

ARTICLE

Taxonomy and biological properties of Ascomycota on *Bidens pilosa* and *Chromolaena odorata* in Northern Thailand with a global checklist

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Abstract

Bidens pilosa and *Chromolaena odorata* are widespread weeds in Asteraceae, recognized as invasive species in many regions worldwide. Comparative research on fungal diversity across Asteraceae weeds remain limited, with only a few studies conducted on the diversity of saprobic fungi on these weeds. Further research is necessary to discover the potential ecological or biotechnological benefits of these taxa. In this study, saprobic fungi collected from *Bidens pilosa* and *Chromolaena odorata* in northern Thailand comprises 44 species, distributed across 30 genera, 20 families, and six orders within Dothideomycetes and Sordariomycetes. Among them, 17 species are identified as novel (*Albifimbria bidentis*, *Austropleospora chromolaenae*, *Bahusandhika bidentis*, *Dothiorella asteracearum*, *D. chromolaenae*, *Diaporthe asteracearum*, *D. chromolaenicola*, *Forliomyces bidentis*, *Fusarium bidentis*, *F. chromolaenae*, *Kalmusia thailandica*, *Pseudothyridariella asteracearum*, *Ps. thailandica*, *Pseudolophiostoma chromolaenae*, *Pseudoneoconiothyrium chromolaenae*, *Pseudo. thailandicum*, *Sarocladium bidentis*). In addition, 20 new host records (*Acrocalymma pterocarpi*, *Bahusandhika indica*, *Colletotrichum gigasporum*, *C. truncatum*, *Diaporthe biconispora*, *Dictyocheirospora nabanheensis*, *Dendryphion hydei*, *Fusarium hainanense*, *Lasiodiplodia henanica*, *L. theobromae*, *Leptospora thailandica*, *Montagnula chromolaenae*, *Neodendryphiella mali*, *Neorousoella entadae*, *Periconia byssoides*, *Pseudopithomyces chartarum*, *Remotididymella anthropophila*, *R. fici-microcarpae*, *Torula canangae*, and *T. mackenziei*) are documented. The species boundaries were delineated based on morphology and multi-gene phylogenetic approaches. Additionally, the preliminary assays revealed antibacterial activity in 36 species against *Bacillus subtilis*, *Escherichia coli*, and *Staphylococcus aureus*, highlighting their biotechnological potential. Furthermore, a global checklist documented 76

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fungal taxa on *Bidens pilosa* and 161 fungal taxa on *Chromolaena odorata*, highlighting their roles as reservoirs of fungal diversity. This study expands the taxonomic and ecological understanding of microfungi associated with invasive Asteraceae weeds in Thailand and the host-fungal relationships in a global context by encouraging future mycological and ecological research efforts.

Keywords – 17 new taxa – antibacterial properties – fungal checklist – Dothideomycetes – multi-gene phylogeny – Sordariomycetes.

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The taxa reported in this study are classified according to the outline of fungi and fungus-like taxa provided by Hyde et al. (2024), with updates incorporated from recent relevant literature.

Phylum Ascomycota

Class Dothideomycetes sensu O.E. Erikss & Winka

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Aplosporellaceae Slippers, Boissin & Crous

1. *Aplosporella hesperidica* Speg.

Botryosphaeriaceae Theiss. & H. Syd.

2. *Dothiorella asteracearum* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**
3. *Dothiorella chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**
4. *Lasiodiplodia henanica* Z.P. Dou, Y. Wang & Y. Zhang **ter, a new host record and a new geographical record**
5. *Lasiodiplodia theobromae* (Pat.) Griffon & Maubl., **a new host record**

Hysteriales Lindau

Hysteriaceae Chevall

6. *Rhytidhysterion bruguierae* Dayarathne, **a new host record**

Pleosporales Luttr. ex M.E. Barr

Acrocallymmaceae Crous & Trakun

7. *Acrocallymma pterocarpi* Jayasiri, E.B.G. Jones & K.D. Hyde, **a new host record**

