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Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits

Jayasiri SC[1-3], Hyde KD[1,2], Jones EBG[4], McKenzie EHC[5], Jeewon R[6], Phillips AJL[7], Bhat DJ[8], Wanasinghe DN[1,2], Liu JK[9], Lu YZ[2,10], Kang JC[10], Xu J[1], Karunarathna SC[1]

[1]*Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, P.R. China*
[2]*Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[3]*School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[4]*Department of Botany and Microbiology, College of Science, King Saud University, P.O Box 2455 Riyadh 11451, Kingdom of Saudi Arabia*
[5]*Manaaki Whenua Landcare Research, Private Bag 92170, Auckland, New Zealand*
[6]*Department of Health Sciences, Faculty of Science, University of Mauritius, Reduit, Mauritius*
[7]*Universidade de Lisboa, Faculdade de Ciências, Biosystems and Integrative Sciences Institute (BioISI), Campo Grande, 1749-016 Lisbon, Portugal*
[8]*Formerly, Department of Botany, Goa University, Goa, India; No. 128/1-J, Azad Housing Society, Curca, P.O. Goa Velha, 403108, India*
[9]*School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu 611731, P.R. China*
[10]*Engineering and Research Center for Southwest Bio-Pharmaceutical Resources of National Education Ministry of China, Guizhou University, Guiyang, Guizhou Province 550025, P.R. China*

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Abstract

Dothideomycetes is one of the largest and most diverse class of ascomycetes. Its members are reported from many plant parts, but less has been reported from wild seed pods and fruits. Dothideomycetes can be seed-borne or colonize fruits and seed pods when they fall to the ground. We studied the Dothideomycetes found on wild fruits and seed pods, mainly in Thailand (tropical), and to a lesser extent, in China (temperate) and UK (temperate). We describe eight new genera, 50 new species, provide 38 new host records and propose seven new combinations. The new genera are: *Amorocoelophoma* (Amorosiaceae), *Cylindroaseptospora* (Didymosphaeriaceae), *Discotubeufia* (Tubeufiaceae), *Leucaenicola* (Bambusicolaceae), *Neolindgomyces* (Lindgomycetaceae), *Pleohelicoon* (Pleomonodictydaceae), *Quercicola* (Astrosphaeriellaceae) and *Xenoastrosphaeriella* (Astrosphaeriellaceae). The new species are: *Acrocalymma pterocarpi*, *Allophoma siamensis*, *Amorocoelophoma cassiae*, *Anteaglonium gordoniae*, *Atrocalyx krabiensis*, *Austropleospora keteleeriae*, *Caryospora quercus*, *Cladosporium entadae*, *C. magnoliigena*, *Cycasicola leucaenae*, *Cylindroaseptospora leucaenae*, *C. siamensis*, *Delitschia nypae*, *Dictyocheirospora lithocarpi*, *Didymella magnoliae*, *Didymocrea leucaenae*, *Diplodia magnoliensis*, *Discotubeufia browneae*, *Dothiorella lampangensis*, *Ernakulamia krabiensis*, *Gloniopsis fluctiformis*, *G. leucaenae*, *Lasiodiplodia avicenniarum*, *L. swieteniae*, *Leucaenicola*

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Corresponding Author: Karunarathna SC – e-mail – samakaru931@yahoo.com

aseptata, *L. phraeana*, *Neodeightonia planchoniae*, *Neolindgomyces pandanae*, *Neopyrenochaeta cercidis*, *Neoroussoella entadae*, *N. leucaenae*, *Ochroconis ailanthi*, *Periconia delonicis*, *Phaeosphaeria sinensis*, *Pleohelicoon fagi*, *Psedochaetosphaeronema siamensis*, *Pseudoberkleasmium acaciae*, *Pseudocoleophoma bauhiniae*, *Pseudofusicoccum calophylli*, *Pseudohelicomyces quercus*, *Pseudopithomyces entadae*, *Quercicola fusiformis*, *Q. guttulospora*, *Remotididymella bauhiniae*, *Spegazzinia radermacherae*, *Stagonosporopsis pini*, *Stomiopeltis phyllanthi*, *S. sinensis*, *Tubeufia entadae* and *Vaginatispora nypae*. These novelties represent both sexual and asexual morphs of species in 35 families of this class. Taxonomic novelties are morphologically illustrated and phylogeny investigated based on multi-gene sequence data. Our results indicate that the plant genus *Leucaena* harbours higher species diversity.

Keywords – 58 new taxa – *Amorocoelophoma* – ascomycete – bitunicate – *Leucaenicola* – *Neolindgomyces*

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Introduction

About 90% of all food crops grown on earth are propagated through seed (Neergaard 1977). Seeds thus play a vital role in the total biological yield. However, fungal deterioration of crop seed

is a major problem (Christensen 1957, Christensen & Kaufmann 1965). Seeds are colonised by various types of fungi, many of which are plant pathogens (Joshi & Mukerji 1999). There is also some evidence of a relationship between seed size and susceptibility to fungal attack (Moles et al. 2003). Previous studies have led to an international perception that small seeds persist for longer in the soil than large seeds (Thompson 2000). While many fungal diversity studies have investigated various plant substrata, few have focused on fruits and seeds (Somrithipol et al. 2002). Therefore, we herein investigate the fungal diversity on fruits and seeds exposed on the forest floor. Seeds may be infected internally, resulting in the destruction of endosperm and embryo or externally on the seed coat. Fungi exist in seeds as spores and hyphae, and they can survive for a long time on the seed coat and in the internal, diseased seed tissue (Cram & Fraedrich 2010).

Factors affecting colonization of seeds and fruits by fungi

Seeds and fruits are filled with stored foods intended to help the embryo germinate and grow or to attract an animal to eat the fruit and inadvertently carry the seeds away to spread them elsewhere (Waldron 2014). The highly nutritious nature of fruits aids in their dispersal and is a source of nutrients for microbes (Tang et al. 2003). Moisture content is the main factor affecting fungal colonization. Somrithipol et al. (2002) followed the sequential occurrence of fungi on exposed pods of *Delonix regia*, under different conditions, i.e. dry and attached to a tree (termed classical seed fungi) or those on the forest floor. Dry attached pods were colonized by *Aspergillus, Chaetomium, Cladosporium, Penicillium* and *Rhizopus* species, while those on the forest floor were colonized by litter fungi, such as *Dictyochaeta, Helicosporium, Phaeoisaria* and *Sporoschisma* species. The moisture content of the pods exposed on the forest floor increased with time of exposure, which may account for the decline in typical seed fungi and the dominance of litter fungi (Sinha 1992, Somrithipol et al. 2002). Specific fungi, however, can be limited in their range because of climatic conditions and host type. For example, *Fusarium circinatum* (pitch canker fungus) has been associated with southern pine and Monterey pine seeds in California maritime areas. In contrast, *Sirococcus conigenus* and *Caloscypha fulgens* are only associated with conifer seeds in the Northern United States (Sutherland et al. 1987).

Importance and application of seeds and fruit fungi

Seed decay fungi play an important role in recycling of nutrients in the forest ecosystem. Seed fungi are involved in the breakdown of dead tissues and their conversion into simpler organic forms. These materials are the food source for many species, including fungi, at the base of ecosystem (Buczacki 1989, Coleman et al. 2004, Boberg 2009).

Much importance has been attached to seed and seedling health. Infection refers to the penetration of seeds by an organism followed by the establishment of a relationship (i.e., saprobic or parasitic) with the seeds. Some fungi are potentially pathogenic given the right environmental conditions, while others are relatively harmless. Some saprobic fungal species may produce toxic substances that control certain active pathogens (Malone & Muskett 1997). Therefore, studies on fungal genera on seeds are of special importance to studies on seed and seedling health.

Many seed fungi are an important source of bioactive compounds. For example, *Kionochaeta pughii*, isolated from decaying dipterocarp seeds, was shown to produce 'pughiinin A' and 'pycnidione' exhibiting anti-plasmodium activity against *Plasmodium falciparum*. Pycnidione also possesses anti-cancer activity (Pittayakajonwut et al. 2002). Another example is *Menisporopsis theobromae*, which produces 'menisporopsin A' that exhibits activity against *Mycobacterium tuberculosis* (Chinworrungsee et al. 2004).

Seed-borne pathogens of woody trees affect nursery seedlings and reduce seed germination and seedling vigor (Abdul-Baki & Anderson 1973, Rai & Mamatha 2005, Bewley & Black 2012). They also decrease the longevity of stored seeds (Mittal et al. 1990). Several species of fungi that are generally considered as saprobes behave as pathogens under certain circumstances while endophytes can switch to a saprobic lifestyle (Promputtha et al. 2007). This happens following injury to the seed or seed coat and when moisture and temperature are favourable and conducive to

fungal growth (Mittal et al. 1990). An example is *Phoma* spp., which can cause seed rot, and suppress growth of seeds of *Araucaria angustifolia*, *Acacia mangium*, *Eucalyptus camaldulensis*, *Casuarina equisetifolia* and *Ficus bengalensis* under favourable conditions (Procházková et al. 2003). It is difficult to predict damage from seed-borne fungi. The most common fungi are saprobes and these may even be beneficial because they compete with other potentially pathogenic species. However, some are consistently associated with reduced germination rates and vigor (Bloomberg 1969). *Diplodia pinea*, *Lasiodiplodia theobromae*, *Sirococcus conigenus*, and *Fusarium* species (e.g. *F. circinatum* and *F. oxysporum*) are pathogenic and routinely associated with conifer seeds (Sutherland et al. 1987, Cram & Fraedrich 2010). In general, fungi that are present within seeds are more damaging than those that merely contaminate the outer seed coat (Cram & Fraedrich 2010). Common genera, such as *Aspergillus*, *Mucor*, *Penicillium*, *Pestalotiopsis*, *Rhizopus* and *Trichoderma* are associated with various tree seeds (Sutherland et al. 1987). Fungi are ubiquitous in soil and may affect seed survival directly by decomposition or pathogenesis (Crist & Friese 1993).

Ali (1993) worked on fungi associated with forest seeds, but literature on seed mycota and its significance, especially on tropical forest seeds, is still rudimentary.

Seed and fruit fungal diversity in Thailand

Fungi associated with wild seeds and fruits are one of the less well-defined assemblages of Dothideomycetes. Fungi associated with seeds of economically important plant hosts have been widely studied (Giatgong 1980, Sontirat et al. 1994) but there are few records of fungi on seeds of wild hosts (Somrithipol et al. 2004, Udayanga et al. 2013, Jayasiri et al. 2017a, b, 2018a, b, Perera et al. 2018a, b). Pongpanich (1990), Thienhirun (1997), Somrithipol et al. (1998), Réblóva (2000) and Udayanga et al. (2013) reported about 200 species of seed-borne and seed decay fungi from Thailand. Most of them are asexual morph species with fewer sexual morphs (Réblová 2000, Somrithipolet al. 2004). In this study, we isolated and identified Dothideomycetes as both sexual and asexual morphs from several Provinces in Thailand using morphology and DNA sequence data.

Dothideomycetes on wild seeds and fruits

Dothideomycetes comprises a highly diverse range of fungi characterized by bitunicate asci, usually with fissitunicate dehiscence (Kodsueb et al 2007, Jeewon et al 2013, Hyde et al. 2013, McKenzie et al. 2014). Members of Dothideomycetes occur as pathogens, endophytes or epiphytes of living plants and also as saprobes degrading cellulose and other complex carbohydrates in dead or partially digested plant matter in leaf litter or dung (Tang et al 2005, Schoch et al. 2006). Dothideomycetes comprises 33 orders and 175 families and highly diverse on various hosts, and in different ecosystems (Hyde et al. 2013, Wijayawardene et al. 2016, 2017a, b, 2018). Somrithipol et al. (2004) reported 15 seed decay and 30 seed-borne Dothideomycetes species from wild seeds.

Materials and Methods

Sample collection and specimen examination

Seeds and fruits samples were collected from Thailand, China and the United Kingdom (UK) and incubated in moist conditions at room temperature (25°C). Samples were collected from southern and northern parts in Thailand (Figs 1, 2), Guizhou and Yunnan Provinces in China; and Bishops Waltham in the UK.

A morphological investigation was carried out as follows. The fungi mounted in water were examined using a Nikon ECLIPSE 80i compound microscope and images recorded with a Canon 450D digital camera fitted to the microscope. Measurements (≥10 for each) were made with the Tarosoft (R) Image Frame Work program and images used for figures were processed with Adobe Photoshop CS6 Extended version 10.0 (Adobe Systems, The United States). Single ascospore or conidium was isolated on malt extract agar (MEA) following a modified method of Chomnunti et al. (2014).

Type voucher specimens were deposited in the herbarium of Mae Fah Luang University (Herb. MFLU) with isotypes and duplicates in Herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (KUN-HKAS), China. Ex-type cultures were deposited in the Mae Fah Luang University Culture Collection (MFLUCC) with duplicates in Kunming Institute of Botany Culture Collection (KUMCC). Facesoffungi and Index Fungorum numbers were registered (Jayasiri et al. 2015, Index Fungorum 2018). New taxa were established based on the guidelines of Jeewon & Hyde (2016).

Culture studies and asexual morphs

Pure cultures were maintained for studying colony characters and for inducing asexual morph growth (Vijaykrishna et al. 2004, Liu et al 2010). In addition, pine needle or wooden tooth picks were added to water agar medium to stimulate asexual morph sporulation. Pure cultures were grown on MEA at 18°C or 25°C.

DNA extraction, PCR amplification and sequencing

Pure fungal isolates were grown on MEA for 14–30 days at 18/25°C in the dark. Genomic DNA were extracted from the growing mycelia using the Biospin Fungus Genomic DNA Extraction Kit (BioFlux) following the manufacturer's protocol (Hangzhou, P.R. China). For some strains DNA was extracted directly from ascomata using a DNA extraction kit (E.Z.N.A. Forensic DNA kit, D3591- 01, Omega Bio-Tek) following the manufacturer's instructions and Zeng et al. (2018). DNA amplifications were performed by polymerase chain reaction (PCR). Part of the large subunit nuclear rRNA gene (LSU) was amplified with primer pairs LROR and LR5 (Vilgalys & Hester 1990). The small subunit nuclear rRNA gene (SSU) was amplified with primer pairs NS1 and NS4 (White et al. 1990). Primer pairs ITS4 and ITS5 were used to amplify the 5.8S rDNA gene and flanking internal transcribed spacers (ITS) (White et al. 1990). The translation elongation factor 1-alpha gene (*tef1*) was amplified by using primers EF1-983F and EF1-2218R (Rehner 2001) or the primers EF1-728F and EF1-986R (Carbone & Kohn 1999). The RNA polymerase II second largest subunit (*rpb2*) gene was amplified with primers fRPB2 and fRPB2-7cR (Liu et al. 1999, Sung et al. 2007). The beta-tubulin (*tub2*) gene was amplified by using primers Btub2fdG and Btub4fd (Woudenberg et al. 2009). The Glyceraldehyde-3- Phosphate Dehydrogenase (*gapdh*) region was amplified with the primers GDP 1 and GDP 2 (Berbee et al. 1999), actin region with ACT-512F and ACT-783R (Carbone & Kohn 1999) and calmodulin region with CAL-228F and CAL-737R (Damm et al. 2012).

The amplification procedures were carried out in a final volume of 50 µl containing 2 µl DNA, 25 µl PCR mix, 19 µl distilled water and 2 µl of each primer. The PCR reactions for amplification of SSU, ITS, LSU, *tef1*, *rpb2*, *tub2*, *gadph*, actin and calmodulin were performed under standard conditions (Vilgalys & Hester 1990, White et al. 1990, Carbone & Kohn 1999, Liu et al. 1999, Myllys et al. 2002, Rehner 2001, Hong et al. 2005, Woudenberg et al. 2009). Purification and sequencing of PCR products were carried at Shanghai Sangon Biological Engineering Technology and Services Co. (China).

Phylogenetic analysis

The SSU, ITS and LSU and protein coding genes were used for different groups of fungi where necessary. All reference sequences were retrieved from GenBank based on the latest references for each group of fungi. Sequences were aligned with Bioedit version 5.0.6 (Hall 1999) and ClustalX v. 1.83 (Thompson et al. 1997) or with MAFFT v. 6.864b (http://mafft.cbrc.jp/alignment/server/index.html). The alignments were checked visually and improved manually where necessary. Phylogenetic analyses were carried with and MrBayes v. 3.0b4 (Ronquist & Huelsenbeck 2003) for Bayesian analyses (BY). A maximum likelihood analysis (ML) was performed at the CIPRES webportal (Miller et al. 2010) using RAxML v.7.2.8 as part of the "RAxML-HPC2 on TG" tool (Stamatakis 2006) or implemented in raxmlGUIv.0.9b2 (Silvestro & Michalak 2010). Other phylogenetic details are outlined in Jeewon et al (2002, 2003),

Cai et al. (2006) and Hongsanan et al. (2017). Phylogenetic trees were drawn with FigTree v. 1.4 (Rambaut 2014). Maximum likelihood bootstrap support (MLBS) equal or greater than 70% and Bayesian posterior probabilities (BYPP) equal or greater than 0.95 are indicated on the resulting tree topology in each figure. Newly generated sequences were deposited at NCBI GenBank. GenBank accession numbers for sequenced genes are given in the descriptions for materials examined.

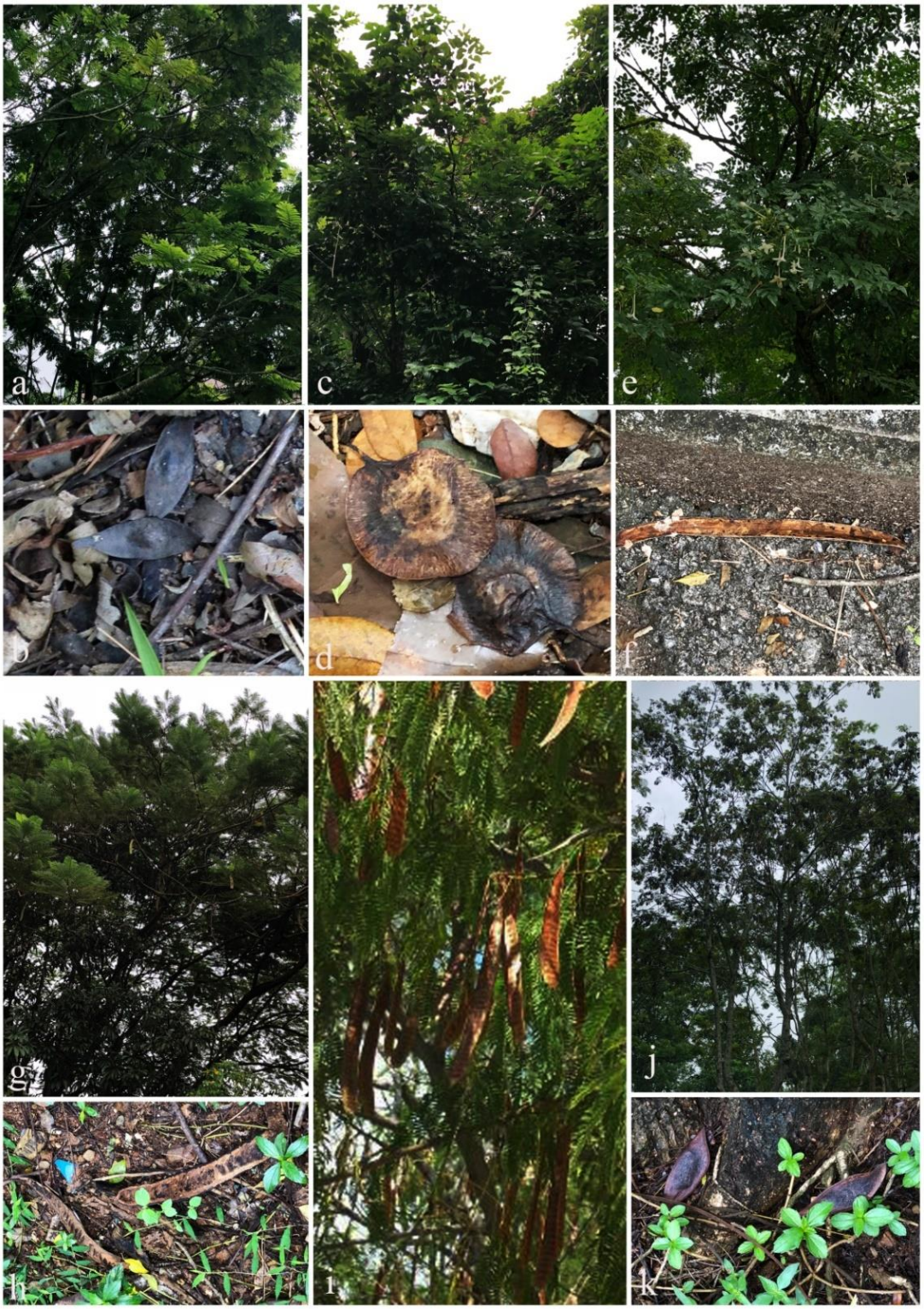


Figure 1 – Common host species in terrestrial environment in Thailand with their fruits or seed pods. a, b *Ailanthus* sp. c, d *Pterocarpus* sp. e, f *Radermachera sinica*. g, h *Delonix regia*. i *Leucaena leucocephala*. j, k *Peltophorum* sp.

Figure 2 – Host and collected fruits from intertidal zone in Thailand. a, d *Avicennia marina*. b, e *Pandanus* sp. c, f *Nypa fruticans*.

Taxonomy

We describe eight new genera, 50 new species, provide 38 new host records and propose seven new combinations. The novel strains were all collected as saprobic taxa. Sixteen species were isolated from decaying seed pods of *Leucaena* sp. and Fabaceae was the family that supported the most diverse mycota, while Fagaceae, Pinaceae and Bignoniaceae from Thailand supported fewer taxa (Fig. 1). We also isolated species from fruits from intertidal zone plant species (Fig. 2) and Dothideomycetes from *Magnolia grandiflora* (Magnoliaceae) in China and *Fagus sylvatica* (Fagaceae) in the UK.

Novelties are morphologically illustrated and phylogenies based on multi-gene sequence data are reported below to accommodate species in their orders, families and genera where appropriate.

Subclass Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker, Mycologia 98 (6): 1048 (2007)

Gloniales Jayasiri & K.D. Hyde, Mycosphere 9 (4): 809 (2018)

Gloniaceae E. Boehm, C.L. Schoch & Spatafora, Mycological Research 113 (4): 468 (2009)

This family comprises three genera, namely *Glonium* (saprobes), *Cenococcum* (ectomycorrhizae) and *Purpurepithecium* (saprobes) (Boehm et al. 2009a, Spatafora et al. 2012, Jayasiri et al. 2017b). In a previous study we introduced the sexual morph of *Purpurepithecium murisporum* from a decaying pine cone as well as the asexual morph from culture (Jayasiri et al. 2017b). In this study, we isolated the asexual morph from the same host at a different locality in Thailand (Fig. 3).

1. *Purpurepithecium murisporum* Jayasiri & K.D. Hyde Cryptogamie Mycologie 38: 246 (2017) Fig. 4

Saprobic on pine cone. Sexual morph: see Jayasiri et al. (2017). Asexual morph: Hyphomycetous. *Colonies* on natural substrate scattered. *Mycelium* immersed, composed of brown, smooth, septate hyphae. *Conidiomata* sporodochial, dark brown to black. *Conidiophores* macronematous, pale brown, smooth. *Conidiogenous cells* holoblastic, integrated, terminal, pale brown, cylindrical, smooth-walled. *Conidia* 20–25 × 20–30 µm ($\bar{x}$ = 23 × 25 µm, n = 20), solitary, acrogenous, cheiroid, pale brown to brown, consisting of 4–5 rows of cells, rows digitate, cylindrical, narrow at the tip, arising from a basal cell, without appendages, with each row composed of 4–5 cells, euseptate, guttulate, slightly constricted at septa.

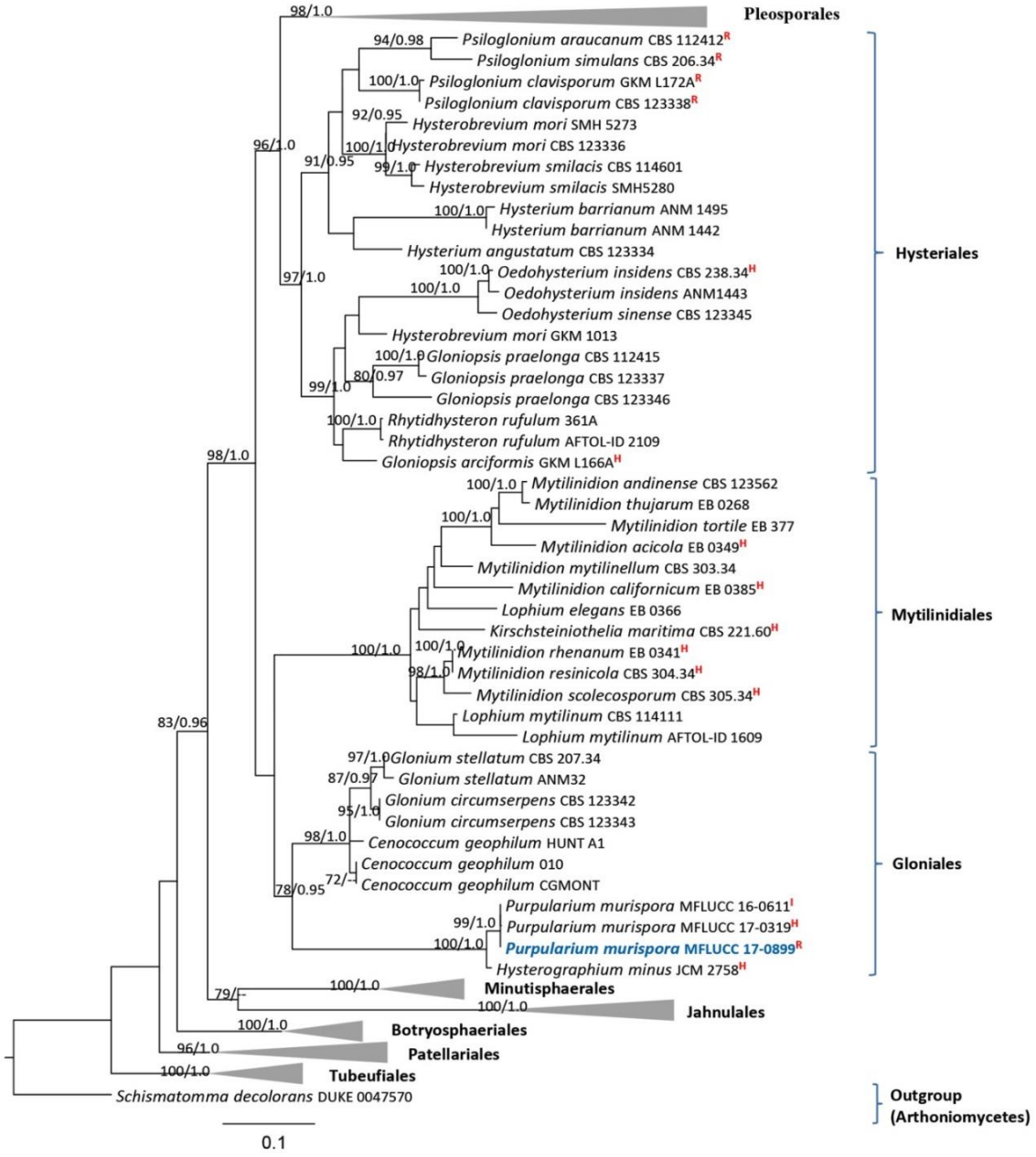


Figure 3 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, *tef1* and *rpb2* partial sequence data for Gloniales and related orders. One hundred and seventeen strains were included in the sequence analysis, which comprised 4271 characters including alignment gaps. *Schismatomma decolorans* (DUKE 0047570) was used as the outgroup taxon. Single gene analyses were carried out and topology of the tree and clade stability were compared. Tree topology of the ML tree was similar to the Bayesian tree. The best scoring RAxML tree with a final likelihood value of -62775.294525 is presented. The matrix had 2524 distinct alignment patterns, with 35.12% of undetermined characters or gaps. Estimated base frequencies

were as follows; A = 0.254015, C = 0.233955, G = 0.273482, T = 0.238548; substitution rates AC = 1.484534, AG = 4.072097, AT = 1.299365, CG = 1.098990, CT = 8.182420, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strain is in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I} and ^{R} respectively.

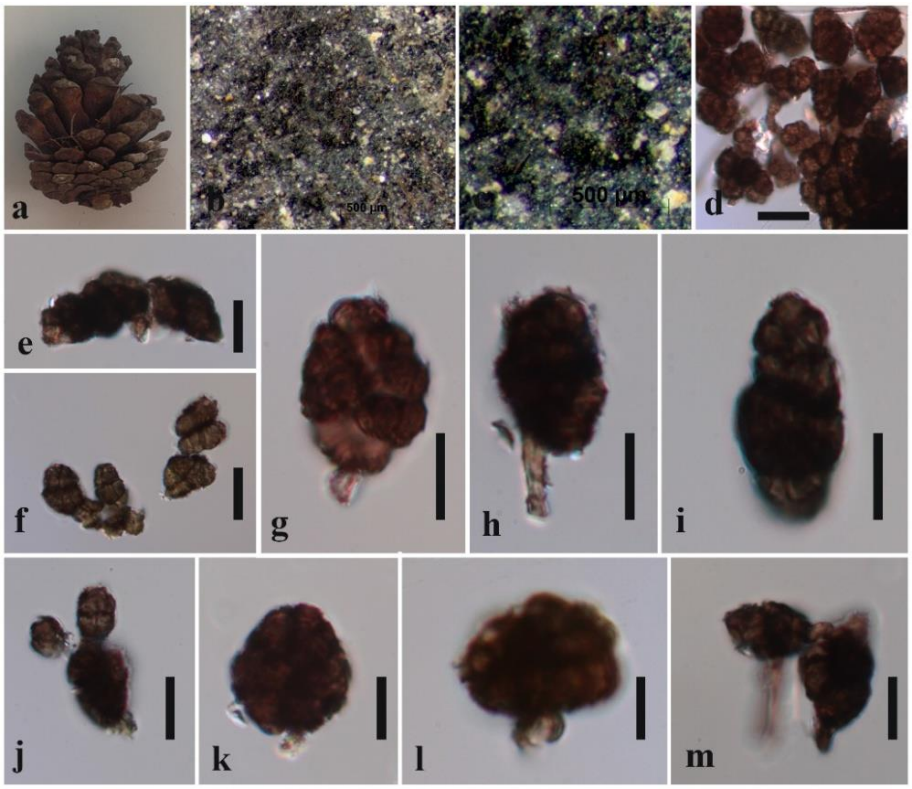


Figure 4 – *Purpurepithecium murisporum* (MFLU 18–2094). a Host seed cone. b, c Conidiomata on host material. d–m Conidia, conidiogenous cells and conidiophores. Scale bars: d–f, j = 20 µm, g–i, k–m = 20 µm.

Culture characters – Conidia germinated on MEA within 18 hr. Colonies reaching 20 mm diam. after 4 weeks at 18ºC, circular, effuse, dense, dark brown, diffuse into media, many layers, outer layer slightly undulate edge, spreading yellow pigment.

Material examined – THAILAND, Huai Namdag, on decaying pine cone, 25 September 2016, S.C. Jayasiri, C 172 (MFLU 18–2094, KUN-HKAS 102411), living culture MFLUCC 17–0899, KUMCC 18–0293.

GenBank numbers – SSU: MK347827, LSU: MK347936, *tef1*: MK360084

Hysteriales Lindau, Die Natürlichen Pflanzenfamilien nebst ihren Gattungen und wichtigeren Arten 1 (1): 265 (1897)

Hysteriaceae Chevall., Flore Générale des Environs de Paris 1: 432 (1826)

Jayasiri et al. (2018) provided an updated backbone tree for this family. We present an updated tree for the genus *Gloniopsis* and introduce two new species, *Gloniopsis fluctiformis* and *Gloniopsis leucaenae* (Fig 5).

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

This genus was introduced by Boehm et al. (2009b) and comprises five species based on morphological and phylogenetic data (Boehm et al. 2009a, b, Hyde et al. 2016). However, the genus is polyphyletic (Boehm et al. 2009a).

2. *Gloniopsis fluctiformis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 6

Index Fungorum number: IF555526; Facesoffungi number: FoF05226

Holotype – MFLU 18–2186

Etymology – Latin 'fluctus', a wave, referring to the wave like hysterothecia.

Saprobic on fruit of unknown plant. Sexual morph: *Ascomata* 500–1000 µm long × 350–370 µm high × 200–230 µm diam. ($\bar{x}$ = 820 × 365 × 220 µm, n = 10), hysterothecia erumpent, with a longitudinal slit, which is wave-like on substrate, scattered. *Peridium* 50–100 µm wide ($\bar{x}$ = 78, n = 20), composed of small pseudoparenchymatous cells, heavily pigmented on the surface, not showing distinct layers, outer surface continuous with plant tissues, inner layer thin and hyaline. *Hamathecium* 1.5–2 µm wide ($\bar{x}$ = 1.8, n = 30), cellular pseudoparaphyses, hyaline, septate, branched above the asci, borne in a gelatinous matrix. *Asci* 53–75 × 13–16 µm ($\bar{x}$ = 68 × 14 µm, n = 20), bitunicate, cylindrical to clavate, stipe, sinuous stipe. *Ascospores* 14–18 × 5–7 µm, ($\bar{x}$ = 16 × 6 µm, n = 30), uni to bi-seriate, pale brown to dark brown, asymmetric, dictyosporous, mostly with 3–4 transverse and 1–3 vertical septa, thin-walled, constricted at septa, asymmetric. Asexual morph: Undetermined.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies on MEA reaching 25–30 mm diam. after 2 weeks at 18°C, with irregular, lobate margin, forming two layers, outer layer off-white, center grey, reverse dark brown in center and pale yellow to off-white at margin.

Material examined – THAILAND, Phrae Province (18˚ 26' 32" N, 100˚ 27' 1" E), on decaying fruit pericarp of Combretaceae sp. 10 January 2018, S.C. Jayasiri, C 419 (MFLU 18–2186, holotype; KUN-HKAS 102434, isotype), ex-type living culture MFLUCC 18–0473, KUMCC 18–0242.

GenBank numbers – SSU: MK347894, ITS: MK347787, LSU: MK348005, *tef1*: MK360055, *rpb2*: MK434865

Notes – *Gloniopsis fluctiformis* is sister to *G. arciformis* in the multi-gene phylogenetic analysis with moderate bootstrap support (75% MLBS/ 0.95 BYPP). These two species are similar in having cylindrical to clavate asci with a sinuous stalk and dictyospores (Fig. 6). However, *G. fluctiformis* differs from *G. arciformis* in having wave-like, erumpent hysterothecia, absence of pigmented epithecium, and straight ascospores with vertical septa in both middle and end cells (Boehm et al. 2009a). ITS, *tef1* and *rpb2* sequence data are not available for *Gloniopsis arciformis* and a comparison of the LSU nucleotides of these two strains reveals 22 (2.5%) nucleotide differences which indicates that these two isolates are two distinct taxa (Jeewon & Hyde 2016).

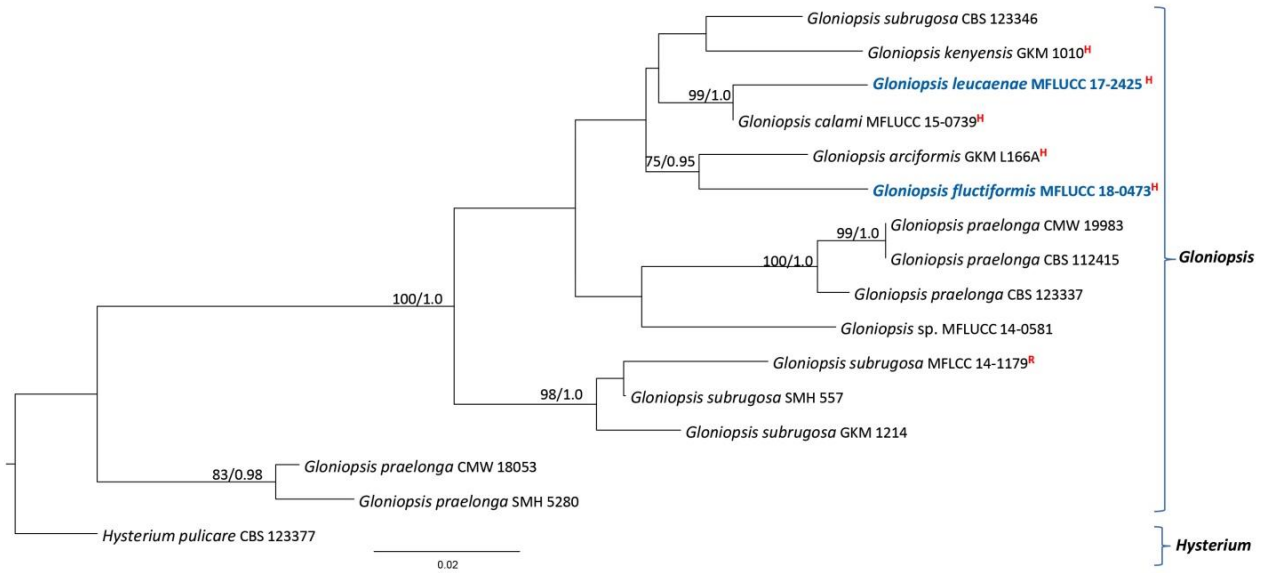


Figure 5 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, *tef1* and *rpb2* partial sequence data for *Gloniopsis* species. Sixteen strains were included in the sequence analysis, which comprised 3880 characters including gaps. *Hysterium pulicare* (CBS 123377) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -9402.630911 is presented. The matrix had 525 distinct alignment patterns, with 41.87% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.253146, C = 0.230090, G = 0.276291, T = 0.240472; substitution rates AC = 1.684242, AG = 3.682892, AT = 1.317889, CG = 0.710989, CT = 8.985446, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strains are in blue. Strains isolated from the holotype indicated in red superscript ^{H}.

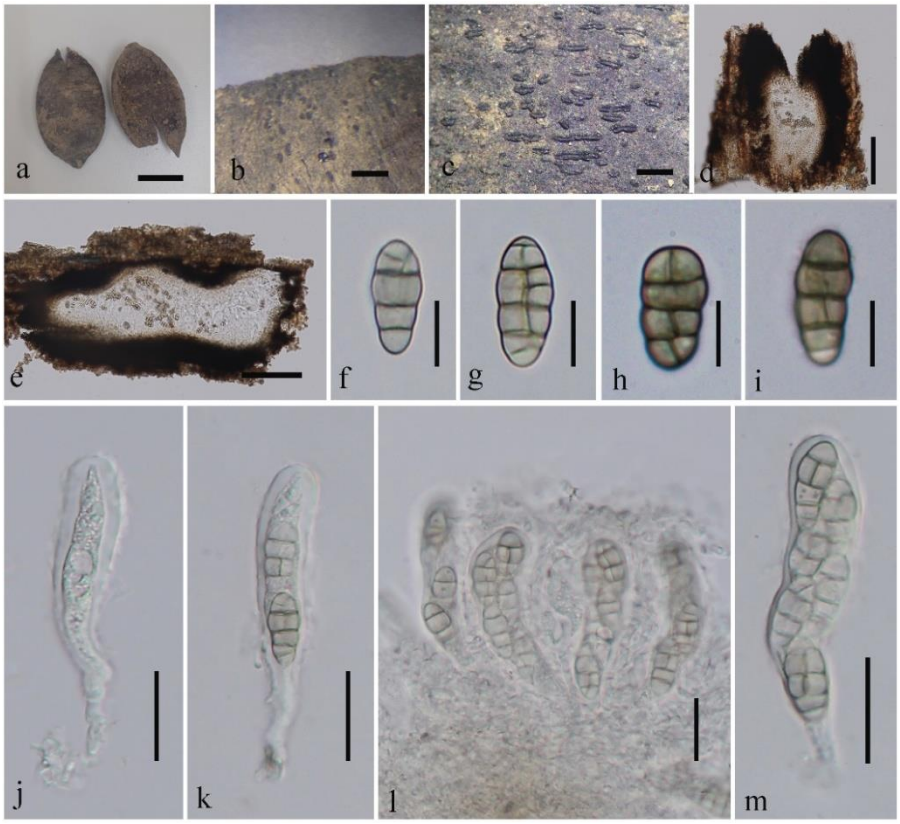


Figure 6 – *Gloniopsis fluctiformis* (MFLU 18–2186, holotype). a Host seeds. b, c Ascomata on substrate. d Cross section of ascoma. e Longitudinal section of ascoma. f–i Ascospores. j–m Asci. Scale bars: a = 1 cm, b = 2 mm, e = 500 µm, d, e = 100 µm, f–i = 10 µm, j–m = 20 µm.

3. *Gloniopsis leucaenae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 7

Index Fungorum number: IF555527; Facesoffungi number: FoF05227

Holotype – MFLU 18–2135

Etymology – Referring to the host on which the fungus was collected, *Leucaena* sp. (Fabaceae)

Saprobic on *Leucaena* sp. pod. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 95–160 µm high × 155–217 µm diam. ($\bar{x}$ = 147 × 182 µm, n = 10), pycnidial, globose to subglobose, on surface of the substrate, olivaceous to brick coloured, later become olivaceous black, solitary or aggregated, lacking setose-like surface outgrowths, with prominent ostiole. *Conidiomata wall* 8–34 µm wide ($\bar{x}$ = 28 µm, n = 20), consisting of brown outer layers to hyaline inner cell layers. *Conidiogenous cells* 6–9 × 1.5–2.5 µm ($\bar{x}$ = 7.5 × 2.2 µm, n = 20), enteroblastic, phialidic, cylindrical to flask-shaped, hyaline, aseptate, smooth-walled. *Conidia*

3–4 × 1.5–2 µm ($\bar{x}$ = 3.5 × 1.8 µm, n = 30), ellipsoidal to allantoid, hyaline, symmetric, with rounded at ends, lacking prominent guttlues.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 25–30 mm diam. after 2 weeks at 18ºC, colonies with irregular growth, lobate margin, forming two layers, outer layer off white, grey at centre, reverse dark brown in center and pale yellow to off white at margin.

Material examined – THAILAND, Chiang Mai Province, Doi Pui, on decaying pod septum of *Leucaena* sp. (Fabaceae), 20 July 2017, S.C. Jayasiri, C 289 (MFLU 18–2135, holotype), ex-type living culture MFLUCC 17–2425, KUMCC 18–0243.

GenBank numbers – SSU: MK347857, ITS: MK347750, LSU: MK347967, *tef1*: MK360056, *rpb2*: MK434888

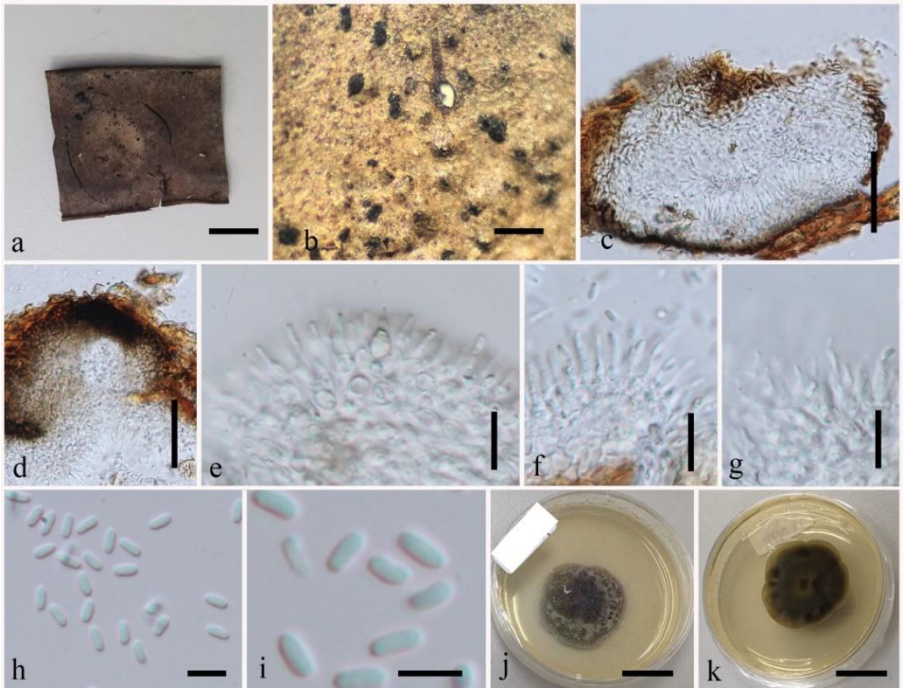


Figure 7 – *Gloniopsis leucaenae* (MFLU 18–2135, holotype). a Part of host seed pod. b Conidiomata on host surface. c Section through conidioma. d Ostiole. e–g Conidiogenous cells. h–i Conidia. j Top view of culture in MEA. k Reverse view of culture. Scale bars: a, j, k = 1 cm, b = 500 µm, c, d = 50 µm, e–g = 10 µm, h, i = 5 µm.

Notes – *Gloniopsis leucaenae*, is a sister species to *G. calami* (MFLUCC 15–0739) with high statistical support (99% MLBS/1.0 BYPP). However, *G. leucaenae* is an asexual morph (Fig. 7) and while *G. calami* is known from only its sexual morph. It is therefore not possible to make a morpholgical comparison of the two species. We have previously observed a similar coelomycetous asexual morph in *G. subrugosa* (MFLCC 14–1179) (Jayasiri et al. 2018). A comparison of the ITS and *tef1* nucleotides of these two strains reveals 14 (2.2%) and 15 (1.6%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Rhytidhysteron Speg., Anales de la Sociedad Científica Argentina 12 (4): 188 (1881)

Thambugala et al. (2016) revised this genus introducing two new species. The genus comprises six species (Spegazzini 1881, Samuels & Müller 1979, Doilom et al. 2017, Thambugala et al. 2016, Vinit et al. 2019). We provide new host records of *Rhytidhysteron rufulum* from decaying fruit of *Swietenia mahagoni* (Fig. 8).

4. *Rhytidhysteron rufulum* (Spreng.) Speg., Anales de la Sociedad Científica Argentina 90(1–6): 177 (1921) [1920] Fig. 9

=*Hysterium rufulum* Spreng., K. svenska Vetensk-Akad. Handl. 46: 50 (1820)

Saprobic on decaying wood and pericarp of *Swietenia mahagoni* fruits. Sexual morph: *Hystherothecia* 1200–1800 µm long × 300–550 high × 750–1000 µm diam. ($\bar{x}$ = 1600 × 450 × 850 µm, n = 10), arising singly or in small groups, sessile, slightly erumpent from the substrate. *Receptacle* cupulate, black, flat or slightly concave, magenta-coloured when fresh, with slightly dentate margin. *Excipulum* 55–65 µm wide ($\bar{x}$ = 61 µm, n = 10), ectal excipulum narrow layered, 3–4 cells deep, thick-walled, with black cells of *textura globulosa* to *textura angularis*; medullary excipulum composed of narrow, long, thin-walled, hyaline to brown cells of *textura porrecta*. *Hamathecium* 1.5–2.2 µm wide ($\bar{x}$ = 1.8 µm, n = 20), numerous, propoloid, exceeding asci in length, apically branched and pigmented, branched apices form a layer on hymenium to develop epithecium. *Asci* 160–200 × 10–17 µm ($\bar{x}$ = 188 × 15 µm, n = 30), 8-spored, long cylindrical, short pedicellate, rounded at apex. *Ascospores* 23–34 × 5–7 µm ($\bar{x}$ = 29.8 × 6.4 µm, n = 40), uniseriate, dark brown, ellipsoid with slightly pointed ends, regularly 3-septate, smooth walled.

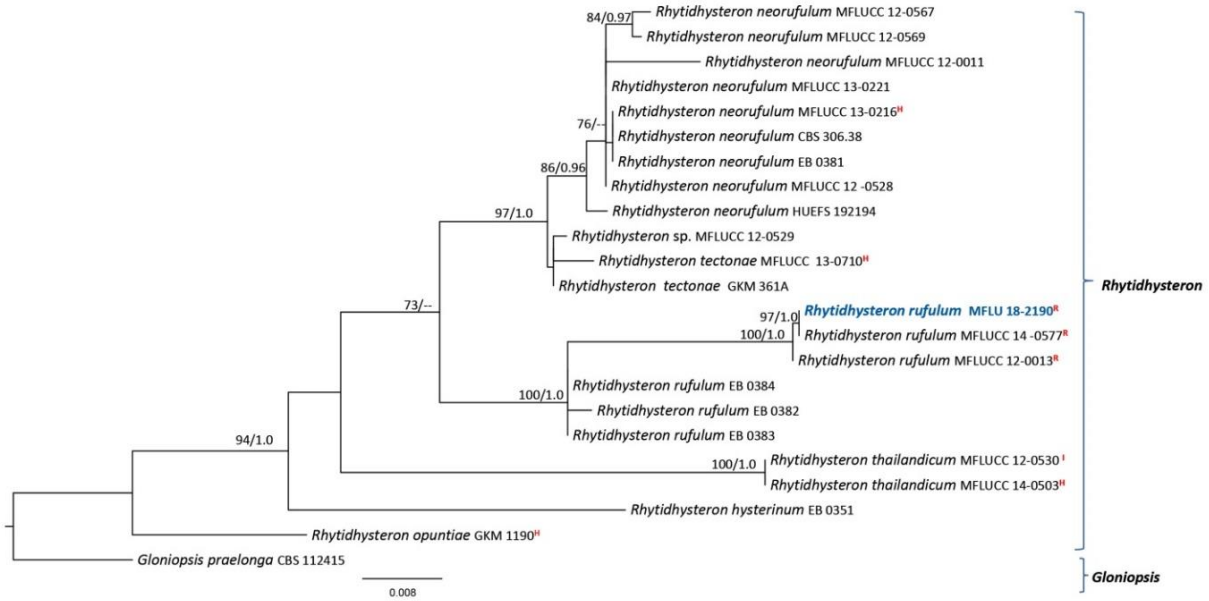


Figure 8 – Phylogram generated from maximum likelihood analysis based on combined LSU, ITS and *tef1* partial sequence data for *Rhytidhysteron* species. Twenty-three strains were included in the sequence analysis, which comprised 2334 characters including alignment gaps. *Gloniopsis praelonga* (CBS 112415) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -5195.407321 is presented. The matrix had 292 distinct alignment patterns, with 36.23% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.235530, C = 0.249898, G = 0.291686, T = 0.222886; substitution rates AC = 2.052756, AG = 2.918220, AT = 1.727617, CG = 0.661795, CT = 9.849620, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strain is in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I}, and ^{R} respectively.

Material examined – THAILAND, Phrae Province (18˚ 26' 32" N, 100˚ 27' 1" E), on decaying fruit pericarp of *Swietenia mahagoni* (Meliaceae) 10 January 2018, S.C. Jayasiri, C 426 (MFLU 18–2190).

GenBank numbers – SSU: MK347897, LSU: MK348008, *tef1*: MK360087

Notes – Our new strain clusters with *Rhytidhysteron rufulum* (MFLUCC 14–0577) with high

statistical support (97% MLBS/1.0 BYPP) and they are morphologically similar in having hystherothecia with receptacle and excipulum, hamathecium apically branched and pigmented, branched apices form a layer on hymenium to develop epithecium. (Thambugala et al. 2016). A comparison of the ITS and *tef1* nucleotides differences of the new strain (MFLU 18–2190) and *Rhytidhysteron rufulum* (MFLUCC 14–0577) reveals no nucleotide differences, which indicates that they are same species (Jeewon & Hyde 2016). There are many records of *Rhytidhysteron rufulum* from different hosts (https://nt.ars-grin.gov/fungaldatabases/). This is a species complex with similar morphology and few base pair differences. This is the first report from *Swietenia mahagoni* (Meliaceae).

Figure 9 – *Rhytidhysteron rufulum* (MFLU 18–2190). a, b Hystherothecia on host seed. c Cross section of hystherothecium. d Peridium. e Paraphyses. f–i Asci. j–m Ascospores. Scale bars: a = 1 cm, b = 2 mm, e = 500 µm, d, e = 100 µm, f–i = 10 µm, j–m = 20 µm.

Pleosporales Luttr. ex M.E. Barr, Prodromus to class Loculoascomycetes: 67 (1987)

This is the largest order in class Dothideomycetes, comprising 75 families and 52 Pleosporales genera *incertae sedis* (Wijayawardene et al. 2017, 2018). Our newly recovered taxa are distributed in 25 families of Pleosporales and one Pleosporlaes *genus incertae sedis*.

Acrocalymmaceae P.W. Crous & T. Trakunyingcharoen, IMA Fungus 5 (2): 404 (2014)

Currently the family comprises the genus, *Acrocalymma*. We present an updated tree for the family and introduce a new species, *Acrocalymma pterocarpi* (Fig. 10).

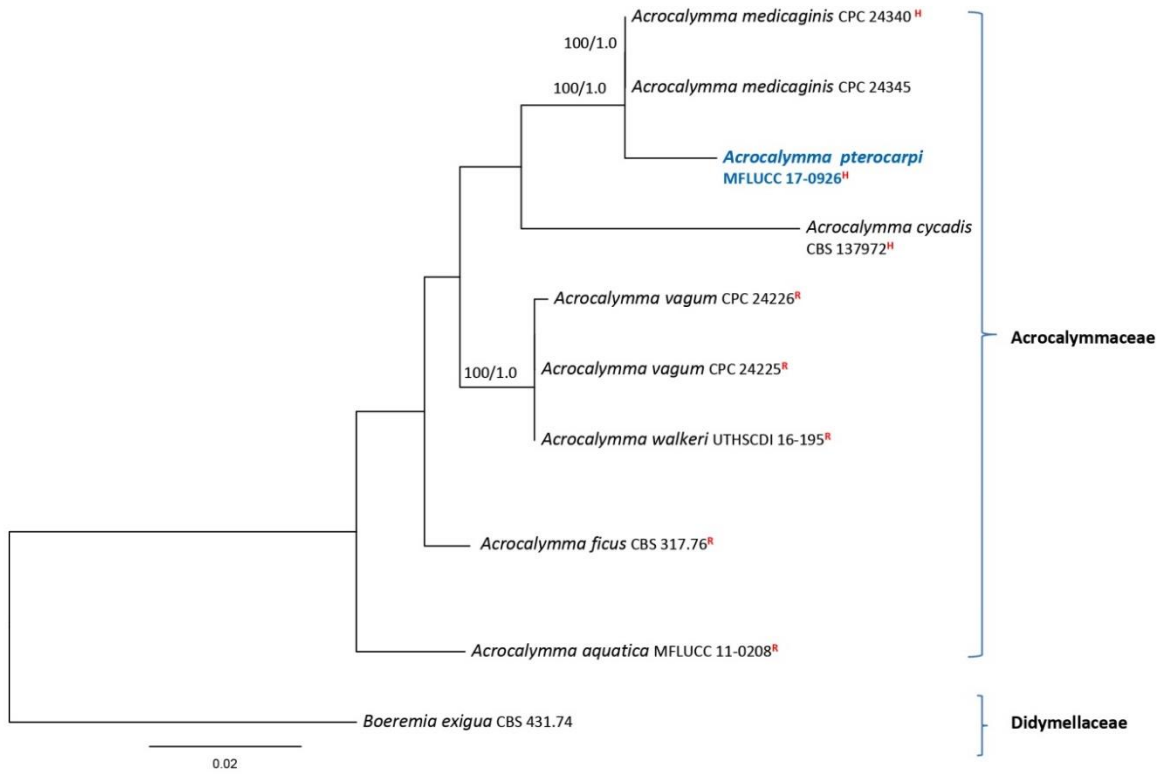


Figure 10 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined ITS and LSU matrix of eleven taxa including related species of the family Acrocalymmaceae. The matrix comprised 1388 characters including alignment gaps. The tree was rooted with *Boeremia exigua* CBS 431.74 (Didymellaceae). The best scoring RAxML tree with a final likelihood value of -3200.844946 is presented. The matrix had 184 distinct alignment patterns, with 14.74% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242740, C = 0.220613, G = 0.274968, T = 0.261679; substitution rates AC = 1.795991, AG = 2.125348, AT = 2.997208, CG = 0.662801, CT = 8.524144, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

Acrocalymma Alcorn & J.A.G. Irwin, Transactions of the British Mycological Society 88 (2): 163 (1987)

This genus was established to accommodate a root pathogen, *Acrocalymma medicaginis* on *Medicago* in Australia (Alcorn & Irwin 1987, Farr et al. 1998). Later five species were introduced to this genus (Zhang et al. 2012, Crous et al. 2014, Trakunyingcharoen et al. 2014) (Table 1). *Acrocalymma medicaginis* has been linked to "*Massarina*" *walkeri* as the sexual morph (Shoemaker et al. 1991). However, Trakunyingcharoen et al. (2014) noticed that they are phylogenetically distinct, and *A. medicaginis* has somewhat smaller conidia than those of *A. walker* (*Massarina walkeri*), which are 11–21 × 3.5–5 µm (Shoemaker et al. 1991).

5. *Acrocalymma pterocarpi* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 11, 12

Index Fungorum number: IF555528; Facesoffungi number: FoF05228

Holotype – MFLU 18–2112

Etymology – Referring to the host genus on which the fungus was collected, *Pterocarpus*

(Fabaceae).

Saprobic on fallen pod of *Pterocarpus indicus*. *Ascomata* 140–150 μm high × 130–145 μm diam. ($\bar{x}$ = 143 × 141 μm, n = 10), scattered, erumpent to nearly superficial, with basal wall remaining immersed in host tissue, globose or subglobose, often laterally flattened, with a flattened base, black, roughened, without ostiole. *Peridium* 15–25 μm wide ($\bar{x}$ = 22 μm, n = 20), composed of heavily pigmented pseudoparenchymatous cells of *textura angularis*. *Hamathecium* 1–2 μm wide ($\bar{x}$ = 1.4 μm, n = 30), dense, broad, very long, septate pseudoparaphyses, anastomosing and branching between and above asci, embedded in gel matrix. *Asci* 65–75 × 7–12 μm ($\bar{x}$ = 70 × 10 μm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, with a short, narrowed, furcate pedicel, and with a small ocular chamber. *Ascospores* 17–21 × 3–5 μm ($\bar{x}$ = 19.5 × 4 μm, n = 30), obliquely biseriate and partially overlapping to triseriate, hyaline, fusiform, 1–3-septate, with narrowly rounded ends, sheath present in immature stage.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies reaching 30 mm diam. after 4 weeks at 18ºC, circular, effuse, dense, white, middle rough, edge smooth surface with entire to slightly undulate edge with yellow pigment lower surface.

Material examined – THAILAND, Chiang Rai Province, Doi Pui (19˚ 49' 31" N, 99˚ 52' 23" E) on fallen pod of *Pterocarpus indicus* (Fabaceae), 2 February 2017, S.C. Jayasiri, C 233 (MFLU 18–2112, holotype), ex-type living culture MFLUCC 17–0926, KUMCC 18–0210.

GenBank numbers – SSU: MK347840, ITS: MK347732, LSU: MK347949, *tef1*: MK360040

Notes – *Acrocalymma walkeri* is the only species with a sexual morph, the other five species being coelomycetous. We isolated the sexual morph of *A. pterocarpi* from a decaying *Pterocarpus indicus* seed pod from Thailand. We failed to obtain an asexual morph from the culture and could only observe chlamydospores (Fig. 12). Our isolate shares similar morphological characters (Fig. 12) of asci and ascospores with *A. walker* but differs in having light greyand warted hairs on the ascomata with a beak and long ostiole (Shoemaker et al. 1991). Phylogenetic analysis of ITS and LSU gene sequences shows that *A. pterocarpi* is a sister clade to *A. medicaginis* with high statistical support (100% MLBS/1.0 BYPP). A comparison of the ITS nucleotides of these two species reveals 12 (2.3%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Table 1 Comparison of habitats and localities of *Acrocalymma* spp.

Species	**Habitat**	**Locality**	**Reference**
Acrocalymma aquatica (coelomycetous)	Submerged wood in a freshwater stream	Thailand	Zhang et al. (2012)
Acrocalymma cycadis (coelomycetous)	Leaf litter of *Cycas calcicola*	Australia	Crous et al. (2014)
Acrocalymma fici (coelomycetous)	*Ficus* sp.	India	Trakunyingcharoen et al. (2014)
Acrocalymma medicaginis (coelomycetous)	*Medicago sativa*	Australia	Alcorn & Irwin (1987)
***Acrocalymma pterocarpi* (sexual morph)**	***Pterocarpus indicus* seed pod**	**Thailand**	**In this study**
Acrocalymma vagum (coelomycetous)	*Amaranthusm* sp., *Citrullus lanatus, Cucumis melo, C. sativus*, *Cucurbita* rootstock, *Vitis vinifera*	Spain, USA	Trakunyingcharoen et al. (2014)
Acrocalymma walker (sexual morph)	*Medicago sativa*	Australia	Trakunyingcharoen et al. (2014)

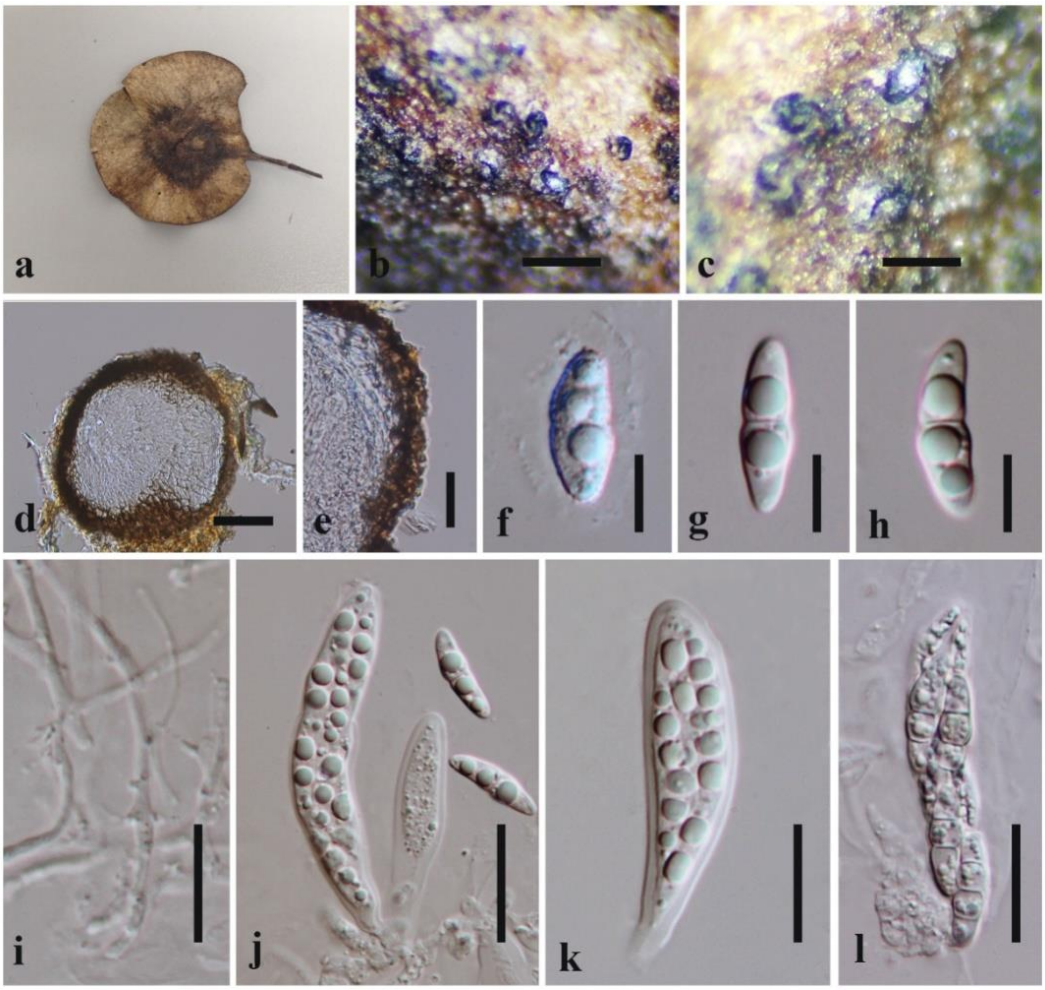


Figure 11 – *Acrocalymma pterocarpi* (MFLU 18–2112, holotype). a *Pterocarpus indicus* pod. b, c View of ascomata on host surface. d Section through ascoma. e Peridium. f–h Ascospores. i Pseudoparaphyses. j–l Asci. Scale bars: b = 500 µm, c = 200 µm, d = 50 µm, e = 20 µm, f–i = 10 µm, j–l = 20 µm.

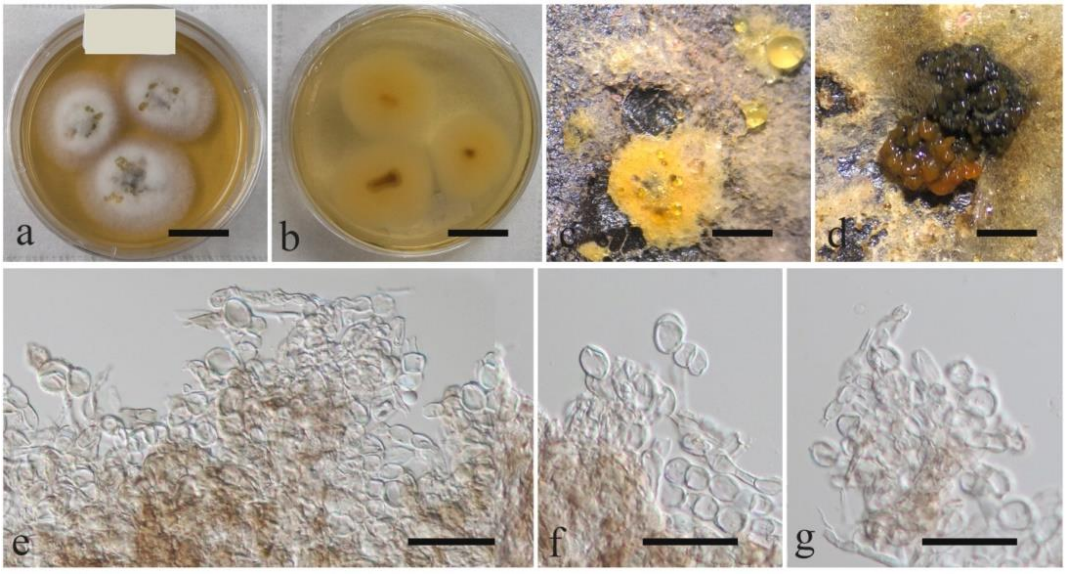


Figure 12 – *Acrocalymma pterocarpi*. (MFLUCC 17–0926, ex-type). a Top view of colony on MEA. b Reverse view of colony. c, d Structures formed in culture. e–g Chlamydospores. Scale bars: a, b = 1 cm, c, d = 100 µm, e–j = 20 µm.

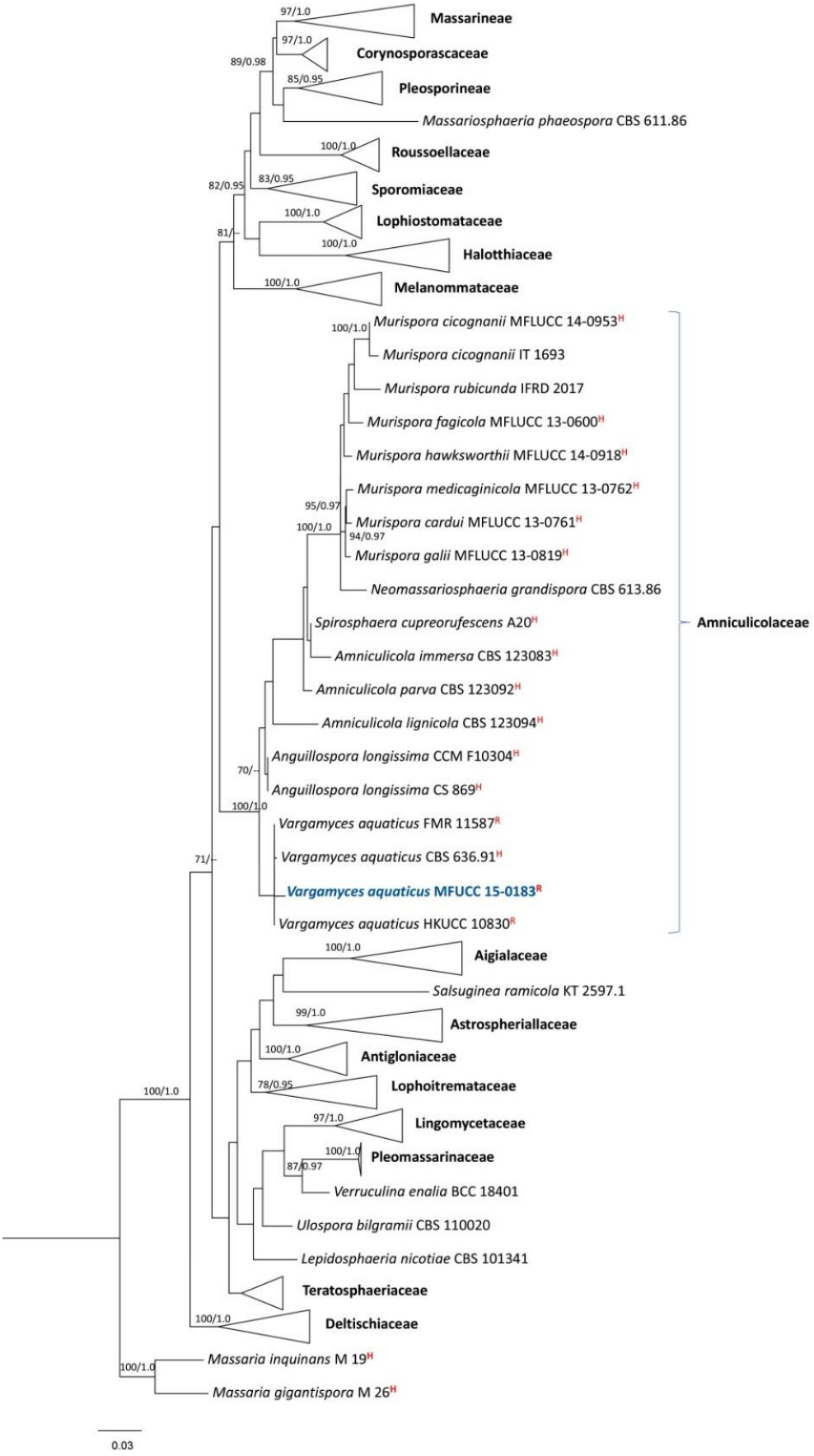


Figure 13 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS and LSU matrix of ninety taxa including related species of the family

Amniculicolaceae and related families. The matrix comprised 3000 characters including alignment gaps. The tree was rooted with *Massaria gigantispora* (M 19) and *Massaria inquinans* (M 26). The best scoring RAxML tree with a final likelihood value of -5459.143248 is presented. The matrix had 1330 distinct alignment patterns, with 24.95% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245853, C = 0.224850, G = 0.286226, T = 0.243071; substitution rates AC = 2.002529, AG = 2.305031, AT = 1.738469, CG = 1.307794, CT = 10.135469, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype, epitype, paratype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

Amniculicolaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde, Studies in Mycology 64: 95 (2009)

Currently the family comprises five genera, *Amniculicola*, *Anguillospora*, *Murispora*, *Neomassariosphaeria* and *Vargamyces* (Zhang et al. 2009a, b, Hyde et al. 2013, Wanasinghe et al. 2015, Hernández-Restrepo et al. 2017). We present an updated tree for the family and introduce a new host record of *Vargamyces aquaticus* from cupule of *Fagus sylvatica* (Fig. 13).

Vargamyces Tóth, Acta Botanica Hungarica 25: 403 (1980)

Vargamyces species form a well-supported subclade in Pleosporales. *Repetophragma ontariense* was previously shown to be related to the Amniculicolaceae, which includes saprobic freshwater fungi (Zhang et al. 2009a, b). *Vargamyces aquaticus* (FMR 11587) was also collected from a freshwater habitat. Révay et al. (2014) suggested that *Vargamyces aquaticus* and *Repetophragma ontariense* could be considered conspecific, but they did not propose any taxonomic changes. Subsequently, Hernández-Restrepo et al. (2017) synonymized *Repetophragma ontariense* as *Vargamyces aquaticus* based on morphological and molecular data.

6. *Vargamyces aquaticus* (Dudka) Tóth., Acta Botanica Hungarica 25: 403 (1980) Fig. 14

Facesoffungi number: FoF05229

Saprobic on decaying wood and cupule of *Fagus sylvatica.* Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Conidiophores* macronematous, mononematous, erect, simple, subhyaline or pale brown, some short conidiophores with few percurrent elongations present, but sympodial conidiogenesis predominant. *Conidia* 90–110 × 12–15 µm ($\bar{x}$ = 102.5 × 13 µm, n = 30), brown, fusiform, apical and basal cells slightly paler, 8–10 septate.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 30–40 mm diam. after 2 weeks at 18ºC, colonies circular, medium dense, flattened, slightly raised near centire, dull, surface smooth, colony from above, grey to dark brown, rough, sponge-like areas in middle; from below: pale brown at the margin, dark brown at the center.

Material examined – UK, Bishops Waltham, Hampshire, on cupule of *Fagus sylvatica* (Fagaceae), 29 September 2014, E.B.G. Jones, GJ 062-A (MFLU 18–2225, new host record), living culture MFUCC 15–0183, KUMCC 18–0303.

GenBank numbers – SSU: MK347927, ITS: MK347818, LSU: MK348038, *rpb2*: MK434849

Notes – Our strain clusters with *Vargamyces aquaticus* (FMR 11587, CBS 636.91 and HKUCC 10830) with low support (Fig. 13). All these *Vargamyces aquaticus* isolates are morphologically similar in having macronematous, mononematous, erect conidiophores, sympodial conidiogenesis and fusiform, brown, apical and basal cells slightly paler, 8–10 septate conidia (Fig. 14). A comparison of the LSU nucleotides of the new strain and existing strains reveals only 3 (0.3 %) nucleotide differences, which indicates that they are not distinct taxa (Jeewon & Hyde 2016). Sequence data for other gene regions are not available. With morphological and multigene phylogenetic support, we report a new host record of *Vargamyces aquaticus* from *Fagus sylvatica* from a terrestrial habitat.

Amorosiaceae Thambug. & K.D. Hyde, Fungal Diversity 74: 252 (2015)

This family was introduced by Thambugala et al. (2015) to accommodate *Amorosia* and *Angustimassarina*. The type genus *Amorosia,* is a hyphomycetous species. Family Amorosiaceae differs from Lophiostomataceae, Teichosporaceae and Sporormiaceae in having hyphomycete asexual morphs and appears to grow within other ascomata (Thambugala et al. 2015). In this study we isolated a coelomycetous fungus and accommodate it in a new genus *Amorocoelophoma* based on multigene phylogenetic analysis of SSU, ITS, LSU and *tef1* gene sequence-data and its distinct morphology (Fig. 15).

7. *Amorocoelophoma* Jayasiri, E.B.G. Jones & K.D. Hyde, gen. nov.

Index Fungorum number: IF555529; Facesoffungi number: FoF05230

Etymology – Referring to the first coelomycetous species was found in family Amorosiaceae.

Saprobic on *Cassia* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, solitary to gregarious, ovoid to globose, brown, covered with hyaline to pale brown, septate, branched hyphal growth as a layer with outer brown layer. *Conidiomata wall* thick, two layers, inner hyaline *textura angularis* 1–2 cell layers, outer brown *textura angularis* brown 1–2 cell layers. *Conidiogenous cells* phialidic, doliform, hyaline, smooth-walled. *Conidia* hyaline, cylindrical, aseptate, smooth- and thin-walled, guttulate concentrated to ends.

Notes – We isolated this coelomycetous species from a decaying pod of *Cassia* sp. This is the first report of a coelomycetous species in family Amorosiaceae. Multigene phylogeny of SSU, ITS, LSU and *tef1* gene sequence data coupled with morphological observations confirm that the new isolate is a novel genus in family Amorosiaceae. The novel species, *Amorocoelophoma cassiae* constitutes an independent lineage close to the type species (*Amorosia littoralis*) of the family, with high statistical support (97% MLBS/1.0 BYPP). *Amorosia* is characterized by a hyphomycetous form.

Type species – ***Amorocoelophoma cassiae*** Jayasiri, E.B.G. Jones & K.D. Hyde

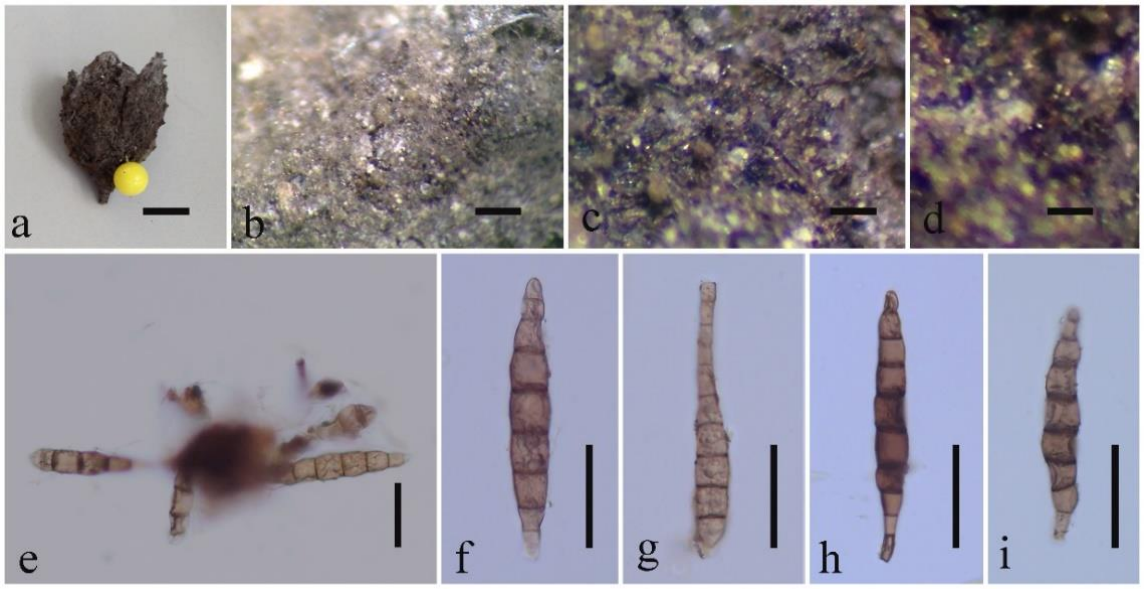


Figure 14 – *Vargamyces aquaticus* (MFLU 15–1398). a Host cupule. b–d Hyphomycetes on host surface. e–i Conidia. Scale bar: a = 1 cm, b = 300 µm, c, d = 200 µm, e–i = 50 µm.

8. *Amorocoelophoma cassiae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 16

Index Fungorum number: IF555530; Facesoffungi number: FoF05231

Holotype – MFLU 18–2121

Etymology – Referring to the host genus on which the fungus was collected, *Cassia* (Fabaceae)

Saprobic on *Cassia* sp. pod. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 130–150 µm high × 110–130 µm diam. ($\bar{x}$ = 140 × 125 µm, n = 10), pycnidial, solitary to gregarious, ovoid to globose, brown, covered with hyaline to pale brown, septate, branched hyphal growth as an outer brown layer. *Conidiomata wall* 17–22 µm wide ($\bar{x}$ = 19 µm, n = 10), two layered, inner hyaline *textura angularis* 1–2 cell thickness, outer layer *textura angularis* brown 1-2 cell thickness. *Conidiogenous cells* 6–8 × 2.3–3.7 µm ($\bar{x}$ = 7.5 × 3.2 µm, n = 30), phialidic, doliform, hyaline, smooth-walled. *Conidia* 9–11 × 2–3 µm ($\bar{x}$ = 10 × 2.5 µm, n = 30), hyaline, aseptate, cylindrical, smooth- and thin-walled, guttulate concentrated at ends.

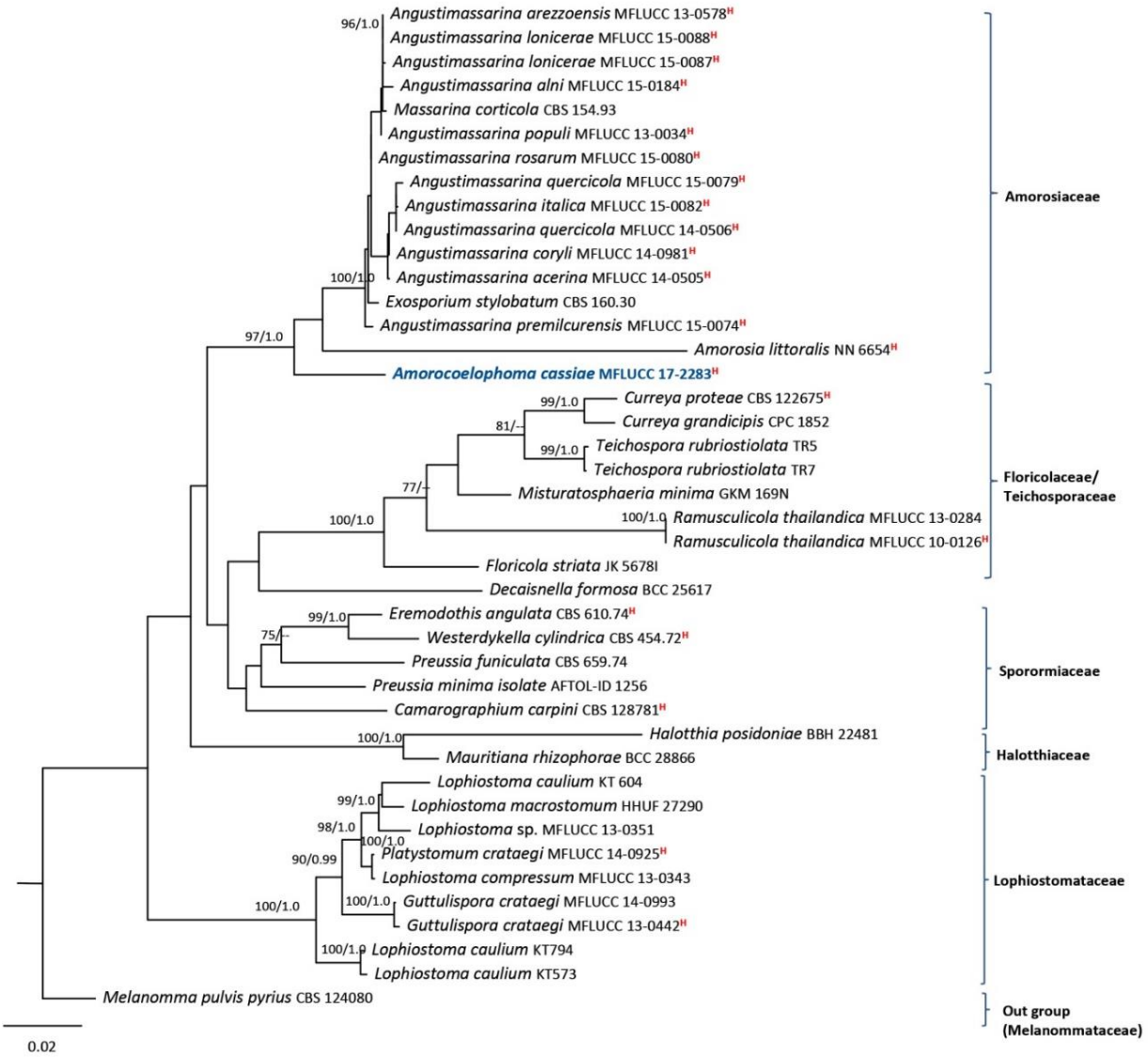


Figure 15 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS, LSU and *tef1* matrix of fourty-two taxa including families in order Pleosporales, which comprised 3416 characters including alignment gaps. The tree was rooted with *Melanomma pulvis pyrius* (CBS 124080). The best scoring RAxML tree with a final likelihood value of -12603.498252 is presented. The matrix had 1054 distinct alignment patterns, with 26.45% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245164, C = 0.246917, G = 0.271282, T = 0.236637; substitution rates AC = 1.203764, AG = 2.379392, AT = 1.581674, CG = 1.158826, CT = 8.203268, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

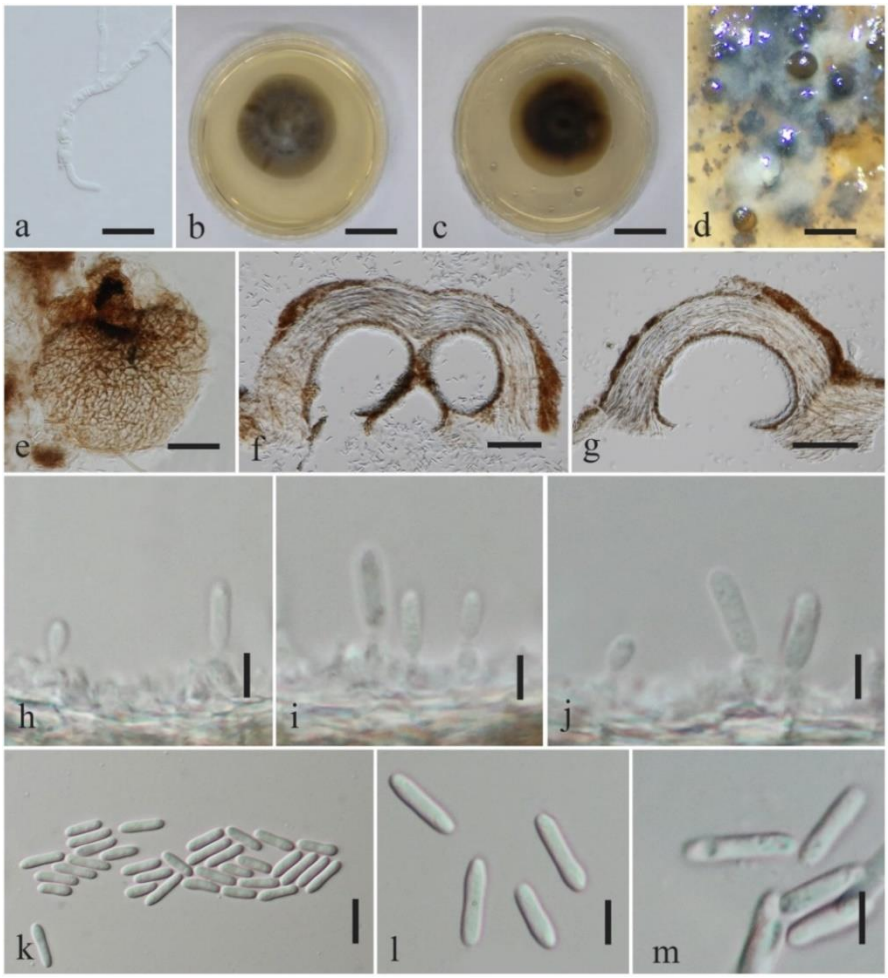


Figure 16 – *Amorocoelophoma cassiae* (MFLUCC 17–2283, ex-type). a Germinated spore. b Top view of the culture. c Reverse view of the culture. d Conidiomata on the culture. e Conidioma wall. f Section through conidiomata. g Section through conidioma. h–j Conidiogenous cells. k–m Conidia. Scale bars: b, c = 1 cm, d = 500 μm, e–h = 100 μm, h–j, l, m = 5 μm, k = 10 μm.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 30–40 mm diam. after 2 weeks at 18 ° C. Colonies circular, medium dense, flattened, slightly raised near centire, dull, surface smooth, from above, pale brown to grey, rough, off white, sponge-like areas in middle; from below pale brown at the margin, dark brown at the center.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on fallen pod of *Cassia* sp. (Fabaceae), 3 July 2017, S.C. Jayasiri C 259 (MFLU 18–2121, holotype; KUN-HKAS 102420, isotype), ex-type living culture MFLUCC 17–2283, KUMCC 18–0213.

GenBank numbers – SSU: MK347847, ITS: MK347739, LSU: MK347956, *tef1*: MK360041, *rpb2*: MK434894

Antigloniaceae K.D. Hyde & A. Mapook, Fungal Diversity 63 (1): 33 (2013)

Two genera are included in this family *Anteaglonium* and *Flammeascoma* (Hyde et al. 2013, Liu et al. 2015). Morphologically they are quite similar to species in *Psiloglonium* (Hysteriaceae), although phylogenetically distinct from Hysteriales and placed in Pleosporales (Hyde et al. 2013). Herein we introduce a new species in *Anteaglonium* and provide an updated tree (Fig. 17).

Anteaglonium Mugambi & Huhndorf, Systematics and Biodiversity 7 (4): 460 (2009)

Anteaglonium includes seven species and our new isolate is well separated from other species in the genus.

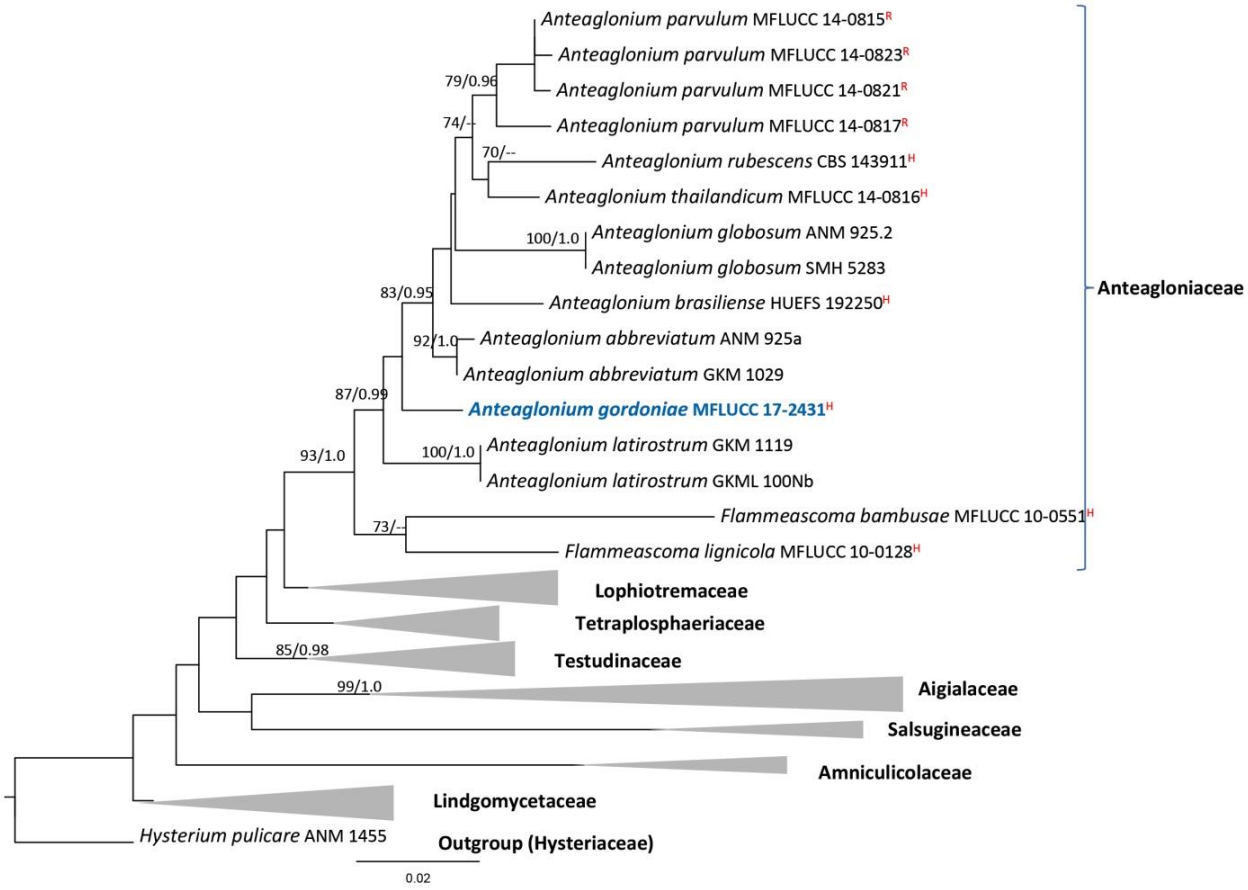


Figure 17 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, LSU and *tef1* matrix of fourty-one taxa including families in order Pleosporales, which comprised 2876 characters including alignment gaps. The tree was rooted with *Hysterium pulicare* (ANM 1455). The best scoring RAxML tree with a final likelihood value of -12603.498252 is presented. The matrix had 790 distinct alignment patterns, with 33.13% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.246630, C = 0.242408, G = 0.280474, T = 0.230488; substitution rates AC = 1.051659, AG = 3.085252, AT = 1.189543, CG = 1.159137, CT = 12.902430, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

9. *Anteaglonium gordoniae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 18

Index Fungorum number: IF555531; Facesoffungi number: FoF05232

Holotype – MFLU 18–2149

Etymology – Referring to the host genus on which the fungus was collected, *Gordonia* (Gordoniaceae)

Saprobic on cupule of *Gordonia* sp. Sexual morph: *Hysterothecia* 400–500 µm long × 250–290 µm high × 260–300 µm diam. ($\bar{x}$ = 448 × 264 × 275 µm; n = 10), superficial, carbonaceous, black, subglobose to oblong, straight, smooth or slightly striate laterally, with a longitudinal slit, sulcus shallow, gregarious, lying at irregular angles, occurring on a black thin crust, tending to darken the substratum, without KOH extractable pigments. *Peridium* 30–50 µm wide ($\bar{x}$ = 43 µm; n = 20), carbonaceous, brittle with age, longitudinally striated at the margins, equally thickened, the inner layer compressed and pallid, the outer layer thickened, comprising pigmented cells of *textura angularis*. *Hamathecium* 1–1.5 µm wide ($\bar{x}$ = 1.3 µm; n = 30), comprising numerous, aseptate pseudoparaphyses, branched above the asci. *Asci* 60–70 × 7–10 µm ($\bar{x}$ = 64 × 8 µm; n = 20), 8-

spored, bitunicate, cylindrical, short pedicellate, obliquely to irregularly uniseriate. *Ascospores* 20–22 × 1.5–3 μm ($\bar{x}$ = 21 × 2.2 μm; n = 30), uni to biseriate, hyaline, fusiform, straight, 1–3 septate, constricted at the middle septum, swollen near to middle
septum, smooth-walled, tapering towards the end, guttulate. Asexual morph: Undetermined.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies on MEA 20 mm diam. after 1 week at 18°C, raised, with lobate margin, finely floccose to woolly aerial mycelium in outer layer. Reverse off white with dark brown.

Material examined – THAILAND, Lampang Province (19˚ 6' 23" N, 99˚ 41' 26" E), on decaying cupule of *Gordonia* sp. (Gordoniaceae), 18 August 2017, S.C. Jayasiri C 332 (MFLU 18–2149, holotype), ex-type culture MFLUCC 17–2431, KUMCC 18–0214.

GenBank numbers – SSU: MK347864, ITS: MK347758, *tef1*: MK360042, *rpb2*: MK434881

Notes – *Anteaglonium gordoniae* shares similar morphology with *Anteaglonium latirostrum* but differs, in having shorter asci (60–70 vs. 115–124 μm) and ascospores (20–22 vs. 22–28 μm) (Fig. 18). *Anteaglonium latirostrum* also has a sheath in immature ascospores and pale brown mature ascospores (Mugambi & Huhndorf 2009). Our phylogeny also supports that *A. gordoniae* as a new species as it constitutes an independent lineage (Fig. 17).

Astrosphaeriellaceae Phookamsak & K.D. Hyde, Fungal Diversity 74: 161 (2015)

Notes – This family consists of four genera: *Astrosphaeriella*, *Astrosphaeriellopsis*, *Pteridiospora*, and *Pithomyces* (Wanasinghe et al. 2018a). We introduce a fifth genus, *Quercicola* (Figs 19, 20). Caryosporaceae was introduced to accommodate *Caryospora* and *Acrocordiopsis* (Ariyawansa et al. 2015) based on sequences available at that time. However, with increased taxon sampling herein, *Caryospora* and *Acrocordiopsis* group with other genera in Astrosphaeriellaceae and further studies are needed to resolve this group. *Acrocordiopsis*, *Astrosphaeriella*, *Astrosphaeriellopsis*, *Caryospora*, *Pithomyces*, *Pteridiospora*, *Quercicola* and *Xenoastrosphaeriella* are also similar due to their carbonaceous ascostromata, and trabeculate pseudoparaphyses (Hawksworth 1981, Hyde & Fröhlich 1998, Liu et al. 2011, Zhang et al. 2012b).

