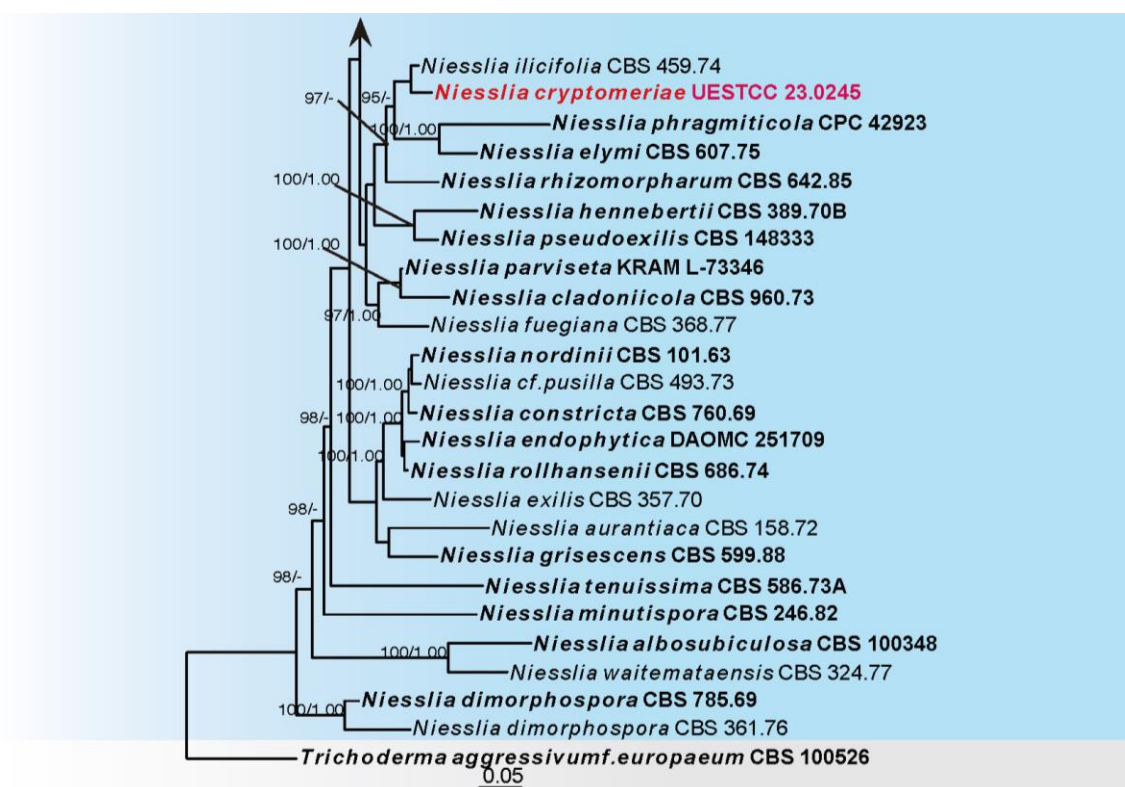


Figure 47 – Continued.

Saprobic on dead leaves of *Podocarpus macrophyllus*. Sexual morph: *Ascomata*, epiphyllous, scattered, black, glossy, globose, collapsing into a cup-like shape when dry, 80–95 μm ($\bar{x}$ = 83 μm , n = 20) diam, surrounded with setae. Setae 30–55 μm ($\bar{x}$ = 43 μm , n = 25) long, numerous, dark brown to black, smooth- and thick-walled. Asci cylindrical-clavate, with slightly truncate apex, 4- or 8-spored, 20–40 $\times$ 4–8 μm ($\bar{x}$ = 24 $\times$ 6 μm , n = 25), with short pedicel. Ascospores ellipsoid allantoid, 1-septate, smooth-walled, with a median septum, slightly constricted or not at the septum, 6.5–9.5 $\times$ 2–2.5 μm ($\bar{x}$ = 8 $\times$ 2 μm , n = 30). Asexual morph: Undetermined.

Material examined – China, Sichuan Province, Chengdu City, Xiyuan Avenue, N 30°52'51", E 103°43'51", elevation 595 m, 8 December 2022, on dead leaves of *Podocarpus macrophyllus*, W.H. Tian XY14_2 (HKAS 131283, holotype).

GenBank numbers – ITS: OR887404, LSU: OR887114, *tef1- α* : PP076829, *tub2*: PP150074, *act*: PP150070

Notes – *Niesslia podocarpi* (HKAS 131283) clustered with *Niesslia aterrima* (CBS 388.85) clade (Fig. 47). Based on pairwise nucleotide comparisons, *N. podocarpi* (HKAS 131283) shows 96.92% sequence identity (504/520 bp, gaps = 3/520 bp) in ITS to *N. aterrima* (CBS 388.85), 99.15% sequence identity (816/823 bp, gaps = 3/823 bp) in LSU to *N. aterrima* (CBS 388.85), 93.90% sequence identity (385/410 bp, no gaps) in *tef1- α* to *N. aterrima* (CBS 388.85), no sequence identity in *act* to *N. aterrima* (CBS 388.85), 96.77% sequence identity (120/124 bp, no gaps) in *tub2* to *N. aterrima* (CBS 388.85). Moreover, *N. aterrima* is only known by asexual morph (Gams et al. 2019). *Niesslia podocarpi* shares similar characteristics with *N. barbula* in having globose and collapsing perithecia, cylindrical asci, and ellipsoid allantoid, 1-septate ascospores, but *N. podocarpi* has longer setae (30–55 μm vs. 25–35 $\times$ 4 μm), smaller asci (20–40 $\times$ 4–8 μm vs. 35–50 $\times$ 6–8 μm) and smaller ascospores (6.5–9.5 $\times$ 2–2.5 μm vs. 8–10 $\times$ 4.5 μm) (Gams et al. 2019). Therefore, based on morphological and phylogenetic distinction, we introduce *N. podocarpi* as a new species from China.

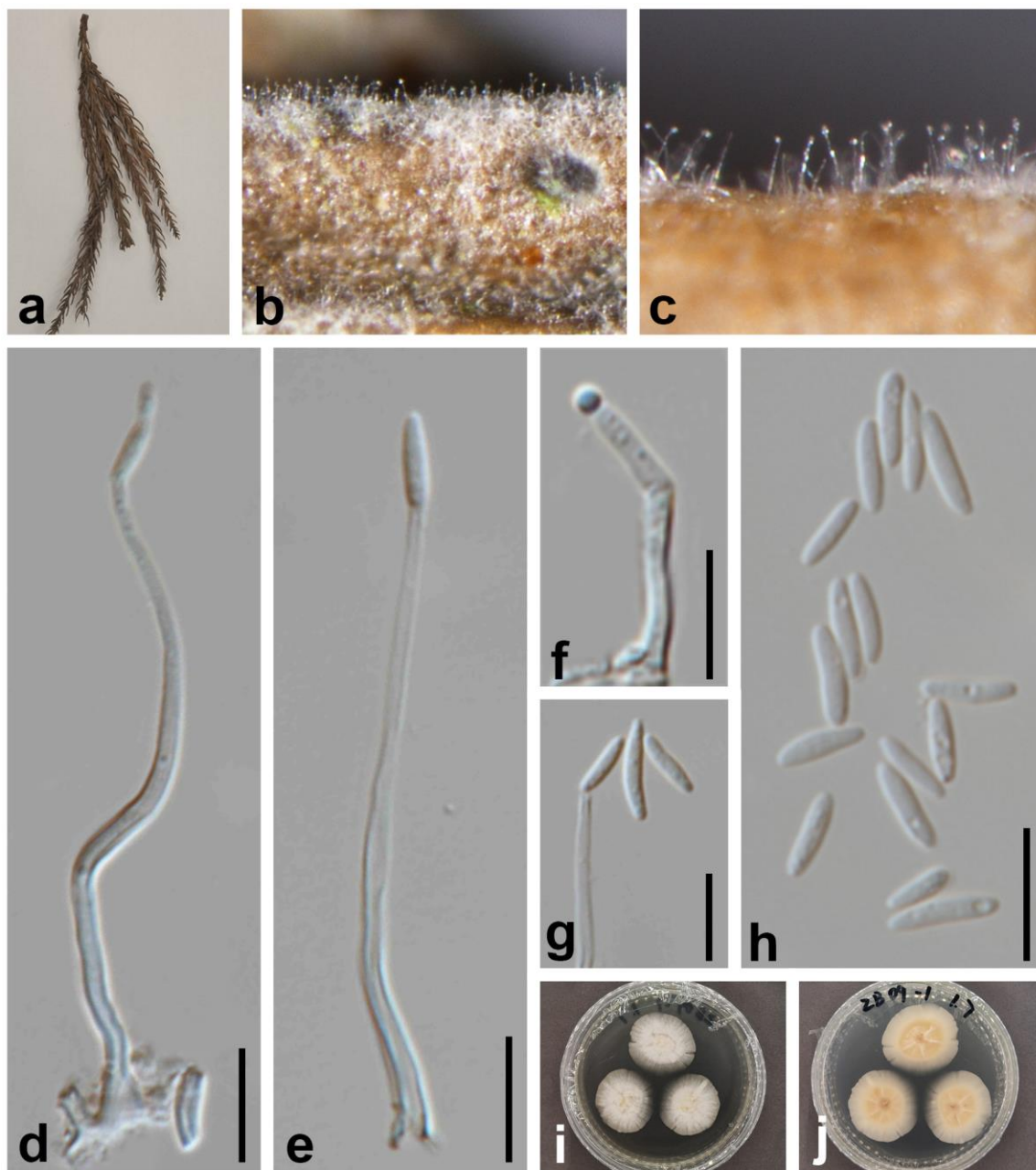


Figure 48 – *Niesslia cryptomeriae* (HKAS 131286, holotype). a Specimen. b, c Colonies on dead leaves of *Cryptomeria japonica*. d–f Conidiophores with conidia. g Germinating conidium. h Conidia. i, j Culture characteristics. Scale bars: d–h = 10 μ m.

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

MycoBank number: MB90922; Facesoffungi number: FoF05320

Notes – The family *Stachybotryaceae* was proposed by Crous et al. (2014) to accommodate the genera *Myrothecium*, *Peethambara* and *Stachybotrys*. *Stachybotryaceae* comprises 39 genera, including significant plant and human pathogens, along with several species utilized in industrial and commercial applications as biodegraders and biocontrol agents (Lombard et al. 2016). This family also includes saprophytic fungi isolated from soil and decaying plant material (Castlebury et al. 2004).

Memnoniella Höhn., Centbl. Bakt. ParasitKde, Abt. II 60: 16 (1923)

MycoBank number: MB8900; Facesoffungi number: FoF05558

Notes – The genus *Memnoniella* was introduced by von Höhnelt (1923) with *M. echinata* as the type species. Species in *Memnoniella* are common saprobic microfungi with predominantly anamorphic development in outdoor and indoor environments (Wang et al. 2015). The genus is characterized by macronematous, mononematous, unbranched conidiophores, phialidic conidiogenous cells with conspicuous collarettes, and unicellular, aseptate, smooth to verrucose conidia arranged in dry chains or slimy masses (Zheng et al. 2019).