Dictyosporiaceae Boonmee & K.D. Hyde

8. *Dictyocheiropora nabanheensis* Tibpromma & K.D. Hyde, **a new host record**
9. *Neodendryphiella mali* Iturr.-Gonz., Gené & Dania García, **a new host record**

Didymellaceae Gruyter, Aveskamp & Verkley

10. *Remotididymella anthropophila* Valenz. Lopez, Cano, Guarro & Stchigel, **a new host record and a new geographical record**
11. *Remotididymella fici-microcarpae* Kular, **a new host record and a new geographical record**

Didymosphaeriaceae Munk

12. *Austropleospora chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**
13. *Chromolaenicola nanensis* Mapook & K.D. Hyde
14. *Kalmusia thailandica* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**
15. *Montagnula chromolaenae* Mapook & K.D. Hyde, **a new host record**
16. *Montagnula donacina* (Niessl) Wanas., E.B.G. Jones & K.D. Hyde
17. *Pseudopithomyces chartarum* (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, **a new host record**

Lentimurisporaceae N.G. Liu, J.K. Liu & K.D. Hyde

18. *Bahusandhika bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**
19. *Bahusandhika indica* (Subram.) Subram, **a new host record and a new geographical record**

Lophiostomataceae Sacc.

20. *Pseudocapulatispora longiappendiculata* Mapook & K.D. Hyde

21. *Pseudolophiostoma chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Periconiaceae Nann

22. *Periconia byssoides* Pers., **a new host record**

Phaeosphaeriaceae M.E. Barr

23. *Leptospora thailandica* Phukhams. & K.D. Hyde, **a new host record**

24. *Murichromolaenicola thailandensis* Htet, Mapook & K.D. Hyde

Roussoellaceae Jian K. Liu, Phook., D.Q. Dai & K.D. Hyde

25. *Neoroussoella entadae* Jayasiri, E.B.G. Jones & K.D. Hyde, **a new host record**

26. *Pseudoneoconiothyrium chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

27. *Pseudoneoconiothyrium thailandicum* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Sporormiaceae Munk

28. *Forliomyces bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Thyridariaceae Q. Tian & K.D. Hyde

29. *Pseudothyridariella asteracearum* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

30. *Pseudothyridariella thailandica* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

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33. *Torula fici* Crous, **a new host record**

34. *Torula mackenziei* Jun F. Li, Phook. & K.D. Hyde, **a new host record**

Class Sordariomycetes O.E. Erikss. & Winka

Diaporthales Nannf.

Diaporthaceae Höhn. ex Wehm

35. *Diaporthe asteracearum* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

36. *Diaporthe biconispora* F. Huang, K.D. Hyde & Hong Y. Li, **a new host record and a new geographical record**

37. *Diaporthe chromolaenicola* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Subclass Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert

Glomerellaceae Locq. ex Seifert & W. Gams

38. *Colletotrichum gigasporum* Rakotonar & Munaut, Mycological Progress 12(2): 407 (2012)

39. *Colletotrichum truncatum* (Schwein) Andrus & W. D. Moore, Phytopathology 25:121 (1935)

Hypocreales Lindau

Nectriaceae Tul. & C. Tul

40. *Fusarium bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

41. *Fusarium chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

42. *Fusarium hainanense* M.M. Wang, Qian Chen & L. Cai, **a new host record and a new geographical record**

Sarocladiaceae L. Lombard

43. *Sarocladium bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Stachybotryaceae L. Lombard & Crous

44. *Albifimbria bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

INTRODUCTION

Asteraceae is a globally distributed plant family, occurring across tropical to temperate regions (Xu & Chang 2017, Yu et al. 2025). The family includes both economically important plants and aggressive weed species (Karlsson et al. 2008, Jayasundera 2021). Invasive Asteraceae weeds, such as *Bidens pilosa* L. and *Chromolaena odorata* (L.) R.M. King & H. Rob., negatively impact native plant communities and lead to significant economic losses in agricultural sectors (Weidlich et al. 2020, Zungsontiporn 2007). Both plants have been reported to harbor a high diversity of weed-associated fungi (Guatimosim et al. 2015, Mapook et al. 2020).