Acrocordiopsis, with the type *Acrocordiopsis patilii* is a marine taxon. *Caryospora aquatica* and the putative strain of *C. minima* are from freshwater. We identified another new species in *Caryospora quercus* from wild fruit in a terrestrial habitat. Therefore, *Caryospora* species are both freshwater and terrestrial.

Zopfia rhizophila also clusters with genera in Astrosphaeriellaceae and requires further studies to resolve its taxonomic placement.

10. *Quercicola* Jayasiri, EBG Jones & K.D. Hyde, gen. nov.

Index fungorum number: IF555532; Facesoffungi number: FoF05233

Etymology – Referring to the host genus on which the fungus was collected, *Quercus* (Fagaceae).

Saprobic on *Quercus* sp. Sexual morph: *Ascomata* gregarious, semi-immersed beneath host epidermis, visible as numerous, raised, dome-shaped areas on the host surface, hemispherical, flattened or wedge-shaped at the base, uni-loculate, dark brown, carbonaceous, glabrous with rough walls, ostiolate. *Ostioles* central, apapillate, with carbonaceous, and thin, slit-like opening. *Peridium* of unequal thickness, poorly developed at the base, thick at sides towards the apex, composed of several layers of dark brown to black, pseudoparenchymatous cells, with host cells plus fungal tissue, arranged in *textura angularis* to *textura prismatica*. *Hamathecium* composed of dense, filiform, trabeculate pseudoparaphyses, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, cylindric-clavate, or obclavate, with short furcate to truncate pedicel, apically rounded, with a truncate ocular chamber. *Ascospores* overlapping, 1–3-seriate at the base, uni-seriate at the apex, hyaline, fusiform with acute ends, 1–5-septate, constricted at the medium septum, upper cell wider than lower cell, guttulate, surrounded by thick asymmetric wall. Asexual morph: Undetermined.

Notes – The two new *Quercicola* species constitute an independent clade close to

Caryospora. These two species share similar morphological characters with other genera in this family in having carbonaceous ascostromata, and trabeculate pseudoparaphyses (Zhang et al. 2012b, Phookamsak et al. 2015, Wanasinghe et al. 2018a). However, *Quercicola* differs from the other genera in having hyaline fusiform ascospores. Therefore, we introduce a new genus, *Quercicola.*

Type species – *Quercicola fusiformis* Jayasiri, EBG Jones & K.D. Hyde

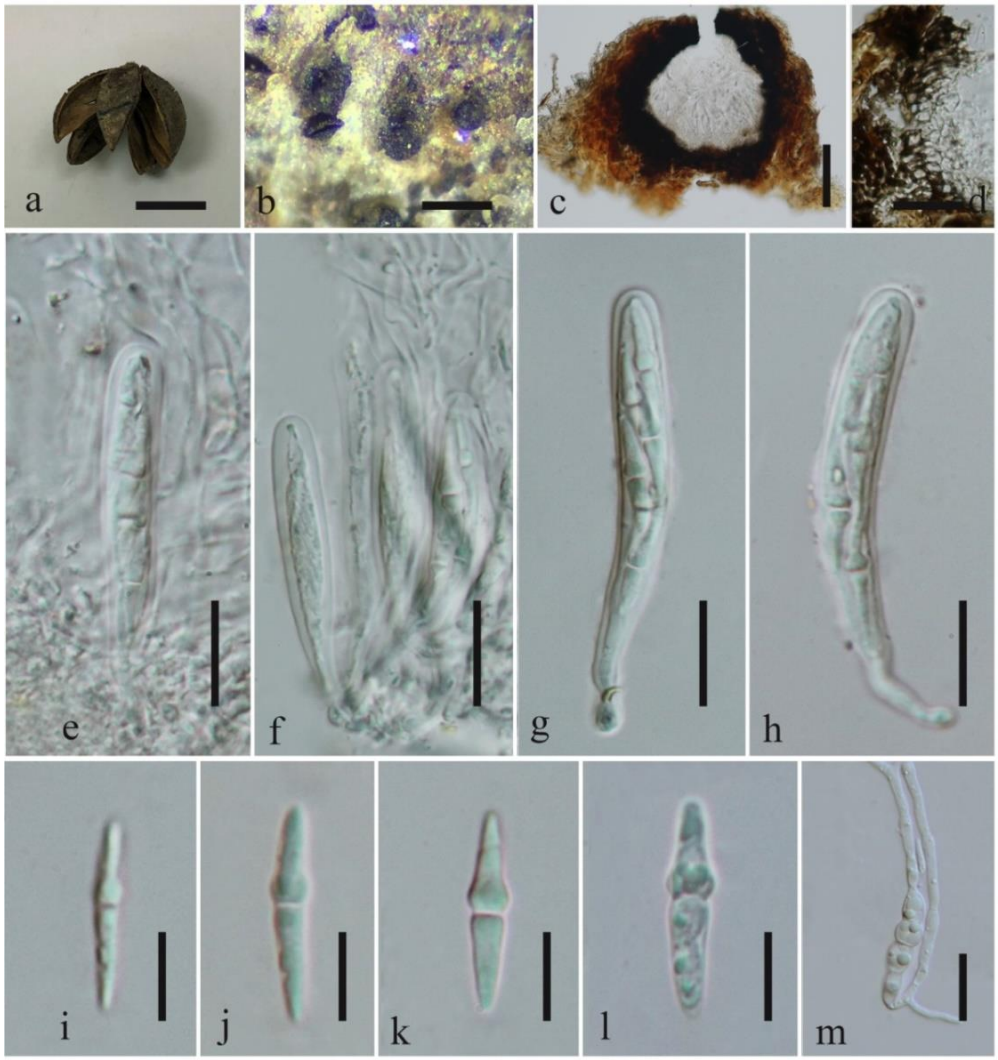


Figure 18 – *Anteaglonium gordoniae* (MFLU 18–2149, holotype). a The host of *Gordonia* sp. fruit. b Hysterothecia on substrate. c Section through hysterothecium. e, f Asci with pseudoparaphyses. g, h Ascus. i–l Ascospores. m Germinated spore. Scale bar: a, b = 1 cm, b = 500 µm, c, d = 100 µm, e = 30 µm, f, h–k = 10 µm, g = 20 µm.

11. *Quercicola fusiformis* Jayasiri, EBG Jones & K.D. Hyde, sp. nov. Fig. 21

Index fungorum number: IF555533; Facesoffungi number: FoF05234

Holotype – MFLU 18–2191

Etymology – Referring to the fusiform shaped ascospores of the identified fungus.

Saprobic on *Quercus* sp. fruit. Sexual morph: *Ascomata* 300–350 µm high × 340–390 µm diam. ($\bar{x}$ = 330 × 360 µm; n = 5), dark brown, gregarious, surface on host epidermis, visible as numerous, raised, dome-shaped areas on the host surface, hemispherical, narrow at the base, uni-loculate, glabrous with rough walls, carbonaceous, ostiolate. *Ostiole* central, apapillate, thin and narrow. *Peridium* 43–68 µm wide ($\bar{x}$ = 56 µm; n = 20), unequal thickness, carbonaceous, poorly developed at the base, thick at sides towards the apex, composed of several layers of dark brown to

black, pseudoparenchymatous cells, base with host cells plus fungal tissue, arranged in a *textura angularis* to *textura prismatica*. *Hamathecium* 0.8–1.5 µm wide ($\bar{x}$ = 1.2 µm; n = 20), composed of dense, filiform, trabeculate pseudoparaphyses, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* 100–130 × 10–13 µm ($\bar{x}$ = 120 × 11 µm; n = 20), 8-spored, bitunicate, cylindric-clavate, or obclavate, with short furcate to truncate pedicel, apically rounded, with a truncate ocular chamber. *Ascospores* 22–27 × 5–7 µm ($\bar{x}$ = 24 × 6 µm; n = 30), overlapping, 1–3-seriate at the base, uni-seriate at the apex, hyaline, fusiform with acute ends, 1–5 septate, constricted at the medium septum, upper cell wider than lower cell, guttulate, surrounded by thick, rough wall. Asexual morph: Undetermined.

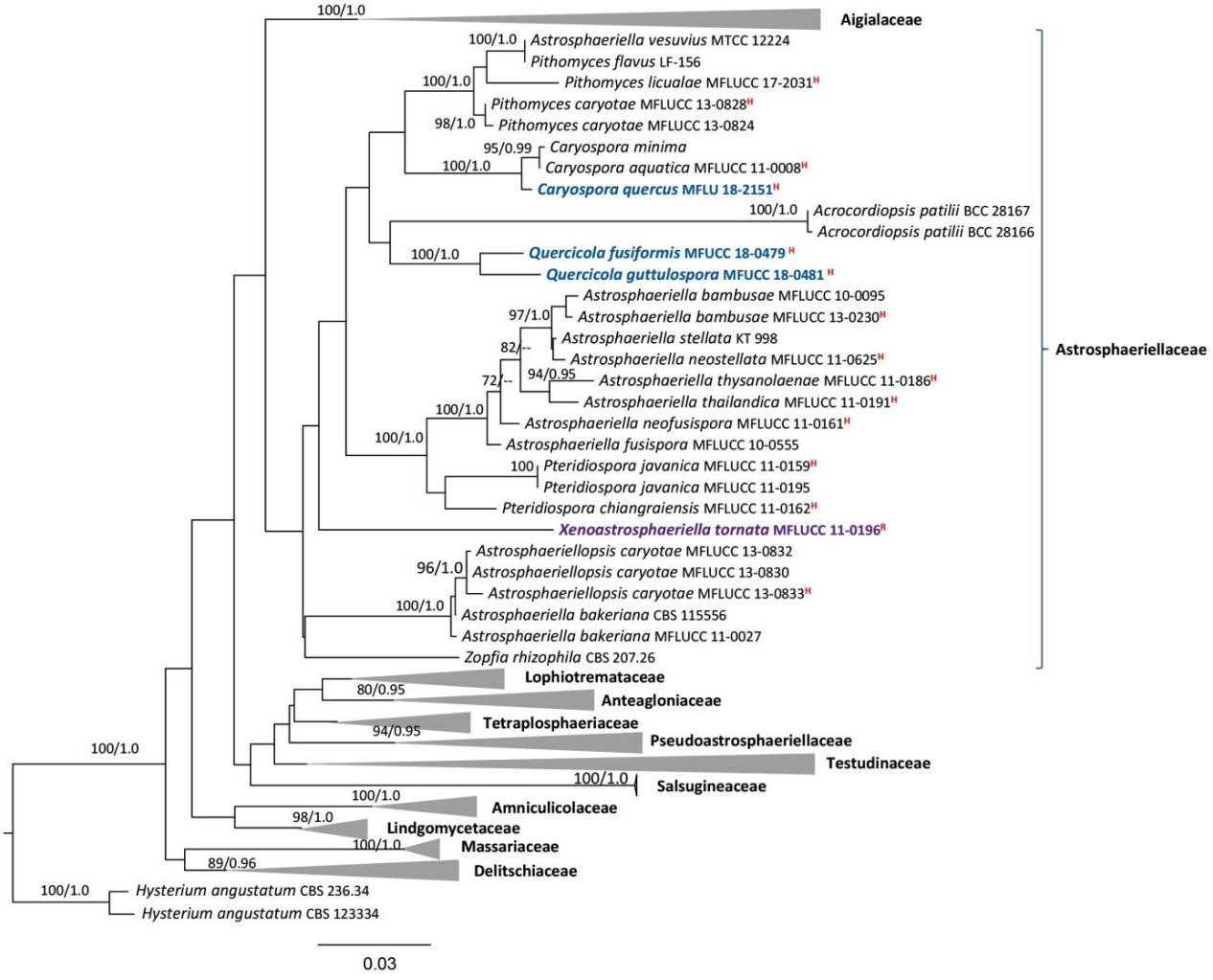


Figure 19 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, LSU and *tef1* matrix of ninety-eight taxa including families in order Pleosporales, which comprised 2853 characters including alignment gaps. The tree was rooted with *Hysterium angustatum* (CBS 236.34/CBS 123334). The best scoring RAxML tree with a final likelihood value of -23760.928529 is presented. The matrix had 1237 distinct alignment patterns, with 21.85% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245539, C = 0.243122, G = 0.282056, T = 0.229283; substitution rates AC = 0.987487, AG = 3.393598, AT = 1.101006, CG = 1.234618, CT = 9.918774, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue and the new combination is in purple. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

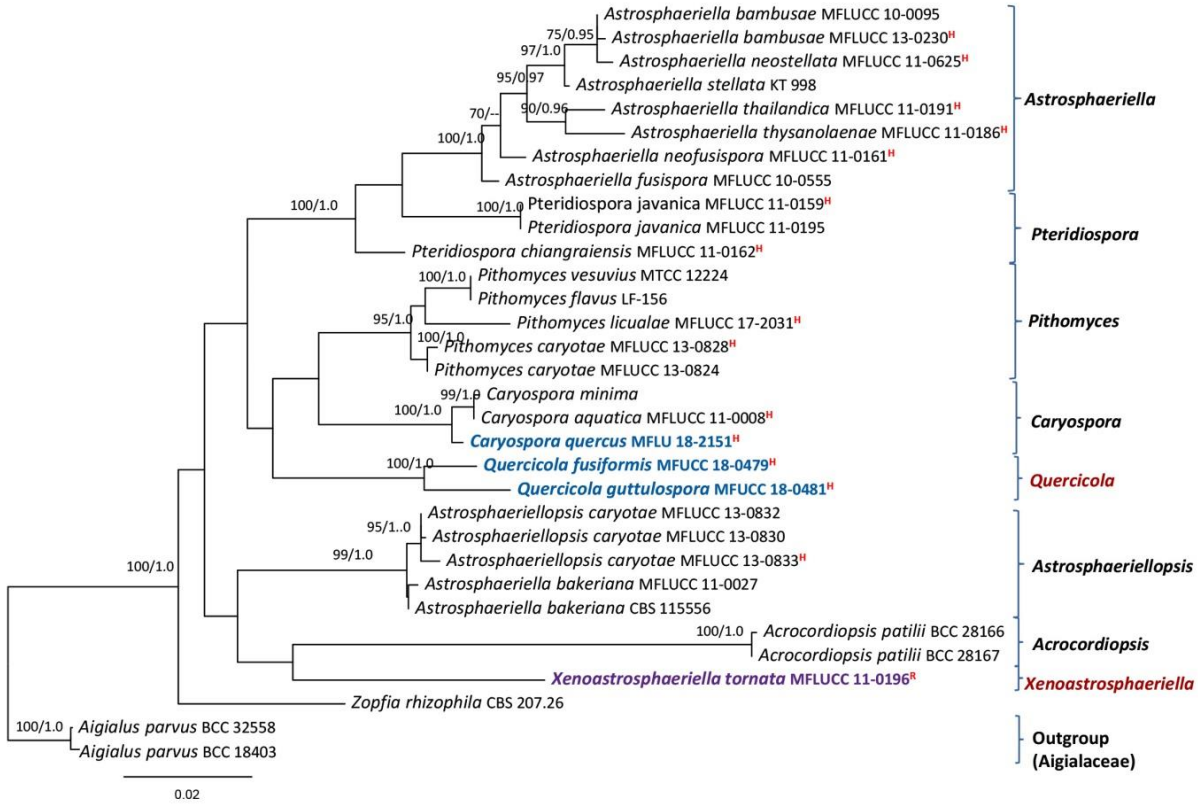


Figure 20 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, LSU and *tef1* matrix of thirty-one taxa including speces belong to Astrosphaeriellaceae, which comprised 2772 characters including alignment gaps. The tree was rooted with *Aigialus parvus* (BCC 32558/BCC 18403). The best scoring RAxML tree with a final likelihood value of -8699.864067 is presented. The matrix had 546 distinct alignment patterns, with 25.55% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245381, C = 0.241016, G = 0.284595, T = 0.229008; substitution rates AC = 1.369230, AG = 3.813023, AT = 0.930144, CG = 1.503050, CT = 15.300231, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue and the new combination is in purple. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies on MEA reaching 30–40 mm diam. after 2 weeks at 18 ° C. Colonies circular, medium dense, slightly raised in middle, dull, bluish grey, surface slightly smoth with flattened margin, reverse dark brown.

Material examined – THAILAND, Chiang Rai Province, Khun Korn waterfall (19˚ 52' 5" N, 99˚ 38' 5" E), on decaying fruit pericarp of *Quercus* sp. (Fagaceae), 24 January 2018, S.C. Jayasiri, C 437 (MFLU 18–2191, holotype; KUN-HKAS 102436, isotype), ex-type living culture MFUCC 18–0479, KUMCC 18–0294.

GenBank numbers – SSU: MK347898, ITS: MK347790, LSU: MK348009, *tef1*: MK360085, *rpb2*: MK434864

12. *Quercicola guttulospora* Jayasiri, EBG Jones & K.D. Hyde, sp. nov. Fig. 22

Index fungorum number: IF555534; Facesoffungi number: FoF05235

Holotype – MFLU 18–2192

Etymology – Referring to the prominent guttule in ascospores of the identified fungus.

Saprobic on fruit of Fagaceae plant. Sexual morph: *Ascomata* 275–300 µm high × 325–352

μm diam. ($\bar{x}$ = 290 × 340 μm; n = 10), gregarious, visible as numerous, raised, dome-shaped areas on the host surface, hemispherical, narrow at the base, uni-loculate, dark brown, glabrous with rough walls, coriaceous, ostiolate. *Ostiole* central, apapillate, carbonaceous, not prominent. *Peridium* 50–76 μm wide ($\bar{x}$ = 66 μm; n = 20), unequal thickness, carbonaceous, poorly developed at the base, thick at sides towards the apex, composed of several layers of dark brown to black, pseudoparenchymatous cells, base with host cells plus fungal tissue, arranged in a *textura angularis* to *textura prismatica*. *Hamathecium* 0.7–1.6 μm wide ($\bar{x}$ = 1.4 μm; n = 20), composed of dense, filiform, trabeculate pseudoparaphyses, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* 135–160 × 8–9 μm ($\bar{x}$ = 148 × 8.5 μm; n = 20), 8-spored, bitunicate, cylindric-clavate, or obclavate, with short furcate to truncate pedicel, apically rounded, with a truncate ocular chamber. *Ascospores* 23–29 × 6–7 μm ($\bar{x}$ = 24 × 6.5 μm; n = 30), uni to biseriate, hyaline, fusiform, 1-septate, thin wall with rounded end, constricted at the septum, assymetric two cells, guttulate; 2–4 big guttlues. Asexual morph: Undetermined.

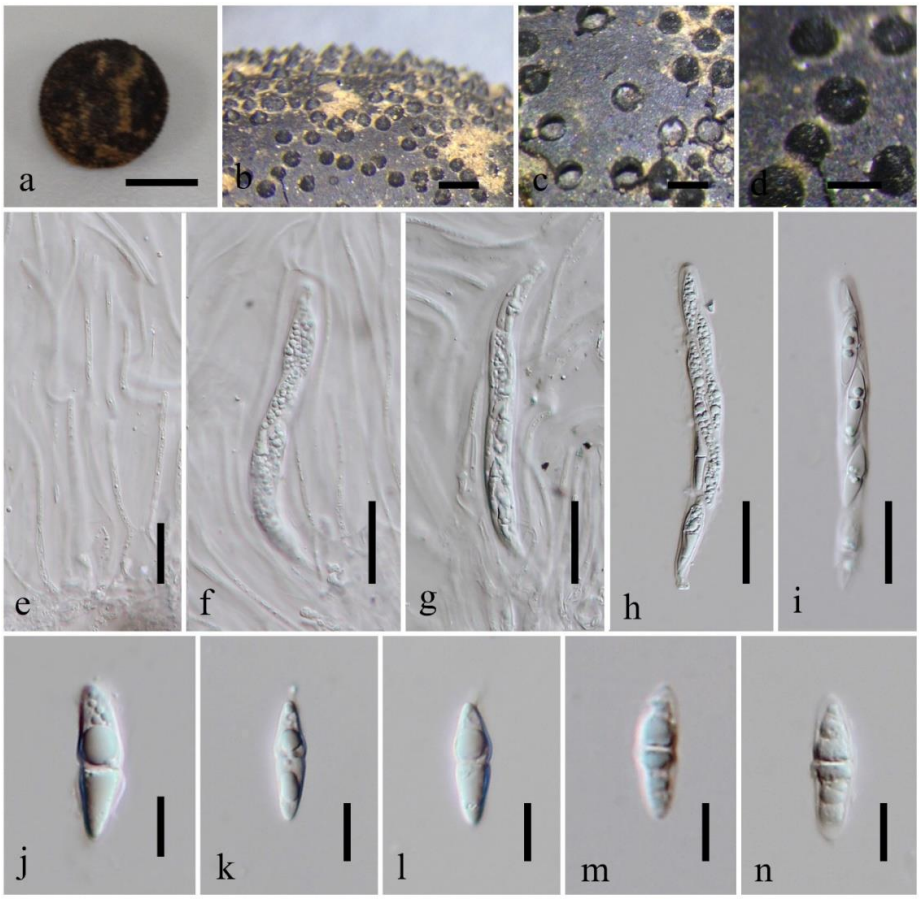


Figure 21 – *Quercicola fusiformis* (MFLU 18–2191, holotype). a Fruit of *Lithocarpus* sp. b, d Ascoma on substrate. c Cross section of ascomata. e Pseudoparaphyses. f–i Asci. j–n Ascospores. Scale bar: a, b = 1 cm, b = 500 μm, c, d = 100 μm, e = 30 μm, f, h–k = 10 μm, g = 20 μm.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies on MEA reaching 3–4 cm diam. after 4 weeks at 25 ° C. Colonies circular, flattened, surface with hyphal growing, with irregular edge, pale brown to grey, radially arranged, middle dark brown, reverse pale brown to grey outer layer and center dark brown to black.

Material examined – Thailand, Chiang Rai Province, Huai-Chomphu, on decaying fruit pericarp of Fagaceae sp., 24 January 2018, S.C. Jayasiri, C 439 (MFLU 18–2192, holotype; KUN-HKAS 102437, isotype), ex-type living culture MFUCC 18–0481, KUMCC 18–0295

GenBank numbers – SSU: MK347899, ITS: MK347791, LSU: MK348010, *tef1*: MK360086

Notes – *Quercicola guttulospora* is sister to *Q. fusiformis* with high statistical support (100% MLBS/1.0 BYPP). These two species share similar morphology in having dome-shaped, carbonaceous ascomata with poorly developed base, cylindric-clavate, or obclavate asci and hyaline, fusiform ascospores (Fig. 21, 22). However, *Q. guttulospora* has longer asci (up to 160 µm vs. up to 130 µm), 1-septate, round end ascospores with prominent guttule even in mature stage. *Quercicola fusiformis* is characterized by 1–5-septate ascospores with acute ends and a thick wall. Culture characters are different in these two species. A comparison of the *tef1* nucleotides of these two strains reveals 41 (4.7%) nucleotide differences and significant morphological differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

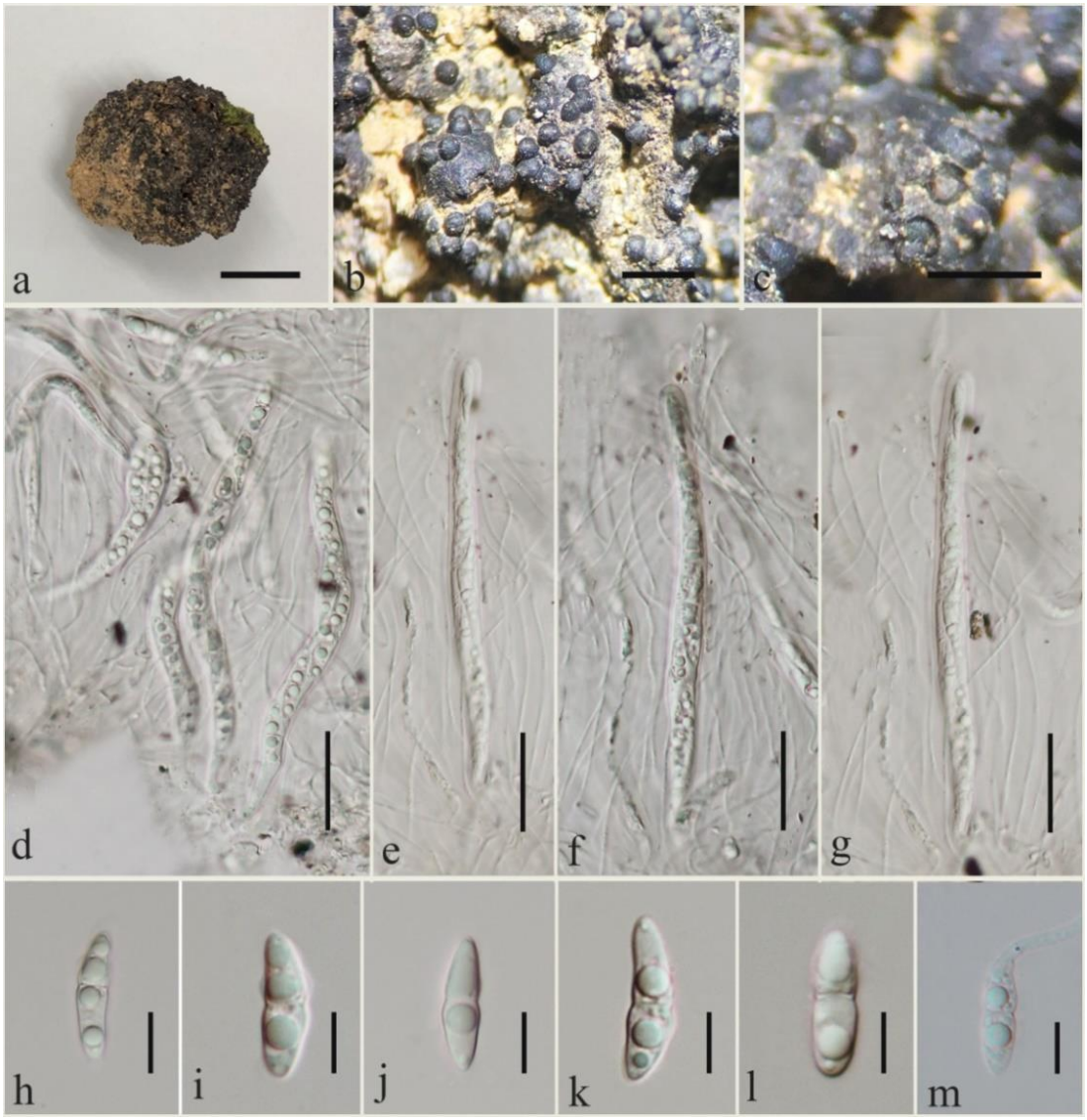


Figure 22 – *Quercicola guttulospora* (MFLU 18–2192, holotype). a The host fruit. b, c Ascomata on substrate. d–g Asci. h–l Ascospores. m Germinated spore. Scale bar: a = 1 cm, b, c = 500 µm, d–g = 30 µm, h–m = 10 µm.

Caryospora De Not., Micromyc. Ital. Novi: 7 (1855)

Caryospora is placed under family Astrosphaeriellaceae based on our multigene phylogenetic analysis (Figs. 19, 20). Only two *Caryospora* species have molecular data, but in this study, we introduce another species (Ariyawansa et al. 2015).

13. *Caryospora quercus* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 23

Index Fungorum number: IF555535; Facesoffungi number: FoF05236

Holotype – MFLU 18–2151

Etymology – Referring to the host genus on which the fungus was collected, *Quercus* (Fagaceae).

Saprobic on *Quercus* sp. fruits. Sexual morph: *Ascomata* 300–420 μm high × 450–483 μm diam. ($\bar{x}$ = 334 × 430 μm, n = 10), solitary or gregarious, conical or semiglobose, immersed becoming erumpent, ostiolate, eupapillate, carbonaceous. *Peridium* 0.8–1.4 μm wide, carbonaceous, black, fragile. *Hamathecium* 0.8–1.4 μm wide ($\bar{x}$ = 1.2 μm; n = 20), septate, branched, trabeculate pseudoparaphyses, numerous, persistent. *Asci* (69)–110 –147 μm × 30–35 μm ($\bar{x}$ = 122 × 33 μm, n = 20), 8-spored, cylindrical, bitunicate, fissitunicate, persistent, with an ocular chamber. *Ascospores* 41–54 μm × 18–28 μm ($\bar{x}$ = 48 × 24 μm, n = 30), uni-seriate, hyaline, pale brown to dark brown, ellipsoidal, diamond-shaped, apex pointed, 1- septate, with a dark band around the septum, slightly constricted at the septum, with walls thickened at both ends, guttulate, present polar germ pores, surrounded by a sheath 3.6–5.5 μm wide. Asexual morph: Undetermined.

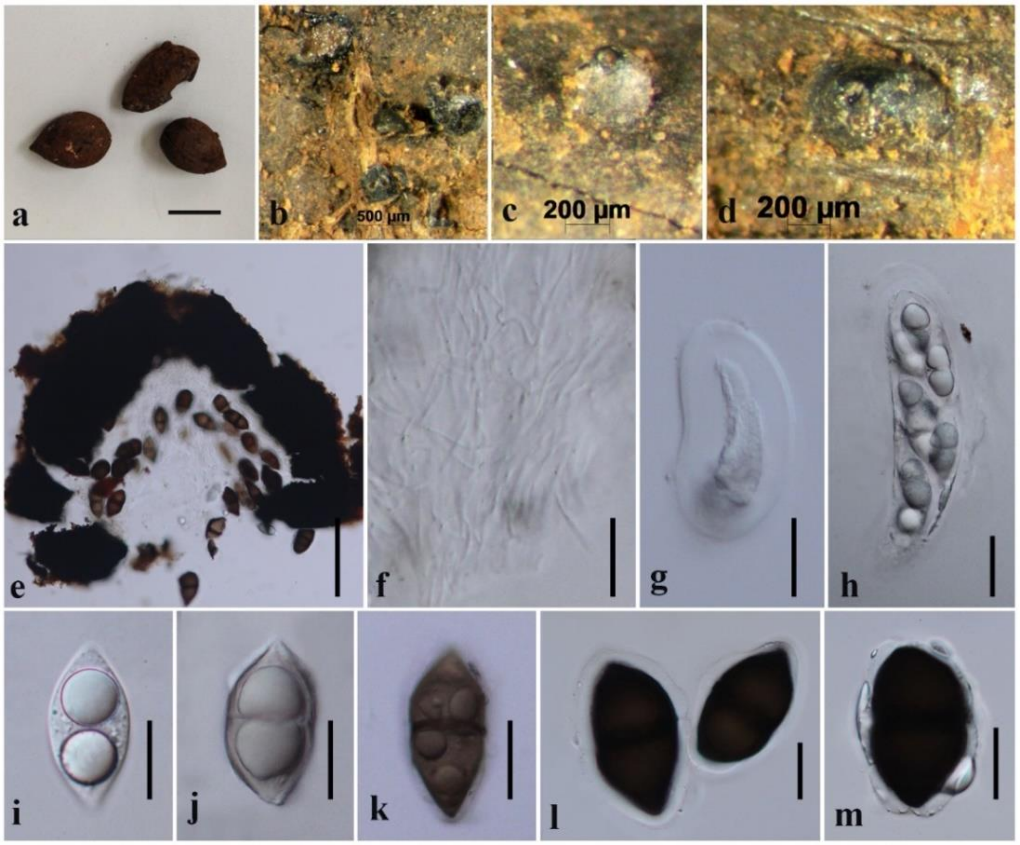


Figure 23 – *Caryospora quercus* (MFLU 18–2151, holotype). a *Quercus* sp. seeds host. b Ascomata on host fruit. c, d Ascoma on host fruit. e Section of ascoma. f Pseudoparaphyses. g, h Asci. i–m Ascospores. Scale bars: a = 1 cm, e = 100 μm, f = 10 μm, g, h = 30 μm, i–m = 20 μm.

Material examined – THAILAND, Lampang Province (19˚ 6' 23" N, 99˚ 41' 26" E), on decaying fruit pericarp of *Quercus* sp. (Fagaceae), 18 August 2017, S.C. Jayasiri C 338 (MFLU 18–2151, holotype: KUN-HKAS 102428, isotype)

GenBank numbers – SSU: MK347869, LSU: MK347979

Notes – *Caryospora quercus* forms a sister clade (Fig. 19, 20) to *C. minima* and *C. aquatica* with high statistical support (100% MLBS/1.0 BYPP, Figs 19, 20). In addition, *Caryospora quercus* fits within the generic concept of *Caryospora* species having erumpent, superficial, dark brown to black, carbonaceous, ostiolate ascomata, a thick and carbonized peridium, and relatively large and thick-walled ascospores (Jeffers 1940). *Caryospora quercus* has smaller ascomata compaired to *C. putaminum* (up to 420 vs. up to 1200 μm) and 8-spored asci (2-spored in *C.*

putaminum). *Caryospora aquatica* also differs from *C. quercus* as it is from a freshwater habitat (Ariyawansa et al. 2015). *Caryospora minima* differs from *Caryospora quercus* as the mature ascospores of *C. minima* are light brown with 3 septa, while in *C. quercus* they become irregularly diamond-shaped and dark brown with polar germ pores. No DNA sequences from protein coding genes are available for three species (*Caryospora aquatica*, *Caryospora minima* and *C. quercus*) and ITS sequence data is available only for *Caryospora aquatica*. However, significant morphological differences and statistical support establishment of our novel species, *Caryospora quercus* (Jeewon & Hyde 2016).

14. *Xenoastrosphaeriella* Jayasiri, EBG Jones & K.D. Hyde, gen. nov.

Index fungorum number: IF555536; Facesoffungi number: FoF05237

Etymology – Referring to the Xeno = ξένος in Greek, distinct; *Astrosphaeriella* = *Astrosphaeriella*-like taxon.

Saprobic on bamboo and palms. Sexual morph: *Ascostromata* dark opaque, gregarious, erumpent to superficial, conical with ruptured, reflexed, stellate, host remnants around the base, uni-loculate, glabrous, brittle, carbonaceous, ostiole central, with pore-like opening. *Peridium* unequal thickness, poorly developed at the base, thick at the sides towards the apex, composed of thick, opaque and melanized cells. *Hamathecium* 1–2 μm wide ($\bar{x}$ = 1.4 μm; n = 20), composed of dense, branching, rough-walled, distinctly septate, trabeculate pseudoparaphyses, anastomosing among the asci, embedded in a hyaline gelatinous matrix. *Asci* 8-spored, bitunicate, cylindrical, subsessile to short pedicellate, apically rounded with an ocular chamber. *Ascospores* overlapping uni- to bi-seriate, brown to reddish brown, fusiform with acute ends, 3-septate, slightly constricted at the central septum, widest at the middle, smooth-walled. Asexual morph: Undetermined.

Notes – *Xenoastrosphaeriella* is distinct from all other genera in the family Astrosphaeriellaceae (Phookamsak et al. 2015, Wanasinghe et al. 2018a, this study) in multi-loci phylogenetic analysis of SSU, LSU and *tef1* genes. Therefore, we introduce it as a new genus within this family (Figs. 19, 20). *Xenoastrosphaeriella tornata* shares similar morphological characters with *Astrosphaeriella lenticularis*, *A. splendida*, *A. trochus* and *A. vesuvius* in having broadly fusiform, reddish brown ascospores. *Xenoastrosphaeriella tornata* is most similar to *A. splendida*, but differs in having smaller ascospores with paler end cells (Phookamsak et al. 2015). Wanasinghe et al. (2018a) synonymized *Astrosphaeriella vesuvius* under *Pithomyces vesuvius* (MTCC 12224). There is no DNA sequence data for *Astrosphaeriella lenticularis*, *A. splendida* and *A. trochus*. Therefore, we introduce *Xenoastrosphaeriella* as a new genus to accommodate *Astrosphaeriella tornata*.

Type species – ***Xenoastrosphaeriella tornata*** (D. Hawksw. & Boise) Jayasiri & K.D. Hyde

15. *Xenoastrosphaeriella tornata* (Berk. & M.A. Curtis) Jayasiri & K.D. Hyde comb. nov.

Index fungorum number: IF555537; Facesoffungi number: FoF05238

≡ *Sphaeria tornata* Berk. & M.A. Curtis, Journal of the Linnean Society. Botany 10: 290 (1868)

= *Astrosphaeriella tornata* (Berk. & M.A. Curtis) D. Hawksw. & Boise, Sydowia 38: 119 (1986)

= *Trematosphaeria tornata* Cooke, Grevillea 16: 91 (1888)

Notes – The type specimen of *Xenoastrosphaeriella tornata* is in poor condition and Phookamsak et al. (2015) introduced a reference specimen for this species with molecular data (MFLUCC 11–0196). *Xenoastrosphaeriella tornata* is distinct from all other species in genus *Astrosphaeriella* and weakly supported to other genera in the family Astrosphaeriellaceae in multi-loci phylogenetic analysis (Phookamsak et al. 2015, Wanasinghe et al. 2018a, this study, Fig. 19). We introduce the new genus mainly based on *Astrosphaeriella tornata* (MFLUCC 11–0196) phylogeny. *Xenoastrosphaeriella tornata* is morphologically similar to *Astrosphaeriella* spp. and the only difference is the paler end cells of ascospores (Phookamsak et al. 2015). *Xenoastrosphaeriella tornata* clusters with *Acrocordiopsis patilii* with low bootstrap support (Fig.

20). *Xenoastrosphaeriella tornata* differs from *Acrocordiopsis patilii* in having reddish brown, fusiform, 3-septate ascospores with wide middle part (Borse & Hyde 1989).

Bambusicolaceae D.Q. Dai & K.D. Hyde, Fungal Diversity 63 (1): 49 (2013)

The family Bambusicolaceae was introduced by Hyde et al. (2013), with the type genus *Bambusicola*. This family has three genera *Bambusicola*, *Neobambusicola* and *Palmiascoma* (Dai et al. 2012, Hyde et al. 2013, Crous et al. 2014b, Liu et al. 2015). We present an updated tree for the family and introduce a new genus and two new species (Fig. 24).

16. *Leucaenicola* Jayasiri, E.B.G. Jones & K.D. Hyde, gen. nov.

Index Fungorum number: IF555538; Facesoffungi number: FoF05239

Etymology – Referring to the host genus on which the fungus was collected, *Leucaena* (Fabaceae).

Saprobic on *Leucaena* sp. pod. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, solitary, immersed in substrate to superficial, visible as black dots covered by epidermal tissues, uniloculate, globose to subglobose, glabrous, ostiolate centrally, with minute papilla. *Conidiomata wall* thin-walled equal thickness, composed of several layers of hyaline to dark brown, pseudoparenchymatous cells, outer layers comprising 2–3 cell layers of thick-walled, dark brown to black cells, organized in a *textura angularis* to *textura prismatica*, with inner layers comprising 1–2 layers of thin-walled, hyaline, and organized in *textura angularis*. *Conidiophores* arising from basal cavity of conidiomata mostly reduced to conidiogenous cells. *Conidiogenous cells*, enteroblastic, phialidic, hyaline to brown, globose to flask-shaped, smooth-walled. *Conidia*, solitary, one-celled, initially hyaline, becoming brown at maturity, oblong to ellipsoidal, with rounded or obtuse ends, aseptate, smooth-walled.

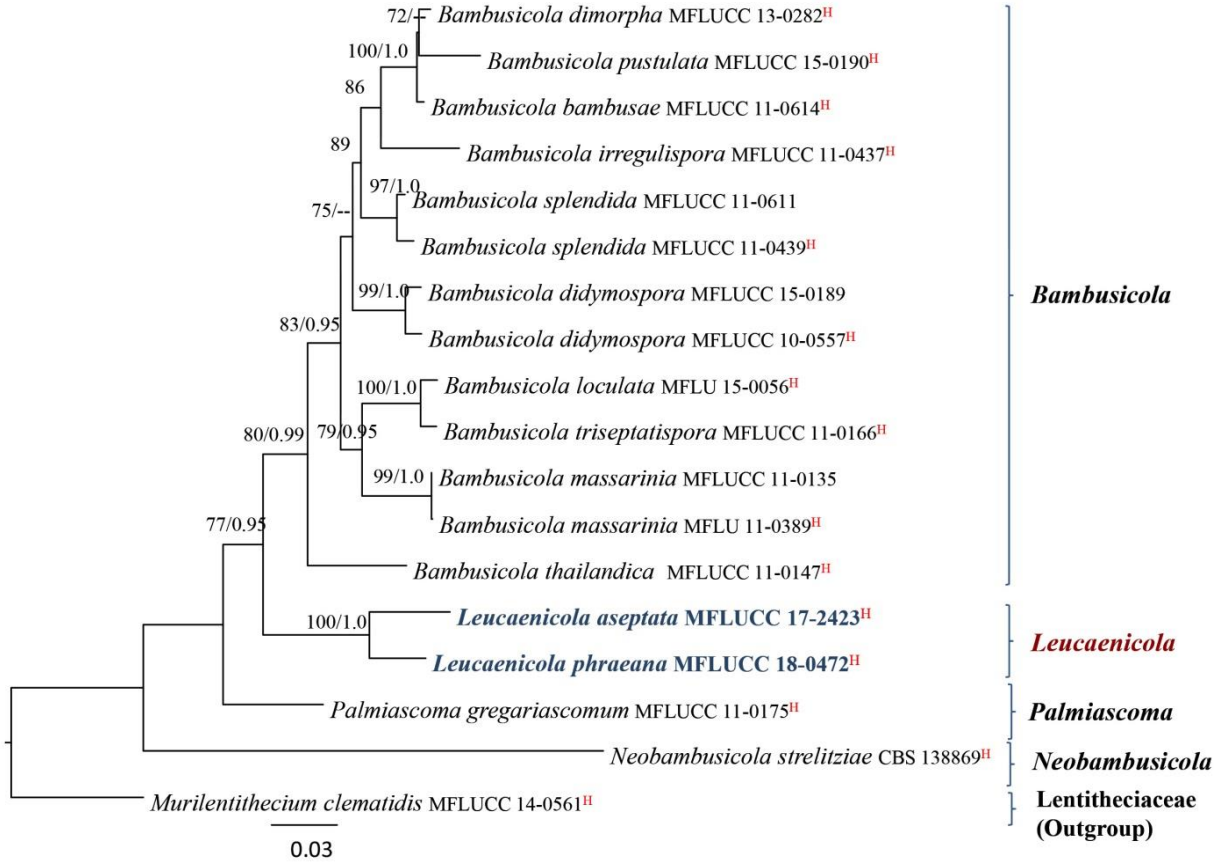


Figure 24 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS LSU and *rpb2* sequenced data of Bambusicolaceae. Related sequences were obtained from

GenBank. Eighteen strains were included in the combined sequence analyses, which comprised 3511 characters including alignment gaps. *Murilentithecium clematidis* (MFLUCC 14–0561) was used as the outgroup taxon. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -11724.282862 is presented. The matrix had 752 distinct alignment patterns, with 21.23% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.249293, C = 0.246762, G = 0.272901, T = 0.231045; substitution rates AC = 1.454764, AG = 3.096539, AT = 0.856027, CG = 1.288498, CT = 6.726041, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. Newly generated sequences are in blue and bold. Strains isolated from the holotype indicated in red superscript ^{H}.

Type species – ***Leucaenicola aseptata*** Jayasiri, E.B.G. Jones & K.D. Hyde

Notes – We isolated two species of this genus, both from a decaying pod of *Leucaena* sp. (Fabaceae). The two *Leucaenicola* species form a sister clade to *Bambusicola* species with high statistical support (77% MLBS/ 0.95 BYPP, Fig. 24) in the multigene phylogenetic analysis. All *Bambusicola* spp. were isolated from dead bamboo culms (Poaceae) while *Neobambusicola* and *Palmiascoma* were from leaves of *Strelitzia nicolai* (Strelitziaceae) and a dead frond of a palm (Arecaceae), respectively (Table 2).

Bambusicolaceae comprises both sexual and asexual morph species. Although our two *Leucaenicola* species have asexual morphs similar to *Bambusicola thailandica* (Thambugala et al. 2017), they differ from *B. thailandica* in having micro- and macro- conidia. *Leucaenicola* is characterized by conidial morphology, size and colour that are similar to those of the micro-conidia of *B. thailandica* but are phylogenetically distinct. We did not observe macro-conidia in *Leucaenicola*.

Table 2 Synopsis of host and genera in family Bambusicolaceae

Genera	**Species**	**Host**
Bambusicola	*Bambusicola dimorpha* (both morph) *Bambusicola pustulata* (sexual morph) *Bambusicola bambusae* *Bambusicola irregulispora* (asexual morph) *Bambusicola splendida* (asexual morph) *Bambusicola didymospora* (both morph) *Bambusicola loculata* (sexual morph) *Bambusicola triseptatispora* (both morph) *Bambusicola massarinia* (both morph) *Bambusicola thailandica* (sexual morph)	Dead culm of bamboo (Poaceae)
Leucaenicola	***Leucaenicola aseptata*** ***Leucaenicola phraeana***	**Decaying pod of *Leucaena* sp. (Fabaceae)**
Neobambusicola	*Neobambusicola strelitziae*	Leaves of *Strelitzia nicolai*

		(Strelitziaceae)
Palmiascoma	*Palmiascoma gregariascomum*	Dead frond of palm species in family Arecaceae

17. *Leucaenicola aseptata* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 25, 26

Index Fungorum number: IF555539; Facesoffungi number: FoF05240

Holotype – MFLU 18–2129

Etymology – Referring to the aseptate conidia, which the fungus was identified.

Saprobic on pod of *Leucaena* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 80–100 μm high × 100–125 μm diam. ($\bar{x}$ = 93 × 117 μm, n = 10), pycnidial, solitary, immersed in substrate to superficial, visible as black dots covered by epidermal tissues, uniloculate, globose to subglobose, glabrous, ostiole central, with minute papilla. *Conidiomata wall* 5–12 μm wide ($\bar{x}$ = 10.2 μm, n = 20), thin-walled, of equal thickness, composed of several layers of hyaline to dark brown, pseudoparenchymatous cells, outer layers comprising 2–3 cell layers of thin-walled, dark brown to black, organized in a *textura angularis* to *textura prismatica*, inner layers comprising 1–2 layers of thin-walled, hyaline, organized in a *textura angularis*. *Conidiophores* arising from basal cavity of conidiomata mostly reduced to conidiogenous cells. *Conidiogenous cells* 2.5–3 × 1.5–2 μm ($\bar{x}$ = 2.7 × 1.7 μm, n = 30), enteroblastic, phialidic, hyaline to brown, globose to flask-shaped, aseptate, smooth-walled. *Conidia* 3–4 × 1.5–2 μm ($\bar{x}$ = 3.5 × 1.7 μm, n = 30), solitary, initially hyaline, becoming brown at maturity, one-celled, oblong to ellipsoidal, with rounded or obtuse ends, aseptate, smooth-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 60–70 mm diam. after 4 weeks at 18 ° C. Colonies grey to brown surface, slightly radiating; reverse yellow to brown in the center, off white to yellow at margin; medium dense, circular, flattened to slightly raised, dull to rough with entire edge, fairly fluffy to velvety, slightly radially furrowed.

Material examined – THAILAND, Chiang Rai Province, Doi Pui, on decaying pod of *Leucaena* sp. (Fabaceae), 20 July 2017, S.C. Jayasiri, C 278 (MFLU 18–2129, holotype; KUN-HKAS 102423, isotype), ex-type living culture MFLUCC 17–2423, KUMCC 18–0256.

GenBank numbers – SSU: MK347853, ITS: MK347746, LSU: MK347963, *tef1*: MK360059, *rpb2*: MK434891

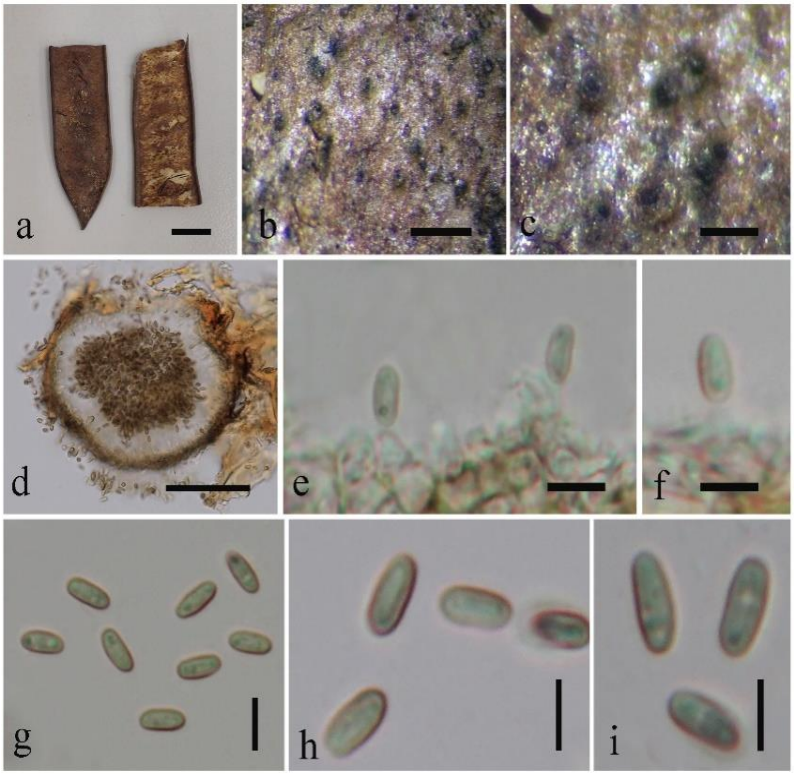


Figure 25 – *Leucaenicola aseptata* (MFLU 18–2129, holotype). a Host pods. b, c Conidiomata in substrate. d Section through conidioma. e, f Conidiogenous cells. g–i Conidia. Scale bars: a, b = 2 cm, c = 500 μm, d–g = 10 μm.

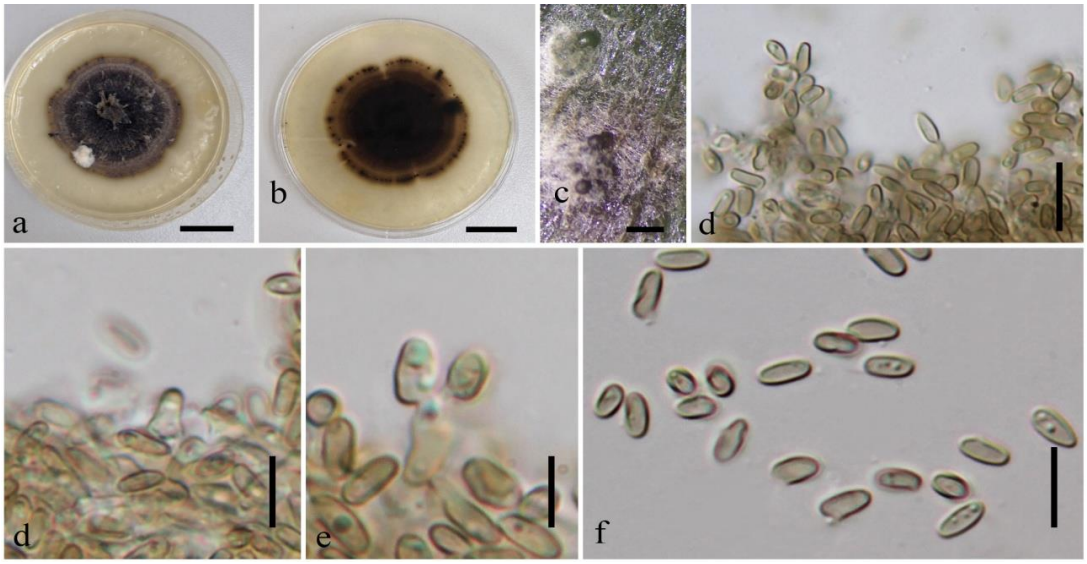


Figure 26 – *Leucaenicola aseptata* in culture (MFLUCC 17–2423, ex-type). a Top view of culture. b Reverse view of culture. c–f Conidiogenous cells and conidia. Scale bars: a, b = 1 cm, c, f = 10 μm, d, e = 5 μm.

18. *Leucaenicola phraeana* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 27

Index Fungorum number: IF555540; Facesoffungi number: FoF05241

Holotype – MFLU 18–2184

Etymology – Referring to the location where the specimen was collected, Phrae Province, Thailand.

Saprobic on *Leucaena* sp. pod. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 90–115 μm high × 130–150 μm diam. ($\bar{x}$ = 105 × 135 μm, n = 10), pycnidial, solitary, immersed in substrate to superficial, visible as black dots covered by epidermal tissues, uniloculate, globose to subglobose, glabrous, ostiole central, with minute papilla, *Conidiomata wall* 10–20 μm wide ($\bar{x}$ = 16.4 μm, n = 20), thin-walled, of equal thickness, composed of several layers of hyaline to brown, pseudoparenchymatous cells, outer layers comprising 2–3 cell layers of thick-walled, dark brown, organized in a *textura angularis* to *textura prismatica*, inner layers comprising 1–2 layers of thin-walled, hyaline, organized in a *textura angularis*. *Conidiophores* arising from basal cavity of conidiomata mostly reduced to conidiogenous cells. *Conidiogenous cells* 3–4 × 1.5–2 μm ($\bar{x}$ = 3.5 × 1.8 μm, n = 30), enteroblastic, phialidic, hyaline, globose to flask-shaped, aseptate, smooth-walled. *Conidia* 3–4 × 1.5–2 μm ($\bar{x}$ = 3.5 × 1.8 μm, n = 30), solitary, initially hyaline, becoming brown at maturity, oblong to ellipsoidal, with rounded or obtuse ends, aseptate, smooth-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 20–30 mm diam. after 4 weeks at 18 ° C. Colonies forming white tufts on surface in the center, outer layer pale brown, reverse dark brown, brown to yellow layers, pale yellow at margin; circular, flattened, dull with entire edge.

Material examined – THAILAND, Phrae Province, on decaying pod of *Leucaena* sp. (Fabaceae), 10 January 2018, S.C. Jayasiri, C 416 (MFLU 18–2184, holotype), ex-type living culture MFLUCC 18–0472, KUMCC 18–0257.

GenBank numbers – SSU: MK347892, ITS: MK347785, LSU: MK348003, *tef1*: MK360060, *rpb2*: MK434867

Notes – Based on the multi-gene sequence analysis, *Leucaenicola phraeana* (MFLUCC 18–

0472) clusters with *L. aseptata* with strong bootstrap support (Fig. 24). A comparison of the ITS, *tef1* and *rpb2* nucleotides of these two strains reveals 24 (5.0%), 86 (8.2 %) and 23 (2.2%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016). *Leucaenicola phraeana* has a prominent ostiole and different culture morphology to *L. phraeana. Leucaenicola phraeana* is also characterized by white tufts surface (Fig. 26), but *L. aseptata* comprised grey to brown surface in culture (Fig. 27).

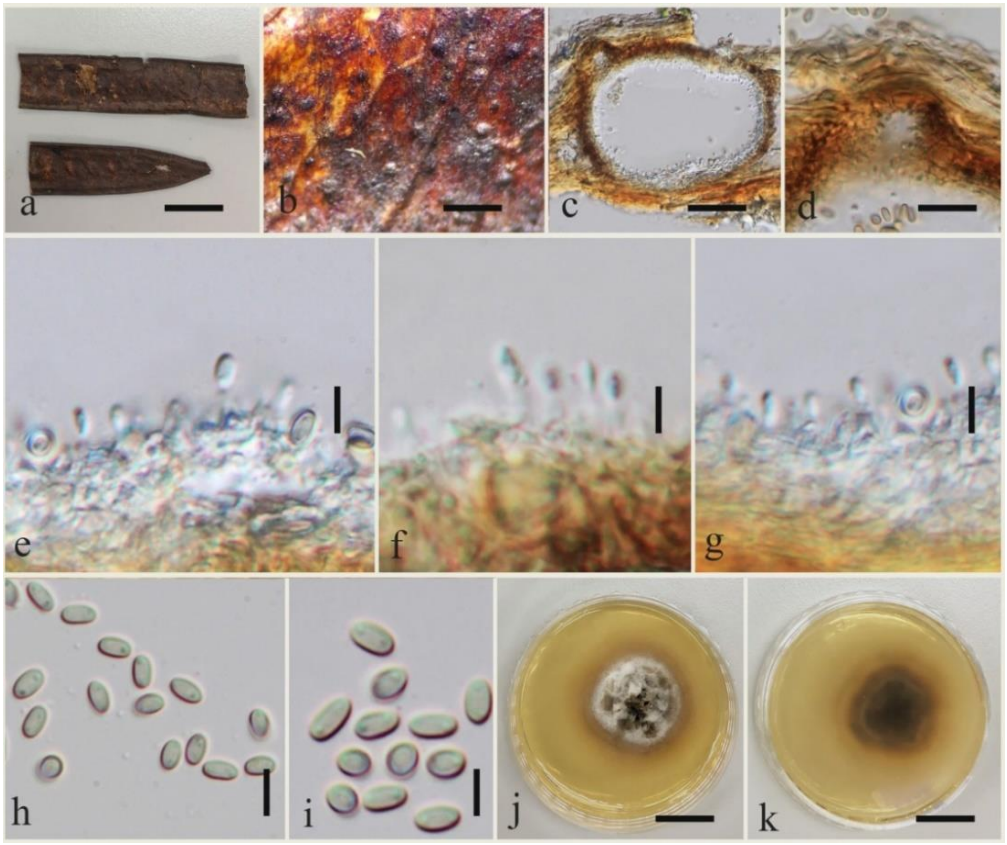


Figure 27 – *Leucaenicola phraeana* (MFLU 18–2184, holotype). a Host pods. b Conidiomata in the substrate. c Section through conidioma. d Ostiole. e–g Conidiogenous cells. h–i Conidia. j Top view of the culture. k Reverse view of the culture. Scale bars: a, b = 2 cm, c = 500 μm, d–g = 10 μm.

Delitschiaceae M.E. Barr, Mycotaxon 76: 109 (2000)

The family Delitschiaceae, typified by *Delitschia*, occurs on bovine dung (Doveri 2011), or rarely on aged wood or plants (Hyde et al. 2013). Recent studies by Rivera-Chávez et al. (2018) reported *Delitschia* species from submerged wood in freshwater habitat and *Delitschia bispora* from a water-cooling tower (Eaton & Jones 1970). Wijayawardene et al. (2018) reported three genera in this family (*Delitschia*, *Ohleriella* and *Semidelitschia*), but sequence data is available only for *Delitschia.* Recently identified *Delitschia* strains from submerged wood show a diversity of important chemicals (Rivera-Chávez et al. 2018) that show activity towards prostate cancer cell lines. Study of the bioactive from sample accessioned as G858 (*Delitschia* sp.) led to the isolation of eight new α-pyrone derivatives (Rivera-Chávez et al. 2018). In this study, we introduce a new species *Delitschia nypae*, from *Nypa fruticans* in Thailand (Fig. 28).

19. *Delitschia nypae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 29, 30

Index Fungorum number: IF555540; Facesoffungi number: FoF05242

Holotype – MFLU 18–2184

Etymology – Referring to the host genus on which the fungus was collected, *Nypa*

(Arecaceae).

Saprobic on *Nypa fruticans* (Arecaceae) fruit. Sexual morph: *Ascomata* 420–500 µm high × 375–425 µm diam. ($\bar{x}$ = 445 × 410 µm; n = 10), solitary or gregarious, subepidermal, conical or semiglobose, immersed becoming erumpent, black, carbonaceous, without ostiole. *Peridium* 38–85 µm wide ($\bar{x}$ = 64 µm; n = 20), many layered; outer layer of small, irregular, thick-walled cells, inner layer with larger lumina, black. *Hamathecium* 1.5–2 µm wide ($\bar{x}$ = 1.7 µm; n = 20), septate, simple, persistent, numerous pseudoparaphyses. *Asci* 130–150 × 15–19 µm ($\bar{x}$ = 145 × 17 µm; n = 30), 8-spored, cylindrical, pedicel, bitunicate, fissitunicate, persistent, with an ocular chamber. *Ascospores* 24–30 × 9–14 µm ($\bar{x}$ = 28 × 12 µm; n = 30), uni-seriate, hyaline to dark brown, ellipsoidal, 1- septate, with a dark band around the septum, constricted at the septum, fragment when mature, thin-walled, guttulate. Asexual morph: Undetermined.

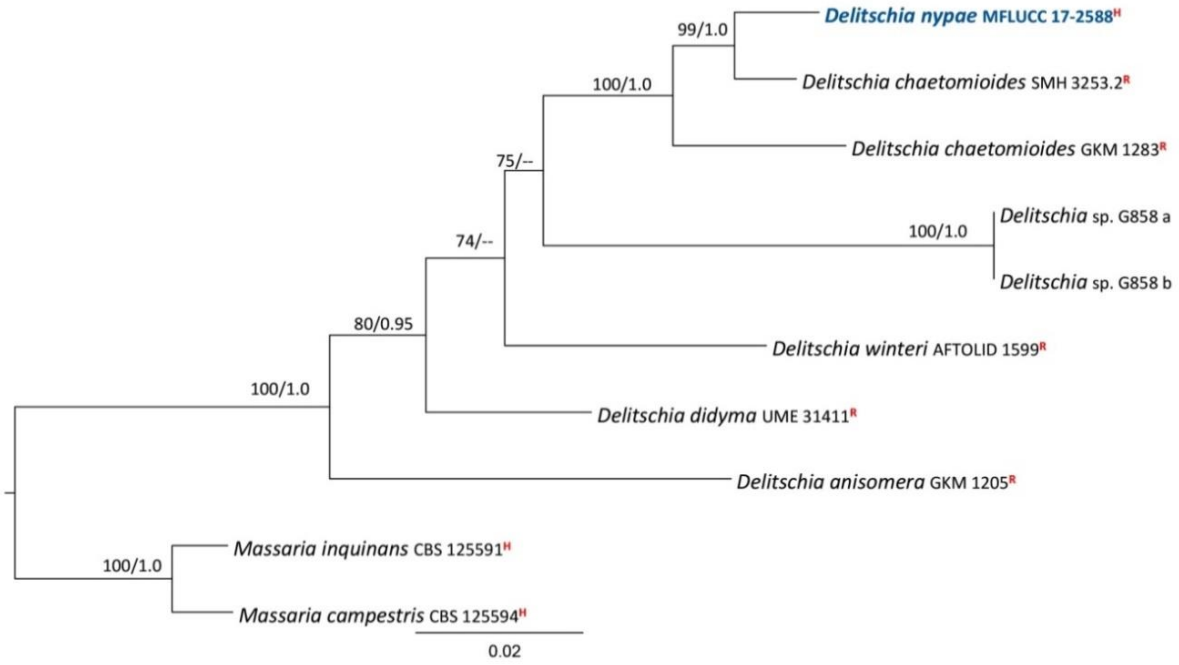


Figure 28 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU and *tef1* sequenced data of Delitschiaceae. Related sequences were obtained from GenBank. Ten strains were included in the combined sequence analyses, which comprised 2950 characters including alignment gaps. *Massaria* spp. (WU 30527 and WU 30611) are used as the outgroup taxon. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -11724.282862 is presented. The matrix had 300 distinct alignment patterns, with 37.12% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245487, C = 0.237535, G = 0.285962, T = 0.231015; substitution rates AC = 0.506809, AG = 1.576045, AT = 0.733037, CG = 1.093869, CT = 6.657433, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. Newly generated sequence is in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I} and ^{R} respectively.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies on MEA reaching 25–30 mm diam. after 4 weeks at 18°C, with irregular, lobate margin, forming two layers; outer layer yellow to pale brown, center dark brown, reverse dark brown in center and off white to pale yellow at margin.

Material examined – THAILAND, Krabi Province, Mueang Krabi District, on decaying fruit pericarp of *Nypa fruticans* (Arecaceae), 31 August 2017, S.C. Jayasiri, C 349 (MFLU 18–2155,

holotype); ex-type living culture MFLUCC 17–2588, KUMCC 18–0228.

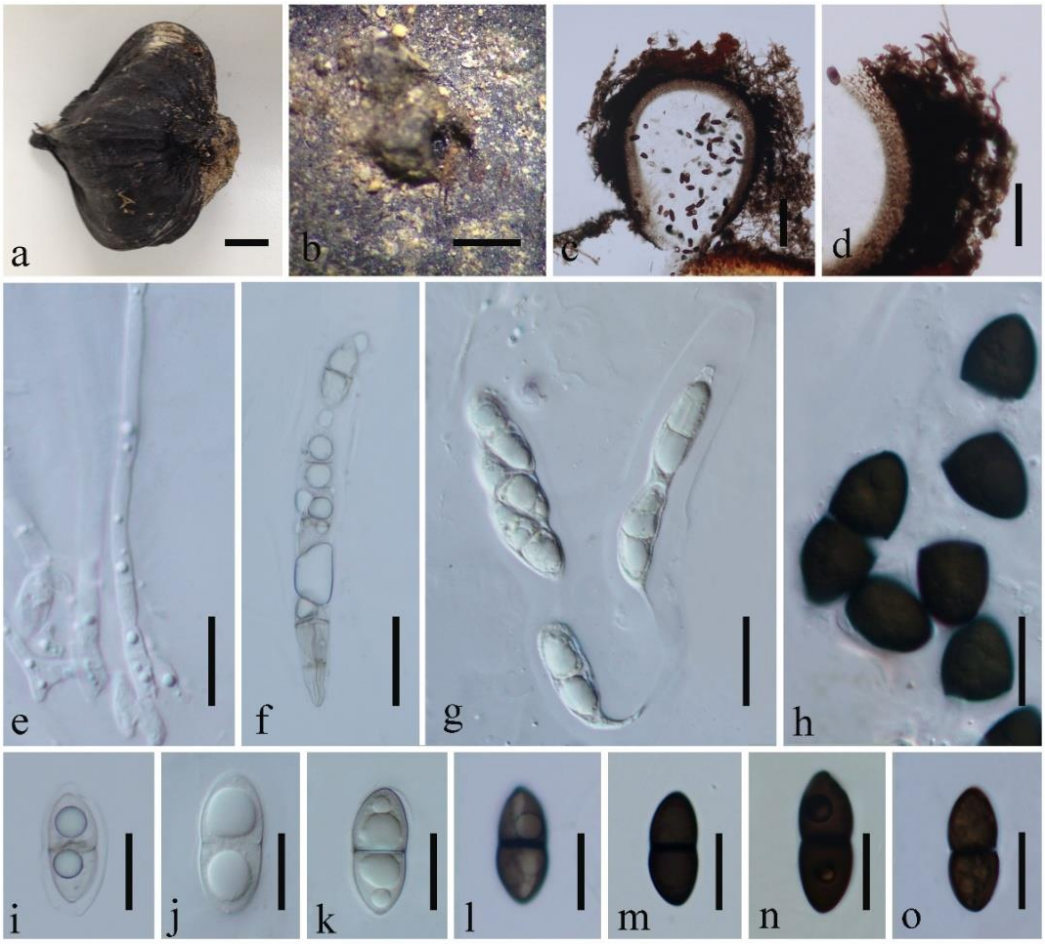


Figure 29 – *Delitschia nypae* (MFLU 18–2155, holotype). a Host fruit. b Ascoma on substrate. c Section through the ascomata. d Peridium. e Pseudoparaphyses. f, g Asci. h Separation of ascospores in to two parts. i–o Ascospores. Scale bars: a = 1 cm, b = 500 µm, c, d = 50 µm, e = 10 µm, f–h = 30 µm, i–o = 20 µm.

GenBank numbers – SSU: MK347871, LSU: MK347981, *tef1*: MK360049, *rpb2*: MK434878

Notes: Our collection shares similar morphological (Fig. 29) characters with *Delitschia* in having darkly pigmented, 2-celled, constricted ascospores with germ slits (Barr 2000, Luck-Allen & Cain 2011). In the multigene phylogenetic analysis, *Delitschia nypae* forms a sister clade to *Delitschia chaetomioides* (SMH 3253.2) with high statistical support (99% MLBS/1.0 BYPP). A comparison of the *tef1* nucleotides of these two strains reveals 30 (4.5%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016). Morphologically *Delitschia nypae* differs from type species of *Delitschia chaetomioides* in having smaller ascospores (24–30 × 9–14 µm vs. 38–50 × 17–20 µm) and asci (145 × 17 µm vs 250 × 30 µm) (Karsten 1873). Type species of *Delitschia chaetomioides* identified from Mustiala and two strains in GenBank identified from Costa Rica (SMH 3253.2) and Kenya (GKM1283). *Delitschia nypae* identified from decaying fruits of *Nypa fruticans* associated with estuarine habitats in Thailand.

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

Boonmee et al. (2016) introduced this family to accommodate mostly aquatic lignicolous species. The family comprises 12 genera and the type genus is *Dictyosporium*, which has been reported from decaying wood and plant litter in terrestrial and aquatic habitats, and is worldwide in distribution (Hyde & Goh 1998, Pinnoi et al. 2006, Tsui et al 2006, Pinruan et al. 2007). We

present an updated tree for the family and introduce two new species and a new host record (Fig. 31).

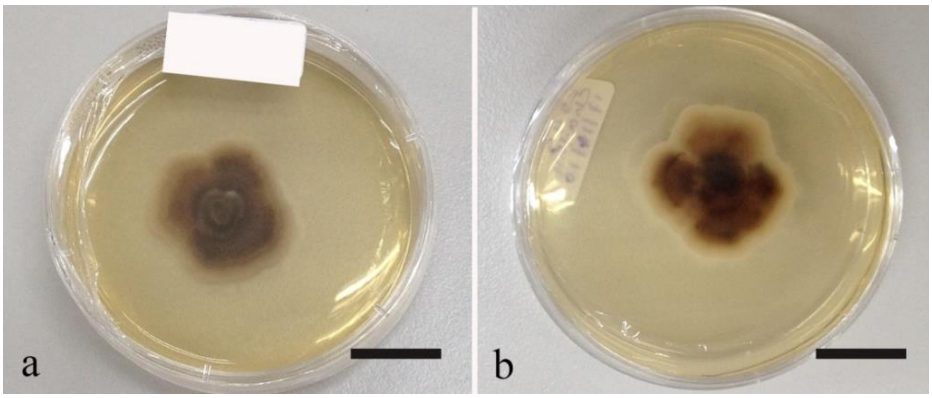


Figure 30 – *Delitschia nypae* culture in MEA (MFLUCC 17–2588, ex-type). a Top view of the culture in MEA. b Reverse view of the culure in MEA. Scale bars: a, b = 1 cm.

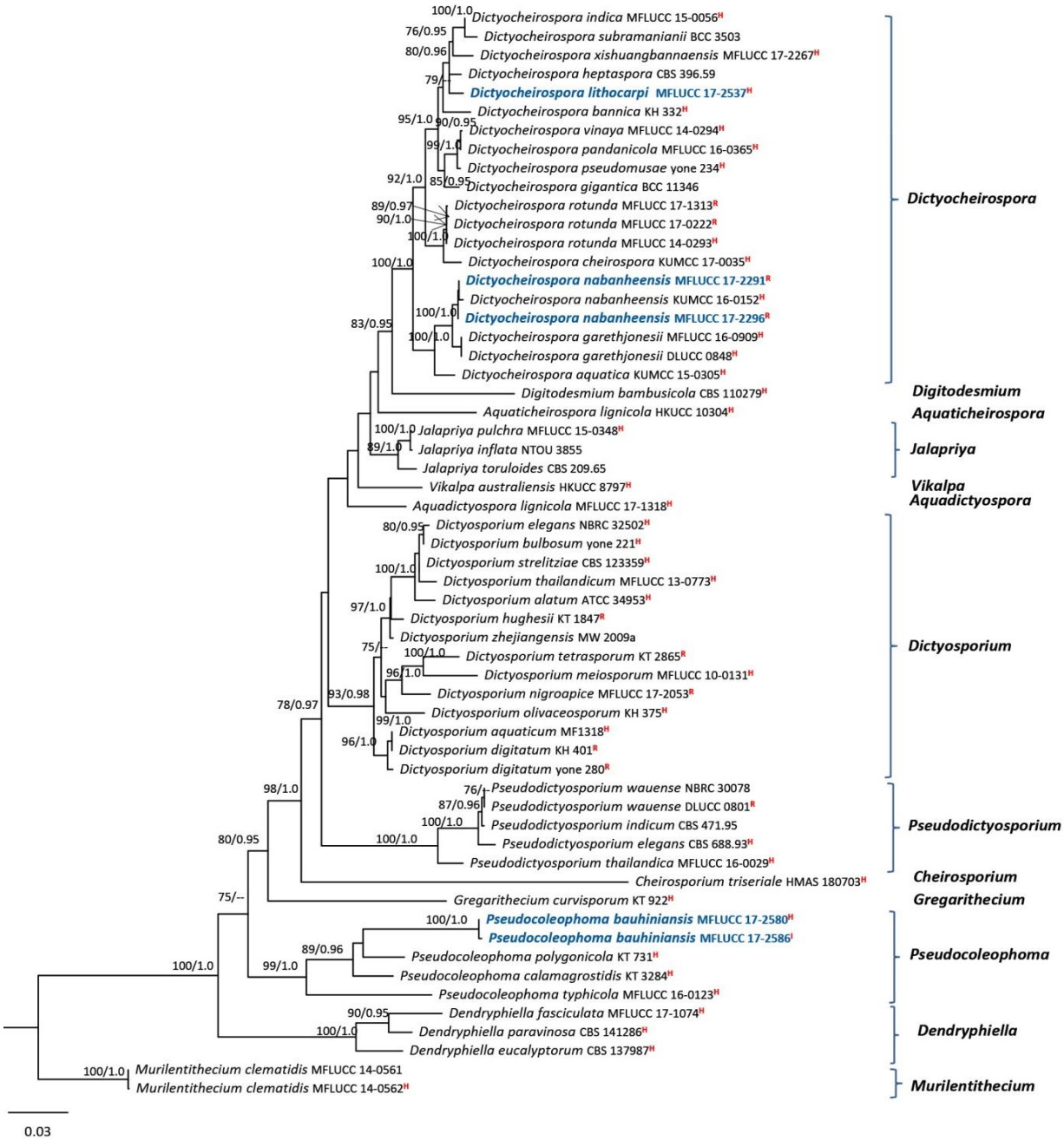


Figure 31 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *tef1* partial sequence data. Fifty-eight strains were included in the sequence analysis, which comprised 2881 characters including alignment gaps. *Murilentithecium clematidis* (Lentitheciaceae) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -7545.505967 is presented. The matrix had 876 distinct alignment patterns, with 37.76% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.237662, C = 0.253136, G = 0.270383, T = 0.238820; substitution rates AC = 1.495111, AG = 3.041974, AT = 2.409593, CG = 0.651257, CT = 7.837986, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strains are in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I} and ^{R} respectively.

Dictyocheirospora M.J. D'souza, Boonmee & K.D. Hyde, Fungal Diversity 80: 465 (2016)

Eleven species are accepted in the genus (Boonmee et al. 2016, Wang et al. 2016, Hyde et al. 2017, Li et al. 2017, Tibpromma et al. 2018, Yang et al. 2018). During our survey one new species and a previously described species were added based on phylogeny and morphology.

20. *Dictyocheirospora lithocarpi* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 32

Index Fungorum number: IF555548; Facesoffungi number: FoF05250

Holotype – MFLU 18–2178

Etymology – Referring to the host genus on which the fungus was collected, *Lithocarpus* (Fagaceae).

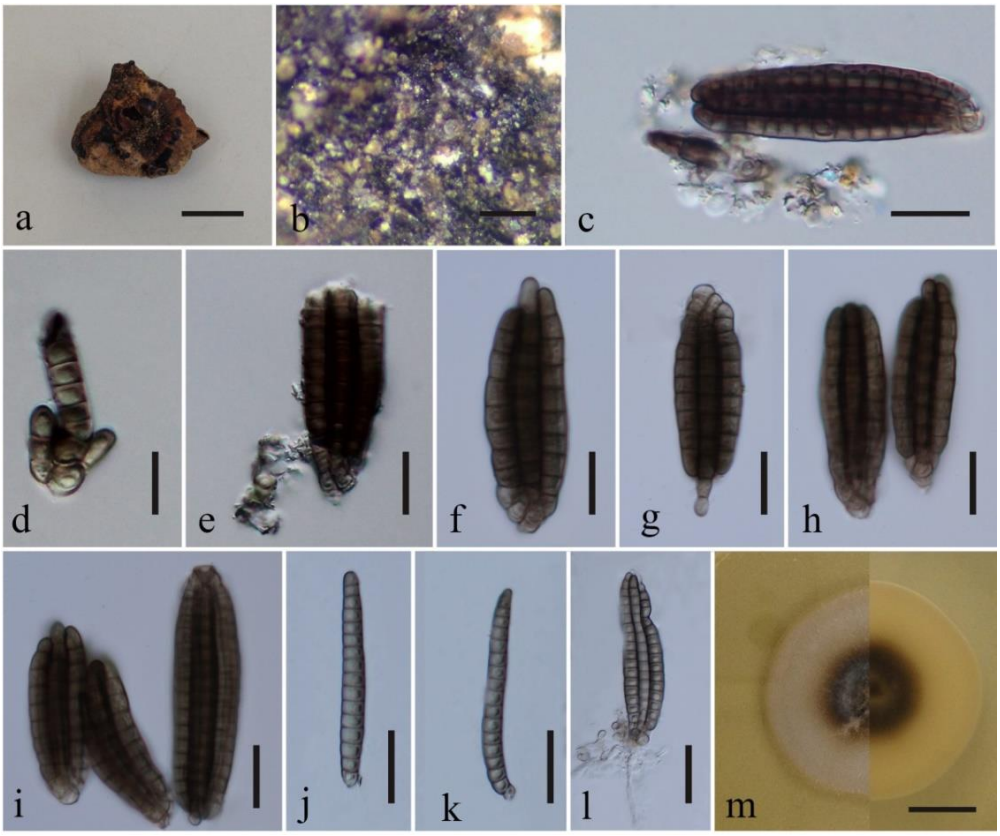


Figure 32 – *Dictyocheirospora lithocarpi* (MFLU 18–2178, holotype). a *Lithocarpus* sp. fruit. b Conidiomata on the substrate. c–e Squash mount of conidioma with conidiogenous cells. f–m Conidia. l Germinated conidium. m Top and reverse view of culture. Scale bars: a, m = 1 cm, b = 500 μm, c–i = 20 μm.

Saprobic on *Lithocarpus* sp. fruit. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, scattered. *Mycelium* immersed, composed of pale brown, smooth, septate, branched hyphae. *Conidiomata* 225–248 μm wide ($\bar{x}$ = 232 μm, n = 10), sporodochial, dark brown to black. *Conidiophores* micronematous, short, unbranched, hyaline to pale brown. *Conidiogenous cells* holoblastic, integrated, terminal, pale brown, smooth-walled. *Conidia* 35–40 × 12–18 μm ($\bar{x}$ = 38 × 16 μm, n = 30), solitary, acrogenous, cheiroid, olivaceous brown, consisting of 6 rows of cells, with rows cylindrical, palmately divergent, inwardly not curved at the tip, arising from a basal cell, without appendages, each row composed of 10–16 cells, euseptate, slightly constricted at the septa, guttulate, smooth.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced from base of conidia. Colonies on MEA reaching 28–32 mm diam. after 2 weeks at 18 ° C, grow with circular, entire edge, off white margin and pale brown to dark brown in the central, raised in Center.

Material examined – THAILAND, Payao Province, on decaying fruit pericarp of *Lithocarpus* sp. (Fagaceae), 20 July 2017, S.C. Jayasiri, C 408 (MFLU 18–2178, holotype); ex-type living culture MFLUCC 17–2537, KUMCC 18–0229.

GenBank numbers – SSU: MK347888, ITS: MK347781, LSU: MK347999, *rpb2*: MK434869

Notes – Phylogenetic analysis based on concatenated LSU, ITS and *tef1* sequence data indicated that *Dictyocheirospora lithocarpi* is related to *D. heptaspora* (CBS 396.59) with low statistical support (Fig. 31). However, only an ITS gene sequence is available for *D. heptaspora* (CBS 396.59) and there is no morphological description of this strain (Boonmee et al. 2016). Goh et al. (1999) provided a description for *Dictyosporium heptaspora*, which was transferred by Boonmee et al. (2016) to *Dictyocheirospora*, and is characterized by conidia that are olivaceous brown, broadly ellipsoidal, with 7 curved rows of cells and 50–80 μm × 20–30 μm size. *Dictyocheirospora lithocarpi* and *Dictyosporium heptasporum* share similar morphology in having olivaceous brown, broadly ellipsoidal conidia (Fig. 32), but *Dictyocheirospora lithocarpi* lacks a hook-like apex and has only 6 curved rows and smaller conidia (35–40 × 12–18 μm vs. 50–80 × 20–30 μm) (Goh et al. 1999). A comparison of the ITS regions reveals *Dictyocheirospora lithocarpi* differs from *D. heptaspora* by 9 (1.7%) nucleotide differences of ITS gene that warrants separate species status (Jeewon & Hyde 2016).

21. *Dictyocheirospora nabanheensis* Tibpromma & K.D. Hyde, Fungal Diversity 92: 10 (2018), Fig. 33

Saprobic on *Leucaena* sp. pod. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on natural substrate superficial, scattered. *Mycelium* immersed, composed of pale brown, smooth, septate, branched hyphae. *Conidiomata* 245–290 μm wide ($\bar{x}$ = 265 μm, n = 10), sporodochial, dark brown to black. *Conidiophores* micronematous, short. *Conidiogenous cells* holoblastic, integrated, terminal, pale brown, smooth-walled. *Conidia* 39–42 × 15–20 μm ($\bar{x}$ = 41 × 16 μm, n = 30), solitary, acrogenous, cheiroid, pale brown to brown, consisting of 5–6 rows of cells, with rows cylindrical, palmately divergent, inwardly curved at the tip, arising from a basal cell, rounded to cylindrical appendage, each row composed of 8–10 cells, euseptate, slightly constricted at septa, guttlue in each cell, smooth.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced from base of conidia. Colonies on MEA reaching 25–30 mm diam. after 2 weeks at 18^{o}C, with circular entire edge, white margin and cream to yellow orange in the centre, raised on surface.

Material examined – THAILAND, Chiang Rai Province, Doi Pui, on decaying pod of *Leucaena* sp. (Fabaceae), 20 July 2017, S.C. Jayasiri, C 285-A (MFLU 18–2132, new host record); living culture, MFLUCC 17–2291, KUMCC 18–0230; THAILAND, Lampang Province, 19° 3' 44" N, 99° 46' 54" E, on decaying pod of *Leucaena* sp. (Fabaceae), 18 August 2017, S.C. Jayasiri, C 317 (MFLU 18–2142), living culture MFLUCC 17–2296, KUMCC 18–0231.

GenBank numbers – MFLUCC 17–2291: SSU: MK347855, ITS: MK347748, LSU:

MK347965, *tef1*: MK360050; MFLUCC 17–2296: SSU: MK347862, ITS: MK347756, LSU: MK347973, *tef1*: MK360051

Notes – The two new strains grouped in the *Dictyocheirospora nabanheensis* clade with high and low bootstrap support. In addition, they share similar morphological characters with *D. nabanheensis* (Tibpromma et al. 2018). A comparison of the ITS and *tef1* regions reveals *Dictyocheirospora nabanheensis* (KUMCC 16–0152) differs from new strains (MFLUCC 17–2291 and MFLUCC 17–2296) by 1 (0.19%) and 3 (0.34%) nucleotide differences of ITS and *tef1* genes that suggest that our new records is *Dictyocheirospora nabanheensis* (Jeewon & Hyde 2016). The *D. nabanheensis* strains grouped as a sister clade to *D. garethjonesii* in an unsupported clade (Fig. 31). Therefore, this is a new record of *D. nabanheensis* from decaying pod of *Leucaena* sp. The type of *D. nabanheensis* was isolated from *Pandanus* sp. (Tibpromma et al. 2018).

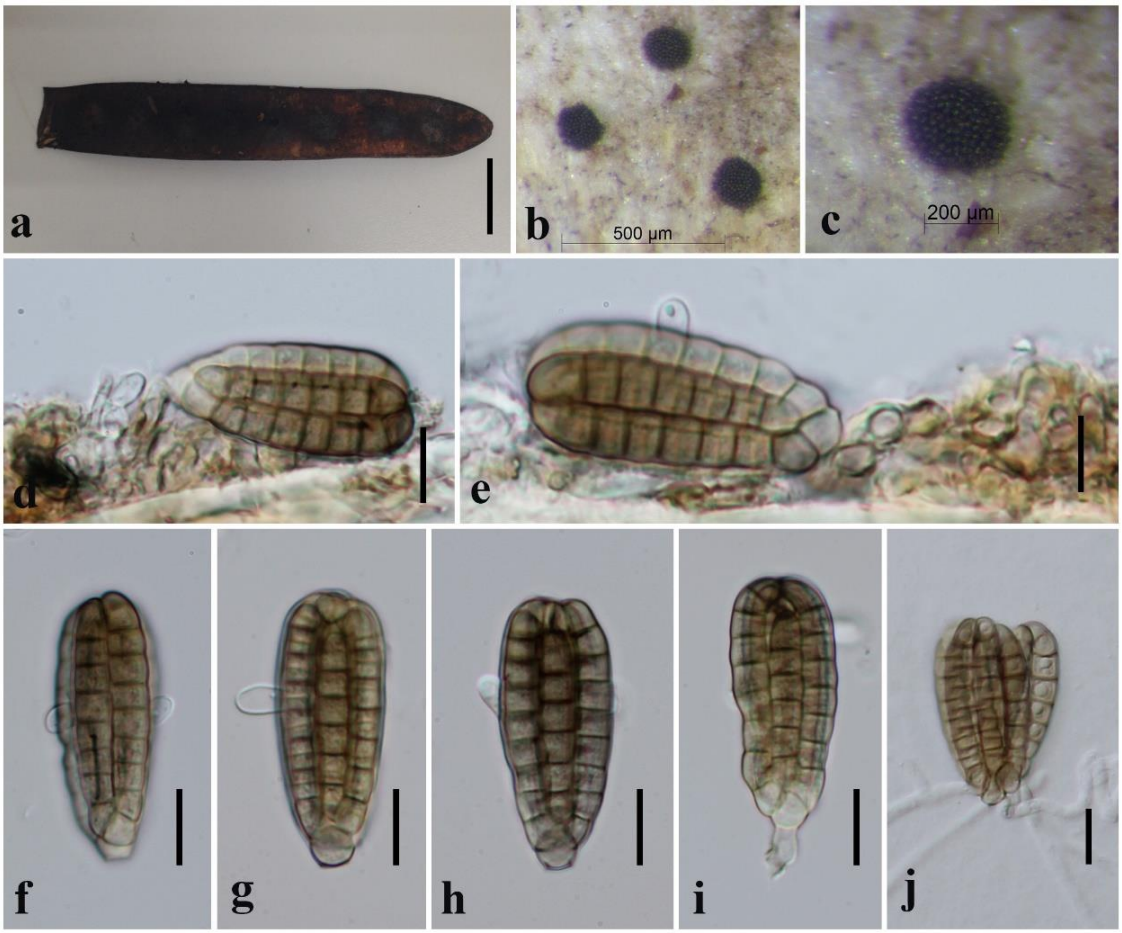


Figure 33 – *Dictyocheirospora nabanheensis* (MFLU 18–2132). a *Leucaena* sp. seed pod. b, c Sporodochia on the substrate. d, e Squash mount of conidioma with conidiogenous cells. f–i Conidia. j Germinated conidium. Scale bars: a = 2 cm, d–j = 10 µm.

Pseudocoleophoma Kaz. Tanaka & K. Hiray., Studies in Mycology 82: 89 (2015)

This genus comprises three species (Tanaka et al. 2015, Hyde et al. 2016) and here we introduce a new species from decaying pod of *Bauhinia* sp. in Thailand.

22. *Pseudocoleophoma bauhiniae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 34, 35

Index Fungorum number: IF555549; Facesoffungi number: FoF05251

Holotype – MFLU 18–2178

Etymology – Referring to the host genus on which the fungus was collected, *Bauhinia* (Fabaceae).

Saprobic on *Bauhinia* sp. pod. Sexual morph: *Ascomata* 125–145 µm high × 100–120 µm

diam. ($\bar{x}$ = 133 × 105 µm; n = 5), immersed to erumpent through host tissue, solitary or scattered, coriaceous, subglobose to obpyriform, dark brown. Ostiolar neck protruding. *Peridium* 22–32 µm wide, comprising many layers of thick-walled, dark brown cells to hyaline inner layers of *textura angularis*. *Hamathecium* 1.5–2 µm wide ($\bar{x}$ = 1.8 µm; n = 10), septate, branching, pseudoparaphyses. *Asci* 65–80 × 5–8 µm ($\bar{x}$ = 75 × 7 µm; n = 10), 8-spored, bitunicate, fissitunicate, clavate to cylindric-clavate, slightly curved, short-pedicellate with an ocular chamber. *Ascospores* 17–20 × 3.5–4.5 ($\bar{x}$ = 18 × 4 µm; n = 10), overlapping, 1–2 seriate, hyaline, cylindric-fusiform, tapering towards the rounded ends, straight to slightly curved, 1–3-septate, smooth-walled, without terminal appendages and sheath. Asexual morph: Coelomycetous. *Conidiomata* 90–115 µm high × 130–150 µm diam. ($\bar{x}$ = 105 × 135 µm; n = 10), pycnidial, solitary, immersed in substrate to superficial, visible as black dots covered by epidermal tissues, multiloculate, globose to subglobose, glabrous, ostiole central, with minute papilla. *Conidiomata wall* 20–25 µm wide ($\bar{x}$ = 23.2 µm; n = 20), thin-walled, of equal thickness, composed of several layers of hyaline to brown, pseudoparenchymatous cells, outer layers comprising 1–2 cell layers of thick-walled, dark brown, organized in a *textura angularis*, inner layers comprising 3–4 layers of thin-walled, hyaline, organized in a *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–5.5 × 2–3 µm ($\bar{x}$ = 3.5 × 1.8 µm; n = 30), phialidic, doliiform to lageniform, hyaline, aseptate, smooth-walled. *Conidia* 7.5–11 × 2–3 µm ($\bar{x}$ = 10 × 2.5 µm; n = 30), solitary, hyaline, oblong to ellipsoidal, with rounded or obtuse ends, smooth-walled, guttlue concentrated to ends.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 20–30 mm diam. after 4 weeks at 18 ° C, with irregular, forming two layers, outer layer grey to black, center dark brown, reverse dark brown in center and greenish brown at margin.

Figure 34 – *Pseudocoleophoma bauhiniae* (MFLU 18–2178, holotype). a Host decaying pod. b Ascomata on substrate. d Section through ascoma. e Cellular pseudoparaphyses. f–h Ascospores. i–m Asci. Scale bars: a = 1 cm, d = 50 µm, e–h = 10 µm, i–m = 20 µm.

Material examined – THAILAND, Payao Province, on decaying pod of *Bauhinia* sp. (Fabaceae), 27 June 2017, S.C. Jayasiri, C 251 (MFLU 18–2117, holotype; KUN-HKAS 102419, isotype), ex-type living culture MFLUCC 17–2586, KUMCC 18–0280; C 248 (MFLU 18–2116); living culture MFLUCC 17–2280, KUMCC 18–0281.

GenBank numbers – MFLUCC 17–2280: SSU: MK347843, ITS: MK347735, LSU: MK347952, *tef1*: MK360075; MFLUCC 17–2586: SSU: MK347844, ITS: MK347736, LSU: MK347953, *tef1*: MK360076

Notes – *Pseudocoleophoma bauhiniae* forms a sister clade to *P. polygonicola* with moderate support. *Pseudocoleophoma bauhiniae* also shares similar morphology with *P. polygonicola* in having scattered 2–4 grouped, immersed to erumpent ascomata and fusiform, 1-septate ascospores with a sheath (Fig. 34). In addition, these two species have an asexual morph with similar morphology. *Pseudocoleophoma polygonicola* differs from *P. bauhiniae* in having larger ascomata with a long ostiolar neck, equally thickening peridium, 2–3 seriately arrange ascospores in asci, wide hamathecium (2–2.5 µm vs. 1.5–2 µm) and large ascospores (20.6 × 4.8 µm vs. 18 × 4 µm). A comparison of the ITS regions reveals *Pseudocoleophoma bauhiniae* differs from *P. polygonicola* by 27 (5.1%) nucleotide difference that warrants separate species status (Jeewon & Hyde 2016). Therefore, based on the morphological differences and with phylogenetic support, we introduce the new species.

Furthermore, we isolated the asexual morph of *Pseudocoleophoma bauhiniae* (Fig. 35) from the same substrate and this strain (MFLUCC 17–2280) sister clades to sexual morph strain (MFLUCC 17–2286) with high statistical support (100% MLBS/1.0 BYPP, Fig. 31). These two strains had only one nucleotide difference in ITS regions. Thefore, we confirm MFLUCC 17–2280 is the asexual morph of *Pseudocoleophoma bauhiniae*.

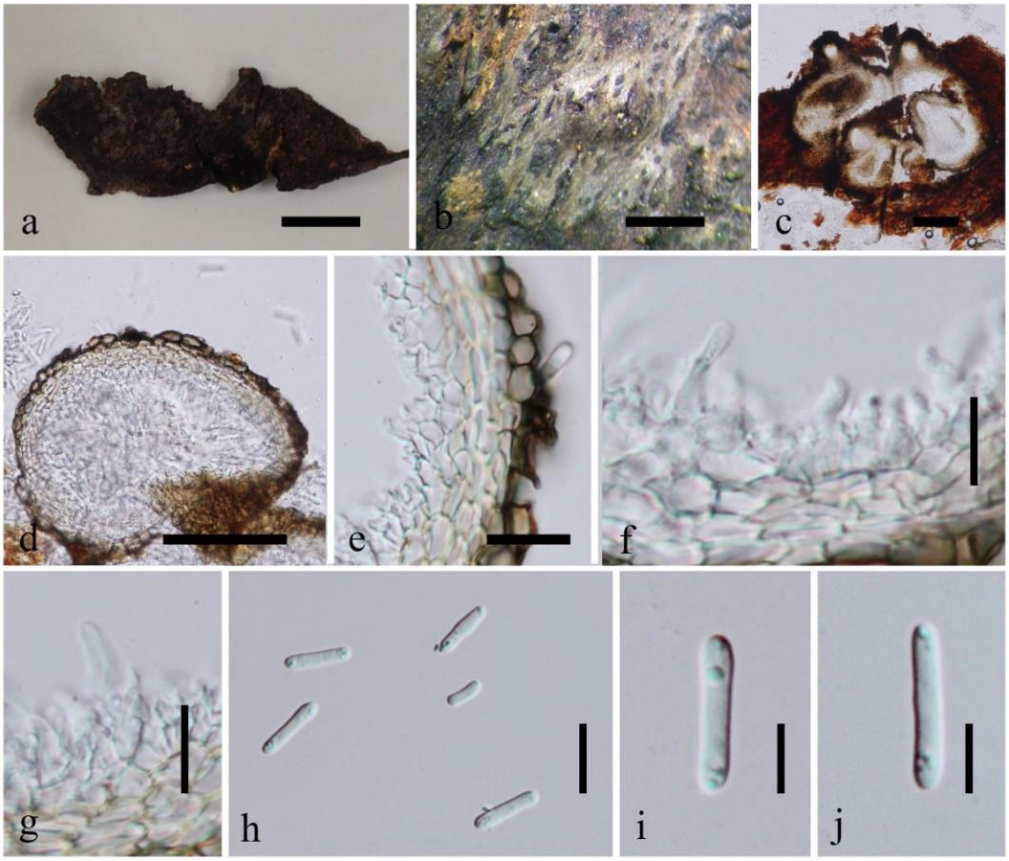


Figure 35 – Asexual morph of *Pseudocoleophoma bauhiniae* (MFLUCC 17–2280). a Seed pods of *Bauhinia* sp. b Conidiomata in the substrate. c Section through conidiomata. d Section through conidioma. e Conidioma wall. e Appendages. f, g Conidiogenous cells. h–j Conidia. Scale bars: a = 1 cm, b = 500 µm, c, d = 100 µm, e = 20 µm, f–h = 10 µm, i, j = 5 µm.