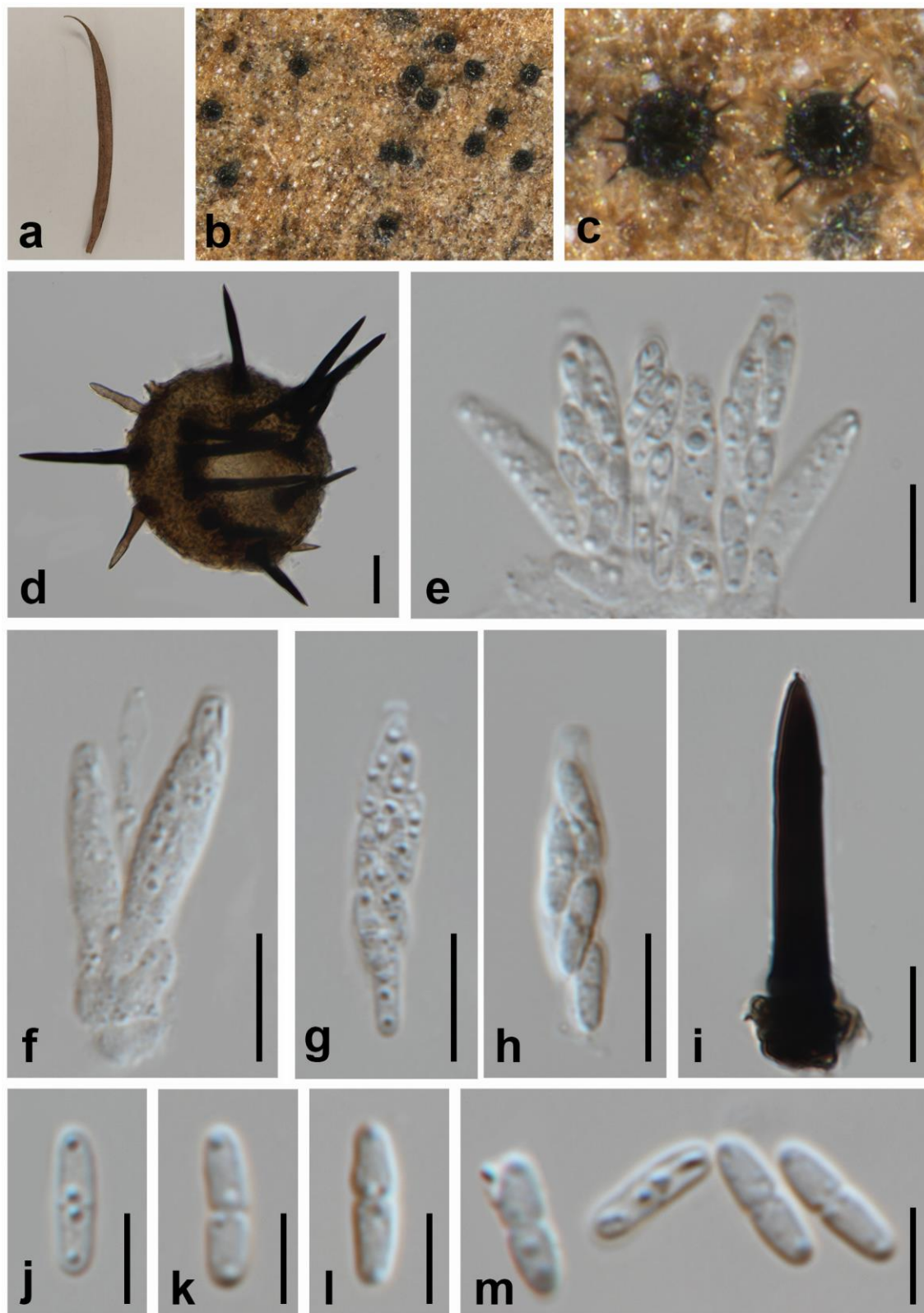


Figure 49 – *Niesslia podocarpi* (HKAS 131283, holotype). a Specimen. b, c Ascomata scattered on

the dead leaves surface of *Podocarpus macrophyllus*. d Ascomata. e–h Asci. i Setae. j–m Ascospores. Scale bars: d = 20 μm , e–i = 10 μm , j–m = 5 μm .

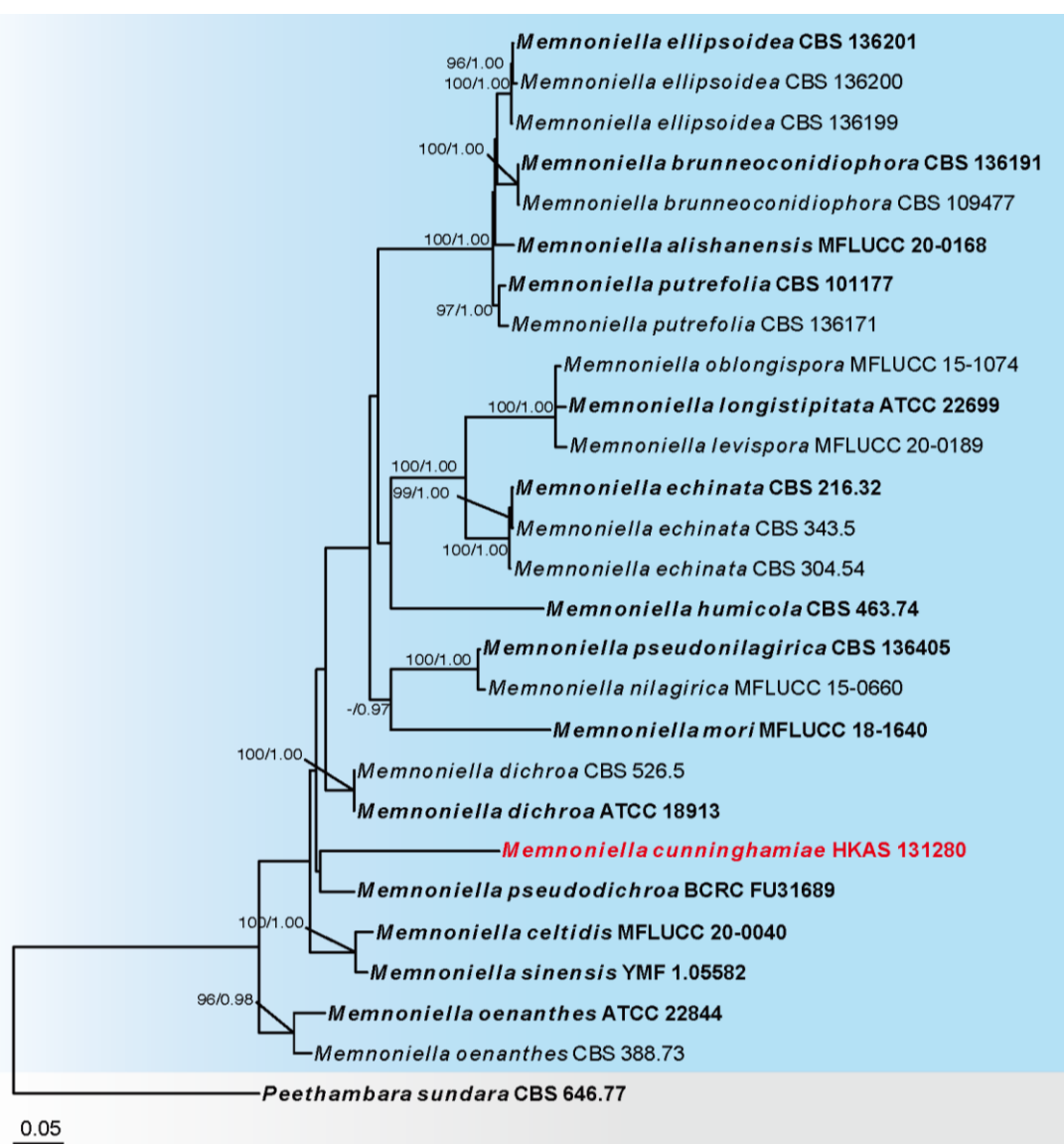


Figure 50 – Phylogram of the best ML tree based on a combined dataset (*ACT*, *ITS*, *tub2*, *cmdA*, *rpb2* and *tef1- α*) of *Memnoniella*. The scale bar indicates 0.05 changes. The tree is rooted with *Peethambara sundara* (CBS 646.77) (Stachybotryaceae, Hypocreales). The best ML tree with a final likelihood value of -14178.288 is presented. The alignment dataset comprises 27 taxa with 2825 sites, including 1095 distinct patterns, 371 singleton sites and 1686 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Memnoniella cunninghamiae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 51

Mycobank number: MB851895; Facesoffungi number: FoF16285

Etymology – Named after the host genus where the fungus was isolated.

Holotype – HKAS 131280

Saprobic on dead leaves of *Cunninghamia lanceolata*. Asexual morph: *Conidiophores* macronematous, mononematous, simple, single or in groups, erect, wider towards the base, straight or slightly flexuous, 3–7-septate, thick-walled, smooth to slightly verrucose, hyaline, 70–250 $\times$ 2–4.5 μm ($\bar{x}$ = 130 $\times$ 2.7 μm , n = 15), bearing a whorl of 4–10 conidiogenous cells. *Conidiogenous*

cells phialidic, discrete, terminal, elongate doliiform to clavate, pale brown, smooth to slightly verrucose, $7.5\text{--}13.5 \times 3\text{--}5 \text{ }\mu\text{m}$ ($\bar{x} = 9.7 \times 3.6 \text{ }\mu\text{m}$, $n = 30$), with conspicuous collarette. *Conidia* acrogenous, aseptate, ellipsoidal, verrucose, gluttulate, thick-walled, hyaline to olivaceous brown to dark brown, $3\text{--}5.5 \times 2\text{--}3 \text{ }\mu\text{m}$ ($\bar{x} = 4.7 \times 2.6 \text{ }\mu\text{m}$, $n = 30$), rounded at both ends. Sexual morph: Undetermined.

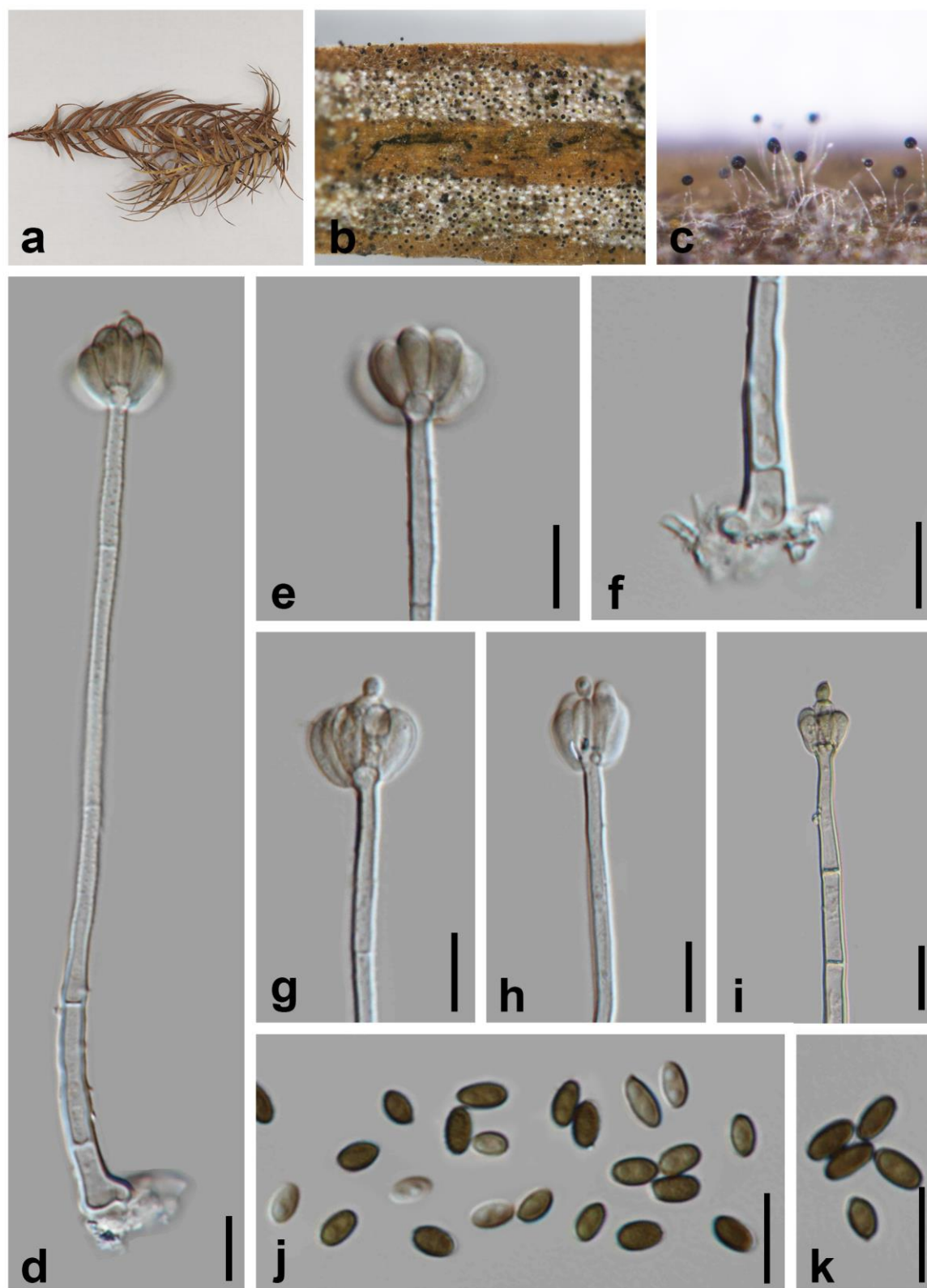


Figure 51 – *Memnoniella cunninghamiae* (HKAS 131280, holotype). a Specimen. b, c Colonies on dead leaves of *Cunninghamia lanceolata*. d Conidiophores with conidiogenous cells.

e Conidiogenous cells f Conidiophore base. g–i Conidiogenous cells with conidia. j, k Conidia. Scale bars: d–k = 10 μ m.