Bidens pilosa is considered one of the most invasive weeds worldwide. This is also known as “blackjack” due to its small, black, stiff bristles. *Bidens pilosa* L. was first formally described by Carl Linnaeus in 1753 (Karis & Ryding 1994). There are 230 to 240 species in *Bidens* distributed across tropical to temperate regions (Norton 1991, Bartolome et al. 2013, Lizarazu et al. 2024). *Bidens pilosa* is native to America and it has become an invasive weed globally (Mahmoud et al. 2015, Shiba et al. 2024). By the 1990s, *B. pilosa* was already considered as one of the worst invasive weeds in Latin America and eastern Africa (Mitich 1994, Wagner et al. 1999). Currently, this invasiveness has increased aggressively across Asia, Africa, Australia, South America and the Pacific islands (Shiba et al. 2024). Despite its invasive nature, *Bidens pilosa* has been widely used as a traditional medicine to treat diarrhoea, enteritis, and malaria in Africa and South America (Chih et al. 1995, Alvarez et al. 1999, Adia et al. 2014). In Brazil, *B. pilosa* is locally known as picão-preto, which is recommended for its anti-inflammatory, anti-infective (for urinary tract), anti-diabetic, and anti-bronchitis properties, as well as for treating muscular pain, rheumatism, sore throat, and stomach pain (Borges et al. 2023). In western Uganda, the aqueous leaf extracts of *B. pilosa* are used in indigenous medicine for therapeutic uses and in herbal remedies for childbirth (Kamatenesi-Mugisha et al. 2007). Beside medicinal applications, Poonpaiboonpipat & Poolkum (2019) discussed the use of *B. pilosa* combined with water irrigation for weed control and rice production.

Bidens pilosa was reported to have a high weed-associated fungal diversity (Guatimosim et al. 2015). Guatimosim et al. (2015) investigated fungal pathogens associated with this host and provided a list of fungi reported. A comparative study conducted on arbuscular mycorrhizal fungal diversity on *Ambrosia artemisiifolia* and *B. pilosa* revealed that *Septoglomus viscosum*, *S. constrictum*, and *Glomus perpusillum* are common in both weeds (Zhang et al. 2018). Li et al. (2020) carried out research on herbaceous litter in Thailand, and *Dendryphion hydei* was isolated on *B. pilosa*. Htet et al. (2024a) studied fungi on Asteraceae and introduced *Pseudorousoella bidenticola* on *B. pilosa*. Htet et al. (2024b) studied the diversity of *Chromolaenicola* species on *B. pilosa* with the potential antibacterial activity of *Chromolaenicola* taxa.

Chromolaena odorata (Asteraceae) is an invasive weed affecting many tropical countries, including Thailand (Goodall & Erasmus 1996, Muniappan et al. 2005, Zachariades et al. 2009, Catarino et al. 2019). The invasiveness of this weed has led to many negative impacts on natural biodiversity and the economy (Hu & Zhang 2013, Sinha et al. 2022). Li et al. (2017) described a new species, *Torula chromolaenae* and a new host record for *T. fici* from *C. odorata* in northern Thailand. Crous et al. (2018) introduced a new genus, *Neocochlearomyces* from *C. odorata*, while Li et al. (2020) reported *Torula hydei* from its leaves and dead branches in Thailand. Mapook et al. (2020) studied microfungi from *C. odorata*, resulting in the discovery of 60 new fungal taxa, with their potential biological properties. The results showed that several members of Phaeosphaeriaceae on *C. odorata*, such as *Leptospora chromolaenae*, *L. phraeana*, *Murichromolaenicola chromolaenae*, *Paraleptospora chromolaenae*, *P. chromolaenicola*, *Pseudoophiosphaerella huishuiensis*, *Pseudostaurosphaeria chromolaenae*, *Ps. chromolaenicola*, and *Yunnanensis chromolaenae* have antimicrobial properties. Moreover, different solvent extracts from various plant parts of *C. odorata* have demonstrated significant antimicrobial properties (Vital & Rivera 2009, Thophon et al. 2016, Hridhya & Kulandhaivel 2017, Mathew et al. 2022), highlighting its potential for biotechnological applications.