Pseudodictyosporium Matsush., Bulletin of the National Science Museum Tokyo 14 (3): 473 (1971)

Matsushima et al. (1971) introduced this genus based on the type species, *Pseudodictyosporium wauense*. We introduce a new host record for this species based on morphological similarities.

23. *Pseudodictyosporium wauense* Matsush. Bulletin of the National Science Museum Tokyo 14(3): 473 (1971) Fig. 36

Saprobic on leaf, stem and cupule of *Fagus sylvatica*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Conidiomata* on natural substratum sporodochia, superficial, punctiform to effuse, scattered, sometimes coalescing, pale brown to dark brown, without mucilage covering, rarely inconspicuous. *Mycelium* immersed, composed of septate, branched, subhyaline to pale brown, smooth-walled hyphae. *Conidiophores* micronematous, aseptate, simple, hyaline to pale brown, smooth. *Conidiogenous cells* integrated, holoblastic, terminal, determinate, doliiform to cylindrical. *Conidia* 17–19 × 10–14 μm, ($\bar{x}$ = 17.5 × 13 μm, n = 30), acrogenous, solitary, dry, cheiroid, pale brown, euseptate or distoseptate, with three rows of cells arising parallelly from truncate basal cell with three rows in different planes, smooth-walled.

Material examined – UK, Bishop Waltham, Hampshire from standing water in a moat, on decaying cupule fruits of *Fagus sylvatica* (Fagaceae), 12 August 2017, EBG Jones, GJ 416 (MFLU 18–2228, new host record).

Known distribution – Papua New Guinea (Matsushima 1971), China (Li et al. 2017a), UK (this study)

Notes – *Pseudodictyosporium wauense* was observed on decaying fruits of *Fagus sylvatica* in UK. This strain shares similar morphology with *Pseudodictyosporium wauense* in having pale brown to dark brown sporodochia, integrated, holoblastic, doliiform to cylindrical conidiogenous cells and cheiroid, pale brown, euseptate or distoseptate conidia (Fig. 36). In addition, conidia consist of a truncate basal cell with three rows of cells arise in parallel (Matsushima et al. 1971, Li et al. 2017a). Our collection identified based only on morphology as single spore isolation was unsuccessfull.

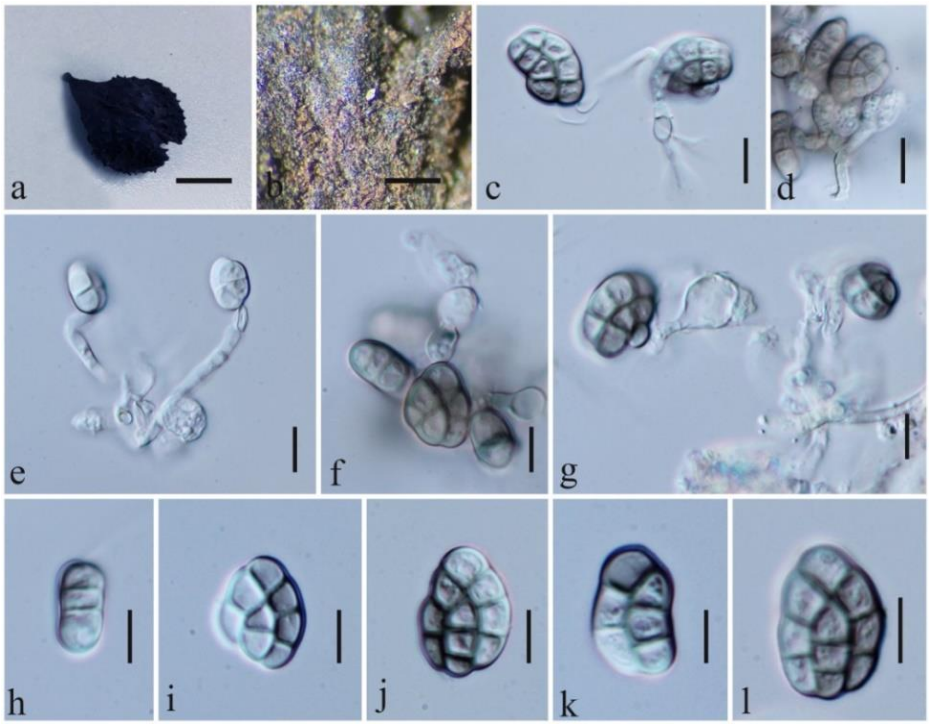


Figure 36 – *Pseudodictyosporium wauense* (MFLU 18–2228). a Host cupule of *Fagus sylvatica*. b Colonies on host fruit. c–g Conidiogenous cells. h–l Conidia. Scale bars: a = 1 cm, c–l = 10 μm.

Didymellaceae Gruyter, Aveskamp & Verkley, Mycological Research 113 (4): 516 (2009)

Family contains economically important plant pathogens (de Gruyter et al. 2013, Valenzuela-Lopez et al. 2018), diverse endophytic, fungicolous and lichenicolous members (Aveskamp et al. 2010), as well as a few human pathogens (de Hoog et al. 2011). This family comprises 26 genera (Fig. 44) (Valenzuela-Lopez et al. 2018). We introduce 4 new species and three new records for this family.

Allophoma Q. Chen & L. Cai, Studies in Mycology 82: 162 (2015)

Based on phylogenetic data, the genus *Allophoma* was introduced to accomodate the type species, *Allophoma tropica* (Chen et al. 2015). Presently, this genus comprises nine species and here we introduce a new species, *Allophoma siamensis* (Fig. 37).

24. *Allophoma siamensis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 38

Index Fungorum number: IF555550; Facesoffungi number: FoF05252

Holotype – MFLU 18–2124

Etymology – Referring to the country (Siam former name for Thailand) where specimen was collected.

Saprobic on *Radermachera sinica* pod. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 70–90 µm high × 68–85 µm diam. ($\bar{x}$ = 86 × 75 µm, n = 10), pycnidial, brown to dark brown, confluent, superficial and immersed (in seed pods), glabrous, ovoid, with a single papillate ostiolar neck. *Conidiomata wall* 8–26 µm wide ($\bar{x}$ = 22 µm, n = 10), 2–4-layered, composed of brown to dark brown *textura angularis* cells. *Conidiogenous cells* 3–6 × 4–5 µm ($\bar{x}$ = 4.5 × 4.8 µm, n = 10), phialidic, hyaline, ampulliform, smooth-walled. *Conidia* 3–4 × 2–3 µm ($\bar{x}$ = 3.5 × 2.8 µm, n = 10), solitary, hyaline, cylindrical, aseptate, smooth- and thin-walled, guttulate. Chlamydospores absent.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 36 mm diam. after 1 week at 18 ° C, flattened, top grey; reverse dark brown.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on decaying pod of *Radermachera sinica* (Bignoniaceae), 3 July 2017, S.C. Jayasiri, C 270 (MFLU 18–2124, holotype; KUN-HKAS 10242, isotype), dry culture 18–2125, ex-type living culture MFLUCC 17–2422, KUMCC 18–0211.

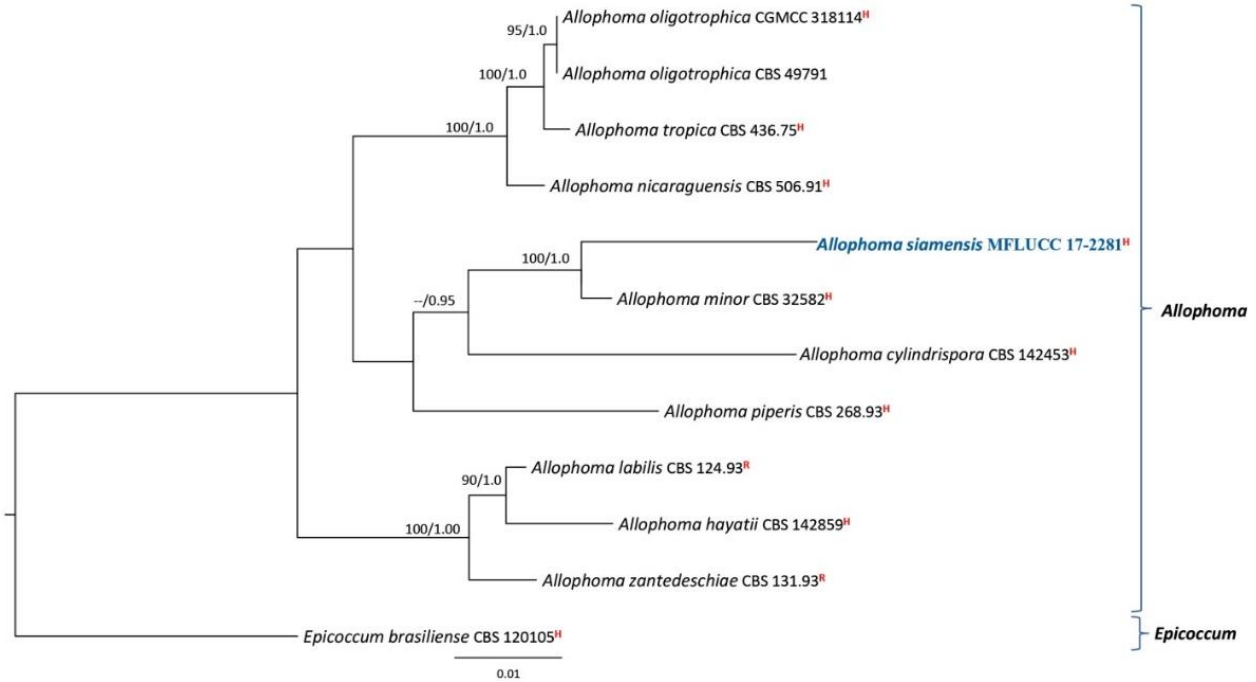


Figure 37 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined ITS, LSU, *rpb2* and *tub2* matrix of twelve taxa including related species of the genus *Allophoma* (Valenzuela-Lopez et al. 2018). The matrix comprised 2713 characters including alignment gaps. The tree was rooted with *Epicoccum brasiliense* (CBS 120105). The best scoring RAxML tree with a final likelihood value of -6509.571102 is presented. The matrix had 294 distinct alignment patterns, with 10.91% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244802, C = 0.240941, G = 0.273868, T = 0.240389; substitution rates AC = 1.284768, AG = 2.506107, AT = 1.125523, CG = 0.949740, CT = 8.024084, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}and ^{R} respectively.

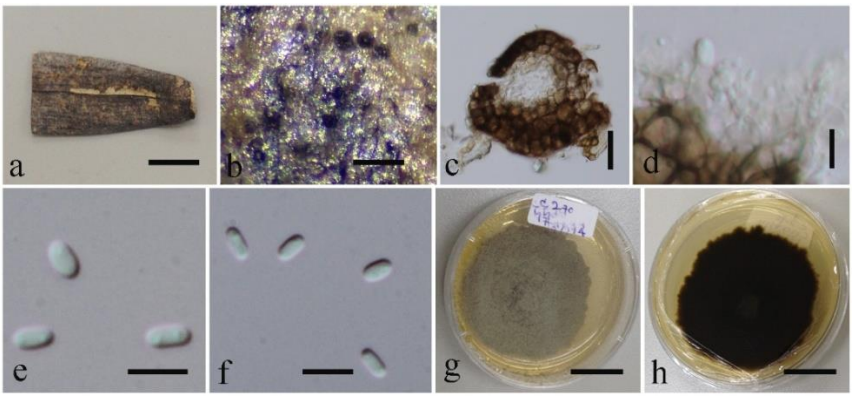


Figure 38 – *Allophoma siamensis* (MFLU 18–2124, holotype). a Host pod. b Conidiomata in the substrate. c Section through conidioma. d Conidiogenous cells. e, f Conidia. g Top view of colony on MEA. h Reverse view of colony. Scale bars: a, g, h = 1 cm, b = 500 μm, c = 20 μm, d–f = 5 μm.

GenBank numbers – SSU: MK347850, ITS: MK347742, LSU: MK347959, *tef1*: MK340859, *rpb2*: MK434912, *tub2*: MK412867, actin: MK412890

Notes – *Allophoma siamensis* forms a distinct clade from its closest relative, *Allophoma minor* (CBS 32582) with high support (100% MLBS/1.0 BYPP, Fig. 37). Most of the species in the family Didymellaceae share similar morphology and species segregation is based on molecular data of protein coding genes (Aveskamp et al. 2010, Chen et al. 2015). *Allophoma siamensis* and *A. minor* also share similar morphology in having phialidic, hyaline, smooth-walled conidiogenous cells and aseptate, hyaline, cylindrical, conidia with guttules (Fig. 38). (Chen et al. 2015). A comparison of the *rpb2* and *tub2* nucleotides of these two species reveal 60 (16.6%) and 7 (2.2%) nucleotide differences, respectively, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Didymella Sacc., Michelia 2 (6): 57 (1880)

Didymella contains very important and serious plant pathogenic species, as well as species that are endophytic and saprobic on a wide range of plant (Aveskamp et al. 2010, Chen et al. 2015, Jayasiri et al. 2017, Valenzuela-Lopez et al. 2018). We introduce a new host record from decaying seed pod of *Leucaena* sp. and a new species from cones of *Magnolia grandiflora* (Fig. 39).

25. *Didymella coffeae-arabicae* (Aveskamp, Verkley & Gruyter) Qian Chen & L. Cai, Studies in Mycology 82: 175 (2015) Fig. 40

Facesoffungi number: FoF05254

Saprobic or *pathogenic* on *Coffea Arabica*, *Euphorbia* sp., *Lagerstroemia indica* and *Leucaena* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 81–111 μm long × 65–78 μm diam. ($\bar{x}$ = 98 × 72 μm, n = 10), pycnidial, solitary or in chains, on the agar

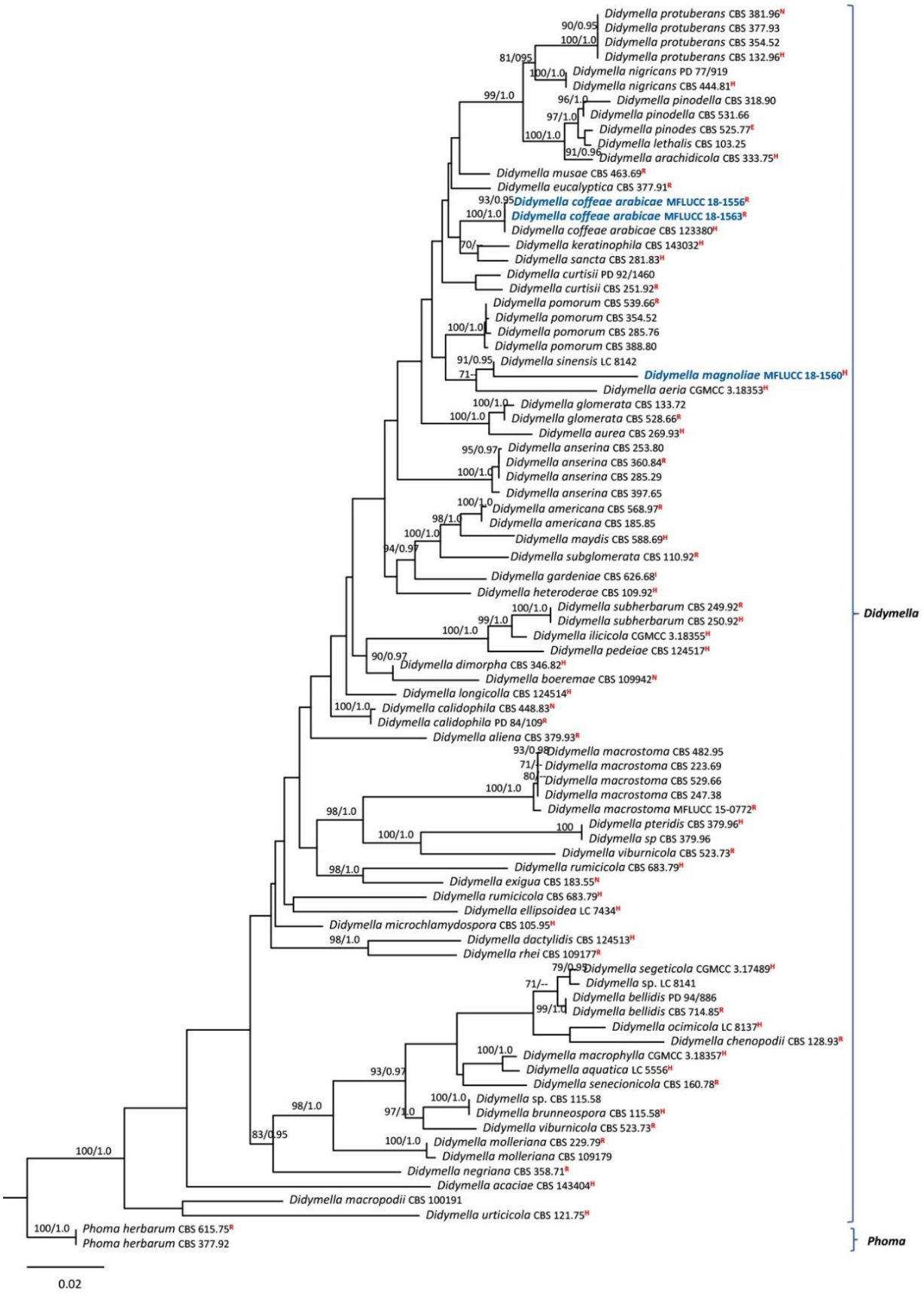


Figure 39 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined ITS, LSU, *rpb2* and *tub2* matrix of eighty-six taxa including related species of the genus *Didymella* (Valenzuela-Lopez et al. 2018). The matrix comprised 2770 characters including alignment gaps. The tree was rooted with *Phoma herbarum* (CBS 615.75, CBS 377.92).

The best scoring RAxML tree with a final likelihood value of -14265.646619 is presented. The matrix had 569 distinct alignment patterns, with 11.70% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241244, C = 0.239343, G = 0.275964, T = 0.243448; substitution rates AC = 1.071831, AG = 4.726251, AT = 1.430141, CG = 0.673042, CT = 9.723633, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolates are in bold and blue. Strains isolated from the holotype, isotype, neotype and reference specimens are indicated in red superscript ^{H}, ^{I}, ^{N} and ^{R} respectively.

surface or submerged, variable in shape, ovoid to subglobose or elongated, glabrous, ostiolate. *Conidiomata wall* 11–15 µm wide ($\bar{x}$ = 12.5 µm, n = 20), pseudoparenchymatous, composed of *textura angularis*. *Conidiogenous cells* 6–7.2 × 5.3–7 µm ($\bar{x}$ = 6.8 × 6.3 µm, n = 30), phialidic, hyaline, simple, smooth, flask-shaped to globose. *Conidia* 4–6.4 × 2.3–3.6 µm ($\bar{x}$ = 5.8 × 3.3 µm, n = 30), hyaline, ellipsoidal to ovoid, variable in length, aseptate, thin-walled, smooth, with minute guttules.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA 57–70 mm diam. after 2 weeks at 18 ° C, with entire, smooth, distinct margin. Aerial mycelium condensed, white with rosy-vinaceous tinges. Agar surface iron-grey. Reverse fulvous to amber, but leaden black in zones with abundant pycnidia.

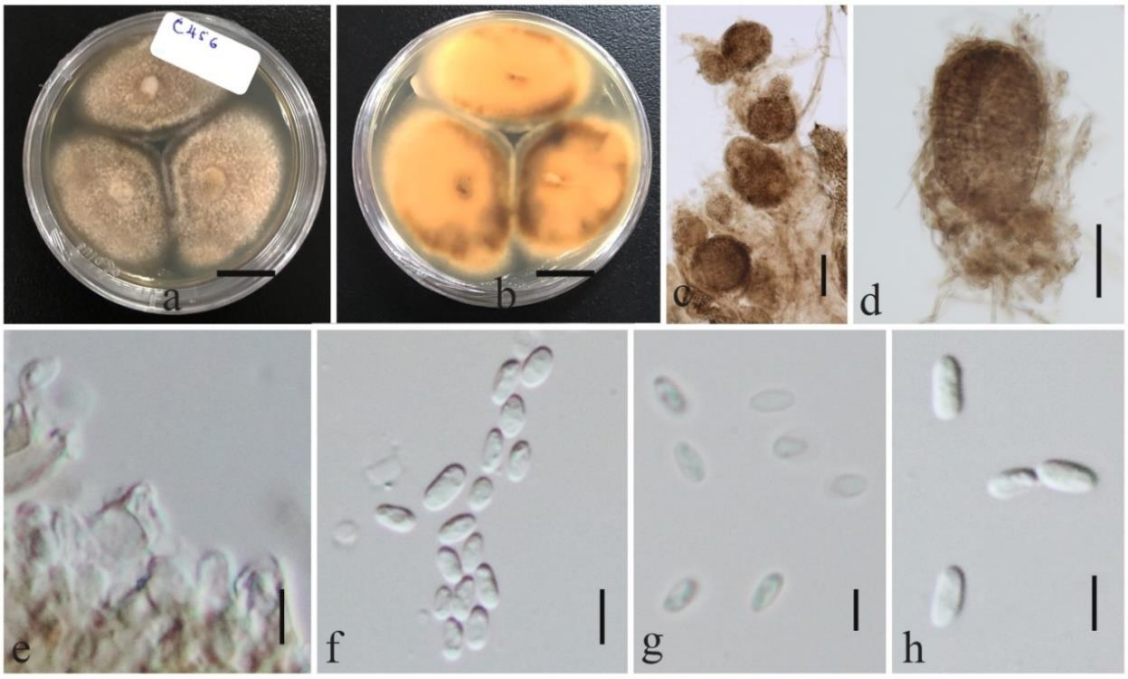


Figure 40 – *Didymella coffeae-arabicae* from the culture (MFLUCC 18–1563). a Top view of culture. b Reverse view of culture. c Conidioamata. d Conidioama. e Conidiogenous cells. f–h Conidia. Scale bars: a, b = 1 cm, c, d = 50 µm, e–h = 5 µm.

Material examined – CHINA, Kunming, Kunming Institute garden, on decaying pod of *Leucaena* sp. (Fabaceae), 25 May 2018, S.C. Jayasiri, C 456 (MFLU 18–2211, new host record), living culture MFLUCC 18–1563, KUMCC 18–0232; C 461-A (MFLU 18–2217) living culture MFLUCC 18–1556, KUMCC 18–0233.

GenBank numbers – MFLUCC 18–1563: SSU: MK347913, ITS: MK347805, LSU: MK348024, *rpb2*: MK434859, *tub2*: MK412869, actin: MK412887; MFLUCC 18–1556: SSU: MK347918, ITS: MK347810, LSU: MK348029, *rpb2*: MK434913, *tub2*: MK412871, actin: MK412889

Known distribution – Italy, on *Lagerstroemia indica* (Chen et al. 2017); Ethiopia, on *Coffea*

arabica (Aveskamp et al. 2009); Russia, on phyllosphere of *Euphorbia* sp.; China on decaying pod of *Leucaena* sp. (this study).

Notes – Our two new strains form a sister clade to *Didymella coffeae-arabicae* (CBS 123380) with high statistical support (100% MLBS/1.0 BYPP, Fig. 39) and share similar morphological characters with the type strain of *D. coffeae arabicae* (Aveskamp et al. 2009). *Didymella coffeae-arabicae* is characterized by solitary or chains of pycnidia, which are flask-shaped to globose; ellipsoidal to ovoid conidiogenous cells and hyaline, aseptate conidia (Fig. 40). These charcaters are shared with our strains with chlamydospores in culture as described in Aveskamp et al. (2009). A comparison of ITS, *rpb2* and *tub2* nucleotides of new strains (MFLUCC 18–1563 and MFLUCC 18–1556) and existing strain (CBS 123380) reveals no nucleotide differences, which indicates that they are not distinct taxa (Jeewon & Hyde 2016). Therefore, a new record of *Didymella coffeae-arabicae* from seed pod of *Leucaena* sp. host in China is documented.

26. *Didymella magnoliae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 41

Index Fungorum number: IF 555552; Facesoffungi number: FoF 05255

Holotype – MFLU 18–2222

Etymology – Referring to the host on which the fungus was collected, *Magnolia* (Magnoliaceae).

Saprobic on *Magnolia grandiflora* cone. Asexual morph: Coelomycetous. *Conidiomata* 90–130 µm long × 80–95 µm diam. ($\bar{x}$ = 122 × 88 µm; n = 30), pycnidial, mostly solitary, on the agar surface or submerged, mostly ovoid but also subglobose or elongated, glabrous, papillate or with an elongated neck. *Ostioles* variable in size, and sometimes relatively wide. *Conidiomata wall* 10–17 µm wide ($\bar{x}$ = 13.5 µm; n = 30), pseudoparenchymatous, composed of oblong to isodiametric cells, 3–5 layers. *Conidiogenous cells* 7.2–9 × 5–7 µm ($\bar{x}$ = 8.5 × 6.4 µm; n = 30), phialidic, hyaline, simple, smooth, flask-shaped to globose. *Conidia* 4.5–6 × 3–4 µm ($\bar{x}$ = 5.5 × 3.4 µm; n = 30), hyaline, ellipsoidal to ovoid, variable in length, aseptate, thin-walled, smooth, eguttulate or with 1–4-minute guttules.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA 57–70 mm diam. after 2 weeks at 18ºC, with entire, smooth, distinct margin. Aerial mycelium condensed, white with rosy-vinaceous tinges. Agar surface iron-grey. Reverse fulvous to amber, but leaden black in zones with abundant pycnidia.

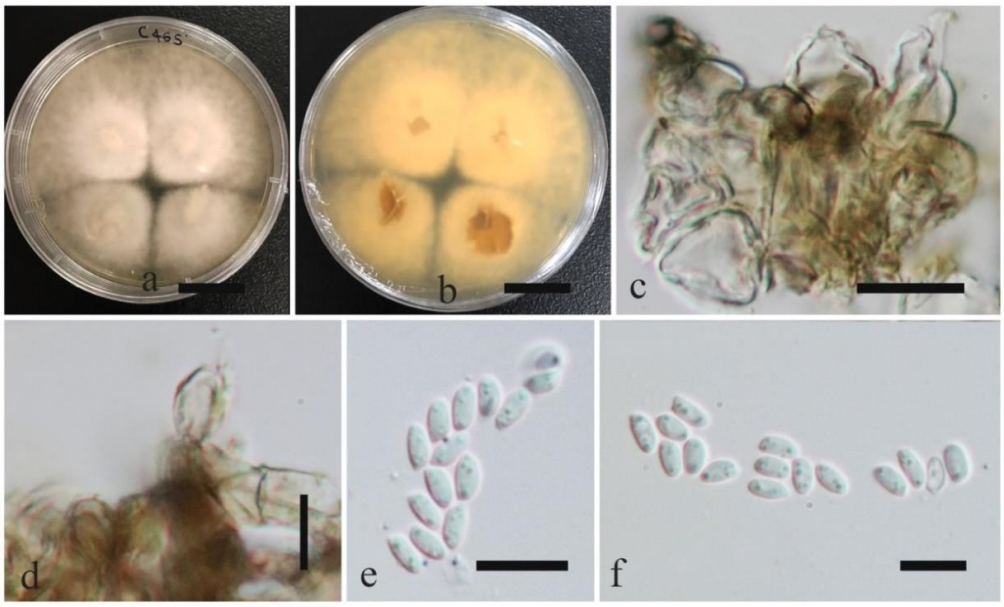


Figure 41 – *Didymella magnoliae* from culture (MFLUCC 18–1560, ex-type). a Top view of culture. b Reverse view of culture. c, d Formation of conidiogenous cells. e, f Conidia. Scale bars: a, b = 1 cm, c–f = 10 µm.

Material examined – CHINA, Yunnan Province, Kunming Institute garden, on decaying cone of *Magnolia grandiflora* (Magnoliaceae), 25 May 2018, S.C. Jayasiri, C 465 (MFLU 18–2222, holotype, MFLU 18–2223, isotype), ex-type living culture MFLUCC 18–1560, KUMCC 18–0236.

GenBank numbers – SSU: MK347922, ITS: MK347814, LSU: MK348033, *rpb2*: MK434852

Notes – *Didymella magnoliae* groups in a sister clade to *Didymella sinensis* with high support (91% MLBS/0.95 BYPP, Fig. 39). *Didymella sinensis* is reported only as the sexual morph from diseased leaves of three host families (Rosaceae, Orchidaceae and Urticaceae) indicative of an opportunistic pathogenic lifestyle (Chen et al. 2017). *Didymella magnoliae* asexual morph is reported here from a decaying cone of *Magnolia grandiflora* (Fig. 41). Therefore, only sequence data can be used to separate these strains. However, *D. magnoliae* fits with the generic description of *Didymella* in having amphigenous, separate, globose, brown, uni- locular pycnidia, phialidic, determinate, doliiform to lageniform conidiogenous cells and hyaline, thinwalled, smooth-walled, guttulate, cylindrical to irregular conidia (Saccardo 1880). A comparison of the ITS, *rpb2* and *tub2* nucleotides of these two strains reveals 6 (1.2%), 27 (4.5%) and 12 (3.9%) nucleotide differences which indicates that they are two distinct taxa (Jeewon & Hyde 2016).

Nothophoma Q. Chen & L. Cai, Studies in Mycology 82: 212 (2015)

This genus is typified by *Nothophoma infossa* and was established to accommodate five *Phoma* species which clustered in a monophyletic clade in Didymellaceae (Chen et al. 2015). This genus is ubiquitous and includes many important plant pathogens, some of which are of quarantine concern (Aveskamp et al. 2008, 2010, Chen et al. 2015). We introduce a new record of *Nothophoma quercina* from decaying cone of *Keteleeria fortune* in China. Many strains of this species have been reported as pathogens of different host plant species (Jianyu et al. 2016, Yun & Oh 2016, Chen et al. 2017, Jiao et al. 2017, Moral et al. 2017, Liu et al. 2018, Valenzuela-Lopez et al. 2018), as well as from human superficial foot lesion (Valenzuela-Lopez et al. 2018). An updated phylogenetic tree for the genus is presented in Fig. 42 and a new host record for *Nothophoma quercina* is introduced.

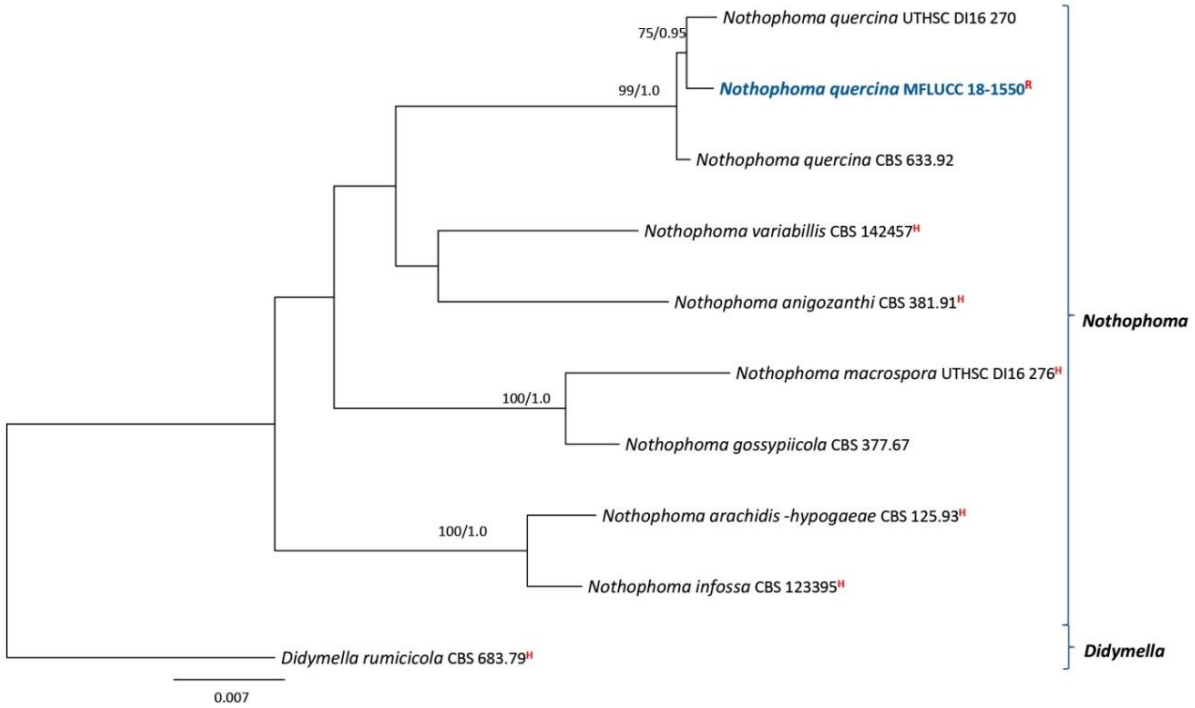


Figure 42 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined ITS, LSU, *rpb2* and *tub2* matrix of eight strains including related species of the

genus *Nothophoma* (Valenzuela-Lopez et al. 2018). The matrix comprised 2698 characters including alignment gaps. The tree is rooted with *Didymella rumicicola* (CBS 683.79). The best scoring RAxML tree with a final likelihood value of -5686.669693 is presented. The matrix had 175 distinct alignment patterns, with 7.93% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242029, C = 0.239130, G = 0.277174, T = 0.241667; substitution rates AC = 1.025250, AG = 3.394380, AT = 1.310418, CG = 0.819358, CT = 12.753666, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

27. *Nothophoma quercina* (Syd. & P. Syd.) Qian Chen & L. Cai, Studies in Mycology 82: 213 (2015) Fig. 43

Facesoffungi number: FoF05256

Saprobic or *fungicolous* on *Quercus* sp., *Keteleeria fortune* and human superficial foot lesion. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 76–140 µm high × 95–165 µm diam. ($\bar{x}$ = 125 × 132 µm, n = 10), pycnidial, solitary, produced on the agar surface, globose to subglobose, conspicuous, non-papillate ostiolate. *Conidiomata wall* 12–16 µm wide ($\bar{x}$ = 14.5 µm, n = 20), pale brown, pseudoparenchymatous, 3–5 layers. *Conidiogenous cells* 7.7–8.6 × 5.2–6.7 µm ($\bar{x}$ = 8.2 × 6.3 µm, n = 30), phialidic, hyaline, simple, smooth, doliiform to ampulliform. *Conidia* 5.1–6.5 × 3.3–4.5 µm ($\bar{x}$ = 6.2 × 4.1 µm, n = 30), initially hyaline, pale brown at maturity, variable in shape, subglobose to oval or obtuse, aseptate, thin-walled, smooth, guttulate.

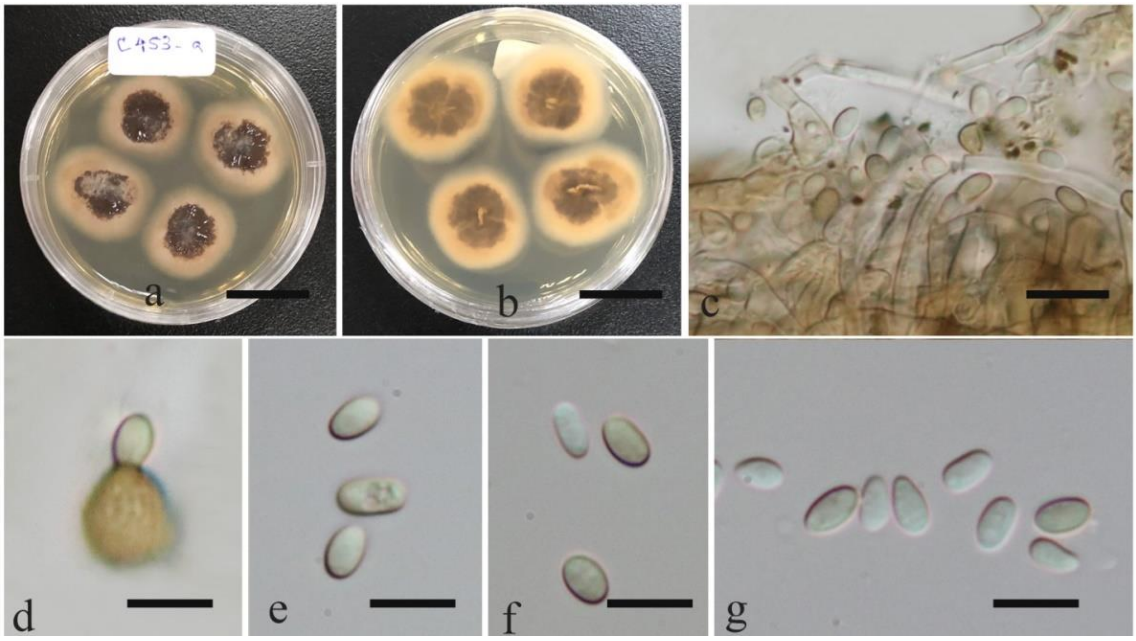


Figure 43 – *Nothophoma quercina* from culture (MFLUCC 18–1550). a Top view of culture. b Reverse view of the culture. c Hyphae and formation of conidia. d Conidiogenous cell. e–g Conidia. Scale bars: a, b = 1 cm, c–g = 10 µm.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA 60 mm diam. after 2 weeks at 18°C, margin regular. Aerial mycelium covering the whole colony, compact, white to pale grey, with olivaceous tinges near the colony centre; reverse olivaceous-black in centre, margin yellow to pale brown.

Material examined – CHINA, Kunming, Kunming Institute garden, on decaying cone of *Keteleeria fortunei* (Pinaceae), 25 May 2018, S.C. Jayasiri, C 453-A (MFLU 18–2206-A, new host

record), living culture MFLUCC 18–1550, KUMCC 18–0269.

GenBank numbers: SSU: MK347909, ITS: MK347801, LSU: MK348020, *tef1*: MK340876, *rpb2*: MK434911, *tub2*: MK412880, actin: MK412891, calmodulin: MK412897

Known Distribution – China, causing brown spot on *Ziziphus jujube* (Jianyu et al. 2016); China, and leaf spot disease of *Phellodendron amurense* (Jiao et al. 2017), causing trunk canker on *Malus micromalus* (Liu et al. 2018), on decaying cone of *Keteleeria fortunei* (this study); Italy, on dead branch of *Ulmus* × *hollandica* (Tibpromma et al. 2017), Korea, causing shoot canker on *Chaenomeles sinensis* in China (Yun & Oh 2016), Spain and Tunisia, dieback of *Olea europaea* (Moral et al. 2017), Ukraine, on *Quercus* sp. (Chen et al. 2017, Moral et al. 2017, Valenzuela-Lopez et al. 2018), USA, from human superficial foot lesion (Valenzuela-Lopez et al. 2018).

Notes – *Nothophoma quercina* forms a sister clade to *N. quercina* (UTHSC DI16 270) with high statistical support (75% MLBS/0.95 BYPP, Fig. 42). It also shares similar morphological characters with the type strain of *N. quercina* in having solitary, globose to subglobose pycnidia with non-papillate ostiole, doliform conidiogenous cells and variable shaped, hyaline or pale brown conidia (Fig. 43). A comparison of the ITS, *rpb2* and *tub2* nucleotides of these two strains reveals less than ≤ 1.5% nucleotide differences which indicates that our isolate is *Nothophoma quercina* (Jeewon & Hyde 2016).

Remotididymella Valenz.-Lopez, Crous, J.F. Cano, Guarro & Stchigel, Studies in Mycology 90: 35 (2017)

This genus was introduced by Valenzuela-Lopez et al. (2018) based on a phylogenetic study, which showed it was distinctness from other genera in family Didymellaceae. Currently, this genus comprises two species namely, *Remotididymella anthropophila* (isolated from human sample) and *R. destructiva* (from fruit of *Lycopersicon esculentum*). Both species are known only as coelomycetous asexual morphs (Valenzuela-Lopez et al. 2018), but we introduce a new, sexual morph species (Fig. 44).

28. *Remotididymella bauhiniae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 45, 46

Index Fungorum number: IF555553; Facesoffungi number: FoF05257

Holotype – MFLU 18–2118

Etymology – Referring to the host on which the fungus was collected, *Bauhinia* (Fabaceae).

Saprobic on *Bauhinia* sp. pod. Sexual morph: *Ascomata* 125–150 μm high × 110–125 μm diam. ($\overline{x}$ = 135 × 115 μm; n = 10), immersed or superficial, globose, conical globose to lenticular, scattered or clustered, papillate or apapillate, ostiolate. *Peridium*15–30 μm wide ($\overline{x}$ = 24 μm; n = 20), composed of several layers of brown to hyaline cells of *textura angularis*, fusing at the outside with the host tissue. *Hamathecium* with 1.5–2 μm wide ($\overline{x}$ = 1.7 μm; n = 20), dense, filamentous, septate, branching and hyaline, cellular pseudoparaphyses. *Asci* 70–80 × 5–9 μm ($\overline{x}$ = 75 × 7.5 μm; n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, short-pedicellate, rounded at apex, with an ocular chamber. *Ascospores* 22–26 × 3–6 μm ($\overline{x}$ = 23.5 × 4.5 μm; n = 20), overlapping 2–3-seriate, hyaline, fusiform, 1–3-septate, constricted at middle septum, containing up to four refractive oil globules, irregular, hyaline, gelatinous sheath observed when mounted in Indian ink. Asexual morph: Conidiomata not observed in culture. *Chlamydospores* 8–12 × 3–4 μm ($\overline{x}$ = 10 × 3.5 μm; n = 20), intercalary or terminal, solitary, subhyaline to dark brown, variable, irregular, verruculose or incidentally tuberculate, 1–2 cells, smooth.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies reaching 15 mm diam. after 1 week, flattened, top and reverse olive brown to dark grey, top white mass of hyphal growth, NaOH spot test negative. Crystals absent.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on decaying pod of *Bauhinia* sp. (Fabaceae), 27 June 2017, S.C. Jayasiri, C 254 (MFLU 18–2118, holotype), ex-type living culture MFLUCC 17–2281, KUMCC 18–0296.

GenBank numbers – SSU: MK347845, ITS: MK347737, LSU: MK347954, *rpb2*: MK434914, *tub2*: MK412884, actin: MK412894

Notes – *Remotididymella bauhiniae* forms a sister clade to *R. anthropophila* (CBS 142462) with high support (100% MLBS/1.0 BYPP, Fig. 44). *Remotididymella bauhiniae* is the first record of sexual morph taxon for this genus; we failed to isolate the asexual morph in culture. Therefore, we compared morphology of *R. bauhiniae* (Fig. 45) with family descriptions of Didymellace; characters such as immersed or superficial, globose, conical globose ascomata, filamentous, septate, branched, cellular pseudoparaphyses, clavate to cylindrical, short-pedicellate asci and fusiform, hyaline, 1–3-septate ascospores occur in both (Chen et al. 2015, Valenzuela-Lopez et al. 2018). Base pair difference of ITS, *rpb*2 and *tub*2 genes are 13 (2.6%), 57 (7.8%) and 33(9.9%), respectively, which separates *R. anthropophila* and the new species.

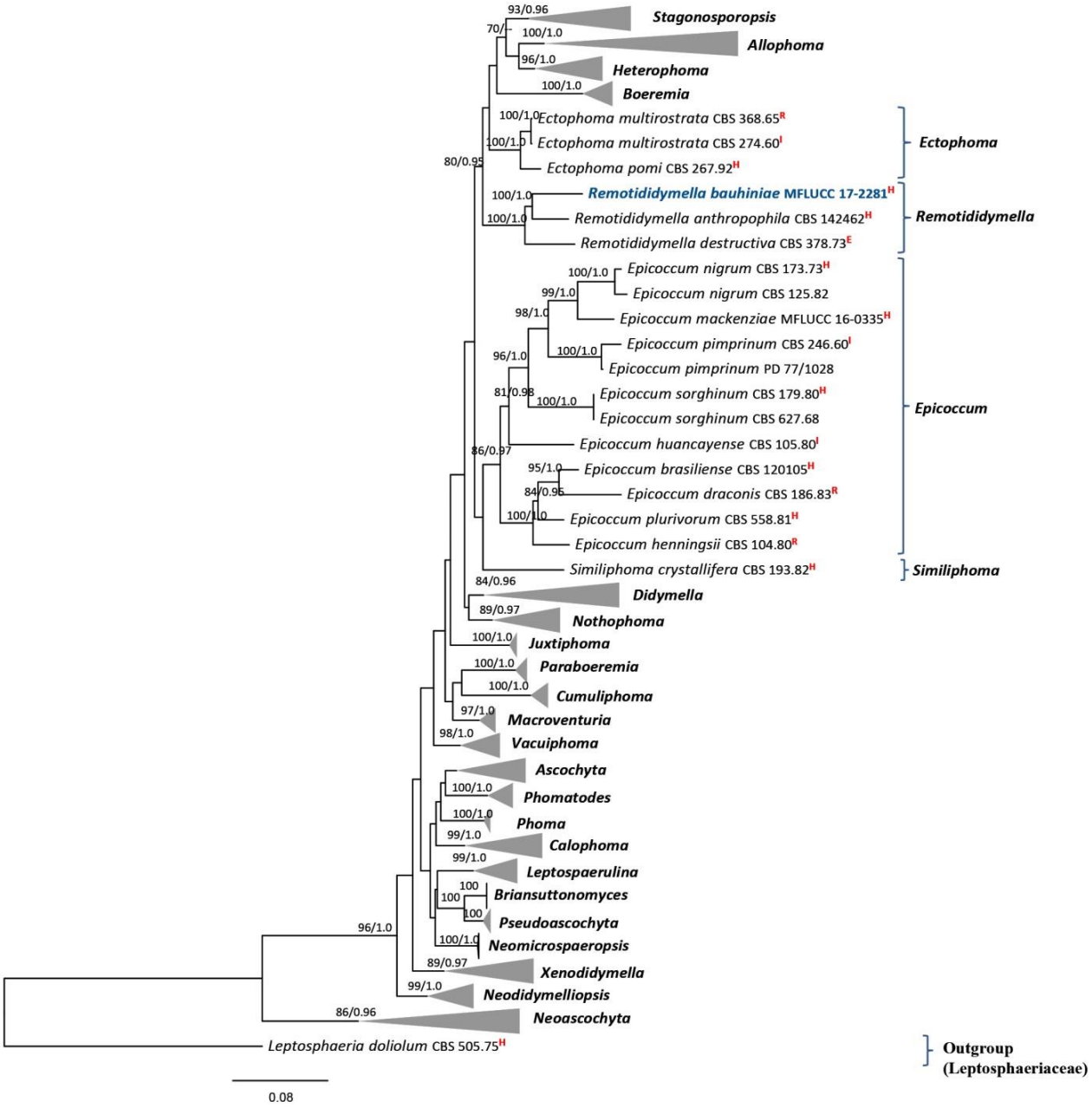


Figure 44 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined ITS, LSU, *rpb*2 and *tub*2 matrix of 246 taxa including related species of the family Didymellaceae (Valenzuela-Lopez et al. 2018). The matrix comprised 2524 characters including alignment gaps. The tree was rooted with *Leptosphaeria doliolum* CBS 505.75 (Leptosphaeriaceae). The best scoring RAxML tree with a final likelihood value of -35336.736875 is presented. The matrix had 942 distinct alignment patterns, with 17.25% of undetermined

characters or gaps. Estimated base frequencies were as follows; A = 0.237767, C = 0.243586, G = 0.273352, T = 0.245295; substitution rates AC = 1.587839, AG = 5.660755, AT = 1.923812, CG = 0.840031, CT = 11.057417, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the epitype, holotype, isotype and reference specimens are indicated in red superscript ^{E}, ^{H}, ^{I} and ^{R} respectively.

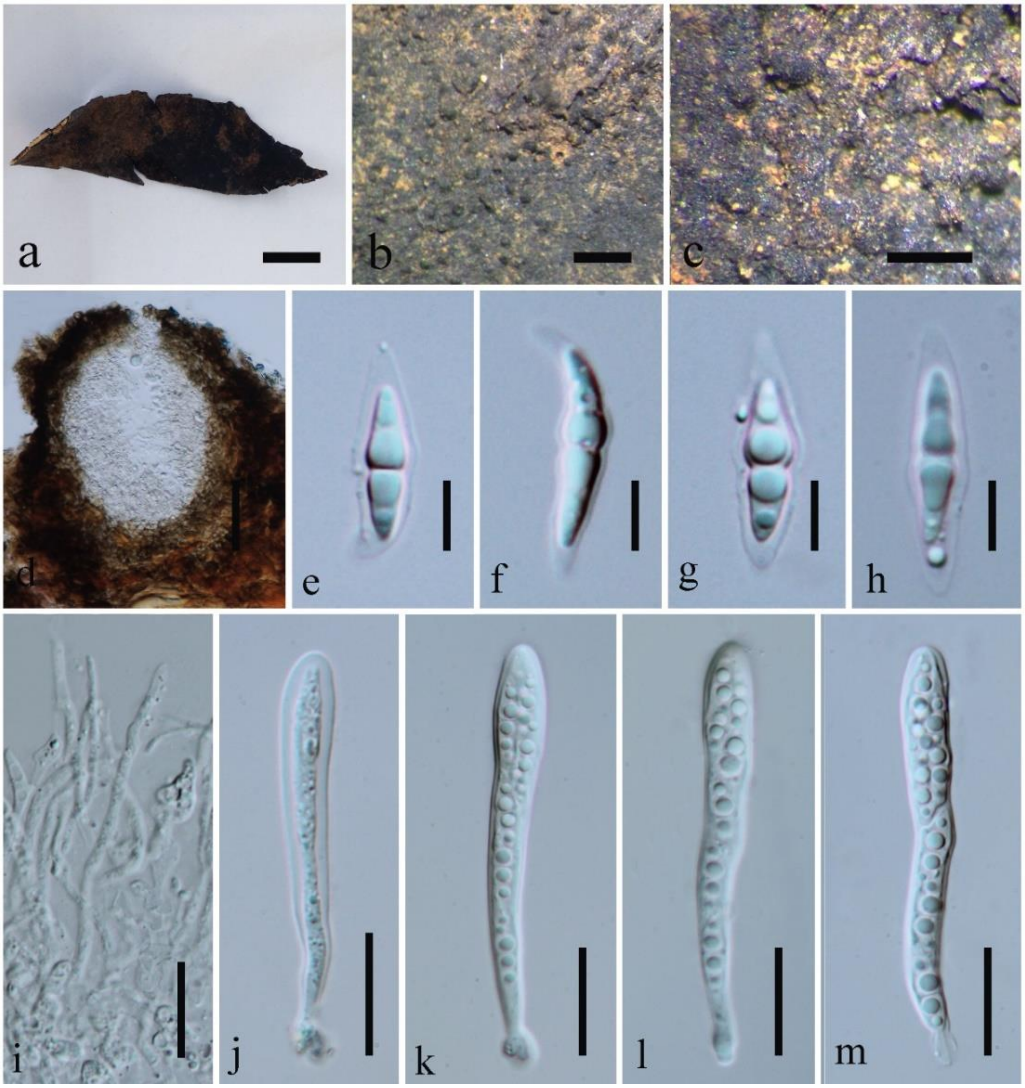


Figure 45 – *Remotididymella bauhiniae* (MFLU 18–2118, holotype). a Host of decaying pod. b, c Ascoma on substrate. d Section through ascoma. e–h Ascospores. i Cellular pseudoparaphyses. j–m Asci. Scale bars: a = 1 cm, b, c = 200 µm, d = 50 µm, e–i = 10 µm, i–k = 20 µm.

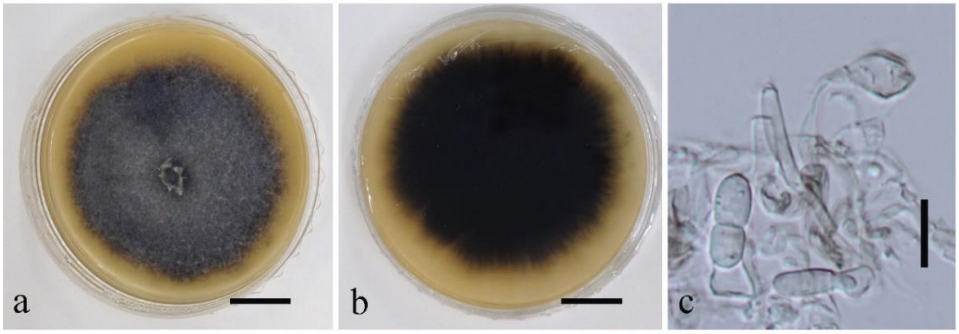


Figure 46 – *Remotididymella bauhiniae* in culture (MFLUCC 17–2281, ex-type). a Top view of colony on MEA. b Reverse view of colony. c Chlamydospores. Scale bars: a, b = 1 cm, c = 10 µm.

Stagonosporopsis Died., Annales Mycologici 10 (2): 142 (1912)

Stagonosporopsis is a coelomycetous genus in Didymellaceae (De Gruyter et al. 2009), accommodating several important phytopathogenic species, some of which have sexual forms in *Didymella* (Diedicke 1912, Aveskamp et al. 2010). Many *Stagonosporopsis* species are considered serious quarantine organisms in parts of the world (Pethybridge et al. 2008, Vaghefi et al. 2012, EPPO 2014). An updated phylogenetic tree for the genus is presented in Fig. 47 and a new species of *Stagonosporopsis* is introduced.

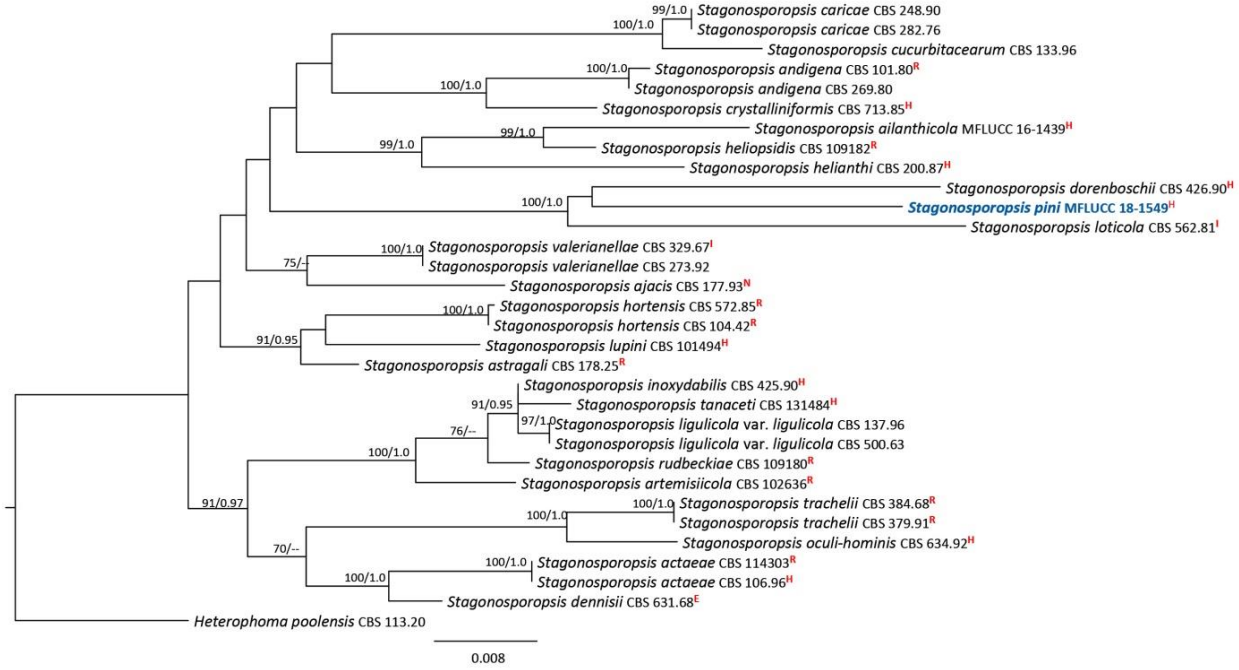


Figure 47 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined ITS, LSU, *rpb2* and *tub2* matrix of thirty-two taxa including related species of the genus *Stagonosporopsis* (Crous et al. 2015). The matrix comprised 2756 characters including alignment gaps. The tree is rooted with *Heterophoma poolensis* (CBS 113.20). The best scoring RAxML tree with a final likelihood value of -8386.622374 is presented. The matrix had 388 distinct alignment patterns, with 11.83% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245798, C = 0.237676, G = 0.273178, T = 0.243348; substitution rates AC = 1.882600, AG = 4.123164, AT = 2.015920, CG = 0.907833, CT = 12.626910, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the epitype, holotype, isotype, neotype and reference specimens are indicated in red superscript ^{E}, ^{H}, ^{I}, ^{N} and ^{R} respectively.

29. *Stagonosporopsis pini* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 48

Index Fungorum number: IF555554; Facesoffungi number: FoF05258

Holotype – MFLU 18–2204

Etymology – Referring to the host on which the fungus was collected, *Pinus* (Pinaceae).

Saprobic on *Pinus* sp. cone. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 105–140 µm high × 122–153 µm diam. ($\bar{x}$ = 125 × 143 µm, n = 10), pycnidial, globose to subglobose, on agar surface or immersed, solitary or confluent, ostiolate or poroid. *Conidiomata wall* 9–26 µm wide ($\bar{x}$ = 19.5 µm, n = 20), pseudoparenchymatous, 2–6 cell layers of which the outer 1–3 are brown/olivaceous. *Conidiogenous cells* 4–7.5 × 3–6 µm ($\bar{x}$ = 5.8 × 4.5 µm, n = 10), lining the inner cavity, ampulliform, hyaline, smooth, with prominent periclinal thickening at apex. *Conidia* 5–6.7 × 2.7–2.9 µm ($\bar{x}$ = 6.1 × 2.8 µm, n = 10), hyaline, ellipsoidal to subglobose, aseptate, thin-walled, smooth, two prominent guttules.

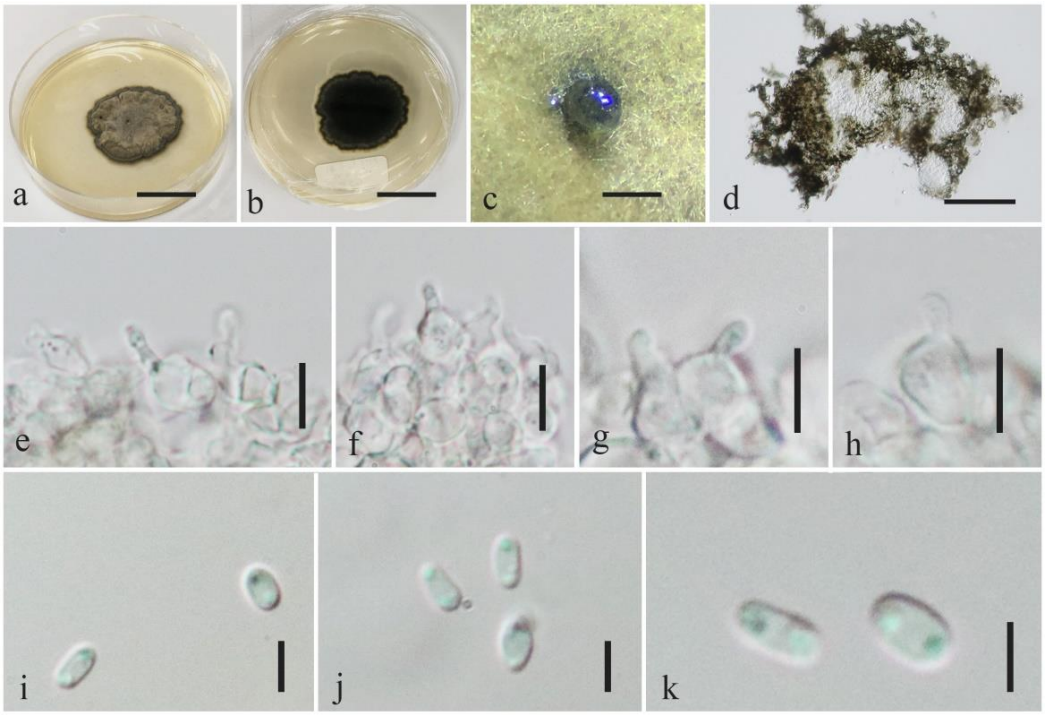


Figure 48 – *Stagonosporopsis pini* (MFLUCC 18–1549, ex-type). a Top view of culture in MEA. b Reverse view of culture in MEA. c Conidioma in culture. d Section through a conidiomata. e–h Conidiogenous cells. i–k Conidia. Scale bars: a, b = 1 cm, c = 200 μm, d = 100 μm, e–k = 5 μm.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced at the end of the conidia. Colonies on MEA reaching 30–40 mm diam. after 2 weeks at 18 ° C, circular, edge lobate, raised, fluffy, dense, convex shaped with white to grey papillate surface, to superficial at the center, flat or effuse at the edge, greyish brown centire and edge brown from above, reverse; olivaceous green centire.

Material examined – CHINA, Yunnan Province, Kunming, Kunming Institute, on decaying cone of *Pinus* sp. (Pinaceae) 15 May 2018, S.C. Jayasiri, C 452 (MFLU 18–2204, holotype, MFLU 18–2205, isotype), ex-type living culture MFLUCC 18–1549; KUMCC 18–0298.

GenBank numbers – SSU: MK347908, ITS: MK347800, LSU: MK348019, *rpb2*: MK434860, *tub2*: MK412886, Calmodulin: MK412896, actin: MK412895

Notes – *Stagonosporopsis pini* groups as sister clade to *Stagonosporopsis dorenboschii* (CBS 426.90) with moderate support (Fig. 47). *S. dorenboschii* has been reported as an opportunistic pathogen (Boerema et al. 2004) from different plant families including Asteraceae (*Callistephus* sp.), causing leaf spots and anthracnose. *Stagonosporopsis pini* is a saprobe on cone of *Pinus* sp. Although the morphological descriptions of *S. dorenboschii* are inadequate, our species fits with the generic description of *Stagonosporopsis* in possessing globose to subglobose pycnidia, ampulliform conidiogenous cells and aseptate, hyaline, ellipsoidal to subglobose conidia with guttules (Fig. 48).

Species in this family are mainly based on molecular data as the morphotaxonomic characters are sparse (Chen et al. 2015). Base pair differences between *S. dorenboschii* and *S. pini* are 12 (2.5%), 54 (9.1%) and 26 (8.3%) for ITS, *rpb2* and *tub2* genes respectively. Therefore, a new species is introduced based primarily on molecular data (Jeewon & Hyde 2016).

Didymosphaeriaceae Munk, Dansk botanisk Arkiv 15 (2): 128 (1953)

Ariyawansa et al. (2014) revised the family Didymosphaeriaceae with 20 genera and listed Montagnulaceae as a synonym of Didymosphaeriaceae. We provide an updated tree for this family with a new genus, five new species and five new host records (Fig. 49).

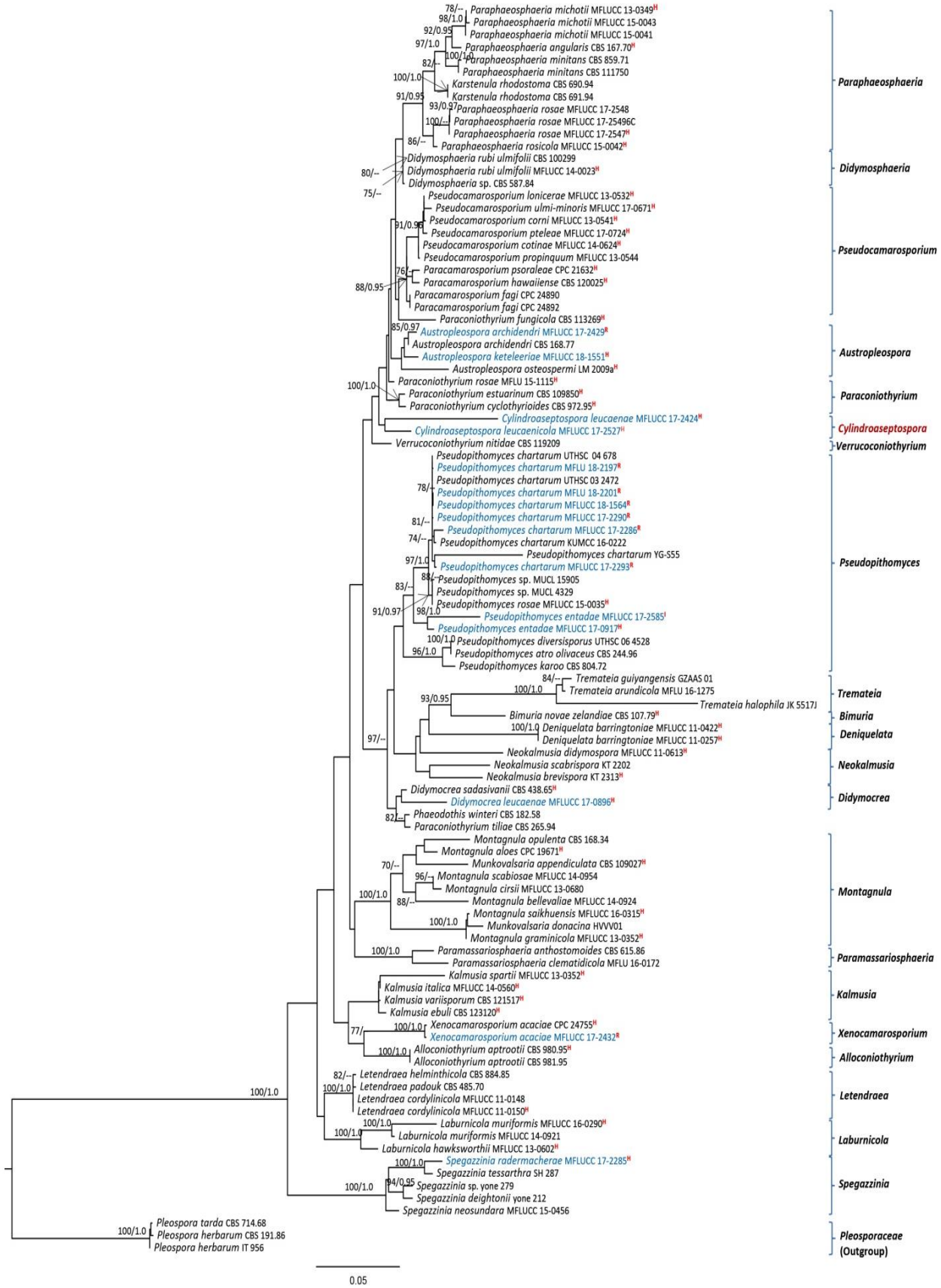


Figure 49 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU and *tef1* sequenced data of Didymosphaeriaceae. Related sequences were obtained from Wanasinghe et al. (2018b). Ninety-six strains were included in the combined sequence analyses, which comprised 3300 characters including alignment gaps. *Pleospora herbarum* (CBS 191.86 and IT 956) and *P. tarda* (CBS 714.68) are used as the outgroup taxa. Tree topology of the ML tree was

similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -18303.530692 is presented. The matrix had 1159 distinct alignment patterns, with 33.72% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240711, C = 0.244769, G = 0.273737, T = 0.240783; substitution rates AC = 1.476563, AG = 2.183231, AT = 1.233338, CG = 0.923088, CT = 6.926094, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolates are in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I} and ^{R} respectively.

Austropleospora R.G. Shivas & L. Morin, Fungal Diversity 40 (1): 70 (2010)

This genus comprises two species namely *Austropleospora archidendri* and *A. osteospermi* (Morin et al. 2010, Verkley et al. 2014, Ariyawansa et al. 2015). We introduce a new species *A. keteleeriae* and a new record of *A. archidendri* (Fig. 49).

30. *Austropleospora archidendri* (Verkley, Göker & Stielow) Ariyaw. & K.D. Hyde, Fungal Diversity 75: 64 (2015) Figs 50, 51

Facesoffungi number: FoF05243

= *Paraconiothyrium archidendri* Verkley, Göker & Stielow, Persoonia 32: 37 (2014)

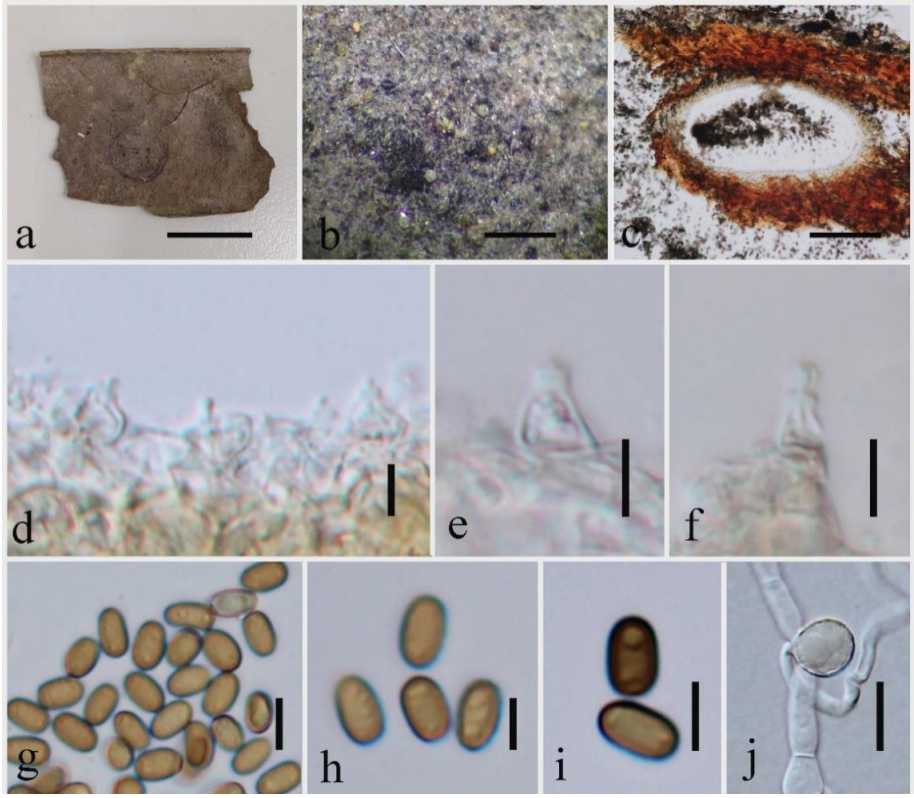


Figure 50 – *Austropleospora archidendri* (MFLU 18–2143). a Part of decaying host pod. b Conidiomata in the substrate. c Section through conidioma. d–f Conidiogenous cells. g–i Conidia. j Germinated spore. Scale bars: a = 1 cm, b = 500 µm, c = 100 µm, d–j = 5 µm.

Pathogenic on *Archidendron bigeminum* leaf and saprobic on *Leucaena* sp. pod. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 250–350 µm high × 200–300 µm diam. ($\bar{x}$ = 310 × 275 µm, n = 10), pycnidial, solitary, immersed, globose, unilocular, centrally ostiolate. *Conidiomata wall* 15–25 µm wide ($\bar{x}$ = 22 µm, n = 20), 4–5-layered, composed of outer 3–4-layers brown and inner 1–2-layers hyaline, thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidioma. *Conidiogenous cells* 3.5–6.5 × 3–4 µm ($\bar{x}$ = 5.2 × 3.5 µm, n = 10), phialidic, with minute collarette,

globose to doliiform, lining the inner wall layer of the pycnidium, hyaline, smooth. *Conidia* 4.5–6.5 × 3–4.5 µm ($\bar{x}$ = 5.7 × 3.8 µm; n = 30), solitary, hyaline when attached to conidiogenous cells, becoming dark brown, globose to obovate, one-celled, thick and, smooth-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Culture on MEA reaching 55–60 mm diam. after 2 weeks at 18°C, colonies colourless to buff margin; immersed mycelium, dense moderately high mat of woolly-floccose, white to greyish, in the centre weakly hazel aerial mycelium; conidiomata observed. Reverse predominantly ochreous, in the centre olivaceous-black with reddish brown margin.

Material examined – THAILAND, Lampang Province (19˚ 41' 45" N, 99˚ 34' 55" E), on decaying pod of *Leucaena* sp. (Fabaceae), 18 August 2017, S.C. Jayasiri, C 321 (MFLU 18–2143, new host record), living culture MFLUCC 17–2429, KUMCC 18–0216.

GenBank numbers – SSU: MK347863, ITS: MK347757, LSU: MK347974, *tef1*: MK360044, *rpb2*: MK434884

Notes – Our new isolate forms a sister clade to *Austropleospora archidendri* with high statistical support (85% MLBS/0.97 BYPP, Fig. 49). In addition, the new strain (Figs. 50, 51) morphologically fits with the description of *A. archidendri* in having globose pycnidia, globose to doliiform conidiogenous cells, olivaceous-brown aseptate conidia and similar culture characters (Verkley et al. 2014). Furthermore, there is no nucleotide difference in ITS regions between the two. Therefore, we introduce this collection as a new host record of *Austropleospora archidendri* from decaying pod of *Leucaena* sp. and the holotype was recorded from leaf spots in *Pithecellobium bigeminum* in Burma on (Verkley et al. 2014). However, arrangements of conidiomata change with the substrate texture.

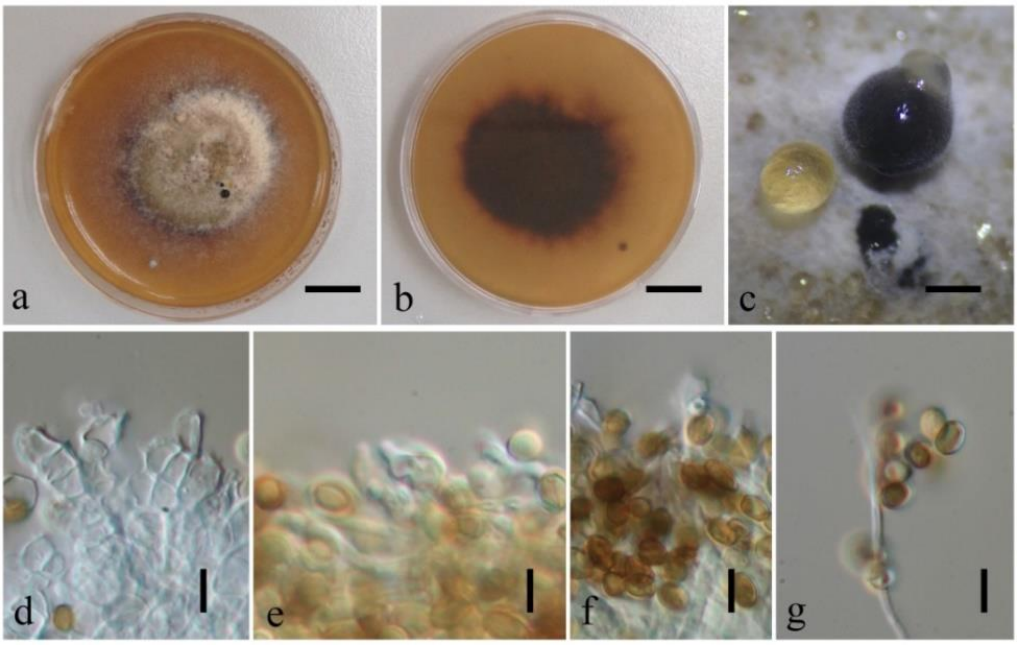


Figure 51 – *Austropleospora archidendri* in culture (MFLUCC 17–2429). a Top view of the culture. b Reverse view of the culture. c Conidiomata in culture. d, e Conidiogenous cells. f, g Conidia. Scale bars: a, b = 1 cm, c = 500 µm, d–g = 5 µm.

31. *Austropleospora keteleeriae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 52

Index Fungorum number: IF555541; Facesoffungi number: FoF05244

Holotype – MFLU 18–2206

Etymology – Referring to the host on which the fungus was collected, *Keteleeria* (Pinaceae).

Saprobic on decaying cone of *Keteleeria fortunei*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 210–240 µm high × 220–255 µm diam. ($\bar{x}$ = 228× 242 µm, n = 30), pycnidial, solitary, immersed, globose to obpyriform, unilocular, centrally ostiolate. *Conidiomata*

wall 33–55 µm wide ($\bar{x}$ = 44 µm; n = 20), thick, 5-6-layers, composed of an outer 4–5 layers, brown and inner 1–2-layers hyaline, thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, arising from the base and sides of the conidioma. *Conidiogenous cells* 5–7 µm × 4–5 µm ($\bar{x}$ = 6.2 × 4.5 µm, n = 30), phialidic, enteroblastic, determinate, ampulliform, lining the inner wall layer of the pycnidium, hyaline, smooth, thin walled. *Conidia* 4–5.5 × 5–6 µm ($\bar{x}$ = 5 × 5.5 µm; n = 10), solitary, hyaline when young, becoming dark brown at maturity, globose to obovate, one-celled, thick andsmooth-walled.

Culture characters – Culture on MEA fast growing, reaching 25–30 mm diam. after 1 week at 18ºC, circular, irregular margin, colonies grow in four layers, center grey, next brown layer, pinkish grey and dark brown at margin, reverse center brown, middle off white and dark brown at margin.

Material examined – CHINA, Yunnan Province, Kunming Institute garden (19˚ 41' 45" N, 99˚ 34' 55" E), on decaying cone of *Keteleeria fortunei* (Pinaceae), 25 May 2018, S.C. Jayasiri, C 453-B (MFLU 18–2206-B, holotype), ex-type living culture MFLUCC 18–1551, KUMCC 18–0217.

GenBank numbers – SSU: MK347910, ITS: MK347802, LSU: MK348021, *tef1*: MK360045, *rpb2*: MK434909

Notes – *Austropleospora keteleeriae* clustered with *A. archidendri* (CBS 168.77 and MFLUCC 17–2429) in the phylogenetic analysis (Fig. 49). *Austropleospora archidendri* has similar shape and size of conidiogenous cells to *A. keteleeriae* but has hyaline conidia attached to the thin-walled conidiogenous cells (Fig. 52). A comparison of the ITS nucleotides of these two species reveals 9 (1.9%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016). Therefore, our isolate is introduced as a new species from *Keteleeria fortunei* collected in China.

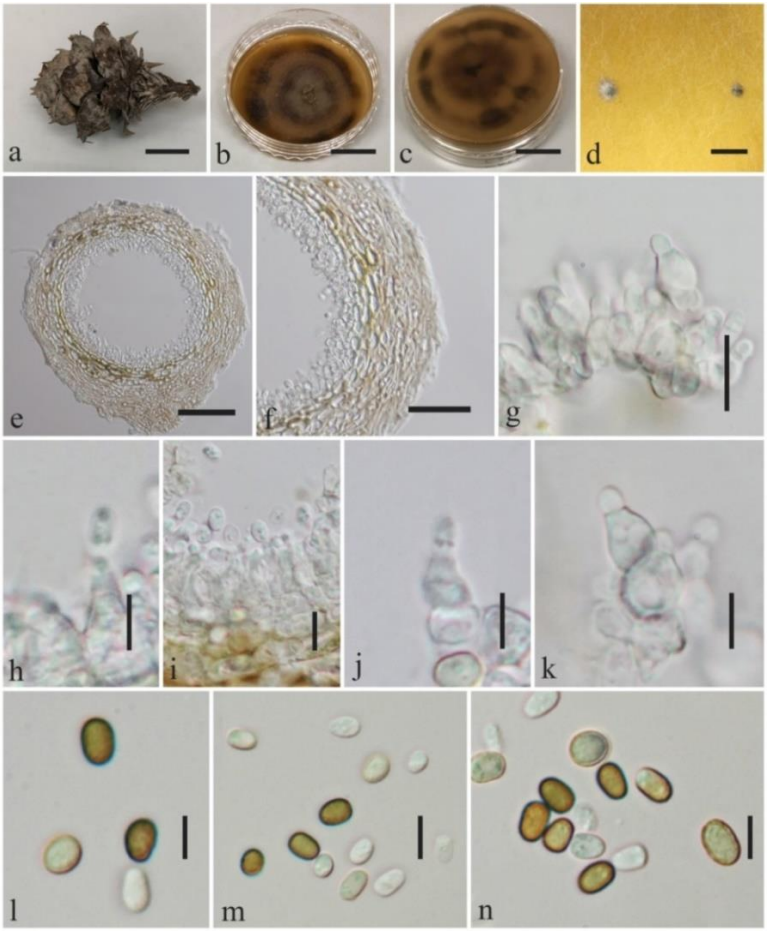


Figure 52 – *Austropleospora keteleeriae* (MFLUCC 18–1551, ex-type). a Host cone. b Top view of the culture. c Reverse view of the culture. d Conidiomata in culture. e Section through conidioma. f Conidioma wall. g–k Conidiogenous cells. l–n Conidia. Scale bars: a–c = 1 cm, d = 500 µm, e = 50 µm, f = 30 µm, g–k = 10 µm, l–n = 10 µm.

32. *Cylindroaseptospora* Jayasiri, E.B.G. Jones & K.D. Hyde, gen. nov.

Index Fungorum number: IF555542; Facesoffungi number: FoF05243

Etymology – Referring to the cylindrical aseptate conidia in isolated fungus.

Saprobic on decaying pod of *Leucaena* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* superficial or immersed in the agar, eustromatic, dark brown to black, more often complex with several merging cavities, without ostioles, opening by dissolution of upper cells; conidiomatal wall composed of a thick outer layer of *textura angularis* with relatively thin, dark brown walls, thin inner layer of *textura angularis*, pale yellow to hyaline walls. *Conidiogenous cells* discrete or assembled into protruding masses, indeterminate, phialidic, formed from the inner cells all over the conidiomatal wall, hyaline, broadly ampulliform to globose, with distinct periclinal thickening. *Conidia* hyaline, cylindrical, rounded at both ends, 1-celled, with thin and smooth walls, with contents minutely granular or with a few small polar guttules.

Type species – ***Cylindroaseptospora leucaenae*** Jayasiri, E.B.G. Jones & K.D. Hyde

Notes – Two asexual morph species clustered in Didymospheriaceae as a monophyletic clade (Fig. 49) in both ML and BY analyses. Both of these specimens were collected from two provinces in Thailand on decaying pod of *Leucaena* species. Since fungi collected herein clearly form an independent lineage and are phylogenetically segregated from other genera, we introduce, *Cylindroaseptospora*, as a new genus to accommodate these species.

33. *Cylindroaseptospora leucaenae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 53

Index Fungorum number: IF555543; Facesoffungi number: FoF05244

Holotype – MFLU 18–2133

Etymology – Referring to the host on which the fungus was collected, *Leucaena* (Fabaceae).

Saprobic on decaying pod of *Leucaena* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 95–170 µm high × 150–210 µm diam. ($\bar{x}$ = 145 × 180 µm, n = 10), pycnidial, superficial or immersed in the agar, eustromatic, dark brown to black, more often complex with several merging cavities, ostioles absent, opening by dissolution of upper cells. *Conidiomata wall* 12–35 µm wide ($\bar{x}$ = 28 µm, n = 20), composed of a thick outer layer of *textura angularis* with relatively thin, dark brown walls, thin inner layer of *textura angularis*, pale yellow to hyaline walls. *Conidiogenous* cells 5–10 × 4–6 µm ($\bar{x}$ = 7.5 × 5.2 µm, n = 20), discrete or assembled into protruding masses, indeterminate, phialidic, formed from the inner cells all over the conidiomatal wall, hyaline, broadly ampulliform to globose, with distinct periclinal thickening. *Conidia* 12–19 × 2–2.5 µm ($\bar{x}$ = 15 × 2.2 µm, n = 5), hyaline, cylindrical, rounded at both ends, 1-celled, with thin and smooth walls, with contents minutely granular or with a few small polar guttules.

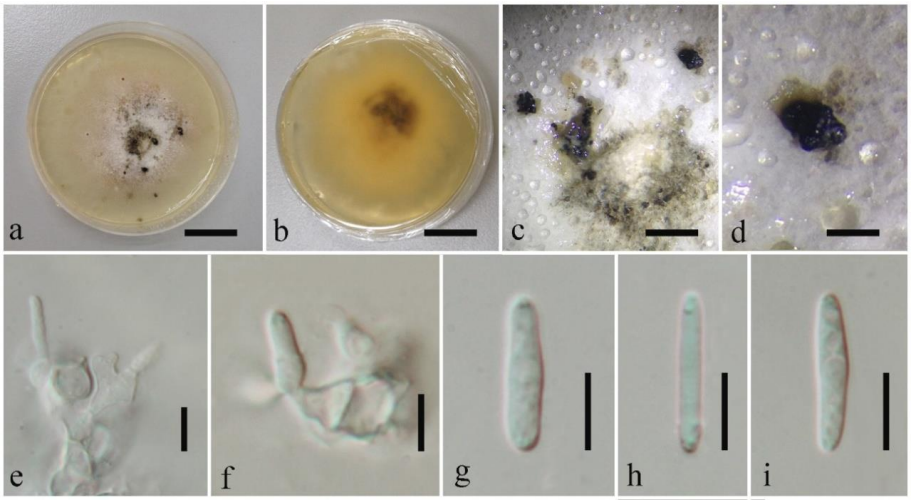


Figure 53 – *Cylindroaseptospora leucaenae* (MFLUCC 17–2424, ex-type). a Top view of colony on MEA. b Reverse view of the colony. c, d Pycnidia in culture. e, f Conidiogenous cells. g–i Conidia. Scale bars: a, b = 1 cm, c = 500 µm, d = 200 µm, e–i = 10 µm.

Culture characters – Conidia germinated on MEA and reaching of 55–60 mm diam. in 2 weeks at 18ºC, spreading, with an even, colourless to buff, glabrous margin; colony surface almost entirely covered by a dense mat of woolly floccose aerial mycelium that remains pure white except in the centre, where it becomes olivaceous buff, visible as scattered black dots in top view; reverse mostly ochreous, but with fulvous zones around a rust centre.

Material examined – THAILAND, Chiang Rai Province, Doi Pui, on decaying pod of *Leucaena* sp. (Fabaceae), 20 June 2017, S.C. Jayasiri, C 286 (MFLU 18–2133, holotype, MFLU 18–2134, isotype); ex-type living culture MFLUCC 17–2424, KUMCC 18–0226.

GenBank numbers – SSU: MK347856, ITS: MK347749, LSU: MK347966, *tef1*: MK360047, *rpb2*: MK434882

Notes – *Cylindroaseptospora leucaenae* and *C. siamensis* share phialidic, determinate, ampulliform conidiogenous cells but *C. siamensis* differs in having globose to subglobose, dark brown, 1-septate conidia at maturity (Figs. 53, 54). A comparison of the ITS and *tef1* nucleotides of these two fungi revealed 23 (4.7%) and 81 (8.8%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

34. *Cylindroaseptospora siamensis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 54

Index Fungorum number: IF555544; Facesoffungi number: FoF 05245

Holotype – MFLU 18–2147

Etymology – Referring to country (‘Siam’ earlier name of Thailand) where the specimen was collected.

Saprobic on *Leucaena* sp. pod. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 110–165 µm high × 140–190 µm diam. ($\bar{x}$ = 142 × 175 µm, n = 10), pycnidial, solitary, immersed, globose to obpyriform, unilocular, thick-walled. *Conidiomata wall* 15–38 µm wide ($\bar{x}$ = 29 µm, n = 20), comprised of brown outer layer, hyaline inner layer, with thin-walled cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells, arising from the base. *Conidiogenous cells* 6.5–7.4 × 3.2–4.7 µm ($\bar{x}$ = 7.1 × 4.1 µm; n = 10), phialidic, determinate, ampulliform, lining the inner wall layer of the pycnidium, hyaline, smooth. *Conidia* 7.2–9.4 × 5.4–6.5 µm ($\bar{x}$ = 8.6 × 6.1 µm; n = 30), hyaline when young, becoming dark brown, globose to subglobose, aseptate, 1-septate at maturity, thick and smooth-walled.

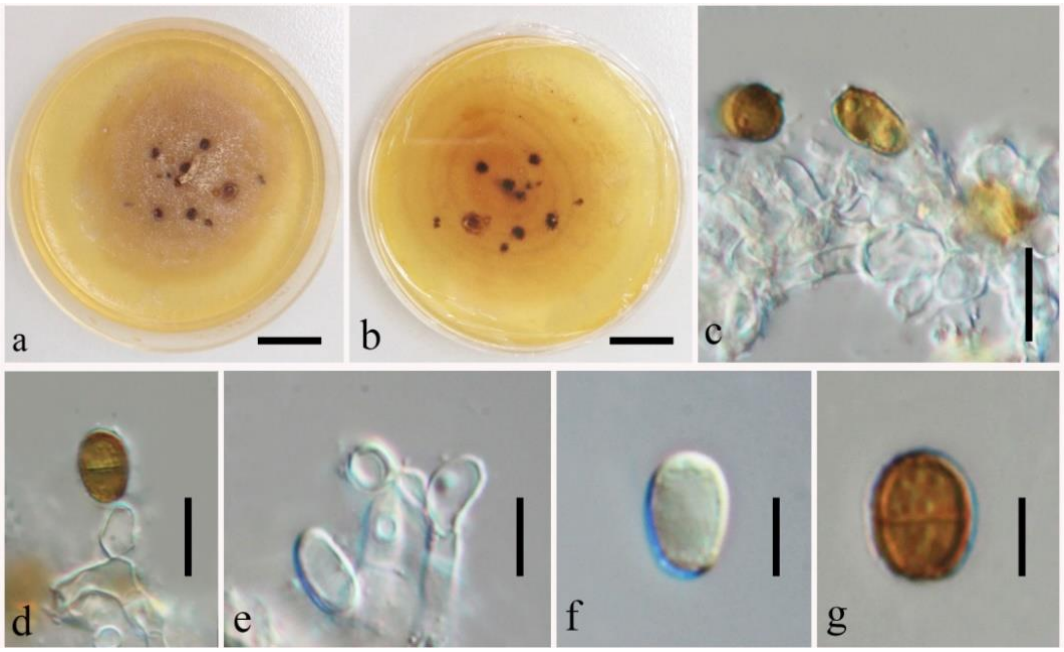


Figure 54 – *Cylindroaseptospora siamensis* (MFLUCC 17–2527, ex-type). a Top view of the colony on MEA. b Reverse view of the colony. c–e Conidiogenous cells. f, g Conidia. Scale bars: a, b = 1 cm, e–g = 10 µm.

Culture characters – Culture on MEA reaching 40–50 mm diam. after 2 weeks at 18ºC, circular, entire margin, colourless to buff, colony surface almost entirely covered by a mat of woolly floccose aerial mycelium that remains off-white except in the centre, where it later becomes olivaceous buff, visible as scattered black dots in top view; reverse mostly ochraceous, but with fulvous zones around a rusty centre.

Material examined – THAILAND, Lampang Province (19° 3' 44" N, 99° 46' 54" E), on decaying pod of *Leucaena* sp. (Fabaceae), 18 August 2017, S.C. Jayasiri, C 329 (MFLU 18–2147, holotype; KUN-HKAS 102427, isotype), ex-type living culture MFLUCC 17–2527, KUMCC 18–0227.

GenBank numbers – SSU: MK347866, ITS: MK347760, LSU: MK347976, *tef1*: MK360048

Didymocrea Kowalski, Mycologia 57 (3): 405 (1965)

Aptroot (1995) suggested placement of this genus under family Zopfiaceae. Kruys et al. (2006) confirmed *Didymocrea* individual lineage within this family but Tanaka et al (2015) placed this genus under Didymospheriaceae with support of multi-loci analysis of SSU and LSU and *tef1* genes (Fig. 49).

35. *Didymocrea leucaenae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 55

Index Fungorum number: IF555546; Facesoffungi number: FoF05247

Holotype – MFLU 18–2092

Etymology – Referring to the host on which the fungus was collected, *Leucaena* (Fabaceae).

Saprobic on *Leucaena* sp. pod. Sexaul morph: Undetermined. Asexual morph: Hyphomycetous. *Sporodochia* on substrate punctiform, pulvinate, granular, black, shining. *Mycelium* immersed in the substrate, composed of branched, septate, smooth, subhyaline to pale brown, hyphae. *Conidiophores* 32–47 × 2.5–3.5 μm ($\bar{x}$ = 40 × 3 μm; n = 20), micronematous or semi-macronematous, mononematous, fasciculate, simple or sometimes branched. *Conidiogenous cells* 12–17 × 11–15 μm ($\bar{x}$ = 15 × 13 μm; n = 20), integrated, holoblastic, terminal, determinate. *Conidia* 15–17 × 16–19 μm ($\bar{x}$ = 16.5 × 18.5 μm; n = 20), acrogenous, solitary, reddish brown to brown, broadly ellipsoidal to obovoid in surface view, fusiform to obclavate in lateral view, flattened, muriform, 3–4 rows of transverse septa, constricted at the septa, dark and thickly banded atthe septa, canals in the septa obscured by dark pigmentation in face view, and visible inside view, thin and smooth-walled. The number of cells per conidium varies from 9 to 11. Basal cell subhyaline to pale brown, cuneiform.

Culture characteristics – Conidia germinating on MEA within 24 hr. Germ tubes produced an end of conidia. Colonies on MEA reaching 36–40 mm diam. after 2 weeks at 18ºC, circular, edge entire, raised, fluffy, dense, convex or dome-shaped with white papillate surface, to superficial at the center, flat or effuse at the edge, greyish brown from above, dark brown from below.

Material examined – THAILAND, Lumphang Province, on decaying pod of *Leucaena* sp. (Fabaceae), 30 August 2016, S.C. Jayasiri, C 150 (MFLU 18–2092, holotype), ex-type living culture MFLUCC 17–0896, KUMCC 18–0235.

GenBank numbers – SSU: MK347826, ITS: MK347721, LSU: MK347935, *tef1*: MK360052, *rpb2*: MK434905

Notes – Our isolate clades with *Didymocrea sadasivanii* which is the type and only species in this genus. However, *Didymocrea sadasivanii* is a sexual morph species and our isolate is an asexual morph (Fig. 55). Therefore, there is no morphological data to compare the two species. There is low bootstrap support for this relationship (Fig. 49). A comparison of the ITS nucleotides of these two strains reveals 38 (6%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Morphology of *Didymocrea leucaenae* bears similarities to species in *Canalisporium* (Sordariomycetes), but phylogenetically they are distinct (Zhao et al. 2013).

Pseudopithomyces Ariyaw. & K.D. Hyde, Fungal Diversity 75: 64 (2015)

Pseudopithomyces was introduced to accommodate *Pithomyces chartarum* and characterized by fusiform, verruculose dark conidia and producing brown to black colonies on the host (Ariyawansa et al. 2015).

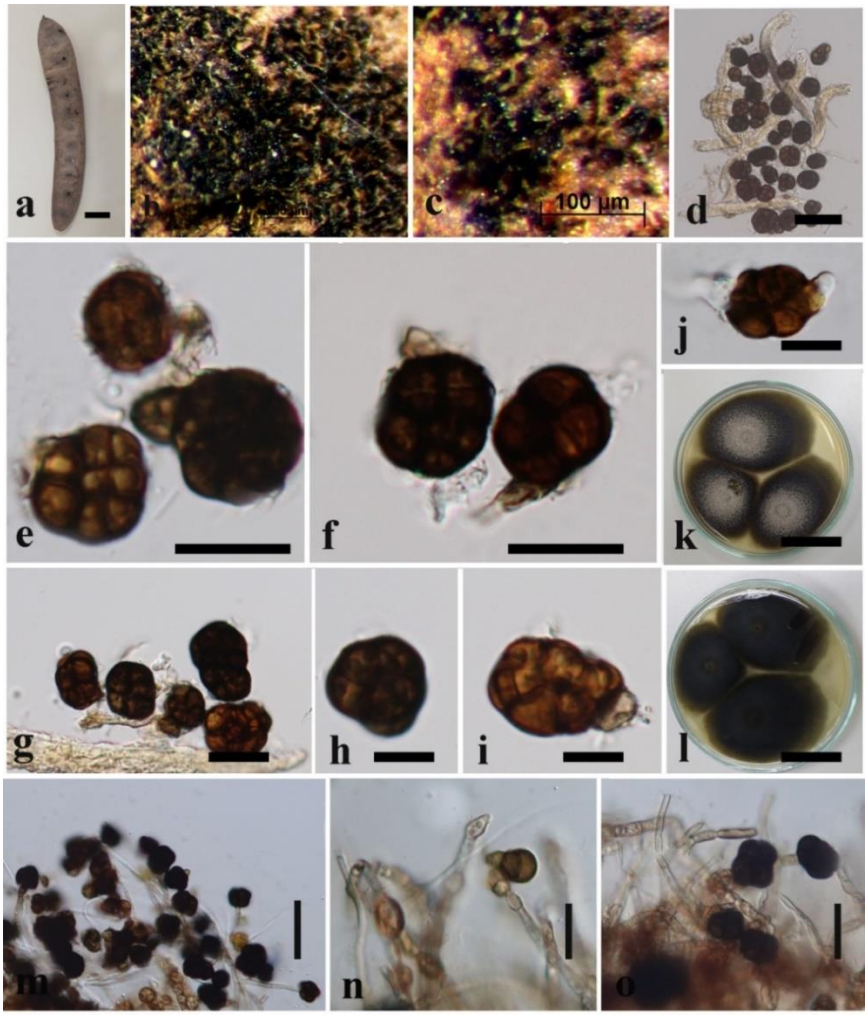


Figure 55 – *Didymocrea leucaenae* (MFLU 18–2092, holotype). a Host *Leucaena leucocephala* pod. b–d Sporodochia and conidia. e–i Conidia. j Germinated conidium. k Top view of culture in MEA. l Reverse view of culture in MEA. m–o Conidia and conidiogenous cells in culture. Sale bars: a = 1 cm, d, n, o = 50 µm, e –g = 20 µm, h–j = 10 µm, k, l = 3 cm, m = 100 µm.