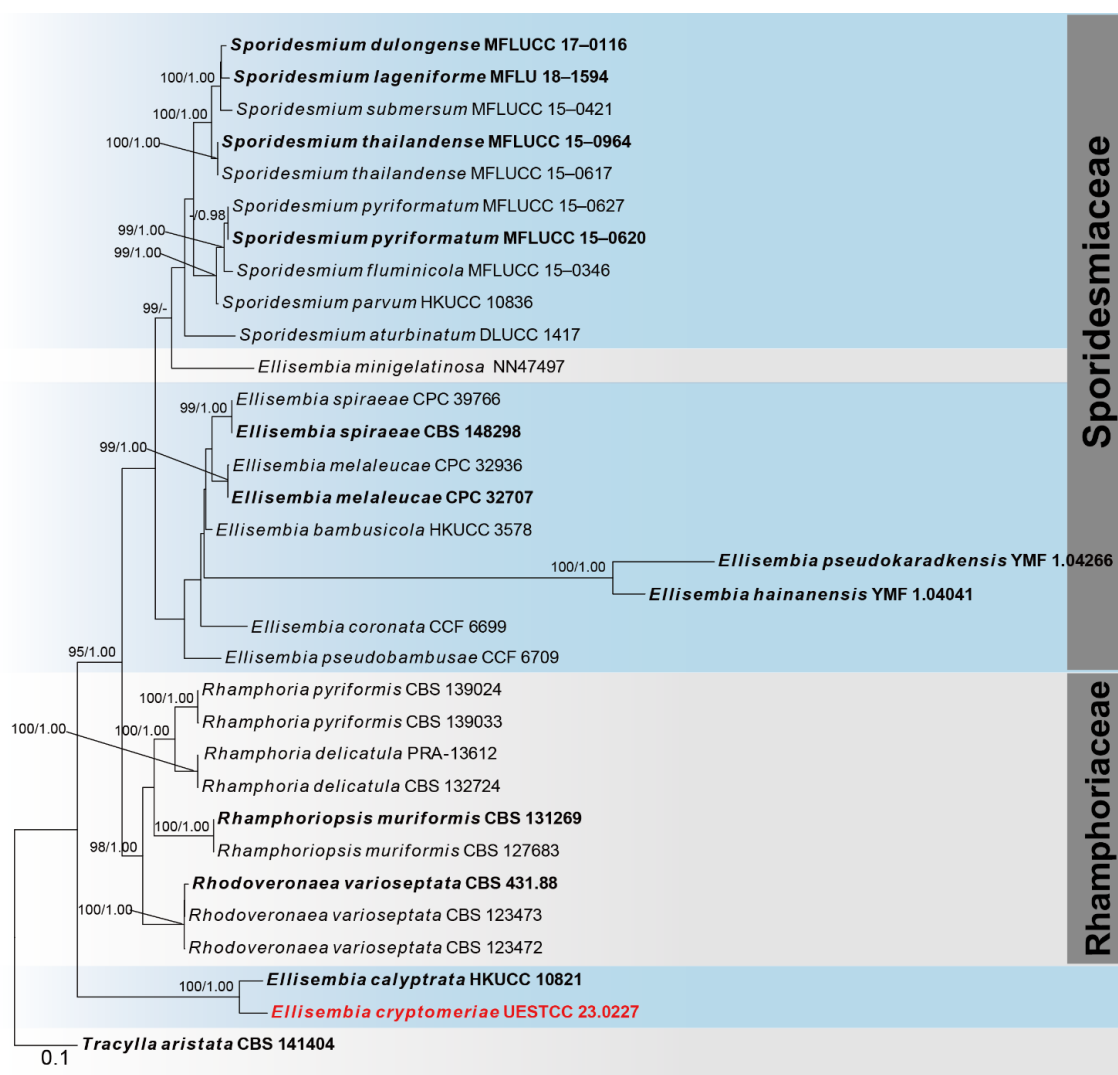


Figure 52 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU and *rpb2*) of Sordariomycetes. The scale bar indicates 0.1 changes. The tree is rooted with *Tracylla aristata* (CBS 141404) (Tracyllaceae, Tracyllales). The best ML tree with a final likelihood value of -16003.629 is presented. The alignment dataset comprises 32 taxa with 2459 sites, including 1168 distinct patterns, 173 singleton sites and 1367 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, on dead leaves of *Cunninghamia lanceolata*, W.H. Tian LCGS39_5 (HKAS 131280, holotype).

GenBank numbers – ITS: OR887402, *rpb2*: PP076810, *tef1- α* : PP076819, *tub2*: PP150072, *camdA*: PP150071

Notes – According to the multi-locus phylogeny, our collection *Memnoniella cunninghamiae* (HKAS 131280) forms clade sister to the *M. pseudodichroa* (BCRC FU31689) (Fig. 50). *Memnoniella cunninghamiae* is differed from *M. pseudodichroa* in having shorter and thinner conidiophores (70–250 $\times$ 2–4.5 μ m vs. 135–255 $\times$ 10–16 μ m) and smaller conidia (3–5.5 $\times$ 2–3 μ m vs. 13–17 $\times$ 6–7 μ m) (Yeh et al. 2023). *Memnoniella cunninghamiae* is morphologically similar to

M. sinensis (YMF 1.05582) and *M. levispora* (MFLUCC 20-0189), but they differ in the size of conidiophores ($70\text{--}250 \times 2\text{--}4.5 \mu\text{m}$ vs. $50\text{--}113 \times 4.3\text{--}6.0 \mu\text{m}$ vs. $43.6\text{--}60 \times 2.5\text{--}4.7 \mu\text{m}$) and conidia ($3\text{--}5.5 \times 2\text{--}3 \mu\text{m}$ vs. $10.1\text{--}13.4 \times 5.1\text{--}8.1 \mu\text{m}$ vs. $2.5\text{--}4.3 \times 1.5\text{--}3.6 \mu\text{m}$) (Zheng et al. 2019, Zhang et al. 2023). Comparisons of the ITS, *cmdA*, *rpb2* and *tub2* sequences data between the type strain of *M. sinensis* (YMF 1.05582) and *M. cunninghamiae* (HKAS 131280) showed 97.56% sequence identity (519/532 bp, gaps: 2/532 bp) in ITS, 85.92% sequence identity (421/490 bp, no gaps) in *cmdA*, 90.43% sequence identity (983/1087 bp, gap: 1/1087) in *rpb2*, and 87.6% sequence identity (219/250 bp, gaps: 10/250 bp) in *tub2*. Based on its morphological characteristics, phylogenetic analysis, and nucleotide polymorphism comparison results, *M. cunninghamiae* is identified as a new species.

Ellisembia Subram., Proc. Indian natn Sci. Acad., Part B. Biol. Sci. 58(4): 183 (1992)

MycoBank number: MB22423; Facesoffungi number: FoF12809

Notes – The genus *Ellisembia* was established by Subramanian (1992) to accommodate *Sporidesmium*-like species, with *Embellisia coronata* ($\equiv$ *Sporidesmium coronatum*) as the type species. Based on the relative similarity of morphology, Su et al. (2016) classified *Ellisembia* into *Sporidesmium*. However, subsequent reports preferred to retain *Ellisembia* as a separate genus until molecular data were available for the type species of both genera (Hyde et al. 2019a, Yang et al. 2021, Wu & Diao 2022). Delgado et al. (2024) supported the retention of the genus *Ellisembia* and obtained the epitype of *E. coronata* from its original host at the type locality in Germany and provided molecular data. Several studies showed that *Embellisia* is polyphyletic (Hyde et al. 2019a, Yang et al. 2021, Wu & Diao 2022, Delgado et al. 2024). Based on phylogenetic analysis, Delgado et al. (2024) identified the *Ellisembia sensu stricto* clades and proposed four new combinations within *Ellisembia sensu stricto*. In this study, we introduce a new species within the *Ellisembia sensu lato*. *Ellisembia* is mainly characterized by acrogenous, solitary, septate conidia seceding schizolytically from monoblastic, integrated, terminal, determinate or irregularly percurrently extending conidiogenous cells (Subramanian 1992, Seifert et al. 2011).

Ellisembia cryptomeriae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 53

MycoBank number: MB851897; Facesoffungi number: FoF16286

Etymology – Named after the host genus from the fungus was collected.

Holotype – HKAS 131276

Saprobic on dead twigs of *Cryptomeria fortunei*. Asexual morph: *Mycelium* superficial, septate, brown to dark brown, numerous, scattered, cylindrical, single or in groups. *Conidiophores* macronematous, mononematous, solitary or caespitose, erect, verruculose, straight or slightly curved, becoming slightly narrower towards the apex, smooth-walled, unbranched, $45\text{--}140 \times 5\text{--}10 \mu\text{m}$ ($\bar{x} = 92 \times 6 \mu\text{m}$, $n = 15$), 4–12-septate. *Conidiogenous cells* monoblastic, integrated, pale brown, terminal, cylindrical, $4\text{--}15 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 9 \times 4 \mu\text{m}$, $n = 30$). *Conidia* solitary, acrogenous, verruculose, obclavate, truncate at the base, tapering to the apex, pale brown to dark brown, with or without a mucilaginous cap, 6–17-septate, $20\text{--}85 \times 7\text{--}14 \mu\text{m}$ ($\bar{x} = 60 \times 9 \mu\text{m}$, $n = 30$), $2\text{--}4 \mu\text{m}$ ($\bar{x} = 2.6 \mu\text{m}$, $n = 30$) wide at apex, $4.5\text{--}5 \mu\text{m}$ ($\bar{x} = 4.5 \mu\text{m}$, $n = 30$) wide at base. Sexual morph: Undetermined.

Culture characters – Colonies on PDA reaching 20 mm diam in 2 weeks at 25 °C in the dark, colonies from above: circular, margin entire, even entire, with thin white aerial mycelium, zonate; from below: luteous, zonate, brown in the center.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, on dead leaves of *Cryptomeria fortunei*, W.H. Tian LCGS08_1 (HKAS 131276, holotype), ex-type CGMCC 3.25638 = UESTCC 23.0227.