Despite recent molecular advances, many Ascomycota associated with *B. pilosa* and *C. odorata* remain poorly characterized genetically, while their biological and biochemical potential is

largely unexplored. In this study, we aim to document Ascomycota diversity on *B. pilosa* and *C. odorata* through integrated morphological and multi-gene phylogenetic analyses and explore their potential biological properties. Our study also provided a worldwide checklist of fungi associated with both plant species, serving as a foundational resource for future taxonomic, ecological, and applied research on weed-associated fungi. By bridging these knowledge gaps, our work provides a systematic framework for understanding plant-fungal relationships in invasive Asteraceae hosts while highlighting underexplored microbial resources.

MATERIALS AND METHODS

Field collection and preservation of samples

Dead stems of *Bidens pilosa* and *Chromolaena odorata* were collected from different collecting sites in Chiang Mai, Chiang Rai and Phayao Provinces, Thailand (Fig. 1). The collecting sites map (Fig.1) was created using DIVA-GIS (v.7.4) using provincial boundaries of Thailand. All specimens were kept in plastic bags labeled with collection details and taken into the laboratory. Living cultures were kept at the Mae Fah Luang University Culture Collection (MFLUCC), while specimens were placed at the Herbarium (Herb. MFLU). As directed by Jayasiri et al. (2019) and Index Fungorum (2025), Faces of Fungi (FoF) numbers and Index Fungorum (IF) numbers were acquired. Additionally, the species descriptions were uploaded to the GMS Microfungi database (Chaiwan et al. 2021).