36. *Pseudopithomyces chartarum* (Berk. & M.A. Curtis) Jin F. Li, Ariyaw. & K.D. Hyde, Fungal Diversity 75: 66 (2015) Figs 56, 57

≡*Sporidesmium chartarum* Berk. & M.A. Curtis, in Berkeley, Grevillea 3: 50 (1874)

≡*Piricauda chartarum* (Berk. & M.A. Curtis) R.T. Moore, Rhodora 61: 96 (1959)

=*Sporidesmium bakeri* Syd. & P. Syd., Annales Mycologici 12 (2): 204 (1914)

Saprobic and *endophytic* on wide host range. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Conidiophores* mononematous, micronematous, mostly intercalary, sometimes denticulate, aseptate. *Conidiogenous cells* mono or polyblastic, light brown, smooth, with upto 2 µm broad conidial attachment, with rhexolytic cesession. *Conidia* 16–22 × 8–12 µm ($\bar{x}$ = 18 × 10 µm, n = 30), solitary, dark brown, obovate to oblong, verruculose to spinulose, slightly constricted at the septa, 3–4 vertical septa, mostly 1–2 longitudinal dark septa.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced at end cells of conidia. Colonies cottony, pinkish white, light brown to brown, reaching 40–50 mm diam. after 2 weeks at 18°C. Mycelium superficial, effuse and radially striated with regular edge. Sporulation observed after 4 weeks at 18°C.

Figure 56 – *Pseudopithomyces chartarum* (MFLU 18–2123). a Host seed pods. b, c Conidiomata on host material. d, e Conidiophores and conidiogenous cells. f–j Conidia. k Germinated spore. Scale bars: a = 2 cm, b = 500 µm, c = 200 µm, d–g, k = 20 µm, f–j = 10 µm.

Figure 57 – *Pseudopithomyces chartarum* from culture (MFLUCC 17–2290). a Germinated spore. b, c Top view of culture. c Reverse view of culture. e–h Conidiophores and conidiogenous cells. d, i–m Conidia. Scale bars: a, d–m = 10 µm, b, c = 1 cm.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on decaying pod of *Radermachera sinica* (Bignoniaceae), 7 July 2017, S. C. Jayasiri, C-268 (MFLU 18–2123, new host record); living culture, MFLUCC 17–2286, KUMCC 18–0287; *ibid.*, Doi Pui (19˚ 52' 5" N; 99˚ 38' 5" E), on decaying pod of *Bauhinia* sp. (Fabaceae), 20 July 2017, S. C. Jayasiri, C 284 (MFLU 18–2131, new host record), living culture, MFLUCC 17–2290, KUMCC 18–0288; THAILAND, Koland, on decaying pod of *Leucaena* sp. (Fabaceae), 6 August 2017, S. C. Jayasiri, C 300 (MFLU 18–2137, new host record) living culture, MFLUCC 17–2293, KUMCC 18–0289; CHINA, Yunnan Province, Kunming Institute garden, on decaying cone of *Magnolia grandiflora* (Magnoliaceae), 25 May 2018, S. C. Jayasiri, C 459 (MFLU 18–2215), living culture MFLUCC 18–1564, KUMCC 18–0290.

GenBank numbers – MFLUCC 17–2286: SSU: MK347849, ITS: MK347741, LSU: MK347958, *tef1*: MK360079, *rpb2*: MK434892; MFLUCC 17–2290: SSU: MK347854, ITS: MK347747, LSU: MK347964, *tef1*: MK360080, *rpb2*: MK434890; MFLUCC 17–2293: SSU: MK347859, ITS: MK347752, LSU: MK347969, *tef1*: MK360081, *rpb2*: MK434887; MFLUCC 18–1564: SSU: MK347916, ITS: MK347808, LSU: MK348027, *tef1*: MK360082, *rpb2*: MK434857

Notes – Four strains of *Pseudopithomyces chartarum* were isolated from decaying wild seed pods and a cone of *Magnolia grandiflora*. These are well supported in the phylogenetic tree (Fig. 49) and morphs are in agreement with the type descriptions (Berkeley & Curtis 1874). *Pseudopithomyces chartarum* has been reported from different hosts (Ariyawansa et al. 2015), but this is the first report from *Bauhinia* sp., *Leucaena* sp., *Magnolia grandiflora* and *Radermachera sinica* species. This species appears as a species complex with many records worldwide but we suggest more gene sequences are needed for further resolve this complex (Fig. 49).

37. *Pseudopithomyces entadae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 58

Index Fungorum number: IF555545; Facesoffungi number: FoF05246

Holotype – MFLU 18–2103

Etymology – Referring to the host on which the fungus was collected, *Entada* (Fabaceae).

Saprobic on pod of *Entada phaseoloides*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Conidiophores* differentiated, arising from creeping hyphae, unbranched, with thin septa, straight to flexuous, hyaline to pale brown, thick-walled, producing conidium-bearing denticles that are widely spaced in the apical region, with rhexolytic conidial cesession. *Conidia* 10–14 × 6–9 μm ($\bar{x}$ = 12 × 8 μm, n = 30), solitary, dark brown, obovate to oblong, verruculose, slightly constricted at the septa, with 1–2 septa, rarely 1 longitudinal septum in the middle cell.

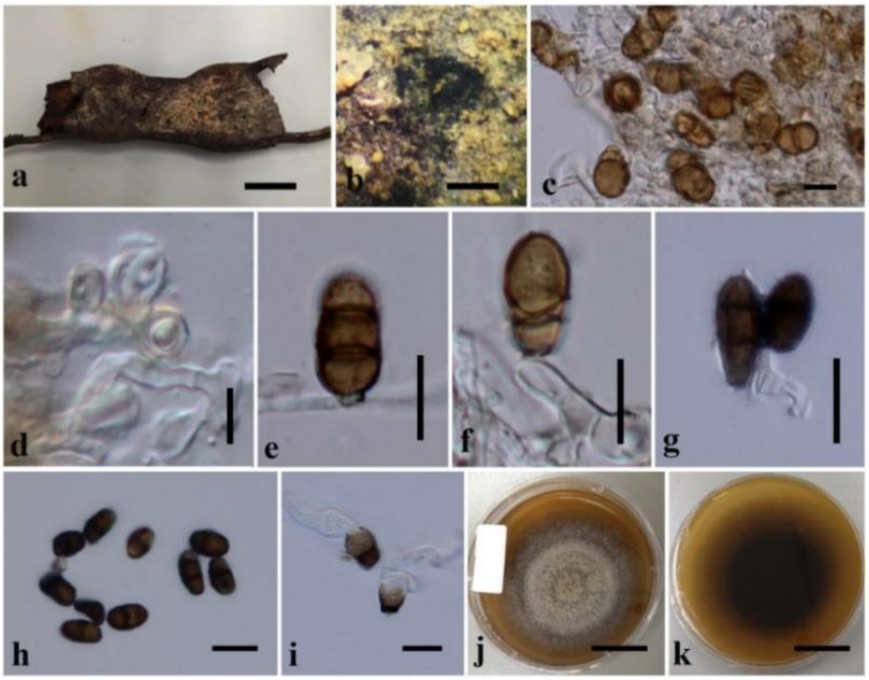


Figure 58 – *Pseudopithomyces entadae* (MFLU 18–2103, holotype). a Part of host seed pod. b Conidiomata on host material. c–g Conidiophores and conidiogenous cells. h Conidia. i Germinated conidia. j Top view of culture. k Reverse view of culture. Scale bars: a, j, k = 2 cm, b = 200 μm, c–g = 10 μm, h, i = 20 μm.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced at end of conidia. Colonies cottony, pinkish white, light brown to brown, reaching 45–52 mm diam. after 2 weeks at 18°C. Mycelium superficial, effuse and radially striate with regular edge.

Material examined – THAILAND, Chiang Rai Province, Khun Korn waterfall (19˚ 52' 5" N; 99˚ 38' 5" E), on decaying pod of *Entada phaseoloides* (Fabaceae), 2 February 2017, S.C. Jayasiri, C 219 (MFLU 18–2103, holotype), ex-type living culture MFLUCC 17–0917, KUMCC 18–0291; C 227 (MFLU 18–2107, paratype), MFLUCC 17–2585, KUMCC 18–0292.

GenBank numbers – MFLUCC 17–0917: SSU: MK347835, LSU: MK347944, *tef1*: MK360083, *rpb2*: MK434899

Notes – *Pseudopithomyces entadae* constitutes an independent subclade to *P. chartarum* strains with high support (83% MLBS, Fig. 49). Morphologically *P. chartarum* differs from *P. entadae* in having conidium-bearing denticles in the apical region of the conidiophore and 1–2 septa, rarely longitudinal septa to the conidia (Fig. 58). However, *Pseudopithomyces chartarum* is characterized by mono or polyblastic conidiogenous cells and 3–4 septa, 1–2 longitudinal septate conidia (Berkeley & Curtis 1874, Ariyawansa et al. 2015). A comparison of the ITS and *tef1* nucleotides of these two strains reveals 18 (3.9%) and 23 (2.6%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Spegazzinia Sacc., Michelia 2 (6): 37 (1880)

Spegazzinia was classified in the Apiosporaceae (Sordariomycetes) based on its morphological traits (Hyde et al. 1998). Tanaka et al. (2015) placed this genus in Didymosphaeriaceae based on molecular evidence. We introduce a new species of *Spegazzinia* from fallen pod of *Radermachera sinica* in Thailand (Fig. 49).

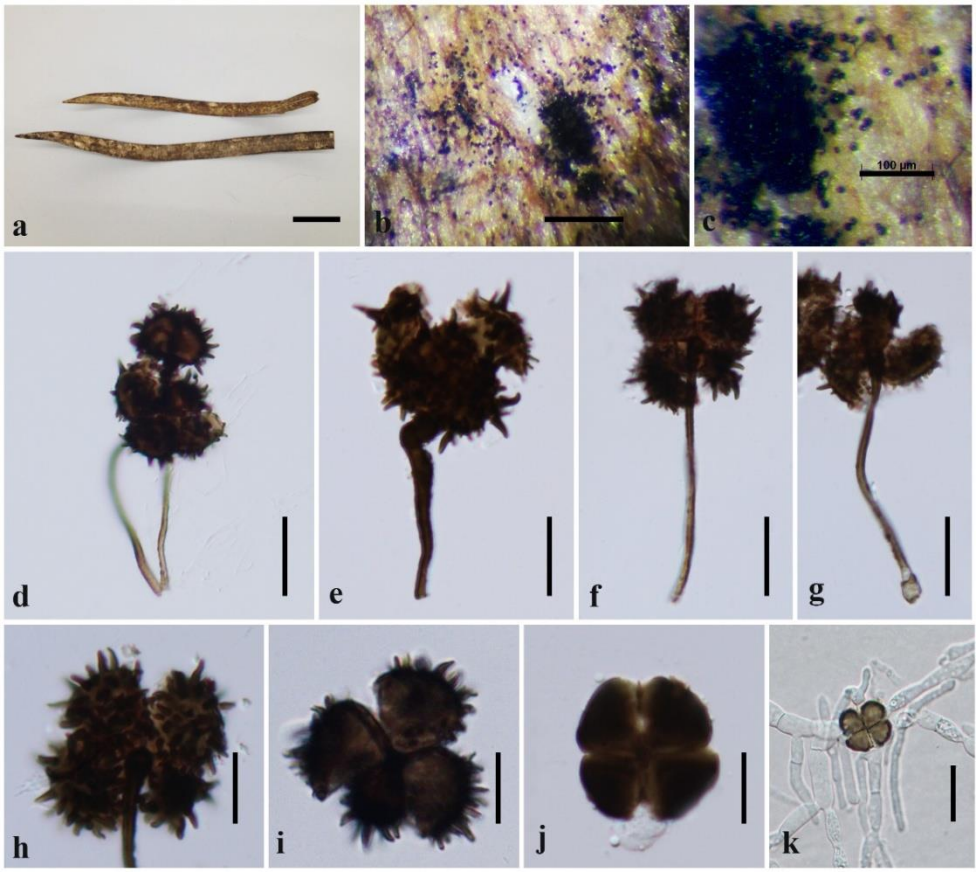


Figure 59 – *Spegazzinia radermacherae* (MFLU 18–2122, holotype). a Host seed pods. b, c Sporodochia on the host surface. d–g Conidiogenous cells and conidia (note conidiogenous mother cell in g). h, i α conidia. j β conidia. k Germinated conidium. Scale bars: a = 2 cm, b = 500 µm, d–g, k = 20 µm, h–j = 20 µm.

38. *Spegazzinia radermacherae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 59

Index Fungorum number: IF555547; Facesoffungi number: FoF05249

Holotype – MFLU 18–2122

Etymology – Referring to the host on which the fungus was collected, *Radermachera* (Bignoniaceae).

Saprobic on *Radermachera sinica*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Sporodochia dark, dense, dry, powdery, velvety. *Conidiophores* micronematous. *Conidiogenous cells* 4–5 µm × 3.5–4.5 µm ($\bar{x}$ = 4.5 × 3.7 µm; n = 10), basauxic, ampulate, verrucose, producing an erect, verruculose unbranched filament up to 43–52 × 1.5–2.5 µm ($\bar{x}$ = 48 × 1.8 µm; n = 20), pale, or golden brown. *Conidia* of two kinds: α conidia 4-celled, brown to black brown, 18–22 × 17.5–20 µm ($\bar{x}$ = 19 × 18 µm; n = 30), with conspicuous spines 2–3 µm, scattered; β conida 15–17 × 8–10 µm ($\bar{x}$ = 16.5 × 9.2 µm; n = 30), 4-celled, pale brown to dark brown, subglobose, flattened in one plane, cuciately septate, smooth to verrucose.

Culture characters – Conidia germinated on MEA within 24 hr and germ tubes produced from several cells. Colonies growing on MEA, reaching 15–20 mm diam. after 2 weeks at 18°C, flat, surface smooth, with entire edge, white to pale greenish-olivaceous, moderately dense, circular; reverse white to greenish olivaceous.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on fallen pod of *Radermachera sinica* (Bignoniaceae), 7 July 2017, S.C. Jayasiri, C 264 (MFLU 18–2122, holotype); ex-type living culture MFLUCC 17–2285, KUMCC 18–0297.

GenBank numbers – SSU: MK347848, ITS: MK347740, LSU: MK347957, *tef1*: MK360088, *rpb2*: MK434893

Notes – *Spegazzinia radermacherae* and *S. tessarthra* are related with high statistical support in the multigene phylogenetic analysis of SSU, ITS, LSU and *tef1* gene sequences (Fig. 49). *Spegazzinia radermacherae* is characteristic of *Spegazzinia* in having two types of conidia (Fig. 59). However, the type species of *Spegazzinia tessarthra* has longer spines (up to 10 µm) while in *S. radermacherae*, they are only 2–3 µm long. To further support the establishment a new taxon, as proposed by Jeewon & Hyde (2016), we examined the nucleotide differences of ITS and *tef1* gene regions. There were 10 (3.1%) and 18 (2.0%) nucleotide differences between *S. radermacherae* and *S. tessarthra* for ITS and *tef1* gene regions.

Xenocamarosporium Crous & M.J. Wingf., Persoonia 34: 185 (2015)

This genus was added to *Camarosporium* complex by Crous et al. (2015). *Xenocamarosporium acacia* is the only species in the genus and it differs from *Paracamarosporium* in lacking paraphyses and from *Pseudocamarosporium* by not having muriformly septate conidia.

39. *Xenocamarosporium acaciae* Crous & M.J. Wingf., Persoonia 34: 185 (2015) Fig. 60

Facesoffungi number: FoF05248

Saprobic on decaying *Leucaena* sp. pods. Sexual morph: *Ascomata* 150–170 µm high × 160–200 µm diam. ($\bar{x}$ = 164 × 185 µm, n = 10), scattered, solitary, immersed, visible as small, brown spots surrounded by pale yellowish region, uniloculate, subglobose, glabrous, with central black ostiole penetrating through host surface. *Peridium* 14–18 µm wide ($\bar{x}$ = 14.5 µm; n = 20), thin-walled, of unequal thickness, composed of 3–4 layers of thickened, brown, pseudoparenchymatous cells, arranged in a *textura angularis*. *Hamathecium* 1–3 µm wide ($\bar{x}$ = 2.2 µm; n = 20), composed of sparse, filiform, frequently anastomosing, broad cellular pseudoparaphyses, with distinct, constricted septa. *Asci* 60–75 × 8–10 µm ($\bar{x}$ = 70 × 9 µm; n = 20), bitunicate, 8-spored, broadly cylindrical to cylindric-clavate, subsessile to short pedicellate, apically rounded with indistinct ocular chamber. *Ascospores* 15–20 × 3.5–5 µm ($\bar{x}$ = 17 × 4 µm; n = 30), overlapping 1–3-seriate, phragmosporous, hyaline to brown, cylindrical, narrower and longer at the lower cell, 4-5-septate, often enlarged at the forth cell, rough-walled. Asexual morph: See Crous et al. (2015).

Culture characters – Ascospores germinated in MEA. Colonies reaching 40 mm diam. after 2 weeks at 18°C, spreading with moderate aerial mycelium and smooth, margins, surface dirty white, reverse with cinnamon centire and margin in yellow layer.

Material examined – THAILAND, Krabi Province, Mueang Krabi District (8˚ 3' 22" N, 98˚ 46' 28" E), on decaying pod of *Leucaena* sp. (Fabaceae), 31 August 2017, S.C. Jayasiri, C 354 (MFLU 18–2157, new host record); living culture MFLUCC 17–2432, KUMCC 18–0306.

GenBank numbers – SSU: MK347873, ITS: MK347766, LSU: MK347983, *tef1*: MK360093

Figure 60 – *Xenocamarosporium acacia* (MFLU 18–2157). a Pod of *Leucaena* sp. host. b, c Ascomata on host pod. d Section of ascoma. e Pseudoparaphyses. f–i Asci. j–n Ascospores. o Germinated ascospore. Scale bars: a = 2 cm, d = 50 µm, e = 10 µm, g, f–i = 20 µm, j–o = 10 µm.

Notes – The sexual morph of *Xenocamarosporium acacia* is reported here and it groups with *Alloconiothyrium aptrootii* with moderate support. A sequence from our recent collection of *X. acacia* (MFLUCC 17–2432) groups with sequence of *X. acacia* (CPC 24755) with high statistical support (100% MLBS/1.0 BYPP, Fig. 49). Our isolate of *X. acacia* did not produce the asexual morph in culture. A comparison of the ITS nucleotides of the new strain (MFLUCC 17–2432) and *Xenocamarosporium acacia* (CPC 24755) reveals only 1 (0.2%) nucleotide differences, which indicates that they are not distinct taxa (Jeewon & Hyde 2016).

Hermatomycetaceae Locq. ex A. Hashim. & Kaz. Tanaka, Persoonia 39: 56 (2017)

The family Hermatomycetaceae was introduced to accommodate the single genus *Hermatomyces* and two species, *H. iriomotensis* and *H. nabanheensis* (Hashimoto et al. 2017, Hyde et al. 2017). However, there are now 13 species in this genus (Tibpromma et al. 2016, 2017, Hyde et al. 2017, Koukol et al. 2018).

Hermatomyces Speg., Anales del Museo Nacional de Historia Natural Buenos Aires ser. 3, 13: 445 (1911)

Some *Hermatomyces* species, such as *H. sphaericus* or *H. tucumanensis*, are seemingly common, but others are specific for one locality (Tibpromma et al. 2016, 2017b, Hyde et al. 2017, Koukol et al. 2018). We collected a specimen in Thailand and it is a new host record of *H. sphaericus* from decaying pod of *Entada phaseoloides.*

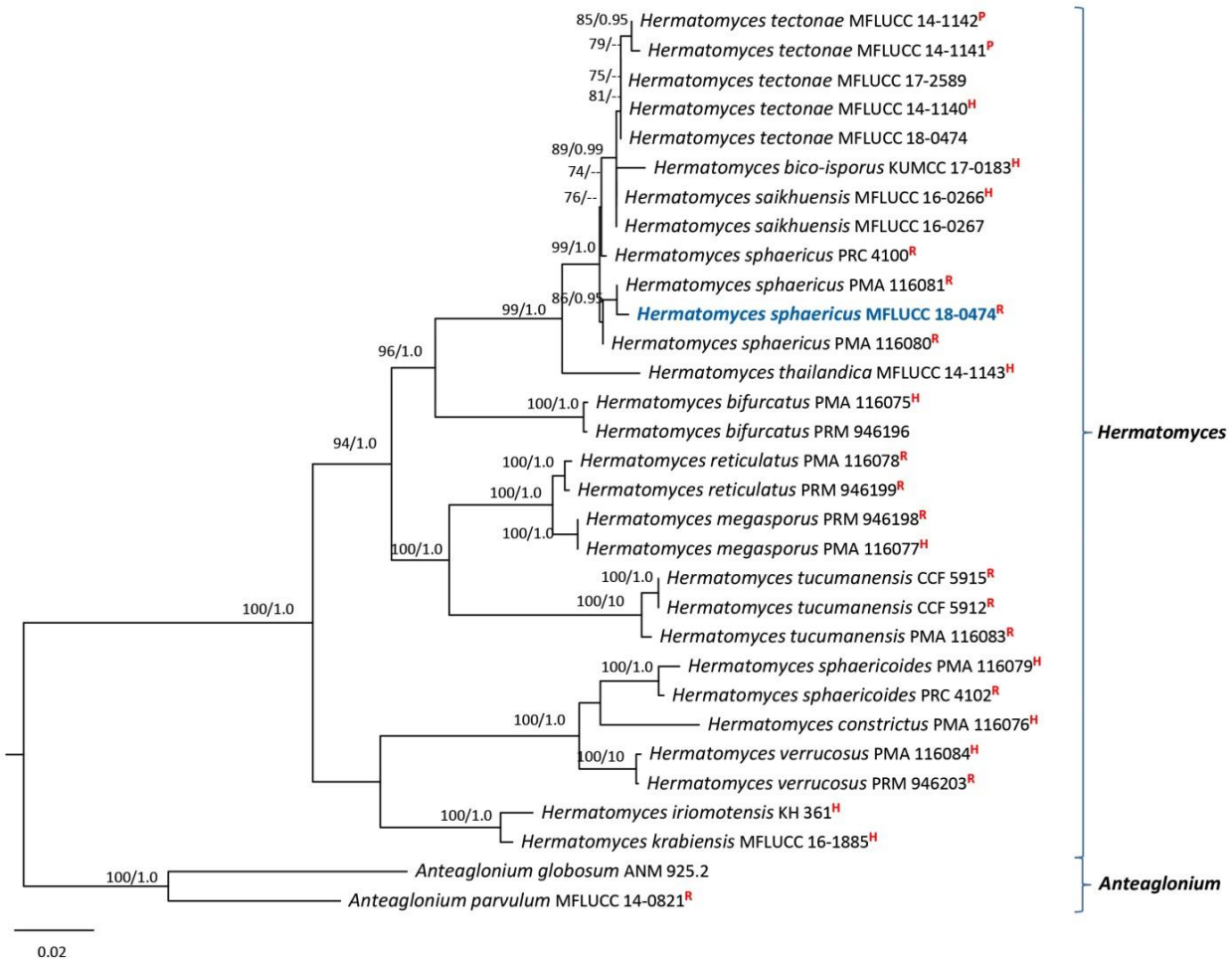


Figure 61 – The best scoring RAxML tree from the maximum likelihood analysis based on combined LSU, ITS, *tef1* and *rpb2* sequence data for Hermatomycetaceae. Forty-three strains were included in the sequence analysis, which comprised 3322 characters including alignment gaps. Two strains of *Anteaglonium* (Anteagloniaceae) were used as the outgroup taxa. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -9995.716043 is presented. The matrix had 642 distinct alignment patterns, with 16.43% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.246000, C = 0.264750, G = 0.260783, T = 0.228466; substitution rates AC = 1.113195, AG = 4.383677, AT = 1.052816, CG = 0.868872, CT = 13.097676, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strain is in blue. Strains isolated from the holotype, paratype and reference specimens are indicated in with a red superscript ^{H}, ^{P} and ^{R} respectively.

40. *Hermatomyces sphaericus* (Sacc.) S. Hughes, Mycological Papers 50: 100 (1953) Fig 62

Facesoffungi number: FoF05259

Saprobic on decaying branch, leaves and pods. Sexual morph: Undetermined. Asexual

morph: Hyphomycetous. *Colonies* on natural substrate scattered, *Mycelium* 2–4 μm wide ($\bar{x}$ = 3.2 μm; n = 20), immersed, composed of brown, smooth, septate hyphae. *Conidiomata* 300–800 μm wide ($\bar{x}$ = 585 μm, n = 20), sporodochial, dark brown to black. *Conidiophores* 8–13 μm long × 2–4 μm diam. ($\bar{x}$ = 11.5 × 3.4 μm; n = 20), micronematous, mononematous, pale brown, smooth. *Conidiogenous cells* 4.5–10 × 3–4 μm ($\bar{x}$ = 7.5 × 3.5 μm, n = 20), monoblastic, integrated, terminal, pale brown, cylindrical, smooth-walled. *Conidia* 25–31 × 20–30 μm ($\bar{x}$ = 28 × 25 μm; n = 20), solitary, acrogenous, cheiroid, pale brown to brown, globose, subglobose, inwardly curved at the tip, arising from a basal cell, consisting of 4–5 rows of cells, rows digitate, without appendages, with each row composed of 4–5 cells, euseptate, constricted at the septa, guttulate.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 20–30 mm diam. after 1 week in 18 ° C, irregular in shape, undulate to lobate, flat or effuse to rise at the edge, convex with papillate surface on old mycelium plugs, aerial, medium sparse, grey above, pastel grey from below.

Material examined – THAILAND, Chiang Rai Province, Khun Korn waterfall (19˚ 52' 5" N; 99˚ 38' 5" E), on decaying pod of *Entada phaseoloides* (Fabaceae), 2 February 2017, S.C. Jayasiri, C 415 (MFLU 18–2183, new host record), living culture MFLUCC 17–0915, KUMCC 18–0246.

GenBank numbers – SSU: MK347891, ITS: MK347784, LSU: MK348002, *tef1*: MK360058, *rpb2*: MK434868

Notes – *Hermatomyces sphaericus* has been reported from different plant families and different plant parts (Koukol et al. 2018). We introduce a new host record from decaying pods of *Entada phaseoloides* (Fabaceae) in Thailand. The new strain groups with other strains of *H. sphaericus* in the multigene analysis (Fig. 61). Morphology of the new strain (Fig. 62) matches the type collection (K(M)–IMI 37763) in having dark brown to black sporodochia, micronematous, mononematous, pale brown, smooth, monoblastic, integrated, terminal, pale brown, cylindrical conidiogenous cells and globose to subglobose, acrogenous, cheiroid conidia with one cell type (Hughes 1953). A comparison of the ITS and *tef1* nucleotides of *Hermatomyces sphaericus* (PMA 116081) and the new strain (MFLUCC 17–0915) revealed 3 (0.5%) and 3 (0.34%) nucleotide differences, which indicates that the new strain is *Hermatomyces sphaericus* (Jeewon & Hyde 2016).

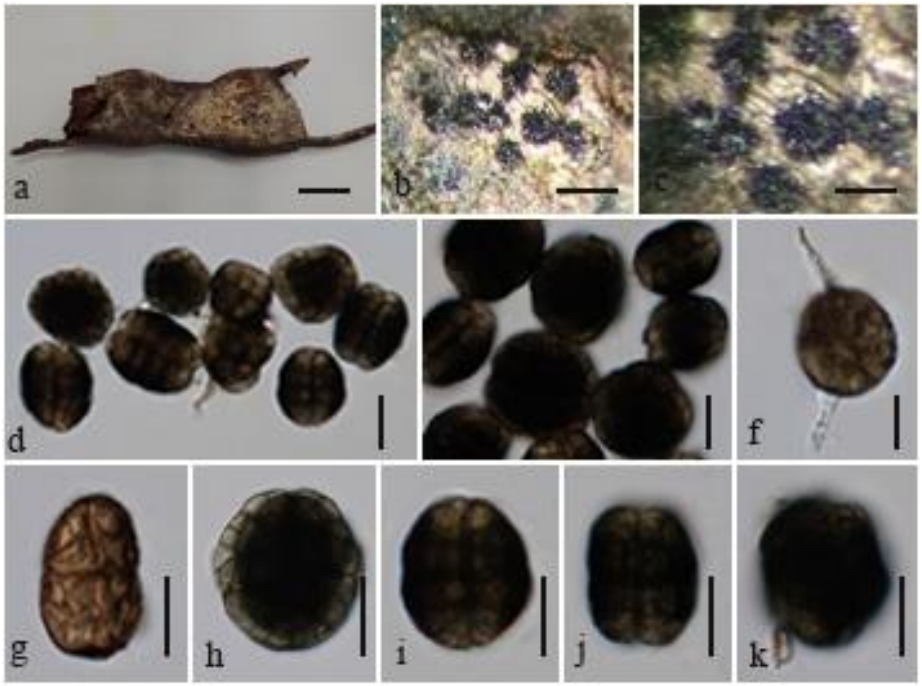


Figure 62 – *Hermatomyces sphaericus* (MFLU 18–2183). a Part of host seed pod. b, c Conidiomata on host material. d, f conidia and conidiophores arrangement. e, g–k Conidia. Scale bars: a = 1 cm, b = 200 μm, c = 500 μm, d–k = 20 μm.

Figure 63 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, LSU and *tef1* matrix of 101 taxa including related families of the order

Pleosporales (Raja et al. 2017). The matrix comprised 2853 characters including alignment gaps. The tree was rooted with *Hysterium angustatum* (Hysteriaceae). The best scoring RAxML tree with a final likelihood value of -23438.322933 is presented. The matrix had 1240 distinct alignment patterns, with 23.56% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.246725, C = 0.239974, G = 0.281460, T = 0.231841; substitution rates AC = 0.949077, AG = 3.313709, AT = 1.082049, CG = 1.230345, CT = 9.959676, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolates are in blue and the new combination is in purple. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I} and ^{R} respectively.

Lindgomycetaceae K. Hiray., Kaz. Tanaka & Shearer, Mycologia 102 (3): 733 (2010)

This family contains four genera, *Arundellina*, *Clohesyomyces*, *Hongkongmyces* and *Lolia*. Most members in this family have been recorded from freshwater habitats, while *Hongkongmyces* is associated with IgG4-related sclerosing disease of humans (Tsang et al. 2014). We introduce a new genus to this family namely, *Neolindgomyces* with *N. pandanae* as the type species (Fig. 63). *Quintaria submersa* is transferred to *Neolindgomyces* as a second species.

41. ***Neolindgomyces*** Jayasiri, E.B.G. Jones & K.D. Hyde, gen. nov.

Index Fungorum number: IF555555; Facesoffungi number: FoF05260

Etymology – Referring to the morphological similarity of new taxon with genus *Lindgomyces.*

Saprobic on *Pandanus* sp. Sexual morph: *Ascomata* scattered to gregarious, immersed, coriaceous, dark brown to black, surrounded by large, carbonaceous parenchymatous cells, clypeus present. *Ostiole* slit-like, central, with a reduced crest and a pore-like opening, plugged by gelatinous tissue, made up of lightly pigmented, pseudoparenchymatous cells. *Peridium* circular, symmetric, dark brown to black layers, somewhat flattened cells of *textura angularis*, fusing and indistinguishable from the host tissues, with inner stratum comprising hyaline cell layers of *textura angularis*. *Hamathecium* comprising numerous, filamentous, branched septate, pseudoparaphyses. *Asci*, 8-spored, bitunicate, fissitunicate, cylindrical, short-pedicellate, apex rounded with a minute ocular chamber. *Ascospores* uniseriate to bi-seriate, overlapping, hyaline, fusiform with narrow, acute ends, 8-septate, constricted at the septa, smooth-walled, guttulate, with a wide mucilaginous sheath. Asexual morph: Undetermined.

Type species – ***Neolindgomyces pandanae*** Jayasiri, E.B.G. Jones & K.D. Hyde

Notes – *Neolindgomyces* is introduced as a new genus belonging to family Lindgomycetaceae based on the multigene phylogenetic analysis of LSU, SSU and *tef1* sequence data and morphological characters. *Neolindgomyces* forms a new lineage in the Lindgomycetaceae distinct from other genera in the family with high statistical support (83% MLBS/0.95 BYPP, Fig. 63). Morphology of our strains are in line with the family descriptions in having subglobose to globose ostiolate ascomata, filamentous, branched, anastomosing pseudoparaphyses, cylindrical to clavate bitunicate asci with an ocular chamber, multi-septate, hyaline ascospores with a gelatinous sheath (Figs. 64, 65). *Neolindgomyces* differs from other genera in this family in having carbonaceous peridium and presence of clypeus (Zhang et al. 2009, Hirayama et al. 2010, Hyde et al. 2014).

42. ***Neolindgomyces pandanae*** Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 64, 65

Index Fungorum number: IF 555556; Facesoffungi number: FoF 05261

Holotype – MFLU 18–2161

Etymology – Referring to the host on which the fungus was collected, *Pandanus* (Pandanaceae).

Saprobic on *Pandanus* sp. fruits. Sexual morph: *Ascomata* 230–255 high × 220–248 µm diam. ($\bar{x}$ = 235 × 225 µm; n = 10), scattered to gregarious, immersed, carbonaceous, globose to subglobose, dark brown to black, clypeus present, ostiolate. *Ostiole* pore-like opening, with

periphyses made up of lightly pigmented, pseudoparenchymatous cells. *Peridium* 13–25 µm wide ($\bar{x}$ = 21 µm; n = 20), circular, symmetric, dark brown to black layers, somewhat flattened cells of *textura angularis*, fusing and indistinguishable from the host tissues, inner stratum comprising hyaline cell layers of *textura angularis*. *Hamathecium* 1.0–1.5 µm wide ($\bar{x}$ = 1.3 µm; n = 30), comprising numerous, filamentous, branched, septate pseudoparaphyses. *Asci* 100–140 × 11–13 µm ($\bar{x}$ = 125 × 11.9 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short-pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 40–50 × 5–7 µm ($\bar{x}$ = 43 × 6.2 µm; n = 30), uniseriate to bi-seriate, overlapping, hyaline, brown when speciemen dry, fusiform with narrow, acute ends, 8-septate, constricted at the septa, smooth-walled, with many guttules, surrounded by prominent mucilaginous sheath. Asexual morph: Undetermined.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 30–40 mm diam. after 4 weeks at 18°C, colonies irregular, medium dense, brown to grey in top view with dark brown edge. Lower surface dark brown with radially arrange margin.

Material examined – THAILAND, Ranong Province (9˚ 35' 43" N, 98˚ 80' 43" E), on decaying fruit pericarp of *Pandanus* sp. (Pandanaceae), 29 August 2017, S.C. Jayasiri, C 358 (MFLU 18–2161, holotype; KUN-HKAS 102431, isotype); ex-type living culture MFLUCC 18–0245, KUMCC 18–0262; *ibid.*, C 363 (MFLU 18–2162), living culture MFLUCC 18–1546, KUMCC 18–0263; *ibid.*, 380-A (MFLU 18–2174); living culture MFLUCC 18–1539, KUMCC 18–0264.

GenBank numbers – MFLUCC 18–0245: SSU: MK347875, ITS: MK347768, LSU: MK347985, *tef1*: MK360062, *rpb2*: MK434875; MFLUCC 18–1546: SSU: MK347877, ITS: MK347770, LSU: MK347987, *tef1*: MK360064, *rpb2*: MK434874; MFLUCC 18–1539: SSU: MK347877, ITS: MK347778, LSU: MK347995, *tef1*: MK360063

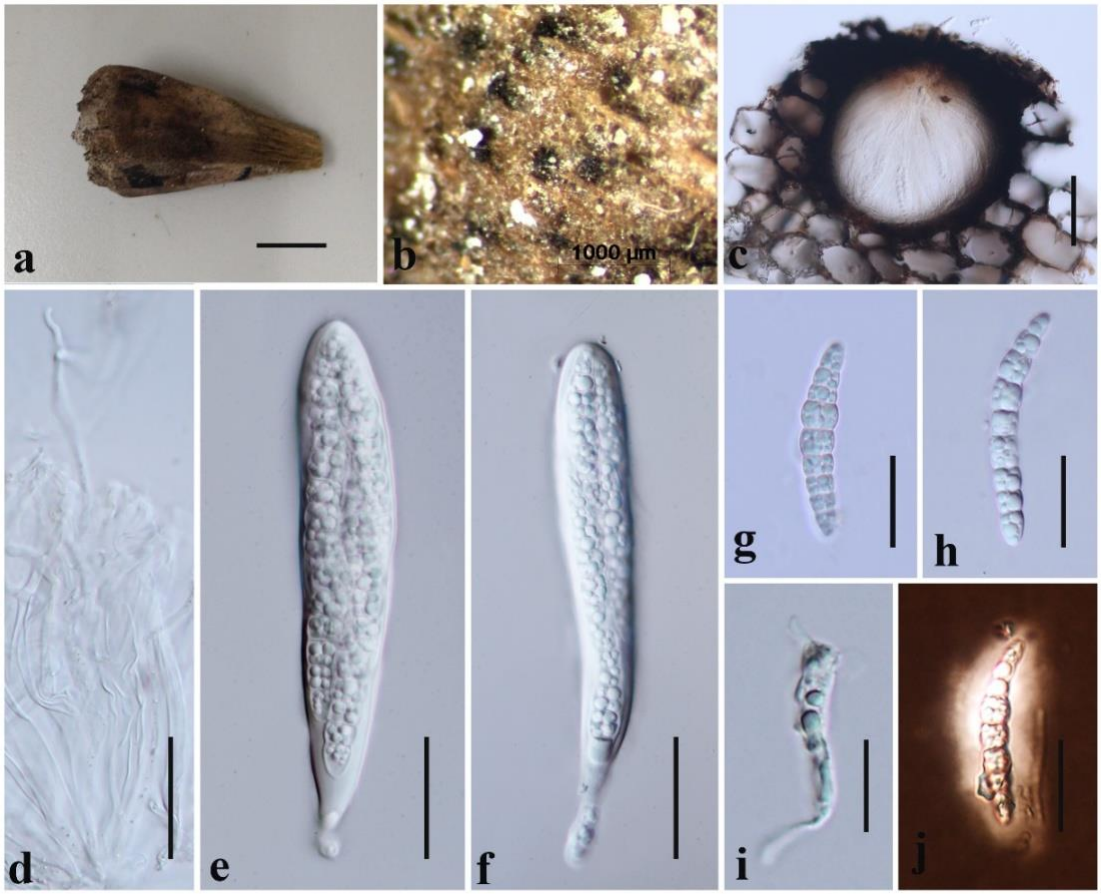


Figure 64 – *Neolindgomyces pandanae* (MFLU 18–2161, holotype). a *Pandanus* sp. host. b Ascomata on host seed. c Section of ascoma. d Pseudoparaphyses. e, f Asci. g, h Ascospores. i Germinated spore. j Sheath in Indian ink. Scale bars: a = 2 cm, c = 100 µm, d = 20 µm, e, f = 30 µm, g–j = 20 µm.

Figure 65 – *Neolindgomyces pandanae* in culture (MFLUCC 18–0245, ex-type). a Top view of culture. b Reverse view of culture. c Ascomata. d Hypha coils. e Section of ascoma. f Peridium. g Ostiolar neck. h–j Asci. k, l Ascospore. Scale bars: a = 2 cm, c = 300 µm, d = 10 µm, e = 100 µm, f, k, l = 20 µm, g–j = 30 µm.

43. ***Neolindgomyces submersa*** (K.D. Hyde & Goh) Jayasiri & K.D. Hyde, comb. nov.

≡ *Quintaria submersa* K.D. Hyde & Goh, Nova Hedwigia 68(1–2): 262 (1999)

Index Fungorum number: IF555557; Facesoffungi number: FoF05262

Description – Refer to Hyde & Goh (1999)

Notes – *Quintaria submersa* (CBS 115553) forms a sister clade to our three strains (MFLUCC 18–0239, MFLUCC 18–0246 and MFLUCC 18–0253) of *Neolindgomyces pandanae* with high statistical support (100% MLBS/1.0 BYPP, Fig. 65). *Quintaria submersa* shares similar morphology with *Neolindgomyces pandanae* in having globose to subglobose ascomata with clypeus and ostiolar canal filled with periphyses, cylindrical, short-pedicellate asci and hyaline, fusiform, guttulate ascospores with sheath (Hyde & Goh 1999). Therefore, we transfer *Quintaria submersa* to the genus *Neolindgomyces*. *Neolindgomyces pandanae* diffes from *N. submera* in having 8-septate, smaller ascospores (40–50 × 5–7 µm vs. 50–68 × 10–14 µm) and smaller asci (100–140 × 11–13 µm vs. 144–212 × 22–33 µm) (Hyde & Goh 1999). To further support the establishment a new taxon, as proposed by Jeewon & Hyde (2016), we examined the nucleotide differences of *tef1* gene region. There was 53 (6.1%) nucleotide difference between *Neolindgomyces pandanae* and *N. submersa* for *tef1* gene region.

Neolindgomyces submersa differs from the type species of *Quintaria* (*Quintaria lignatilis*) in having coriaceous ascomata, presence of clypeus and ascospores with a sheath (Hyde & Goh 1999). *Quintaria lignatilis* groups with species in family Testudinaceae (Schoch et al. 2009, this study). However, LSU sequence data in GenBank blast with Lophiotremataceae species, while SSU and

rpb2 sequence data in GenBank blast with Testudinaceae. Recent studies of these families did not consider *Q. lignatilis* and further sampling is required to confirm the placement of this species.

Two additional species, *Q. aquatica* and *Q. microsporum* have no sequence data available. *Quintaria aquatica* differs from *Neolindgomyces pandanae*, in having 11–13 septate ascospores with a thin sheath and asci with a ring-like apical thickening (Hyde & Goh 1999). *Quintaria microsporum* is characterized by short ascospores without a sheath and shorter asci compared to other species of *Quintaria* and *Neolindgomyces pandanae* (Zhang et al. 2008).

Lophiostomataceae Sacc., Sylloge Fungorum 2: 672 (1883)

Species of the family are recognised by their carbonaceous ascomata with a slit-like ostiolar neck (Zhang et al 2009, Hashimoto et al. 2018). They are saprobes on woody plants from terrestrial, freshwater, and marine environments (Thambugala et al. 2015, Hashimoto et al. 2018, Tennakoon et al. 2018). We introduce a new host record of *Flabellascoma minimum* from fallen pods of *Leucaena leucocephala* and describe a new species, *Vaginatispora nypae* from fallen fruit of *Nypa fruticans* in intertial zone in Thailand (Fig. 66).

44. *Flabellascoma minimum* A. Hashim., K. Hiray. & Kaz. Tanaka, Studies in Mycology 90: 169 (2018) Fig. 67

Facesoffungi number: FoF05263

Saprobic on dead herbaceous twigs and pods. Sexual morph: *Ascomata* 228–310 µm high × 245–325 µm diam. ($\overline{x}$ = 265 × 286 µm, n = 20), solitary, immersed, papilla erumpent through host surface, coriaceous to carbonaceous, black, subglobose, ostiolate. *Ostiole* slit-like, variable in shape, central, papillate, with a crestlike apex and an irregular porelike opening, plugged by gelatinous tissue, made up of hyaline, periphyes and occasionally lighter coloured. *Peridium* 22–45 µm wide, wider at the apex and thinner at the base, composed of a single stratum, with several layers of lightly pigmented to brown cells of *textura prismatica*, cells towards the inside lighter and somewhat broad, at the outside, darker, fusing and indistinguishable from the host tissues. *Hamathecium* 1.5–2.5 µm wide ($\overline{x}$ = 2.2 µm; n = 30), comprising numerous, filamentous, branched, septate, pseudoparaphyses, situated between and above the asci, embedded in a gelatinous matrix. *Asci* 65–79 × 7–9.5 µm ($\overline{x}$ = 74 × 8.3 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate, long pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 19–22 × 3–5 µm ($\overline{x}$ = 21 × 4.2 µm, n = 20), overlapping 1–2 seriate, hyaline, fusiform, with narrow, acute ends, mostly curved, 1-3 septate, constricted at the central septum, cell above central septum widest, smooth-walled, guttulate, with polar appendages at each end. Asexual morph: See Hashimoto et al. (2018).

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 35–45 mm diam. after 4 weeks at 18°C, colonies irregular, medium dense, brown to grey in top view with pale grey edge. Lower surface grey to brown with radially arrange margin.

Material examined – THAILAND, Lampang Province, 19° 3' 44" N, 99° 46' 54" E, on fallen pod of *Leucaena leucocephala* (Fabaceae), 18 August 2017, S.C. Jayasiri, C 328 (MFLU 18–2146, new host record; KUN-HKAS 102426), living culture MFLUCC 18–0233, KUMCC 18–0241.

GenBank numbers – SSU: MK347865, ITS: MK347759, LSU: MK347975, *tef1*: MK360054, *rpb2*: MK434883

Notes – Our isolate forms a sister clade to two strains of *Flabellascoma minimum* (CBS 143645 and CBS 143645) with high statistical support (100% MLBS/ 1.0 BYPP, Fig. 66), and shares similar morphological characters (Hashimoto et al. 2018). *Flabellascoma minimum* has coriaceous to carbonaceous, black, subglobose ascomata with ostiole, bitunicate, fissitunicate, clavate asci and fusiform, 1-3 septate, guttulate ascospores with polar appendages at each end (Hashimoto et al. 2018). A comparison of the ITS, *tef1* and *rpb2* nucleotides of *Flabellascoma minimum* (CBS 143646) and the new strain (MFLUCC 18–0245) revealed 3 (0.57%), 5 (0.56%) and 10 (0.9%) nucleotide differences, which indicates that the new strain is *Flabellascoma minimum* (Jeewon & Hyde 2016). Therefore, we introduce this as a new record of *Flabellascoma*

minimum on *Leucaena leucocephala* in Thailand. Previously, this species was reported on petioles of *Arenga engleri* and pods of *Bauhinia purpurea* in Taiwan (Hashimoto et al. 2018).

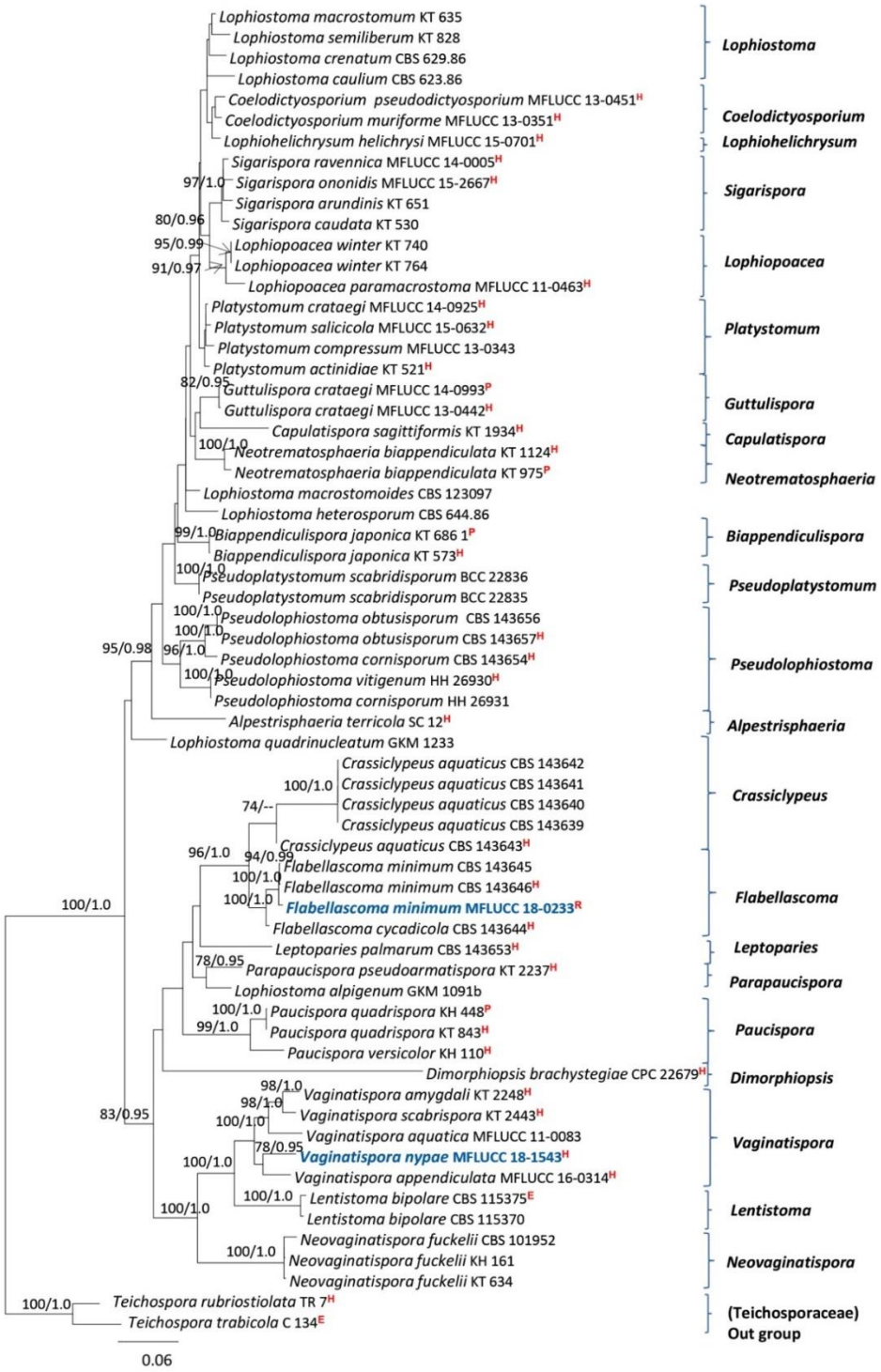


Figure 66 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, *tef1* and *rpb2* partial sequence data. Sixty-four strains are included in the sequence analysis, which comprised 3645 characters including alignment gaps. *Teichospora rubriostiolata* and *Teichospora trabicola* (Teichosporaceae) were used as the outgroup taxa. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML analysis was similar to the BY. The best scoring RAxML tree with a final likelihood value of -24365.760802 is presented. The matrix had 1489 distinct alignment patterns, with 31.29% of undetermined characters or gaps. Estimated base frequencies were as

follows; A = 0.244512, C = 0.262058, G = 0.270451, T = 0.222979; substitution rates AC = 1.513226, AG = 4.132155, AT = 1.335161, CG = 1.306726, CT = 8.580096, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolates are in blue. Strains isolated from the epitype, holotype, partype and reference specimens are indicated in red superscript ^{E}, ^{H}, ^{P} and ^{R} respectively.

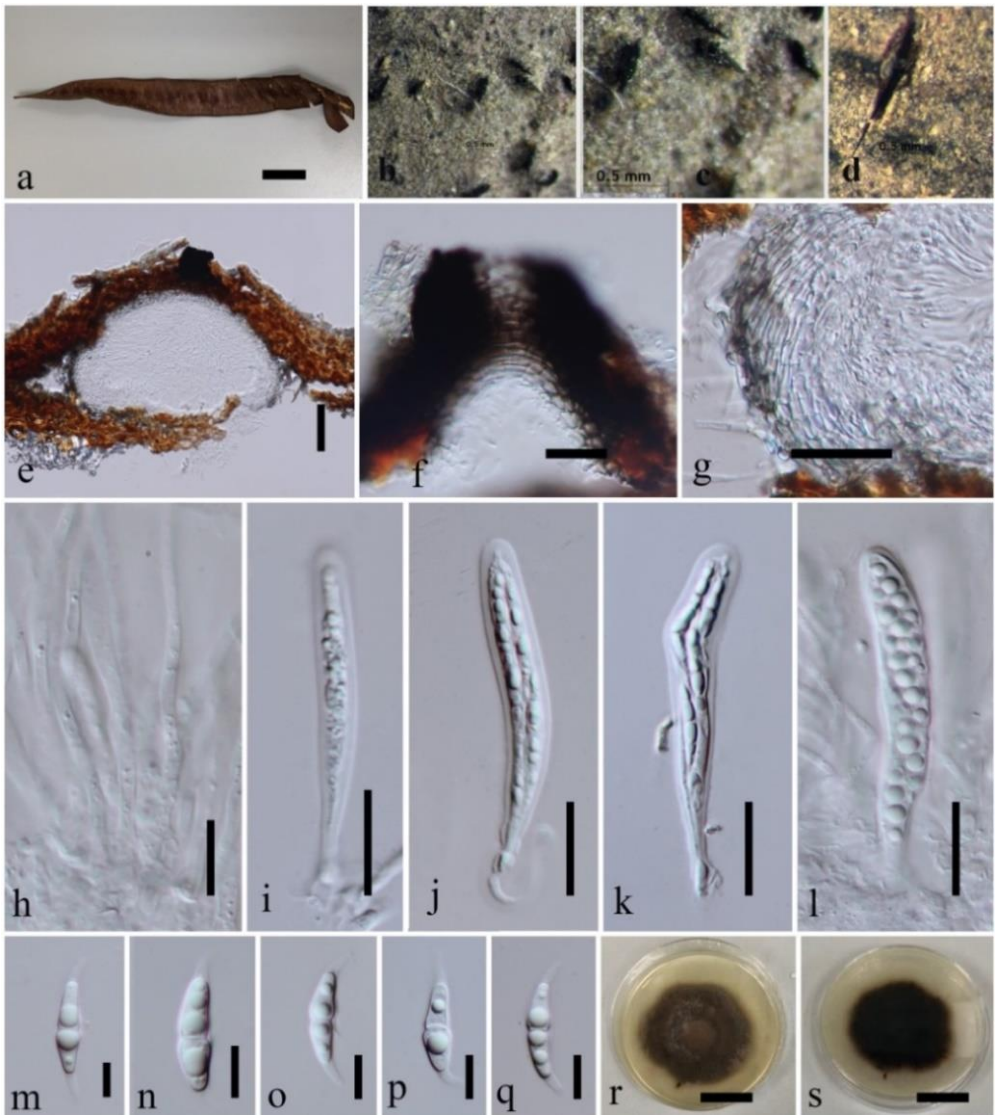


Figure 67 – *Flabellascoma minimum* (MFLU 18–2146). a Host seed pod. b–d Ascomata in host. e Section through ascoma. f Ostiole. g Peridium. h Pseudoparaphyses. i–l Asci. m–q Ascospores. r Top view of culture. s Reverse view of culture. Scale bars: a = 2 cm, e, u = 50 µm, f, g, i–l = 20 µm, h, m–q = 10 µm, r, s = 1 cm.

45. ***Vaginatispora nypae*** Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 68

Index Fungorum number: IF555558; Facesoffungi number: FoF05264

Holotype – MFLU 18–2156

Etymology – Referring to the host on which the fungus was collected, *Nypa* (Arecaceae).

Saprobic on brackish water palm *Nypa fruticans*. Sexual morph: *Ascomata* 305–360 µm high × 280–405 µm diam. ($\bar{x}$ = 344 × 365 µm; n = 30), scattered to gregarious, immersed, coriaceous, dark brown to black, surrounded by large, blackened parenchymatous cells, ostiolate. *Ostiole* slit-like, central, with a reduced crest and a pore-like opening, plugged by gelatinous tissue, made up of lightly pigmented, periphyes. *Peridium* 22–30 µm wide, circular, symmetric, dark brown to black

layers, somewhat flattened cells of *textura angularis*, fusing and indistinguishable from the host tissues, inner stratum comprising hyaline cell layers of *textura angularis*. *Hamathecium* 1.0–1.5 µm wide ($\bar{x}$ = 1.3 µm; n = 30), comprising numerous, filamentous, branched septate, pseudoparaphyses. *Asci* 75–85 × 11–13 µm ($\bar{x}$ = 82 × 11.9 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical-clavate, short-pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 22–26 × 10–13 µm ($\bar{x}$ = 24 × 12 µm; n = 30), uniseriate to bi-seriate, overlapping, hyaline, fusiform with narrow, acute ends, 8-septate, constricted at the septa, smooth-walled, guttulate, with a prominent mucilaginous sheath. Asexual morph: Undetermined.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 3–4 mm diam. after 4 weeks at 18°C, colonies irregular, medium dense, brown to grey in top view with pale brown edge. Lower surface dark brown with radially arrange margin.

Material examined – THAILAND, Krabi Province, Mueang Krabi District, on fallen fruit pericarp of *Nypa fruticans* (Arecaceae), 31 Aug 2017, S.C. Jayasiri C 350 (MFLU 18–2156, holotype), ex-type living culture MFLUCC 18–1543, KUMCC 18–0302.

GenBank numbers – SSU: MK347872, ITS: MK347765, LSU: MK347982, *tef1*: MK360091, *rpb2*: MK434877

Notes – *Vaginatispora nypae* forms a sister clade to *V. appendiculata* (MFLUCC 16–0314) with good statistical support (78 % MLBS/0.95 BYPP, Fig. 67) and shares similar morphological characters. Both species have cylindrical to clavate asci and hyaline, narrow fusiform ascospores with sheaths (Fig. 68). However, *V. nypae* lacks a slit-like ostiole, appendages and ascospores with a wing like sheath seen in *V. appendiculata* (Wanasinghe et al. 2016). *Vaginatispora nypae* was collected from estuarine zone in Thailand, while *V. appendiculata* is known from a fresh water environment in Thailand. A comparison of the ITS nucleotides of these two strains reveals 58 (10.7%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

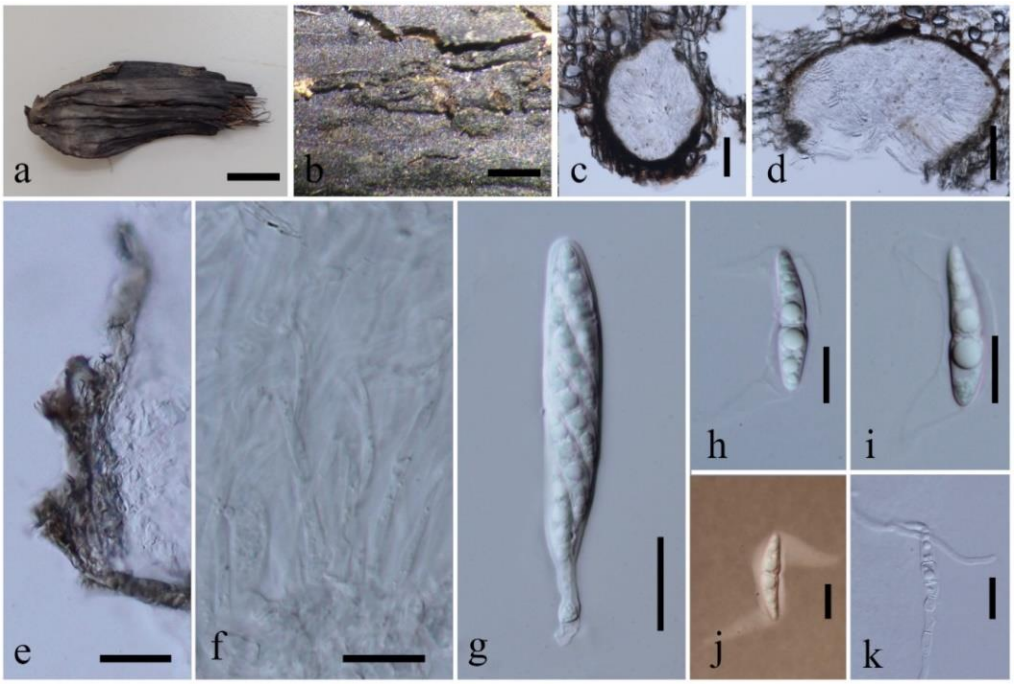


Figure 68 – *Vaginatispora nypae* (MFLU 18–2156, holotype). a Host fruit. b Ascoma on substrate. c, d Section through ascoma. e Peridium. f Pseudoparaphyses. g Ascus. h–i Ascospore. j Ascospore stained with Indian ink. k Germinated ascospore. Scale bars: a = 1 cm, b = 500 µm, c, d = 100 µm, e = 30 µm, f, h–k = 10 µm, g = 20 µm.

Lophiotremataceae K. Hiray. & Kaz. Tanaka, Mycoscience 52: 405 (2011)

The taxonomic placement of Lophiotremataceae was reassessed by Hashimoto et al. (2017) and this family comprises six genera, *Atrocalyx*, *Crassimassarin*a, *Cryptoclypeus*, *Galeaticarpa*,

Lophiotrema and *Pseudocryptoclypeus.* An updated phylogenetic tree for the family is presented in Fig. 69 and a new species of *Atrocalyx* is introduced.

Atrocalyx A. Hashim. & Kaz. Tanaka, Persoonia 39: 59 (2017)

This genus was introduced with the type *Atrocalyx acutisporus* (Hashimoto et al. 2017). Species in this genus inhabit twigs or bark of woody plants in Belgium, China and Japan (Hashimoto et al. 2017, De Silva et al. 2018).

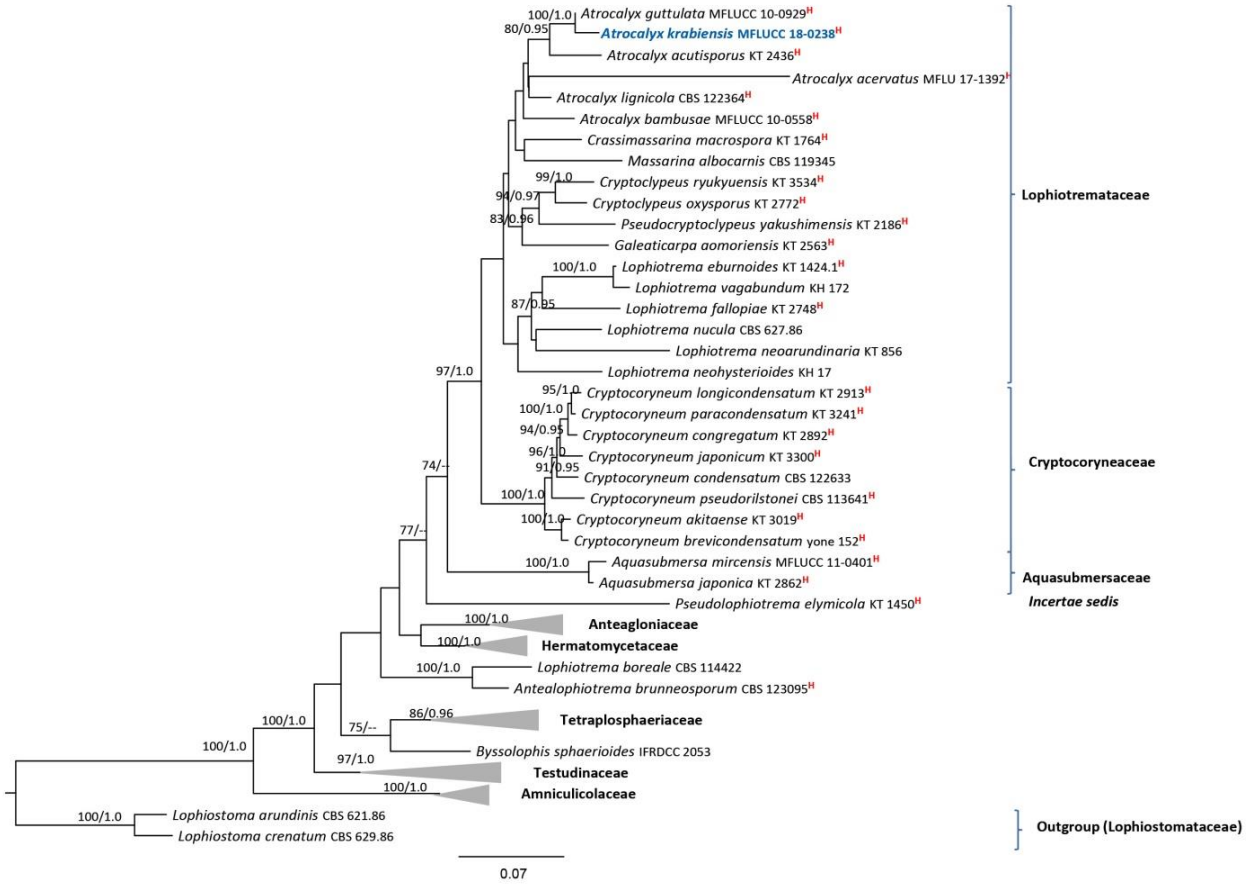


Figure 69 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, *tef1* and *rpb2* partial sequence data. Fifty-one strains were included in the sequence analysis, which comprised 4908 characters including alignment gaps. *Lophiostoma* spp. (Lophiostomataceae) were used as the outgroup taxa. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -34728.193523 is presented. The matrix had 1750 distinct alignment patterns, with 19.64% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250766, C = 0.249259, G = 0.268459, T = 0.231517; substitution rates AC = 1.562313, AG = 4.270025, AT = 1.434787, CG = 1.201086, CT = 9.281437, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strain is in blue. Strains isolated from the holotype are indicated in red superscript ^{H}.

46. ***Atrocalyx krabiensis*** Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 70, 71

Index Fungorum number: IF555559; Facesoffungi number: FoF05265

Holotype – MFLU 18–2167

Etymology – Referring to the location where the specimen was collected, Krabi province, Thailand.

Saprobic on *Acacia* sp. pods. Sexual morph: *Ascomata* 260–350 µm high × 250–320 µm diam. ($\bar{x}$ = 315 × 288 µm, n = 10), solitary, scattered, immersed, slightly erumpent through host surface, visible as raised, black spots on host surface, globose to subglobose, glabrous, uni-loculate. *Ostiole* apical slit-like opening with periphyses. *Peridium* 40–50 µm wide ($\bar{x}$ = 47 µm, n = 10), carbonaceous, fragile, thick at aside, composed of hyaline and dark brown layers, inner layers hyaline to light brown cells, arranged in a *textura prismatica*, outer layers thick, arranged in a *textura angularis*, dark brown cells. Pseudoparaphyses dense, 0.6–1.2 µm wide ($\bar{x}$ = 0.9 µm, n = 10), indistinctly septate, branched, anastomosing at the apex, embedded in a hyaline gelatinous matrix. *Asci* 75–90 × 7–9 µm ($\bar{x}$ = 80 × 8 µm, n = 25), bitunicate, fissitunicate, cylindrical, apically round, with well-developed ocular chamber, with short furcate pedicel and 8-spored. *Ascospores* 18–23 × 2–3 µm ($\bar{x}$ = 20 × 2.5 µm, n = 30), fusiform with acute ends, hyaline, 1–6-septate constricted at the medium septum, enlarged near medium septum at the upper cell, smooth, 4–6 guttules, surrounded by a thick mucilaginous sheath in immature stage (Fig. 70i). Asexual morph: *Conidiomata* pycnidial, brown to dark brown, confluent, immersed. *Hyphae* hyaline, branched, septate, reddish brown pigmented, *Conidiogenous cells* 3–6 × 4–5 µm ($\bar{x}$ = 4.8 × 4.5 µm; n = 20), phialidic, hyaline, smooth-walled, ampulliform. *Conidia* 3–4 × 2–3 µm ($\bar{x}$ = 3.8 × 2.6 µm, n = 30), hyaline, aseptate, cylindrical, smooth- and thin-walled, guttulate (Fig. 71).

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 20–30 mm diam. after 4 weeks at 18°C, colonies irregular, medium dense, dull, off-white to brown in top view, reverse pale brown, pale yellow in margin.

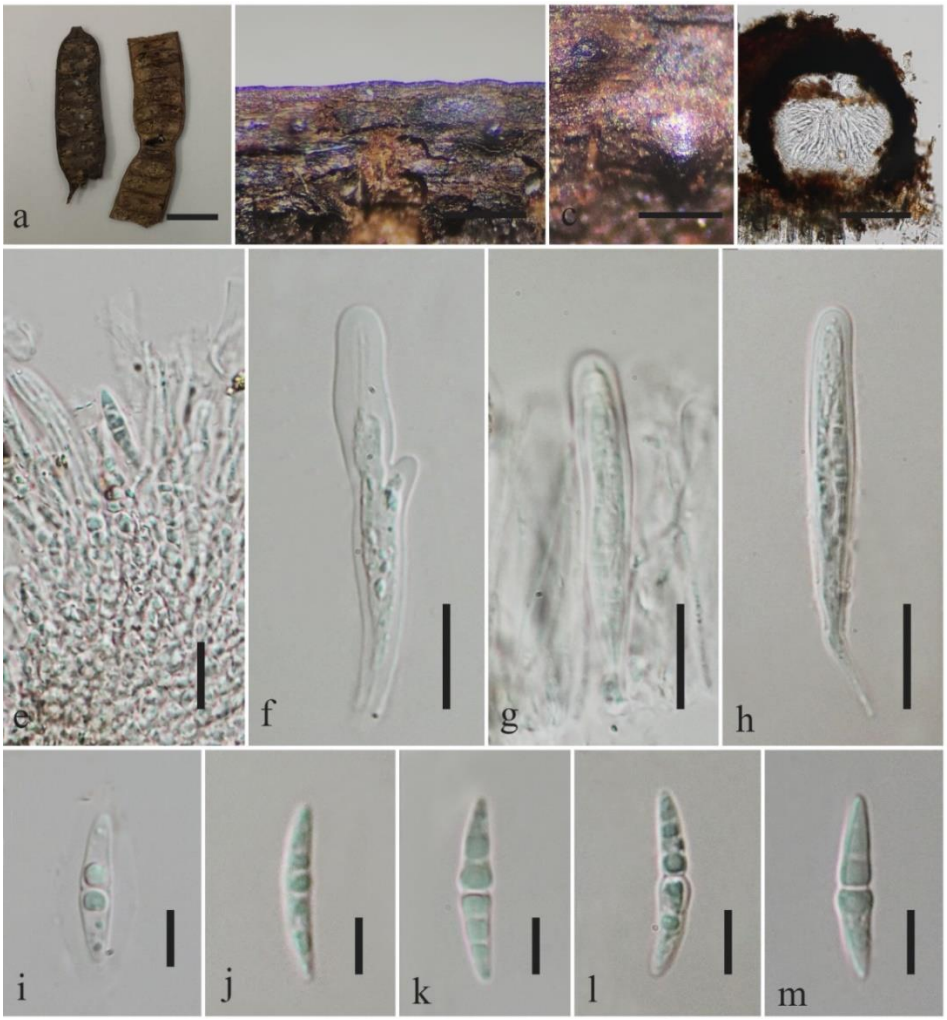


Figure 70 – *Atrocalyx krabiensis* (MFLU 18–2167, holotype). a Host seed pods. b, c Ascomata on substrate. d Section through ascoma. e Paraphyses. f–h Asci. i–m Ascospores. Scale bars: a = 1 cm, b, c = 500 cm, d, e, i = 50 µm, f–h = 20 µm, i–m = 30 µm.

Material examined – THAILAND, Krabi Province, Mueang Krabi District, on fallen pod septum of *Acacia* sp. (Fabaceae), 31 August 2017, S.C. Jayasiri, C 372-B (MFLU 18–2167, holotype, MFLU 18–2168, isotype), ex-type living culture MFLUCC 18–0237, KUMCC 18–0215.

GenBank numbers – SSU: MK347881, ITS: MK347774, LSU: MK347991, *tef1*: MK360043

Notes – *Atrocalyx krabiensis* fits the generic description of *Atrocalyx* (Hashimoto et al. 2017, de Silva et al. 2018) forming a sister clade to *A. guttulata* (MFLUCC 10–0929) with high statistical support (100% MLBS/ 1.0 BYPP, Fig. 69). They also share similar asexual morphs. Unfortunately, *Atrocalyx guttulata* does not have sequence data for ITS or any protein coding genes for nucleotide comparison with the new species. *Atrocalyx krabiensis* differs from *A. guttulata* in having smaller ascospores (20 × 2.5 μm vs. 26 × 5 μm) with a sheath in immature stage and lacking any appentages (Fig. 70).

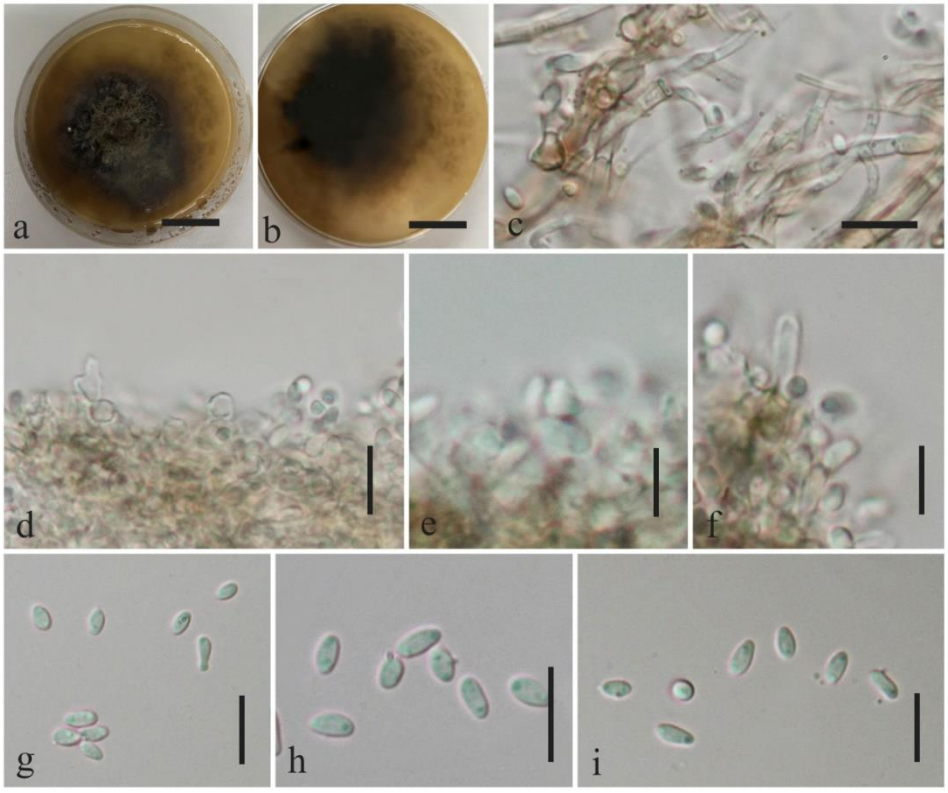


Figure 71 – *Atrocalyx krabiensis* asexual morph from culture (MFLUCC 18–0237, ex-type). a Top view of colony on MEA. b Reverse view of colony. c Conidiomata in the substrate. d–f Conidiogenous cells. g–i Conidia. Scale bars: a, b = 1 cm, c = 20 μm, d–i = 5 μm.

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

This is a family of suborder Massarineae and was introduced by Crous et al. (2015); it contains two genera *Macrodiplodiopsis* and *Pseudochaetosphaeronema.*

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

This genus is recorded as a human pathogen (Ahmed et al. 2014) and as saprobic species on plants (Verkley et al. 2005, Tibpromma et al. 2018). We introduce a new species from fallen pod of *Tamarind* sp. (Fig. 72).

47. *Pseudochaetosphaeronema siamensis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 73

Index Fungorum number: IF555560; Facesoffungi number: FoF05266

Holotype – MFLU 18–2126

Etymology – Referring to country (‘Siam’ synonyms of Thailand) where the specimen was collected.

Saprobic on tamarind pods. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 85–100 µm high × 80–90 µm diam. ($\bar{x}$ = 87 × 84 µm, n = 5), pycnidial, scattered to gregarious, superficial, dark brown, shiny, solitary, uniloculate, globose to subglobose, without papilla and ostiole. *Conidiomata wall* 12–18 µm wide, composed of several layers of thick-walled, dark brown cells of *textura prismatica*. *Conidiogenous cells* 8–17 × 1–2.5 µm ($\bar{x}$ = 11 × 2 µm, n = 20), monophialidic, cylindrical, thick-walled, smooth, each with a small collarette at the tip. *Conidia* 3–5 × 2.5–3 µm ($\bar{x}$ = 3 × 2 µm, n = 30), hyaline to subhyaline, subglobose to oval, aseptate, guttulate.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 30–40 mm diam. after 4 weeks at 18 °C, colonies irregular, medium dense, dull, fluffy to floccose, slightly radiating with concentric ring of cottony mycelium at edge of colony; colony from above different layers in brown and grey; from below: pale brown at the margin, dark brown at the center. Material examined – THAILAND, Payao Province, Amphoe Phu Sang, on fallen pod of *Tamarind* sp. (Fabaceae), 20 July 2017, S.C. Jayasiri, C 273 (MFLU 18–2126, holotype; KUN-HKAS 102422, isotype), ex-type living culture MFLUCC 17–2287, KUMCC 18–0279.

GenBank numbers – SSU: MK347851, ITS: MK347743, LSU: MK347960, *tef1*: MK360074

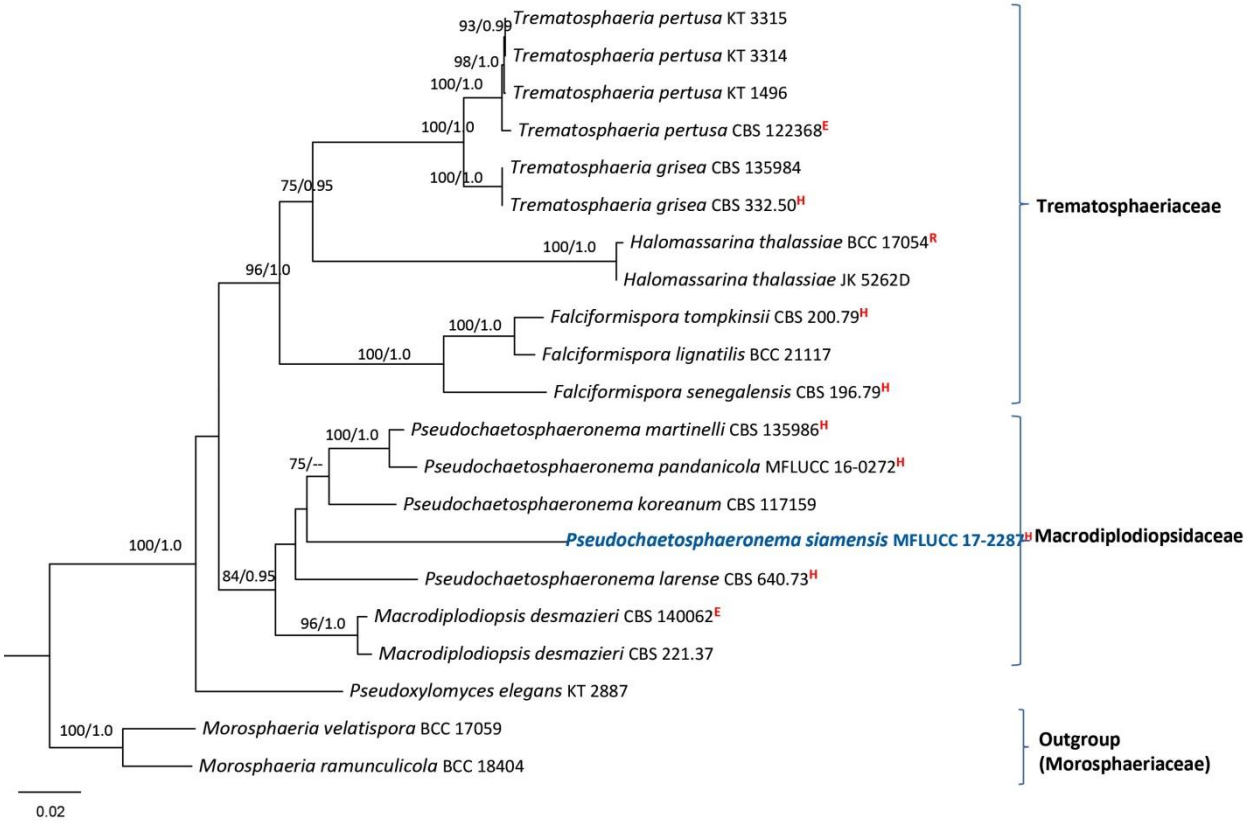


Figure 72 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, LSU and *tef1* matrix of nineteen taxa including species of family Trematosphaeriaceae and Macrodiplodiopsidaceae, which comprised 2855 characters including alignment gaps. The tree is rooted with *Morosphaeria* spp. (Morosphaeriaceae). The best scoring RAxML tree with a final likelihood value of -34728.193523 is presented. The matrix had 789 distinct alignment patterns, with 20.02% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.240358, C = 0.246501, G = 0.271028, T = 0.242112; substitution rates AC = 1.087996, AG = 2.523011, AT = 1.574829, CG = 1.095648, CT = 6.682636, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian

posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the epitype, holotype and reference specimens are indicated in red superscript ^{E}, ^{H} and ^{R} respectively.

Notes – In the phylogenetic analysis, *Pseudochaetosphaeronema siamensis* clusters with other species of *Pseudochaetosphaeronema*. *Pseudochaetosphaeronema siamensis* shares similar morphology with other species in being coelomycetous with uniloculate, globose to subglobose pycnidia, monophialidic and cylindrical conidiogenous cells and subglobose to oval, aseptate, hyaline conidia with guttules (Fig. 73). However, pycnidia of *P. siamensis* do not have a papilla and/or ostiole while *P. koreanum* (CBS 117159) and *P. larense* (CBS 640.73) are characterized by prominent ostiolar necks (Punithalingam 1979, Verkley et al. 2005, Ahmed et al. 2014). In addition, *P. koreanum* has two types of conidia (Verkley et al. 2005). A comparison of the ITS nucleotides of *Pseudochaetosphaeronema siamensis* with *P. koreanum* and *P. larense* reveal 28 (5.2%) and 32 (5.9%) nucleotide differences respectively for each species and which indicates that *P. siamensis* is distinct from *P. koreanum* and *P. larense* (Jeewon & Hyde 2016).

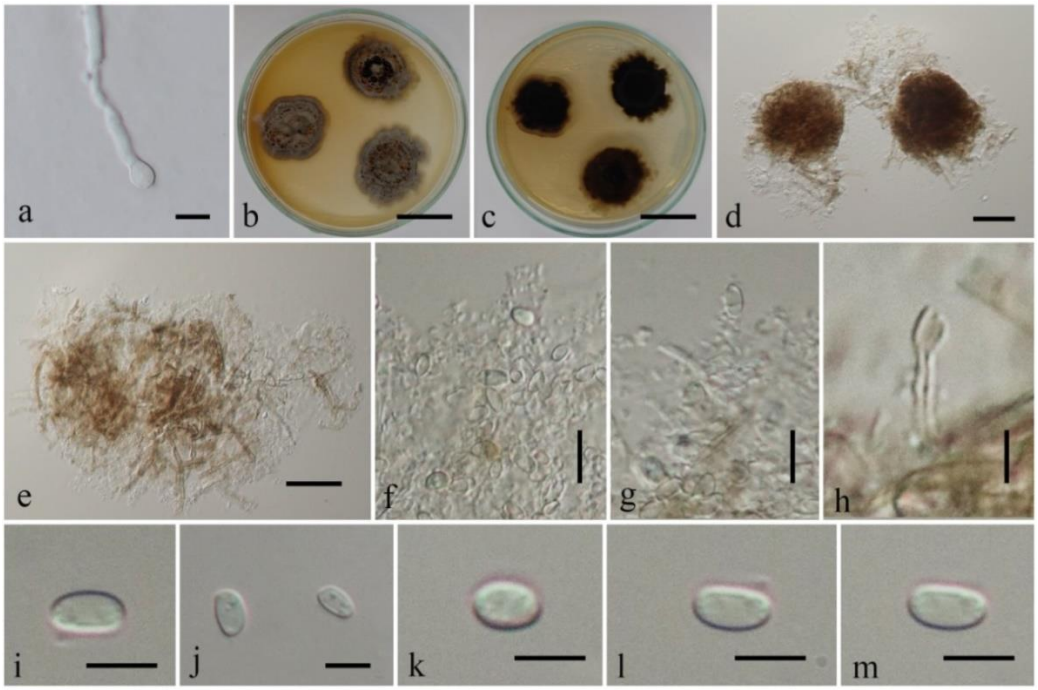


Figure 73 – *Pseudochaetosphaeronema siamensis* (MFUCC 17–2287, ex-type). a Germinated conidium. b Top view of culture. c Reverse view of culture. d, e Conidiomata. f–h Conidia with conidiogenous cells. i–m Conidia. Scale bars: a, i–m = 5 µm, b, c = 2 cm, d, e = 50 µm, f–h = 10 µm.

Neopyrenochaetaceae Valenz.-Lopez, Crous, J.F. Cano, Guarro & Stchigel, Studies in Mycology 90: 54 (2017)

Valenzuela-Lopez et al. (2018) introduced this family based on multigene phylogenetic analyses. Previously Neopyrenochaetaceae species were included in family Cucurbitariaceae (Crous et al. 2015b). Neopyrenochaetaceae is a monophyletic family (Valenzuela-Lopez et al. 2018, Jaklitsch et al. 2018). We present an updated tree for the family and introduce a new species, *Neopyrenochaeta cercidis* (Fig. 74).

Neopyrenochaeta Valenz.-Lopez, Crous, Stchigel, Guarro & J.F. Cano, Studies in Mycology 90: 54 (2017)

Neopyrenochaeta includes four species *N. acicula*, *N. fragariae*, *N. inflorescentiae* and *N.*

telephoni (Valenzuela-Lopez et al. 2018). We introduce a new species to this genus based on morphological and molecular data.

48. ***Neopyrenochaeta cercidis*** Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 75

Index Fungorum number: IF555561; Facesoffungi number: FoF05267

Holotype – MFLU 18–2089

Etymology – Referring to the host genus on which the fungus was collected, *Cercis* (Fabaceae).

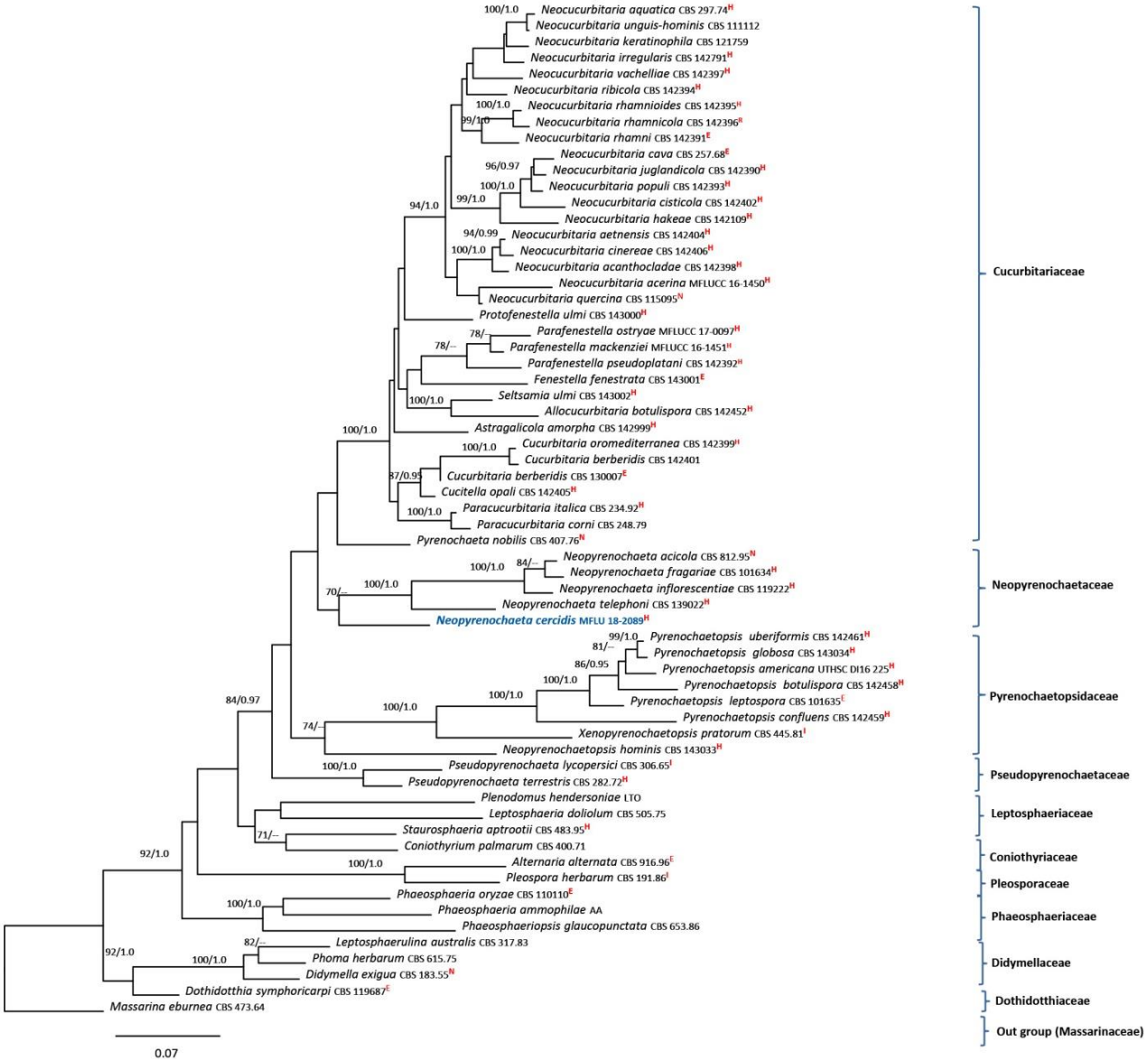


Figure 74 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS, LSU and *rpb2* matrix of sixty-three taxa including related families of order Pleosporales, which comprised 2834 characters including aligment gaps. The tree is rooted with *Massarina eburnea* (Massarinaceae). The best scoring RAxML tree with a final likelihood value of -32269.150713 is presented. The matrix had 1413 distinct alignment patterns, with 30.12% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.253495, C = 0.232719, G = 0.268626, T = 0.245160; substitution rates AC = 1.944563, AG = 5.652011, AT = 2.157548, CG = 1.277423, CT = 9.738451, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near

to each branch. New isolate is in blue. Strains isolated from the epitype, holotype, isotype, neotype and reference specimens are indicated in red superscript ^{E}, ^{H}, ^{I}, ^{N} and ^{R} respectively.

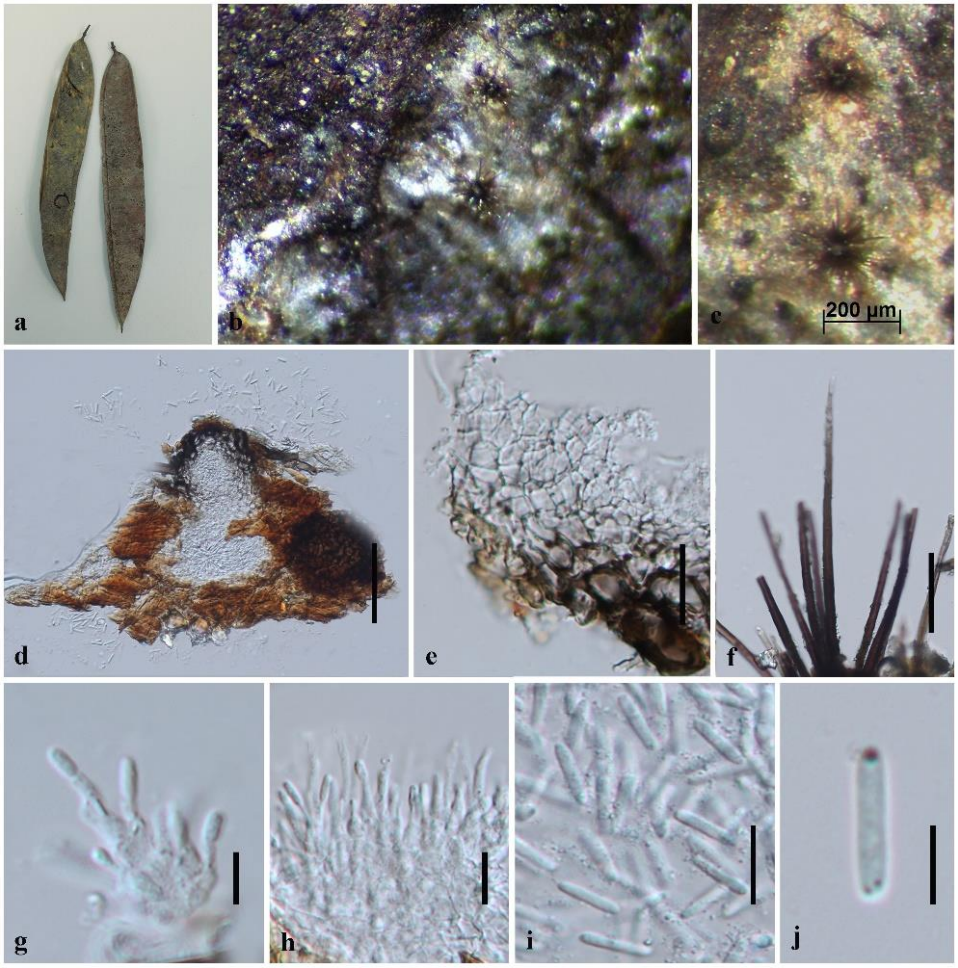


Figure 75 – *Neopyrenochaeta cercidis* (MFLU 18–2089, holotype). a Seed pods of *Cercis chinensis*. b, c Conidiomata in the substrate. d Section through conidioma. d Conidioma wall. f Appendages. g, h Conidiogenous cells. i, j Conidia. Scale bars: a = 1 cm, b = 500 µm, d = 50 µm, e = 20 µm, f = 30 µm, g–j = 5 µm.

Saprobic on pods of *Cercis chinensis.* Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 130–150 µm high × 110–130 µm diam. ($\bar{x}$ = 140 × 120 µm, n = 10), pycnidial, brown to dark brown, solitary, ovoid to globose, covered with brown to dark brown, septate, erect, smooth and thick-walled setae tapering towards the apex, mainly around the ostiole, with a single papillate ostiolar neck. *Conidiomata wall* 20–40 µm wide, 3–8 cell layers of *textura angularis*, composed of brown, flattened polygonal cells. *Conidiogenous cells* 4.5–7 × 3.5–4 µm ($\bar{x}$ = 5.8 × 3.7 µm, n = 30), phialidic, ampulliform, hyaline, smooth-walled. *Conidia* 8–10 × 1.7–2 µm ($\bar{x}$ = 9 × 1.8 µm, n = 30), hyaline, cylindrical, aseptate, smooth and thin-walled, guttulate; concentrated to ends.