GenBank numbers – ITS: OR887405, LSU: OR887115, *rpb2*: PP076811, *tef1- α* : PP076818

Notes – Multi-locus phylogenetic analysis indicated that *Ellisembia cryptomeriae* forms a sister clade to *Ellisembia calyptrata* with 100% ML/1.00 BYPP support (Fig. 52). Only LSU/ *rpb2*

sequence data are accessible for *E. calyptrata*. A comparison of sequence data of the ITS and *rpb2* between *E. cryptomeriae* (UESTCC 23.0227) and *E. calyptrata* (HKUCC 10821) show 98.17%

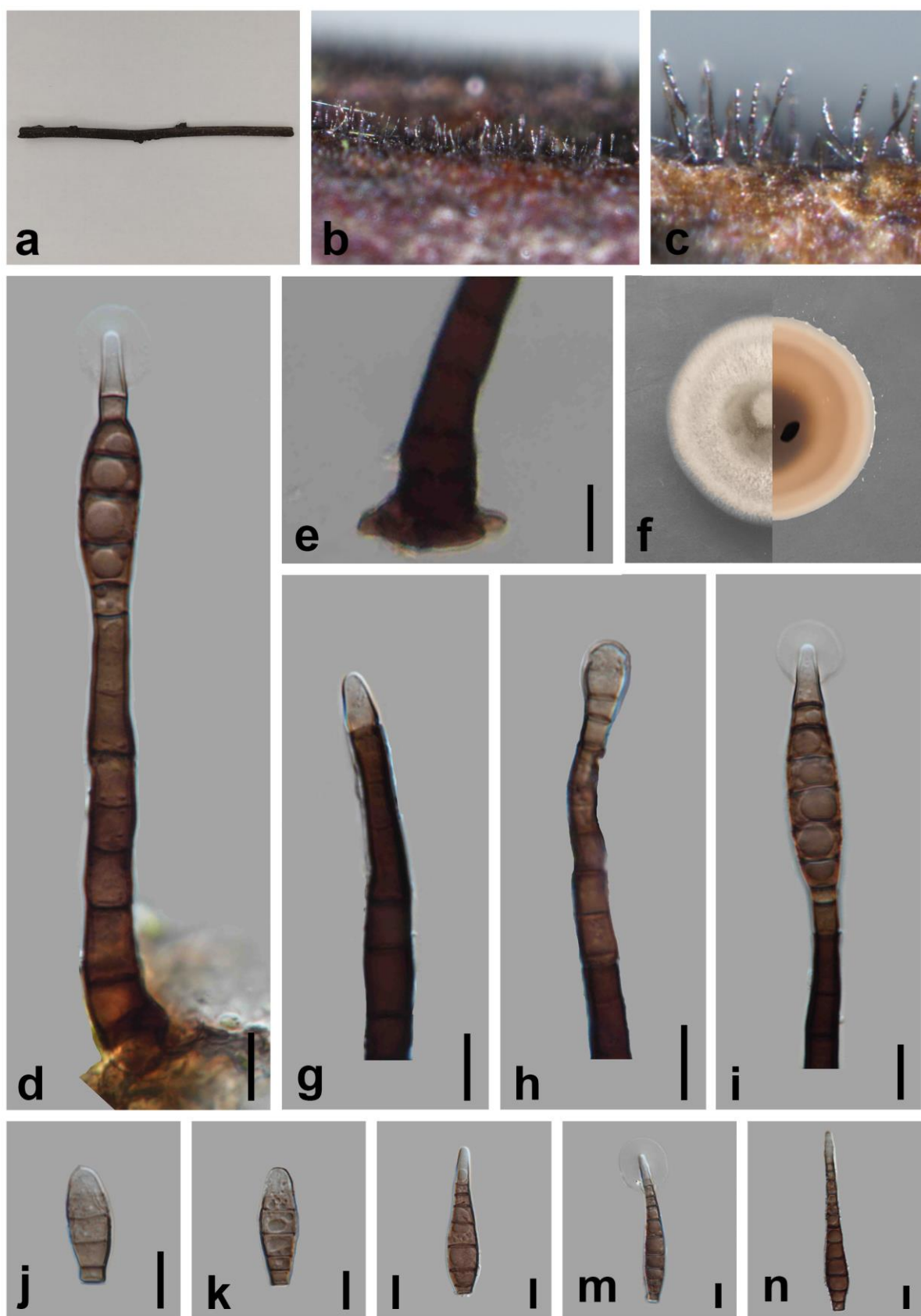


Figure 53 – *Ellisembia cryptomeriae* (HKAS 131276, holotype). a Specimen. b, c Colonies on dead twigs of *Cryptomeria fortunei*. d, Conidiophores, conidiogenous cells with conidia. e Conidiophore

base. f Culture characteristics. g–i Conidiogenous cells with conidia j–m Conidia. n Germinating conidium. Scale bars: d–n = 10 μ m.

sequence identity (804/819 bp, gap: 1/819 bp) in LSU, 86.87% sequence identity (721/830 bp, gaps: 4/830 bp) in *rpb2*. Additionally, there are significant morphological differences between *E. cryptomeriae* and *E. calyptrata*. *Ellisembia cryptomeriae* differs from *E. calyptrata* in having longer conidiophores ($45\text{--}140 \times 5\text{--}10 \mu\text{m}$ vs. $30\text{--}50 \times 6.0\text{--}7.0 \mu\text{m}$) and smaller conidia ($20\text{--}85 \times 7\text{--}14 \mu\text{m}$ vs. $60\text{--}90 \times 9.0\text{--}12.0 \mu\text{m}$) (Cabello et al. 1990). Based on its morphological characteristics, phylogenetic analysis, and nucleotide polymorphism comparison results, *E. cryptomeriae* has been identified as a new species within the *Ellisembia* s. l.

Parasymphodiellales Hern. -Restr., Gené, R.F. Castañeda & Crous, Stud. Mycol. 86: 87 (2017)

MycoBank number: MB820297; Facesoffungi number: FoF06518

Notes – The monotypic order Parasymphodiellales was proposed by Hernández-Restrepo et al. (2017) to accommodate Parasymphodiellaceae. The members of Parasymphodiellales are characterized by *stylaspergillus*-like syn asexual morphs, supporting this order as a distinct taxonomic (Cheewangkoon et al. 2009, Hernández-Restrepo et al. 2017).

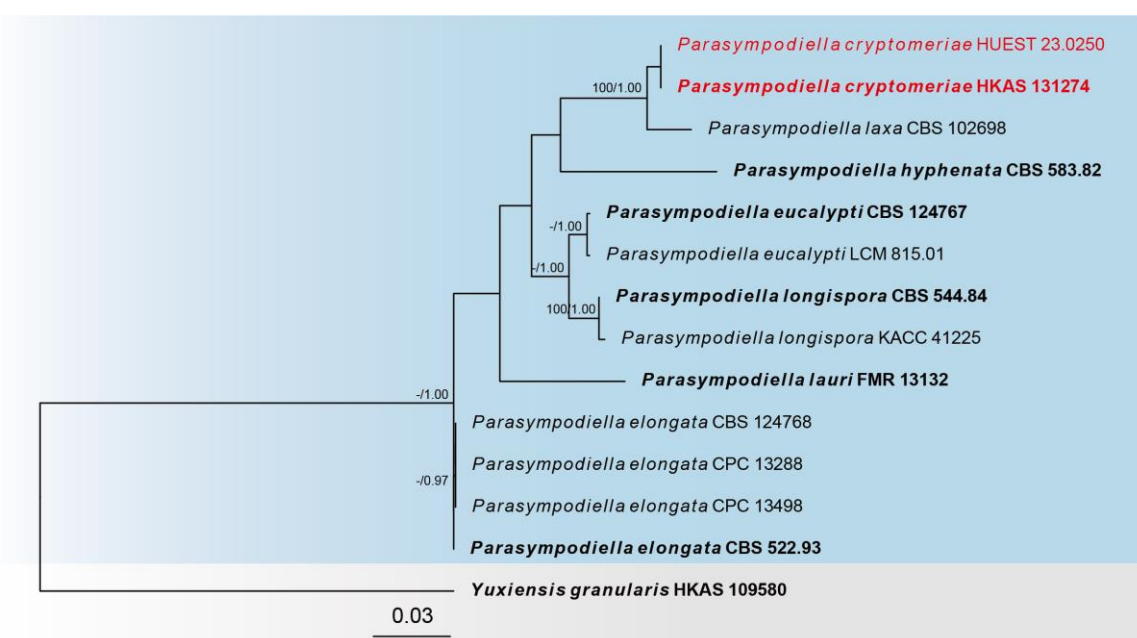


Figure 54 – Phylogram of the best ML tree based on a combined dataset (ITS and LSU) of *Parasymphodiella*. The scale bar indicates 0.03 changes. The tree is rooted with *Yuxiensis granularis* (HKAS 109580) (Scortechiniaceae, Coronophorales). The best ML tree with a final likelihood value of -3761.491 is presented. The alignment dataset comprises 14 taxa with 1438 sites, including 248 distinct patterns, 139 singleton sites and 1188 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Parasymphodiellaceae Hern. -Restr., Gené, Guarro & Crous, Stud. Mycol. 86: 87 (2017)

MycoBank number: MB820298; Facesoffungi number: FoF05187

Notes – Parasymphodiellaceae was introduced for the clade that encompasses four *Parasymphodiella* species, with *Parasymphodiella* as the type genus, previously accommodated in *Symphodiella* (Ponnappa 1975, Hernández-Restrepo et al. 2017). Taxa of this family most commonly grow as saprobes on plant litter, conifers and dicotyledons (Subramanian & Vittal 1973, Crous et al. 1995, Cheewangkoon et al. 2009, Seifert et al. 2011, Hernández-Restrepo et al. 2017).

Parasymphodiella Ponnappa, Trans. Br. mycol. Soc. 64(2): 344 (1975)

MycoBank number: MB9226; Facesoffungi number: FoF05188

Notes – *Parasymphodiella* was established by Ponnappa (1975) with *P. laxa* as the type species. *Parasymphodiella* was mainly characterized by distinct, single conidiophores with terminal and intercalary, integrated, indeterminate, sympodially extending conidiogenous cells that produce catenate, cylindrical, thallic conidia by disarticulations of the fertile hyaline branches (Li et al. 2014).

Parasymphodiella cryptomeriae W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 55

MycoBank number: MB851896; Facesoffungi number: FoF16287

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

Holotype – HKAS 131274.

Saprobic on dead leaves of *Cryptomeria japonica*. Asexual morph: *Mycelium* consisting of branched, septate, smooth, hyaline to black. *Conidiophores* macronematous, mononematous, scattered, erect, solitary, unbranched, cylindrical, septate; sterile part dark brown to black, thick-walled, $140\text{--}355 \times 5\text{--}12\ \mu\text{m}$ ($\bar{x} = 264 \times 9\ \mu\text{m}$, $n = 15$), 8–14 septa; fertile part brown, becoming paler toward the apex, comprising 2–6 conidiogenous cells; swollen base $11\text{--}30\ \mu\text{m}$ ($\bar{x} = 20\ \mu\text{m}$, $n = 10$) wide. *Conidiogenous cells* holoblastic, terminal and intercalary, integrated, indeterminate, sympodial proliferation, smooth, pale brown to brown, becoming hyaline toward the apex, $22\text{--}45 \times 5\text{--}10\ \mu\text{m}$ ($\bar{x} = 35 \times 7\ \mu\text{m}$, $n = 20$) between conidiogenous loci. *Conidia* thallic-arthric, forming in loose unbranched chains, hyaline, dry, smooth, becoming verruculose with age, guttulate, thin-walled, cylindrical, $23\text{--}50 \times 6\text{--}10\ \mu\text{m}$ ($\bar{x} = 35 \times 8\ \mu\text{m}$, $n = 30$), 0–4-septate, apex and base of intercalary conidia truncate, apical conidia with obtuse or rounded apex, occurring in unbranched conidial chains. *Stylaspergillus* state. Sexual morph: Undetermined.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N $29^{\circ}37'36''$, E $102^{\circ}53'13''$, elevation 628 m, 28 July 2022, within dead bark of *Cryptomeria japonica*, W.H. Tian LCGS02_3 (HKAS 131274, holotype); *ibid.*, Zhougong Mountain, N $29^{\circ}58'1''$, E $103^{\circ}2'8''$, elevation 1196 m, 16 November 2022, on dead leaves of *Pinus* sp., W.H. Tian ZGS76 (HUEST 23.0250).