Material examined – CHINA, Guizhou Province, Guizhou University, on fallen pod of *Cercis chinensis* (Fabaceae), 30 July 2016, S.C. Jayasiri C 136 (MFLU 18–2089, holotype; KUN-HKAS, isotype)

GenBank numbers – SSU: MK347823, ITS: MK347718, LSU: MK347932, *rpb2*: MK434908

Notes – *Neopyrenochaeta cercidis* forms an independent lineage to other *Neopyrenochaeta* species with moderate statistical support (70% MLBS, Fig. 74) and forms a basal terminal clade in *Neopyrenochaeta. Neopyrenochaeta cercidis* (Fig. 77) differs from *N. telephoni* in having smaller conidiomata (120 × 140 µm vs. 160 × 186 µm), cylindrical conidia and only one type of setae

(Crous et al. 2015b). In *N. telephoni* one type of seta formed on the outer wall is long and mainly concentrated around the ostiole, while the second type around the pycnidia consists of non-stiff hairs or setae-like outgrowths (Crous et al. 2015b). *Neopyrenochaeta cercidis* differs (Fig. 75) from *N. acicola* in having cylindrical conidia (Boerema et al. 2004) and from *N. fragariae* in having longer (8–10 vs. 3.5–5 µm) cylindrical conidia (Valenzuela-Lopez et al. 2018).

Periconiaceae (Sacc.) Nann., Repertorio sistematico dei miceti dell' uomo e degli animali 4: 482 (1934)

The family Periconiaceae was introduced by Nannizzi (1934) with *Periconia* as the type genus, and revised by Hyde et al. (2017, 2018), Liu et al. (2017) and Thambugala et al. (2017).

Periconia Tode, Fungi Mecklenburgenses Selecti 2: 2 (1791)

The genus *Periconia* was introduced by Tode (1791) with *P. lichenoides* as the type species. Herein we introduce a new species and two host records in *Periconia* and provide an updated tree (Fig. 76).

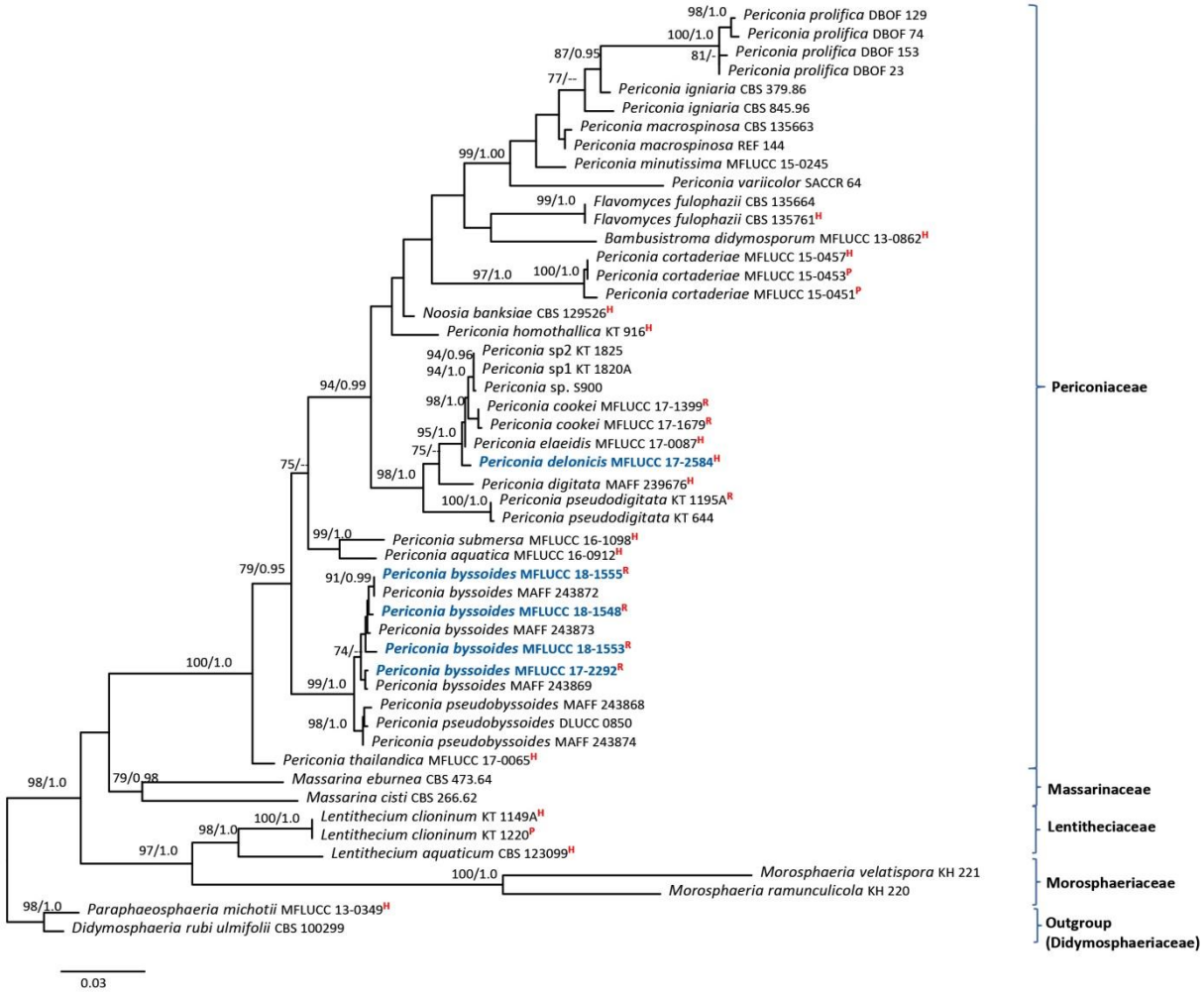


Figure 76 – Phylogram generated from maximum likelihood analysis based on combined ITS, LSU and *tef1* partial sequence data. Fifty strains were included in the sequence analysis, which comprised 2284 characters including aligment gaps. Didymosphaeriaceae spp. (MFLUCC 13–0349/CBS 100299) were used as the outgroup taxa. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -10448.537270 is presented. The matrix had 672 distinct alignment patterns, with 26.95%

of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.224485, C = 0.272782, G = 0.273778, T = 0.228955; substitution rates AC = 1.621763, AG = 2.587602, AT = 1.797216, CG = 1.264889, CT = 11.353607, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in bold and blue. Strains isolated from the holotype, paratype and reference specimens are indicated in red superscript ^{H}, ^{P} and ^{R} respectively.

49. *Periconia byssoides* Pers., Syn. meth. fung. (Göttingen) 2: 686 (1801) Fig. 77

Saprobic on pods of *Peltophorum* sp. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colony effuse, powdery, gregarious, black. *Mycelium* composed of cottony, branched, hyphae forming dark clusters with conidia scattered on the host surface. *Conidiophores* 350–420 μm long × 4.5–5.5 μm diam. ($\bar{x}$ = 385 × 5 μm, n = 20), macronematous, mononematous, single or rarely 2–3 together on stromata, brown to dark brown, erect, or bent, septate, smooth, thick-walled. *Conidiogenous cells* monoblastic, discrete on stipe. *Conidia* 9–12 × 8–12 μm ($\bar{x}$ = 10 × 11 μm, n = 20), catenate, globose, one-celled, hyaline to pale brown when immature, becoming brown to dark brown at maturity, verruculose.

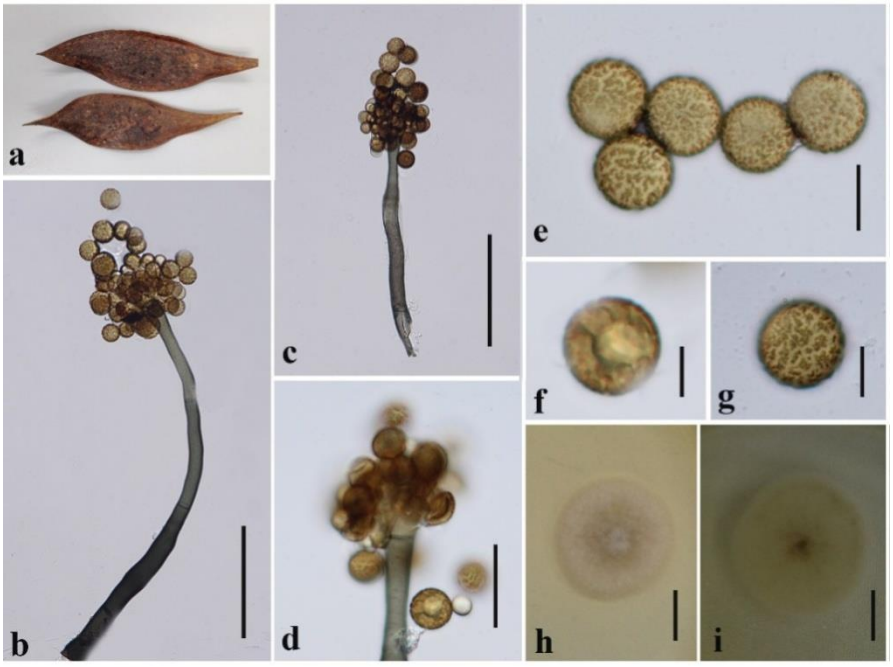


Figure 77 – *Periconia byssoides* (MFLU 18–2136). a Seed pod of *Peltophorum* sp. b–c Conidiophore with conidia. d Conidia attached to conidiogenous cells. e–g Conidia. h Top view of colony on MEA. i Reverse view of colony. Scale bars: b, c = 50 μm, d = 50 μm, e–g = 5 μm, h, i = 1 cm.

Culture characters – Conidia germinated on MEA within 18 hr. Colonies growing on MEA, reaching 20 mm diam. after 1 week at 18°C, flat, surface smooth, with entire edge, white to pinkish, pale white near the margin, moderately dense, circular; reverse white to yellow.

Material examined – THAILAND, Ko Larn island, on decaying pod of *Peltophorum* sp. (Fabaceae), 6 August 2017, S.C. Jayasiri, C 292 (MFLU 18–2136, new host record); living culture, MFLUCC 17–2292, KUMCC 18–0272; CHINA, Yunnan Province, Kunming, Kunming Institute garden, on decaying cone of *Magnolia grandiflora* (Magnoliaceae), 10 May 2018, S.C. Jayasiri, C 445-B (MFLU 18–2195, new host record), living culture MFLUCC 18–1548, KUMCC 18–0271; *ibid.*, 25 May 2018, S.C. Jayasiri, C 457 (MFLU 18–2213), living culture MFLUCC 18–1553, KUMCC 18–0273, C 460 (MFLU 18–2216), living culture MFLUCC 18–1555, KUMCC 18–0274.

GenBank numbers – MFLUCC 17–2292: SSU: MK347858, ITS: MK347751, LSU: MK347968, *tef1*: MK360069, *rpb2*: MK434886; MFLUCC 18–1548: SSU: MK347902, ITS: MK347794, LSU: MK348013, *tef1*: MK360070, *rpb2*: MK434863; MFLUCC 18–1553: SSU: MK347914, ITS: MK347806, LSU: MK348025, *tef1*: MK360068, *rpb2*: MK434858; MFLUCC 18–1555: SSU: MK347917, ITS: MK347809, LSU: MK348028, *rpb2*: MK434856.

Notes – Our four strains of *Periconia byssoides* group with other *P. byssoides* strains forming a sister clade to *Periconia paseuobyssoides* with high statistical support (Fig. 76). A comparison of the ITS and *tef1* nucleotides of *Periconia byssoides* and new strains (MFLUCC 18–0245, MFLUCC 18–1548, MFLUCC 18–1553 and MFLUCC 18–1553) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *Periconia byssoides* (Jeewon & Hyde 2016). Morphologically our strains (Fig. 77) of *P. byssoides* are similar to the type species in having macronematous, mononematous, brown, septate conidiophores and one-celled, pale brown conidia (Persoon 1801). Morphologically and phylogenetically there are no significant differences between our new strains and other strains. Therefore we document two new records of *Periconia byssoides* from a decaying cone of *Magnolia grandiflora* and decaying pod of *Peltophorum* sp. *Periconia byssoides* has been reported from many plant species but these are the first reports for the hosts sampled in this study (https://nt.ars-grin.gov/fungaldatabases/).

50. *Periconia delonicis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 78

Index Fungorum number: IF555562; Facesoffungi number: FoF05268

Holotype – MFLU 18−2100

Etymology – Referring to the host genus on which the fungus was collected, *Delonix* sp. (Fabaceae)

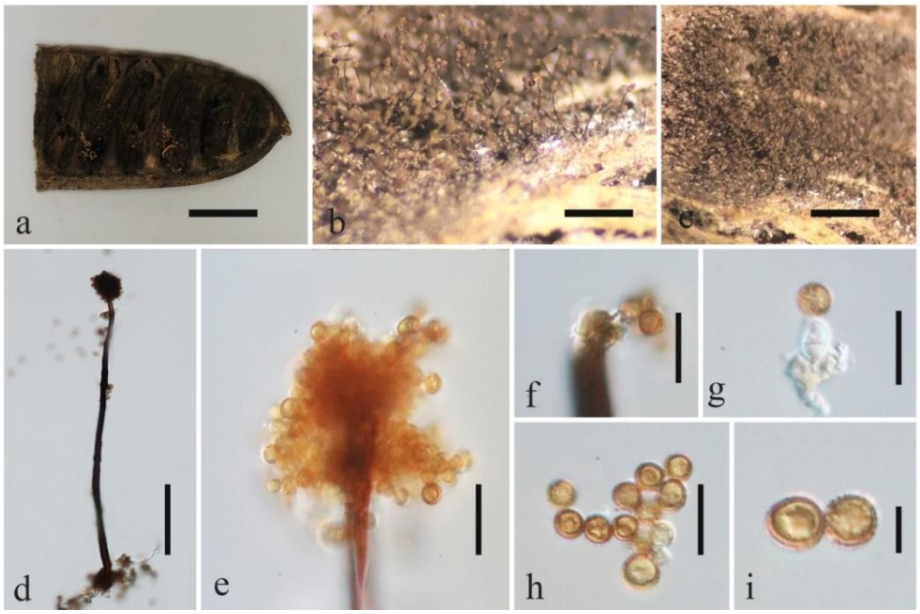


Figure 78 – *Periconia delonicis* (MFLU 18−2100, holotype). a Part of seed pod of *Delonix regia*. b, c Colonies on host substrate. d Conidiophore with conidia. e Conidia on conidiophore. f, g Conidiogenous cells with conidia. h, i Conidia. Scale bars: a, c = 1 cm, b = 500 μm, d = 100 μm, e = 20 μm, f–h = 10 cm, i = 5 cm.

Saprobic on pods of *Delonix regia*. Asexual morph: Hyphomycetous. *Colonies* on substrate numerous, effuse, dark brown to black. *Conidiophores* 360−420 μm high × 8−12 μm diam. ($\bar{x}$ = 398 × 11 μm, n = 10), macronematous, mononematous, unbranched, erect, straight or slightly flexuous, single, greyish brown to dark brown, septate, smooth to minutely verruculose, thick-walled. *Conidiogenous cells* monoblastic, proliferating, hyaline, terminal, blunt end, ovoid to globose, thick-walled. *Conidia* 5.5−7 μm diam. ($\bar{x}$ = 6.4 μm, n = 30), solitary, subhyaline to pale brown, subglobose to globose, verruculose, aseptate. Sexual morph: Undetermined.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies reaching about 50 mm diam. in 2 weeks at 18 °C. Colonies on MEA with sparse white mycelia on the surface. The reverse of colony dark brown and yellow in the center with a white margin.

Material examined – THAILAND, Chiang Rai Province, on decaying pod of *Delonix regia* (Fabaceae), 28 January 2017, S.C. Jayasiri, C 199-B, (MFLU 18−2100, holotype), ex-type living culture MFLUCC 17−2584, KUMCC 18−0275

GenBank numbers – SSU: MK347832, LSU: MK347941, *tef1*: MK360071, *rpb2*: MK434901

Notes – *Periconia delonicis* is introduced based on morphological and phylogenetic data. It groups with other *Periconia* species in the family Periconiaceae with high statistical support (95% MLBS/1.0 BYPP, Fig. 76). *Periconia delonicis* differs from *P. elaeidis* by 5 base pairs in both ITS and LSU genes. *tef1* gene sequence data are not available for *P. elaeidis* in GenBank. Morphologically, *P. delonicis* differs from *P. elaeidis* in having hyaline conidiogenous cells with blunt end and pale brown conidia (Fig. 78). *Periconia elaeidis* is characterized by pale brown, smooth conidiogenous cells and subhyaline to pale brown conidia (Hyde et al. 2018).

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

This is a highly diverse and large family in the order Pleosporales (Hyde et al. 2013) with 42 genera (Phookamsak et al. 2014, Hyde et al. 2017, Senanayake et al. 2018, Wanasinghe et al. 2018b). We introduce a new species from the genus *Phaeosphaeria* based on the multigene phylogeny coupled with morphological characters (Fig. 79).

51. *Phaeosphaeria sinensis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 80

Index Fungorum number: IF555564; Facesoffungi number: FoF05270

Holotype – MFLU 18–2208

Etymology – Referring to country where the specimen was collected, China.

Saprobic on decaying pod of *Wisteria* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 155–198 µm long × 139–159 µm diam. ($\bar{x}$ = 172 µm × 143 µm, n = 20), pycnidial, erumpent, brown, globose, solitary, with central ostiole. *Conidiomata wall* 21–25 µm, 3 layers, dark brown outer layer with 1–2 layers of *textura angularis*, middle hyaline pale brown 4–5 layers of *textura angularis*, inner single layer of brown cells. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–5.5 × 2.5–3.3 µm ($\bar{x}$ = 4.7 µm × 3.2 µm, n = 20), phialidic, ampulliform, lining the inner cavity, hyaline, smooth. *Conidia* 3.5–4.1 × 1.9–2.4 µm ($\bar{x}$ = 3.9 µm × 2.1 µm, n = 20), solitary, red-brown in mass, smooth, globose to subglobose, rounded ends, aseptate, guttulate.

Culture characters – Conidia germinated on MEA within 18 hr. Colonies growing on MEA reaching 20–30 mm diam. after 1 week at 18°C, aerial mycelia present, surface smooth, with entire edge, white, moderately dense, circular; reverse yellow to pale brown.

Material examined – CHINA, Yunnan Province, Kunming, Kunming Institute garden, on decaying pod of *Wisteria* sp. (Fabaceae), 25 May 2018, S.C. Jayasiri, C 454 (MFLU 18–2208, holotype), MFLUCC 18–1552, KUMCC 18–0276.

GenBank numbers – SSU: MK347911, ITS: MK347803, LSU: MK348022, *tef1*: MK360072

Notes – In the phylogenetic analysis, *Phaeosphaeria sinensis* forms a sister clade to *P. podocarpi* (CBS 138903) with moderate support (71% MLBS/ 0.95 BYPP, Fig. 79). These two species share similar morphological characters in having erumpent, brown, globose, solitary pycnidia with a central ostiole, phialidic, ampulliform conidiogenous cells and conidia red-brown in mass. There are significant differences between *Ph. podocarpi* and the new species (Fig. 80). *P. podocarpi* has conidia that are 1-septate, fusoid-ellipsoidal, with an obtuse apex, and a truncate base while *P. sinensis* is characterized by globose to subglobose conidia, rounded ends, and with prominent guttules (Crous et al. 2014). *Phaeosphaeria sinensis* and *P. podocarpi* differ by 6 base pairs in ITS gene. *tef1* gene sequence data are not available for *P. podocarpi* in GenBank. *Phaeosphaeria podocarpi* was reported from leaves of *Podocarpus latifolius* while *P. sinensis* occurred on decaying pod of *Wisteria* sp. (Crous et al. 2014).

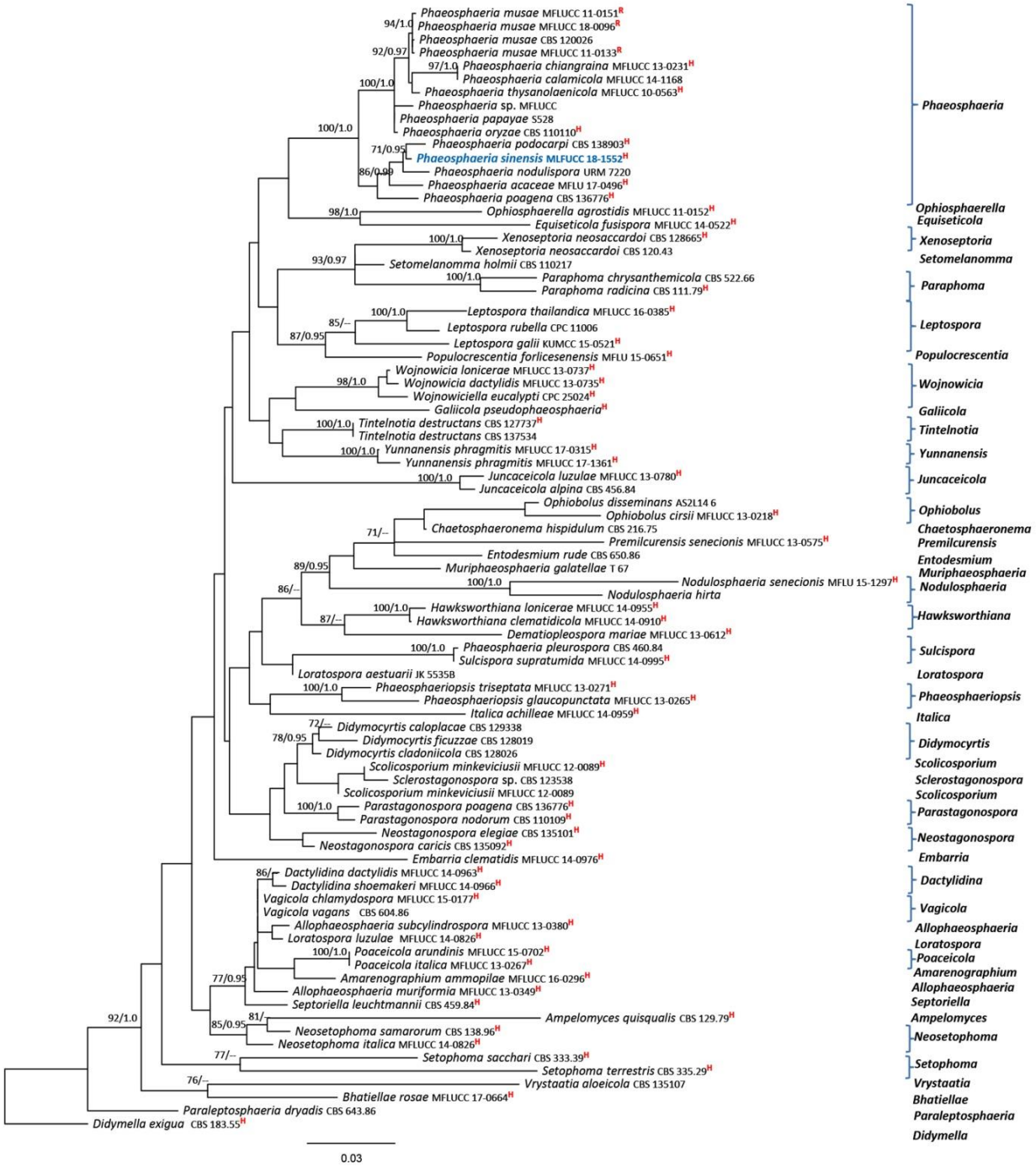


Figure 79 – The best scoring RAxML tree from the maximum likelihood analysis based on combined SSU, ITS, LSU and *tef1* sequence data for Phaeosphaeriaceae. Eightyfive strains were included in the sequence analysis, which comprised 3366 characters including alignment gaps. The *Didymella exigua* (CBS 183.55) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -32087.882436 is presented. The matrix had 1027 distinct alignment patterns, with 33.63% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.244013, C = 0.231082, G = 0.267422, T = 0.257483; substitution rates AC = 1.891915, AG = 3.688826, AT = 3.749101, CG = 0.833773, CT = 9.399134, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolate is in bold and blue. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

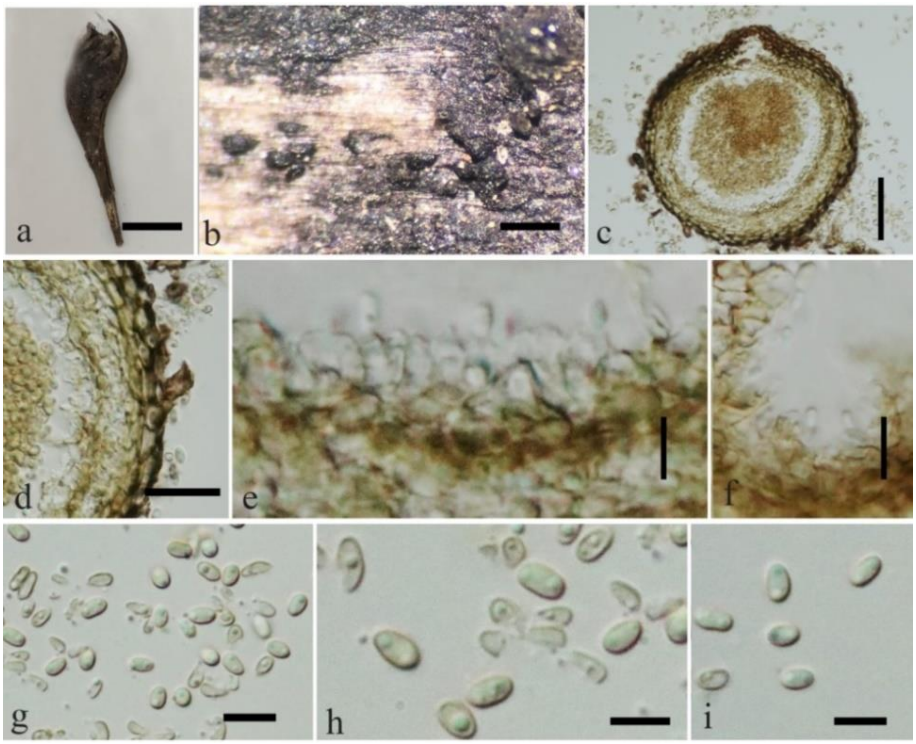


Figure 80 – *Phaeosphaeria sinensis* (MFLU 18–2208, holotype). a Host seed pod. b Conidiomata in the substrate. c Section through conidioma. d Conidioma wall. e, f Conidiogenous cells. g–i Conidia. Scale bars: a = 1 cm, b = 500 μm, c = 5 μm, d = 20 μm, e–i = 5 μm.

Pleomonodictydaceae Hern.-Restr., J. Mena & Gené, Studies in Mycology 86: 76 (2017)

This family was introduced by Hernàndez-Restrepo et al. (2017) based on the type genus *Pleomonodictys* and single species *P. descalsii*. Herein we introduce a new genus and species and rename *Pleohelicoon richonis* in Pleomonodictydaceae and provide an updated tree (Fig. 81).

52. *Pleohelicoon* Jayasiri, D.J. Bhat, E.B.G. Jones & K.D. Hyde, gen. nov.

Index Fungorum number: IF 555565; Facesoffungi number: FoF05271

Etymology – Referring "Pleo" to Pleosporales; and "helicon" referring to the morphological similarity to the genus *Helicoon*.

Saprobic on *Fagus sylvatica.* Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* on substrate scattered or in groups, arising terminally from short, undifferentiated, superficial, hyaline hyphal branches, shiny black, ellipsoidal conidia are visible. *Mycelium* scanty mostly immersed. *Conidiophores* macronematous, mononematous, unbranched, straight, hyaline to brown, smooth. *Conidiogenous cells* monoblastic, integrated, terminal and determinate. *Conidia* solitary, acrogenous, simple, pale brown to dark fuscous, nearly always clockwise tightly coiled 7–9 times in 3 planes to form an ovoid, spherical, ellipsoidal, hollow, doliiform spore body, with multiseptate conidial filament multiseptate, with 5–12 septa per coil, slightly constricted at the septa, 7–9 μm thick. *Microcoidia* hyaline, globose, aggregated, guttulate, located inside macroconidia.

Type species – ***Pleohelicoon fagi*** Jayasiri, D.J. Bhat, E.B.G. Jones & K.D. Hyde

Notes – Morgan (1892) established genus *Helicoon* to accommodate helicosporous species with developing nonproliferating, ellipsoidal to doliiform conidia. The type species of this genus, *H. sessile*, arose from the Orbiliales (Goh & Kuo 2018). However, species of *Helicoon* were placed in different ordinal lineages, namely Orbiliales, Pleosporales, Pleurotheciales, Tubeufiales and Venturiales. Given the polyphyletic nature of *Helicoon*, we suggest that there is a need to revisit the

taxonomy with additional support from new collections and DNA sequence data. Lu et al. (2018) introduced *Pseudohelicoon*, for helicoon-like species belonging to order Tubeufiales. We introduce a new genus, to *Pleohelicoon* to accommodate *Helicoon* species belonging to order Pleosporales.

Pleohelicoon forms a sister clade to *Pleomonodictys* (Pleomonodictydaceae) with moderate bootstrap support (Fig. 81). *Pleomonodictys* has blastic conidia that are formed solitary or in short chains, muriform, verrucose to tuberculate and variable in shape. Therefore, we introduce a second genus of family Pleomonodictydaceae based on the type species, *Pleohelicoon fagi.*

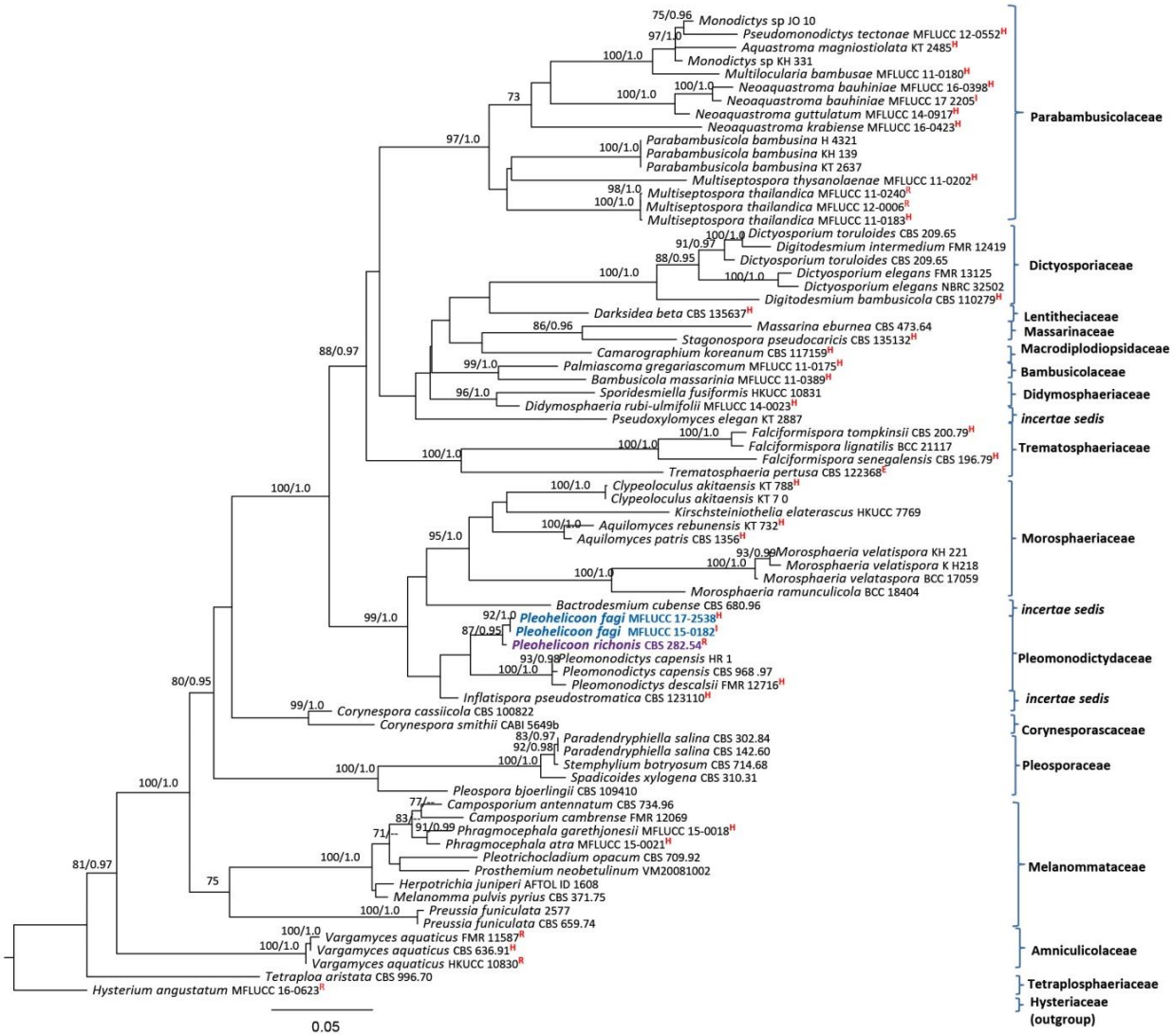


Figure 81 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS and LSU matrix of seventy-four taxa including related families of order Pleosporales. The matrix comprised 2627 characters including alignment gaps. The tree was rooted with *Hysterium angustatum* (Hysteriaceae). The best scoring RAxML tree with a final likelihood value of -21385.064811 is presented. The matrix had 1145 distinct alignment patterns, with 26.79% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250635, C = 0.221769, G = 0.275500, T = 0.252096; substitution rates AC = 1.415901, AG = 2.608795, AT = 1.406746, CG = 0.901746, CT = 5.284979, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolates are in blue and the new combination is in purple. Strains isolated from the epitype, holotype, isotype and reference specimens are indicated in red superscript ^{E}, ^{H}, ^{I} and ^{R} respectively.

53. *Pleohelicoon fagi* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 82

Index Fungorum number: IF555566; Facesoffungi number: FoF05272

Holotype – MFLU 18–2224

Etymology – Referring to the host genus on which the fungus was collected, *Fagus* (Fagaceae)

Saprobic on cupule of *Fagus sylvatica.* Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on substrate individually scattered or in groups, arising terminally from short, undifferentiated, superficial, hyaline hyphal branches, shiny black, ellipsoidal conidia are visible. *Mycelium* scanty mostly immersed. *Conidiophores* 22–31 µm high × 3.3–3.7 µm diam. ($\bar{x}$ = 26 × 3.5 µm, n = 30), macronematous, mononematous, unbranched, straight, hyaline to brown, smooth. *Conidiogenous cells* monoblastic, integrated, terminal and determinate. *Conidia* 57–90 µm × 35–50 µm ($\bar{x}$ = 68 × 42 µm, n = 30), solitary, acrogenous, pale brown to dark fuscous, nearly always clockwise tightly coiled 7–9 times in 3 planes to form an ovoid, spherical, ellipsoidal, hollow, doliiform spore body; conidial filament multiseptate, with 5–12 septa per coil, slightly constricted at septa, 7–9 µm thick. *Microcoidia* 4.2–4.8 × 4.3–5.2 µm ($\bar{x}$ = 4.5 × 4.8 µm, n = 30), globose, aggregated, hyaline, guttulate, located inside macroconidia.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 18–20 mm diam. after 2 weeks at 18°C, elevated, velvety, with moderate amount of short mycelium, mouse grey, margin fimbriate, greyish; reverse dark mouse grey.

Material examined – UK, Bishops Waltham, Hants., on decaying cupule of *Fagus sylvatica* (Fagaceae), 3 September 2014, E.B.G. Jones, GJ 50 (MFLU 18–2224, holotype; KUN-HKAS 102441, isotype), ex-type living culture MFLUCC 15–0182, KUMCC 18–0277; *ibid*., Hampshire from standing water, on decaying cupule of *Fagus sylvatica*, 12 August 2017, E.B.G. Jones, GJ 415 (MFLU 18– 2227, paratype), living culture MFLUCC 17– 2538, KUMCC 18–0278.

GenBank numbers – MFLUCC 18–0182: SSU: MK347926, ITS: MK347817, LSU: MK348037, *rpb2*: MK434853; MFLUCC 17– 2538: SSU: MK347925, ITS: MK347816, LSU: MK348036, *rpb2*: MK434851

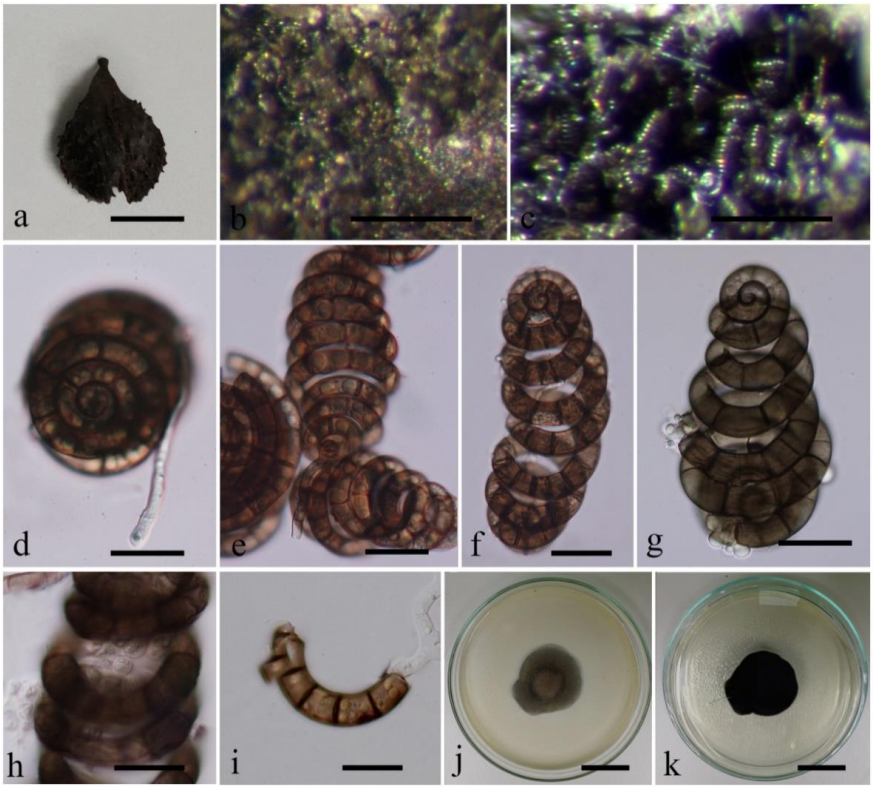


Figure 82 – *Pleohelicoon fagi* (MFLU 18–2224, holotype). a Cupule of *Fagus sylvatica.* b, c Colonies on substrate. d–h Conidia. i Germinated conidium. j Top of culture. k Reverse of culture. Scale bars: d–i = 30 µm.

54. *Pleohelicoon richonis* (Boud.) Jayasiri, E.B.G. Jones & K.D. Hyde, comb. nov.

Index Fungorum number: IF555567; Facesoffungi number: FoF05273

≡*Helicosporium richonis* Boud., Icones mycologicae 26-30: t. 599 (1907)

≡*Helicoon richonis* (Boud.) Linder, Annals of the Missouri Botanical Garden 16: 323 (1929)

Saprobic on dead branch of *Populus* sp. Sexual morph: Unknown. Asexual morph: Hyphomycetous. *Colonies* on substrate blackening. *Hyphae* dark brown, giving rise to short conclorous filaments, septate. *Conidiophore*s 1–1.5 µm long. *Conidia* 50–60 × 50–80 µm, 8–10 seriate, brown, irregularly oval or rounded, filaments, multiseptate (Linder 1929).

Notes – *Pleohelicoon richonis* (CBS 282.54) forms a sister clade to two strains of *P. fagi* (MFLUCC 17–2538/ MFLUCC 15–0182) with high statistical support (87% MLBS/ 0.95 BYPP, Fig. 81). The holotype of *P. richonis* was collected in France on *Populus* (Linder 1929) but sequence data was derived from a collection made in the Netherlands. *Pleohelicoon richonis* shares morphological characters with *P. fagi* in having coiled, multiseptate, brown conidia. *Pleohelicoon fagi* has much longer conidiophores than *P. richonis* (22–31 vs. 1–1.5 µm). A comparison of the ITS nucleotides of these two species revealed 8 (1.6%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Pleosporaceae Nitschke, Verh. Naturhist. Vereines Preuss. Rheinl.: 74 (1869)

Alternaria Nees, System der Pilze und Schwämme: 72 (1817)

Alternaria species can be serious plant pathogens, causing stem cankers, leaf blight or leaf spots on a wide variety of crops (Peever et al. 2004, Thomma, 2003). *Alternaria alternata* can produce host-specific toxins (Akamatsu et al. 1999). *Alternaria alternata* and *A. solani* are important postharvest pathogens as well as being airborne allergens (El-Goorani & Sommer 1981, Reddy et al. 2000, Mitakakis et al. 2001). Many species are also saprobes (Ariyawansa et al. 2015, Woudenberg et al. 2015, Thambugala et al. 2017, Wanasinghe et al. 2018b). *Alternaria* comprises 24 sections (Woudenberg et al. 2013). We report a new host record for *A. alternata* from decaying cone of *Magnolia grandiflora* in China.

55. *Alternaria alternata* (Fr.) Keissl., Zur Kenntnis der Pilzflora Krains. Beihefte zum Botanischen Centralblatt. 29: 434 (1912) Fig. 84

Facesoffungi number: FoF05274

Pathogeneic and *saprobic* on many plant species, human body, air. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* superficial, composed of septate, branched, smooth, thin-walled, white to pale brown hyphae. *Conidiophores* 18–50(–97) µm high × 4.1–5.3 µm diam. ($\bar{x}$ = 46 × 4.6 µm, n = 20), macronematous, mononematous, light brown to brown, thick-walled, smooth, septate, branched at base, straight or flexuous, cylindrical. *Conidiogenous cells* 6.3–8.5 µm long × 7.1–8 µm diam ($\bar{x}$ = 7.8 × 7.4 µm, n = 20), polytretic, integrated, terminal, determinate or percurrent, cylindrical, doliiform, brown, thin-walled. *Conidia* 14.5–26.6 × 10–15.5 µm ($\bar{x}$ = 23 × 12 µm, n = 30), acrogenous, holoblastic, solitary, brown to dark brown, straight, curved, fusiform, obpyriform or obturbinate, subglobose, catenate, sometimes rostrate, rough, multiseptate, thin-walled, cicatrized at base.

Culture characters – Conidia germinated on MEA within 18 hr and germ tubes produced from upper cells. Colonies growing on MEA, reaching 50 mm diam. in 2 weeks at 18^{o}C, hairy or cottony, white to light brown, mycelium superficial, effuse, radially striate, with regular edge, pale brown hyphae; conidia produced within 2 weeks.

Material examined – CHINA, Yunnan Province, Kunming, Kunming Institute garden, on decaying cone of *Magnolia grandiflora* (Magnoliaceae), 10 May 2018, S.C. Jayasiri, C 445-A (MFLU 18–2194, new host record); *ibid.*, 25 May 2018, S. C. Jayasiri, C 462 (MFLU 18–2218), dry culture MFLU 18–2219, living culture MFLUCC 18–1558, KUMCC 18–0212.

GenBank numbers – MFLU 18–2194: SSU: MK347901, ITS: MK347793, LSU: MK348012, *tef1*: MK340863, *rpb2*: MK434862, *tub2*: MK412868, *gapdh*: MK412898; MFLUCC 18–1558: SSU: MK347920, ITS: MK347812, LSU: MK348031, *tef1*: MK340860, *rpb2*: MK434855, *tub2*:

MK412870, *gapdh*: MK412899

Notes – We collected the asexual morph of *Alternaria alternata* from decaying cone of *Magnolia grandiflora* in China. It sporulated in culture (Fig. 84) producing the same characteristic morphology as in the type description (Ellis 1971). A comparison of the ITS, *tef1*, *rpb2* and *gapdh* nucleotides of *Alternaria alternata* and new strains (MFLU 18–2194 and MFLUCC 18–1558) revealed nucleotide differences ≤ 1.5%, which indicates that the new strains are *Alternaria alternata* (Jeewon & Hyde 2016) and independent lineage of *Alternaria alternata* clade from other species in the section *Alternaria*. Therefore, we introduced new host record from decaying cone of *Magnolia grandiflora* in China.

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

Liu et al. (2014) introduced this family to accommodate *Neoroussoella*, *Roussoella* and *Roussoellopsis*. Wanasinghe et al. (2018b) introduced two genera (*Pararoussoella* and *Neoconiothyrium*) in Thyridariaceae, which we transfer to Roussoellaceae in this study. *Arthopyrenia* sp. in GenBank clusters with species in family Roussoellaceae, but these species do not have a morphological description. The type species of *Arthopyrenia*, *A. cerasi*, belongs to family Arthopyreniaceae. Therefore, we tentatively designate *Arthopyrenia* sp. as *Roussoella* sp. because these strains are not related to any type material and therefore it is inappropriate to rely on it for a phylogenetic discussion (Wanasinghe et al. 2018b). We present an updated tree for the family and introduce two new species and rename two species (Fig. 88).

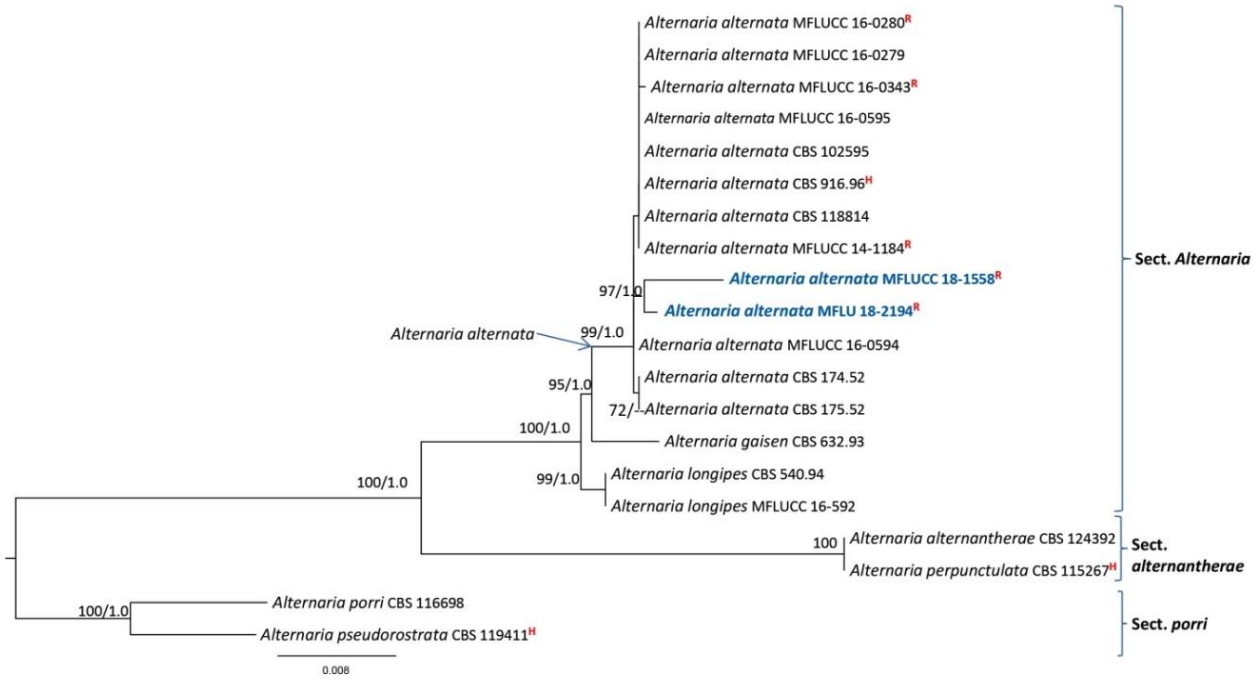


Figure 83 – The best scoring RAxML tree from the maximum likelihood analysis based on combined ITS, LSU, *tef1*, *rpb2* and *gapdh* matrix of twenty strains including related species of the section *Alternaria*. The matrix comprised 3309 characters including alignment gaps. The Section *porri* (CBS 116698/ CBS 119411) was used as outgroup. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -6319.810823 is presented. The matrix had 267 distinct alignment patterns, with 21.34% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.246927, C = 0.251441, G = 0.266231, T = 0.235402; substitution rates AC = 1.583664, AG = 4.074495, AT = 1.496241, CG = 1.430388, CT = 10.663375, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near

to each branch. New isolates are in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

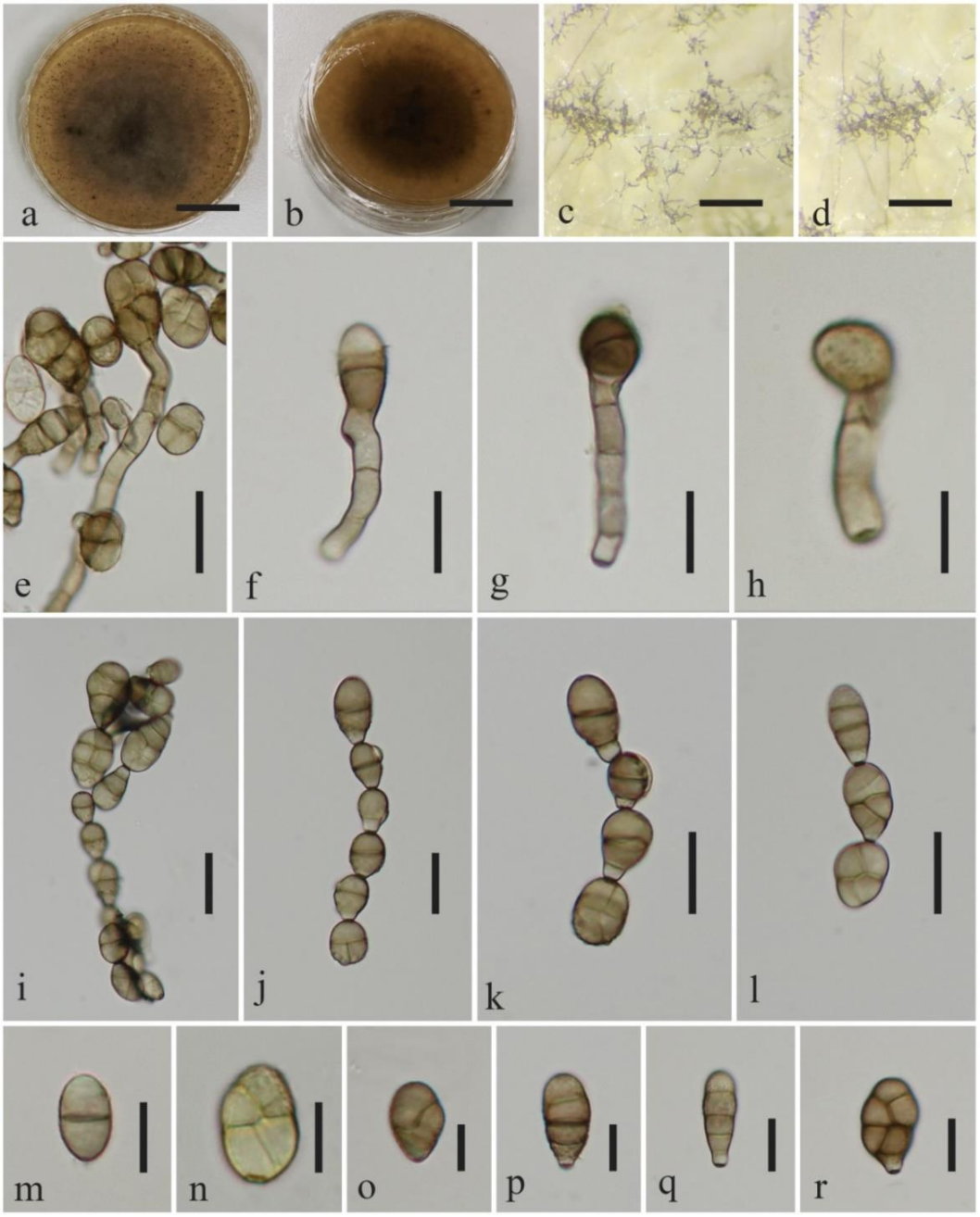


Figure 84 – *Alternaria alternata* from culture (MFLUCC 18–1558). a Top view of culture. b Reverse view of culture. c, d Structures in culture. e–h Conidiophores and conidiogenous cells. i–l Conidial chains. m–r Conidia. Scale bars: a, b = 1 cm, c–j = 20 µm, k, l = 10 µm.

Neoroussoella J.K. Liu, Phookamsak & K.D. Hyde, Phytotaxa 181 (1): 21 (2014)

This genus was introduced based on phylogenetic data coupled with distinct asexual morph from other genera, producing relatively small, hyaline conidia with smooth walls with type species *Neoroussoella bambusae* (Liu et al. 2014). Hyde et al. (2016) added another species to the genus. We introduce two new *Neoroussoella* species and transfer *Roussoella solani* (CPC 26331) to *Neoroussoella* based on the multigene phylogenetic analyses of LSU, SSU, ITS, *rpb2* and *tef1* sequence data coupled with morphological observations. However, *Roussoella solani* (KT 3264 and KT 3265) is distinct from *R. solani* (CPC 26331) and we rename KT 3264 and KT 3265 strains

as *Neoroussoella leucaenae.*

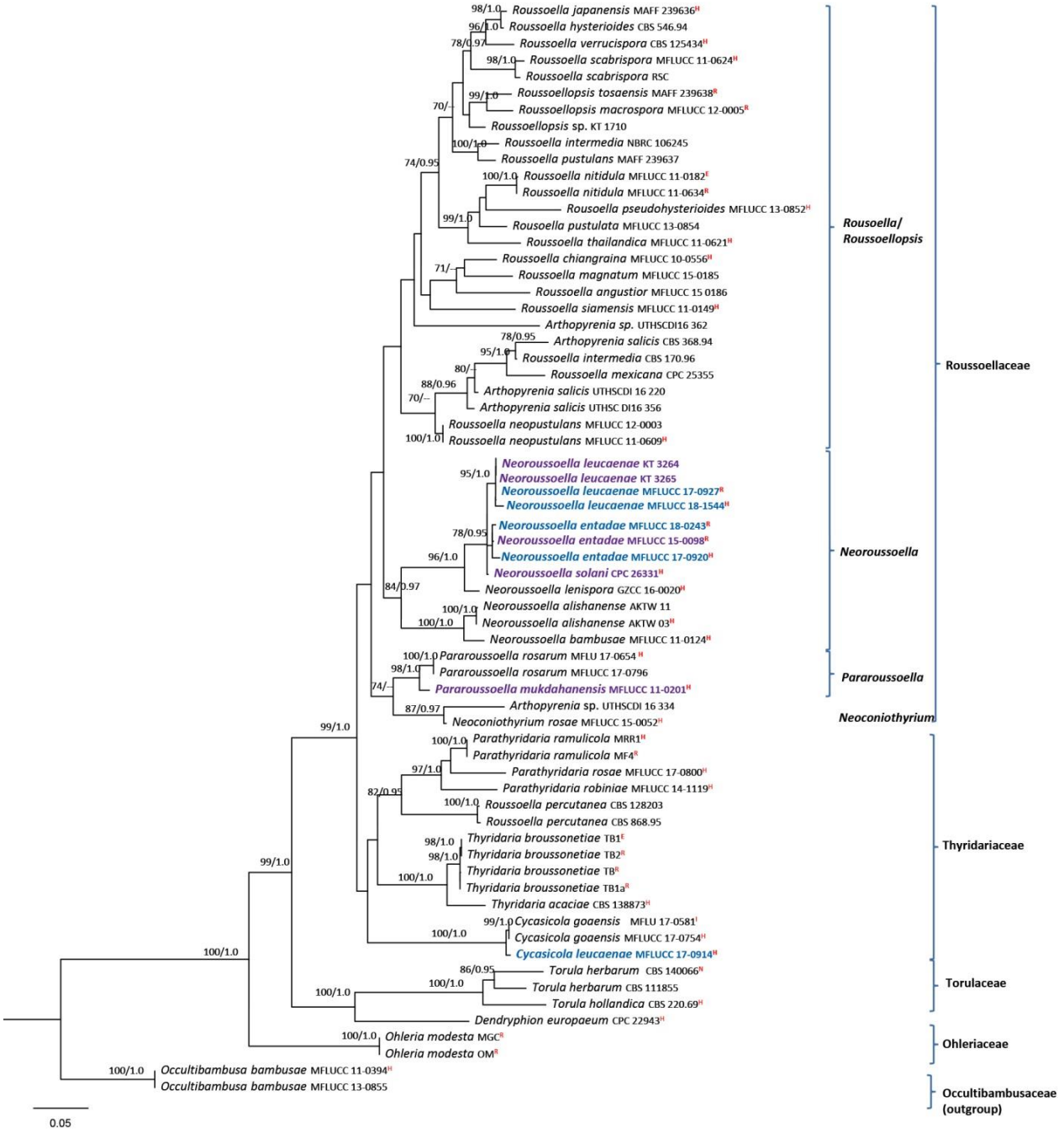


Figure 85 – Phylogram generated from maximum likelihood analysis based on combined SSU, ITS, LSU, *rpb2* and *tef1* partial sequence data. Fifty-one strains were included in the sequence analysis, which comprised 3442 characters with gaps. Two strains of *Occultibambusa bambusae* (Occultibambusaceae) were used as the outgroup taxa. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -14689.599902 is presented. The matrix had 1590 distinct alignment patterns, with 37.79% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.247628, C = 0.256142, G = 0.268302, T = 0.227927; substitution rates AC = 1.684273, AG = 4.305228, AT = 1.881038, CG = 1.378430, CT = 9.209369, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue and new combiinations are in purple. Strains isolated from

the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I} and ^{R} respectively.

56. ***Neoroussoella entadae*** Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 86, 87

Index Fungorum number: IF555568; Facesoffungi number: FoF05275

Holotype – MFLU 18–2106

Etymology – Referring to the host genus on which the fungus was collected, *Entada* (Fabaceae)

Saprobic on *Entada phaseoloides* and *Leucaena* sp. pods. Sexual morph: undetermined. Asexual morph: Coelomycetous. *Conidiomata* 127–192 × 161–190 µm ($\bar{x}$ = 169 × 184 µm, n = 10), pycnidial, solitary to gregarious, occasionally confluent, formed in uni- or multi-loculate stromata, immersed, becoming erumpent at maturity, ostiolate. *Ostiole* papillate, central, circular. *Conidiomata wall* 20–37 µm wide, composed of thick-walled, dark brown cells of *textura angularis*; inner layer thin, hyaline. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 3.5–5.6 × 0.7–1.8 µm ($\bar{x}$ = 4.2 × 1.3 µm, n = 20), phialidic, ampulliform to cylindrical, hyaline, smooth-walled. *Conidia* 3–4 × 1.7–1.9 µm ($\bar{x}$ = 3.5 × 1.8 µm, n = 20), initially hyaline, becoming pale brown when mature, oblong to ovoid, straight, both ends, broadly rounded, aseptate.

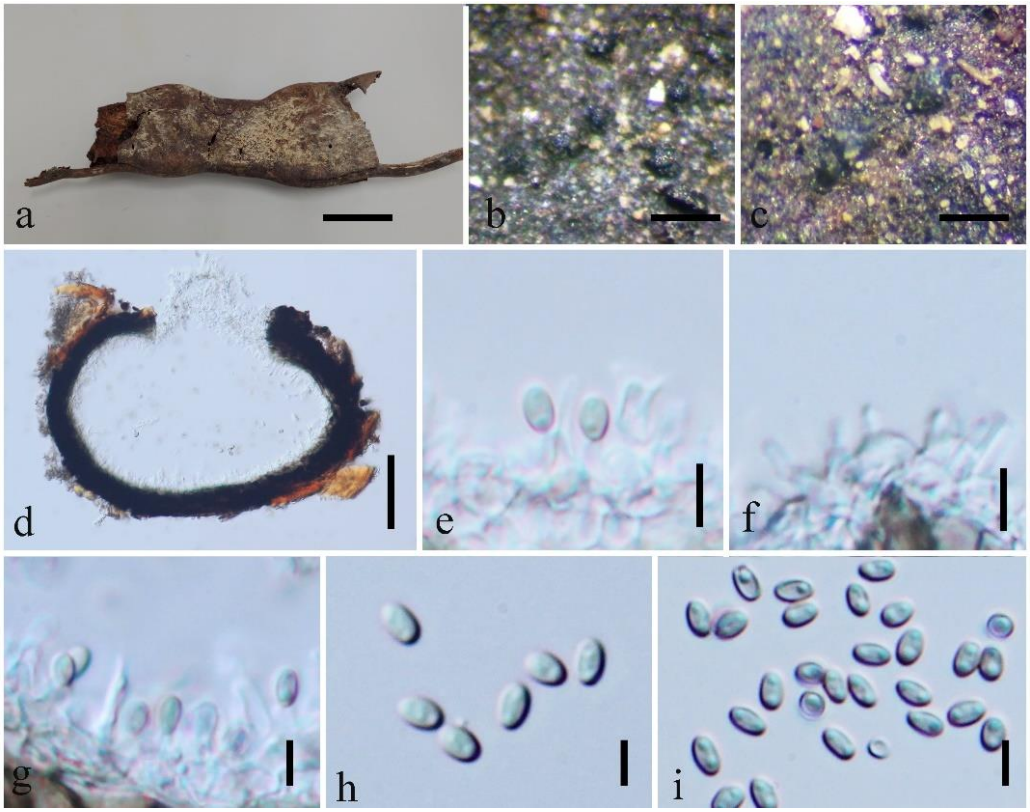


Figure 86 – *Neoroussoella entadae* (MFLU 18–2106, holotype). a Part of host pod. b, c Conidiomata on host material. d Section through conidioma. e–g Conidiogenous cells. h, i Conidia. Scale bars: a = 2 cm, b, c = 500 µm, d = 50 µm, e–i = 5 µm.

Culture characters – Ascospores germinated on MEA within 18 hr. Colonies growing on MEA, reaching 40 mm diam. after 2 weeks at 18°C, with irregular edge and pale thin outer layer embedded in medium, dark brown three clearly visible layers, conidiomata spread throughout the media, reverse dark brown.

Material examined – THAILAND, Chiang Rai Province, Khun Korn waterfall (19˚ 52' 5" N; 99˚ 38' 5" E), on decaying pod of *Entada phaseoloides* (Fabaceae), 2 February 2017, S.C. Jayasiri, C 222 (MFLU 18–2106, holotype; KUN-HKAS 102415, isotype), ex-type living culture, MFLUCC

17–0920, KUMCC 18–0265; THAILAND, Phrae Province, on decaying pod of *Leucaena* sp. (Fabaceae), 10 January 2018, S.C. Jayasiri, C 417 (MFLU 18–2185); living culture MFLUCC 18–0243, KUMCC 18–0267.

GenBank numbers – MFLUCC 17–0920: SSU: MK347837, ITS: MK347729, LSU: MK347946; MFLUCC 18–0243: SSU: MK347893, ITS: MK347786, LSU: MK348004, *tef1*: MK360065, *rpb2*: MK434866

Notes – *Neoroussoella entadae* forms a sister clade to *N. solani* (CPC 26331) with high statistical support (Fig. 85). *Neoroussoella solani* (CPC 26331) has only ITS and LSU sequence data available in GenBank and a comparison of nucleotide difference in ITS regions reveals 9 (1.7%) difference between *N. solani* (CPC 26331) and *N. entadae* (MFLUCC 17–0920). *Neoroussoella entadae* (Figs. 86, 87) has smaller conidia than *N. solani* (3.5 × 1.8 µm vs. 4.5–5(–7) × 2(–3) µm) (Crous et al. 2016).

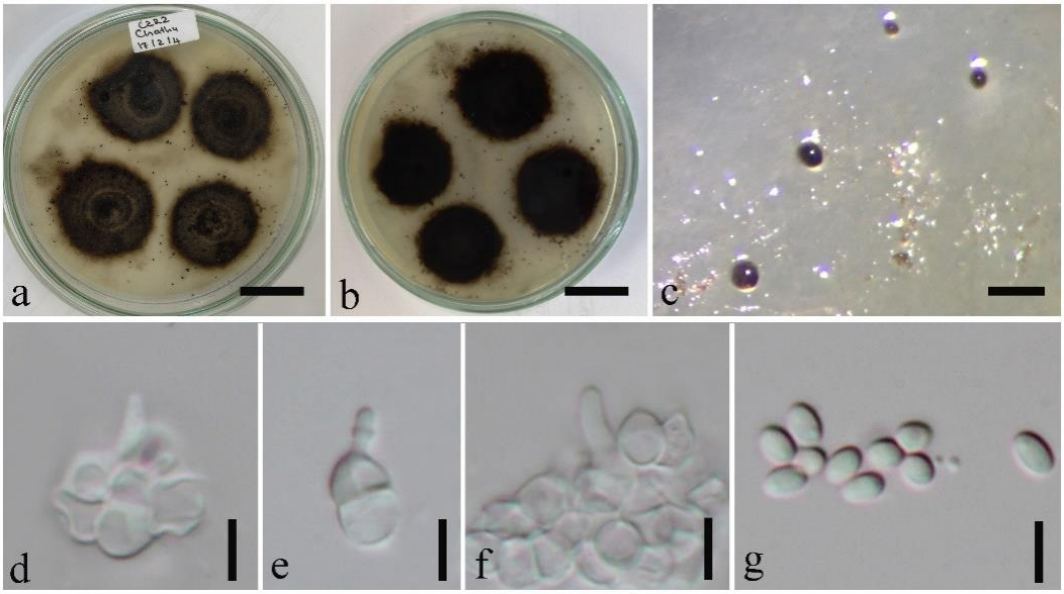


Figure 87 – *Neoroussoella entadae* in culture (MFLUCC 17–0920, ex-type). a Top view of culture. b Reverse view of culture. c Conidiomata in culture. d–f Conidiogenous cells. g Conidia. Scale bars: a, b = 2 cm, c = 500 µm, d–g = 10 µm.

57. *Neoroussoella leucaenae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Figs 88, 89

Index Fungorum number: IF 555570; Facesoffungi number: FoF 05277

Holotype – MFLU 18–2159

Etymology – Referring to the host genus on which the fungus was collected, *Leucaena* (Fabaceae).

Saprobic on *Leucaena* sp. and *Pterocarpus* sp. pods. Sexual morph: *Ascomata* 215–275 µm high × 175–225 µm diam. ($\bar{x}$ = 169 × 184 µm; n = 20), scattered to gregarious, semi-immersed, globose to subglobose, dark brown to black, surrounded by dark brown parenchymatous cells, non-ostiolate. *Peridium* 5–15 µm wide, symmetric, hyaline to brown *textura angularis* cell layers, fusing and indistinguishable from the host tissues. *Hamathecium* 1.1–1.5 µm wide ($\bar{x}$ = 1.4 µm; n = 30), comprising numerous, filamentous, branched septate, pseudoparaphyses. *Asci* 50–60 × 4.5–5.5 µm ($\bar{x}$ = 55 × 5 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, short-pedicellate, apex rounded with a minute ocular chamber. *Ascospores* 8–9 × 2.5–3.5 µm ($\bar{x}$ = 7 × 3 µm; n = 30), uniseriate, hyaline to brown, fusiform with narrow, acute ends, two asymmetric cells with guttules, constricted at the septum, smooth-walled, appendages absent. Asexual morph: Coelomycetous. *Conidiomata* 135–175 µm high × 120–180 µm diam. ($\bar{x}$ = 156 × 134 µm; n = 10), pycnidial, solitary to gregarious, occasionally confluent, formed in uni- or multi-loculate stromata, immersed, covered by hyphae, becoming erumpent at maturity. *Hyphae* 1.5–1.7 µm wide ($\bar{x}$ = 1.6 µm; n =

30), septate, branched, hyaline to pale brown, red pigmented. *Conidiomata wall* 28–35 µm wide ($\bar{x}$ = 31 µm; n = 20), composed of thick-walled, brown cells of *textura angularis*; inner layer thin, hyaline. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 5.5–9 × 3–4 µm ($\bar{x}$ = 7.2 × 3.5 µm; n = 20), phialidic, hyaline, red pigmented, ampulliform to cylindrical, smooth-walled. *Conidia* 3.5–4.5 × 1.9–2.6 µm ($\bar{x}$ = 4.2 × 2.2 µm; n = 20), initially hyaline, pale brown when mature, oblong to ovoid, straight, both ends broadly rounded, aseptate.

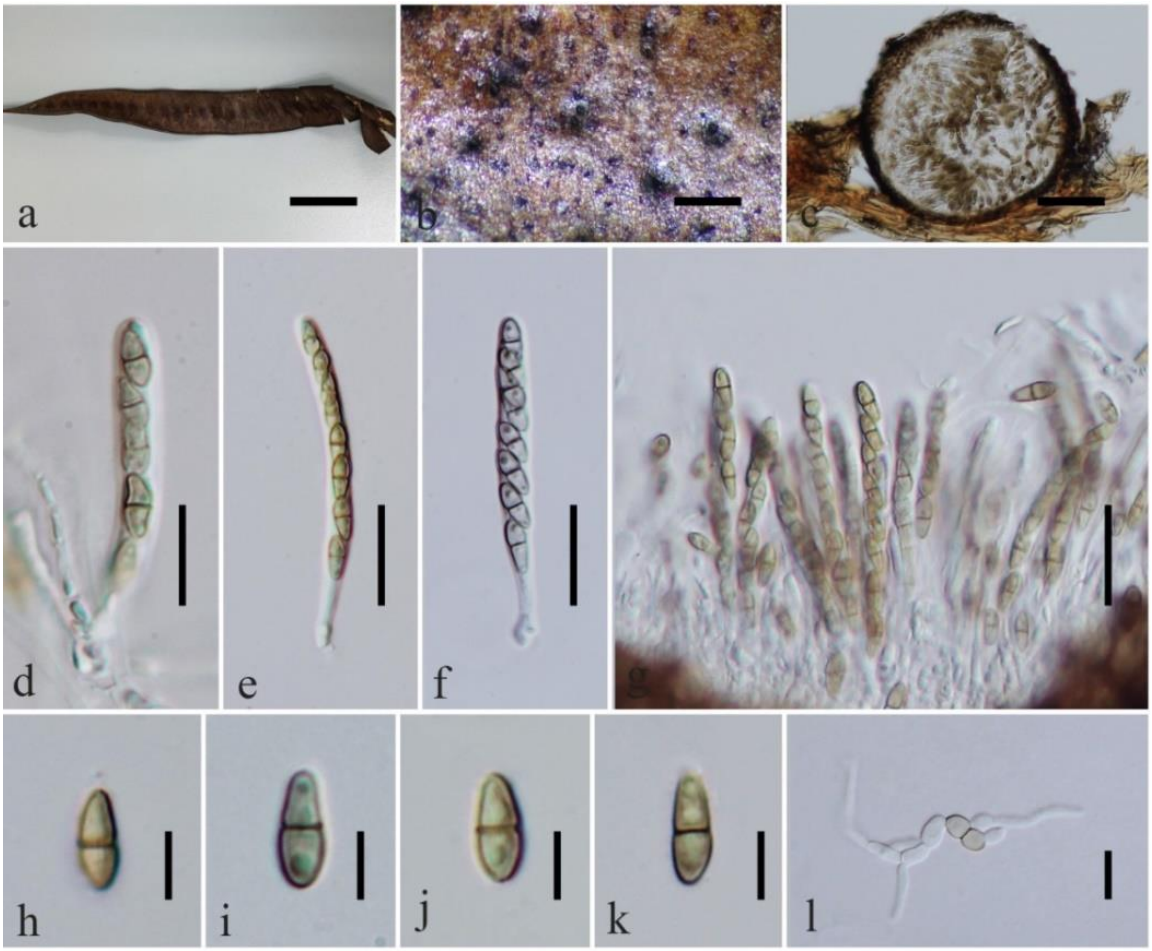


Figure 88 – *Neoroussoella leucaenae* (MFLU 18–2159, holotype). a The host pod. b Ascoma on substrate. c Section through ascoma. d–g Asci. h–k Ascospores. l Germinated ascospore. Scale bars: a = 1 cm, b = 500 µm, c = 50 µm, d–g = 20 µm, h–l = 5 µm.

Culture characters – Ascospores germinated on MEA within 18 hr. Colonies growing on MEA, reaching 30–40 mm diam. after 2 weeks at 18 ° C, surface with grey to brown hyphal growing, radially arranged brown edge, reverse dark brown and brown two layers.

Material examined – THAILAND, Krabi Province, Mueang Krabi District, on decaying pod of *Leucaena* sp. (Fabaceae), 31 August 2017, S.C. Jayasiri, C 356 (MFLU 18–2159, holotype; MFLU 18–2160, isotype), ex-type living culture MFLUCC 18–1544, KUMCC 18–0266; THAILAND, Chiang Rai Province, Doi Pui, on decaying pod of *Pterocarpus* sp. (Fabaceae), 02 January 2017, S.C. Jayasiri, C 235 (MFLU 18–2114, KUN-HKAS 102417); living culture MFLUCC 17–0927, KUMCC 18–0268.

GenBank numbers – MFLUCC 18–1544: SSU: MK347874, ITS: MK347767, LSU: MK347984, *tef1*: MK360067, *rpb2*: MK434876; MFLUCC 17–0927: SSU: MK347841, ITS: MK347733, LSU: MK347950, *tef1*: MK360066, *rpb2*: MK434896

Notes – New strains (MFLUCC 18–1544 and MFLUCC 17–0927) and existing strains (KT 3264 and KT 3265) form a separate clade from *Neoroussoella entadae* and *N. solani* with high

statistical support (99% MLBS/1.0 BYPP, Fig. 85). *Neoroussoella entadae* and *N. solani* only reported as asexual morph, *Neoroussoella entadae* differs from *N. solani* in having smaller conidia (3.5 × 1.8 μm vs. 4.5–5(–7) × 2(–3) μm) (Crous et al. 2016).

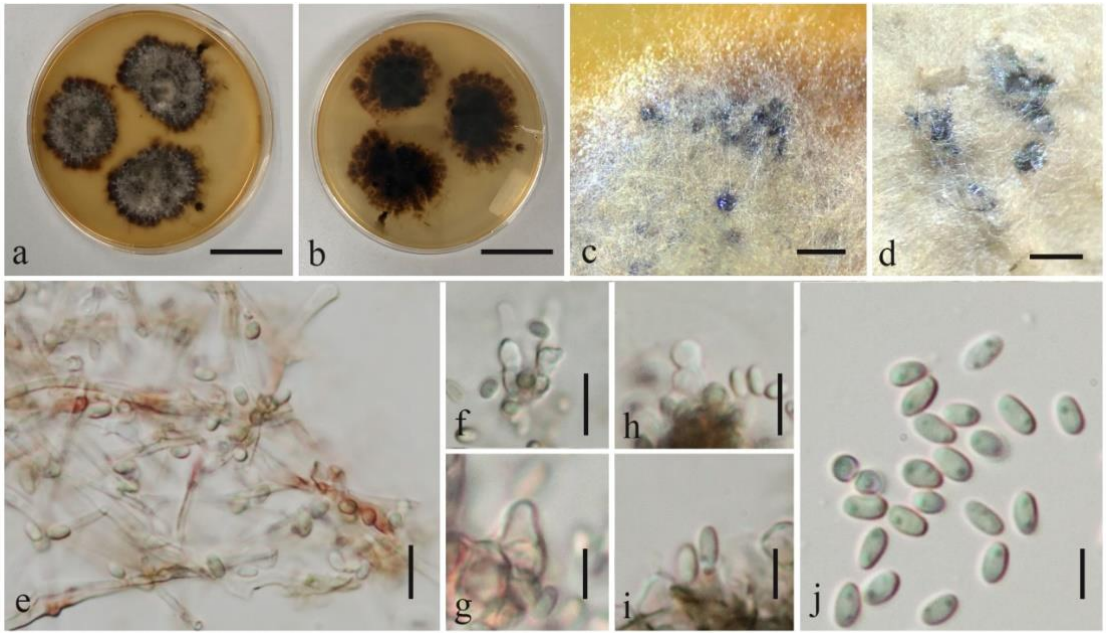


Figure 89 – *Neoroussoella leucaenae* from culture (MFLUCC 18–1544, ex-type). a, b Top and reverse view of culture. c, d Conidiomata. e Red pigmented hyphae. f–i Conidiogenous cells. j Conidia. Scale bars: a, b = 2 cm, c, d = 500 μm, e–i = 10 μm, j = 5 μm.

For the new species *Neoroussoella leucaenae* both asexual and sexual morph are found. This species shares similar morphological characters with other *Neoroussoella* spp., such as phialidic, ampulliform conidiogenous cells and aseptate, pale brown, subcylindrical conidia, but differs in having red pigmented conidiogenous cells and hypha (Fig. 89). A comparison of the ITS and *rpb2* nucleotides of *N. entadae* and *N. leucaenae* strains revealed 8 (1.5%) and 45 (4.3%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016). *Neoroussoella solani* has no molecular data available for protein coding genes and a comparison of the ITS nucleotides of *N. solani* and *N. leucaenae* strains reveal 8 (1.5%) differences which indicates that these two isolates are two distinct taxa (Jeewon & Hyde 2016).

Another two strains (KT 3264 and KT 3265) previously recorded as *Roussoella solani* (Mochizuki et al. 2017) clustered with *Neoroussoella leucaenae*. These two strains were introduced as human pathogenic species (Mochizuki et al. 2017). Morphology of strains KT 3264 and KT 3265 is similar to *N. leucaenae* in having cylindrical, short-pedicellate, asci with minute ocular chamber, hyaline to brown, 1-septate ascospores and phialidic, ampulliform conidiogenous cells and aseptate, pale brown, subcylindrical conidia (Figs. 88, 89).

58. *Neoroussoella solani* (Crous & M.J. Wingf.) Jayasiri & K.D. Hyde comb. nov.

= *Roussoella solani* Crous & M.J. Wingf., Persoonia 36: 341 (2016)

Index Fungorum number: IF555715; Facesoffungi number: FoF 05322

Description – Ref. Crous et al. (2016)

Notes – In our multigene phylogenetic study, *Roussoella solani* (CPC 26331) clustered with other species of *Neoroussoella* with high statistical support (78% MLBS/0.95 BYPP, Fig. 88) and distant from other *Roussoella* sp. This species also shares similar morphological characters with other *Neoroussoella* spp., such as phialidic, ampulliform conidiogenous cells and aseptate, pale brown, subcylindrical conidia. Therefore, we synonymize *Roussoella solani* as *Neoroussoella solani.*

Pararoussoella Wanas., E.B.G. Jones & K.D. Hyde, Fungal Diversity 89: [169] (2018)

Pararoussoella was introduced by Wanasinghe et al. (2018b) to accomodate the type species *Pararoussoella rosarum* from *Rosa* sp. in UK.

59. *Pararoussoella mukdahanensis* (Phookamsak D.Q. Dai & K.D. Hyde) Jayasiri & K.D. Hyde, comb. nov.

≡ *Roussoella mukdahanensis* Phookamsak, D.Q. Dai & K.D. Hyde, Fungal Diversity 82: 32 (2016)

Index Fungorum number: IF555572; Facesoffungi number: FoF05279

Description – Ref. Dai et al. (2016)

Notes – In our multigene phylogenetic study, *Roussoella mukdahanensis* (MFLUCC 11–0201) clusters with *Pararoussoella rosarum* (MFLU 17–0654/ MFLUCC 17–0796) with high statistical support (99% MLBS/1.0 BYPP, Fig. 88) and distant from other *Roussoella* sp. In addition, these two species share similar morphological characters, such as globose, ostiolate ascomata, filamentous, branched, septate, pseudoparaphyses, narrowly ellipsoid, straight to slightly curved, ascospores with 1-septum. *Pararoussoella rosarum* differ from *Roussoella mukdahanensis* in having irregular longitudinal striations ascospores. A comparison of the ITS nucleotides of these two species reveal 14 (3%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016). Therefore, we transfer *Roussoella mukdahanensis* to *Pararoussoella.*

Teichosporaceae M.E. Barr, Mycotaxon 82: 374 (2002)

The family Teichosporaceae was proposed by Barr (2002) in the order Pleosporales to accommodate eight genera. We present an updated tree for the family with eleven genera (Thambugala et al. 2015) and introduce a new host record for *Ramusculicola thailandica* (Fig. 90).

60. *Ramusculicola thailandica* Thambug. & K.D. Hyde, Fungal Diversity 74: 251(2015) Fig. 91

Saprobic on twig of deciduous tree and *Leucaena* sp. pod. Sexual morph: *Ascomata* 180–200 μm high × 250–270 μm diam. ($\bar{x}$ = 190 × 260 μm; n = 10), immersed, solitary, scattered, subglobose to obpyriform, coriaceous, dark brown, without a subiculum covering the host, erumpent ostiole. *Ostiole* papillate, protruding from the substrate. *Peridium* 18–25 μm wide ($\bar{x}$ = 22.5 μm; n = 20), comprising two types of cell layers, dark brown outer layers and hyaline inner layers, covered by plant tissues. *Hamathecium* comprising 1.5–2 μm wide ($\bar{x}$ = 1.8 μm; n = 30), filiform, septate, branching pseudoparaphyses. *Asci* 65–80 × 8–11 μm ($\bar{x}$ = 72 × 9 μm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-subclavate, slightly curved, short pedicellate, apically rounded, with an ocular chamber. *Ascospores* 20–30 × 3–5 μm ($\bar{x}$ = 24 × 4 μm; n = 30), overlapping 2–3-seriate, hyaline, cylindric-fusiform, tapering towards the rounded ends, straight to slightly curved, 1-septate, guttulate, with mucilagenous sheath. Asexual morph: Undetermined.

Culture characters – Ascospores germinated on MEA within 18 hr. Colonies growing on MEA, reaching a diameter of 20 mm diam. after 2 weeks at 25°C, surface with hyphal growing, with entire edge, white, middle grey, dense, circular; reverse white to pale yellow.

Material examined – THAILAND, Mae Pha, on decaying pods of *Acacia* sp. 21 September 2016, S.C. Jayasiri, C 193 (MFLU 18–2097, new host record), living culture MFLUCC 17–0909, KUMCC 18–0299.

GenBank numbers – SSU: MK347830, ITS: MK347724, LSU: MK347939, *tef1*: MK360089

Notes – Our isolate groups with other sequences of *Ramusculicola thailandica* (MFLUCC 10–0126/MFLUCC 13–0284) with high statistical support (100% MLBS/1.0 BYPP, Fig. 90). They are morphologically similar in having immersed, papillate usually erumpent, black, subglobose to globose, coriaceous, uniloculate, ostiolate ascomata, central, rounded, compressed, periphysate, ostiole with a pore-like opening and hyaline, fusiform ascospores with a thin mucilaginous sheath (Thambugala et al. 2015). A comparison of the ITS, *tef1* and *rpb2* nucleotides of *Ramusculicola thailandica* (MFLUCC 10–0126/MFLUCC 13–0284) and the new strain (MFLUCC 17–0909)

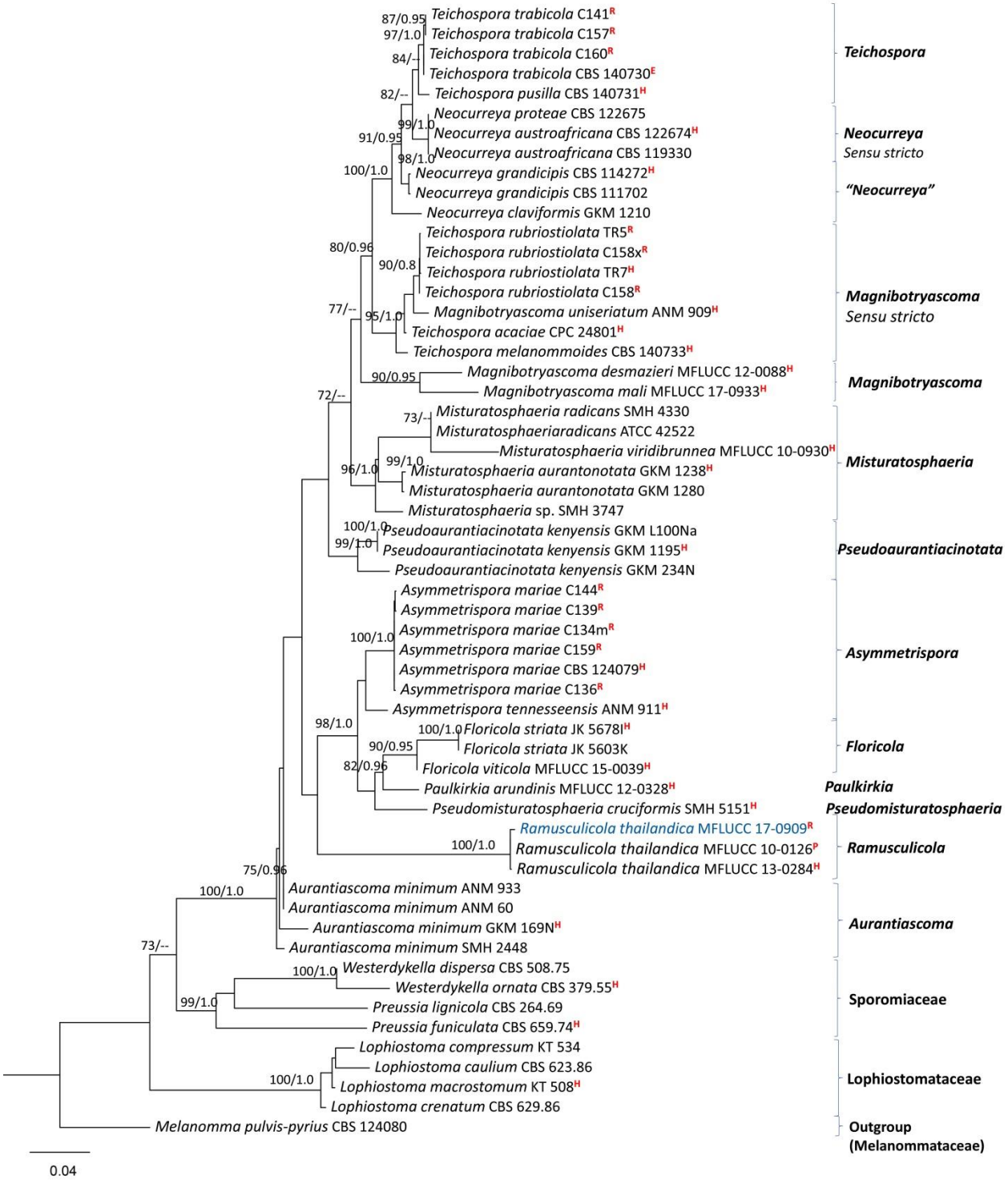


Figure 90 – Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS, *tef1* and *rpb2* sequence data related to family Teichosporaceae. Sixty strains were included in the combined sequence analyses, which comprised 4709 characters with gaps. *Melanomma pulvis-pyrius* (CBS 124080) was used as the outgroup taxon. Single gene analyses were also performed and topology and clade stability compared from combinbed gene analyses. Tree topology of the ML analysis was similar to the BY. The best scoring RAxML tree with a final likelihood value of -22095.570405 is presented. The matrix had 1542 distinct alignment patterns, with 49.68% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242601, C = 0.252145, G = 0.278539, T = 0.226715; substitution rates AC = 1.366345, AG = 3.813280, AT = 1.945628, CG = 1.436558, CT = 9.159549, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95

are given near to each branch. The newly generated sequence is in blue. New isolate is in blue. Strains isolated from the epitype, holotype, paratype and reference specimens are indicated in red superscript ^{E}, ^{H}, ^{P} and ^{R} respectively.

revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *Ramusculicola thailandica* (Jeewon & Hyde 2016). Therefore, our strain is morphologically (Fig. 91) and phylogenetically in agreement with *Ramusculicola thailandica* and we report a new record from decaying pods of *Acacia* sp. in Thailand.

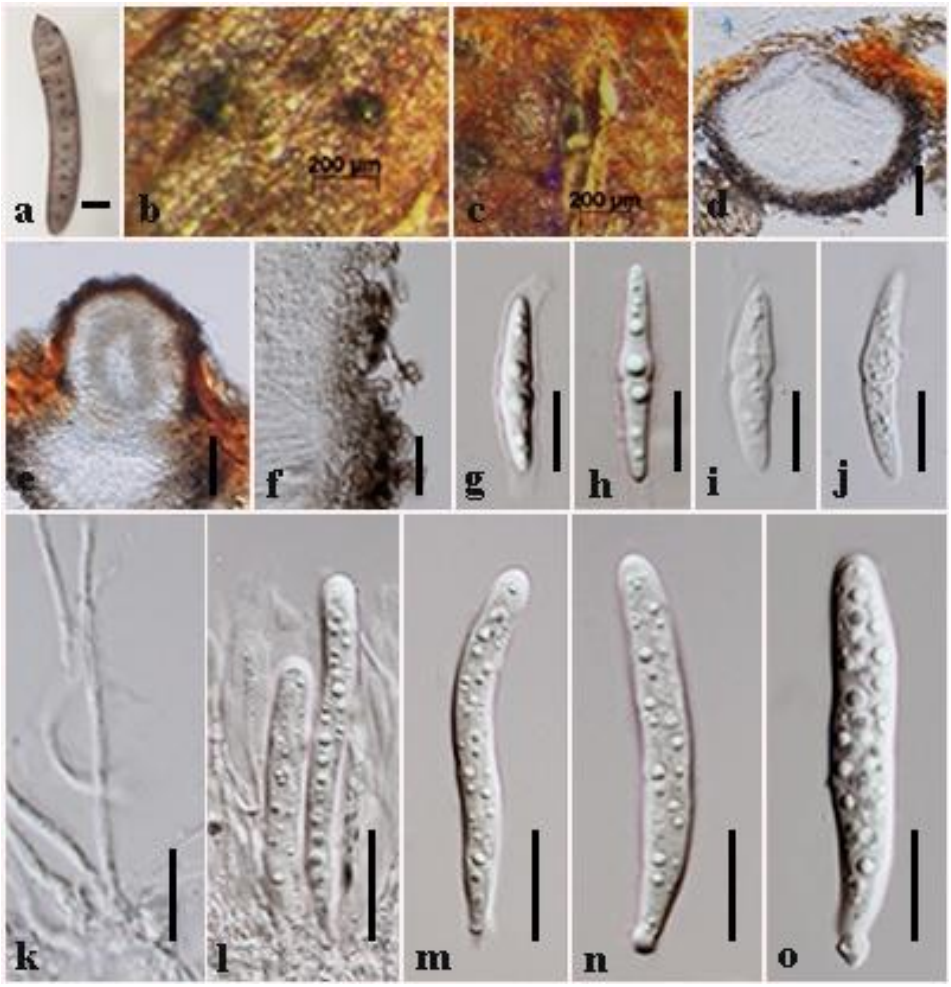


Figure 91 – *Ramusculicola thailandica* (MFLU 18–2097). a Host of decaying pod. b, c Immersed ascomata on substrate. d, e Section through ascoma. f Peridium. g–j Ascospores. k Cellular pseudoparaphyses. l–o Asci. Scale bars: a = 1 cm, d, e = 50 µm, g–k = 10 µm, l–o = 20 µm.

Testudinaceae Arx, Persoonia 6 (3): 366 (1971)

This family is poorly studied and relationships mainly based on DNA sequence analyses of a few species (Wanasinghe et al. 2017). This has resulted in an inadequate understanding of the genera and species in this family (Jeewon & Hyde 2007, Zhang et al. 2012).

Verruculina Kohlm. & Volkm.-Kohlm., Mycological Research 94: 689 (1990)

This genus was introduced to accommodate an obligate marine species, *Verruculina enalia* (Kohlmeyer & Volkmann-Kohlmeyer 1990). In this study, we introduce new host record for *Verruculina enalia* from Thailand (Fig. 92).

61. *Verruculina enalia* (Kohlm.) Kohlm. & Volkm.-Kohlm., Mycological Research 94: 689 (1990) Fig. 93

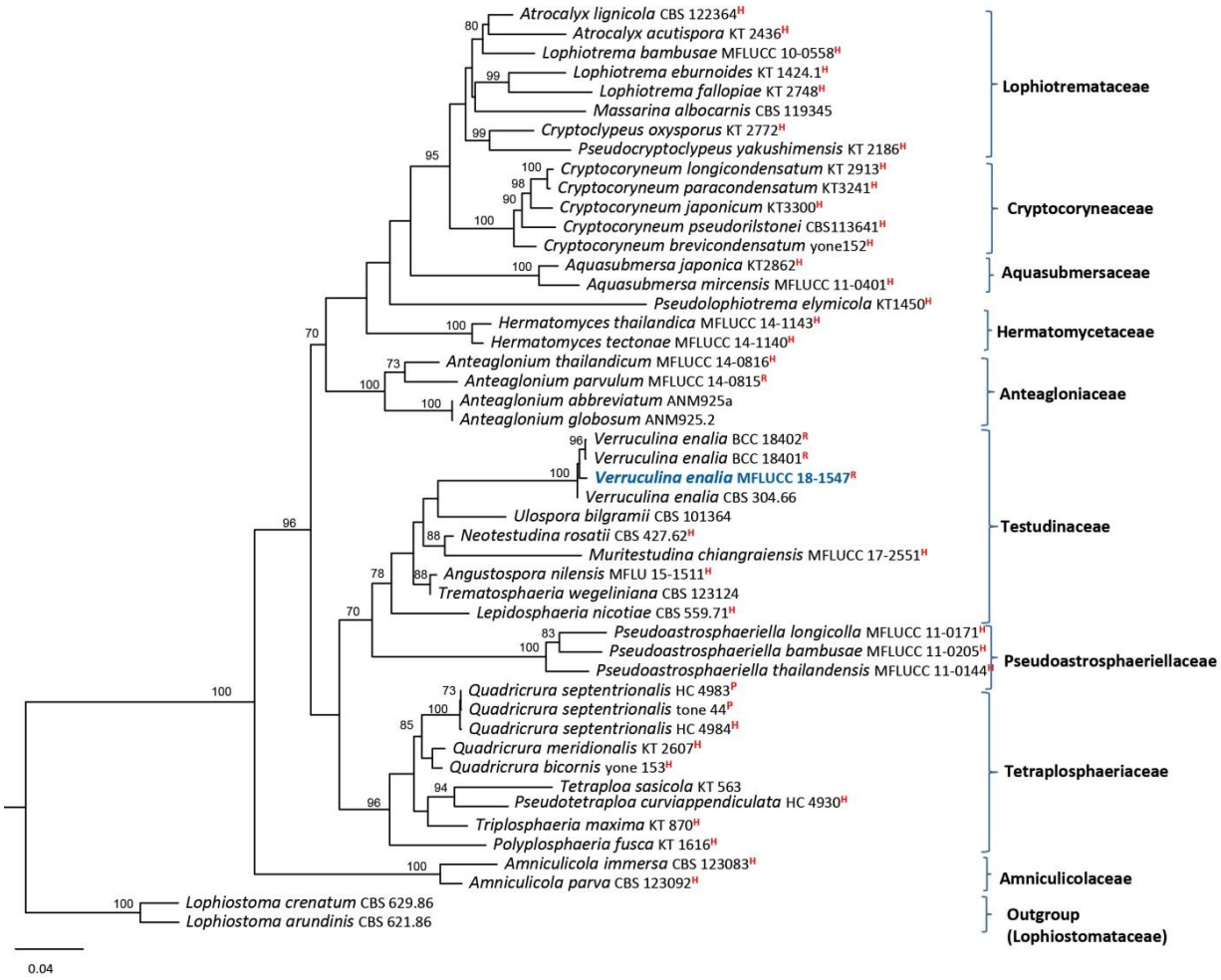


Figure 92 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS, LSU, *tef1* and *rpb2* matrix of fourty-eight strains including related species of the family Testudinaceae and families related to Testudinaceae. *Lophiostoma* spp. were used as the outgroup taxa. The matrix comprised 4944 characters including aligment gaps. The best scoring RAxML tree with a final likelihood value of -13396.714097 is presented. The matrix had 1706 distinct alignment patterns, with 28.45% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.250985, C = 0.245666, G = 0.269693, T = 0.233655; substitution rates AC = 1.621034, AG = 4.550733, AT = 1.588888, CG = 1.284743, CT = 9.542453, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strain is in blue. Strains isolated from the holotype, paratype and reference specimens are indicated in red superscript ^{H}, ^{P} and ^{R} respectively.

Facesoffungi number: FoF05281

Saprobic on *Rhizophora* spp., *Phragmites* sp. and *Pandanus* sp. Sexual morph: *Ascomata* 110–138 µm high × 94–145 µm diam. ($\bar{x}$ = 126 × 121 µm; n = 10), solitary or gregarious, globose, superficial or clypeate, carbonaceous, black, thick-walled, ostiolate. *Peridium* 19–29 µm wide ($\bar{x}$ = 24.2 µm; n = 20), outer layer of small irregular, dark brown, thick-walled cells, inner layer of cells with larger lumina, arranged in a *textura angularis*. *Hamathecium* 1.2–1.5 µm ($\bar{x}$ = 1.3 µm; n = 30), simple or branched, filiform, septate pseudoparaphyses. *Asci* 144–151 × 11–14 µm ($\bar{x}$ = 148 × 12.5 µm; n = 20), 8-spored, bitunicate, broadly clavate, ovoid or ellipsoidal, short pedicellate, apically rounded, without an apical apparatus, asci arising from a hemisphaerical pulvinus composed of radiating hyphae. *Ascospores* 20–21 × 7.7–10 µm ($\bar{x}$ = 20.4 × 8.4 µm; n = 30), uni-

seriate, dark brown to blackish brown, biturbinate to subellipsoidal, 1-septate, with a dark band around the septum, constricted at the septum, apically papillate, with apical germ pores, thick-walledguttulate.

Culture characters – Ascospores germinated on MEA within 18 hr. Colonies growing on MEA, reaching a diameter of 20 mm diam. after 2 weeks at 18°C, surface with hyphal growing, with lobate edge, off-white to grey, dense, circular; reverse grey with pale yellow margin.

Material examined – THAILAND, Krabi Province, Mueang Krabi District (8˚ 3' 22" N, 98˚ 46' 28" E), on decaying fruit pericarp of *Pandanus* sp. (Pandanaceae), 31 August 2017, S.C. Jayasiri, C 364 (MFLU 18–2163, new host record); living culture MFLUCC 18–1547, KUMCC 18–0304.

GenBank numbers – SSU: MK347878, ITS: MK347771, LSU: MK347988, *tef1*: MK360092, *rpb2*: MK434873

Notes – The new isolate groups with three other strains (BCC 18401, BCC 18402 and CBS 304.66) of *Verruculina enalia* in GenBank. The new strain (Fig. 93) is in agreement with the type description in having clypeate or ostiloate, black, carbonaceous ascomata, long cellular, septate, sparsely branching pseudoparaphyses, cylindrical, short pedicel asci and ovoid or ellipsoidal, dark brown, 1-septate, verrucose or verruculose ascospores with germ pore (Kohlmeyer & Volkmann-Kohlmeyer 1990). A comparison of the ITS, *tef1* and *rpb2* nucleotides of *Verruculina enalia* (BCC 18401, BCC 18402 and CBS 304.66) and the new strain (MFLUCC 18–1547) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *Verruculina enalia* (Jeewon & Hyde 2016). Therefore, we document the new record of *Verruculina enalia* from *Pandanus* sp. *Verruculina enalia* was previously reported from *Rhizophora mangle*, *R. racemose*, and *Phragmites* sp. (Kohlmeyer & Volkmann-Kohlmeyer 1990, Suetrong et al. 2009).

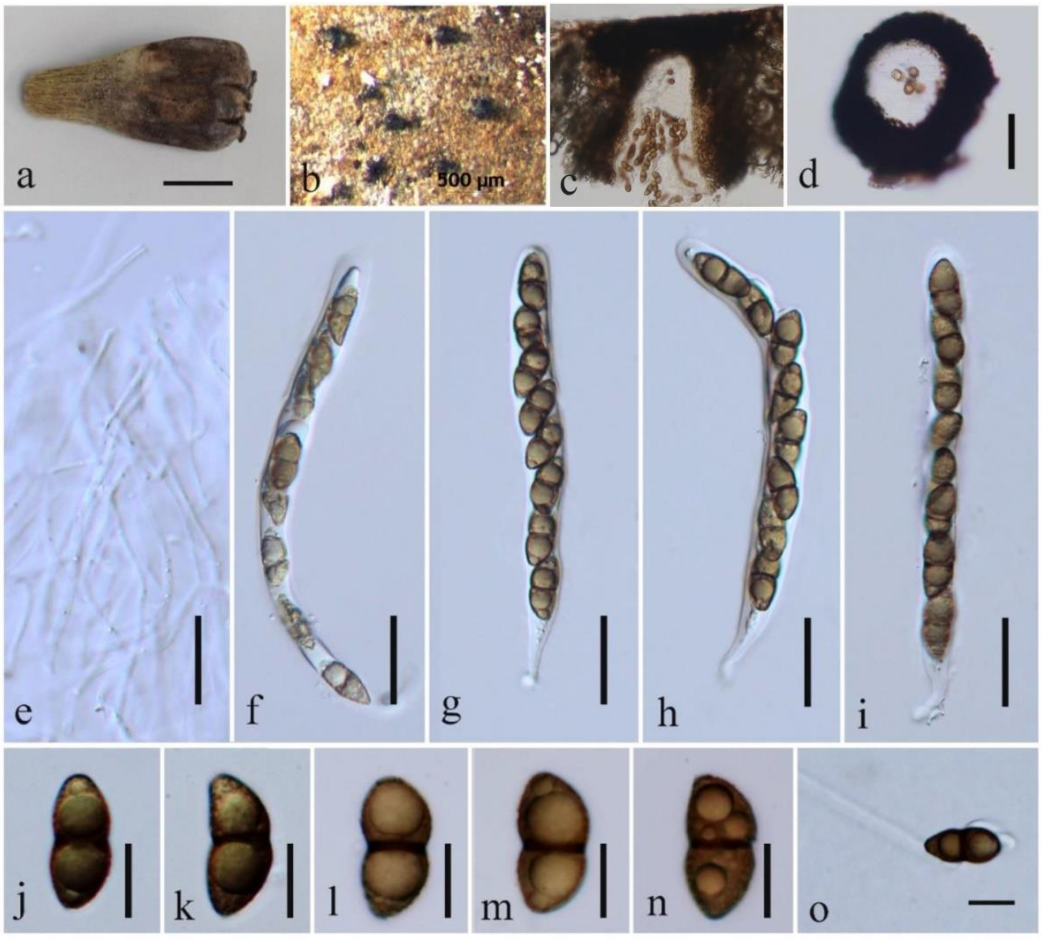


Figure 93 – *Verruculina enalia* (MFLU 18–2163). a Fruit of *Pandanus* sp. host. b Ascomata on host. c Ostiole neck. d Section of ascoma. e Pseudoparaphyses. f–i Asci. j–n Ascospores. o Germinated ascospore. Scale bars: a = 2 cm, d = 100 µm, e = 10 µm, g, f–i = 30 µm, j–o = 10 µm.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray., Studies in Mycology 64: 177 (2009)

This family was introduced to accommodate five genera producing conidia with setose appendages (Tanaka et al. 2009) and *Ernakulamia* was later added (Delgado et al. (2017). We present an updated tree for the family and introduce a new species, *Ernakulamia krabiensis* (Fig. 94).

Ernakulamia Subram., Kavaka 22/23: 67 (1996)

Delgado et al. (2017) introduced this genus based on type species, *Ernakulamia cochinensis* collected from *Strocaryum standleyanum* (Arecaceae) in Panama. We introduce a new species from pods of *Acacia* sp. in Thailand.

62. *Ernakulamia krabiensis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 95

Index Fungorum number: IF555574; Facesoffungi number: FoF05282

Holotype – MFLU 18–2166

Etymology – Referring to the Province where the specimen was collected, Krabi (Thailand).

Saprobic on *Acacia* sp. pod. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on substrate dark brown, effuse. *Conidiophores* arising laterally from cells of intricately branched repent hyphae, crowded, erect, short, cylindrical, subhyaline, simple, thin-walled, rarely septate. *Conidiogenous cells* monoblastic. *Conidia* 46–55 × 36–49 µm ($\bar{x}$ = 53 × 42 µm, n = 30), acrogenous and singly at the tip of conidiophores, dark brown, obconical, ovoid, broad-fusiform or subglobose, muriform. Thin-walled, dark brown, constricted cells attach wth appendages. *Appendages* 21–32 × 3.3–3.7 µm ($\bar{x}$ = 28 × 3.5 µm, n = 30), arising from basel part brown, hyaline tip, straight, septate, wide similar base to tip, 3–4 per conidium. *Spermatia* 2.7–3.4 × 1.6–2.1 µm ($\bar{x}$ = 3.1 × 1.8 µm, n = 30), hyaline, subglobose, two prominent guttules.

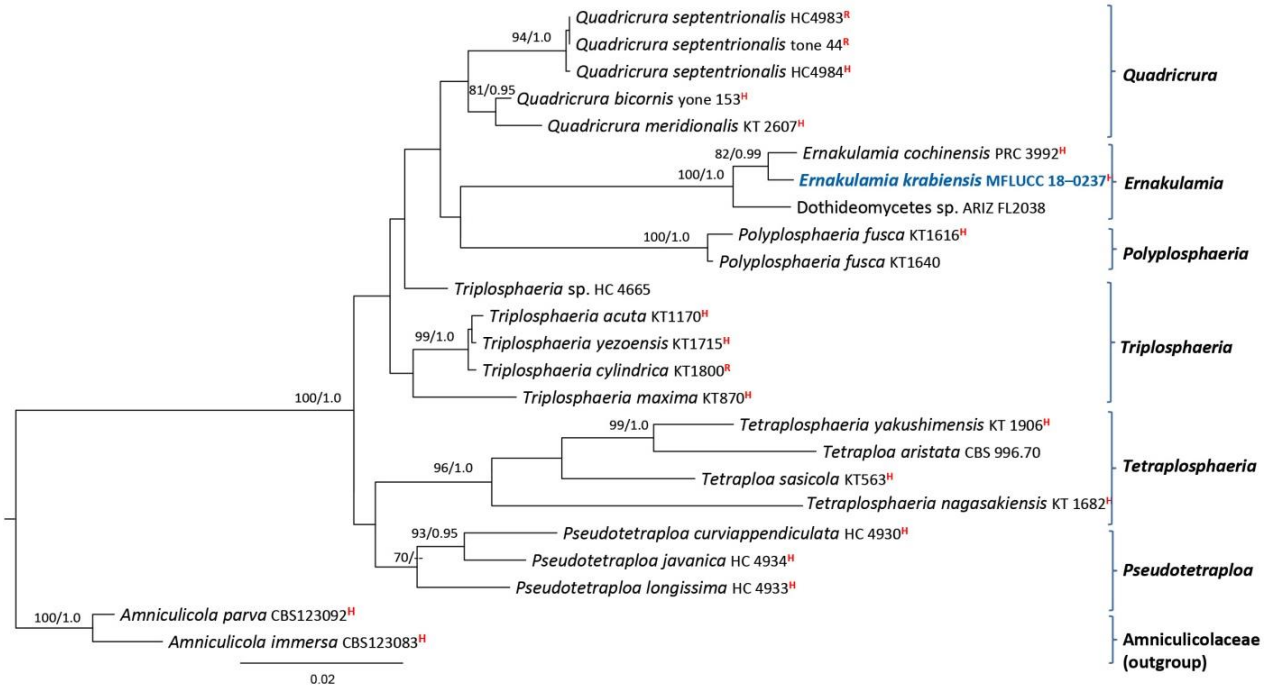


Figure 94 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS and LSU matrix of twenty-three strains including related species of the family Tetraplosphaeriaceae. The matrix comprised 2886 characters including aligment gaps. The tree was rooted with *Amniculicola* spp. (Amniculicolaceae). The best scoring RAxML tree with a final likelihood value of -7792.333429 is presented. The matrix had 367 distinct alignment

patterns, with 12.64% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.252367, C = 0.232260, G = 0.275939, T = 0.239434; substitution rates AC = 3.635512, AG = 3.074785, AT = 2.569761, CG = 1.114076, CT = 13.620941, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

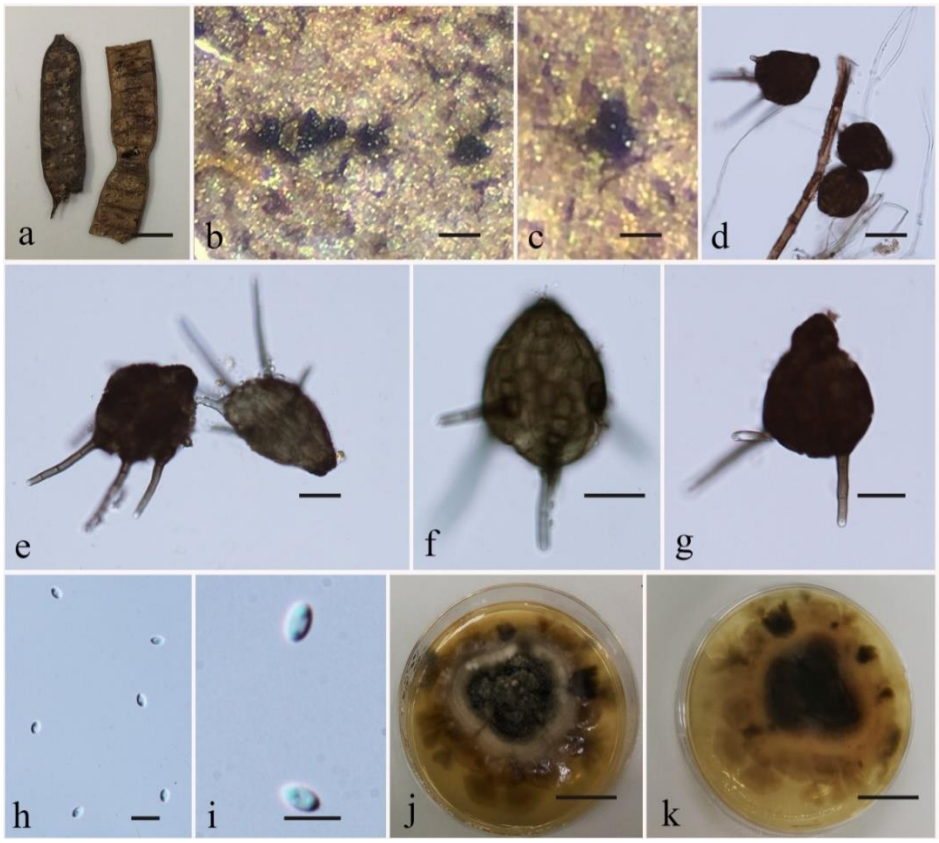


Figure 95 – *Ernakulamia krabiensis* (MFLU 18–2166, holotype). a Host seed pods. b, c Colonies on dead pod. d Hyphae with conidia. e–g Conidia. h, i Spermatia. j Top view of culture. k Reverse view of culture. Scale bars: a, j, k = 1 cm, b = 100 μm, c, d = 50 μm, e–g = 20 μm, h, i = 5 μm.

Culture characters – Conidia germinated on MEA within 18 hr. Colonies growing on MEA, reaching 20 mm diam. after 2 weeks at 18°C, surface with hyphal growing, with irregular edge, different layers, middle grey, off white and brown layers, dense, circular; reverse black, pale brown and dark brown.

Material examined – THAILAND, Krabi Province, Mueang Krabi District, on decaying pods septum of *Acacia* sp., 31 August 2017, S.C. Jayasiri, C 372-A (MFLU 18–2166, holotype), ex-type living culture MFLUCC 18–0237; KUMCC 18–0240.

GenBank numbers – SSU: MK347880, ITS: MK347773, LSU: MK347990, *tef1*: MK360053, *rpb2*: MK434872

Notes – We isolated a tetraploa-like species from decaying *Acacia* sp. seed pod from Krabi province, Thailand. Most tetraploa-like species were identified from bamboo (Tanaka et al. 2009). *Ernakulamia krabiensis* forms a sister clade to *E. cochinensis* (PRC 3992) with high statistical support (82 %MLBS/0.99 BYPP, Fig. 94). A comparison of the ITS nucleotides of these two strains reveals 9 (1.9%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016). Morphologically *E. krabiensis* and *E. cochinensis* are similar in having monoblastic conidiogenous cells, acrogenous, obconical, ovoid or broad-fusiform, dark brown, muriform conidia with appendages (Fig. 95). However, conidia of *E. krabiensis* have 3–4 appendages that are

shorter (21–32 µm) than those of *E. cochinensis* which are up to 150 µm. In addition, the appendages of *E. cochinensis* have a broad base and apex while in *E. krabiensis* they are uniform from base to apex (Subramanian 1957). The holotype of *E. cochinensis* was collected from *Cocos nucifera* in India and later recorded from *Astrocaryum standleyanum* (Arecaceae) in Panama (Subramanian 1957, Delgado et al. 2017).

Another strain (ARIZ FL 2038) in GenBank groups with *E. krabiensis* and *E. cochinensis* with high statistical support (100% MLBS/1.0 BYPP, Fig. 94). This strain was isolated as an endophytic species from a senescent leaf in the canopy of *Serenoa repens* (U'Ren & Arnold 2016).

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

Hyde et al. (2013) introduced Thyridariaceae to accommodate the genus *Thyridaria* based on its unique morphology and phylogenetic placement in the Dothideomycetes. Jaklitsch & Voglmayr (2016) synonymized Roussoellaceae under Thyridariaceae but Tibpromma et al. (2017, 2018) recommended retaining Roussoellaceae based on phylogenetic analysis and its distinct morphology. Currently, Thyridariaceae comprise three genera *Cycasicola*, *Parathyridaria* and *Thyridaria* (Hyde et al. 2013, Jaklitsch & Voglmayr 2016, Wanasinghe et al. 2018b). We present an updated tree for the family and introduce a new species, *Cycasicola leucaenae* (Fig. 85).

Cycasicola Wanas., E.B.G. Jones & K.D. Hyde, Fungal Diversity 89: 89: 161 (2018)

Wanasinghe et al. (2018b) introduced this genus based on phylogeny of the type species, *Cycasicola goaensis.* We isolated a new species from decaying seed pod of *Leucaena* sp.

63. *Cycasicola leucaenae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 96

Index Fungorum number: IF555573; Facesoffungi number: FoF05280

Holotype – MFLU 18–2101

Etymology – Referring to the host genus on which the fungus was collected, *Leucaena* (Fabaceae).

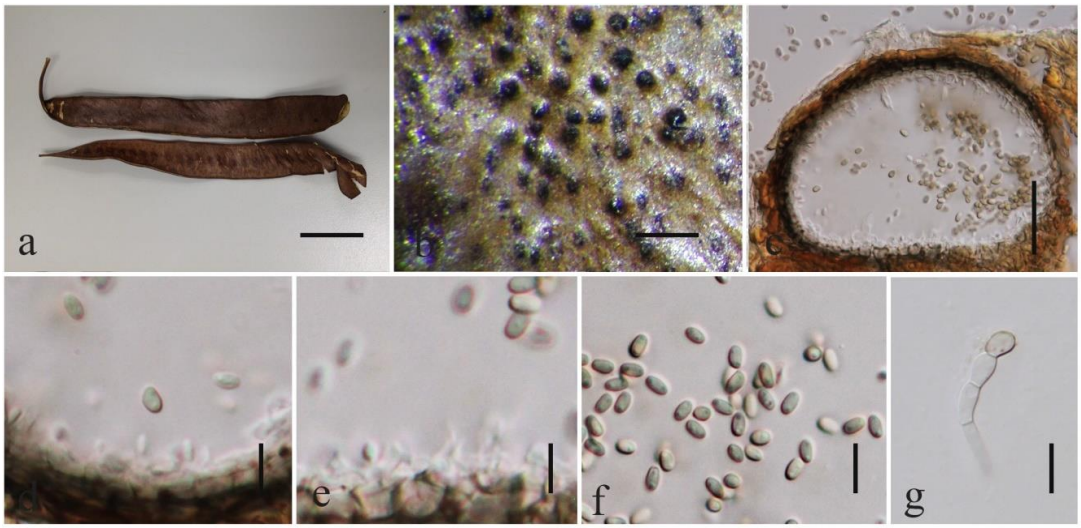


Figure 96 – *Cycasicola leucaenae* (MFLU 18–2101, holotype). a Seed pods of *Leucaena* sp. b Conidiomata in the substrate. c Section through conidioma. d, e Conidiogenous cells. f Conidia. g Germinated conidium. Scale bars: a = 1 cm, b = 500 µm, c = 100 µm, e = 20 µm, f–g = 10 µm.

Saprobic on *Leucaena* sp. pods. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 70–80 µm high 90–120 µm diam. ($\bar{x}$ = 75 × 110 µm; n = 20), pycnidial, solitary, gregarious or confluent, immersed, unilocular, globose, dark brown. *Conidiomata wall* 8–12 µm wide, composed of brown two cell layers and a hyaline cell layer of

textura angularis. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, hyaline, ampulliform, smooth-walled. *Conidia* 3–4 × 1.5–2.5 µm ($\bar{x}$ = 3.5 × 2 µm; n = 30), hyaline or pale brown, fusiform to cylindrical, continuous, straight or slightly curved, obtuse at apex and base, sometimes slightly truncate at base, aseptate, guttulate, smooth-walled.

Culture characters – Ascospores germinated on MEA within 18 hr. Colonies growing on MEA, reaching 50 mm diam. after 2 weeks at 18°C, with pale brown crenate edge, middle grey with crenate edge in margin of layer, reverse dark brown middle and pale brown outer layer.

Material examined – THAILAND, Lumphang Province, on decaying pod of *Leucaena* sp. (Fabaceae), 24 September 2016, S.C. Jayasiri, C 215 (MFLU 18–2101, holotype; KUN-HKAS 102413, isotype); ex-type living culture MFLUCC 17–0914, KUMCC 18–0225.

GenBank numbers – SSU: MK347833, ITS: MK347726, LSU: MK347942, *tef1*: MK360046

Notes – *Cycasicola leucaenae* forms a sister clade to *C. goaensis* with high statistical support (100% MLBS/1.0 BYPP, Fig. 85). *Cycasicola leucaenae* morphologically agrees with the generic description of the type species, *C. goaensis* in having globose, dark brown, gregarious conidiomata, phialidic, ampulliform, hyaline conidiogenous cells and cylindrical, guttulate, aseptate, hyaline to pale brown conidia (Wanasinghe et al. 2018b). *Cycasicola leucaenae* differs from *C. goaensis* in having a thin-walled peridium with two brown and a hyaline layer and lacking an ostiole (Fig. 96). In addition, the substrate around the conidiomata of *C. goaensis* is stained black but this was not observed in *C. leucaena* (Wanasinghe et al. 2018b). A comparison of the ITS nucleotides of these two strains reveals 9 (1.9%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016). Based on these differences we introduce a second species of *Cycasicola.*

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

This consists of five hyphomycetous genera, *Torula*, *Dendryphion*, *Neotorula*, *Rostriconidium* and *Sporidesmioides* (Su et al. 2016, Hyde et al. 2016, Li et al. 2016, Li et al. 2017, Su et al. 2018). Most of the species in this family occur in fresh water habitats (Su et al. 2018). We document two strains of *Torula ficus* from wild mangosteen fruit in Thailand and fruit of *Magnolia grandiflora* in China (Fig. 97).

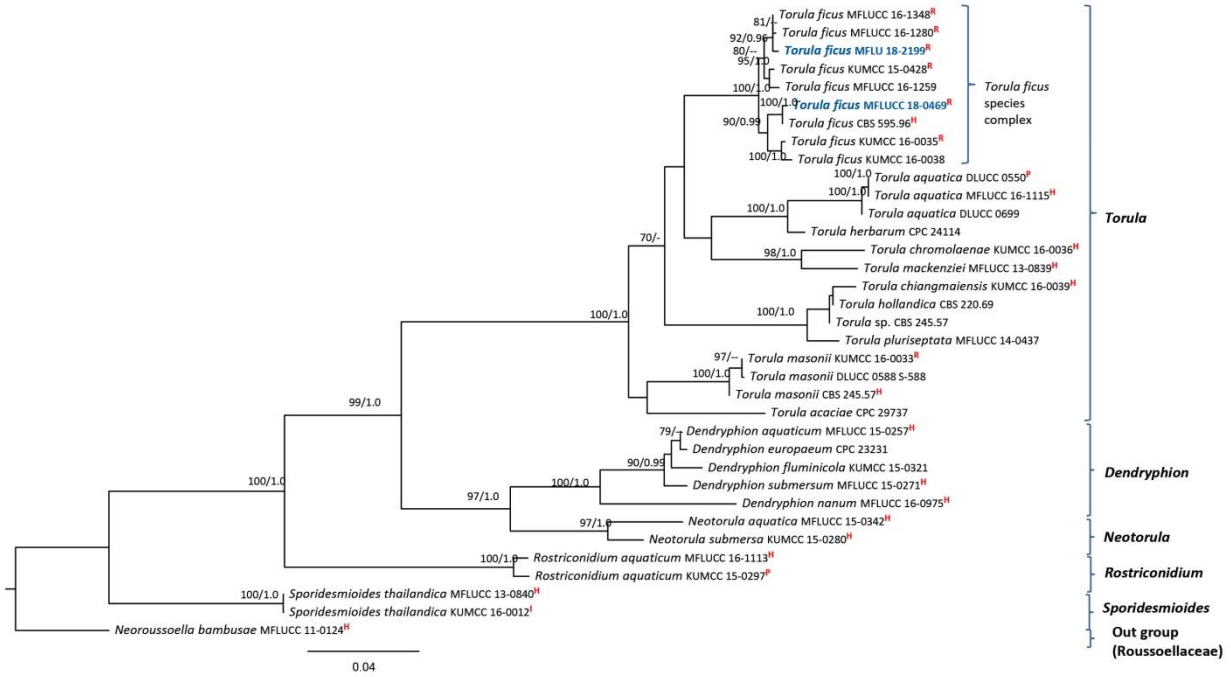


Figure 97 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined ITS, LSU, *tef1* and *rpb2* matrix of 35 strains including related species of the family Torulaceae (Su et al. 2018). The matrix comprised 3130 characters including alignment

gaps. The tree was rooted with *Neoroussoella bambusae* MFLUCC 11 0124 (Roussoellaceae). The best scoring RAxML tree with a final likelihood value of -13396.714097 is presented. The matrix had 996 distinct alignment patterns, with 28.67% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241477, C = 0.270123, G = 0.274045, T = 0.214355; substitution rates AC = 1.730630, AG = 4.254515, AT = 2.022183, CG = 1.205691, CT = 9.382099, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new strains are in blue. Strains isolated from the holotype, isotype, paratype and reference specimens are indicated in red superscript ^{H}, ^{I}, ^{P} and ^{R} respectively.

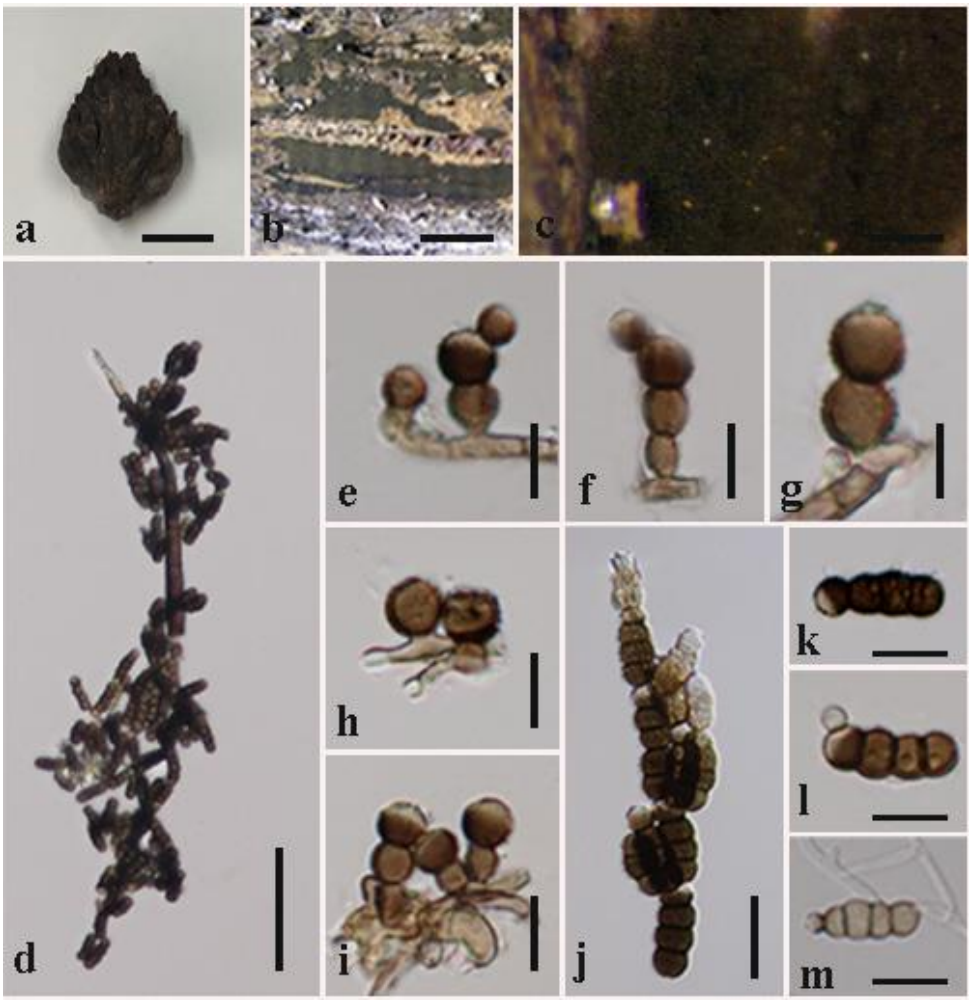


Figure 98 – *Torula ficus* (MFLU 18–2199). a *Magnolia grandiflora* cone. b, c Colonies on dead pod. d Hypha with conidia. e–i Conidiophores with conidiogenous cell. j Conidial chain. k Conidia l Budding on conidium. m Germinated conidium. Scale bars: a = 1 cm, b = 500 μm, c = 200 μm, d = 30 μm, e–m = 10 μm.

64. *Torula ficus* P.W. Crous, IMA Fungus 6 (1): 192 (2015) Fig. 98

Saprobic on a submerged decaying wood and wild fruits. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Colonies* effuse on host, blackish green, powdery. *Mycelium* 1.5–2 μm wide ($\bar{x}$ = 1.8 μm; n = 30), superficial to partly immersed on the substrate, composed of septate, branched, smooth, hyaline to brown hyphae. *Conidiophores* macronematous, mononematous, solitary, erect, light brown, verruculose, thick-walled, consisting of with 1 or 2 cells, without apical branches, ellipsoid to subglobose, arising from hypha. *Conidiogenous cells* 6–11 × 3.5–6 μm ($\bar{x}$ = 8.5 × 4.5 μm; n = 20), polyblastic, terminal, light brown to brown, paler at apex, smooth to minutely verruculose, thick-walled, doliiform. *Conidia* 10–22 × 6–7 μm ($\bar{x}$ = 15.5

× 6.5 μm; n = 30), catenated, acrogenous, simple, light brown to brown, phragmosporous, mainly subcylindrical, smooth to minutely verruculose, rounded at both ends, often paler at apex, 2–3-septate, constricted at septa. Conidial secession schizolytic.

Culture characters – Conidia germinated on MEA within 18 hr. and germ tubes produced from the apex. Colonies growing on MEA, reaching 50 mm diam. in 2 weeks at 18ºC, mycelium partly superficial, partly immersed, slightly effuse, cottony, with regular edge, grayish-brown to brown.

Material examined – THAILAND, Ranong Province (8˚ 45' 5" N; 98˚ 23' 40" E), on decaying fruit pericarp of *Garcinia* sp. (Clusiaceae), 29 August 2017, S.C. Jayasiri, C 374 (MFLU 18–2171, new host record), living culture MFLUCC 18–0469, KUMCC 18–0300; CHINA, Yunnan province, Kunming, Kunming Institute garden, on decaying cone of *Magnolia grandiflora* (Magnoliaceae), 10 May 2018, S.C. Jayasiri, C 448 (MFLU 18–2199, new host record).

GenBank numbers – MFLUCC 18–0469: SSU: MK347883, ITS: MK347776, LSU: MK347993, *tef1*: MK360090, *rpb2*: MK434871; MFLU 18–2199: SSU: MK347905, ITS: MK347797, LSU: MK348016

Known distribution – Europe from *Ficus* sp. (Crous et al. 2015a); Thailand from *Chromolaena odorata* (Li et al. 2017b); China from submerged decaying wood (Su et al. 2017) and from *Magnolia grandiflora* (this study); Thailand from *Garcinia* sp. (this study).

Notes – Our two strains group with other sequences of *Torula ficus* in GenBank (Fig. 97). Morphological characters (Fig. 98) such as macronematous conidiophores, mono- to polyblastic, doliiform conidiogenous cells and dry, acrogenous, brown, constricted at septa, verrucose conidia in chains and consticted at the septa, fit well within the species concept of *T. ficus* (Crous et al. 2015a). Therefore, we report on two new host records for *T. ficus* from terrestrial environments on decaying fruit of *Garcinia* sp. and cone of *Magnolia grandiflora.*

Pleosporales, *incertae sedis*

Pseudoberkleasmium Tibpromma & K.D. Hyde, Fungal Diversity 93:50 (2018)

This genus was established with *Ps. pandanicola* as the type species based on morphology and phylogenetic analyses (Tibpromma et al. 2018). Herein we introduce a new species in *Pseudoberkleasmium* (Fig. 99).

65. *Pseudoberkleasmium acaciae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 100

Index Fungorum number: IF555575; Facesoffungi number: FoF05283

Holotype – MFLU 18–2169

Etymology – Referring to the host genus on which the fungus was collected, *Acacia* (Fabaceae).

Saprobic on *Acacia* sp. pods. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. Colonies on natural substrate, superficial, gregarious, scattered, black, powdery, glistening, with conidia readily liberated when disturbed. *Mycelium* 1.9–3.3 μm wide ($\bar{x}$ = 2.8 μm; n = 30), superficial to immersed, hyaline to pale brown, branched, septate. *Conidiophores* micronematous, mononematous, fasciculate, hyaline, smooth. *Conidiogenous cells* 10–12 × 6–10 μm ($\bar{x}$ = 11 × 8.4 μm; n = 30), globose to subglobose, terminal, thick-walled, determinate, hyaline. *Conidia* 28–38 × 17–24 μm ($\bar{x}$ = 34 × 22 μm; n = 30), initially hyaline, later brown to olivaceous green, hyaline basal cell, muriform, globose to subglobose, rounded at apex.

Culture characters – Ascospores germinated on MEA within 18 hr. Colonies growing on MEA, reaching 15 mm diam. after 2 weeks at 18 ° C, surface with hyphal growing, with irregular edge, pale brown to grey, radially arrange, middle dark brown, muciligenous extudate, reverse three layers, pale brown to grey outer layer, yellowish brown middle layer and center dark brown to black.

Material examined – THAILAND, Krabi Province, Mueang Krabi District (8˚ 3' 22" N, 98˚ 46' 28" E), on decaying pod septum of *Acacia* sp. (Fabaceae), 31 August 2017, S.C. Jayasiri, C 373

(MFLU 18–2169, holotype), ex-type living culture MFLUCC 17–2590, KUMCC 18–0286.

GenBank numbers – SSU: MK347882, ITS: MK347775, LSU: MK347992, *tef1*: MK360073

Notes – *Pseudoberkleasmium acaciae* forms a sister clade to *P. pandanicola* (MFLUCC 17–2264) with high statistical support (Fig. 100). Both species share morphological features (Fig. 101) such as hyphomycetous form, micronematous, mononematous conidiophores and muriform ascospores. However, *P. pandanicola* has conidiogenous cells that remain connected to the base of conidia, with guttules and broadly ellipsoidal to obovoid, flattened, one-cell thick, guttulate conidia (Tibpromma et al. 2018). Therefore, we describe a new species of *Pseudoberkleasmium.* A comparison of the ITS nucleotides of these two species reveal 33 (6.7%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

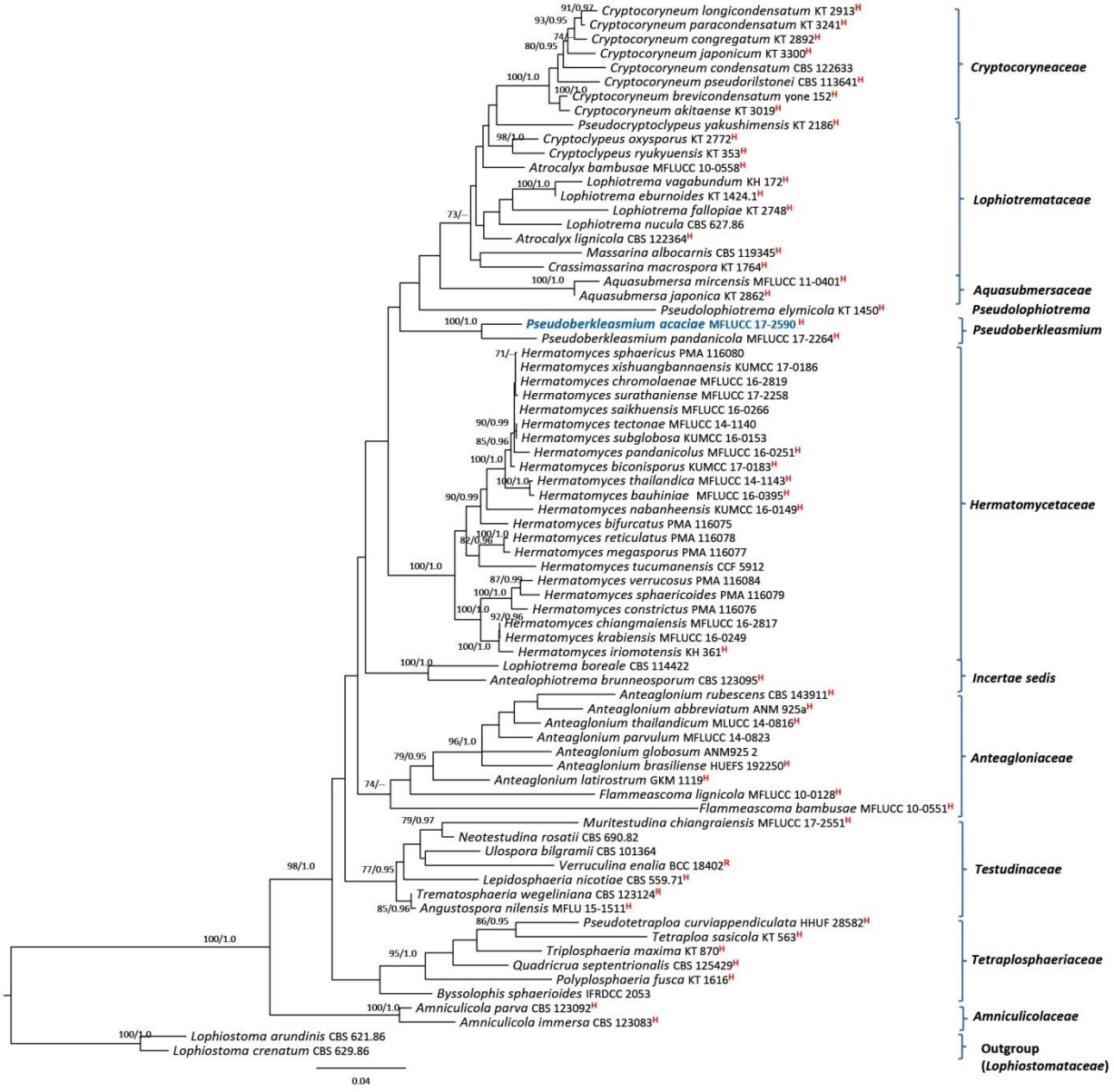


Figure 99 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS, LSU and *tef1* matrix of 74 strains was including related families of order Pleosporales. The matrix comprised 3394 characters including alignment gaps. The tree was rooted with *Lophiostoma* spp. (Lophiostomataceae). The best scoring RAxML tree with a final likelihood value of -21848.231790 is presented. The matrix had 873 distinct alignment patterns, with 22.56% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.242601, C = 0.252145, G = 0.278539, T = 0.226715; substitution rates AC = 0.767335, AG = 2.871799, AT = 1.203512, CG = 1.169423, CT = 11.302775, GT = 1.000000. ML bootstrap

support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolate is in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

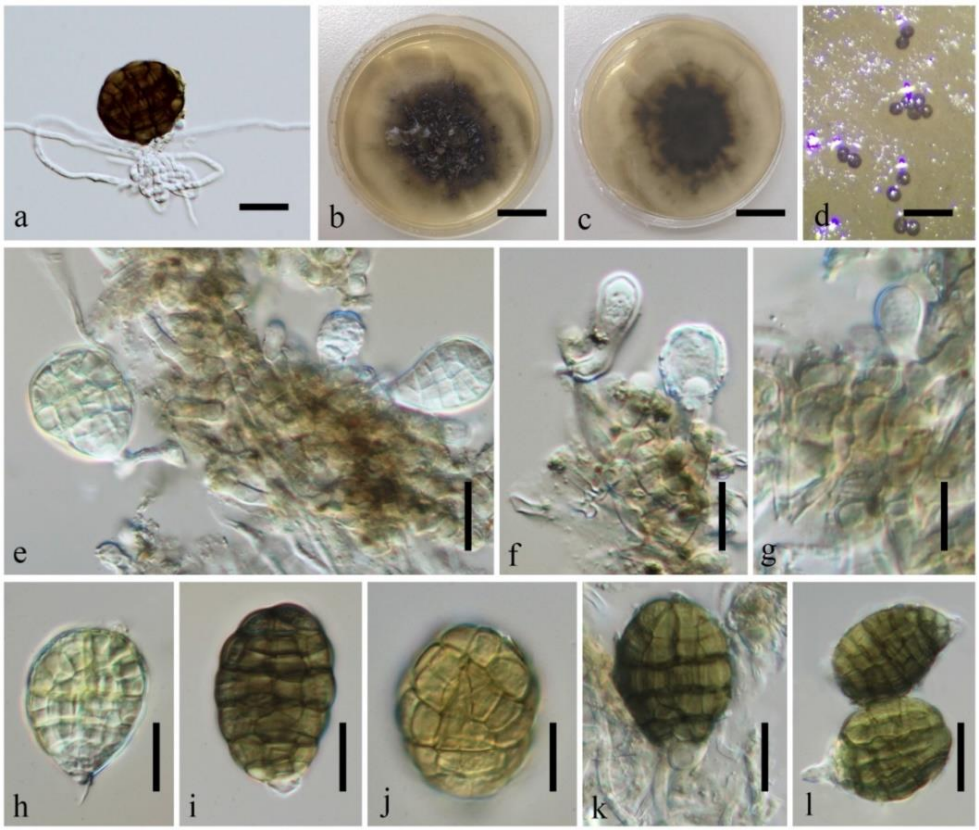


Figure 100 – *Pseudoberkleasmium acaciae* (MFLUCC 17–2590, ex-type). a Germinated conidium. b, c Top and reverse views of culture. d Growth in culture. e–f Conidiophores and conidiogenous cells. g–k Conidia. Scale bars: b, c = 1 cm, a, d–k = 20 μm.

Subclass Dothideomycetidae P.M. Kirk et al. Mycologia 98: 1045 (2007)

Capnodiales Woron., Annales Mycologici 23: 177 (1925)

Capnodiaceae (Sacc.) Höhn. ex Theiss., Verhandlungen der Zoologisch-Botanischen Gesellschaft Wien 66: 363 (1916)

Capnodiaceae contains species of sooty moulds (Hyde et al. 2013, Chomnunti et al. 2011, 2014). The family is commonly found on leaves and associated with the honeydew of insects (Chomnunti et al. 2011).

Leptoxyphium Speg., Physis Revista de la Sociedad Argentina de Ciencias Naturales 4 (17): 294 (1918)

Leptoxyphium is the asexual morph genus in Capnodiaceae. It has elongated pycnidia, with short or long necks, an apical ostiole, and aseptate, hyaline conidia (Chomnunti et al. 2011, 2014). Herein introduce a new host record of *Leptoxyphium kurandae* from Thailand.

66. *Leptoxyphium kurandae* Crous & R.G. Shivas, Persoonia 26: 145 (2011) Fig. 101

Facesoffungi number: FoF05284

Saprobic sooty moulds, forming on the upper surface of leaves and fruits. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Hyphae* olivaceous brown to dark brown, branched, septate, constricted at the septa, bead-like, forming an irregular network. *Conidiomata*

342–422 μm high ($\bar{x}$ = 381 μm; n = 10), synnematal, dark olivaceous-brown to black, straight to slightly flexuous, base 37–47 × 37–43 μm wide ($\bar{x}$ = 44 × 39 μm; n = 20), basal cells dark olivaceous-brown, bulbous, apex 29–37 × 28–32 μm wide ($\bar{x}$ = 34 ×31 μm; n = 20), funnel-shaped, resembling a cupula. *Conidiogenous cells* arising from the inner cell wall of the cupulate apex, olivaceous-brown to hyaline. *Conidia* 6.2–7.4 × 2.7–3.4 μm ($\bar{x}$ = 6.7 × 3 μm; n = 20), hyaline, broadly ellipsoid with rounded ends, aseptate and lacking guttules.

Material examined – THAILAND, Chiang Rai Province, decaying fruits of *Lagerstroemia loudoni* (Lythraceae), 23 October 2015, S.C. Jayasiri, C 67 (MFLU 18–2085, new host record).

Notes – The morphology of this new collection is identical with description of *Leptoxyphium kurandae* (Crous et al. 2011). *Leptoxyphium kurandae* was reported from leaves of *Eucalyptus* sp. (Crous et al. 2011), on extrafloral nectaries of *Hibiscus rosa-sinensis* (Park et al. 2015) and on leaves of *H. cannabinus* (Choi et al. 2015). This is the first report of *L. kurandae* from fruit (*Lagerstroemia loudoni*) and as a saprobe. Our new collection identified based only on morphology (Fig. 107) as single spore isolation was unsuccessfuled.

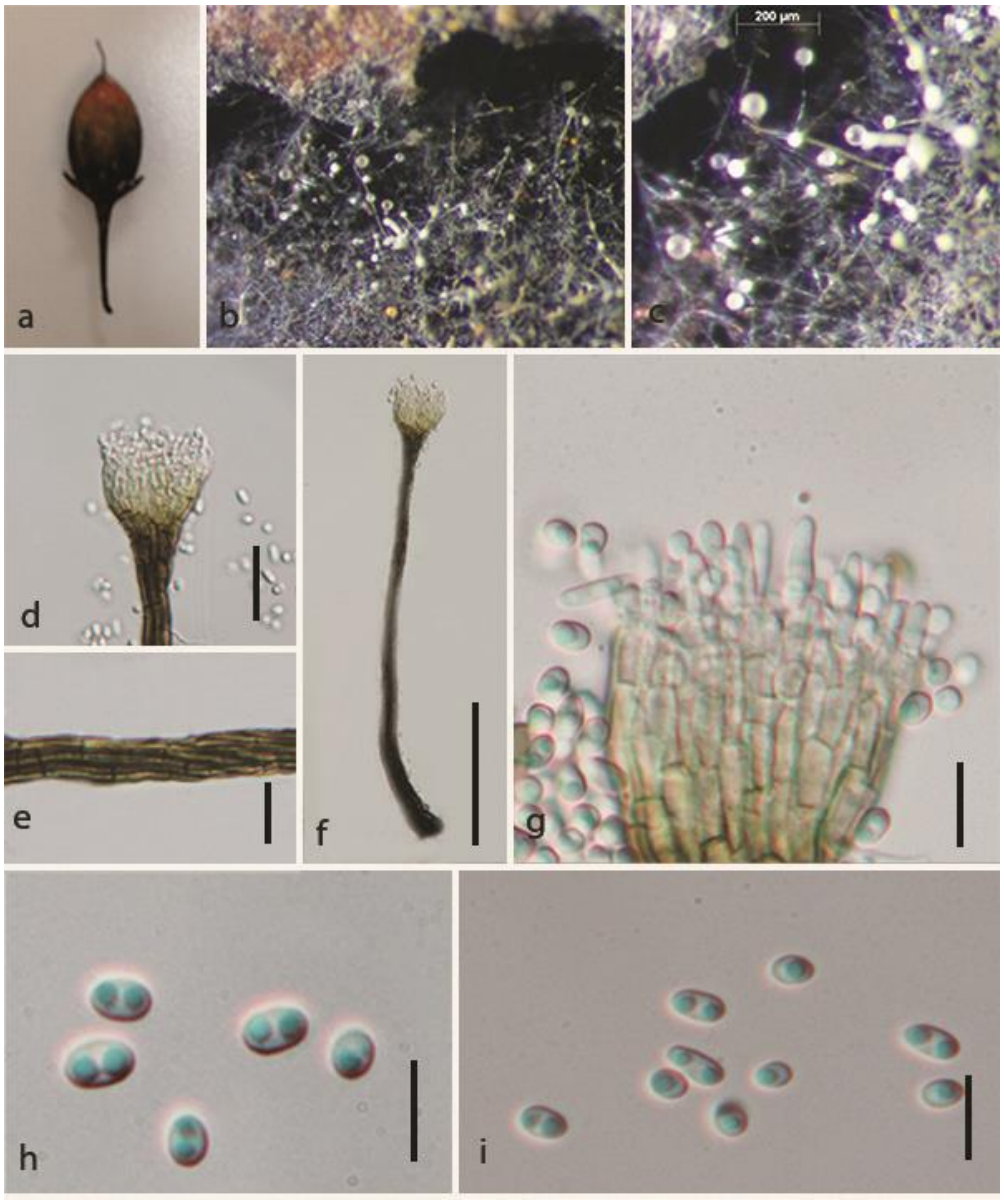


Figure 101 – *Leptoxyphium kurandae* (MFLU 18–2085). a Host seed. b, c Mycelium on host surface. d Apex swelling on synnemata. e Close up of synnematal stalk. f Synnematal stalk. g Condiogenous cells close up view of formation of conidia. h, i Conidia. Scale bars: d, e, g–j = 10 μm, f = 100 μm.

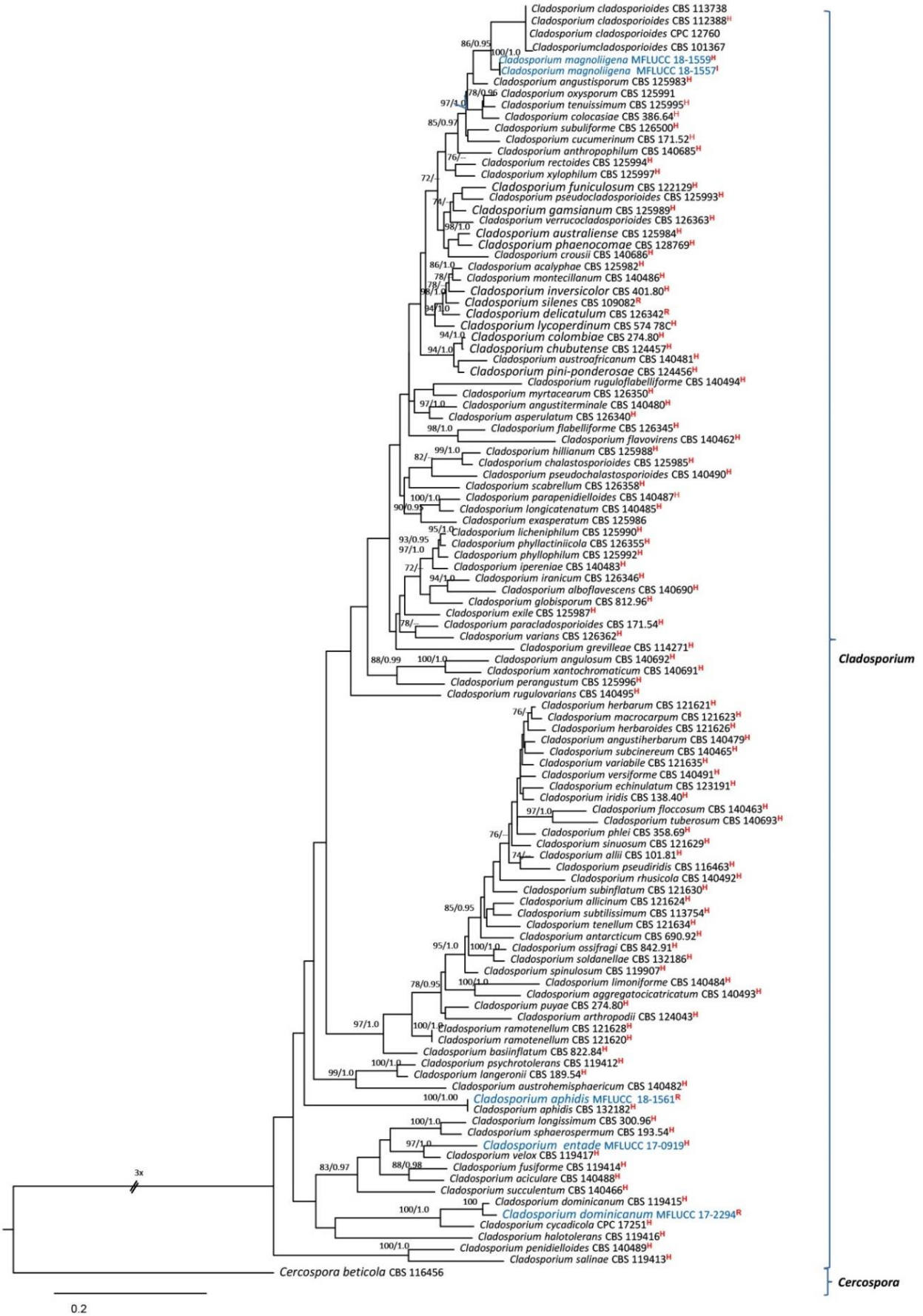


Figure 102 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1* and actin partial sequence data for *Cladosporium* species. One hundred and seven strains were included in the sequence analysis, which comprise 1378 characters including alignment gaps.

Cercospora beticola (CBS 116456) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -20894.787676 is presented. The matrix had 845 distinct alignment patterns, with 23.69% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.226943, C = 0.290615, G = 0.251331, T = 0.231112; substitution rates AC = 1.878021, AG = 3.250831, AT = 1.689030, CG = 1.117942, CT = 5.560854, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue. Strains isolated from the holotype, isotype and reference specimens are indicated in red superscript ^{H}, ^{I} and ^{R} respectively.

Cladosporiaceae Nann., Repertorio sistematico dei miceti dell' uomo e degli animali 4: 404 (1934)

Cladosporiaceae contains eight genera (Wijayawardene et al. 2018) including the divese and species rich genus, *Cladosporium.*

Cladosporium Link, Magazin der Gesellschaft Naturforschenden Freunde Berlin 8: 37 (1816)

This genus mostly comprises saprobes with a worldwide distribution, and growing on a wide range of substrates (Bensch et al. 2012, Crous et al. 2014, Sandoval-Denis et al. 2016). We collected three host records and two new species of *Cladosporium*.

67. *Cladosporium aphidis* Thüm., Oesterr. Landwirtsch. Wochenbl. 2(43): 505 (1876) Fig. 103

Facesoffungi number: FoF05285

Saprobic on aphids, *Aphis symphyti* and pods of *Laburnum anagyroides*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* 2–3 μm wide ($\bar{x}$ = 2.2 μm; n = 30), superficial and immersed composed of septate, branched, subhyaline to pale green-brown, rough- and thick-walled, anastomosing hyphae. *Conidiophores* 43–58 μm high × 3–3.5 μm diam. ($\bar{x}$ = 52 × 3.2 μm; n = 30), erect, cylindrical, nodulose, septate, simple or branched, brown, roughened to verruculose, thick-walled. *Conidiogenous cells* 4.5–7.5 × 1–2 μm ($\bar{x}$ = 6.8 × 1.8 μm; n = 20), terminal or intercalary, subcylindrical or cylindrical, bearing up to four conidiogenous loci, darkened and refringent. *Ramoconidia* 11–20 × 3–3.5 μm ($\bar{x}$ = 15 × 3.2 μm; n = 30), pale brown to brown, ellipsoidal to cylindrical, smooth or finely verruculose, 1–4-septate. *Conidia* 5–9 × 3–4 μm ($\bar{x}$ = 6 × 3.5 μm; n = 30), pale brown to brown, obovoidal to short ellipsoid, aseptate, smooth- and thick-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies reaching a diam. of 50 mm after 2 weeks at 18°C. Colonies olivaceous-grey to olivaceous, pale olivaceous-grey due to aerial mycelium, iron-grey reverse, sometimes zonate, velvety or powdery, margin colourless or white, regular, radially furrowed, feathery, colony centre often forming a crater like structure, immersed, aerial mycelium sparse, diffuse or dense, numerous small prominent exudates formed, appear almost blackish, profuse sporulation.

Material examined – UK, Southsea, on decaying pods of *Laburnum anagyroides* (Fabaceae), 8 November 2015, E.B.G. Jones, GJ 210 (MFLU 18–2226, new host record); living culture MFLUCC 18–1561, KUMCC 18–0219.

GenBank numbers – SSU: MK347924, ITS: MK347815, LSU: MK348035, *rpb2*: MK434850

Notes – In the phylogenetic analysis, the new strain grouped in a clade with *Cladosporium aphidis* (CBS 132182) with high support (100 % MLBS/1.0 BYPP, Fig. 102). A comparison of the ITS, *tef1* and actin nucleotides of *Cladosporium aphidis* and the new strain (MFLUCC 18–1561) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *Cladosporium aphidis* (Jeewon & Hyde 2016). *Cladosporium aphidis* has erect, cylindrical, nodulose, septate, simple or branched, brown conidiophores, terminal or intercalary, subcylindrical or cylindrical conidiogenous cells, 1–4-septate, ellipsoidal to cylindrical ramoconidia and obovoidal to short ellipsoid, aseptate, pale green-brown conidia (Bensch et al. 2012). *Cladosporium aphidis* is the only example of a *Cladosporium* species on aphids. However, in our study we isolated the same

species from wild seed pods of *Laburnum anagyroides*. Lectotype of this species is from *Symphytum officinale* associated with *Aphis symphyti* and a later epitype by Bensch et al. (2012) on dead carcasses of aphids on leaves of *Echium vulgare* (Boraginaceae). It formed colonies on the leaf surface around the carcasses and finally spread over the whole leaf (Bensch et al. 2012). Our sample may be associated with aphids, although we only observed colonies growning on surface of the seed coat.

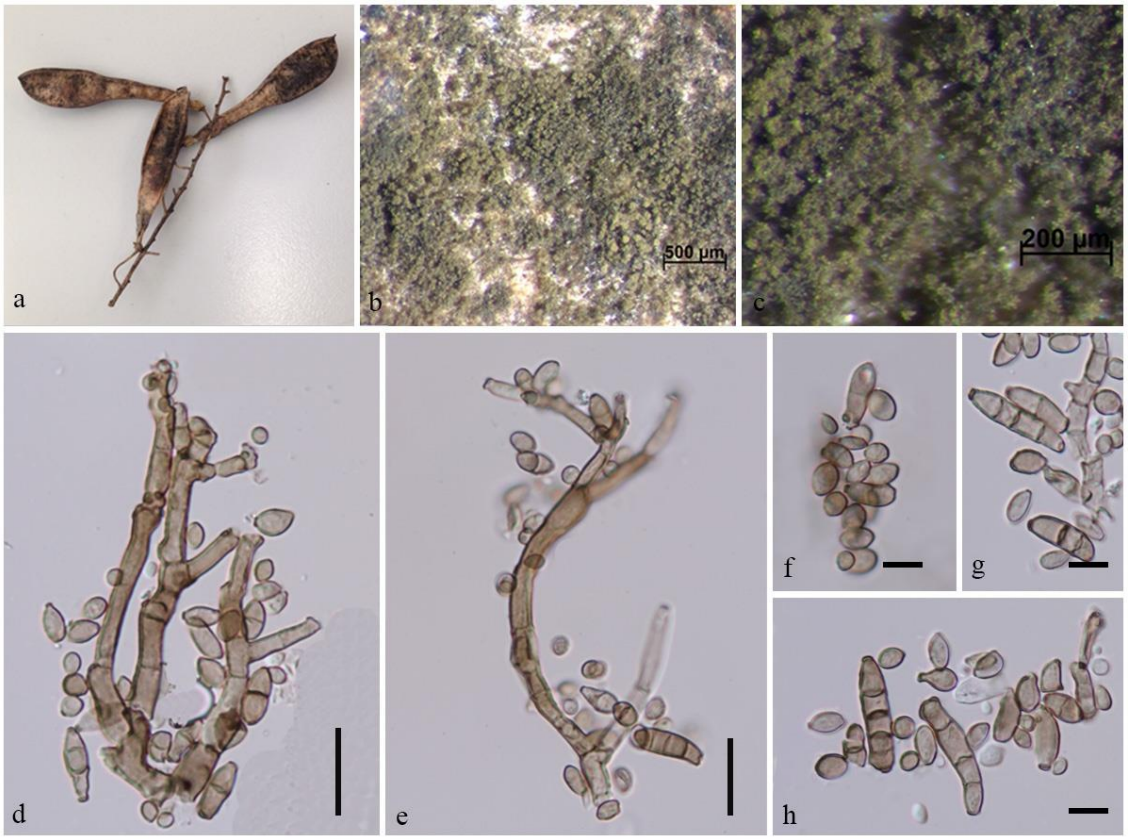


Figure 103 – *Cladosporium aphidis* (MFLU 18–2226). a Host pods of *Laburnum anagyroides*. b, c Appearance of colonies. d, e Conidiophores, conidiogenous cells and conidia. f–g Conidia and ramoconidia. Scale bars: a = 1 cm, d, e = 10 µm, f–h = 5 µm.

68. *Cladosporium dominicanum* Zalar, de Hoog & Gunde-Cimerman, Studies in Mycology 58: 169 (2007) Fig. 104

Facesoffungi number: FoF05323

Saprobic on *Delonix regia* pod and in hypersaline water. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* 2–4 µm wide ($\bar{x}$ = 3.2 µm; n = 30), partly superficial partly submerged; hyphae branched, septate, often with swellings and constrictions, irregular, hyaline to pale brown, smooth, walls, slightly thickened. *Conidiophores* 50–80 (–150) µm long × 2–3 µm diam. ($\bar{x}$ = 72 × 2.5 µm; n = 30), arising laterally or terminally, erect, micronematous and semimacronematous, straight to slightly flexuous, filiform to narrowly cylindrical, unbranched or branched, brown. *Conidiogenous cells* undifferentiated. *Condiogenous scars* thickened and conspicuous, protuberant. *Ramoconidia* rarely formed. *Conidia* 5–6 × 2.5–2.6 µm ($\bar{x}$ = 5.5 × 2.5 µm; n = 30), catenate, in branched chains, hyaline to dark brown, narrower at both ends, straight, guttulate.

Culture characters – Conida germinated on MEA with in 18 hr. Colonies on MEA reaching 30–40 mm diam. after 2 weeks at 18°C, dark green, velvety, furrowed, with undulate margin. Reverse dark green-brown.

Material examined – THAILAND, Ko Larn Island, on decaying pod septum of *Delonix regia*

(Fabaceae), 6 August 2017, S.C. Jayasiri, C 302 (MFLU 18–2138, new host record), living culture MFLUCC 17–2294, KUMCC 18–0222.

GenBank numbers – ITS: MK347753, LSU: MK347970, *tef1*: MK340861, actin: MK412888

Notes – In the phylogenetic analysis, the new strain grouped in a clade with *Cladosporium dominicanum* (CBS 119415) with high support (100 % MLBS/1.0 BYPP, Fig. 102) and shares similar morphology with type description (Zalar et al. 2007). A comparison of the ITS, *tef1* and actin nucleotides of *Cladosporium dominicanum* and the new strain (MFLUCC 17–2294) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *Cladosporium dominicanum* (Jeewon & Hyde 2016). The type of *C. dominicanum* was identified from hypersaline water of salt lake, while our new strain collected from decaying pods of *Delonix regia* (Zalar et al. 2007).

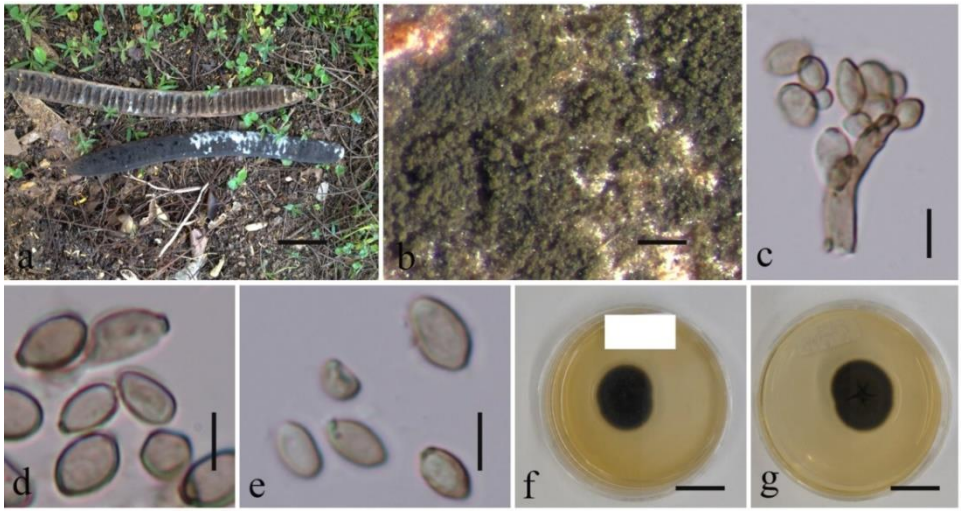


Figure 104 – *Cladosporium dominicanum* (MFLU 18–2138). a Host seed pods of *Delonix regia*. b Appearance of colonies in the substrate. c Conidiogenous cell with conidia. d, e Conidia. Scale bars: a = 2 cm, b = 200 µm, c–e = 5 µm, f–g = 1 cm.

69. *Cladosporium entadae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 105

Index Fungorum number: IF555576; Facesoffungi number: FoF05287

Holotype – MFLU 18–2104

Etymology – Referring to the host genus on which the fungus was collected, *Entada* (Fabaceae).

Saprobic on pod of *Entada phaseoloides.* Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* partly superficial partly submerged; hyphae branched, septate, irregular, often with swellings and constrictions, hyaline to pale brown to, smooth, walls, slightly thickened. *Conidiophores* arising laterally or terminally, erect, straight to slightly flexuous, filiform to narrowly cylindrical, broad towards the base, unbranched or branched, hyaline to pale brown. *Condiogenous scars* thickened and conspicuous, protuberant. *Conidia* 5–6 × 2.5–2.6 µm ($\bar{x}$ = 5.5 × 2.5 µm; n = 30), in branched chains, terminal chains with up to five conidia, hyaline to dark brown, guttulate, flat end, straight. *Ramoconidia* in the culture, hyaline to pale brown, globose, subglobose, ovoid, apex rounded, aseptate, 1-prominent guttule.

Culture characters – Conida germinated on MEA with in 18 hr. Colonies on MEA reaching 30–40 mm diam. after 2 weeks at 18°C, pale green, radially furrowed, with raised, crater-shaped central part, with white, undulate, submerged margin.

Material examined – THAILAND, Chiang Rai Province, Khun Korn waterfall (19˚ 52' 5" N; 99˚ 38' 5" E), on decaying pod of *Entada phaseoloides* (Fabaceae), 2 February 2017, S.C. Jayasiri, C 221 (MFLU 18–2104, holotype, MFLU 18–2105, isotype), living culture MFLUCC 17–0919, KUMCC 18–0223.

GenBank numbers – SSU: MK347836, ITS: MK347728, LSU: MK347945

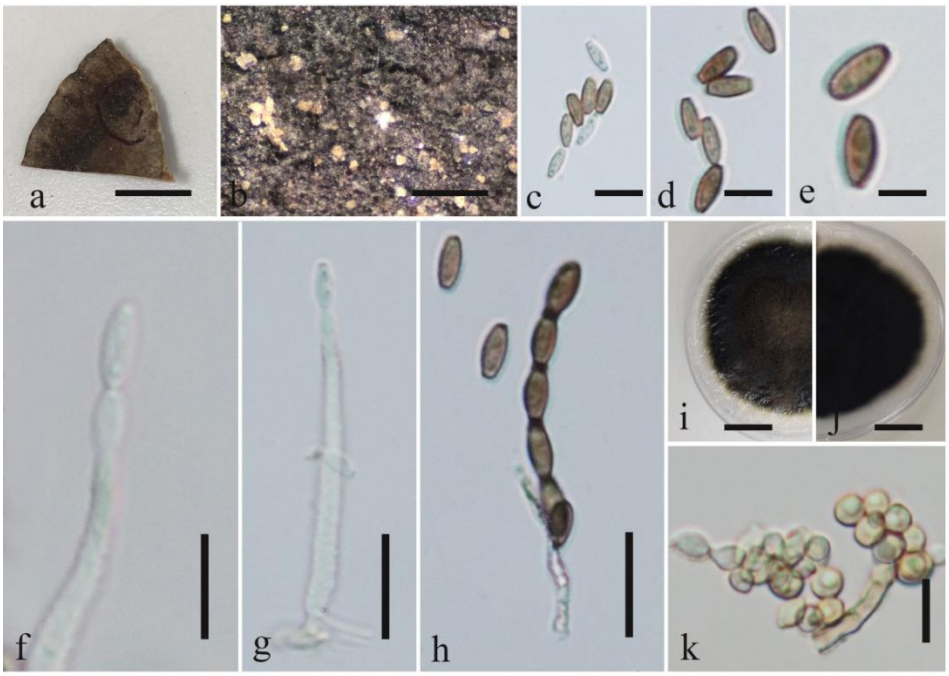


Figure 105 – *Cladosporium entadae* (MFLU 18–2104, holotype). a Part of *Entada phaseoloides* pod. b Appearance of colonies on substrate. c–e Conidia. f, g Conidiophore and conidiogenous cell. h Conidial chain. i, j Top and reverse view of culture. k Conidia in culture (MEA). Scale bars: a, i, j = 1 cm, b = 500 µm, c–e = 5 µm, f–h, k = 10 µm.

Notes – In the phylogenetic analysis, *Cladosporium entadae* formed a sister clade to *C. velox* with high support (97 % MLBS/1.0 BYPP, Fig. 102). *Cladosporium velox* characterized by olivaceous-brown, dichotomously branched conidiophores 5(–7)-septate with 5 conidia in the chain, verruculose, pale brown, non-septate conidia and cylindrical, 0–1-septate ramoconidia (Zalar et al. 2007). *Cladosporium entadae* is characterized by hyaline to pale brown, erect conidiophores, hyaline to dark brown conidia with flat, dark wall ends and globose to subglobose ramoconidia (Fig. 106). With these significant morphological differences and with phylogenetic support we introduce *C. entadae* as a new species. A comparison of the ITS nucleotides of these two strains reveal 8 (1.7%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

70. *Cladosporium magnoliigena* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 106

Index Fungorum number: IFIF555716; Facesoffungi number: FoF05286

Etymology – Referring to the host genus on which the fungus was collected, *Magnolia* (Magnoliaceae).

Saprobic on cone of *Magnolia grandiflora*. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* partly superficial partly submerged, overgrowing entire pod, thin to dense, later often forming colonies on the surface, hyphae straight to strongly flexuous sinuous, branched, subhyaline to olivaceous-brown. *Conidiophores* 50–150 × 3–4.5 µm ($\bar{x}$ = 88 × 3.8 µm; n = 20), erect, stipes, slightly attenuated towards the apex, olivaceous-brown, smooth and thick-walled, arising terminally and laterally from aerial hyphae, dichotomously branched, septate. *Conidia* 4.2–5.5 × 2–5 µm ($\bar{x}$ = 5.1 × 3.5 µm; n = 30), in simple and branched chains, subhyaline to olivaceous-brown, shape and size variable, subglobose, ellipsoid-ovoid, obovoid, fusiform, subcylindrical, aseptate, smooth to faintly rough-walled, conidia thin-walled. *Secondary ramoconidia* 9.5–18 × 2.7–4.2 µm ($\bar{x}$ = 14 × 3.5 µm; n = 30), olivaceous-brown, ellipsoid-ovoid, obovoid, fusiform, subcylindrical, 0–3-septate, smooth to faintly rough-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies on MEA reaching 50–60 mm diam. after 2 weeks at 18°C. Colonies olivaceous-grey to olivaceous, pale olivaceous-

grey due to aerial mycelium, iron-grey reverse, sometimes zonate, velvety or powdery, margin colourless or white, regular, radially furrowed, feathery, colony centre often forming a crater like structure, immersed, aerial mycelium sparse, diffuse or dense, numerous small prominent exudates formed, appear almost blackish, sporulation profuse.

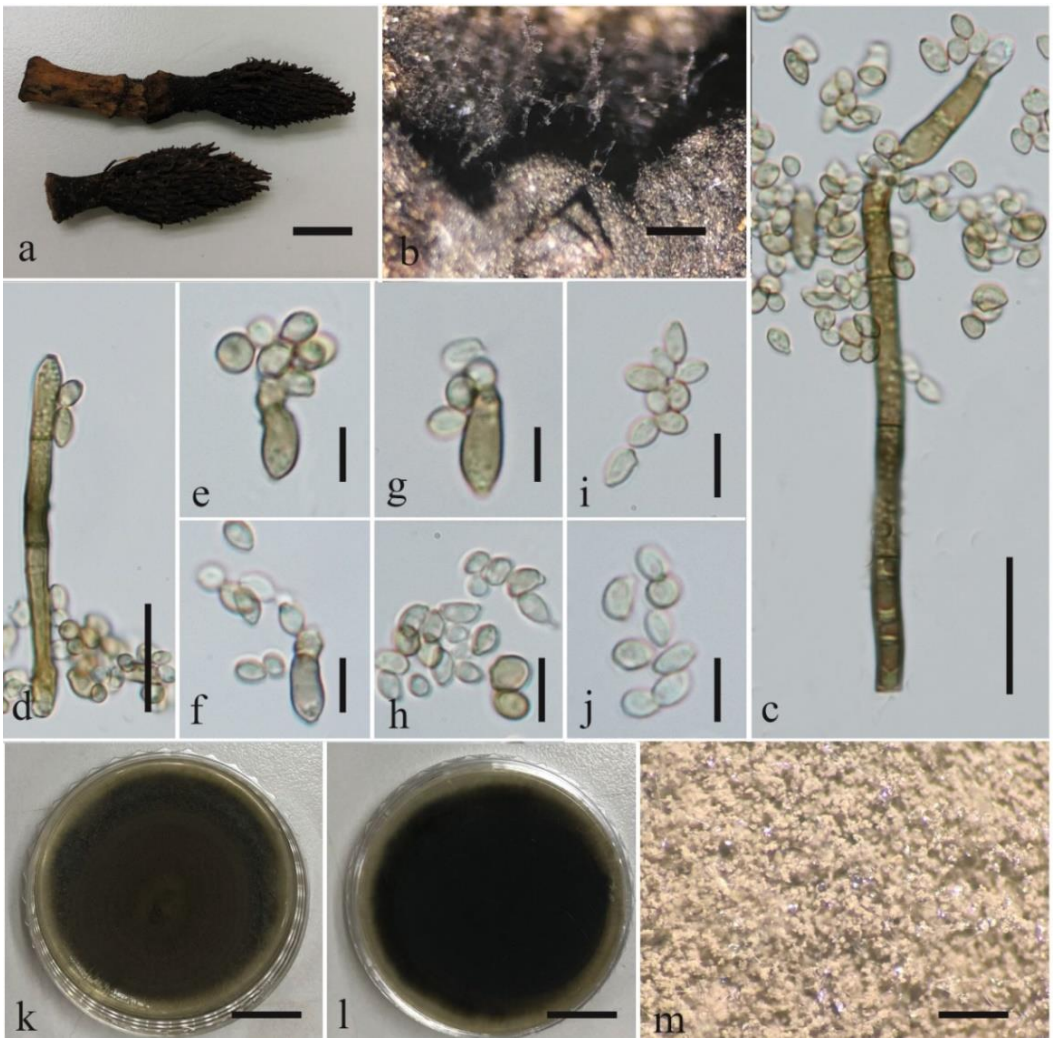


Figure 106 – *Cladosporium magnolicola* (MFLU 18–2220, holotype). a Host fruits of *Magnolia grandiflora*. b Appearance of colonies. d Conidiophore. e–g Conidia and ramoconidia. h–j Conidia. k Top view of culture. l Reverse view of culture. m Sporulation on culture. Scale bars: a, k, l = 1 cm, b, m = 200 µm, c, d = 20 µm, e–j = 10 µm.

Material examined – CHINA, Yunnan Province, Kunming Institute of Botany, on decaying cone of *Magnolia grandiflora* (Magnoliaceae), 25 May 2018, S.C. Jayasiri, C 463 (MFLU 18–2220, holotype; KUN-HKAS102440, isotype); ex-type living culture MFLUCC 18–1559, KUMCC 18–0220; *ibid* C 461-B (MFLU 18–2217-B), living culture MFLUCC 18–1557, KUMCC 18–0221.

GenBank numbers – MFLUCC 18–1559: SSU: MK347921, ITS: MK347813, LSU: MK348032, *tef1*: MK340864, *rpb2*: MK434854; MFLUCC 18–1557: SSU: MK347919, ITS: MK347811, LSU: MK348030, *tef1*: MK340862, *rpb2*: MK434910

Notes – *Cladosporium magnoliigena*, is a sister species to *C. cladosporioides* with high statistical support (86% MLBS/0.95 BYPP, Fig. 102). *Cladosporium magnoliigena* is morphologically (Fig. 107) similar but phylogenetically distant from *C. cladosporioides* (Torres et al. 2017). A comparison of the *tef1* and actin nucleotides of these two strains reveals 39 (17.4%) and 12 (5.2%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

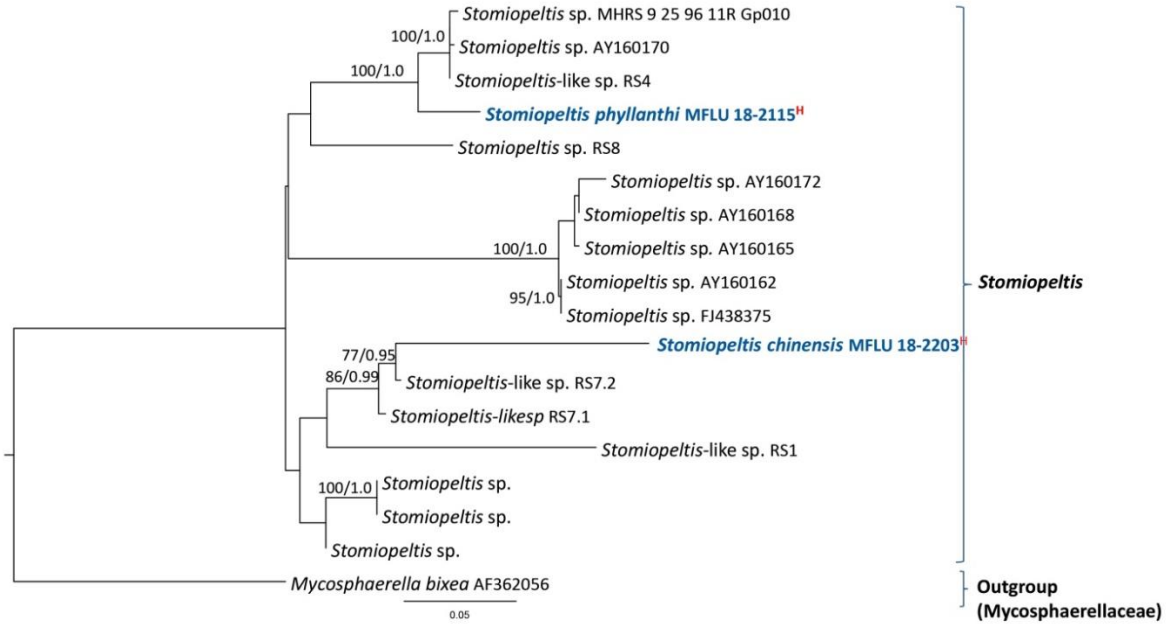


Figure 107 – Phylogram generated from maximum likelihood analysis based on combined ITS and LSU partial sequence data for *Stomiopeltis* species. Eighteen strains were included in the sequence analysis, which comprise 1378 characters including alignment gaps. *Mycosphaerella bixea* (AF 362056) was used as the outgroup taxon. Single gene analysis was carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -4755.099490 is presented. The matrix had 290 distinct alignment patterns, with 41.44% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.225933, C = 0.259155, G = 0.286189, T = 0.228723; substitution rates AC = 1.079318, AG = 1.717967, AT = 1.184400, CG = 1.238487, CT = 4.663407, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue. Strains isolated from the holotype specimens are indicated in red superscript ^{H}.

Phaeothecoidiellaceae K.D. Hyde & Hongsanan, Mycosphere 8 (1): 140 (2017)

This family comprises several species which cause sooty blotch and flyspeck diseases of some economic fruits. We introduce two new species from decaying wild fruits (Fig. 107).

Stomiopeltis Theiss., Brotéria Série Botânica 12: 85 (1914)

Index Fugorum lists 48 records for this genus, with 33 records in USDA Fungal database from different hosts. Many species have been synonymized under different names and few have sequence data with their morphological descriptions. Most species in this genus have been reported as pathogens on fruits (Mayfield et al. 2013, Ajitomi et al. 2017). We introduce two new species from decaying wild fruits from China and Thailand.

71. *Stomiopeltis sinensis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 108

Index Fungorum number: IF555578; Facesoffungi number: FoF05289

Holotype – MFLU 18–2203

Etymology – Referring to the place where the fungus was collected, China.

Saprobic on *Harpephyllum* sp. fruit. Sexual morph: *Thyriothecia* 86–104 μm high × 220–228 μm diam. ($\bar{x}$ = 96 × 225 μm, n = 20), solitary, gregarious, superficial, rounded, easily removed from

the host surface, black, ostiolate. *Peridium* 40–59 μm wide ($\bar{x}$ = 51 μm; n = 20), dark brown *textura angularis* cell layers. *Hamathecium* 2–2.5 μm wide ($\bar{x}$ = 2.2 μm; n = 30), hyaline, filiform, unbranched, septate pseudoparaphyses. *Asci* 44–49 × 15–21 μm ($\bar{x}$ = 45 × 19 μm; n = 20), 4-spored, bitunicate, fissitunicate, oblong to subglobose, with a minute pedicel, arranged vertically, apical region of asci usually with a thick opaque region, without an ocular chamber. *Ascospores* 19–21 × 5–7 μm ($\bar{x}$ = 20 × 5.5 μm; n = 20), uniseriate, hyaline, obovoid to ellipsoid, 1-septate, strongly constricted at the septum, with two different length cells, upper cell slightly broader, asymmetric, guttulate. Sexual morph: Undetermined.

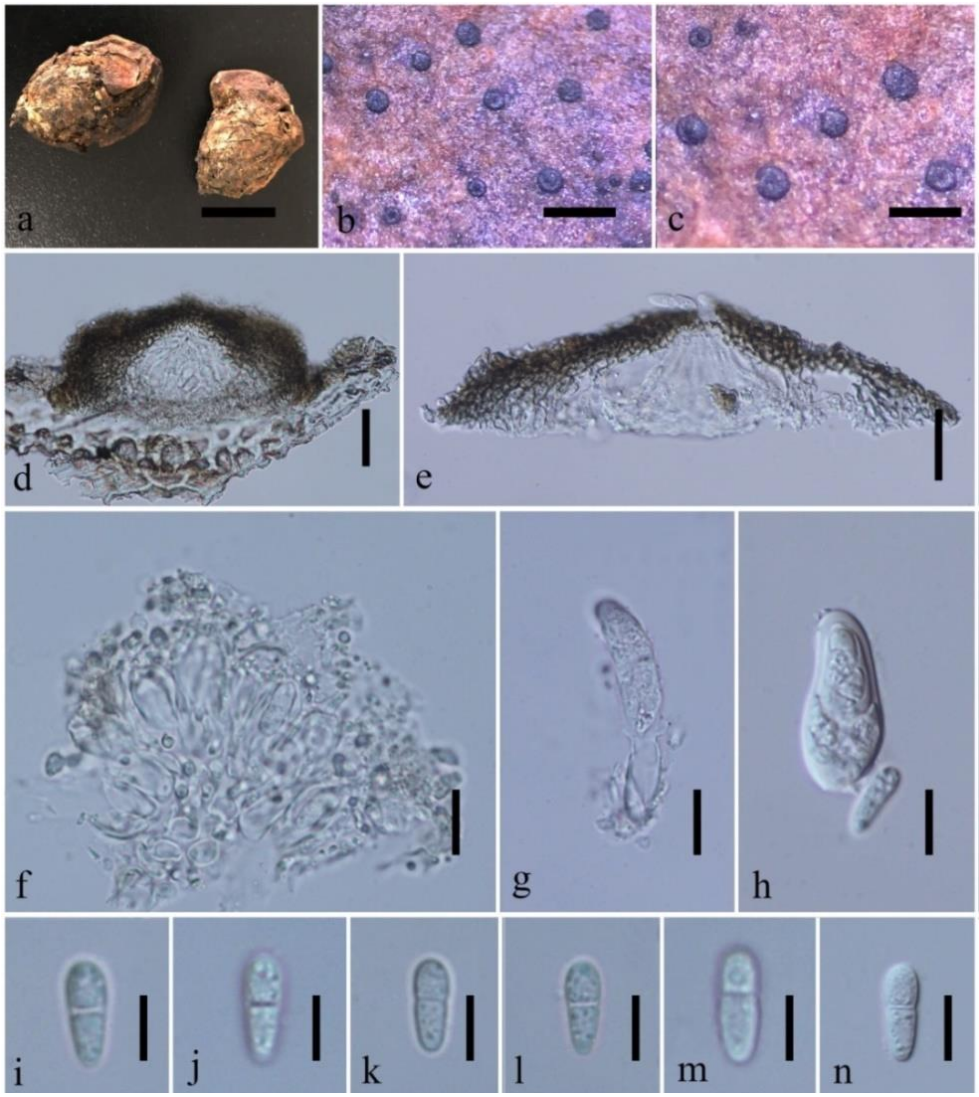


Figure 108 – *Stomiopeltis sinensis* (MFLU 18–2203, holotype). a Host seed. b, c View of thyriothecia on host surface. d, e Section through thyriothecia. f–h Asci. i–n Ascospores. Scale bars: a = 1 cm, b, c = 500 μm, d, e = 30 μm, f–n = 10 μm.

Material examined – CHINA, Yunnan Province, Kunming Institute of Botany, on decaying fruit pericarp of *Harpephyllum* sp. (Anacardiaceae), 25 April 2018, S.C. Jayasiri, C 450 (MFLU 18–2203, holotype; KUN-HKAS 102438, isotype).

GenBank numbers – SSU: MK347907, ITS: MK347799, LSU: MK348018

Notes – *Stomiopeltis sinensis* clusters with *Stomiopeltis* sp. (RS7.1 and RS7.2) introduced from apple sooty blotch and flyspeck (SBFS) disease in northeastern Turkey (Mayfield et al. 2013). However, there is no morphological description of this strain, only described culture morphology. However, we were unable to get a culture of *Stomiopeltis sinensis* and DNA was extracted directly from the fruiting bodies (Zeng et al. 2018). *Stomiopeltis* sp. (RS7.2) has good support in multi-loci

phylogeny (77% MLBS/0.95 BYPP, Fig. 107) with new strain and there were 75 (13.3%) base pair differences for ITS gene region. Therefore, we introduce a new species, *Stomiopeltis sinensis* (Fig. 108) as it fits with the description of the genus in having superficial, orbicular, conical to lenticular, ostiolar, unilocular thyriothecia with pseudoparenchyma cell wall, bitunicate asci with thick neck and hyaline, guttulate ascospores with a transverse septum (Ajitomi et al. 2017).

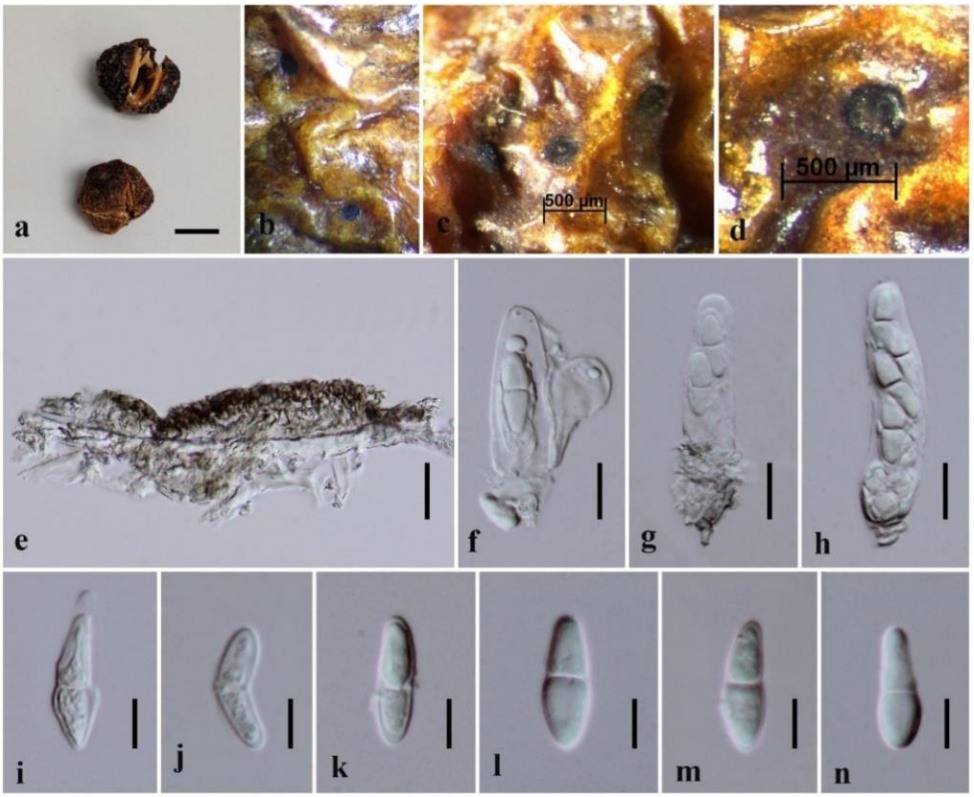


Figure 109 – *Stomiopeltis phyllanthi* (MFLU 18–2115, holotype). a *Phyllanthus emblica* seeds. b–d View of thyriothecia on host surface. e Section through thyriothecium. f–h Asci. i–n Ascospores. Scale bars: a = 1 cm, e = 20 µm, f–h = 10 µm, i–n = 5 µm.

72. *Stomiopeltis phyllanthi* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 109

Index Fungorum number: IF555577; Facesoffungi number: FoF05288

Holotype – MFLU 18–2115

Etymology – Referring to the host genus on which the fungus was collected, *Phyllanthus* (Phyllanthaceae).

Saprobic on *Phyllanthus emblica* fruits. Sexual morph: *Thyriothecia* 19–35 µm high × 67–84 µm diam. ($\bar{x}$ = 23 × 74 µm; n = 20), solitary, gregarious, superficial, rounded, easily removed from the host surface, black; upper wall comprising a thin layer of neatly arranged dark cells of *textura angularis*. *Hamathecium* lacking pseudoparaphyses. *Asci* 44–49 × 7–9 µm ($\bar{x}$ = 45 × 8 µm; n = 20), 4- spored, bitunicate, fissitunicate, oblong to subglobose, with a minute pedicel, arranged vertically, apical region of asci usually with a thick opaque region, ocular chamber not observed. *Ascospores* 15–17 × 4–5 µm ($\bar{x}$ = 16 × 4.5 µm; n = 20), uniseriate, hyaline, obovoid to ellipsoid, 1-septate, strongly constricted at the septum, equal length cells, but upper cell slightly broader, asymmetric. Asexual morph: Undetermined.

Material examined – THAILAND, Chiang Rai, Mae Fah Luang University, on decaying fruit pericarp of *Phyllanthus emblica* (Phyllanthaceae), 20 March 2017, D. Thennakon, C-241 (MFLU 18–2115, holotype; KUN-HKAS 102418, isotype).

GenBank numbers – SSU: MK347842, ITS: MK347734, LSU: MK347951

Notes – *Stomiopeltis phyllanthi* forms a sister clade to *Stomiopeltis* spp. strains (RS4, 11R Gp010 and AY160170) with high statistical support (100% MLBS/1.0 BYPP, Fig. 107), although

these strains do not have any morphological description. However, *S. phyllanthi* (Fig. 109) fits with the description of the genus *Stomiopeltis* in having superficial, orbicular, unilocular thyriothecia with pseudoparenchyma cell wall, bitunicate asci with thicked neck and hyaline ascospores with a transverse septum (Ajitomi et al. 2017). A comparison of the ITS nucleotides of *Stomiopeltis phyllanthi* and *Stomiopeltis* sp. (RS4, 11R Gp010 and AY160170) strains reveals 58 (12.8%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Dothideomycetes orders *incertae sedis*

Botryosphaeriales C.L. Schoch, Crous & Shoemaker, Mycologia 98 (6): 1050 (2007)

Botryosphaeriaceae Theiss. & P. Syd., Annales Mycologici 16 (1–2): 16 (1918)

Among the six families in the order (Phillips et al. 2019), Botryosphaeriaceae is the largest. The species in Botryosphaeriaceae are morphologically diverse and include pathogens, endophytes or saprobes usually associated with woody hosts (Phillips et al. 2013). Interest in this fungal group is mainly because they cause plant diseases (Phillips et al. 2013, Marin-Felix et al. 2017). We introduce novelties within seven of the 22 genera currently recognised in this family. All our isolates came from decaying wild fruits or seed pods.

Cophinforma Doilom, J.K. Liu & K.D. Hyde, Fungal Diversity 57: 174 (2012)

This genus comprises *Cophinforma atrovirens* and *C. mamane*, two species that are morphologically very similar, with significant overlap in conidial dimensions. Phillips et al. (2013) suggested that they can be distinguished based only on DNA data.

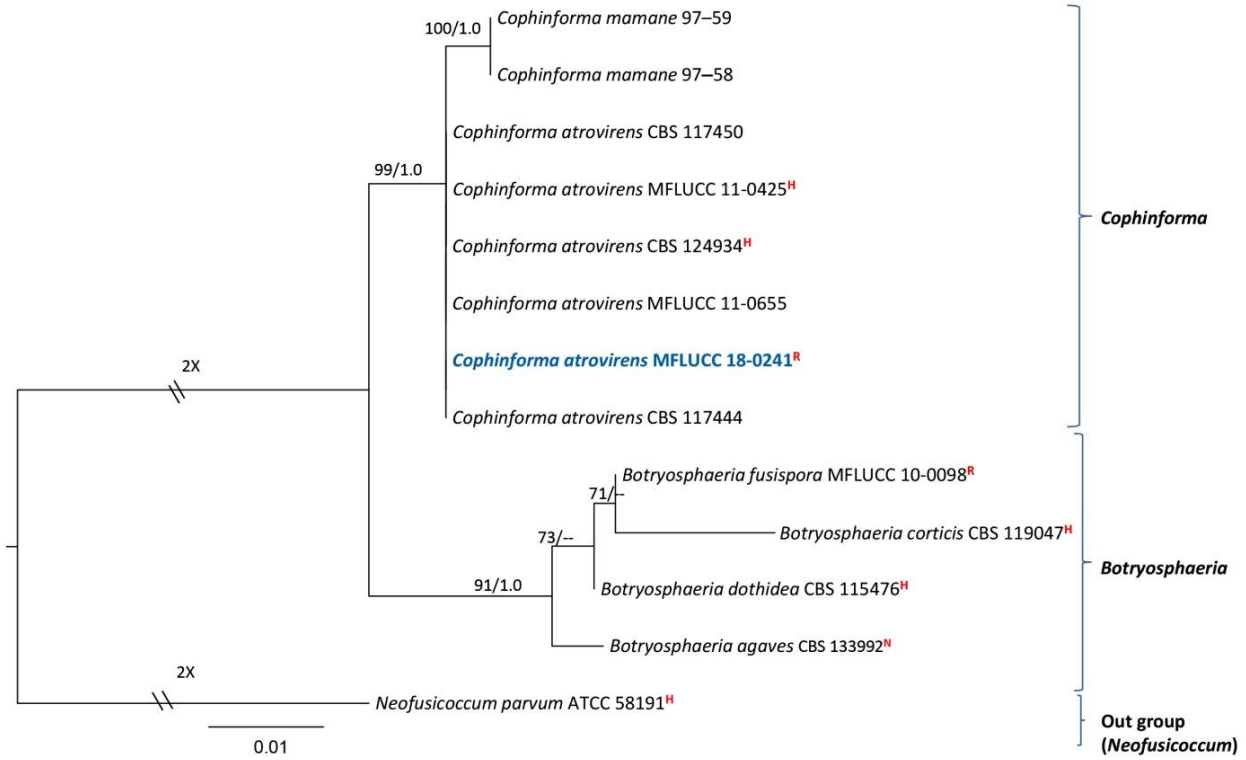


Figure 110 – Phylogram generated from maximum likelihood analysis based on combined ITS partial sequence data. Thirteen strains are included in the sequence analyses that comprise 560 characters including alignment gaps. *Neofusicoccum parvum* (ATCC 58191) was used as the outgroup taxon. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -1101.021888 is presented. The matrix had 82 distinct

alignment patterns, with 5.88% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.218330, C = 0.296118, G = 0.255108, T = 0.230444; substitution rates AC = 1.091606, AG = 3.291473, AT = 2.663012, CG = 2.340074, CT = 11.299261, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype, neotype and reference specimens are indicated in red superscript ^{H}, ^{N} and ^{R} respectively.