GenBank numbers – HKAS 131274 = ITS: OR887407, LSU: OR887117; HUEST 23.0250 = ITS: OR887406, LSU: OR887116

Notes – In the phylogenetic analysis of *Parasymphodiella*, *P. cryptomeriae* clustered with *P. laxa* (CBS 102698) with 100% ML and 1.00 BYPP support (Fig. 54). Comparisons of the LSU and ITS sequences of *P. cryptomeriae* (HKAS 131274) and *P. laxa* (CBS 102698) revealed 99.13% sequence identity (801/808 bp, gaps: 1/808 bp) in LSU and 95.05% sequence identity (461/485 bp, gaps: 4/485 bp) in ITS. Morphologically, *P. cryptomeriae* and *P. laxa* share similar characteristics by solitary, unbranched, and septate conidiophores (Cheewangkoon et al. 2009). These conidiophores possess holoblastic, integrated conidiogenous cells that produce thallic-arthric conidia, forming loose, unbranched chains. However, our collections have smaller conidiophores ($140\text{--}355 \times 5\text{--}12\ \mu\text{m}$ vs. up to $500\ \mu\text{m} \times 8\text{--}10\ \mu\text{m}$), smaller conidiogenous cells ($22\text{--}45 \times 5\text{--}10\ \mu\text{m}$ vs. $35\text{--}75 \times 8\text{--}12\ \mu\text{m}$), smaller conidia ($23\text{--}50 \times 6\text{--}10\ \mu\text{m}$ vs. $35\text{--}60 \times 8\text{--}9\ \mu\text{m}$) and fewer number of septa in conidia (0–4-septate vs. 0–3(–7)-septate) (Cheewangkoon et al. 2009). Thus, we introduce our collection as a novel taxon.

Pleurotheciales Réblová & Seifert, Persoonia 37: 63 (2015)

MycoBank number: MB813228; Facesoffungi number: FoF06531

Notes – Réblová et al. (2016) established the order Pleurotheciales including the single family Pleurotheciaceae, based on a combined dataset of ITS, SSU, LSU, *tub2*, *MCM7* and *rpb2* sequences. Members in this order are common saprobic on wood, rarely human pathogens causing keratomycosis (Réblová et al. 2016). Currently, there are one family and 14 genera in this order (Wijayawardene et al. 2022a).

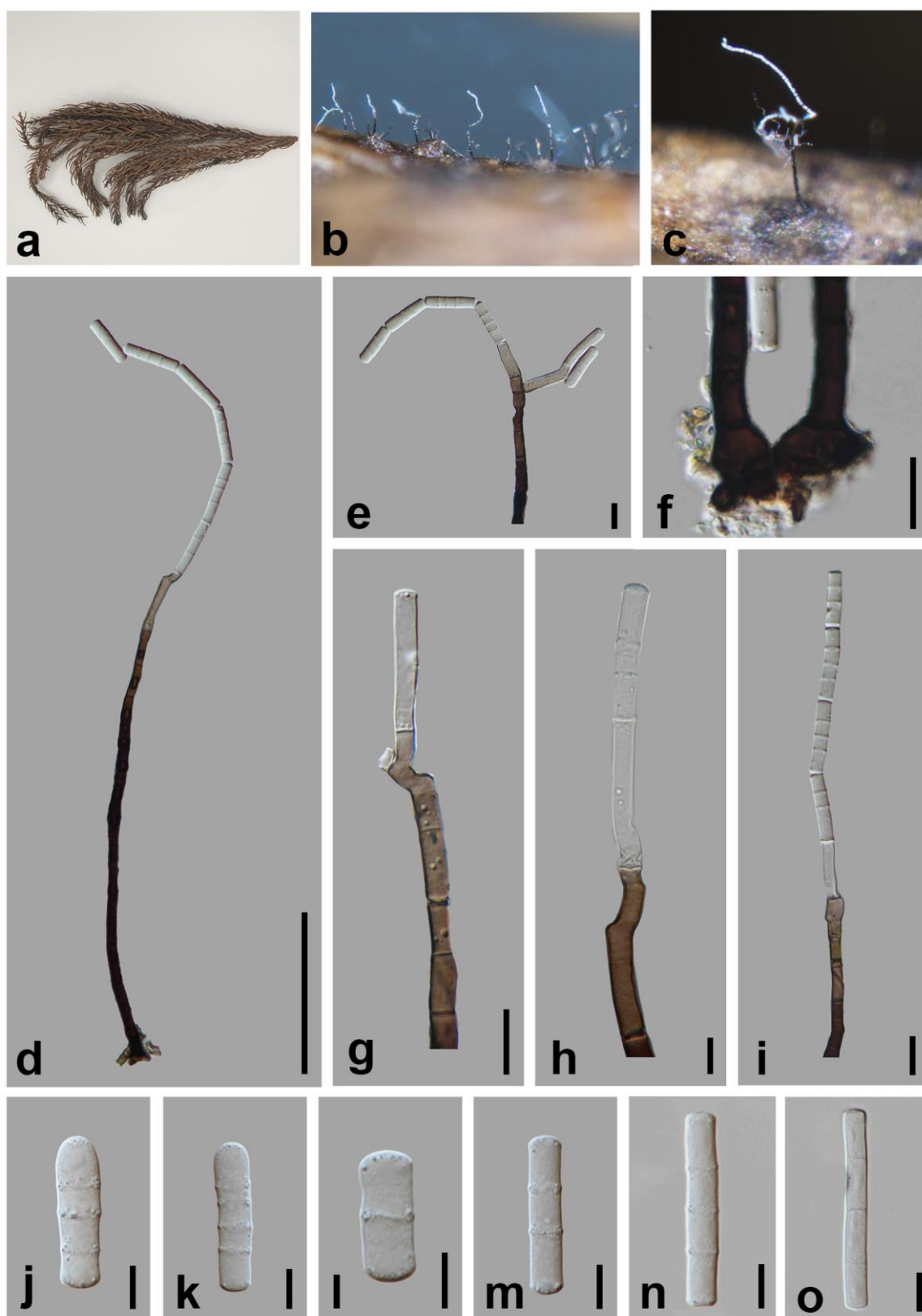


Figure 55 – *Parasympodiella cryptomeriae* (HKAS 131274, holotype). a Specimen. b, c Colonies on dead twigs of *Cryptomeria japonica*. d, Conidiophores, conidiogenous cells with conidia. e, g–i Conidiogenous cells with conidia. f Conidiophores bases. j, k Apical conidia. l–o Conidia. Scale bars: d = 100 μ m. e–g, i = 20 μ m. h, j–o = 10 μ m.

Pleurotheciaceae Réblová & Seifert, Persoonia 37: 63 (2015)

Mycobank number: MB813229; Facesoffungi number: FoF05316

Notes – Pleurotheciaceae was typified by *Pleurothecium*, which was introduced by Höhnelt (1919). Pleurotheciaceae is an assemblage of genera representing a highly diverse morphology that have perithecial ascomata with asexual dematiaceous hyphomycetous stages (Dong et al. 2021). Members of this family have mostly been isolated from decaying wood or plant debris as saprobes, while a few species were also identified as opportunistic human pathogens (Guarro et al. 2000).

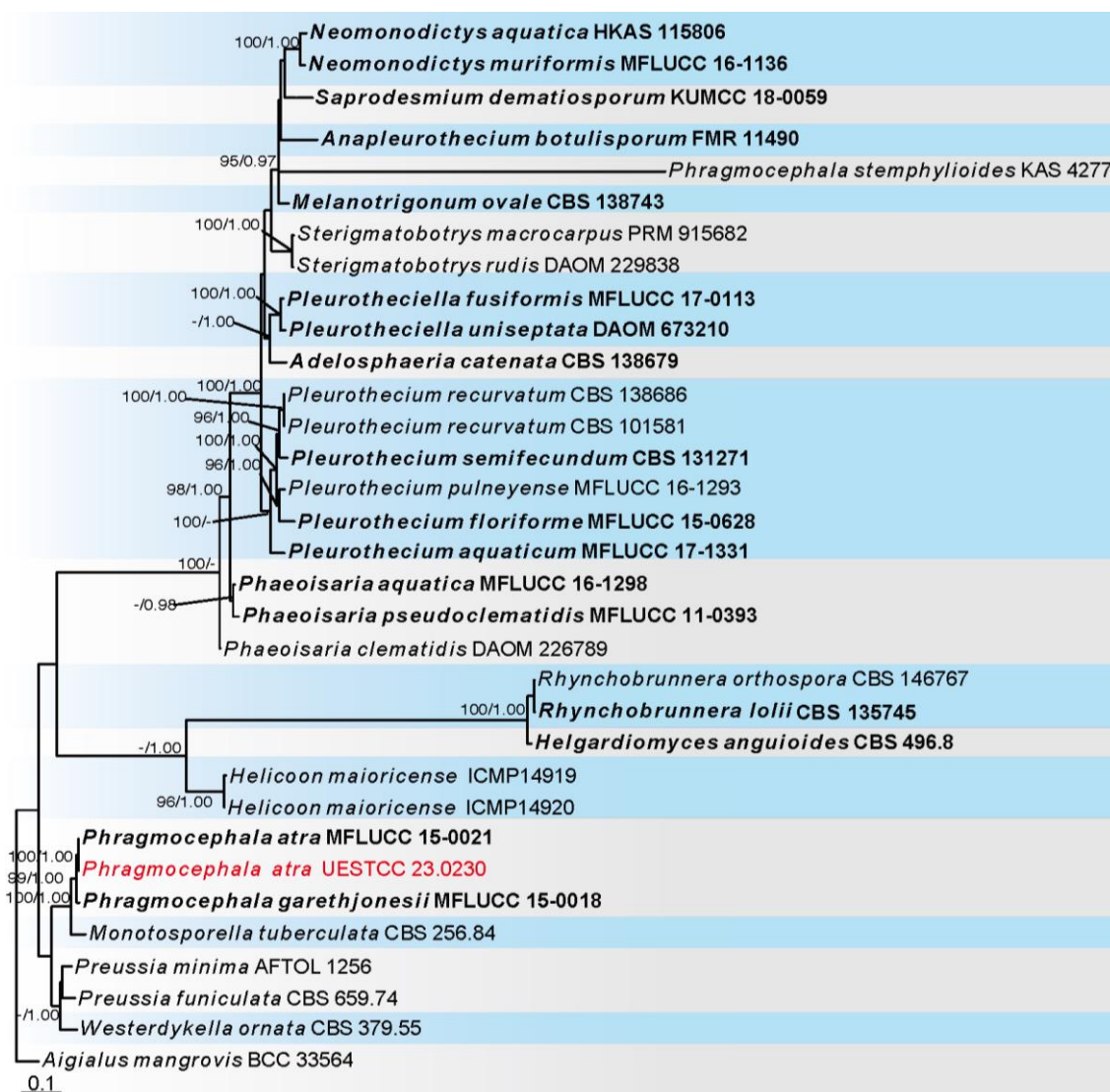


Figure 56 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU and SSU) of Pleurotheciaceae. The scale bar indicates 0.1 changes. The tree is rooted with *Aigialus mangrovis* (BCC 33564) (Aigialaceae, Pleosporales). The best ML tree with a final likelihood value of -16141.143 is presented. The alignment dataset comprises 33 taxa with 2649 sites, including 1215 distinct patterns, 430 singleton sites and 1356 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

Phragmocephala E.W. Mason & S. Hughes, Naturalist (Hull), ser. 3, 1951: 97 (1951)

Mycobank number: MB9367; Facesoffungi number: FoF00783

Notes – *Phragmocephala* was proposed by Mason & Hughes (1951) with *P. elliptica* as the type species. The genus is characterized by macronematous, mononematous, erected more or less straight conidiophores that are terminated by a single integrated holoblastic conidiogenous cell. The conidia are typically ellipsoidal, blastic, solitary, 3–6 septate, seceding with a portion of the

conidiogenous cell by rupture of the wall immediately below the base of the conidium (Mason & Hughes 1951, Whitton et al. 2012).

Phragmocephala atra (Berk. & Broome) E.W. Mason & S. Hughes, Naturalist: 97 (1951) Fig. 57
MycoBank number: MB303243

Saprobic on dead twigs of *Cryptomeria fortunei*. Asexual morph: *Mycelium* partly immersed, composed of septate, dark brown, smooth hyphae. *Conidiophores* synnematos, macronematous, septate, in fascicles, unbranched, erect, dark brown at the base, pale brown at fertile, flared apex, sometimes proliferating, 4–8-septate, $130\text{--}220 \times 4\text{--}8 \mu\text{m}$ ($\bar{x} = 172 \times 6.5 \mu\text{m}$, $n = 30$). *Conidiogenous cells* monoblastic, terminal, integrated, elongated, pale brown. *Conidia* $30\text{--}38 \times 18\text{--}21 \mu\text{m}$ ($\bar{x} = 34 \times 19 \mu\text{m}$, $n = 30$), 1–4-septate, ellipsoidal to subglobose, dark brown, pale brown at apical and basal cells, with dark brown to black central cells, with a thick dark band on the central septum; smooth, rounded at apex, truncate at base, sometimes released with part of conidiogenous cell; conidial secession schizolytic. Sexual morph: Undetermined.