73. *Cophinforma atrovirens* (Mehl & Slippers) A. Alves & A.J.L. Phillips, Studies in Mycology 76: 80 (2013) Fig. 111

≡*Fusicoccum atrovirens* Mehl & Slippers, Mycologia 103: 543 (2011)

=*Cophinforma eucalypti* Doilom, J.K. Liu & K.D. Hyde, Fungal Diversity 57:174 (2012)

Facesoffungi number: FoF05290

Saprobic or *pathogenic* on branches or pod of *Ailanthus* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 78–100 µm high × 82–105 µm diam. ($\bar{x}$ = 85 × 90 µm; n = 10), on host seed pod, superficial, multilocular, dark brown to black, eustromatic, complex, effuse, globose, with wall composed of two layers, an outer layer of thick-walled dark brown cells of *textura angularis*, and inner layer of thin-walled hyaline *textura angularis* cells. *Conidiophores* absent. *Conidiogenous cells* 15–19 × 5–8 µm ($\bar{x}$ = 16 × 6 µm; n = 10), enteroblastic, annellidic, hyaline, smooth, cylindrical, proliferating percurrently to form one or two distinct annellations, or proliferating at the same level giving rise to periclinal thickenings. *Paraphyses* absent. *Conidia* 24–32 × 8–10 µm ($\bar{x}$ = 27 × 9 µm; n = 30), hyaline, ellipsoid to obovoid, unicellular, contents granular, asymmetric, smooth, thin-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies growing on MEA 50 mm diam. after 2 weeks at 18ºC, fluffy, initially white to olivaceous in the center, later becoming black on both sides.

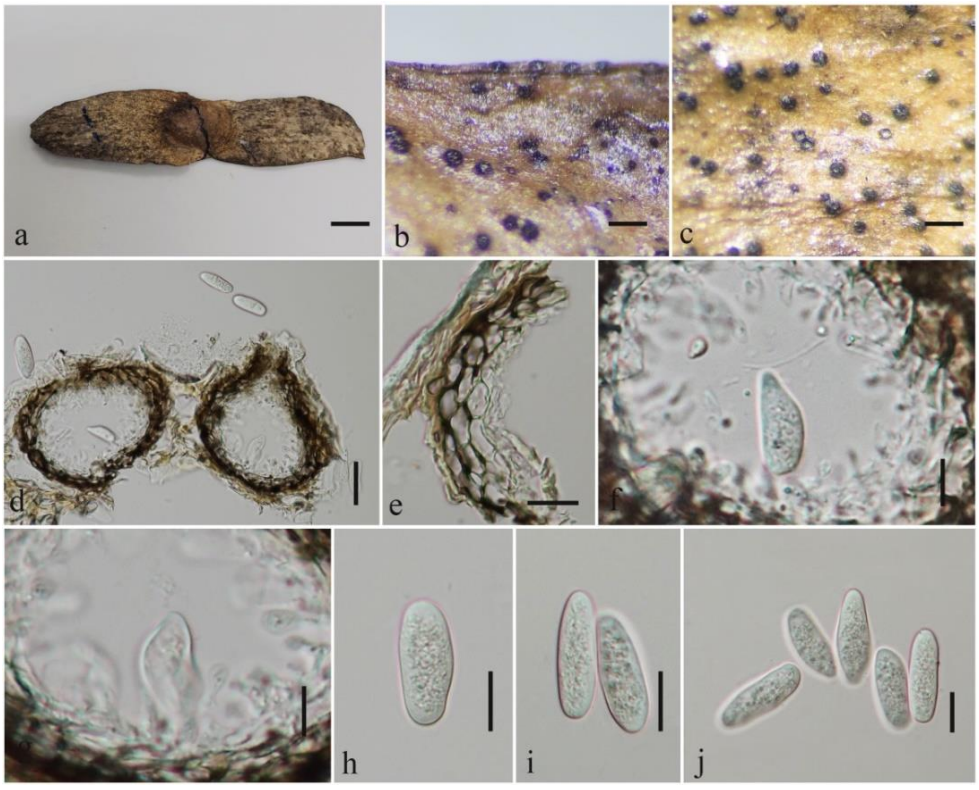


Figure 111 – *Cophinforma atrovirens* (MFLU 18–2179). a *Ailanthus* sp. pod. b, c Conidiomata on host surface. d Section through conidiomata. e Conidioma wall. f, g Conidiogenous cells. h–j Conidia. Scale bars: a = 1 cm, b, c = 200 µm, d = 20 µm, e–j = 10 µm.

Material examined – THAILAND, Phrae Province (18˚ 22' 9" N, 100˚ 21' 12"), on fallen pod of *Ailanthus* sp. (Simaroubaceae), 10 January 2018, S.C. Jayasiri, C 411 (MFLU 18–2179, new host record), living culture MFLUCC 18–0241, KUMCC 18–0224.

GenBank numbers – SSU: MK347889, ITS: MK347782, LSU: MK348000, *tef1*: MK340865

Notes – Species in this genus are recognized mainly based on phylogenetic data and for *Cophinforma mamane* only ITS sequence data are available (Phillips et al. 2013). Our strain groups well with other *C. atrovirens* strains in GenBank (Fig. 110). Therefore, we introduce a new host record for *C. atrovirens*, i.e. seed pods of *Ailanthus* sp. This is the second record of *C. atrovirens* from Thailand. *Cophinforma atrovirens* is reported as a saprobe or pathogen on various plant hosts, namely *Acacia mangium*, *Dimocarpus longan*, *Eucalyptus hybrid*, *Eucalyptus* sp., *E. urophylla* and *Pterocarpus angolensis* from China, South Africa, Thailand and Venezuela (Mohali et al. 2007, Mehl et al. 2011, Liu et al. 2012, Xu et al. 2015, Li et al. 2018). In most of these reports *C. atrovirens* was regarded as a pathogen. We report *C. atrovirens* as a saprobe from *Ailanthus* sp. (Simaroubaceae).

Figure 112 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1* and *tub2* partial sequence data. Forty-seven strains were included in the sequence analysis, which comprise 1308 characters including alignment gaps. *Lasiodiplodia theobromae* (CBS 164.96) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -4780.098792 is presented. The matrix had 394 distinct alignment patterns, with 18.09% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.205692, C = 0.307983, G = 0.260318, T = 0.226007; substitution rates AC = 1.026040, AG = 3.116482, AT = 1.028957, CG = 1.577387, CT = 4.393616, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue. Strains isolated from the epitype, holotype, isotype, neotype and reference specimens are indicated in red superscript ^{E}, ^{H}, ^{I}, ^{N} and ^{R} respectively.

Diplodia Fr., in Montagne, Ann. Sci. Nat., Bot., 2e Sér., 1:302 (1834)

This genus comprises 31 species based of the molecular and morphological data (Dissanayake et al. 2016, Linaldeddu et al. 2016, Yang et al. 2017). We add a new species and a new host record (Fig. 113).

74. *Diplodia magnoliigena* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 113

Index Fungorum number: IF555579; Facesoffungi number: FoF05291

Holotype – MFLU 18–2214

Etymology – Referring to the host genus on which the fungus was collected, *Magnolia* (Magnoliaceae).

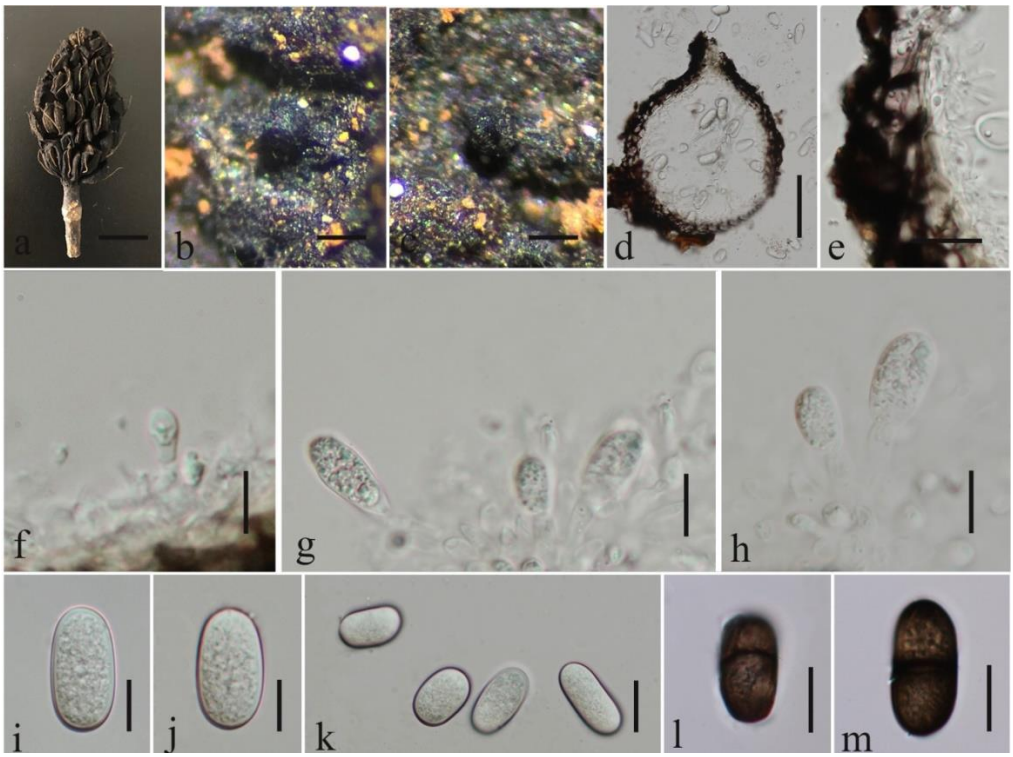


Figure 113 – *Diplodia magnoliigena* (MFLU 18–2214, holotype). a Host cone. b, c Conidiomata on host surface. d Section through conidioma. e Conidioma wall. f–h Conidiogenous cells. i–m Conidia. Scale bars: a = 1 cm, b, c = 200 µm, d = 100 µm, e–h, k–m = 20 µm, i, j = 10 µm.

Saprobic on cone of *Magnolia grandiflora*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 190–210 µm high × 182–212 µm diam. ($\bar{x}$ = 205 × 198 µm; n = 10),

solitary, partly immersed, partially erumpent when mature, dark brown to black, more or less globose, with wall composed of two layers; an outer layer of dark brown, thick-walled cells of *textura angularis* and an inner layer of thin-walled hyaline cells. *Ostiole* 55–65 μm high ($\bar{x}$ = 62 μm; n = 10), central, circular, papillate. *Conidiophores* absent. *Conidiogenous cells* 9–15 × 2–3 μm ($\bar{x}$ = 13 × 2.5 μm; n = 20), holoblastic, integrated, annellidic, hyaline, cylindrical, smooth, indeterminate, proliferating percurrently to form one or two indistinct annellations. *Conidia* 26–30 × 12–14 μm ($\bar{x}$ = 28 × 12.5 μm; n = 30), hyaline and aseptate at first, becoming dark brown and 1-septate, oblong to ovoid, straight, both ends broadly rounded, smooth, thick-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies growing on MEA reaching 40 mm diam. after 2 weeks at 18ºC, with fluffy mycelium, initially white to amber in the centre, after two weeks turning dark amber, white to dark amber, olivaceous with age; reverse submerged mycelium, first yellow, with age dark amber, almost olivaceous, and with age olivaceous center.

Material examined – CHINA, Yunnan Province, Kunming Institute, on fallen cone of *Magnolia grandiflora* (Magnoliaceae), 15 May 2018, S.C. Jayasiri, C 458 (MFLU 18–2214, holotype), ex-type living culture MFLUCC 18–1554, KUMCC 18–0236.

GenBank numbers – SSU: MK347915, ITS: MK347807, LSU: MK348026, *tub2*: MK412873

Notes – *Diplodia magnoliigena* groups sister to *D. mutila* and *Diplodia pyri* with high support (Fig. 112) but differs morphologically (Fig. 113) from the latter by having dark brown, 1-septate, longer conidia and the conidiomatal wall consists of two layers. *Diplodia mutila* is characterized by short conidia, which are rarely pale brown, and a three-layered peridium (Phillips et al. 2013). In addition, these two species can be distinguished by 13 (4.1) and 7 (1.8%) base pair differences in *tef1* and *tub2* gene regions respectively. Confirmed hosts for the *D. mutila* are *Chamaecyparis lawsoniana*, *Fraxinus*, *Malus*, *Populus*, *Taxus baccata* and *Vitis vinifera* (Phillips et al. 2013) together with a recent record on *Juglans regia* (Díaz et al. 2018).

75. *Diplodia sapinea* (Fr.) Fuckel, Jb. nassau. Ver. Naturk. 23–24: 393 (1870) Fig. 114

Facesoffungi number: FoF05292

Saprobic on cone of *Pinus* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 240–550 μm high × 300–500 μm diam. ($\bar{x}$ = 385 × 445 μm, n = 10), pycnidial, stromatic, globose, immersed, sometimes appearing superficial, separate or aggregated, dark brown to black, unilocular. *Conidiomata wall* 30–60 μm wide ($\bar{x}$ = 47 μm; n = 10), 6–8 layered, with outer wall of dark brown, thick-walled cells of *textura angularis*, with wall cells darker around the circular, central ostiole. *Conidiophores* absent. *Conidiogenous cells* arising from inner wall of the locule. *Conidia* 28–33 × 11–16 μm ($\bar{x}$ = 30 × 14 μm; n = 10), dark brown, oblong to clavate, straight to slightly curved, at first aseptate, when old 1-septate. *Spermatogenous cells* 2.5–3.5 × 2–3.5 μm ($\bar{x}$ = 3 × 3 μm; n = 20), holoblastic or proliferating via phialides with periclinal thickenings, hyaline, smooth, cylindrical. *Spermatia* 3.5–5.5 × 1.5–2.5 μm ($\bar{x}$ = 4.7 × 2 μm; n = 20), hyaline, cylindrical with rounded ends, smooth, aseptate.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies growing on MEA 40 mm diam. after 4 weeks at 18ºC, initially off white to grey, when mature becoming black, reverse grey to black.

Material examined – CHINA, Guizhou Province, on decaying cone of *Pinus* sp. (Pinaceae), 25 May 2016, S.C. Jayasiri, C 140 (MFLU 18–2090, KUN-HKAS 102410), living culture MFLUCC 18–1542, KUMCC 18–0237.

GenBank numbers – SSU: MK347824, ITS: MK347719, LSU: MK347933, *tef1*: MK340866, *tub2*: MK412872

Notes – Our isolate clustered with other *Diplodia sapinea* strains (Fig. 112). Base pair differences between our isolate and *D. sapinea* (CBS 109725, CBS 393.84) are 1 and 3 respectively for ITS and *tub2* and no base pair differences for *tef1*. Morphological characters could not be described clearly because the sample was very dry and conidia were not observed in culture. However, we obtained spermatia (Fig. 114). *Diplodia sapinea* has been recorded worldwide,

especially from *Pinus* species as a pathogen (Palmer et al. 1987); in this study it was also isolated it from a pine cone in China, but as a saprobe. Other host species associated with *D. sapinea* include *Abies*, *Larix*, *Picea*, *Thuja* and *Pseudotsuga* (Palmer et al. 1987, Phillips et al. 2013). Considering these features, we introduce another strain of *Diplodia sapinea* with spermatia in culture.

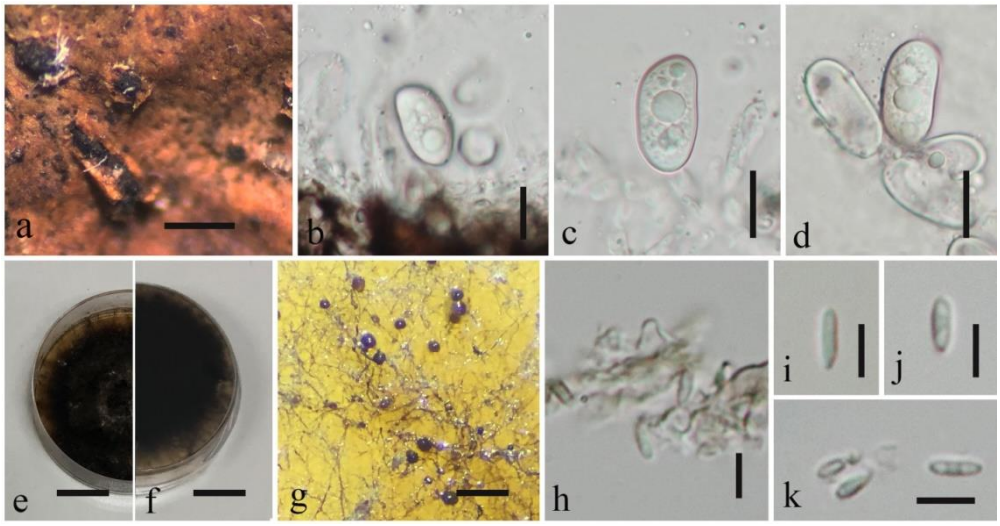


Figure 114 – *Diplodia sapinea* (MFLU 18–2090). a Conidiomata on host surface. b, c Conidiogenous cells. d Conidia. e, f Top and reverse view of culture. g Conidimata in culture. h Spermatogenous cells. i–k Spermatia. Scale bars: a = 200 μm, b–e = 20 μm, f, g = 1 cm, i–l = 5 μm.

Dothiorella Sacc., Michelia 2 (6): 5 (1880)

Based on the most recent study, *Dothiorella* contains 40 species based on molecular and morphological data (Dissanayake et al. 2016, 2017, Yang et al. 2017, You et al. 2017). Yang et al. (2017) concluded that the most useful gene regions for separation of species are ITS and *tef1*.

76. *Dothiorella lampangensis* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 116

Index Fungorum number: IF555580; Facesoffungi number: FoF05293

Holotype – MFLU 18–2145

Etymology – Referring to the place where the specimen was collected, Lampang Province (Thailand).

Saprobic on an unidentified wild fruit. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 265–320 μm high × 260–380 μm diam. ($\bar{x}$ = 295 × 274 μm; n = 10), pycnidial, stromatic, mostly superficial, dark brown to black, globose, solitary, occasionally covered by mycelium. *Conidiomata wall* 40–65 μm wide ($\bar{x}$ = 58 μm; n = 20). *Conidiophores* absent. *Conidiogenous cells* 11–22 × 3–8 μm ($\bar{x}$ = 18.5 × 5.2 μm, n = 20), holoblastic, hyaline, smooth, cylindrical, sometimes slightly swollen at the base. *Conidia* 22–28 × 9–11 ($\bar{x}$ = 25 × 10 μm; n = 30), initially hyaline and aseptate, when mature becoming yellowish brown, orange to dark brown, asymmetric, ellipsoid, obtuse at apex, truncate at base, 1-septate.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies growing on MEA attaining 70 mm diam. after 2 weeks at 18°C, becoming pale olivaceous-grey to dark olivaceous-grey at the surface, and yellowish brown to iron-grey in the reverse, with irregular edges.

Material examined – THAILAND, Lampang Province (19° 6′ 23″ N, 99° 41′ 26″ E), on fallen fruit pericarp of Rutaceae, 18 August 2017, S.C. Jayasiri, C 322 (MFLU 18–2145, holotype; KUN-HKAS102425, isotype), ex-type living culture, MFLUCC 18–0232, KUMCC 18–0239.

GenBank numbers – SSU: MK347864, ITS: MK347758, *tef1*: MK340869, *tub2*: MK412874

Notes – *Dothiorella lampangensis* lies in a clade sister to *D. brevicollis* (CBS 130411) with high bootstrap support (97% MLBS/ 1.0 BYPP, Fig. 115). Base pair differences between these two species are 5 (1.1%) and 18 (4.9%) in ITS and *tub2* gene sequences. Morphologically, *D.*

lampangensis differs from *D. brevicollis* in having asymmetric conidia with obtuse apex and truncate base (Jami et al. 2012, Phillips et al. 2013). *Dothiorella brevicollis* was isolated from healthy wood of *Acacia karroo* (Fabaceae) from South Africa, whereas *D. lampangensis* was isolated from a decaying fruit in Thailand. *Dothiorella lampangensis* clades close to *D. tectonae* with high support (83% MLBS/ 0.95 BYPP, Fig. 115). Base pair differences between these two species are 7 (1.5%), 17 (8.5%) and 20 (5.2%) respectively for ITS, *tef1* and *tub2* gene regions. *Dothiorella lampangensis* has longer conidia than *D. tectonae* (22–28 µm vs. 21–22 µm) and lacks irregular striations on the surface (Fig. 116).

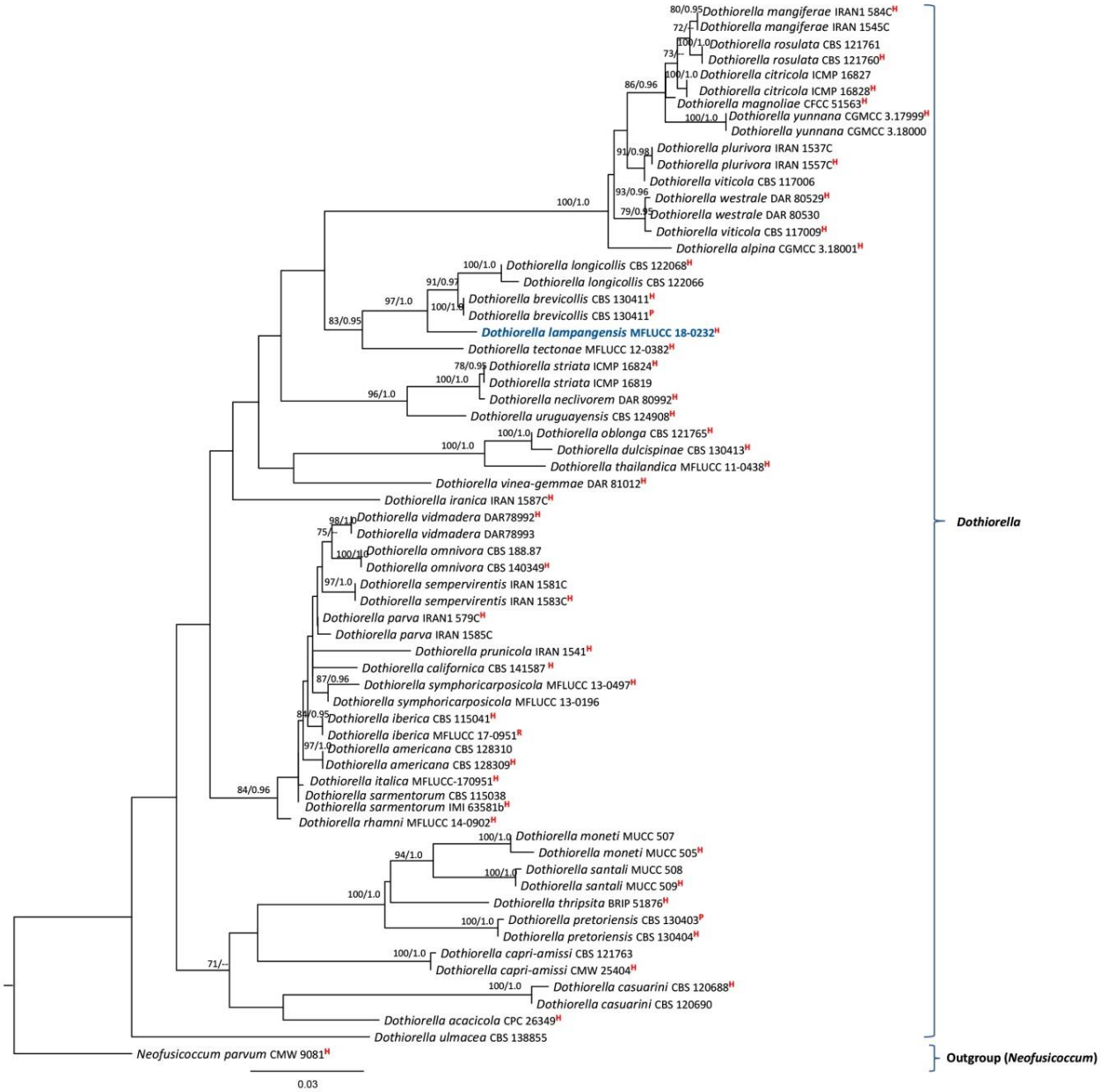


Figure 115 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1* and *tub2* partial sequence data. Sixtythree strains were included in the sequence analysis, which comprised 1184 characters including alignment gaps. *Neofusicoccum parvum* (CMW 9081) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -5766.079927 is presented. The matrix had 442 distinct alignment patterns, with 23.28% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.207748, C = 0.311193, G =

0.249528, T = 0.231530; substitution rates AC = 1.306974, AG = 1.985424, AT = 1.310930, CG = 1.254756, CT = 4.360996, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype, paratype and reference specimens are indicated in red superscript ^{H}, ^{P} and ^{R} respectively.

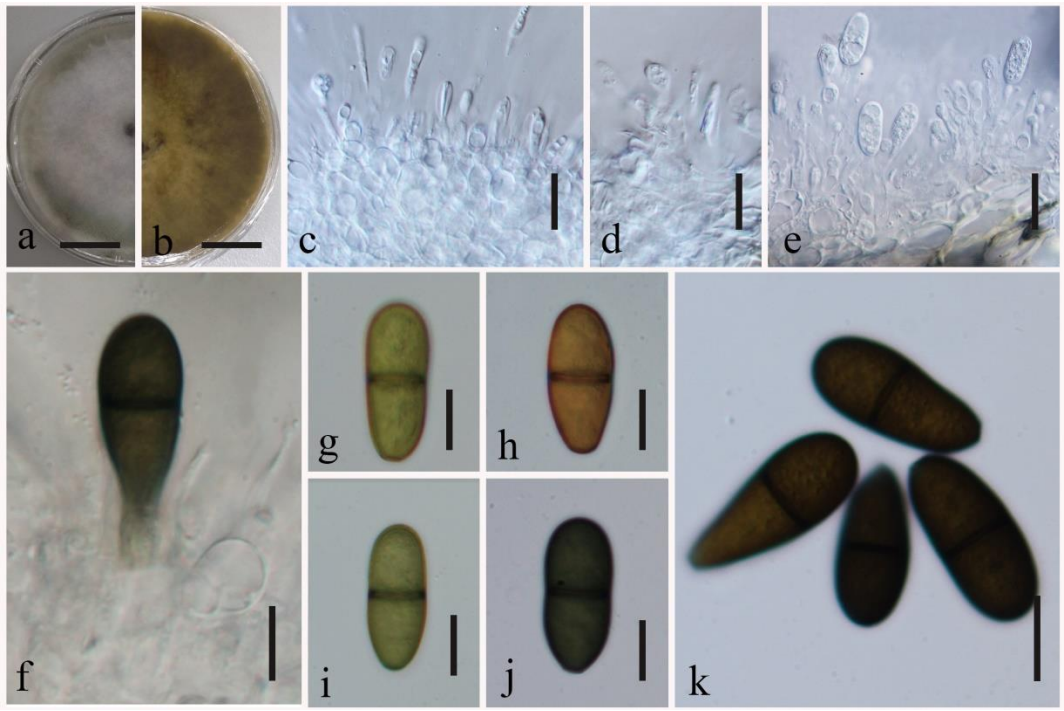


Figure 116 – *Dothiorella lampangensis* (MFLU 18–2145, holotype). a, b Top and reverse view of culture. c–f Conidiogenous cells. g–k Conidia. Scale bars: a, b = 1 cm, c–e = 20 μm, f–k = 10 μm.

Lasiodiplodia Ellis & Everh., Botanical Gazette Crawfordsville 21: 92 (1896)

The latest revisions accept 36 species in this genus based of the molecular and morphological data (Dissanayake et al. 2016, Dou et al. 2017a, b, Yang et al. 2017). Previous studies have shown that morphology alone is not a reliable character for species differentiation and species can be recognized only from combined ITS and *tef1* sequence data (Phillips et al. 2013, Slippers et al. 2014). Yang et al. 2017 found that *tub2* is the most useful gene for separation of species. We used multigene phylogenetic analyses (ITS, *tef1* and *tub2* genes) and established two novel species (Fig. 117).

77. *Lasiodiplodia avicenniarum* Jayasiri, E.B.G. Jones & K.D. Hyde sp. nov. Fig. 118

Index Fungorum number: IF555581; Facesoffungi number: FoF05294

Holotype – MFLU 18–2173

Etymology – Referring to the host genus on which the fungus was collected, *Avicennia* (Acanthaceae).

Saprobic on fruit of *Avicennia marina.* Sexual morph: Not determined. Asexual morph: Coelomycetous. *Conidiomata* 180–220 μm high × 160–180 μm diam. ($\bar{x}$ = 213 × 174 μm; n = 10), pycnidial, solitary to gregarious, occasionally confluent, formed in uni- or multi-loculate stromata, immersed, becoming erumpent at maturity, ostiolate. *Ostiole* papillate, central, circular. *Conidiomata wall* 40–50 μm wide ($\bar{x}$ = 43 μm; n = 20), composed of thick-walled, brown cells of *textura angularis*; inner layer thin, hyaline. *Hamathecium* 2–3 μm wide ($\bar{x}$ = 2.3 μm; n = 30), hyaline, cylindrical, aseptate, not branched, round at apex. *Conidiophores* usually reduced to conidiogenous cells. *Conidiogenous cells* 15–18 × 5–8 μm ($\bar{x}$ = 17 × 7 μm; n = 30), phialidic or annellidic, hyaline, cylindrical, discrete or occasionally integrated, determinate or proliferating at

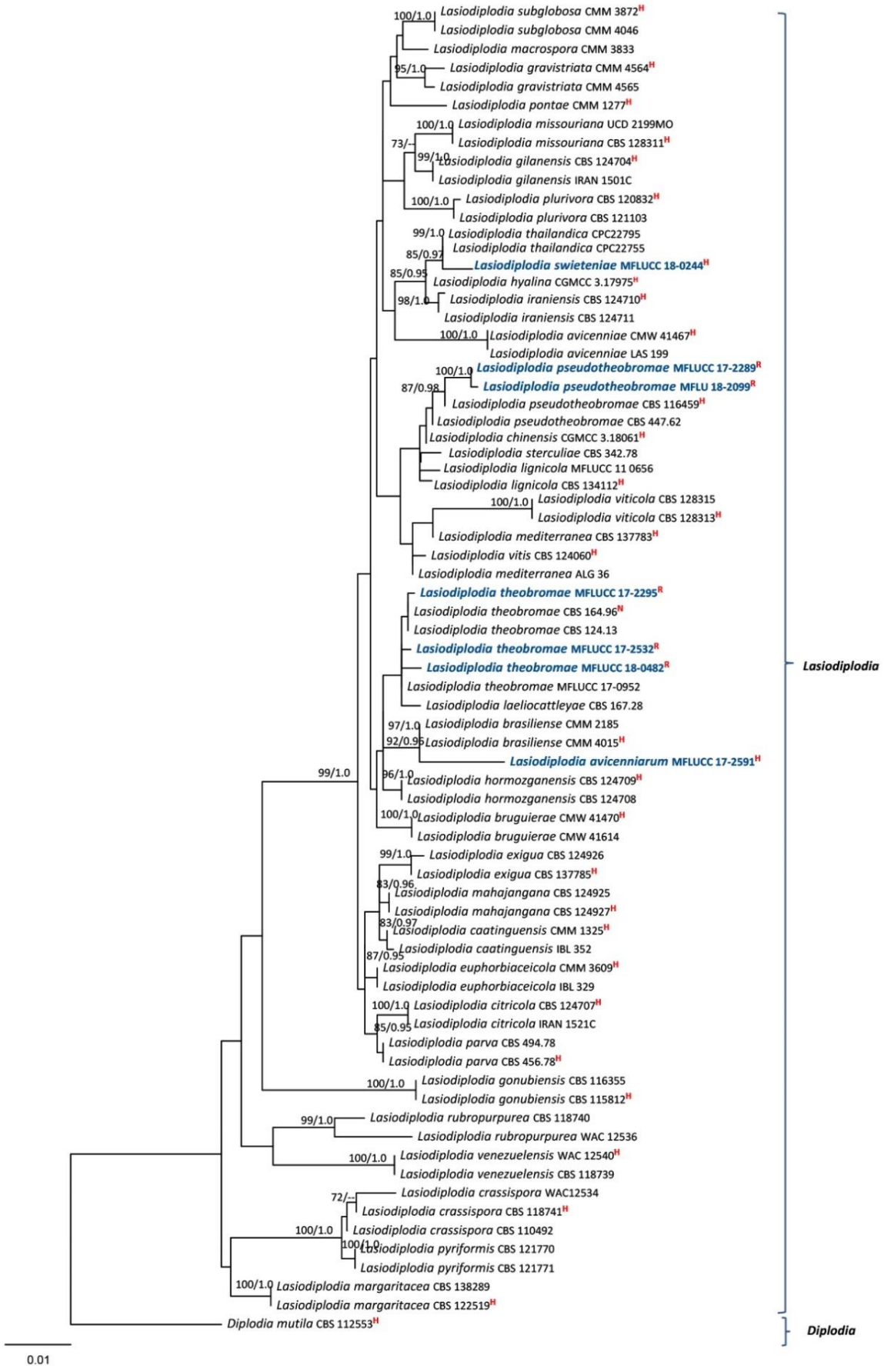


Figure 117 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1* and *tub2* partial sequence data. Sixty-eight strains were included in the sequence analysis,

which comprise 829 characters with gaps. *Diplodia mutila* (CBS 112553) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -3533.673744 is presented. The matrix had 391 distinct alignment patterns, with 15.23% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.209713, C = 0.303667, G = 0.256066, T = 0.230553; substitution rates AC = 1.085553, AG = 2.917602, AT = 1.419541, CG = 1.096504, CT = 4.741431, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in bold and blue. Strains isolated from the holotype, neotype and reference specimens are indicated in red superscript ^{H}, ^{N} and ^{R} respectively.

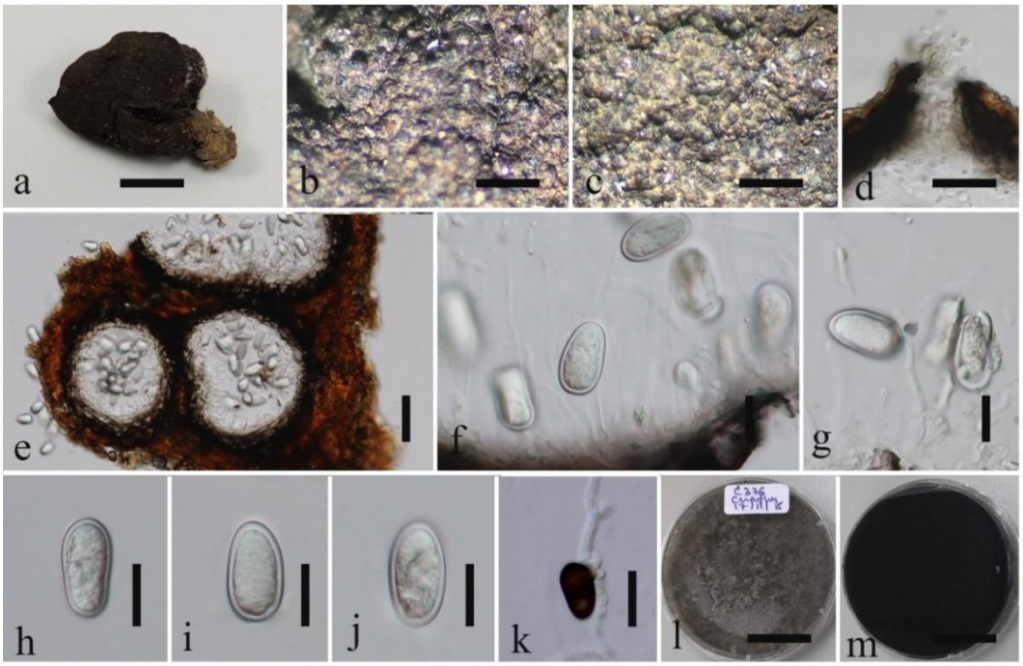


Figure 118 – *Lasiodiplodia avicenniarum* (MFLU 18–2173, holotype). a Fruit of the host, *Avicennia marina*. b, c Conidiomata on host surface. d Ostiole. e Section through conidiomata. f, g Conidiogenous cells and immature conidia. h-j Conidia. k Germinated conidium. l Top view of culture. m Reverse view of culture. Scale bars: a, l, m = 1 cm, b, c = 500 μm, d, e = 50 μm, f–j = 20 μm, k = 30 μm.

the same level giving rise to periclinal thickenings, or proliferating percurrently. *Conidia* 26–32 × 11–14 μm ($\bar{x}$ = 28 × 12 μm; n = 30), initially hyaline, aseptate, at maturity 1-septate and dark brown, ellipsoidal, straight, both ends, broadly rounded, thick-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced at end of conidia. Colonies growing on MEA, reaching 70 mm diam. after 2 weeks at 18ºC. Colonies with aerial mycelia, becoming smoke grey to olivaceous-grey at surface; reverse dark grey to black.

Material examined – THAILAND, Krabi Province, Mueang Krabi District, on decaying fruit pericarp of *Avicennia marina* (Acanthaceae), 30 August 2017, S.C. Jayasiri, C 376 (MFLU 18–2173, holotype), ex-type living culture MFLUCC17–2591, KUMCC 18–0250.

GenBank numbers: SSU: MK347884, ITS: MK347777, LSU: MK347994, *tef1*: MK340867

Notes – *Lasiodiplodia avicenniarum* lies in a clade sister to *L. brasiliense* (CMM 4015 and CMM 2185) with high statistical support (89% MLBS/ 0.96 BYPP, Fig. 118). There are 12 (2.5%) base pair differences in ITS regions between these two species. In addition, *L. avicenniarum* differs from *L. brasiliense* in having multi-loculate stromata and lacking longitudinal striations on conidial wall (Netto et al. 2014). However, *Lasiodiplodia avicenniarum* and *L. brasiliense* have similar

morphology of conidiogenous cells and conidia (Netto et al. 2014).

78. *Lasiodiplodia pseudotheobromae* A.J.L. Phillips, A. Alves & Crous, Fungal Diversity 28: 8 (2008) Fig. 119

Saprobic and *pathogenic* on twigs, fruits and seed pods. Sexual morph: see Tennakoon et al. (2016). Asexual morph: Coelomycetous. *Conidiomata* 320–350 µm high × 215–245 µm diam. ($\bar{x}$ = 332 × 232 µm n = 10), pycnidial, solitary to gregarious, occasionally confluent, formed in uni- or multi-loculate stromata, immersed, becoming erumpent at maturity, ostiolate. *Ostiole* papillate, central, circular. *Conidiomata walls* 26–55 µm wide, composed of thick-walled, brown cells of *textura angularis*; inner layer thin, hyaline. *Conidiophores* usually reduced to conidiogenous cells, when present hyaline, simple, occasionally septate, rarely branched, cylindrical, arising from cells lining the pycnidial cavity. *Conidiogenous cells* 15–19 × 4–8 ($\bar{x}$ = 17 × 6.5 µm, n = 30), phialidic or annellidic, hyaline, cylindrical, discrete or occasionally integrated, determinate or proliferating at the same level giving rise to periclinal thickenings, or proliferating percurrently and forming two or three annellations. *Conidia* 23–30 × 11–13 ($\bar{x}$ = 28 × 12 µm, n = 30), initially hyaline, aseptate, mature 1-septate and pale brown to dark brown, oblong to ovoid, straight, both ends, broadly rounded, thin-walled, with longitudinal striations.

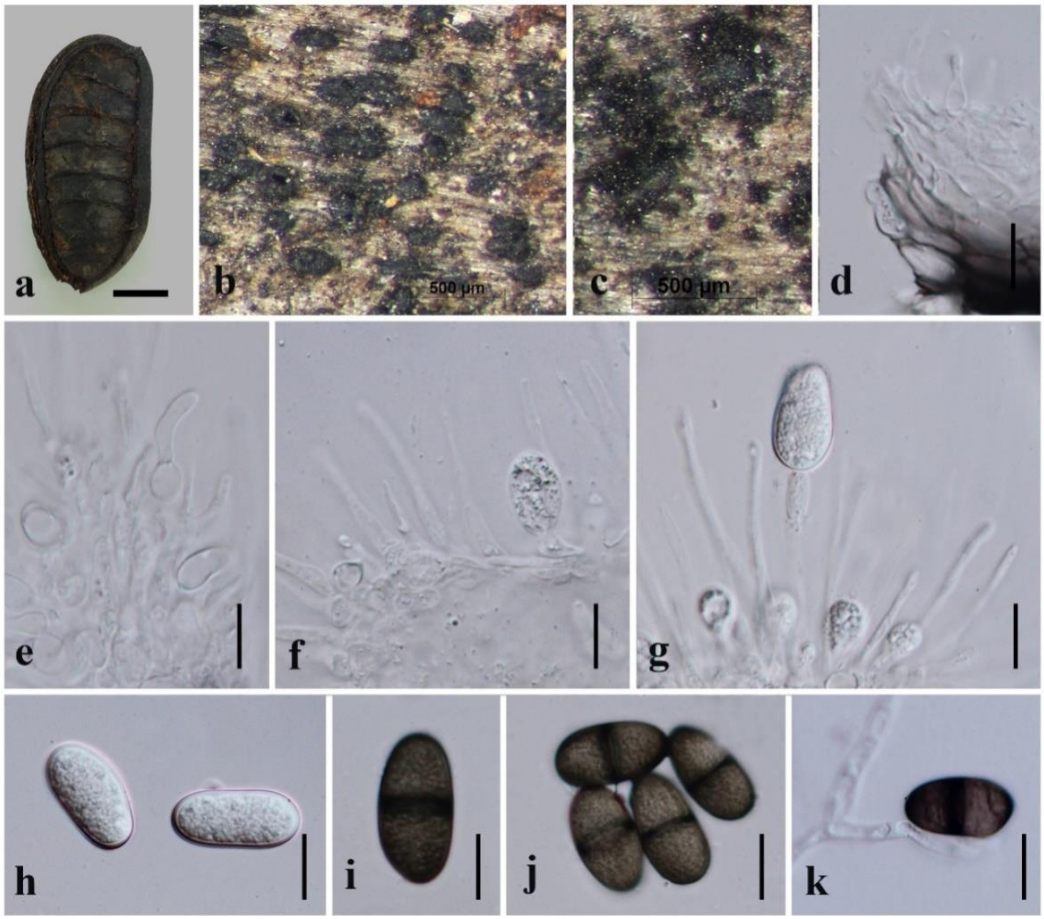


Figure 119 – *Lasiodiplodia pseudotheobromae* (MFLU 18–2128). a Part of *Afzelia xylocarpa* seed pod. b, c Conidiomata on host surface. d–g Conidiogenous cells. h–j Conidia k Germinated conidium. Scale bars: b = 1 cm, d = 500 µm, f–h = 10 µm.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced from end of conidia. Colonies growing on MEA, reaching 60 mm diam. after 2 weeks at 18ºC. Colonies with aerial mycelia, aerial mycelia becoming smoke grey to olivaceous-grey at the surface and reverse dark grey to black.

Material examined – THAILAND, Payao Province, Amphoe Phu Sang, on decaying pod septum of *Afzelia xylocarpa* (Fabaceae), 20 July 2017, S.C. Jayasiri, C 277 (MFLU 18–2128, new host record); living culture MFLUCC 17–2289, KUMCC 18–0249; THAILAND, Mae Hong Son Province, on decaying fruits pericarp of *Quercus* sp. (Fagaceae), 22 September 2016, S.C. Jayasiri, C 197 (MFLU 18–2099, new host record).

GenBank numbers – MFLUCC 17–2289: SSU: MK347852, ITS: MK347745, LSU: MK347962, *tef1*: MK340871, *tub2*: MK412875; MFLU 18–2099: SSU: MK347831, ITS: MK347725, LSU: MK347940, *tub2*: MK412876

Notes – Phylogenetically our two strains clade together with other reported strains of *Lasiodiplodia pseudotheobromae* (Fig. 117). Therefore we herein introduce a new record of *L. pseudotheobromae,* from a decaying pod of *Afzelia xylocarpa* and fruits of *Quercus* sp. in Thailand. *Lasiodiplodia pseudotheobromae* has been previously reported from many host species (Alves et al. 2008, Correia et al. 2013 Pillay et al. 2013, Phillips et al. 2013, Sanchez et al. 2013, Sandoval-Marques et al. 2013a, Castro-Medina et al. 2014, Machado et al. 2014a, b, Mehl et al. 2014, Netto et al. 2014, Dissanayake et al. 2015a, Doilom et al. 2015, Li et al. 2015, Trakunyingcharoen et al. 2015b, Correia et al. 2016a, Li et al. 2016b, Rosado et al. 2016). There were two and one base pair differences between our two strains and CBS 116459/CBS 447.62, respectively, for *tef1* and *tub2* genes, but no difference in ITS.

79. *Lasiodiplodia swieteniae* Jayasiri, E.B.G. Jones & K.D. Hyde sp. nov. Fig. 120

Index Fungorum number: IF555582; Facesoffungi number: FoF05296

Holotype – MFLU 18–2188

Etymology – Referring to the host genus on which the fungus was collected, *Swietenia* (Meliaceae).

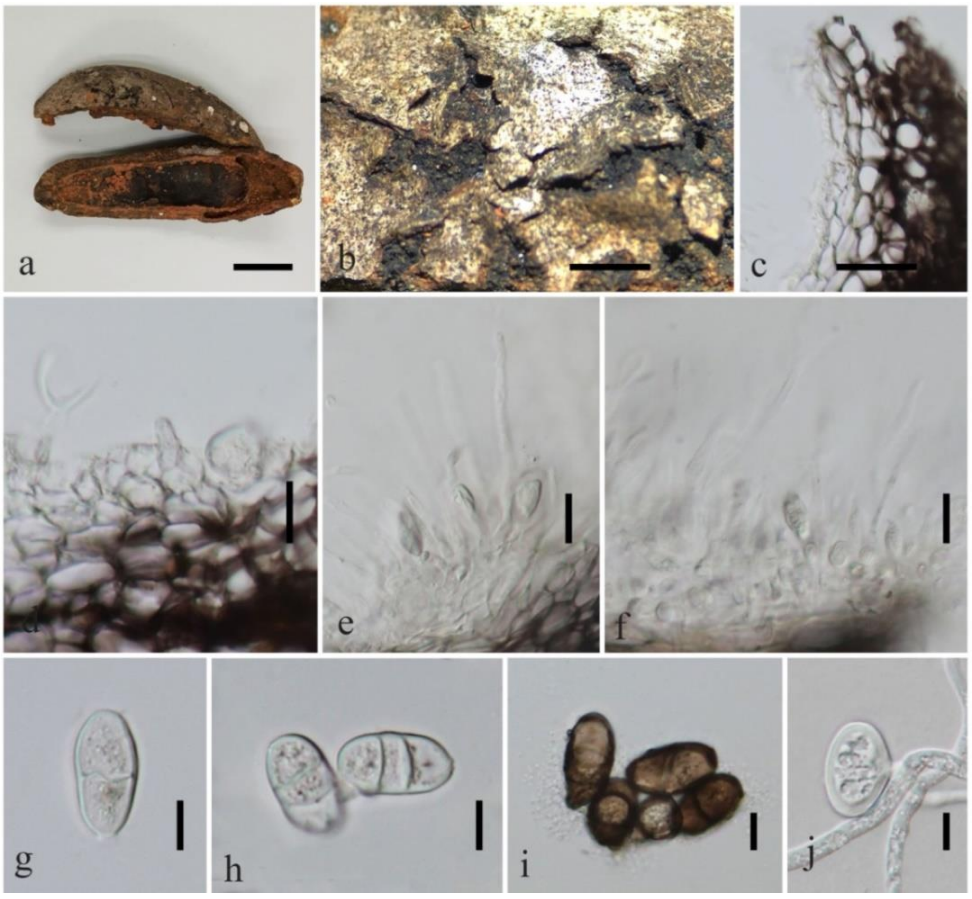


Figure 120 – *Lasiodiplodia swieteniae* (MFLU 18–2188, holotype). a Host fruit of *Swietenia* sp. b Conidiomata on host surface. c Conidioma wall. d–f Conidiogenous cells. g–i Conidia. j Germinated conidium. Scale bars: a = 1 cm, b = 500 μm, c = 20 μm, d–j = 10μm.

Saprobic on fruit of *Swietenia* sp. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 310–330 μm high × 300–370 μm diam. ($\bar{x}$ = 315 × 345 μm; n = 10), pycnidial, semi-immersed, solitary, rarely aggregated, dark brown to black, unilocular, with globose base. *Conidiomata wall* 33–51 μm wide ($\bar{x}$ = 46 μm; n = 20), outer layers composed of dark brown *textura angularis*, becoming thin-walled and hyaline toward the inner region; with brown, septate, hyphal hairs, with rounded tips covering the outer wall of fruiting body. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 11–13 × 7–8.5 μm ($\bar{x}$ = 12 × 7.5 μm; n = 20), hyaline, smooth, thin-walled, discrete, phialidic, proliferating percurrently, arising from hyaline inner conidiomatal wall. *Hamathecium* 2–3 μm wide ($\bar{x}$ = 2.3 μm; n = 30), hyaline, aseptate, smooth, thin-walled, cylindrical, originating from the hyaline inner cells of conidiomata wall, with basal cells slightly swollen and apical cells rounded at tips. *Conidia* 24–32 × 11–14 μm ($\bar{x}$ = 30 × 13 μm; n = 30), initially hyaline, mature conidia turning dark brown, ellipsoid, with granular content, 1–3 septate.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced from end of conidia. Colonies growing on MEA, reaching 60 mm diam. after 2 weeks at 18 ˚ C. Colonies with white fluffy mycelium, slightly dense and flattening at the centre, mycelium turning smoky-grey to olivaceous-grey, mycelium turning greenish olivaceous to black-olivaceous in reverse.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on decaying fruit pericarp of *Swietenia* sp. (Meliaceae), 15 January 2018, S.C. Jayasiri, C 425 (MFLU 18–2188, holotype; KUN-HKAS 102435, isotype), ex-type living culture MFLUCC 18–0244, KUMCC 18–0251.

GenBank numbers – SSU: MK347896, ITS: MK347789, LSU: MK348007, *tef1*: MK340870, *tub2*: MK412877

Notes – *Lasiodiplodia swieteniae* is in a clade sister to *L. thailandica* with high statistical support (83% MLBS/ 0.95 BYPP, Fig. 117) in multigene phylogenetic analysis of *tef1* and *tub2* genes. Base pair differences of the two species are 1 and 7 (2.0%) respectively, for *tef1* and *tub2* genes. Conidia of *L. swieteniae* differ from *L. thailandica* in having 1–3-septate, dark brown conidia without longitudinal striations (Trakunyingcharoen et al. 2015). Therefore, we introduce a new species based on molecular and morphological differences.

80. *Lasiodiplodia theobromae* (Pat.) Griffon & Maubl., Bulletin de la Société Mycologique de France 25: 57 (1909) Fig. 121

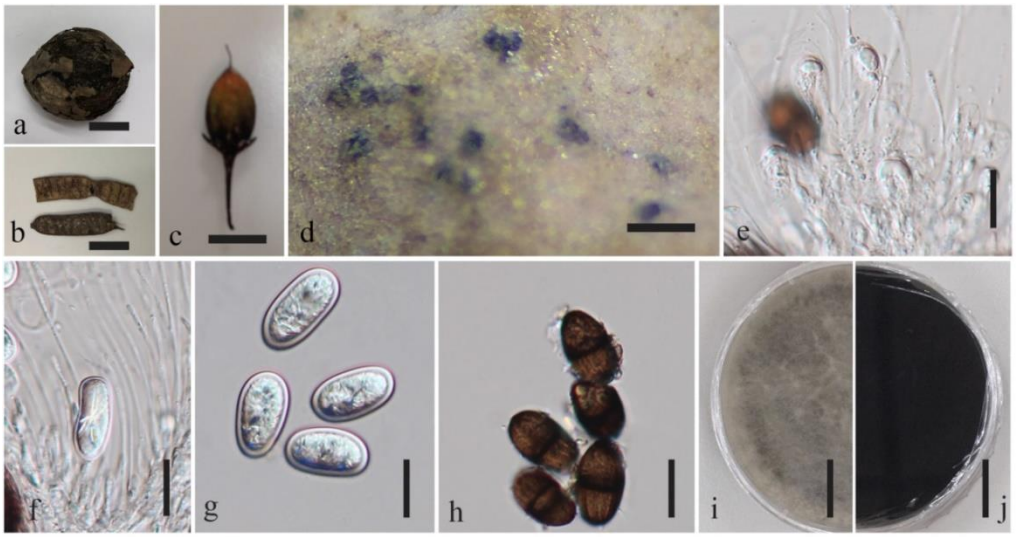


Figure 121 – *Lasiodiplodia theobromae* (MFLU 18–2139). a Host *Calophyllum inophyllum* fruit. b Host decaying *Acacia* sp. pods. c Host decaying fruit. d Conidiomata on host surface. e, f Conidiogenous cells. g, h Conidia. i Top view of culture. j Reverse view of culture. Scale bars: a–c, i, j = 1 cm, d = 200 μm, e–h = 20 μm.

Saprobic or *pathogenic* on wide host range. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 58–80 µm high × 74–90 µm diam. (74 × 80 µm; n = 10), pycnidial, semi-immersed, unilocular, solitary, scattered, globose or subglobose, dark brown. *Conidiomata wall* 12–27 µm wide ($\bar{x}$ = 21.6 µm; n = 20), outer layers dark brown to black, thick-walled, inner layers thin-walled, pale brown to hyaline, comprising 2–3 layers of dark brown cells of *textura angularis*. *Paraphyses* hyaline, septate, cylindrical, occasionally branched, ends rounded. *Conidiogenous cells* 19–23 × 7–8 µm ($\bar{x}$ = 21 × 7.5 µm; n = 20), phialidic, hyaline, cylindrical. *Conidia* 18–24 × 8–9 µm ($\bar{x}$ = 22 × 8.5 µm; n = 30), initially hyaline and aseptate when immature, becoming medianly 1-euseptate, dark brown, ellipsoid to obovoid, truncate or rounded at base, with longitudinal striations from apex to base, thick-walled.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced from end of conidia. Colonies growing on MEA, reaching 50–60 mm diam. after 2 weeks at 18ºC, with white fluffy mycelium, slightly dense and flattening at the centre, turn smoky-grey to olivaceous-grey with age, mycelium turning greenish olivaceous to black-olivaceous in reverse after 1 week.

Material examined – THAILAND, Lampang Province (19˚ 6' 23" N, 99˚ 41' 26" E), on decaying pod of *Acacia* sp. (Fabaceae), 18 August 2017, S.C. Jayasiri, C 311 (MFLU 18–2139, new record); living culture MFLUCC 17–2295, KUMCC 18–0254; THAILAND, Krabi Province (8˚ 2' 27" N, 98˚ 49' 5" E), on decaying fruit pericarp of *Calophyllum inophyllum* (Calophyllaceae), 31 August 2018, S.C. Jayasiri, C 345 (MFLU 18–2152, new host record); living culture, MFLUCC 17–2532, KUMCC 18–0253; THAILAND, Chiang Rai Province, Mae Fah Luang University, on decaying fruit pericarp of unknown plant, 24 January 2018, S.C. Jayasiri, C 443-B (MFLU 18–2193), living culture MFLUCC 18–0482, KUMCC 18–0252.

GenBank numbers – MFLUCC 17–2295: SSU: MK347860, ITS: MK347754, LSU: MK347971, *tef1*: MK340872, *tub2*: MK412878; MFLUCC 17–2532: SSU: MK347870, ITS: MK347763, LSU: MK347980, *tef1*: MK340873, *tub2*: MK412879; MFLUCC 18–0482: SSU: MK347900, ITS: MK347792, LSU: MK348011, *tef1*: MK340874

Notes – We isolated three strains of *Lasiodiplodia theobromae* from decaying wild fruits and pods. The holotype of this species could not be found and a neotype was designated (Phillips et al. 2013) from an unidentified fruit in New Guinea (CBS H-21411). This species has a wide host range in tropical and subtropical regions (Dissanayake 2016).

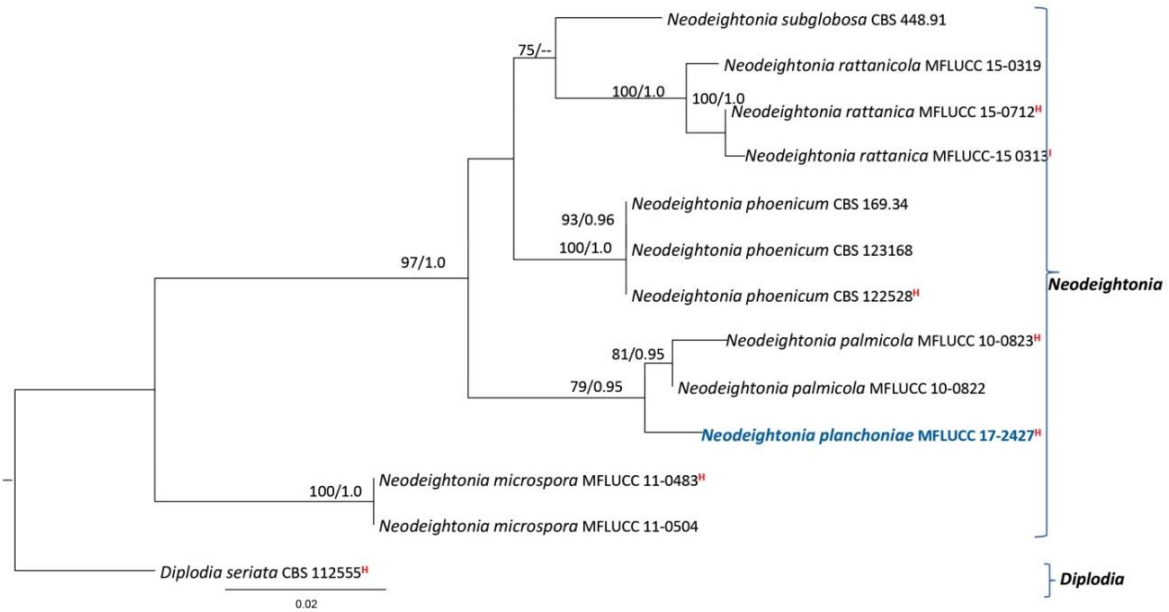


Figure 122 – Phylogram generated from maximum likelihood analysis based on combined ITS and *tef1* partial sequence data. Thirteen strains were included in the sequence analysis, which comprised 872 characters including alignment gaps. *Diplodia seriata* (CBS 112555) was used as

the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -1941.053640 is presented. The matrix had 132 distinct alignment patterns, with 13.53% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.201898, C = 0.303509, G = 0.274434, T = 0.220159; substitution rates AC = 2.133078, AG = 3.446620, AT = 1.016394, CG = 1.506886, CT = 5.661906, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolate is in blue. Strains isolated from the holotype and isotype specimens are indicated in red superscript ^{H} and ^{I} respectively.

We compared base pair differences of our three strains of *L. theobromae* with three other strains (CBS 124.13, CBS 164.96 and MFLUCC 17–0952). ITS sequences were identical for all six strains. However, there were 4, 1 and 1 base pair differences in strains MFLUCC 17–2295, MFLUCC 17–2532 and MFLUCC 18–0482, respectively, for *tef1* gene region. In addition, MFLUCC 18–0482 had 1 base pair difference with CBS 164.96 for *tub2* gene.

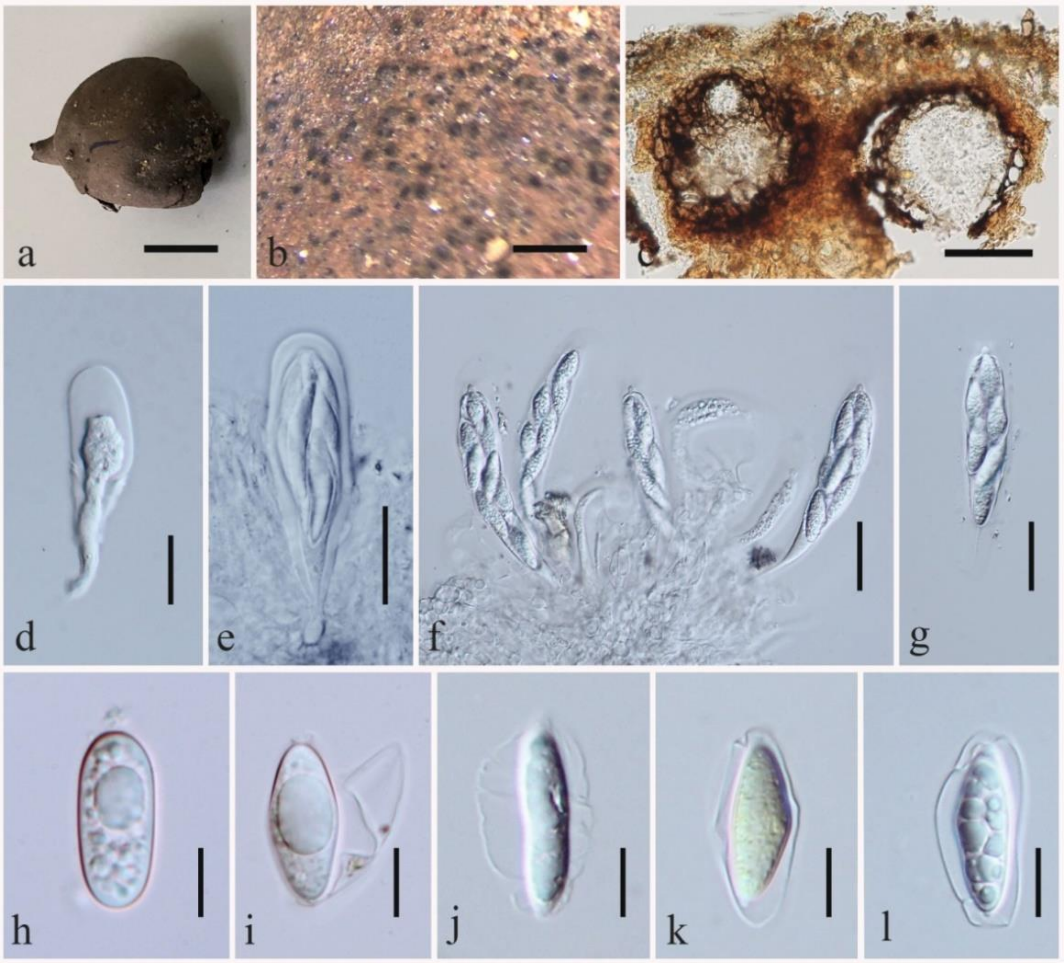


Figure 123 – *Neodeightonia planchoniae* (MFLU 18–2140, holotype). a Host pod. b View of ascomata on host surface. c Section through ascoma. d–g Asci. h–l Ascospores. Scale bars: a = 1 cm, b = 500 µm, c = 100 µm, d–g = 20 µm, h–l = 10 µm.

Neodeightonia in Punithalingam, Mycol. Pap. 19: 17 (1970) [1969]

This genus comprises six species namely *N. licuriensis* from *Syagrus coronate* (Adamčík et al. 2015), *N. palmicola* from *Arenga westerhoutii* (Liu et al. 2012), *N. phoenicum* from *Phoenix* sp. (Phillips et al. 2008, Ligoxigakis et al. 2013), *N. rattanica* from *Calamus* sp. (Konta et al. 2016a),

N. rattanicola from *Calamus* sp. (Konta et al. 2016a) and *N.subglobosa* from *Bambusa arundinacea* (Punithalingam 1970), with both pathogenic and saprobic species (Punithalingam 1970, Liu et al. 2010, Phillips et al. 2008, Ligoxigakis et al. 2013, Konta et al. 2016a). We add another species to this genus from decaying fruit of *Planchonia* sp. from Thailand (Fig. 122).

81. ***Neodeightonia planchoniae*** Jayasiri & K.D. Hyde, sp. nov. Fig. 123

Index Fungorum number: IF555583; Facesoffungi number: FoF05297

Holotype – MFLU 18–2140

Etymology – Referring to the host genus on which the fungus was collected, *Planchonia* (Lecythidaceae).

Saprobic on fruit of *Planchonia* sp. Sexual morph: *Ascomata* 175–210 × 182–250 μm ($\bar{x}$ = 190 × 220 μm; n = 10), immersed, dark brown to black, with a single aparaphysate locule, with wall composed of pseudoparenchymatous cells many layers thick, asci developing amongst partially disintegrating sterile thin-walled tissue in locule. Neck of ascostromata narrow, opening by an apical ostiole, formed by the disintegration of the central thin-walled cells. *Peridium* 28–60 μm wide ($\bar{x}$ = 42 μm; n = 20), dark brown, smooth, two cell layers of *textura angularis*. *Hamathecium* 1.5–2.5 μm wide ($\bar{x}$ = 1.9 μm, n = 30), Pseudoparaphyses, hyphae-like, septate, constricted at the septa. *Asci* 58–70 × 15–21 μm ($\bar{x}$ = 64 × 18 μm; n = 20), parallel, more or less separated from one another by stromatic tissue, clavate to cylindric-clavate, 8-spored, bitunicate with a thick endotunica. *Ascospores* 18–26 × 7–9 μm ($\bar{x}$ = 23 × 8 μm; n = 30), biseriate, hyaline to pale brown, oval to broadly ellipsoidal, when mature muriform, aseptate, with bipolar germ pores, immature with large guttule, surrounded by a thick mucilaginous sheath. Asexual morph: Undetermined.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced from ends of conidia. Colonies growing on MEA, reaching 50–60 mm diam. after 2 weeks at 18ºC. Colonies with aerial mycelia, becoming smoke grey to olivaceous-grey at the surface and reverse dark grey to black.

Material examined – THAILAND, Lampang Province (19˚ 6' 23" N, 99˚ 41' 26" E), on decaying fruit pericarp of *Planchonia* sp. (Lecythidaceae), 18 August 2017, S.C. Jayasiri, C 312 (MFLU 18–2140, holotype; MFLU 18–2141, isotype), ex-type living culture MFLUCC 17–2427, KUMCC 18–0260.

GenBank numbers – SSU: MK347861, ITS: MK347755, LSU: MK347972

Notes – Based on phylogenetic and morphological differences, a new species, *Neodeightonia planchoniae,* is introduced. *Neodeightonia planchoniae,* forms a sister clade to *N. palmicola* with high statistical support (79% MLBS/0.95 BYPP, Fig. 122). There are 8 (1.5%) base pair differences between *N. planchoniae* and *N. palmicola* in the ITS gene sequence. *tef1* gene sequences are not available for *N. palmicola* for comparison. *Neodeightonia palmicola* and *N. planchoniae* share many similar morphological characters e.g. ostiolate ascomata, clavate to cylindric-clavate asci with a thick endotunica, ascospores with bipolar germ pores and thick mucilaginous sheaths (Fig. 123). However, *N. palmicola* differs in having pale brown and muriform mature ascospores and a thin peridium. Taking these differences into account, we identify our strain as a new species.

Neofusicoccum Crous, Slippers & A.J.L. Phillips, Studies in Mycology 55: 247 (2006)

The genus *Neofusicoccum* includes some important plant pathogens, especially those associated with woody crop plant species (Phillips et al. 2013, Marin-Felix et al. 2017). Currently 37 species have been reported from this genus (Dissanayake 2016, Marin-Felix et al. 2017, Zhang et al. 2017, Li et al. 2018). *Neofusicoccum* is morphologically similar to *Botryosphaeria* but phylogenetically distinct (Phillips et al. 2013). Most species of *Neofusicoccum* are morphologically similar and are defined on ITS sequence data, often together with loci of other genes (Phillips et al. 2013). We introduce both morphs of the type species (*Neofusicoccum parvum*) on two different hosts from China (Fig. 124).

Figure 124 – Phylogram generated from maximum likelihood analysis based on combined ITS, *tef1* and *tub2* partial sequence data. Seventyeight strains are included in the sequence analysis, which comprised 1585 characters including alignment gaps. Two *Dothiorella* species were used as the outgroup taxa. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -5063.598833 is presented. The matrix had 423 distinct alignment patterns, with 16.48% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.205999, C = 0.308748, G = 0.265038, T = 0.220215; substitution rates AC = 1.211622, AG = 4.547892, AT = 0.800196, CG = 0.869036,

CT = 8.086004, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue. Strains isolated from the holotype and reference specimens are indicated in red superscript ^{H} and ^{R} respectively.

82. ***Neofusicoccum parvum*** (Pennycook & Samuels) Crous, Slippers & A.J.L. Phillips, Studies in Mycology 55: 248 (2006) Figs 125, 126

Facesoffungi number: FoF05298

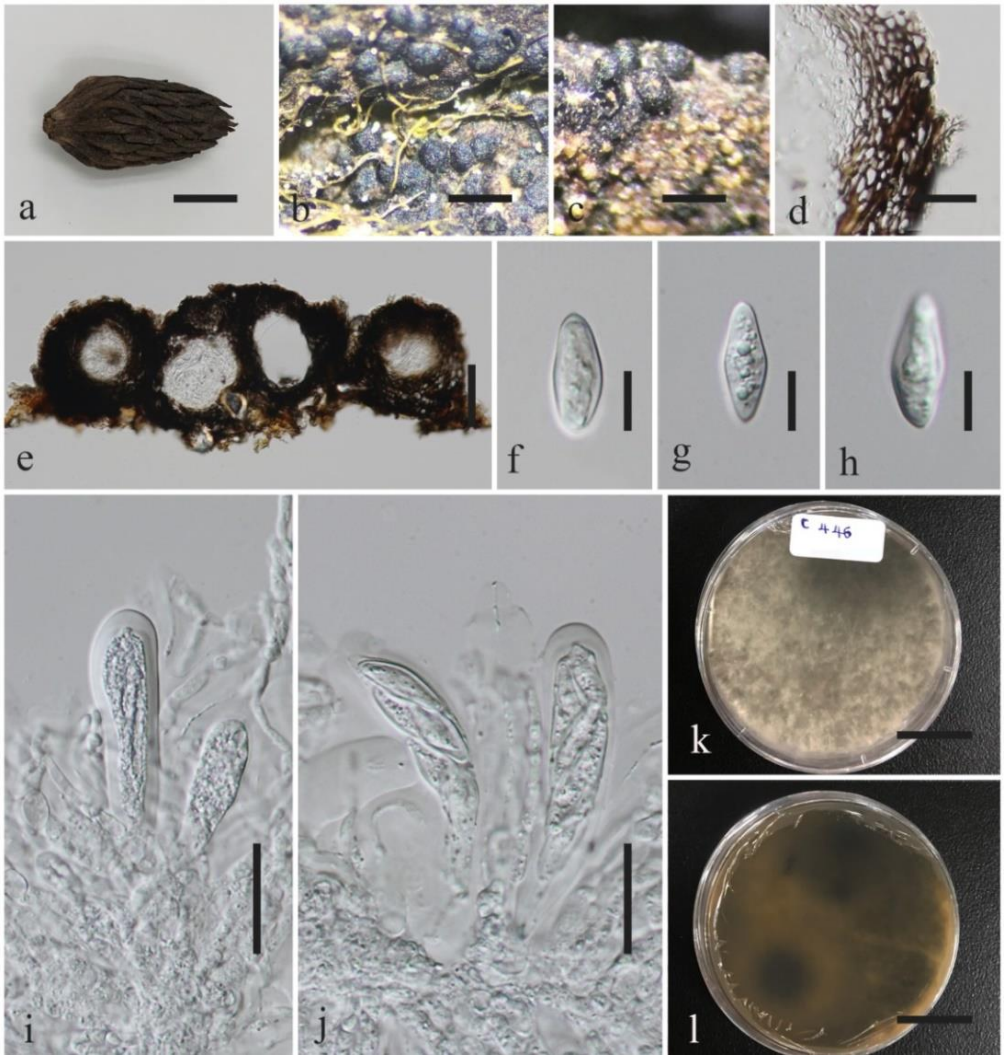


Figure 125 – Sexual morph of *Neofusicoccum parvum* (MFLU 18–2196). a Host cone. b, c View of ascomata on host surface. d Peridium. e Section through ascomata. f–h Ascospores. i, j Asci with cellular paraphyses. k Top view of culture. l Reverse view of culture. Scale bars: a = 1 cm, b, c = 500 µm, d, i, j = 30 µm, f–g = 10 µm.

Saprobic or *pathogenic* on wild host range. Sexual morph: *Ascomata* 170–205 µm high × 139–261 µm diam. ($\bar{x}$ = 184 × 221 µm; n = 10), forming clusters, locules, erumpent through surface of fruit, globose, with a short, sunken ostiole. *Peridium* 30–60 µm wide, dark brown to black, smooth, with wall composed of dark brown thick-walled cells, lined with thin-walled, hyaline cells. *Asci* 106–131 × 19–24 µm ($\bar{x}$ = 124 × 22 µm; n = 20), clavate, 8-spored, bitunicate. *Ascospores* 29–32 × 8–10 µm ($\bar{x}$ = 30.5 × 9 µm; n = 20), broadly ellipsoidal to fusoid, apiculus at each end, hyaline, smooth, aseptate. Asexual morph: Coelomycetous. *Conidiomata* 175–218 µm high × 220–245 µm diam. ($\bar{x}$ = 196 × 231 µm; n = 10), aggregated and morphologically indistinguishable from ascomatal aggregates, individually globose, apapillate to pyriform with a

short, acute papilla, entire locule lined with conidiogenous cells. *Conidiogenous cells* 25–34 × 3–5 µm ($\bar{x}$ = 26 × 4 µm; n = 10), phialidic or annellidic, hyaline, subcylindrical, proliferating percurrently to form 1–2 annellations, or proliferating at the same level to form periclinal thickenings. *Conidia* 16–19 × 4–6 µm ($\bar{x}$ = 17 × 5 µm; n = 30), hyaline, ellipsoidal with apex round and base flat, unicellular.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced at end of conidia. Colonies growing on MEA, reaching 50–60 mm diam. after 2 weeks at 18ºC. Colonies with aerial mycelia, becoming smoke off white to olivaceous-grey at the surface and reverse dark grey to black.

Material examined – CHINA, Guizhou Province, Guizhou University, on fallen pod of *Cercis chinensis* (Fabaceae), 30 July 2016, S.C. Jayasiri, C 133 (MFLU 18–2086, new host record); CHINA, Yunnan Province, Kunming Institute, on fallen cone scale of *Magnolia grandiflora* (Magnoliaceae), 10 May 2018, S.C. Jayasiri, C 446 (MFLU 18–2196, new host record)

GenBank numbers – MFLU 18–2086: SSU: MK347820, ITS: MK347715, LSU: MK347929; MFLU 18–2196: SSU: MK347903, ITS: MK347795, LSU: MK348014, *tef1*: MK340875, *rpb2*: MK434861

Notes – Both sexual and asexual stages of *Neofusicoccum parvum* are reported here for China and are in agreement with descriptions in Phillips et al. (2013). A comparison of the ITS, *tef1* and *tub2* nucleotides of *Neofusicoccum parvum* (CMW 9081) and the new strain (MFLU 18–2086 and MFLU 18–2196) revealed nucleotide differences ≤ 1.5%, which indicates that the new strains are *N. parvum* (Jeewon & Hyde 2016). There are many host records for *N. parvum* from different localities, but this is the first record from *Cercis chinensis* and *Magnolia grandiflora* in China.

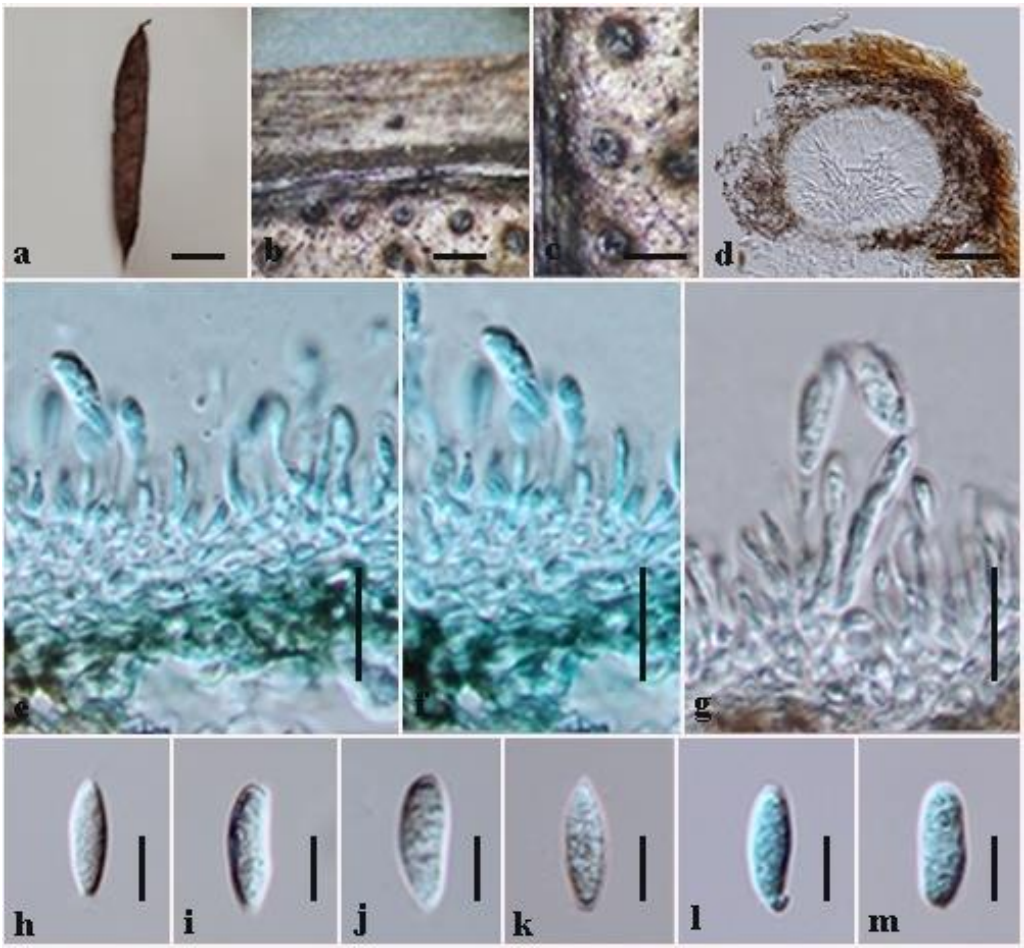


Figure 126 – Asexual morph of *Neofusicoccum parvum* (MFLU 18–2086). a Host pod of *Cercis chinensis.* b, c Conidiomata on host surface. d Section through conidioma. e–g Conidiogenus cells. h–m Conidia. Scale bars: a = 1 cm, b = 500 µm, c = 300 µm, d = 50 µm, e–m = 10 µm.

Phyllostictaceae Fr., Summa vegetabilium Scandinaviae 2: 420 (1849)

Pseudofusicoccum Mohali, Slippers & M.J. Wingf., Studies in Mycology 55: 249 (2006)

This genus is known only as the asexual morph and seven species have been reported. Species are found on different plant families and are not considered to be host specific (Phillips et al. 2013). We introduce another species to this genus, *Pseudofusicoccum calophylli* (Fig. 127).

83. *Pseudofusicoccum calophylli* Jayasiri, E.B.G. Jones & K.D. Hyde sp. nov. Fig. 128

Index Fungorum number: IF555584; Facesoffungi number: FoF05299

Holotype – MFLU 18–2153

Etymology – Referring to the host genus on which the fungus was collected, *Calophyllum* (Calophyllaceae).

Saprobic on *Calophyllum inophyllum*. Asexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* 140–160 µm high × 133–197 µm diam. ($\bar{x}$ = 144 × 160 µm; n = 10), semi-immersed, solitary, globose to subglobose, papillate, covered by host epidermal tissues, lack of ostiole. *Conidiomata wall* 30–50 µm wide ($\bar{x}$ = 47 µm; n = 20), outer pale brown *textura angularis* cell layers, inner hyaline *textura angularis* cell layer, embedded within plant tissues. *Conidiogenous cells* 10–14 × 3–5 µm ($\bar{x}$ = 13 × 4 µm; n = 20), phialidic, ovate to cylindrical, smooth, hyaline. *Conidia* 14–17 × 4–5 µm ($\bar{x}$ = 16 × 4.5 µm; n = 30), hyaline, ellipsoid, occasionally slightly bent or irregularly shaped, apices rounded, smooth with fine granular content, unicellular, thin-walled.

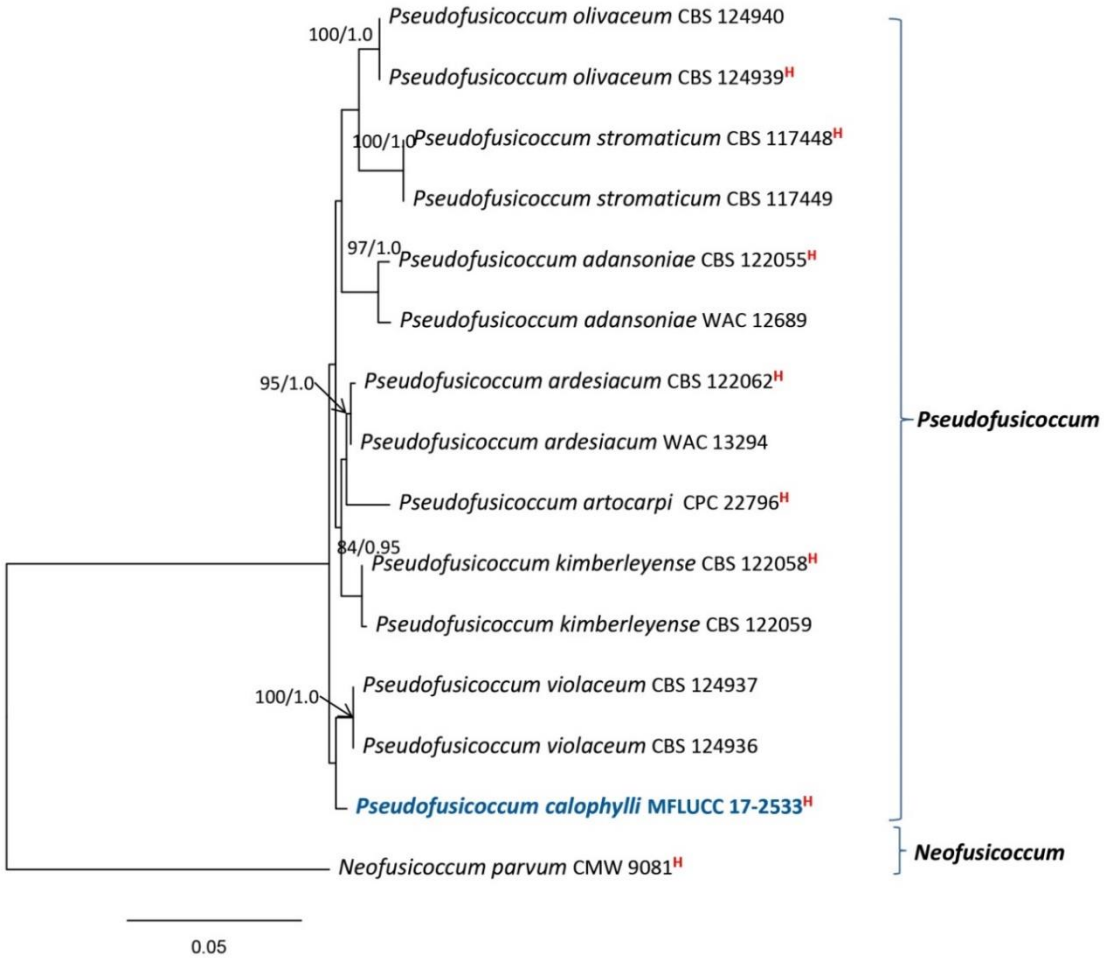


Figure 127 – Phylogram generated from maximum likelihood analysis based on combined ITS and *tef1* partial sequence data. Fifteen strains were included in the sequence analysis, which comprised 896 characters including alignment gaps. *Neofusicoccum parvum* (CBS 110301) was used as the

outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -2088.268519 is presented. The matrix had 120 distinct alignment patterns, with 9.49% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.201315, C = 0.289437, G = 0.269133, T = 0.240115; substitution rates AC = 1.326098, AG = 10.505713, AT = 1.200532, CG = 0.946602, CT = 11.682318, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. The new isolate is in blue. Strains isolated from the holotype specimens are indicated in red superscript ^{H}.

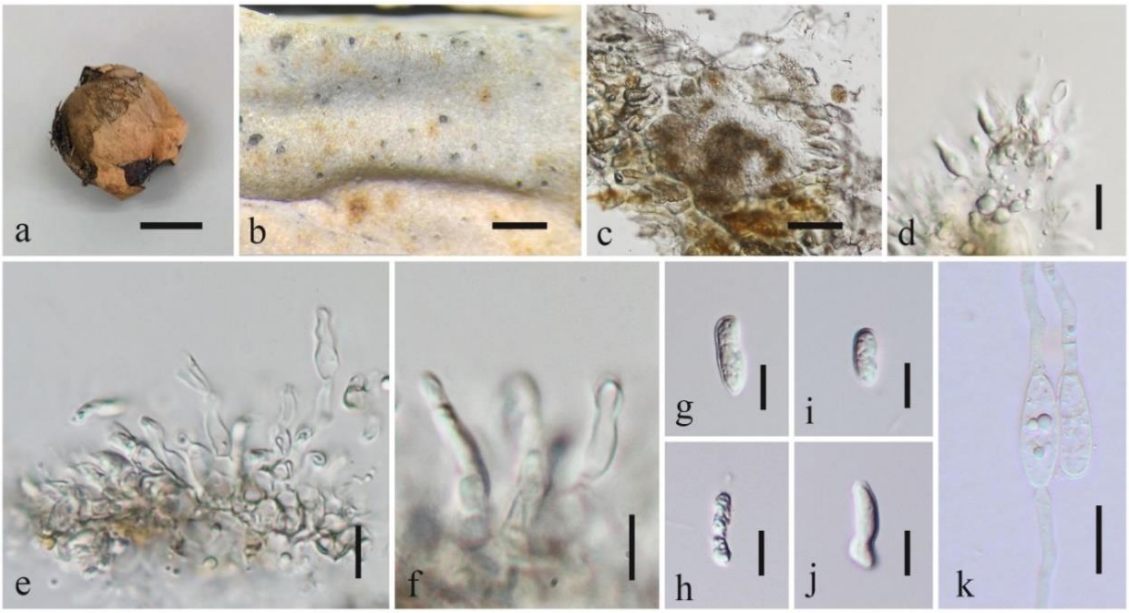


Figure 128 – *Pseudofusicoccum calophylli* (MFLU 18–2153, holotype). a Host fruit. b Conidiomata on host surface. c Section through conidioma. d–f Conidiogenus cells. g–j Conidia. k Germinated conidia. Scale bars: a = 1 cm, b = 500 µm, c = 50 µm, d–k = 10 µm.

Culture characters – Conidia germinated on MEA within 24 hr. Germ tubes produced at one end or both ends of conidia. Colonies growing on MEA, reaching 35–40 mm diam. after 2 weeks at 18^{o}C. Colonies fluffy, initially white to amber at the centre, olivaceous at the edges, becoming white to olivaceous with age.

Material examined – THAILAND, Krabi Province, Mueang Krabi District (8˚ 2' 27" N, 98˚ 49' 5" E), decaying fruit pericarp of *Calophyllum inophyllum* (Calophyllaceae), 31 August 2018, S.C. Jayasiri, C 346 (MFLU 18–2153, holotype; KUN-HKAS102429, isotype), ex-type living culture MFLUCC 17–2533, KUMCC 18–0282.

GenBank numbers – ITS: MK347764, *tef1*: MK340877, *rpb2*: MK434879, *tub2*: MK412885

Notes – *Pseudofusicoccum calophylli* clusters with two strains of *P. violaceum. Pseudofusicoccum violaceum* is characterized by bacilliform conidia with a mucilaginous sheath and larger spores compared to *P. calophylli* (33 × 9.5 vs. 16 × 4.5 µm) (Mehl et al. 2011). However, *Pseudofusicoccum calophylli* has bacilliform conidia in the immature stage but these later become irregular in shape, without a mucilaginous sheath (Fig. 129). A comparison of the ITS and *tef1* nucleotides of these two strains reveals 5 (0.8%) and 5 (1.6%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Muyocopronales Mapook, Boonmee & K.D. Hyde, Phytotaxa 265 (3): 230 (2016)

Muyocopronaceae K.D. Hyde, Fungal Diversity 63 (1): 164 (2013)

This family was introduced for the monotypic genus *Muyocopron* with type species *Muyocopron corrientinum* (Hyde et al. 2013).

Muyocopron Speg., Anales de la Sociedad Científica Argentina 12 (3): 113 (1881)

Species of *Muyocopron* occur worldwide and are associated with a wide variety of plant substrates (Mapook et al. 2016). We record three new host records from fallen pods from China and Thailand (Fig 129).

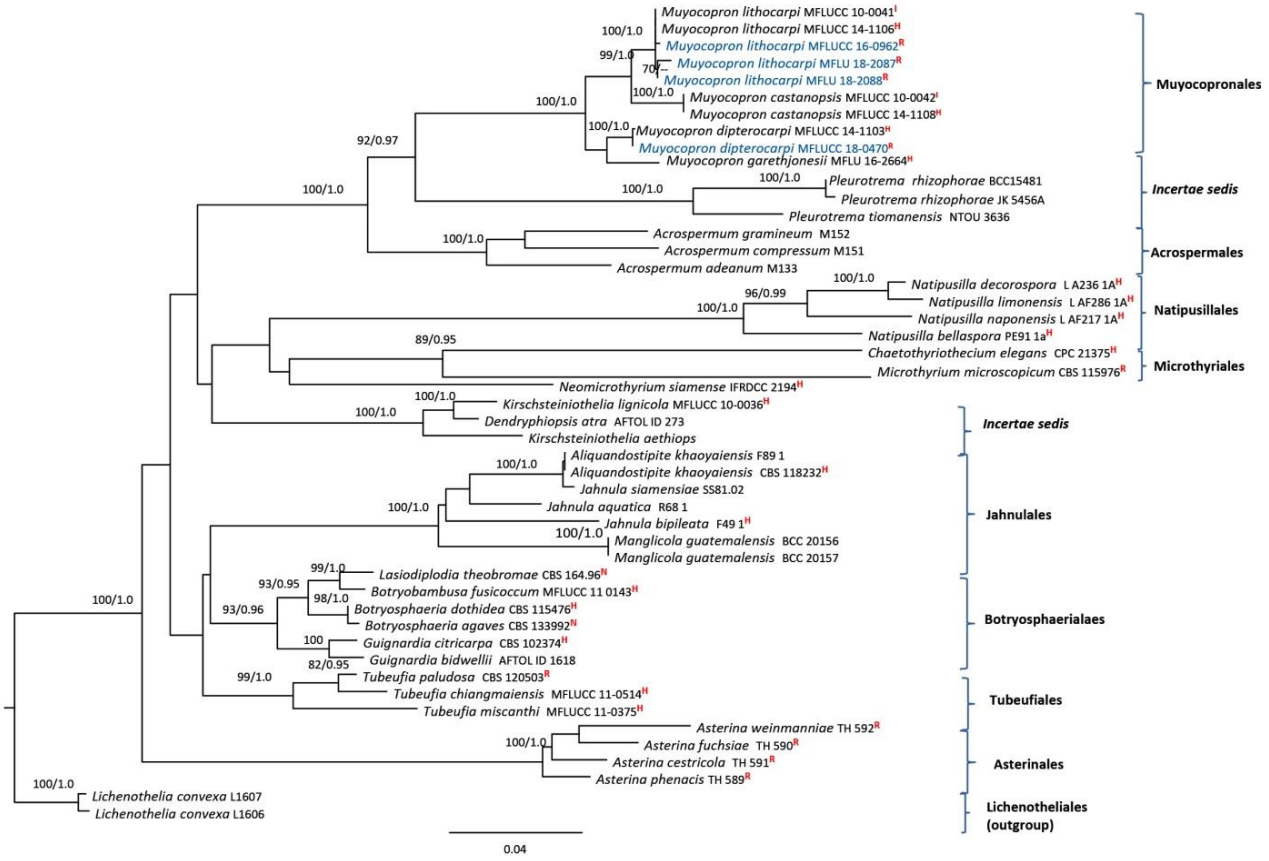


Figure 129 – Phylogram generated from maximum likelihood analysis based on combined SSU and LSU partial sequence data. Fortyeight strains were included in the sequence analysis, which comprise 1883 characters including alignment gaps. *Lichenothelia convexa* (L1606/ L1607) was used as the outgroup taxon. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. Tree topology of the ML tree was similar to the BY tree. The best scoring RAxML tree with a final likelihood value of -13815.005728 is presented. The matrix had 889 distinct alignment patterns, with 14.10% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.251270, C = 0.224786, G = 0.292104, T = 0.231840; substitution rates AC = 0.952432, AG = 2.650848, AT = 1.001097, CG = 1.197500, CT = 6.662515, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue. Strains isolated from the holotype, isotype, neotype and reference specimens are indicated in red superscript ^{H}, ^{I}, ^{N} and ^{R} respectively.

84. ***Muyocopron dipterocarpi*** Mapook, Doilom, Boonmee & K.D. Hyde, Phytotaxa 265 (3): 232 (2016) Fig. 130

Saprobic on twigs and pod of *Delonix regia*. Sexual morph: *Ascomata* 90–140 µm high × 220–270 µm diam. ($\bar{x}$ = 110 × 258 µm; n = 10), superficial, coriaceous, solitary or scattered, appearing as circular, scattered, flattened, brown to dark brown spots, covering the host, without a

subiculum, with a poorly developed basal layer and an irregular margin. *Ostiole* central. *Peridium* 20–30 μm wide, widest at the sides, outer layer comprising dark brown to black pseudoparenchymatous, occluded cells of *textura angularis*, inner layer comprising light brown cells of *textura angularis*. *Hamathecium* 1.5–3 μm wide ($\bar{x}$ = 2.2 μm; n = 30), cylindrical to filiform, septate, pseudoparaphyses. *Asci* 50–70 × 18–20 μm ($\bar{x}$ = 60 × 19 μm; n = 20), 8-spored, bitunicate, saccate or broadly obpyriform, pedicellate, straight or slightly curved, with small ocular chamber. *Ascospores* 15–18 × 7–10 μm ($\bar{x}$ = 16 × 9 μm; n = 30), irregularly arranged, overlapping in the ascus, hyaline, oval to obovoid with obtuse ends, aseptate, with granular appearance. Asexual morph: Undetermined.

Culture characters – Ascospores germinated on MEA within 24 hr. and germ tubes produced from the ends of the ascospore. Colonies on MEA reaching 40 mm diam. after 2 weeks at 18ºC. Initially aerial mycelium white, slightly raised, in old cultures grayish to light brown, flattened on surface, dark to dark brown from below, light brown to white margin.

Material examined – THAILAND, Phrae Province, on decaying pod septum of *Delonix regia* (Fabaceae), 10 January 2018, S.C. Jayasiri, C 412 (MFLU 18–2181, new host record; KUN-HKAS 102433), living culture, MFLUCC 18–0470, KUMCC 18–0258.