Known distribution – China

Culture characteristics – Colonies on PDA reaching 21 mm diam after 10 days at 25 °C, colonies from above: circular, divergent at the margin, dense, slightly raised, pale luteous in the centre, white at the margin; reverse: brownish-yellow in the center, pale luteous at the margin.

Material examined – China, Sichuan Province, Ya'an City, Longcanggou National Forest Park, N 29°37'36", E 102°53'13", elevation 628 m, 28 July 2022, on dead twigs of *Cryptomeria fortunei*, W.H. Tian LCGS09_2 (HUEST 23.0230), living culture UESTCC 23.0230.

GenBank numbers – ITS: OR887408, LSU: OR887118

Notes – In our multi-locus phylogenetic tree, our collection (UESTCC 23.0230) forms a branch sister to *Phragmocephala atra* (MFLUCC 15–0021) with 100% ML/1.00 BYPP support (Fig. 56). Morphologically, our collection (UESTCC 23.0230) is similar to *P. atra* (MFLUCC 15–0021) in the shapes and size of synnematos, septate, unbranched conidiophores, monoblastic, pale brown conidiogenous cells and 4-septate, ellipsoidal to subglobose, dark brown conidia (Su et al. 2015). Hence, we have identified our collection as *P. atra*, marking the first report of its presence on *Cryptomeria fortunei*.

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

MycoBank number: MB90505; Facesoffungi number: FoF12988

Notes – Xylariales was proposed by Nannfeldt (1932) in Sordariomycetes which comprised 20 families (Wijayawardene et al. 2022a). The order was characterized by eight-spored unitunicate asci, usually with an apical J+ apparatus and ellipsoidal, dark ascospores (Smith et al. 2003, Maharachchikumbura et al. 2016). Members of the Xylariales are commonly found on fallen twigs, branches, and trunks, leading to the early perception of their efficiency as lignin degraders (Ferrari et al. 2021). Some species can also cause soft rots (Ferrari et al. 2021).

Coniocessiaceae Asgari & Zare, Mycol. Progr. 10(2): 195 (2011)

MycoBank number: MB518425; Facesoffungi number: FoF00671

Notes – Coniocessiaceae was established by Asgari & Zare (2011) to accommodate *Coniocessia*, which comprises saprobes in plants, soil and dung. Based on morphology and phylogeny and divergence time estimations, Coniocessiaceae was placed in Xylariales (Asgari & Zare 2011, Hyde et al. 2013, Maharachchikumbura et al. 2016).

Circinotrichum Nees, Syst. Pilze (Würzburg) (Ueberbl.): 18 (1816)

MycoBank number: MB7667; Facesoffungi number: FoF13681

Notes – *Circinotrichum*, introduced by Nees von Esenbeck (1817), accommodates taxa characterized by unbranched, circinate or flexuous setae, with conidiophores reduced to conidiogenous cells that aggregate around the bases of setae. The genus is typified by *Circinotrichum maculiforme*. *Circinotrichum* and *Gyrothrix* are very similar in morphology and

both occur as saprophytes on leaves and branches in tropical, subtropical to temperate climate worldwide. The similar morphological characteristics of the two genera often lead to confusion among their species, making classification complex and difficult. Hernández-Restrepo et al. (2022) further classified and identified these similar taxa and distinguished *Circinotrichum* from *Gyrothrix* based on molecular sequences. They proposed that *Circinotrichum* has simple setae, whereas *Gyrothrix* has branched setae (Hernández-Restrepo et al. 2022).

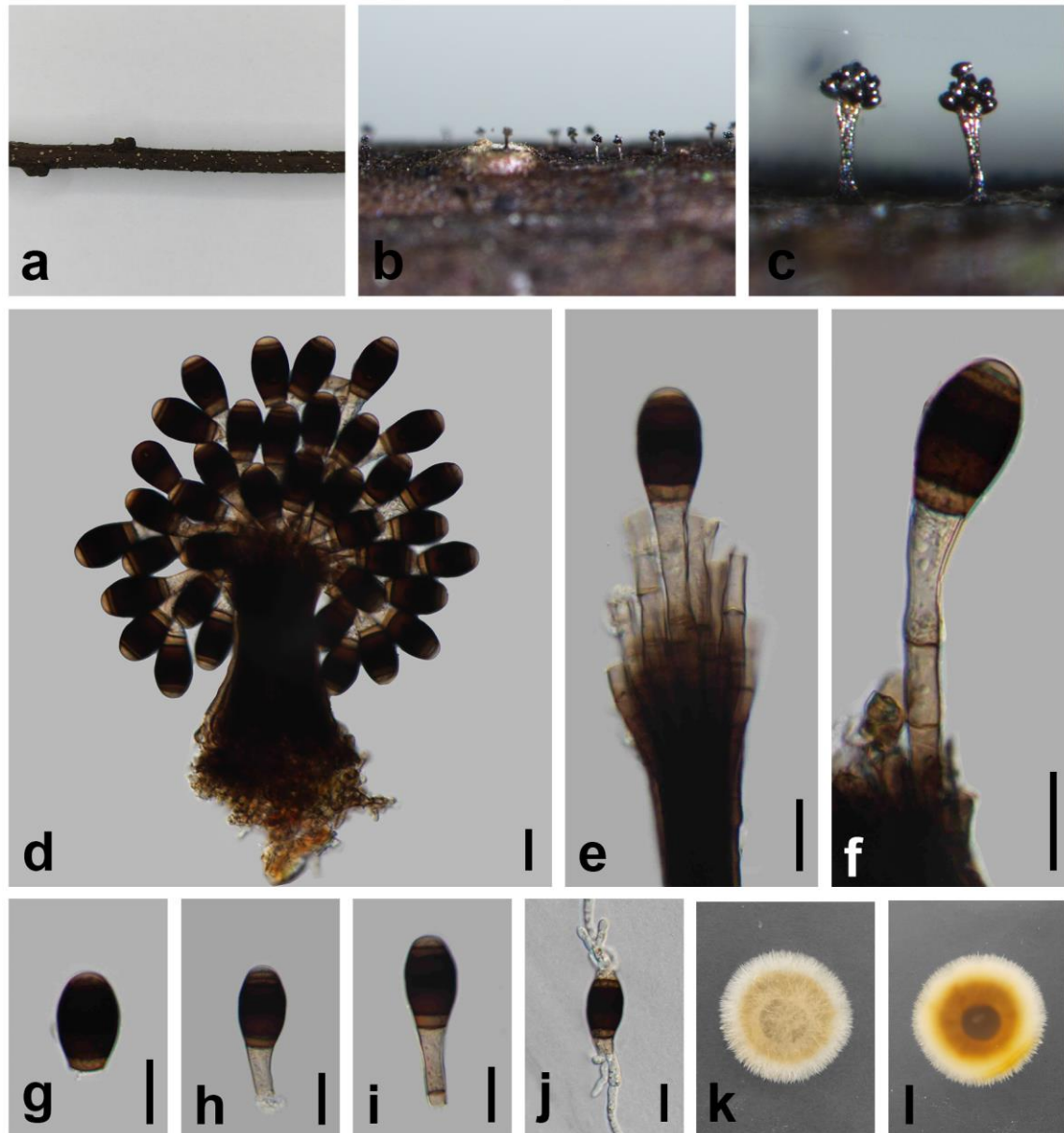


Figure 57 – *Phragmocephala atra* (HUEST 23.0230). a Specimen. b, c Colonies on dead twigs of *Cryptomeria fortunei*. d–f Conidia attached to conidiophores. g–i Conidia. j Germinating conidium. k, l Culture characteristics. Scale bars: d–j = 20 μ m.

Circinotrichum podocarpi W.H. Tian, K.D. Hyde & Maharachch., sp. nov.

Fig. 59

Mycobank number: MB854682; Facesoffungi number: FoF16288

Etymology – Named after the host genus where the fungus was collected.

Holotype – HKAS 134912

Saprobic on dead leaves of *Podocarpus macrophyllus*. Asexual morph: *Mycelium* composed of branched and anastomosing, smooth-walled, septate, brown hyphae, 1–3 μ m wide, bearing setae and conidiogenous cells. *Setae* irregularly branched, in clusters, with L- or T-basal cell giving rise

to a network of aggregated conidiogenous cells, main stipe dark brown, thick-walled, initially smooth, becoming verruculose towards the apex, branches and upper part circinate, $68\text{--}132 \times 2.7\text{--}4 \mu\text{m}$ ($\bar{x} = 110 \times 3.3 \mu\text{m}$, $n = 30$). *Conidiogenous cells* aggregated in tight clusters around the base of setae, pale to medium brown, smooth, subcylindrical to lageniform, $6\text{--}15.5 \times 3\text{--}5.5 \mu\text{m}$ ($\bar{x} = 11 \times 4 \mu\text{m}$, $n = 30$). *Conidia* aggregated in clusters at the apices of conidiogenous cells, hyaline, smooth, multi-guttulate, cylindrical to fusoid, straight to slightly curved, apex subobtuse, $12\text{--}18 \times 1.6\text{--}2.7 \mu\text{m}$ ($\bar{x} = 14 \times 2 \mu\text{m}$, $n = 30$). Sexual morph: Undetermined.

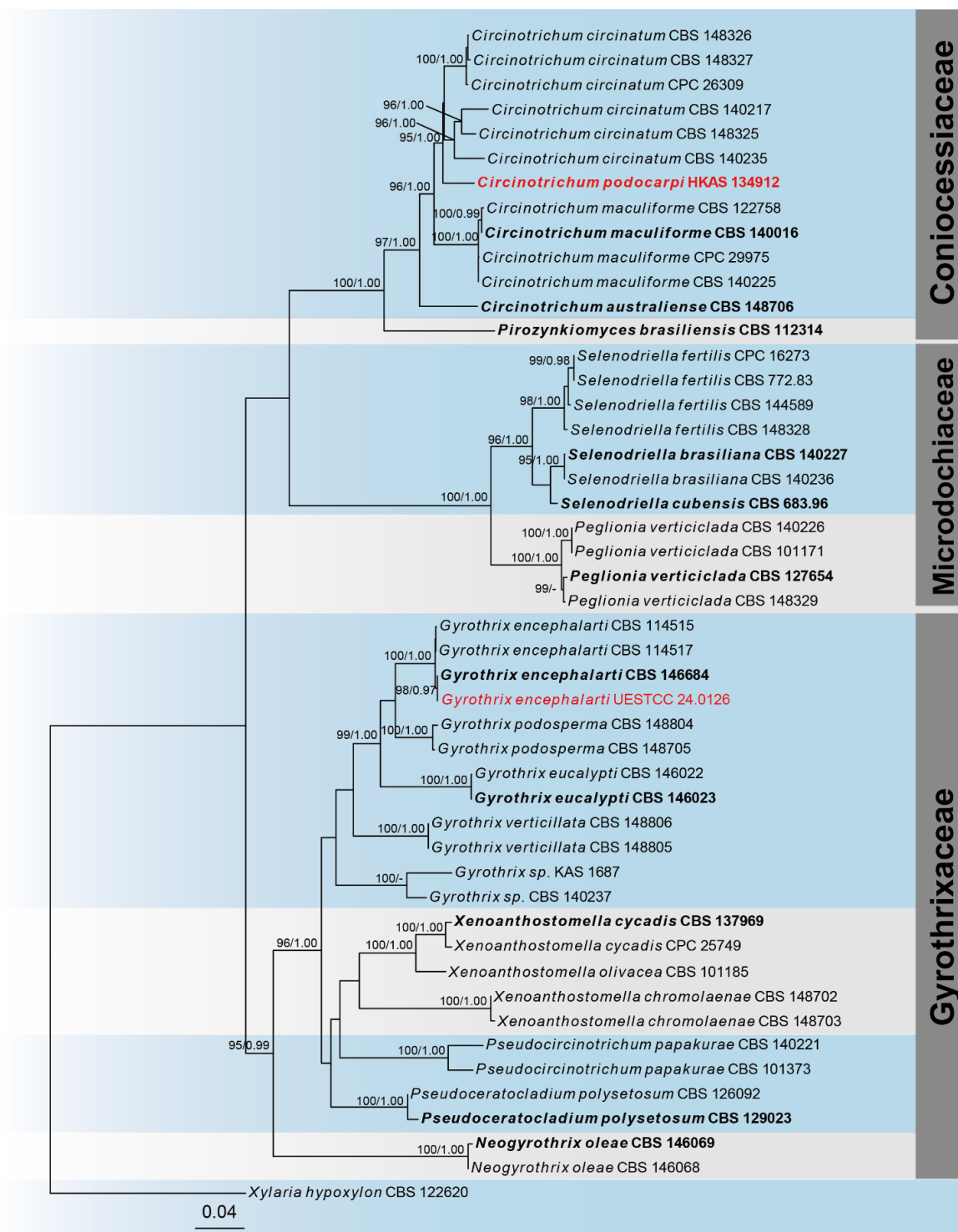


Figure 58 – Phylogram of the best ML tree based on a combined dataset (ITS, LSU and *rpb2*) of Coniocyssaceae, Microdochiaceae and Gyrothrixaceae. The scale bar indicates 0.04 changes. The tree is rooted with *Xylaria hypoxylon* (CBS 122620) (Xylariaceae, Xylariales). The best ML tree