GenBank numbers – SSU: MK347890, ITS: MK347783, LSU: MK348001

Notes – The new strain formed a sister clade to *Muyocopron dipterocarpi* (MFLUCC 14–1103) with high statistical support (100% MLBS/1.0 BYPP, Fig. 129). These two strains share similar morphology in having superficial, coriaceous, circular, scattered, flattened, brown to dark brown spots ascomata, broadly obpyriform asci and irregularly arranged, hyaline, oval to obovoid, aseptate ascospores with granular appearance (Mapook et al. 2016). A comparison of the SSU and LSU nucleotides of *Muyocopron dipterocarpi* (MFLUCC 14–1103) and the new strain (MFLUCC 18–0470) revealed nucleotide differences ≤ 1.5%, which indicates that new strains are *M. dipterocarpi* (Jeewon & Hyde 2016). Therefore, we introduce a new strain of *M. dipterocarpi* from decaying pod of *Delonix regia*; the holotype was recorded from dead twigs of *Dipterocarpus tuberculatus* in Thailand.

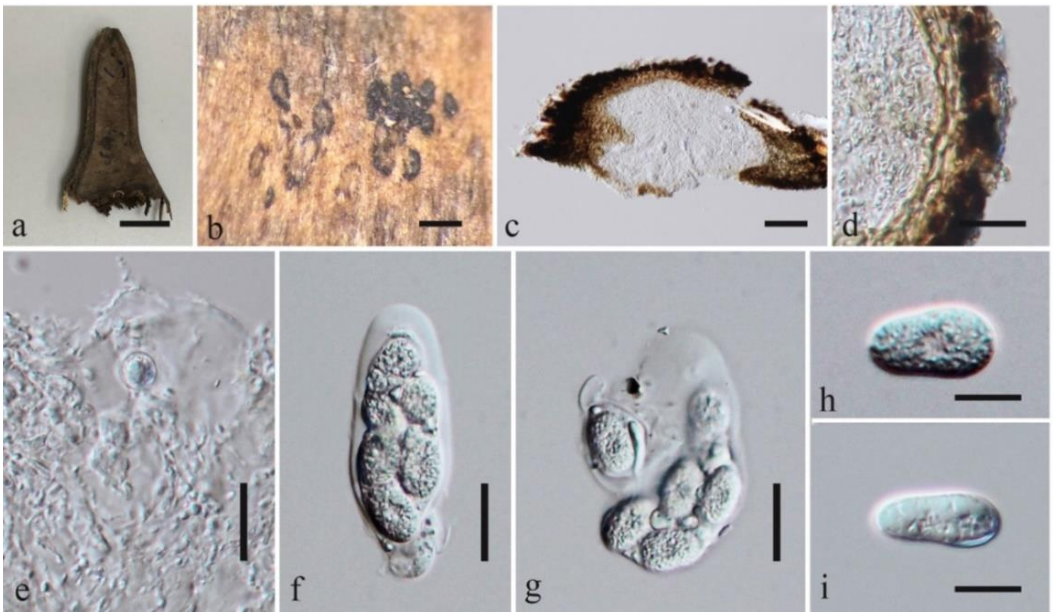


Figure 130 – *Muyocopron dipterocarpi* (MFLU 18–2181). a Part of the host seed pod. b Superficial ascomata on substrate. c Section of ascoma. d Peridium. e Pseudoparaphyses. f, g Asci. h, i Ascospores. Scale bars: a = 1 cm, b = 500 μm, c, d = 50 μm, f, g = 20 μm, e, h, i = 10 μm.

85. *Muyocopron lithocarpi* Mapook, Boonmee & K.D. Hyde, Phytotaxa 265 (3): 235 (2016)

Fig. 131

Saprobic on leaves and wild pods. Sexual morph: *Ascomata* 90–102 µm high × 225–358 µm diam. ($\overline{x}$ = 72 × 275 µm; n = 10), superficial, coriaceous, solitary or scattered, appearing as circular, scattered, flattened, brown to dark brown spots, covering the host, without a subiculum, with a poorly developed basal layer and an irregular margin. *Ostiole* central. *Peridium* 10–27 µm wide ($\overline{x}$ = 23 µm; n = 20), widest at the sides, outer layer comprising dark brown to black pseudoparenchymatous, occluded cells of *textura epidermoidea*, inner layer comprising light brown cells of *textura angularis*. *Hamathecium* 1.5–2.5 µm wide ($\overline{x}$ = 2.1 µm; n = 20), cylindrical to filiform, septate, pseudoparaphyses. *Asci* 55–77 × 19–23 µm ($\overline{x}$ = 65 × 21 µm; n = 20), 8-spored, bitunicate, saccate or broadly obpyriform, pedicellate, straight or slightly curved, with small ocular chamber. *Ascospores* 14–19 × 8–12 µm ($\overline{x}$ = 16 × 10 µm; n = 20), irregularly arranged, overlapping in the ascus, hyaline, oval to obovoid with obtuse ends, aseptate, with granular appearance. Asexual morph: Undetermined.

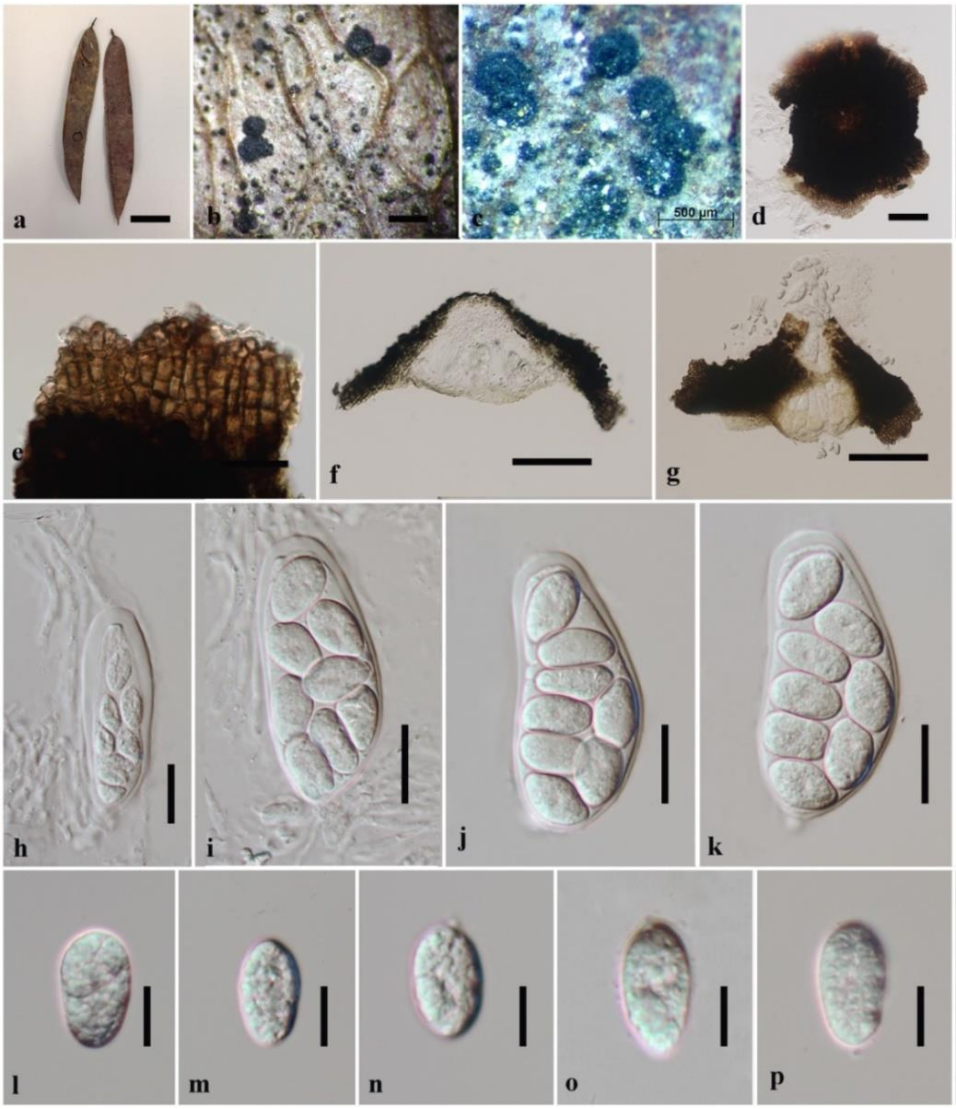


Figure 131 – *Muyocopron lithocarpi* (MFLU 18–2087). a Host pods. b, c Superficial ascomata on substrate. d Top view of ascoma. e Squash mounts showing peridium. f, g Section of ascoma. h–k Asci. l–p Ascospores. Scale bars: a = 1 cm, b, c = 500 µm, d = 50 µm, e = 10 µm, h–k = 20 µm, l–p = 10 µm.

Culture characters – Ascospores germinated on MEA within 18 hr. and germ tubes produced from the ends of the ascospore. Colonies on MEA reaching 20 mm diam. after 2 weeks at 18ºC. Initially aerial mycelium white, slightly rose, in old cultures greyish to light brown, flattened on

surface, brown to dark brown from below, light brown to white margin.

Material examined – THAILAND, Chiang Rai Province, Mae Fah Luang University, on decaying pods of *Peltophorum* sp., 25 August 2015, S.C. Jayasiri, C 61 (MFLU 16–0962, new host record), living culture MFLUCC 16–0962, KUMCC 18–0259; CHINA, Guizhou province, Guizhou University, on fallen pod of *Cercis chinensis* (Fabaceae), 10 May 2106, S.C. Jayasiri, C134/C135 (MFLU 18–2087, MFLU 18–2088, new host record).

GenBank numbers – MFLUCC 16–0962: SSU: MK347923, LSU: MK348034; MFLU 18–2087: SSU: MK347716, ITS: MK347716, LSU: MK347930; MFLU 18–2088: SSU: MK347822, ITS: MK347717, LSU: MK347931

Notes – In the phylogenetic analysis, the three new strains grouped with other strains (MFLUCC 10–0041 and 14–1106) of *Muyocopron lithocarpi.* They are also morphologically identical to the type species (Fig. 131). A comparison of the SSU and LSU nucleotides of *Muyocopron lithocarpi* (MFLUCC 14–1106) and new strains (MFLUCC 16–0962, MFLU 18–2087 and MFLU 18–2088) revealed nucleotide differences ≤ 1.5%, which indicates that new strains are *M. lithocarpi* (Jeewon & Hyde 2016). Therefore, we record new host records of *M. lithocarpi* in *Peltophorum* sp. and *Cercis chinensis* from Thailand and China, respectively.

Tubeufiales Boonmee & K.D. Hyde, Fungal Diversity 68 (1): 245 (2014)

Tubeufiaceae M.E. Barr, Mycologia 71: 948 (1979)

The phylogenetic affinities of this family were initially investigated by Kodsueb et al. (2006) and the latest overview for this order was by Lu et al. (2018) in which 42 genera were recognized in the family Tubeufiaceae (Tubeufiales). We introduce one new genus, three new species and six new records in this group based on morphology and multigene phylogeny. Most species in the family are saprobic on terrestrial woody substrates although some are from aquatic habitats (Boonmee et al. 2011, 2014, Hyde et al. 2016a, Brahamanage et al. 2017, Chaiwan et al. 2017, Doilom et al. 2017, Lu et al. 2017a, b, c, 2018b, Luo et al. 2017, Liu et al. 2018, Phookamsak et al. 2018). We report species isolated from decaying wild seeds and fruits from Thailand. We also introduce a sexual morph genus *Neohelicosporium* (Jayasiri et al. 2017b) from a decaying fruit of Malvaceae sp.

86. *Discotubeufia* Jayasiri, E.B.G. Jones & K.D. Hyde, gen. nov.

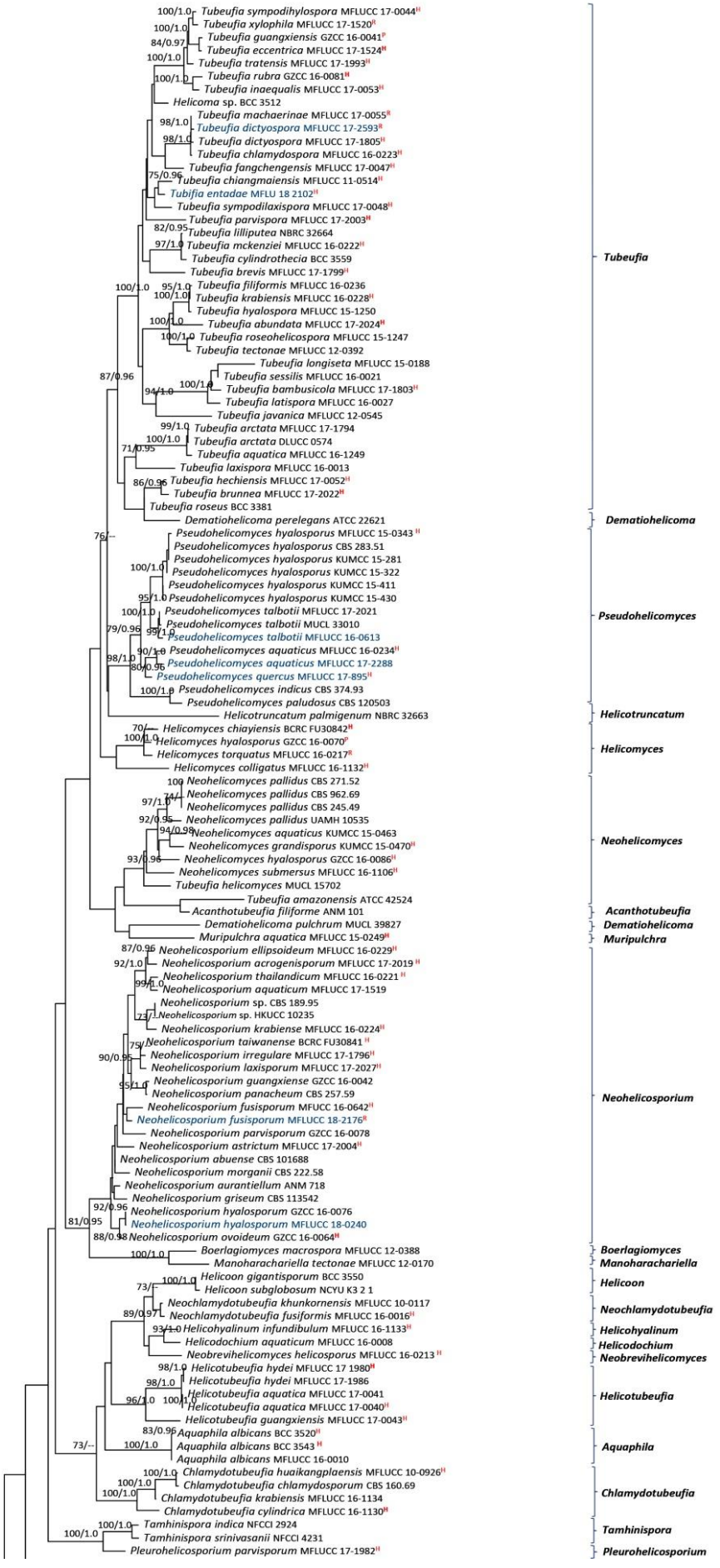
Index Fungorum number: IF555585; Facesoffungi number: FoF05300

Etymology – Referring to the dish shaped ascomata bearing members in order Tubeufiales.

Saprobic on decaying pod of *Brownea* sp. Sexual morph: *Ascomata* globose when dry becoming cup-shaped, erumpent to superficial, light brown to dark, setiferous; setae attached to outer wall, tapering towards the tip, dark brown, rough. *Peridium* composed of pseudoparenchymatous dark brown outer layer, pale brown middle layer and hyaline inner layer, forming a *textura angularis* in surface view, with inner layers *textura angularis* to *textura prismatica*. *Hamathecium* sparse, septate pseudoparaphyses, immersed in a gelatinous matrix. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to sub cylindrical or obclavate, tapering toward the base, with a long stipe, thick-walled at the apex. *Ascospores* uni to biseriate, hyaline, asymmetric, with upper part broader than lower part, fusiform to cylindrical, 3-septate, multi-guttulate, without an appendage. Asexual morph: Unknown.

Type species – ***Discotubeufia browneae*** Jayasiri, E.B.G. Jones & K.D. Hyde

Notes – *Discotubeufia* forms a sister group to *Kamalomyces* species with low bootstrap support (Fig. 132). *Kamalomyces* is characterized by solitary, gregarious, subglobose to lemoniform ascomata on a black hyphal subiculum and broadly cylindrical to clavate asci (Verma et al. 2008, Phookamsak et al. 2017). However, *Discotubeufia* is characterized by cup-shaped, erumpent to superficial, light brown to dark, setiferous ascomata and cylindrical to sub cylindrical asci (Fig. 133). *Discotubeufia browneae* also clusters with *Helicoarctatus aquaticus* and *Neohelicoma fagacearum.* However, *Helicoarctatus aquaticus* is an asexual morph genus.


Tubeufia sympodihylospora MFLUCC 17-0044H
Tubeufia xylophila MFLUCC 17-1520R
Tubeufia guangxiensis GZCC 16-0041P
Tubeufia eccentrica MFLUCC 17-1524H
Tubeufia tratensis MFLUCC 17-1993H
Tubeufia rubra GZCC 16-0081H
Tubeufia inaequalis MFLUCC 17-0053H
Helicoma sp. BCC 3512
Tubeufia machaerinae MFLUCC 17-0055R
Tubeufia dictyospora MFLUCC 17-2593R
Tubeufia dictyospora MFLUCC 17-1805H
Tubeufia chlamydospora MFLUCC 16-0223H
Tubeufia fangchengensis MFLUCC 17-0047H
Tubeufia chiangmaiensis MFLUCC 11-0514H
Tubifia entadae MFLU 18 2102H
Tubeufia sympodilaxispora MFLUCC 17-0048H
Tubeufia parvispora MFLUCC 17-2003H
Tubeufia lilliputea NBRC 32664
Tubeufia mckenziei MFLUCC 16-0222H
Tubeufia cylindrothecia BCC 3559
Tubeufia brevis MFLUCC 17-1799H
Tubeufia filiformis MFLUCC 16-0236
Tubeufia krabiensis MFLUCC 16-0228H
Tubeufia hyalospora MFLUCC 15-1250
Tubeufia abundata MFLUCC 17-2024H
Tubeufia roseohelicospora MFLUCC 15-1247
Tubeufia tectonae MFLUCC 12-0392
Tubeufia longiseta MFLUCC 15-0188
Tubeufia sessilis MFLUCC 16-0021
Tubeufia bambusicola MFLUCC 17-1803H
Tubeufia latispora MFLUCC 16-0027
Tubeufia javanica MFLUCC 12-0545
Tubeufia arctata MFLUCC 17-1794
Tubeufia arctata DLUCC 0574
Tubeufia aquatica MFLUCC 16-1249
Tubeufia laxispora MFLUCC 16-0013
Tubeufia hechiensis MFLUCC 17-0052H
Tubeufia brunnea MFLUCC 17-2022H
Tubeufia roseus BCC 3381
Tubeufia
Dematiohelicoma perelegans ATCC 22621
Dematiohelicoma
Pseudohelicomyces hyalosporus MFLUCC 15-0343H
Pseudohelicomyces hyalosporus CBS 283.51
Pseudohelicomyces hyalosporus KUMCC 15-281
Pseudohelicomyces hyalosporus KUMCC 15-322
Pseudohelicomyces hyalosporus KUMCC 15-411
Pseudohelicomyces hyalosporus KUMCC 15-430
Pseudohelicomyces talbotii MFLUCC 17-2021
Pseudohelicomyces talbotii MUCL 33010
Pseudohelicomyces talbotii MFLUCC 16-0613
Pseudohelicomyces aquaticus MFLUCC 16-0234H
Pseudohelicomyces aquaticus MFLUCC 17-2288
Pseudohelicomyces quercus MFLUCC 17-895H
Pseudohelicomyces indicus CBS 374.93
Pseudohelicomyces paludosus CBS 120503
Pseudohelicomyces
Helicotruncatum palmigenum NBRC 32663
Helicotruncatum
Helicomyces chiayiensis BCRC FU30842H
Helicomyces hyalosporus GZCC 16-0070P
Helicomyces torquatus MFLUCC 16-0217R
Helicomyces colligatus MFLUCC 16-1132H
Helicomyces
Neohelicomyces pallidus CBS 271.52
Neohelicomyces pallidus CBS 962.69
Neohelicomyces pallidus CBS 245.49
Neohelicomyces pallidus UAMH 10535
Neohelicomyces aquaticus KUMCC 15-0463
Neohelicomyces grandisporus KUMCC 15-0470H
Neohelicomyces hyalosporus GZCC 16-0086H
Neohelicomyces submersus MFLUCC 16-1106H
Tubeufia helicomyces MUCL 15702
Neohelicomyces
Tubeufia amazonensis ATCC 42524
Acanthotubeufia filiforme ANM 101
Acanthotubeufia
Dematiohelicoma pulchrum MUCL 39827
Dematiohelicoma
Muripulchra aquatica MFLUCC 15-0249H
Muripulchra
Neohelicosporium ellipsoideum MFLUCC 16-0229H
Neohelicosporium acrogenisporum MFLUCC 17-2019H
Neohelicosporium thailandicum MFLUCC 16-0221H
Neohelicosporium aquaticum MFLUCC 17-1519
Neohelicosporium sp. CBS 189.95
Neohelicosporium sp. HKUCC 10235
Neohelicosporium krabiense MFLUCC 16-0224H
Neohelicosporium taiwanense BCRC FU30841H
Neohelicosporium irregulare MFLUCC 17-1796H
Neohelicosporium laxisporum MFLUCC 17-2027H
Neohelicosporium guangxiense GZCC 16-0042
Neohelicosporium panacheum CBS 257.59
Neohelicosporium fusisporum MFUCC 16-0642H
Neohelicosporium fusisporum MFLUCC 18-2176R
Neohelicosporium parvisporum GZCC 16-0078
Neohelicosporium astrictum MFLUCC 17-2004H
Neohelicosporium abuense CBS 101688
Neohelicosporium morganii CBS 222.58
Neohelicosporium aurantiellum ANM 718
Neohelicosporium griseum CBS 113542
Neohelicosporium hyalosporum GZCC 16-0076
Neohelicosporium hyalosporum MFLUCC 18-0240
Neohelicosporium ovoideum GZCC 16-0064H
Neohelicosporium
Boerlagiomyces macrospora MFLUCC 12-0388
Manoharachariella tectonae MFLUCC 12-0170
Boerlagiomyces
Manoharachariella
Helicoon gigantisporum BCC 3550
Helicoon subglobosum NCYU K3 2 1
Helicoon
Neochlamydotubeufia khunkornensis MFLUCC 10-0117
Neochlamydotubeufia fusiformis MFLUCC 16-0016H
Neochlamydotubeufia
Helicohyalinum infundibulum MFLUCC 16-1133H
Helicohyalinum
Helicodochium aquaticum MFLUCC 16-0008
Helicodochium
Neobrevihelicomyces helicosporus MFLUCC 16-0213H
Neobrevihelicomyces
Helicotubeufia hydei MFLUCC 17 1980H
Helicotubeufia hydei MFLUCC 17-1986
Helicotubeufia aquatica MFLUCC 17-0041
Helicotubeufia aquatica MFLUCC 17-0040H
Helicotubeufia guangxiensis MFLUCC 17-0043H
Helicotubeufia
Aquaphila albicans BCC 3520H
Aquaphila albicans BCC 3543H
Aquaphila albicans MFLUCC 16-0010
Aquaphila
Chlamydotubeufia huaikangplaensis MFLUCC 10-0926H
Chlamydotubeufia chlamydosporum CBS 160.69
Chlamydotubeufia krabiensis MFLUCC 16-1134
Chlamydotubeufia cylindrica MFLUCC 16-1130H
Chlamydotubeufia
Tamhinispora indica NFCCI 2924
Tamhinispora srinivasanii NFCCI 4231
Tamhinispora
Pleurohelicosporium parvisporum MFLUCC 17-1982H
Pleurohelicosporium

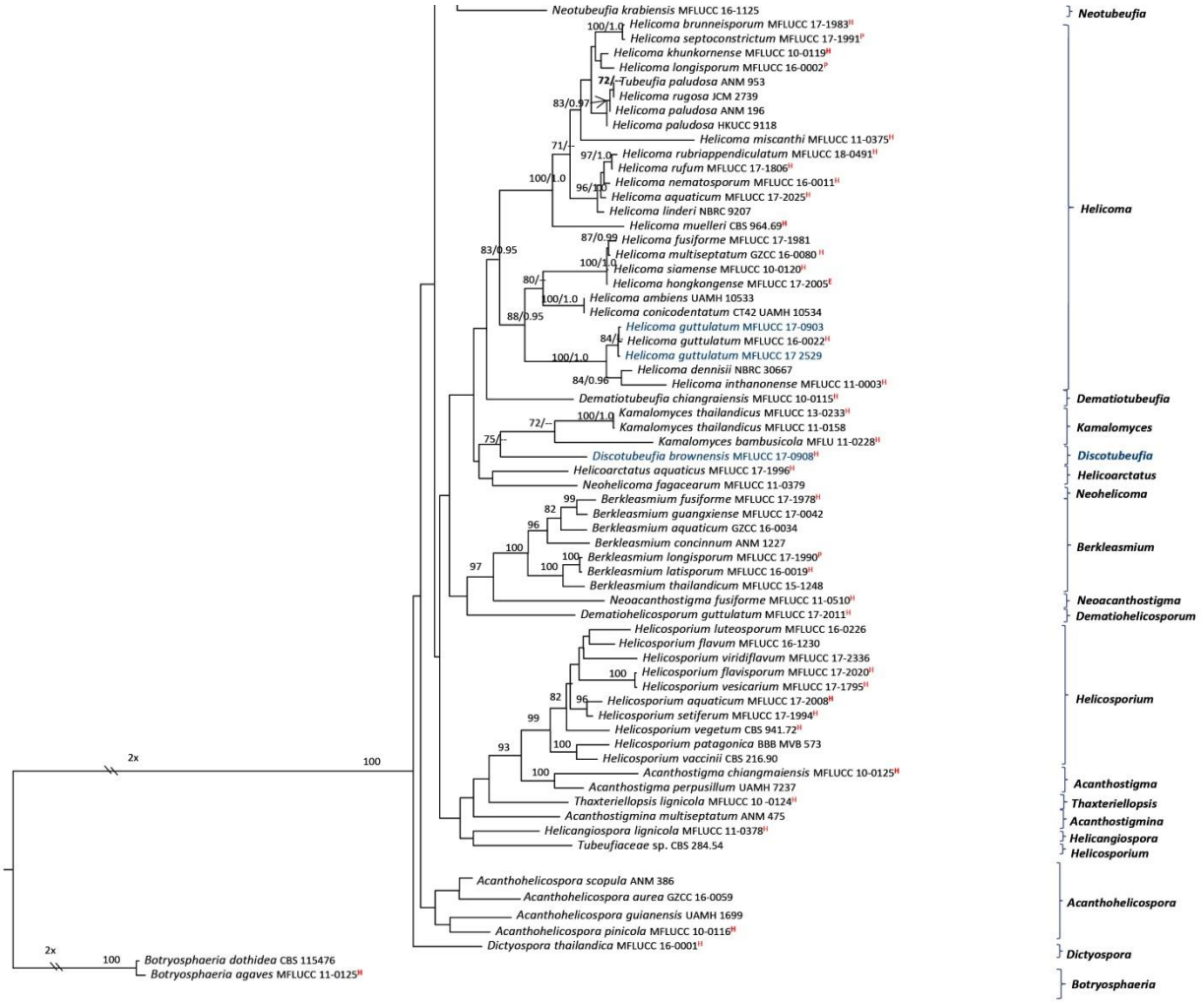


Figure 132 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained using the combined ITS, LSU, *tef1* and *rpb2* matrix of 187 taxa including related species of the order Tubeufiales (Lu et al. 2018b). The matrix comprised 3525 characters including alignment gaps. The tree was rooted with *Botryosphaeria* spp. (Botryosphaeriales). The best scoring RAxML tree with a final likelihood value of -60324.463725 is presented. The matrix had 1790 distinct alignment patterns, with 35.67% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.243594, C = 0.251595, G = 0.260381, T = 0.244430; substitution rates AC = 1.047549, AG = 4.941476, AT = 2.193590, CG = 0.734873, CT = 8.281175, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue. Strains isolated from the holotype, epitype, paratype and reference specimens are indicated in red superscript ^{H}, ^{E}, ^{P} and ^{R} respectively.

Discotubeufia browneae comprises only a sexual morph. Therefore, it was possible to compare its morphology only with *Neohelicoma fagacearum*, the type species of the genus. *Discotubeufia browneae* has cup-shaped, black, setiferous ascomata, and 3-septate, broad ascospores, while *Neohelicoma fagacearum* has globose to subglobose, pale brown, ostiolate ascomata and 9–12-septate narrow ascospores. Although phylogenetic support among these three genera is low, they appear in different lineages. We introduce the new genus based on sequence data and its distinct morphology.

87. *Discotubeufia browneae* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 133
Index Fungorum number: IF555586; Facesoffungi number: FoF05301

Holotype – MFLU 18–2096

Etymology – Referring to the host genus on which the fungus was collected, *Brownea* (Fabaceae).

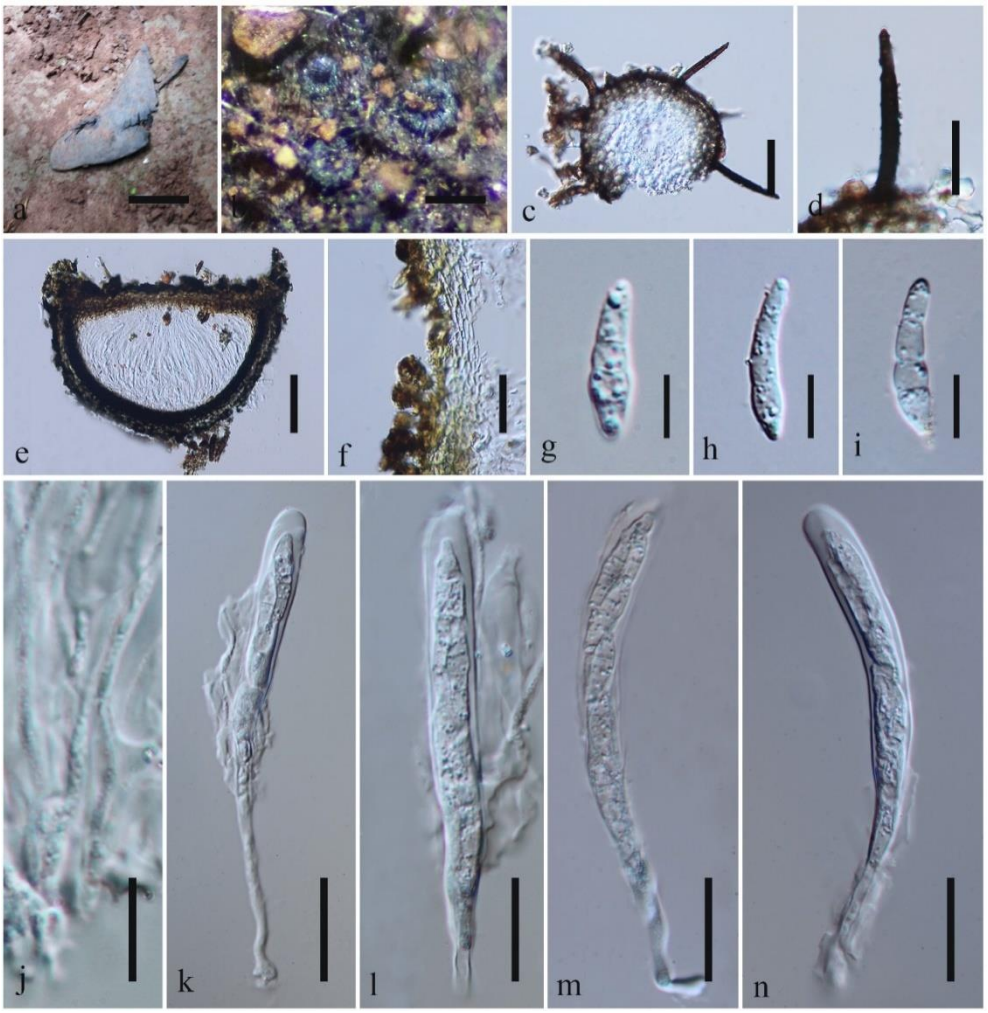


Figure 133 – *Discotubeufia browneae* (MFLU 18–2096, holotype). a Host species on forest floor. b View of ascomata on host. c Section through ascoma with setae. d Setae e Section through ascoma. f Peridium. g–i Ascospores. j Pseudoparaphyses. k–n Asci. Scale bars: a = 4 cm, b = 500 µm, c = 30 µm, d = 20 µm, e = 30 µm, g–j = 10 µm, d, f, k–n = 20 µm.

Saprobic on pod of *Brownea* sp. Sexual morph: *Ascomata* 105–130 µm high × 225–266 µm diam. ($\bar{x}$ = 122 × 252 µm; n = 10), cup-shaped, erumpent to superficial, light brown to dark, setiferous; setae 45–57 µm long ($\bar{x}$ = 52.5 µm; n = 20), attached to outer wall, tapering towards base, dark brown, rough. *Peridium* 18–27 µm wide ($\bar{x}$ = 22 µm; n = 20), composed of pseudoparenchymatous dark brown outer layer, pale brown middle layer and hyaline inner layer, forming a *textura angularis* in surface view, with inner layers *textura angularis* to *textura prismatica*. *Hamathecium* 1.5–2 µm wide ($\bar{x}$ = 1.7 µm; n = 30), composed of sparse, septate pseudoparaphyses, immersed in a gelatinous matrix. *Asci* 83–95 × 6–11 µm ($\bar{x}$ = 87 × 9 µm; n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to sub-cylindrical or obclavate, tapering towards the base, with a long stipe, thick-walled at the apex. *Ascospores* 20–25 × 4–6 µm ($\bar{x}$ = 23 × 5 µm; n = 30), uni- to biseriate, hyaline, asymmetrical, with lower part broader than upper part, fusiform to cylindrical, 3-septate, multi-guttulate, without an appendage. Asexual morph: Unknown.

Culture characters – Ascospores germinated on MEA within 24 hr. Colonies growing on MEA reaching 50 mm diam. after 2 weeks at 18ºC, colonies circular, effuse, dense, dark brown,

many layered and rough on surface with entire to slightly undulate edge with brown yellow diffused pigment in media.

Material examined – THAILAND, Chiang Mai Province, Mae Kam, on decaying pod septum of *Brownea* sp. (Fabaceae), 21 September 2016, S.C. Jayasiri, C 191 (MFLU 18–2096, holotype), ex-type living culture, MFLUCC 17–0908, KUMCC 18–0238.

GenBank numbers – SSU: MK347829, ITS: MK347723, LSU: MK347938

Helicoma Corda, Icones fungorum hucusque cognitorum 1: 15 (1837)

More than 80 records are listed under *Helicoma* in Index Fungorum however, a recent study accepts 57 species and excludes twelve species from this genus (Lu et al. 2018b). We report a new host record for *Helicoma guttulatum,* from decaying wild fruits (Fig. 132).

88. *Helicoma guttulatum* Y.Z. Lu, Boonmee & K.D. Hyde, Fungal Diversity 80: 125 (2016)

Fig. 134

Saprobic on woody substrates and fruit of *Lithocarpus* sp. Sexual morph: Undetermined. Asexual morph: Hyphomycetous, helicosporous. *Colonies* appear as a yellow droplet on host seed. *Mycelium* mostly superficial, septate, branched, smooth, subhyaline to pale brown. *Conidiophores* 91–200 × 4–6 µm ($\bar{x}$ = 120 × 5 µm; n = 20), macronematous, mononematous, cylindrical, unbranched, septate, erect, subhyaline to yellowish, dark brown towards the base, septate, unbranched, smooth-walled. *Conidiogenous cells* holoblastic, monoblastic to polyblastic, subhyaline to pale brown, smooth-walled. *Conidia* 47–58 × 6–8 µm ($\bar{x}$ = 53 × 7.2 µm; n = 20), conidial filament 16–22 µm wide ($\bar{x}$ = 19 µm; n = 20), solitary, acrogenous, helicoid, hyaline to pale brown, tapering toward flat end, rounded at the apex, conico-truncate at the base, tightly coiled 1–1½ times, smooth-walled.

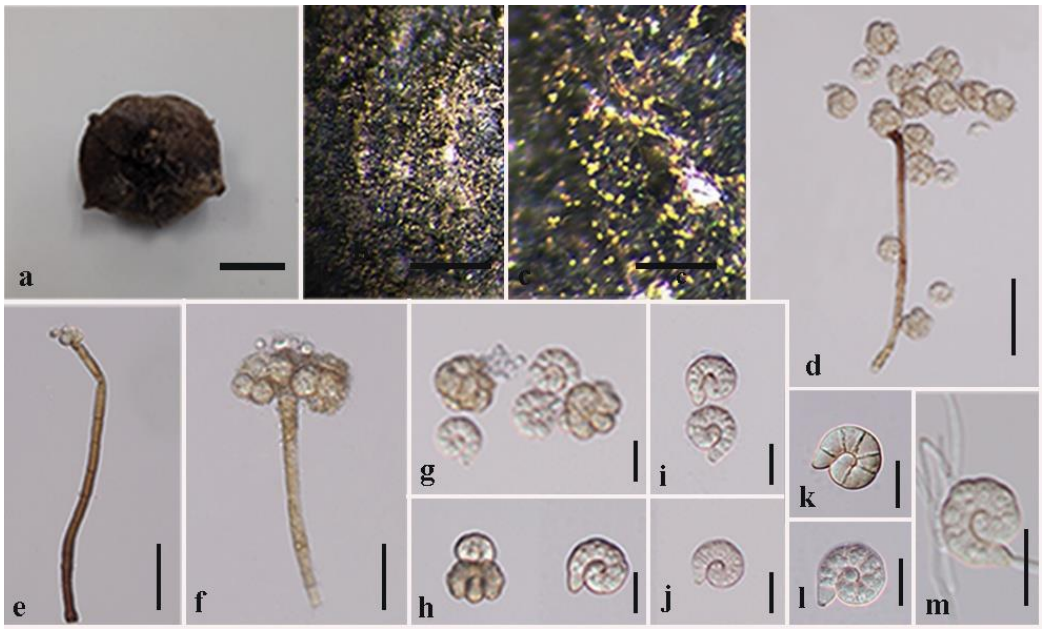


Figure 134 – *Helicoma guttulatum* (MFLU 18–2095). a *Lithocarpus* species host fruit. b, c Colonies on host material. d–f Immature conidia attached to conidiogenous cells. g, h Immature conidia. i–l Mature conidia. m Germinated spore. Scale bars: b = 500 µm, c = 200 µm, d–f = 10 µm, g–m = 20 µm.

Culture characters – Ascospores germinated on MEA within 24 hr. and germ tubes produced from all cells. Colonies growing on MEA reaching 8 mm diam. in 1 week at 18ºC, slightly effuse, edge entire rise or dentate and darkened to blackish.

Material examined – THAILAND, Mae Hong Son Province, on decaying fruit of *Lithocarpus*

sp., 22 September 2016, S.C. Jayasiri, C 177 (MFLU 18–2095, new host record), living culture MFLUCC 17–0903, KUMCC 18–0244; THAILAND, Lampang Province, on fruit of unknown species, S.C. Jayasiri, C 334 (MFLU 18–2150), living culture MFLUCC 17–2529, KUMCC 18–0245.

GenBank numbers – MFLUCC 17–0903: SSU: MK347828, ITS: MK347722, LSU: MK347937, *rpb2*: MK434904; MFLUCC 17–2529: SSU: MK347868, ITS: MK347762, LSU: MK347978, *tef1*: MK360057, *rpb2*: MK434880

Notes – We introduce a new host record for *Helicoma guttulatum* on wild fruit of *Lithocarpus* sp. (Fig. 132). Our new collections resemble *H. guttulatum* (MFLUCC 16–0022) in conidiophores and conidial morphology (Hyde et al. 2016) and in the phylogenetic analyses our new isolates clustered together with *H. guttulatum* (MFLUCC 16–0022). A comparison of the ITS, *tef1* and *rpb2* nucleotides of *Helicoma guttulatum* (MFLUCC 16–0022) and new strains (MFLUCC 17–0903 and MFLUCC 17–2529) revealed nucleotide differences ≤ 1.5%, which indicates that new strain are *H. guttulatum* (Jeewon & Hyde 2016). The conidia are 7 septate in the new collections while they were 8–9 septate in the type specimen (Hyde et al. 2016). With strong molecular evidence, we identified them as the same species.

Neohelicosporium Y.Z. Lu, J.C. Kang & K.D. Hyde, Mycological Progress 17 (5): 637 (2018)

This genus was introduced by Lu et al. (2018a) with 19 species based on a multigene phylogenetic analyses coupled with morphological data (Jayasiri et al. 2017b, Lu et al. 2018a, b). We introduce two new host records, on decaying seed pods from Thailand (Fig. 132).

89. ***Neohelicosporium fusisporum*** Jayasiri & K.D. Hyde, Studies in Fungi 2(1): 212 (2017)

Fig 135

Saprobic on pod of *Oroxylum* sp. Sexual morph: See Jayasiri et al (2017). Asexual morph: Hyphomycetous, helicosporous. *Mycelium* composed of partly immersed, partly superficial, hyaline to pale brown, septate, abundantly branched hyphae, with masses of crowded, glistening conidia. *Conidiophores* macronematous, mononematous, flexuous, cylindrical, long, septate, branched, pale brown, smooth-walled. *Conidiogenous cells* 14–22 × 2–3 μm, holoblastic, mono- to polyblastic, discrete, intercalary, cylindrical, with denticles, pale brown, smooth-walled. *Conidia* 100–150 × 1.8–2.5 μm ($\bar{x}$ = 135 × 2.2 μm; n = 20), conidial filament 18–25 μm wide ($\bar{x}$ = 22 μm; n = 20), solitary, pleurogenous, helicoid, hyaline, rounded at ends, tightly coiled 2½–3¼ times, loosely coiled in water, multi-septate, verruculose, guttulate.

Culture characters – Conidia germinated on MEA. Colonies reaching 10 mm diam. in 2 weeks at 18ºC. Colonies on MEA are adpressed, circular, flat on surface, entire on edge, first cream then becoming dark brown and raised in the centre with mycelium, reverse brown.

Material examined – THAILAND, Amphoe, Prachuap Khiri Khan Province, Bang Saphan District, on decaying pod of *Oroxylum* sp. (Bignoniaceae), 28 August 2017, S.C. Jayasiri, C 397 (MFLU 18–2176, new host record).

GenBank numbers – SSU: MK347887, LSU: MK347997

Notes – Our isolate forms a sister clade to *Neohelicosporium fusisporum* with low statistical support. A comparison of the ITS nucleotides of *Neohelicosporium fusisporum* (MFUCC 16–0642) and the new strain (MFLUCC 17–0903) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *N. fusisporum* (Jeewon & Hyde 2016). New strain shares similar morphology with type strain of *Neohelicosporium fusisporum* (MFUCC 16–0642) in having macronematous, cylindrical, septate, branched, pale brown conidiophores, holoblastic, mono- to polyblastic, cylindrical, pale brown conidiogenous cells with denticles, and helicoid, tightly coiled, multi-septate, verruculose, hyaline conidia with guttules (Jayasiri et al. 2017b). We record *Oroxylum* sp. (Bignoniaceae) in Thailand as a new host for *Neohelicosporium fusisporum* (Fig. 135). In a previous study, we introduced the sexual morph of *Neohelicosporium fusisporum* from decaying fruit of Malvaceae sp. and asexual morph from the resulting culture (Jayasiri et al. 2017b).

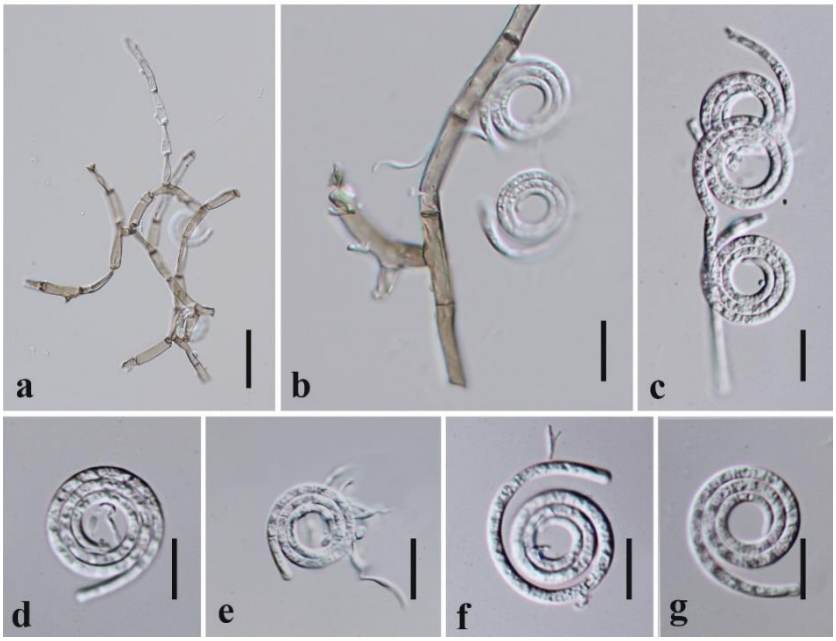


Figure 135 – *Neohelicosporium fusisporum* (MFLU 18–2176). a, b Conidiophores and conidiogenous cells. c–g Conidia. Scale bars: a–g = 10 µm.

90. ***Neohelicosporium hyalosporum*** Y.Z. Lu, J.C. Kang & K.D. Hyde, Mycological Progress 17 (5): 641 (2017) Fig. 136

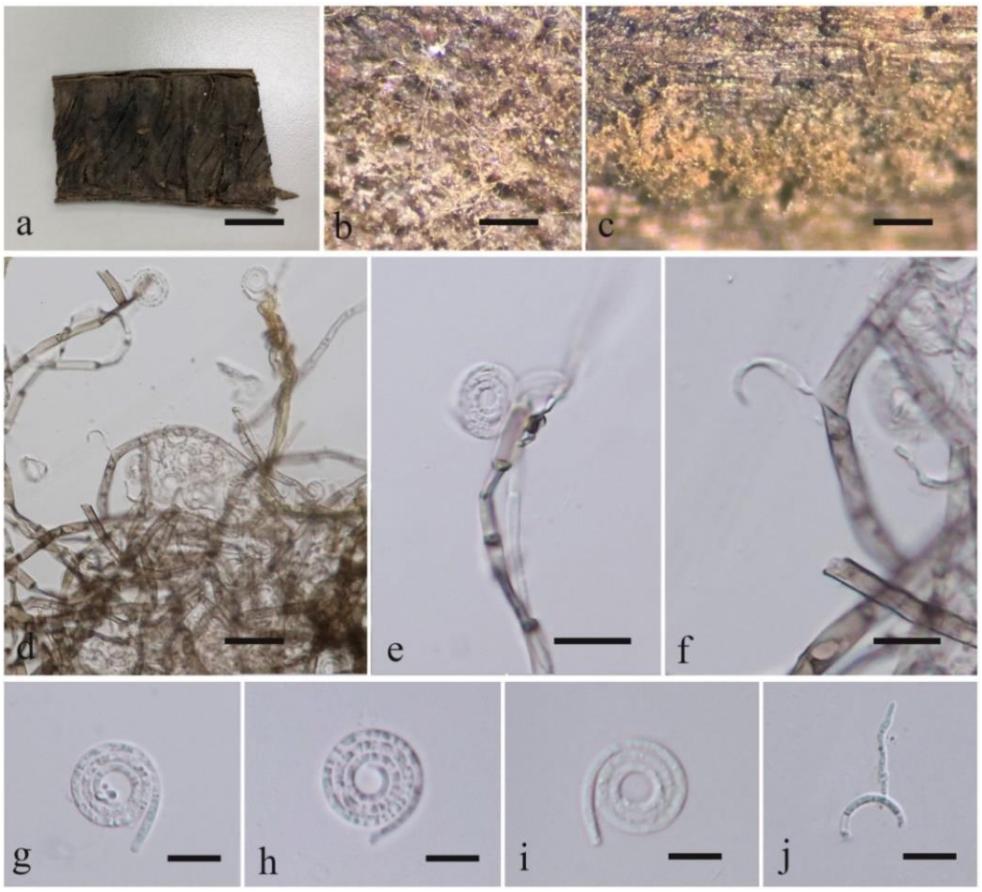


Figure 136 – *Neohelicosporium hyalosporum* (MFLU 18–2175). a Part of seed of pod. b, c Colonies on host material. d–f Hyphal arrangement and conidiogenous cells. g–i Conidia. j Germinated conidium. Scale bars: a = 1 cm, b, c = 500 µm, d, e = 10 µm, f–j = 10 µm.

Saprobic on submerged wood and pods of *Delonix regia.* Sexual morph: Undetermined. Asexual morph: Hyphomycetous, helicosporous. Colonies on the substratum superficial, effuse, gregarious, white. *Mycelium* composed of partly immersed, partly superficial, hyaline to pale brown, septate, abundantly branched hyphae, with masses of crowded, glistening conidia. *Conidiophores* macronematous, mononematous, flexuous, long, cylindrical, branched, septate, smooth-walled. *Conidiogenous cells* holoblastic, mono- to polyblastic, integrated, intercalary, cylindrical, with pale brown, smooth-walled denticles. *Conidia* 130–140 μm long × 3.5–4.5 μm diam. ($\bar{x}$ = 137 × 4.2 μm; n = 30), conidial filament 17–21 μm wide, ($\bar{x}$ = 19 μm; n = 30), solitary, pleurogenous, helicoid, hyaline, rounded at the tip, tightly coiled 3–3½ times, not loosely coiled in water, multi-septate, guttulate.

Culture characters – Conidia germinated on MEA and producing germ tubes within 12 hr. Colonies reaching 11 mm diam. in 2 weeks at 18°C, growing on MEA circular, flat at surface, entire at edge, pale brown to brown. Mycelium superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.

Material examined – THAILAND, Prachuap Khiri Khan Province, Bang Saphan District, decaying pod of *Delonix regia* (Fabaceae), 28 August 2018, S.C. Jayasiri, C 388 (MFLU 18–2175, new host record), living culture MFLUCC 18–0240, KUMCC 18–0261.

GenBank numbers – SSU: MK347886, ITS: MK347779, LSU: MK347996, *tef1*: MK360061, *rpb2*: MK434870

Notes – Our isolate is phylogenetically close (92% MLBS/0.96 BYPP, Fig. 132) to *Neohelicosporium hyalosporum.* Although it exhibits a few differences in morphology with shorter and narrower conidia and not uncoiling in water, its DNA sequences are identical to the holotype of *N. hyalosporum* (Fig. 136). Therefore, we record a new host species *Delonix regia* pod from Thailand for our new collection.

Pseudohelicomyces Y.Z. Lu, J.K. Liu & K.D. Hyde, Fungal Diversity 92: 248 (2018), nom. illegit., non Garnica & E. Valenz. (2000)

Recently introduced, this genus includes five species, *viz*. *P. aquaticus*, *P. hyalosporus*, *P. indicus*, *P. paludosus* and *P. talbotii* (Lu et al. 2018b). *Pseudohelicomyces* is a monotypic genus whose only species, *P. albus*, is based on the asexual morph of *Deconica merdaria* (Valenzuela & Garnica 2000, as "*Psilocybe merdaria*"), the genus is thus a junior heterotypic synonym of *Deconica*. We will be submitting a "Proposal to conserve *Pseudohelicomyces* Y.Z. Lu, J.K. Liu & K.D. Hyde (Tubeufiaceae) against *Pseudohelicomyces* Garnica & Valenz. (Hymenogastraceae)." Here we introduce a new species *Pseudohelicomyces quercus*. In addition, we present new records for *P aquaticus* and *P. talbotii* from decaying pod of *Tamarindus indica* and fruit of a *Meliaceae* sp. respectively.

91. *Pseudohelicomyces aquaticus* Y.Z. Lu, Boonmee & K.D. Hyde, Fungal Diversity 92: 250 (2018) Fig. 137

Index Fungorum number: IF555590; Facesoffungi number: FoF05325

Saprobic on wood and fruit of *Tamarindus indica.* Sexual morph: Undetermined. Asexual morph: Hyphomycetous, helicosporous. *Conidiophores* macronematous, mononematous, setiferous, erect, septate, unbranched, dark-brown, fertile in the middle, tapering to a narrow sub-acute sterile apex, smooth-walled, arising directly from a thick-walled, closely septate, repent hyphae on the substrate, crowded or in fascicles, glistening, light-coloured. *Conidiogenous cells* polyblastic, intercalary, rarely terminal, with lateral conspicuous denticles, each with single conidium. *Conidia* 80–100 μm long × 1–2 μm diam. ($\bar{x}$ = 19 × 1.9 μm; n = 20), conidial filament 18–21 μm wide ($\bar{x}$ = 19.5 μm; n = 30), coiled 3–4 times, tightly to loosely coiled, hyaline, rounded at apical end, truncate at base, septate, slightly constricted at septa, smooth-walled.

Culture characters – Spores germinated on MEA, colonies reaching 15–20 mm diam. in 2 weeks at 18^{o}C, colonies adpressed, circular, first cream-coloured becoming dark brown and rose in the centre of mycelium, reverse brown, slow growing.

Material examined – THAILAND, Chiang Rai Province, Doi Pui, decaying pod of *Tamarindus indica* (Fabaceae), 20 June 2017, S.C. Jayasiri, C 276 (MFLU 18–2127, new host record); living culture MFLUCC 17–2288, KUMCC 18–0283.

GenBank numbers – ITS: MK347744, LSU: MK347961

Notes – Morphologically and phylogenetically, our strain is in agreement with the type strain of *Pseudohelicomyces aquaticus* (Lu et al. 2018b) with high statistical support (90% MLBS/1.0 BYPP, Fig. 132). A comparison of the ITS nucleotides of *Pseudohelicomyces aquaticus* (MFLUCC 16–0234) and the new strain (MFLUCC 17–2288) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *P. aquaticus* (Jeewon & Hyde 2016). Therefore, we introduce pods of *Tamarindus indica* as a new host record the type strain was also reported from Thailand in an aquatic habitat.

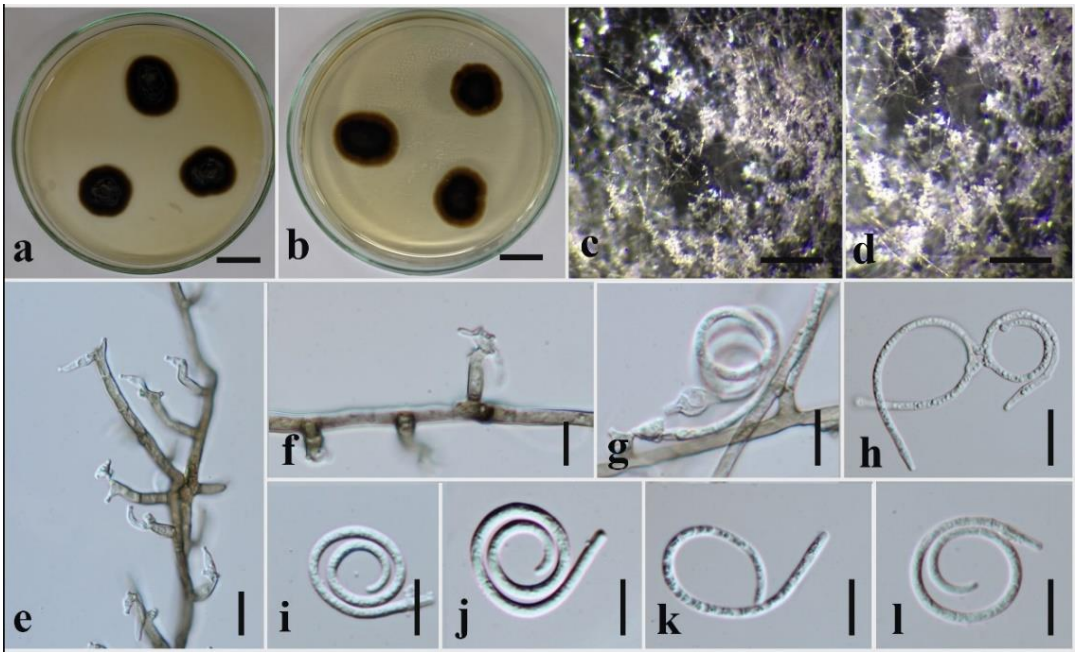


Figure 137 – *Pseudohelicomyces aquaticus* (MFLUCC 17–2288). a Top view of colony on MEA. b Reverse view of colony. c, d Fungus in culture. e–g Conidiophores and conidiogenous cells. h–l Conidia. Scale bars: a, b = 1 cm, c, d = 500 µm, e–l = 20 µm.

92. *Pseudohelicomyces quercus* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 138

Index Fungorum number: IF555587; Facesoffungi number: FoF05302

Holotype – MFLU 18–2091

Etymology – Referring to the host genus on which the fungus was collected, *Quercus* (Fagaceae).

Saprobic on fruit of *Quercus* sp. Sexual morph: *Ascomata* 150–200 µm high × 140–180 µm diam. ($\bar{x}$ = 175 × 160 µm), superficial, solitary, scattered, subglobose, ellipsoidal-ovate, with few hyphae developing from ascomatal base on substrate, pale brown to dark brown, velvety, ostiolate. *Peridium* 25–30 µm wide ($\bar{x}$ = 27 µm; n = 20), comprising 3–4 layers, composed of cells of *textura angularis*, with inner layer cells light brown and outer cells dark brown. *Hamathecium* comprised of 1–2 µm wide ($\bar{x}$ = 1.6 µm; n = 30), numerous, filiform pseudoparaphyses. *Asci* 85–110 × 6–8 µm ($\bar{x}$ = 92 × 7 µm; n = 20), 8-spored, bitunicate, cylindrical, apically thickened and rounded, with a pedicel. *Ascospores* 37–49 × 2–3 µm ($\bar{x}$ = 42 × 2.5 µm; n = 30), overlapping, fasciculate, hyaline, elongate-fusiform, with tapering and rounded ends, straight to slightly curved, 5–6-septate, not constricted at septa, smooth-walled. Asexual morph: Undetermined.

Culture characters – Ascospores readily germinated on MEA. Colonies on MEA reaching 10 mm diam. in 2 weeks at 18ºC, slow growing, circular, flat at surface, entire at edge, first cream-coloured, then becoming dark brown and raised in the centre with mycelium, reverse brown.

Material examined – THAILAND, Lamphang Province, on decaying fruit pericarp of *Quercus* sp. (Fagaceae), 30 August 2016, S.C. Jayasiri, C 143 (MFLU 18–2091, **holotype**), ex-type living culture MFUCC 17–0895, KUMCC 18–0284.

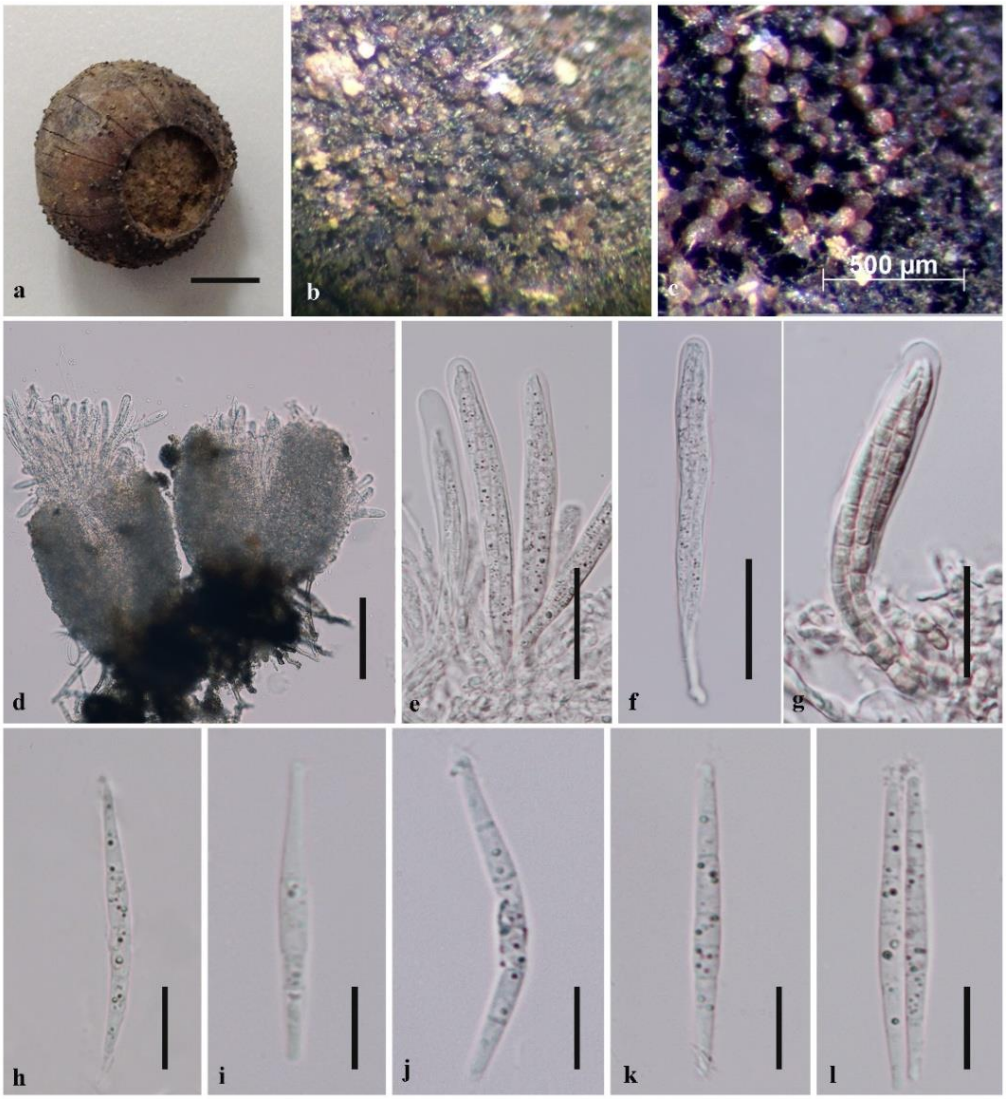


Figure 138 – *Pseudohelicomyces quercus* (MFLU 18–2091, holotype). a The host seed. b, c Superficial ascomata on substrate, oozing mass of ascospores at apex of ascomata. d Squash prepartion of ascomata. e–g Asci. h–l Ascospores. Scale bar: a = 1 cm, b = 100 µm, e–g = 30 µm, h–i = 10 µm.

GenBank numbers – SSU: MK347825, ITS: MK347720, LSU: MK347934, *tef1*: MK360077, *rpb2*: MK434906

Notes – *Pseudohelicomyces quercus* form a sister clade with two strains of *P. aquaticus* with high statistical support (80% MLBS/0.96 BYPP, Fig. 132). We could not induce sporulation of the asexual morph of *R. quercus. Pseudohelicomyces aquaticus* is known only as an asexual morph and therefore a morphological comparison of the two species is not possible. A comparison of the *tef1* nucleotides of these two species reveal 14 (1.5%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Pseudohelicomyces quercus (Fig. 138) fits well with the generic description in having superficial, pale brown to reddish-brown ascomata seated on a subiculum, cylindrical, pedicellate, Morphological and phylogenetic evidence places *Pseudohelicomyces quercus* as the sixth species

apically rounded asci and fusiform, straight or slightly curved, guttulate ascospores (Lu et al. 2018). of the genus *Pseudohelicomyces.*

93. *Pseudohelicomyces talbotii* (Goos) Y.Z. Lu & K.D. Hyde, Fungal Diversity 92: 252 (2018)
Figs 139, 140

≡ *Helicosporium talbotii* Goos, Mycologia 81(3): 368 (1989)

≡ *Helicosporium ramosum* P.H.B. Talbot, Bothalia 6: 493 (1956), nom. illegit., non (Berk. & M.A. Curtis) Massee 1893

Index Fungorum number: IF 555591; Facesoffungi number: FoF05326

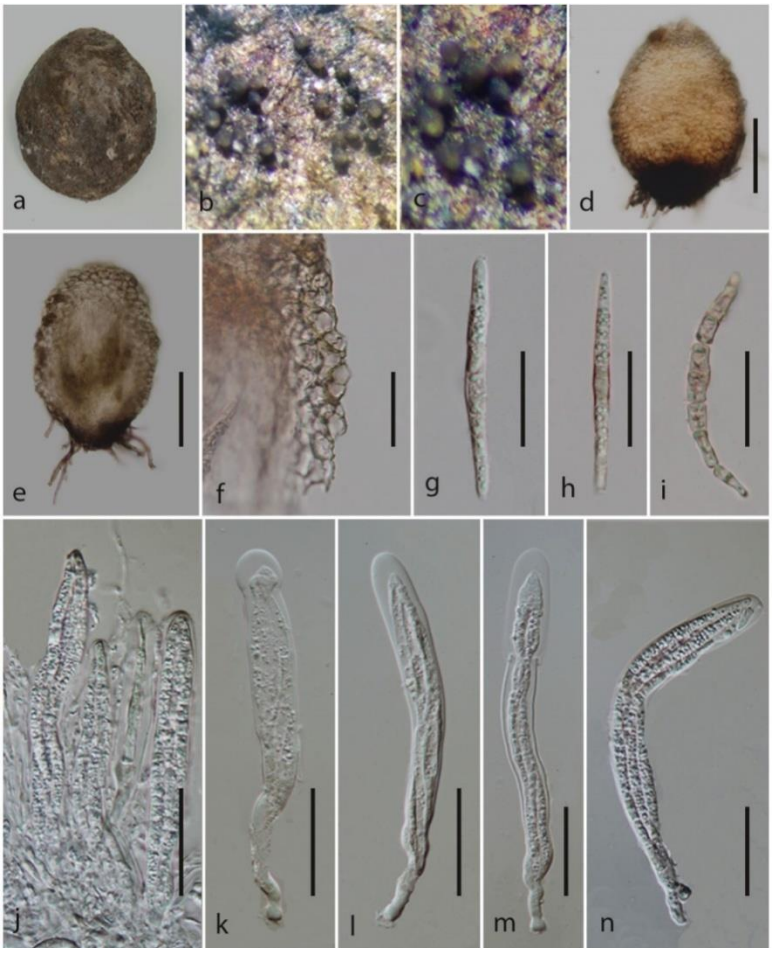


Figure 139 – *Pseudohelicomyces talbotii* (MFLU 16–0959). a Host fruit. b, c Superficial ascomata on substrate. d Close up view of ascoma. e Section through ascoma. f Peridium. g–i Ascospores. j Asci arranged with pseudoparaphyses. k–n Asci with ascospores. Scale bars: d, e = 100 µm, f, j–n = 30 µm, g–i = 20 µm

Saprobic on fruits of Meliaceae sp. Sexual morph: *Ascomata* 225–270 µm high × 138–200 µm diam. ($\bar{x}$ = 250 × 165 µm; n = 10), superficial, solitary, scattered, subglobose, ellipsoidal-ovate, with few hyphae developing from ascomatal base on substrate, dark brown to black, velvety, ostiolate. *Peridium* comprising 4–5 layers, composed of cells of *textura angularis*, with inner cells brown and outer cells dark brown. *Hamathecium* 1–2 µm wide ($\bar{x}$ = 1.7 µm; n = 30), filiform, hyaline, numerous, pseudoparaphyses. *Asci* 104–148 × 10–16 µm ($\bar{x}$ = 128 × 13 µm; n = 20), 8-spored, bitunicate, cylindrical, apically thickened and rounded, with a long pedicel. *Ascospores* 47–62 × 2.5–4.8 µm ($\bar{x}$ = 54 × 3.7 µm; n = 30), overlapping, fasciculate, hyaline to pale brown, cylindric-fusiform, with tapering and rounded ends, straight to slightly curved, 5–6-septate, constricted at septa, smooth-walled. Asexual morph: Hyphomycetous, helicosporous. *Conidiophores* macronematous, mononematous, dark-brown, erect, septate, branched, smooth-

walled, arising directly on substrate from thick-walled, closely septate, repent hyphae, crowded or in fascicles, glistening, light-coloured. *Conidiogenous cells* 7–15 × 3–5 µm ($\bar{x}$ = 13.5 × 4.2 µm; n = 20), polyblastic, intercalary, rarely terminal, with lateral minute denticles each with single conidium. *Conidia* 95–110 µm long × 2–2.5 µm diam. ($\bar{x}$ = 107 × 2.2 µm; n = 30), conidial filament 15–20 µm wide (17.4 µm; n = 30), coiled 3–4 times, tightly to loosely coiled, solitary, acropleurogenous, helicoid, hyaline, rounded at the tip, multi-septate, smooth-walled.

Culture characters – Spores germinated on MEA. Colonies on MEA reaching 15 mm diam. in 2 weeks at 18ºC. Colonies adpressed, circular, first cream-coloured, later becoming dark brown and rose in the centre of mycelium, reverse brown, and slow growing.

Material examined – THAILAND, Chiang Mai Province, Doi Suthep, 22 December 2015, on decaying fruits of Meliaceae sp., S.C. Jayasiri, C 126 (MFLU 16–0959, new host record), living culture MFUCC 16–0613, KUMCC 18–0285.

GenBank numbers – SSU: MK347819, ITS: MK347714, LSU: MK347928, *tef1*: MK360078, *rpb2*: MK434907

Notes – Our collection of *Pseudohelicomyces talbotii* is morphologically (Fig. 139) and phylogenetically (Fig. 132) similar to the fungus referred to as *Pseudohelicomyces talbotii* by Lu et al. (2018). A comparison of the ITS and *tef1* nucleotides of *Pseudohelicomyces talbotii* (MFLUCC 16–0234) and the new strain (MFUCC 16–0613) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *P. talbotii* (Jeewon & Hyde 2016). We record a new host on decaying fruits of Meliaceae sp. The fungus was previously recorded from decaying wood in aquatic and terrestrial habitats in China, Japan, Mexico, South Africa and Thailand (Lu et al. 2018).

Tubeufia Penz. & Sacc., Malpighia 11: 517 (1898)

A recent multigene phylogeny coupled with morphological data, recognised 50 species of *Tubeufia* (Lu et al. 2018). We add a new species and provide a new host record for *Tubeufia dictyospora* from decaying wild seed pods in Thailand (Fig. 132).

Figure 140 – Asexual morph of *Pseudohelicomyces talbotii* (MFUCC 16–0613). a Germinated ascospores. b Top view of colony on MEA. c Reverse view of colony. d–g Conidiophores and conidiogenous cells. h–k Conidia. Scale bars: a = 10µm, b, c = 1 cm, d–f = 30 µm, g = 20 µm, h–k = 10 µm.

94. *Tubeufia dictyospora* Y.Z. Lu, Boonmee & K.D. Hyde, Fungal Diversity 92 (1): 271 (2018)

Fig. 141

Saprobic on submerged wood and pod of *Delonix regia*. Sexual morph: undetermined. Asexual morph: Hyphomycetous, dictyosporous. *Conidiophores* lacking. *Conidiogenous cells* holoblastic, monoblastic, integrated, cylindrical, apical, pale brown. *Conidia* 65–110 × 53–94 µm ($\bar{x}$ = 95 × 70 µm; n = 20), dictyosporous, acrogenous, carbonaceous, friable, solitary, pale brown when young, becoming dark brown to black, variable in shape, globose to subglobose, ovoid to irregular, indistinctly dictyoseptate, verrucose.

Material examined – THAILAND, Phang Nga Province, Thap Put District, on decaying pod of *Delonix regia* (Fabaceae), 31 August 2017, S.C. Jayasiri, C 405 (MFLU 18–2177, new host record), living culture MFLUCC 17–2593, KUMCC 18–0301.

Culture characters – *Conidia* germinated on MEA and producing germ tubes within 24 hr. Colonies growing on MEA and reaching 20 mm diam. in 2 weeks at 18 ° C. Colonies circular, with flat surface, filiform at edge, brown to dark brown. Mycelium superficial and partially immersed, branched, septate, hyaline to pale brown.

GenBank numbers – ITS: MK347780, LSU: MK347998

Notes – *Tubeufia dictyospora* is characterized by dictyosporous conidia which are similar to *T. chlamydospora* (Lu et al. 2018). A comparison of the ITS nucleotides of *Tubeufia dictyospora* (MFLUCC 17–1805) and the new strain (MFLUCC 17–2593) revealed nucleotide differences ≤ 1.5%, which indicates that the new strain is *T. dictyospora* (Jeewon & Hyde 2016). We isolated a new strain of *T. dictyospora* from decaying pod of *Delonix regia* (Fig. 141); it was previously, recorded from decaying wood. *Tubeufia machaerinae* forms a sister clade to *T. dictyospora* and *T. chlamydospora* (MFLUCC 17–0055). *Tubeufia machaerinae* is characterized by helicosporous conidia (Lu et al. 2018).

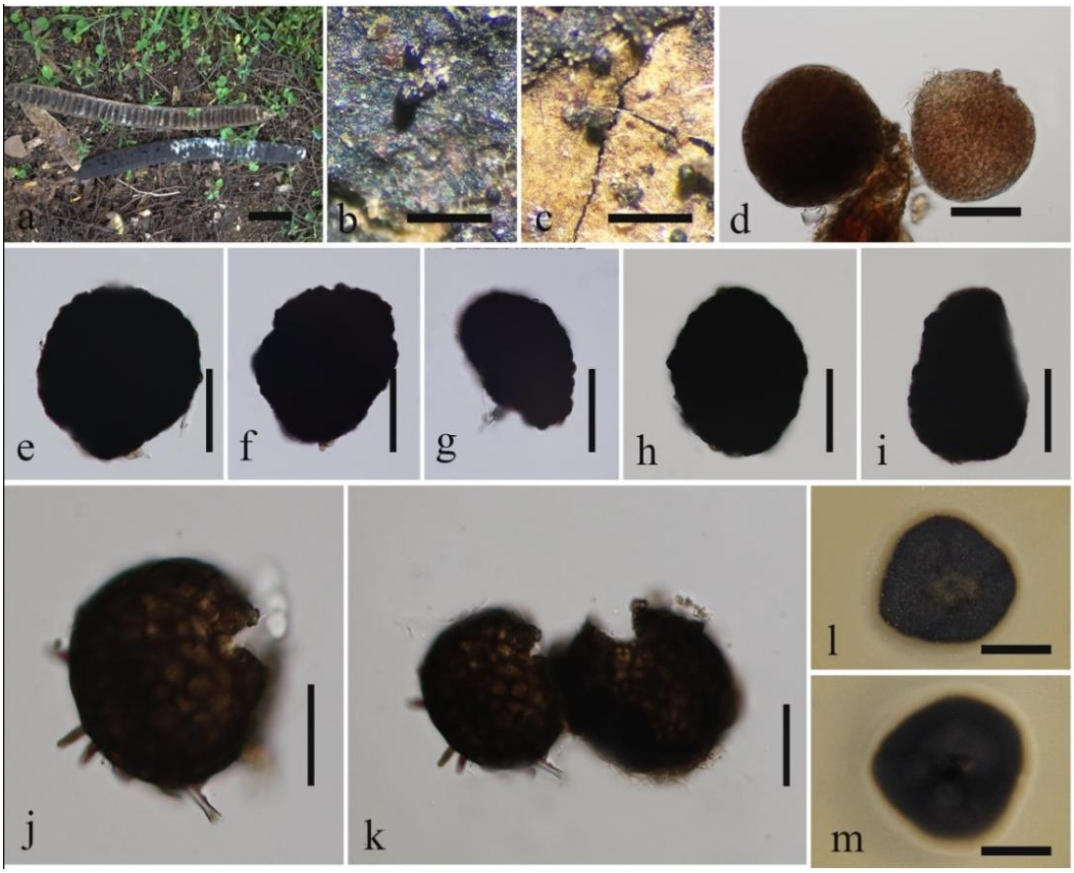


Figure 141 – *Tubeufia dictyospora* (MFLU 18–2177). a Part of host pod. b, c Colonies on decaying pod. d–k Conidia. l, m Colony on MEA from above and below. Scale bars: a = 1 cm, b, c = 500 µm, d–i, k = 50 µm, j = 30 µm, l, m = 1 cm.

95. *Tubeufia entadae* Jayasiri, E. B.G. Jones & K.D. Hyde, sp. nov. Fig. 142

Index Fungorum number: IF555588; Facesoffungi number: FoF05303

Holotype – MFLU 18–2102

Etymology – Referring to the host genus on which the fungus was collected, *Entada* (Fabaceae).

Saprobic on pod of *Entada phaseoloides*. Sexual morph: *Ascomata* 120–145 µm high × 95–105 µm diam. ($\bar{x}$ = 140 × 100 µm; n = 10), superficial, solitary, scattered, subglobose, ellipsoidal-ovate, with a few hyphae developing from ascomatal base on substrate, orange to brown, velvety, without a prominent ostiole. *Peridium* 17–23 µm wide ($\bar{x}$ = 21.5 µm; n = 20), comprising many indistinguishable layers, overlapping, composed of cells of *textura angularis* to *textura prismatica*, with base intermixed with plant tissues and dark brown thickening. *Hamathecium* comprising numerous, 1–2 µm wide ($\bar{x}$ = 1.8 µm; n = 30), filiform, hyaline pseudoparaphyses. *Asci* 104–125 × 10–16 µm ($\bar{x}$ = 120 × 14 µm; n = 20), 8-spored, bitunicate, cylindrical, apically thickened and rounded, short-pedicellate. *Ascospores* 50–64 × 3–5 µm ($\bar{x}$ = 60 × 4 µm; n = 30), overlapping fasciculate, pale pinkish brown, cylindric-fusiform, with tapering and rounded ends, straight to slightly curved, 8–9-septate, constricted at septa, smooth-walled. Asexual morph: Undetermined.

Culture characters – Conidia germinated on MEA, colonies reaching 20 mm diam. in 2 weeks at 18ºC. Colonies on MEA appear, circular, first cream-coloured, later becoming dark brown and raised in the centre with mycelium, reverse brown.

Material examined – THAILAND, Chiang Rai Province, Khun Korn waterfall (19˚ 52' 5" N, 99˚ 38' 5" E), on decaying pod of *Entada phaseoloides* (Fabaceae), 2 February 2017, S.C. Jayasiri, C 218 (MFLU 18–2102, holotype; KUN-HKAS, isotype).

Figure 142 – *Tubeufia entadae* (MFLU 18–2102, holotype). a Part of the host seed pod. b, c Ascomata on substrate. d Ascoma. e Section through ascoma. f–h Ascospores. i–m Asci. Scale bars: a = 1 cm, b, c = 500 µm, d, e, i = 50 µm, f–h = 20 µm, j–m = 30 µm.

GenBank numbers – SSU: MK347834, ITS: MK347727, LSU: MK347943

Notes – *Tubeufia entadae* forms a sister clade to *T. chiangmaiensis* (MFLUCC 11–0514) with high statistical support (75% MLBS/0.96 BYPP, Fig. 132). However, these two species share few morphological characters in common. *Tubeufia chiangmaiensis* has dark brown ascomata with brown to reddish-brown peridial cells and hyaline to pale brown ascospores (Boonmee et al. 2014). *Tubeufia entadae* is characterized by pale brown to orange ascomata with out well developed peridium and pinkish brown ascospores in immature stage (Fig. 142). A comparison of the ITS nucleotides of these two strains reveals 17 (3.4%) nucleotide differences, which indicates that they are distinct taxa (Jeewon & Hyde 2016).

Venturiales Yin. Zhang & K.D. Hyde, Fungal Diversity 51: 249–277 (2011)

Sympoventuriaceae Yin. Zhang, C.L. Schoch & K.D. Hyde, Fungal Diversity 51: 251 (2011)

These fungi exhibit a parasitic or saprobic lifestyle and occur on leaves or stems of dicotyledons (Zhang et al. 2011). Subsequently, Samerpitak et al. (2014) recorded that nearly all members of Venturiales are plant pathogens as well as associated with animals. This order comprises two families Sympoventuriaceae and Venturiaceae. *Ochroconis* is a genus belonging to the family Sympoventuriaceae.

Ochroconis de Hoog & Arx, Kavaka 1: 57 (1973)

Ochroconis is reported as mesophilic, with several species causing infections in cold-blooded animals (Samerpitak et al. 2014). Currently, 28 species have been reported from this genus, including our new species (Fig. 143).

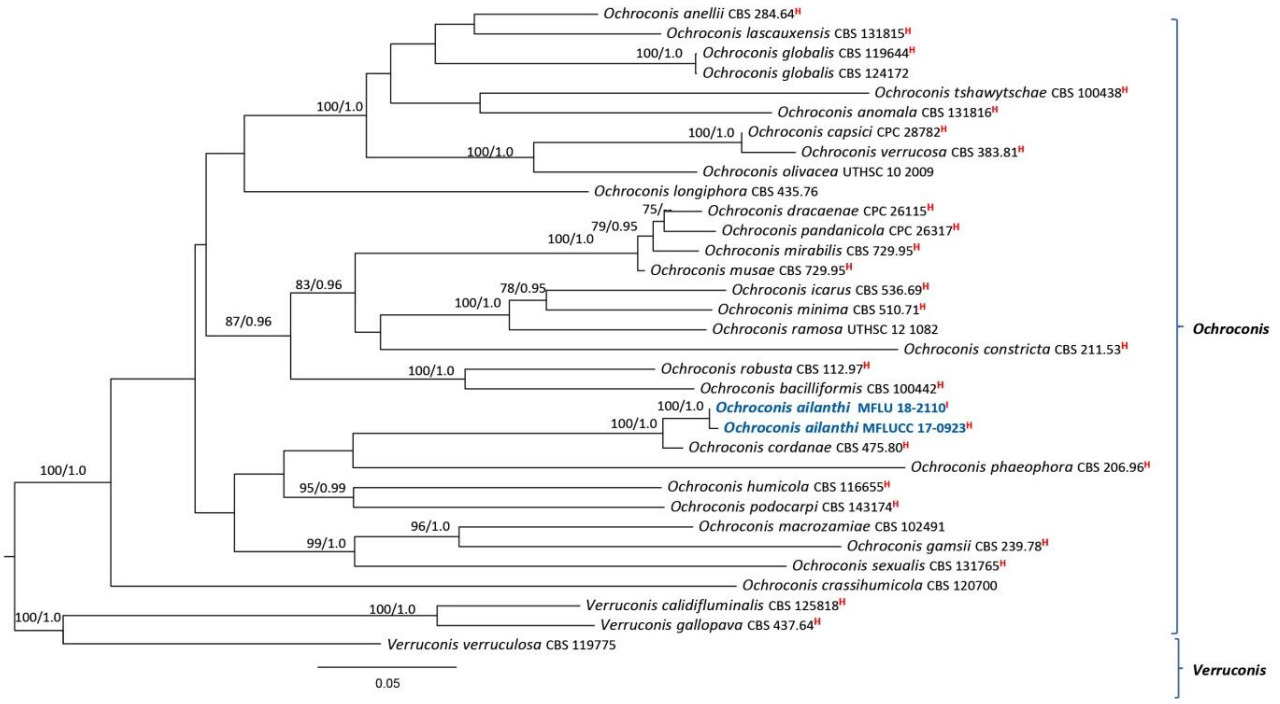


Figure 143 – Simplified phylogram showing the best RAxML maximum likelihood tree obtained from the combined SSU, ITS, LSU, *tub2* and actin matrix of eleven taxa including related species

of the genus *Ochroconis*. The matrix comprised 4379 characters including alignment gaps. The tree was rooted with *Verruconis* spp. (CBS 437.64, CBS 125818 and CBS 119775). The best scoring RAxML tree with a final likelihood value of -3200.844946 is presented. The matrix had 1673 distinct alignment patterns, with 24.27% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238060, C = 0.237325, G = 0.294478, T = 0.230137; substitution rates AC = 0.876705, AG = 1.707991, AT = 0.830163, CG = 0.856733, CT = 2.871062, GT = 1.000000. ML bootstrap support (first set) equal or greater than 70 % and Bayesian posterior probabilities equal or greater than 0.95 are given near to each branch. New isolates are in blue. Strains isolated from the holotype and isotype specimens are indicated in red superscript ^{H}, and ^{I} respectively.

96. *Ochroconis ailanthi* Jayasiri, E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 144

Index Fungorum number: IF555608; Facesoffungi number: FoF05304

Holotype – MFLU 18–2108

Etymology – Referring to the host genus on which the fungus was collected, *Ailanthus* (Simaroubaceae).

Saprobic on pod of *Ailanthus* sp. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Hyphae* 2.0–2.5 µm wide ($\bar{x}$ = 2.2 µm; n = 20), branched, with thin septa, hyaline to pale brown, smooth-walled. *Conidiophores* differentiated, arising at right angles from creeping hyphae, unbranched, with thin septa, straight to flexuous, brown, thick-walled, rhexolytic, producing conidium-bearing denticles that are widely spaced in the apical region. *Conidia* 9–10 × 2.4–2.6 µm ($\bar{x}$ = 9.4 × 2.5 µm; n = 20), solitary, dark brown, fusiform, with a thick median septum, with longitudinally striate, thick-walled.

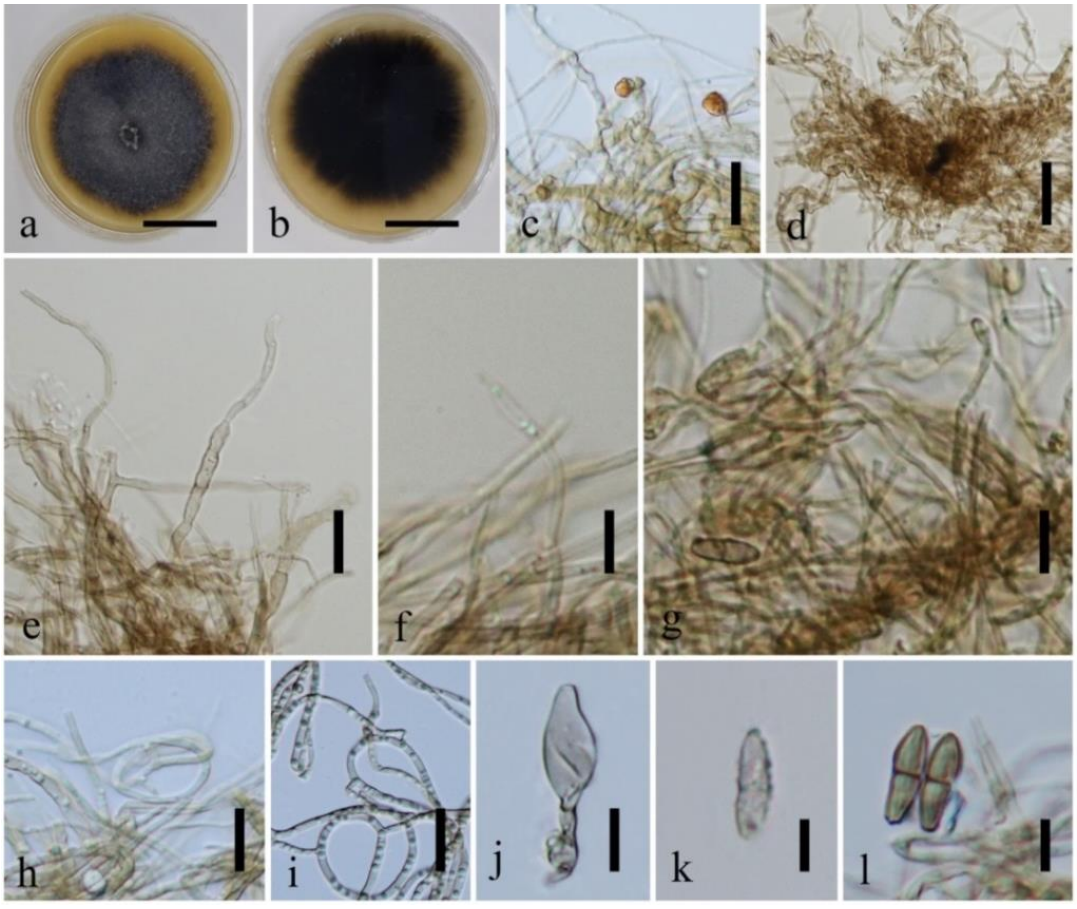


Figure 144 – *Ochroconis ailanthi* (MFLUCC 17–0923, ex-type). a Top view of culture. b Reverse view of culture. c–i Hyphal coils and anastomosing hyphae. j–l Conidia. Scale bars: a, b = 1 cm, c–i = 10 µm, j–l = 5µm.

Culture characters – Conidia germinated on MEA within 24 hr. Colonies growing on MEA 4 mm diam. after 30 days at 18ºC, moderate growth, circular, effuse, dense, dark brown, diffuse into media, rough at surface, with entire to slightly undulate edge, with grey white pigment.

Material examined – THAILAND, Chiang Rai Province, Doi Pui (19˚ 49' 31" N, 99˚ 52' 23") on fallen pod of *Ailanthus* sp. (Simaroubaceae), 2 February 2017, S.C. Jayasiri, C 228 (MFLU 18–2108, holotype; KUN-HKAS 102416, isotype), ex-type living culture MFLUCC 17–0923, KUMCC 18–0270; C 229 (MFLU 18–2110).

GenBank numbers – MFLUCC 17–0923: SSU: MK347838, ITS: MK347730, LSU: MK347947, *tub2*: MK412883, actin: MK412893; MFLU 18–2110: SSU: MK347839, ITS: MK347731, LSU: MK347948, *tub2*: MK412881, ACT: MK412892

Notes – *Ochroconis ailanthi* is introduced based on morphological and phylogenetic differences with other species in the genus. In multi loci phylogenetic analysis of SSU, ITS, LSU, *tub2* and actin genes, *O. ailanthi* forms a sister clade to *O. cordanae* (CBS 475.80) with high statistical support (100% MLBS/1.0 BYPP, Fig. 143). However, *O. ailanthi* (Fig. 144) has dark brown fusiform conidia with longitudinal striations while *O. cordanae* has pale brown, cylindrical conidia without longitudinal striations (Samerpitak et al. 2014). Base pair differences between the two species were 13 (5.1%) and 26 (10.4%) base pairs for *tub2* and actin, respectively.

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

Hymenogastraceae Vittad. [as 'Hymenogastereae'], Monogr. Tuberac. (Milano): 11 (1831)

In this study, we point out that the genus *Pseudohelicomyces* Garnica & E. Valenz (2000) is a junior heterotypic synonym of *Deconica*.

Deconica (W.G. Sm.) P. Karst., Bidr. Känn. Finl. Nat. Folk 32: XXVI (1879)

= *Pseudohelicomyces* Garnica & E. Valenz., Mycological Research 104(6): 739 (2000)

Notes – The monotypic genus *Pseudohelicomyces* Garnica & E. Valenz was established by Valenzuela & Garnica (2000) based on the type species *Pseudohelicomyces albus*, which was introduced as the asexual morph of *Psilocybe merdaria*. Noordeloos (2009) transferred *Psilocybe merdaria* to *Deconica merdaria*. Based on "One Fungus = One Name" (Hawksworth et al. 2011, Hawksworth 2012), *Pseudohelicomyces albus* is a junior synonym of the currently accepted name *Deconica merdaria*. Therefore, the genus *Pseudohelicomyces* Garnica & E. Valenz (not *Pseudohelicomyces* Y.Z. Lu, J.K. Liu & K.D. Hyde) is a junior heterotypic synonym of *Deconica*.

Deconica merdaria (Fr.) Noordel., Öst. Z. Pilzk. 18: 199 (2009)

≡ *Agaricus merdarius* Fr., Syst. mycol. (Lundae) 1: 291 (1821)

≡ *Psilocybe merdaria* (Fr.) Ricken, Die Blätterpilze: 251 (1912)

= *Pseudohelicomyces albus* Garnica & E. Valenz., Mycological Research 104(6): 739 (2000)

Notes – *Agaricus merdarius* was introduced by Fries (1821). Ricken (1912) synonymized it as *Psilocybe merdaria*. *Pseudohelicomyces albus* was introduced as the asexual morph of *Psilocybe merdaria* by Valenzuela & Garnica (2000). Noordeloos (2009) transferred *Agaricus merdarius* and *Psilocybe merdaria* as *Deconica*, thus the currently accepted name for *Agaricus merdarius*, *Psilocybe merdaria* and *Pseudohelicomyces albus* is *Deconica merdaria*.

Discussion

In this paper we document saprobic Dothideomycetes from selected seed pods and fruits in wild plant species. There are 8 new genera, 50 new species and 38 new host records. These novelties are accommodated in 35 families in the class Dothideomycetes. The study was based on decaying wild seed pods and fruits mainly from Thailand and a few from China and the UK. The saprobic species were from 18 host plant families. Fifty species were found on the family Fabaceae, including 16 species from *Leucaena*. Magnoliaceae, Fagaceae, Pinaceae, and Bignoniaceae yielded 12, 10, 5 and 4 species respectively.

In our study 38 new host records are reported based on multigene phylogeny coupled with morphological studies. If fungal occurrence is genus-specific as compared to host-specific, this would have important implications for estimates of fungal numbers (Jeewon et al. 2004, Hyde et al. 2007). In our study, we introduced a new genus in the family Bambusicolaceae with two new species from host genus *Leucaena* and observed that fungal species from other genera of this family could also be associated with other hosts. Based on previous studies, *Leptoxyphium kurandae* was thought to be host specific to *Hibiscus* but we found it on fruit of *Lagerstroemia loudoni* (Crous et al. 2011, Choi et al. 2015). According to Phillips et al. (2013), confirmed hosts for *Diplodia mutila* are *Chamaecyparis lawsoniana*, *Fraxinus*, *Malus*, *Populus*, *Taxus baccata* and *Vitis vinifera* together with a recent record on *Juglans regia* (Díaz et al. 2018). We isolated a new strain from a cone of *Magnolia grandiflora* from China. Some species have been presumed to be host-specific, for instance *Diplodia sapinea* has been recorded worldwide, especially as pathogens from *Pinus* species (Palmer et al. 1987) but in this study we also report *D. sapinea* as a saprobe from a pine cone in China which indicates that this species can exhibit different lifestyle (Promputtha et al. 2007).

Fungi are capable of shifting their modes of nutrition, for instance many endophytic and pathogenic fungi may persist as saprobes once the plant organ, on which they inhabit, has aged and senesced (Zhou & Hyde 2001, Photita et al. 2004, 2005, Promputtha et al. 2005, Promputtha et al. 2010). In our study, a new species (*Austropleospora keteleeriae*) and a new host record (*A. archidendri*) are reported from decaying pod of *Leucaena* sp. as saprobes. However, these are the first report of *Austropleospora* spp. as saprobes. Previous studies have reported *Austropleospora archidendri* as pathogens on *Pithecellobium bigeminum* and *Austropleospora osteospermi* on *Chrysanthemoides monilifera* and *Osteospermum* sp. (Morin et al. 2010, Verkley et al. 2014). These taxa collected herein could also have been pathogens before they become saprobes. *Didymella coffeae-arabicae* has been reported as plant pathogens in the family Didymellaceae but in our study we recorded it as a saprobic species from fallen *Leucaena* sp. pod. *Nothophoma quercina* is also reported as pathogens on many plant species, however we collected it from decaying cone of *Keteleeria fortunei.* Samerpitak et al. (2014) recorded that nearly all members of Venturiales are plant pathogens as well as being associated with animals while in our study we introduced a new saprobic species of *Ochroconis* from decaying seed pods of *Ailanthus* sp. in China.

Vargamyces aquaticus was reported as a saprobic freshwater fungus (Zhang et al. 2009a, b), but we found it on *Fagus sylvatica* cupules in a terrestrial environment. *Delitschia* species are mostly reported from dung, rarely on aged wood or plants, but recently introduced from a freshwater habitat. In the present study we found it on *Nypa fruticans* in estuarine habitats. *Verruculina* was introduced to accommodate an obligate marine species and in our study and we provide a new host record from fallen fruit of *Pandanus* sp. the in intertidal zone in Thailand. *Neofusicoccum* species are important plant pathogens (Phillips et al. 2013, Marin-Felix et al. 2017), but we isolated *N. parvum* from wild seed pod and cone of *Cercis chinensis* and *Magnolia grandiflora* from China.

Dothideomycetes from wild seed pods and fruits are more diverse than expected with possibly a broad range of host association, wide environmental adaptations with a possible transition from pathogenic mode of life to saprobic one. Further studies are needed for other Ascomycetes to obtain a better picture of diversity of fungi from wild seeds and fruits. This study gives a better knowledge about saprobic species that can be associated with wild plant species and it will be important to ecologist and agricultural scientist as well. Therefore, knowledge about these groups is important for sustainability in wild environment.

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