with a final likelihood value of -13446.304 is presented. The alignment dataset comprises 48 taxa with 2144 sites, including 869 distinct patterns, 95 singleton sites and 1464 constant sites. Ultrafast bootstrap values for the maximum likelihood analysis equal to or greater than 95% and posterior probability for Bayesian analysis equal to or greater than 0.95 are indicated at the nodes. Novel isolates are shown in red. Isolates from type materials are in bold.

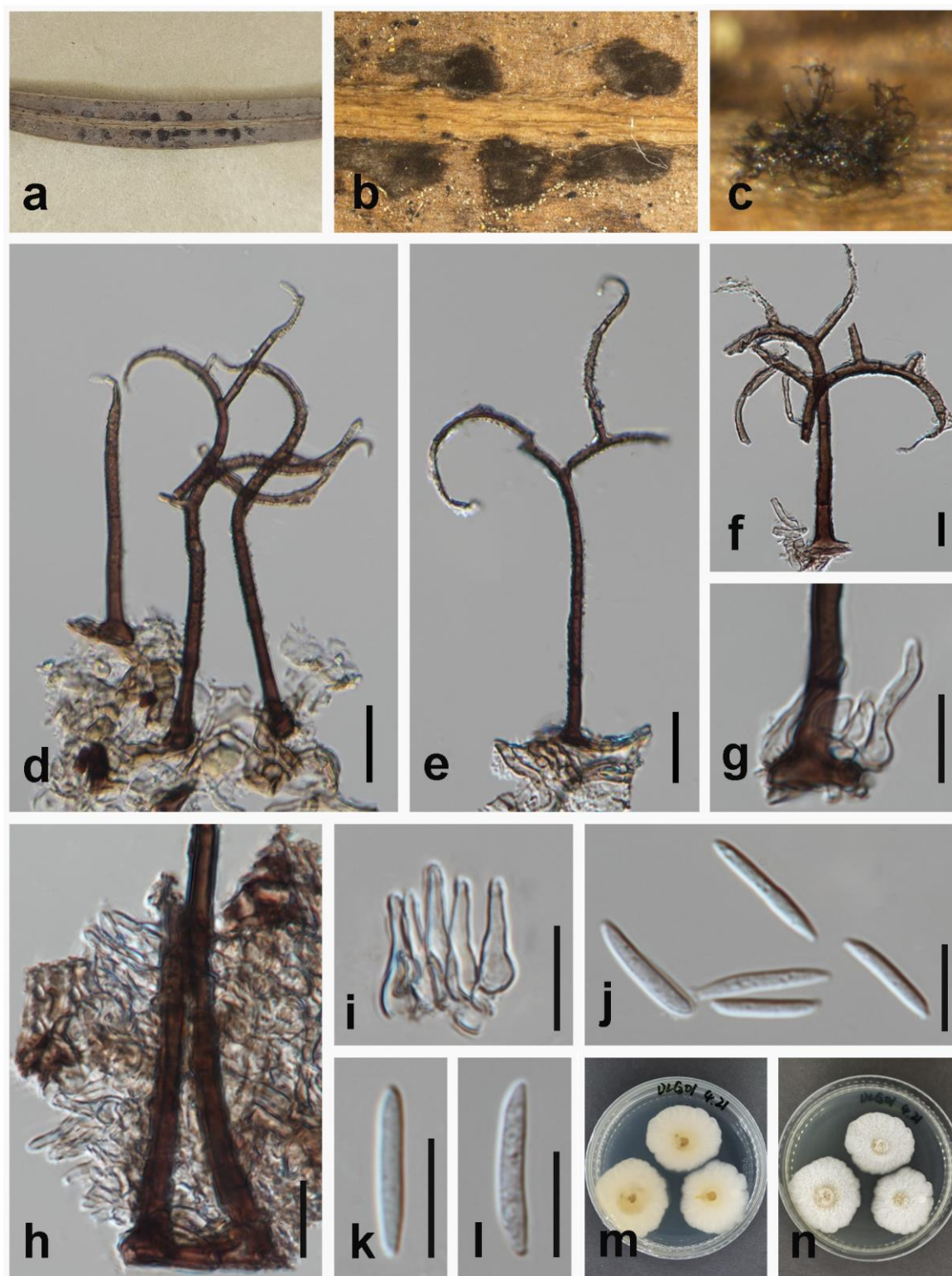


Figure 59 – *Circinotrichum podocarpi* (HKAS 134912, holotype). a Specimen. b, c Colonies on dead leaves of *Podocarpus macrophyllus*. d–f Setae. g, h conidiogenous cells, i–k Conidia. Scale bars: d, e = 20 μ m, f–k = 10 μ m.

Material examined – China, Sichuan Province, Luzhou City, Daolingou, N 29°15'1", E 105°42'1", elevation 405 m, 31 March 2023, on dead leaves of *Podocarpus macrophyllus*, W.H. Tian DLG01 (HKAS 134912, holotype).

GenBank numbers – ITS: PP740386, LSU: PP740392, *rpb2*: PP779425

Notes – Phylogenetic analysis based on the combined dataset of ITS, LSU and *rpb2* genes revealed that our collection (HKAS 134912) forms a separate branch and is sister to *Circinotrichum circinatum* and *Circinotrichum maculiforme* (Fig. 58). They are morphologically similar, but the conidiogenous cells of our strain is slightly larger than *C. circinatum* (6–15.5 × 3–5.5 µm vs. 4–11.5 × 2–4 µm), and the setae are shorter than *C. maculiforme* (68–132 µm vs. up to 350 µm) (Crous et al. 2015a, Hernández-Restrepo et al. 2022). Moreover, based on pairwise nucleotide comparisons, the closest relative to our collection (HKAS 134912) is *C. circinatum* (CBS 148326), comparing the ITS, LSU and *rpb2* of their sequence revealed 96.83% sequence identity (397/410 bp, gaps: 2/410 bp) in ITS, 99.35% sequence identity (766/771 bp, no gaps) in LSU and 92.43% sequence identity (537/581 bp, no gaps) in *rpb2*.

Gyrothrixaceae Hern. -Restr. & Crous, Persoonia. 49: 99–135 (2022)

MycoBank number: MB844015

Notes – Based on multi-locus phylogenetic analysis (ITS, LSU, *rpb2*) and morphological studies Hernández-Restrepo et al. (2022) introduced the family Gyrothrixaceae with *Gyrothrix* as its type genus. Gyrothrixaceae comprises six genera: *Gyrothrix*, *Xenoanthostomella*, *Pseudocircinotrichum*, *Pseudoceratocladium*, *Neogyrothrix* and *Neoanthostomella* (Hernández-Restrepo et al. 2022).

Gyrothrix (Corda) Corda, Anleit. Stud. Mykol., Prag: LXIII (1842)

Fig. 60

MycoBank number: MB8414; Facesoffungi number: FoF13685

Notes – *Gyrothrix* was introduced by Corda (1842) and typified by *G. podosperma*. See notes under *Circinotrichum*.

Gyrothrix encephalarti Crous, in Crous et al., Persoonia 44: 343 (2020)

MycoBank number: MB835410

Saprobic on dead branches of *Pinus* sp. Asexual morph: *Mycelium* consisting of brown, smooth, septate, branched hyphae. *Setae* 74–172 × 2–4.5 µm ($\bar{x}$ = 110 × 3.3 µm, n = 30), erect, brown, multiseptate, thick-walled, verrucose, subcylindrical with apical taper, base bulbous, apex spirally twisted with twisted lateral branches in apical region. *Conidiophores* 5.5–14 × 2.5–4.5 µm ($\bar{x}$ = 9.4 × 3.5 µm, n = 30), reduced to conidiogenous cells around base of setae, ampulliform to subcylindrical, pale brown, smooth, proliferating percurrently at apex. *Conidia* hyaline, smooth, aseptate, fusoid, inaequilateral, inner plane flat, outer plane convex, apex subobtuse, base truncate, 10.5–16.4 × 1.3–2.2 µm ($\bar{x}$ = 13 × 2 µm, n = 30). Sexual morph: Undetermined.

Known distribution – China (this study)

Culture characters – Colonies on PDA reaching 28 mm diam after 19 days at 25 °C, colonies from above: white, circular, dense, fluffy appearance, with denser mycelium at the center and becoming sparser at the edge; colonies from the below: white, pale yellow in the centre, cream at margin.

Material examined – China, Sichuan Province, Chengdu City, Jiudaoguai, N 30°30'21", E 103°53'47", elevation 502 m, 19 October 2023, within dead branches of *Pinus* sp., W.H. Tian JDG02_1 (HUEST 24.0145), living culture UESTCC 24.0126.

GenBank numbers – ITS: PP740387, LSU: PP740393, *rpb2*: PP779426

Notes – Crous et al. (2020) first isolated the *Gyrothrix encephalarti* from *Encephalartos* sp. in South Africa. Multi-locus analyses of combined ITS, LSU, and *rpb2* sequence data showed that our strain clusters with the type strain of *G. encephalarti* (CBS 146684) (Fig. 53). Our new collection (UESTCC 24.0126) shares similar morphological characters to the type of *G. encephalarti* (Crous et al. 2020). Sequence comparison for the ITS, LSU and *rpb2* region

between our isolate (UESTCC 24.0126) and *G. encephalarti* (CBS 146684) showed 99.80% sequence identity (510/511 bp, no gaps) in ITS, 100% sequence identity (758/758 bp, no gaps) in LSU and 100% sequence identity (673/673 bp, no gaps) in *rpb2*. Hence, we treated our isolate as a novel host record of *G. encephalarti* from *Pinus* sp., and this is the first time *G. encephalarti* has been reported from China.

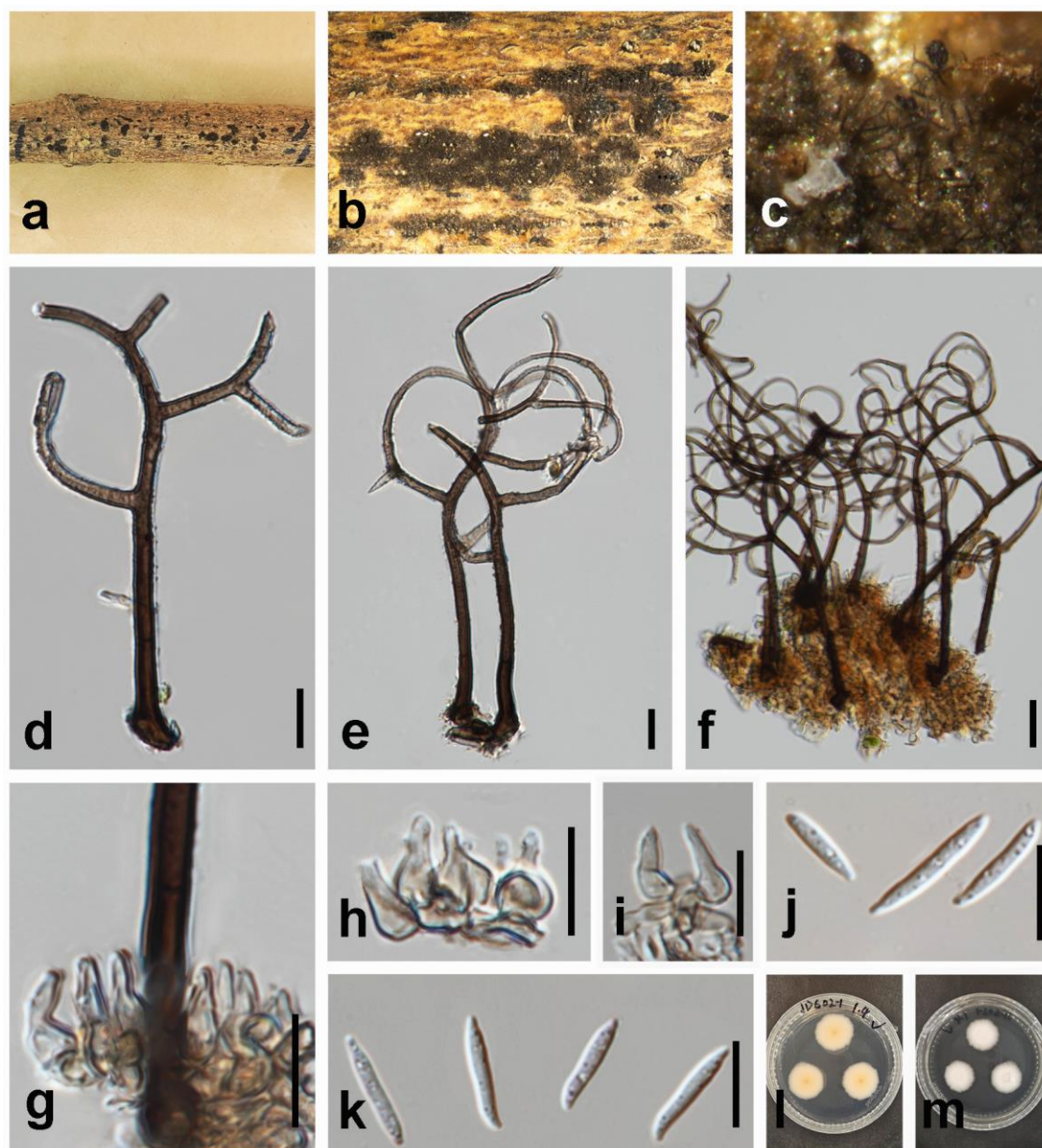


Figure 60 – *Gyrothrix encephalarti* (HUEST 24.0145). a Specimen. b, c Colonies on dead branch of *Pinus* sp. d–f Setae. g–i conidiogenous cells, j, k Conidia. l, m Culture characteristics. Scale bars: d, e, g–k = 10 μ m, f = 20 μ m.

DISCUSSION

Historical investigations into gymnosperms-associated mycota have concentrated on endophytic and pathogenic taxa, yet saprotrophic fungi associated with gymnosperms have relatively little attention from the scholarly. In Italy (Mediterranean biome), 68 fungal species were cataloged on *Juniperus oxycedrus* (Zedda & Sipman 2001). Concurrently, explorations in the North American temperate zones led to the delineation of *Parksia* and *Camaropycnis*, alongside the taxonomic description of three novelties: *Parksia libocedri*, *Camaropycnis libocedri* and *Tryblidiella macrospora*, all isolated from *Libocedrus* in California (Cash 1945). In the boreal

forests, an extensive survey on the endemic *Chamaecyparis nootkatensis* in Alaska reported a consortium of 77 fungal species, amongst which potential phytopathogens were noted (Hennon 1990). In East Asia, a novel pathogen, *Neofusicoccum cryptomeriae*, was identified on *Cryptomeria japonica* in China, underscoring the emerging threats to gymnosperms health in these ecosystems (Si et al. 2023). Moreover, taxonomic reevaluation resulted in the merging of *Leptosphaerulina japonica* from *Cryptomeria japonica* into *Sydowia japonica*, illustrating the dynamic nature of fungal taxonomy (Hirooka et al. 2013).

In European coniferous forests, investigations into *Sequoiadendron giganteum* revealed the presence of Botryosphaeriaceae members, with the discovery of *Neofusicoccum parvum*, capable of causing canker diseases in redwoods (Haenzi et al. 2021). Furthermore, paleomycological studies in China unveiled three fossilized genera of epiphyllous fungi viz. *Stomipeltites*, *Callimothallus* and *Trichothyrites* from *Cunninghamia*, providing insights into the ancient fungal associations (Maslova et al. 2021). In the Australasian region, the documentation of *Gelineostroma* and the novel species *Apiothyrium tasmanicum* and *Gelineostroma athrotaxi* from *Athrotaxis* in Tasmania expanded the geographic and taxonomic scope of gymnosperms-associated fungi (Swart 1988). These findings collectively emphasize the vast diversity and ecological roles of fungi associated with gymnosperms across global biomes.

In our exploration, we documented several distinctive and scarce mycota, some first identified centuries ago. Herein, we introduce *Triposporium cryptomeriae* sp. nov. into this old genus after 187 years, marking the second new species introduced to this genus in the 21st century (Corda 1837, Crous et al. 2014a). *Triposporium cryptomeriae*, isolated from the dead bark of *Cryptomeria japonica*, is the third member of this genus to be characterized using molecular data. Additionally, *Kiflimonium cryptomeriae* sp. nov., isolated from the needles of *Cryptomeria japonica*, marks the third species within this genus supported by molecular sequences. *Nigrocephalum cycadicola* sp. nov., derived from *Cycas revoluta* twigs, introduces the second species to this genus. The genus *Musillium*, which comprises four species, is expanded by the addition of the use of another word, *Musillium elettariae* sp. nov., from *Cycas revoluta* twigs in China, a first for this region. *Fulvoflamma*, previously known for a single species, *F. eucalypti* (Crous et al. 2006), now includes new geographical records from *Cryptomeria japonica* dead bark in China, supplemented by comprehensive morphological characterization.

The morphological convergence observed among fungal taxa, wherein phylogenetically disparate groups exhibit similar structural features, presents a significant taxonomic challenge. Our study also underscores the complexity of fungal taxonomy, where morphologically similar fungi can reside in distinct taxonomic orders or classes. For example, *Velutinus* (Leotiomyces) shares morphological characteristics with *Pleopunctum* (Dothideomycetes) yet belongs to different classes (Liu et al. 2019, Wu et al. 2024). This phenomenon is shown in the superficial morphological congruence between *Conlarium* and *Pseudoconlarium*, despite their distinct phylogenetic placements within *Conlariaceae* (Conlariales, Diaporthomycetidae) and as Diaporthomycetidae genus *incertae sedis*, respectively (Liu et al. 2012, Hyde et al. 2020a). Similarly, *Monodictys* (Dothideomycetes) and *Neomonodictys* (Sordariomycetes), while morphologically analogous, are phylogenetically divergent and classified into different classes (Day et al. 2006, Hyde et al. 2020a). The newly characterized *Neodictyocheirospora* gen. nov (Leotiomyces) further illustrates this pattern, sharing morphological traits with *Dictyocheirospora* (Dothideomycetes) yet belonging to a different class (Boonmee et al. 2016). Such morphological parallelism can be attributed to convergent evolution, where unrelated lineages independently evolve similar traits in response to an analogous selective pressures (Malagnac et al. 2008). The diverse ecological roles, reproductive strategies and life cycles of fungi contribute to this morphological plasticity, allowing for the adaptation to specific environmental niches (Malagnac et al. 2008, Nagy et al. 2018). Consequently, relying solely on morphological criteria for fungal taxonomy can be misleading, underscoring the necessity of accurately integrating genetic and molecular analyses to elucidate phylogenetic relationships. Applying molecular clocks to estimate divergence times offers a quantitative measure to refine fungal taxonomy, aiding in the hierarchical classification of families,

orders and subclasses (Hongsan et al. 2017a, Liu et al. 2017, Chen et al. 2022, Chen et al. 2023). Combining morphological, genetic, and divergent time, this comprehensive approach is essential for resolving the complexities of fungal taxonomy and understanding the evolutionary dynamics within the fungal kingdom.

Taxonomic delineation within certain fungal taxa presents ongoing challenges, particularly when introducing new species does not rigorously integrate morphological and molecular data (Chethana et al. 2021). Instances where species within genera such as *Conidiocarpus*, *Conlarium* and *Phragmocamarosporium* exhibit pronounced morphological disparities yet possessed closely similar molecular sequences exemplify these issues (Jaczewski 1917, Chomnunti et al. 2011, Zhang et al. 2017, Wanasinghe et al. 2018, Phookamsak et al. 2019, Tennakoon et al. 2021, Wanasinghe et al. 2022b). For *Conidiocarpus* species, taxonomic introductions often rely on morphological comparisons, neglecting comprehensive molecular analysis due to the scarcity of molecular data, with limited LSU/ITS sequences available for definitive classification (Abdollahzadeh et al. 2020, Tennakoon et al. 2021). The challenge of achieving clear taxonomic resolution in *Phragmocamarosporium* is similarly reflected, hindered by the scarcity of comprehensive molecular data (Wijayawardene et al. 2015, Wanasinghe et al. 2018, Wijayawardene et al. 2022b). In the case of *Conlarium*, despite the availability of numerous molecular sequences, three species viz. *C. aquaticum*, *C. thailandense* and the newly identified *C. metasequoiae* sp. nov. are differentiated based on significant morphological traits, particularly conidial morphology, despite their high sequence homology (Zhang et al. 2017, Phookamsak et al. 2019). This scenario raises critical questions regarding the sufficiency and justification of current classification criteria, highlighting the need for a more balanced integration of morphological and molecular evidence (Chethana et al. 2021, Maharachchikumbura et al. 2021, Pem et al. 2021). Genome-wide analyses offer a promising avenue to address these inconsistencies. Our prior research involving a systematic comparative genomic study of the *Colletotrichum* genus has underscored the value of genomic insights in clarifying species classification, offering robust support for taxonomic decisions (Chen et al. 2022). Similarly, genomic investigations within the Sordariomycetes have facilitated a more profound comprehension of taxonomic relationships at higher levels, proposing a novel framework for the taxonomy (Chen et al. 2023). Such fungal genomic studies have significantly enhanced the precision and reliability of fungal taxonomy by elucidating genetic relationships and shedding light on evolutionary divergences, thereby establishing a stronger foundation for fungal classification (Kiss et al. 2019, Ryan & Farley 2020).

Our study delves into saprobic fungi associated with gymnosperms, uncovering both rare and distinctive species. However, the potential for these saprobic fungi to synthesize bioactive compounds remains an open question. Studies on the diversity of bioactive secondary metabolites produced by saprophytic fungi in the order Xylariales indicate their significant potential to produce biologically active compounds, many of which remain underexplored (Helaly et al. 2018). These potential merits further investigation to uncover and exploit these bioactive compounds. Research into fungi associated with gymnosperms, including mycorrhizal and soil fungi, has revealed a significant diversity within these fungal communities. This suggests that there are many saprobic fungal species associated with gymnosperms, some of which are either rare or previously undocumented (Zhou & Dai 2012, Kandhasamy et al. 2015, Bradshaw et al. 2016, Tirza et al. 2022). This suggests a vast unexplored territory within gymnosperms-associated saprobic taxa that could yield significant discoveries. Given these findings, it becomes imperative to extend our research to determine whether any saprobic fungi we have identified in association with gymnosperms possess pathogenic capabilities. Such investigations are crucial for understanding the total ecological impact and potential risks of these fungi, as well as for exploring their possible applications in various fields, including medicine, agriculture and biotechnology.

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