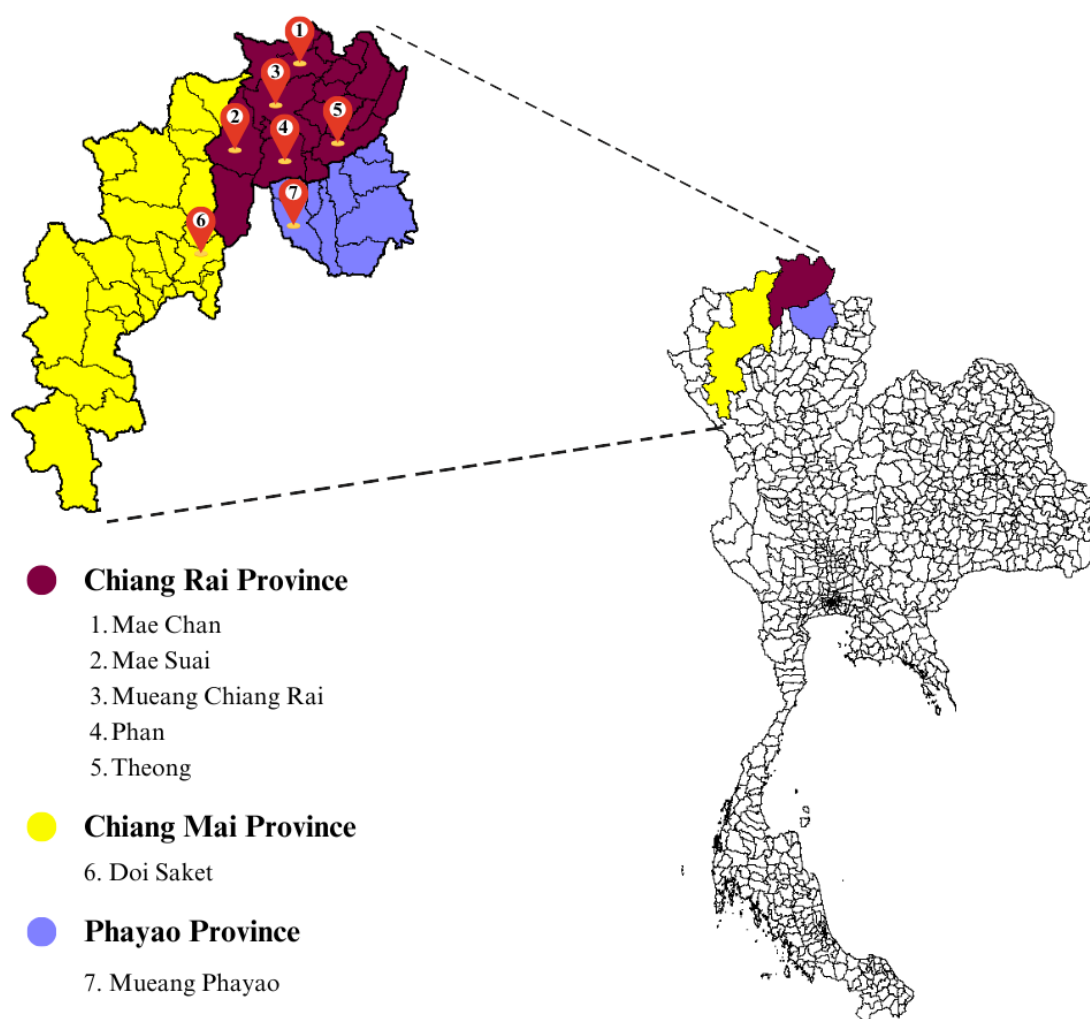


Figure 1 – Geographical locations where samples were collected in northern Thailand. The map was created using DIVA-GIS (v.7.4), using provincial boundaries of Thailand.

Morphological study and isolation of fungi

Vertical sections of fruiting bodies or fungal colonies were examined and photographed using a Nikon ECLIPSE 80i compound microscope (Nikon, Japan) fitted to a Canon 550D digital camera (Canon, Japan). All the measurements were done with Tarosoft Image Framework (v 0. 9.7), and photo plates were prepared using Adobe Photoshop CS6 Extended (v 10.0.) (Adobe Systems, USA). Single spore isolation was carried out on malt extract agar (MEA) and potato dextrose agar (PDA), following the methods described by Senanayake et al. (2020) and kept for 24 h at room temperature. The spore germination was observed within 24 h using a Motic SMZ 168 Series microscope. Germinated spores were transferred to new MEA plates to obtain pure fungal colonies. Colonies were measured and cultural morphology was recorded at 10 days of age.

DNA Extraction, PCR amplification and sequencing

Genomic DNA was extracted from 15–20 fruiting bodies (>500 µm, n=10) or forty-day-old mycelium using E.Z.N.A.® Tissue DNA Kit (Omega Biotek Inc.), following the manufacturer's instructions. DNA amplifications were performed by polymerase chain reaction (PCR), using different gene regions (Table 1). The PCR primers used in this study are also shown in Table 1. The quality of PCR products was confirmed on 1% gel electrophoresis. The PCR products were sent to a commercial sequencing provider (Solgent Co., Ltd, Thailand). The newly generated nucleotide sequences were deposited in GenBank, and accession numbers were obtained.

Table 1 – Primers used in this study

Gene	Primers		References
	Forward	Reverse	
Large subunit (LSU)	LR0R	LR5	Vilgalys & Hester (1990)
Small subunit (SSU)	NS1	NS4	White et al. (1990)
Internal transcribed spacer (ITS)	ITS5	ITS4	White et al. (1990)
Elongation factor-1 alpha (<i>efl-α</i>)	EF1-983F	EF1-22185R	Rehner & Buckley (2005), O'Donnell et al. (1998), Carbone & Kohn (1999)
RNA polymerase II subunit (<i>rpb2</i>)	RPB2-5f	RPB2-7cr	Liu et al. (1999), Reeb et al. (2004)
Beta-tubulin (<i>tub2</i>)	Bt2a	Bt2b	Glass & Donaldson (1995)
Glyceraldehyde-3-Phosphate Dehydrogenase (GAPDH)	GDF	GDR	Templeton et al. (1992)
Chitin synthase (CHS)	CHS79F	CHS345	Carbone & Kohn (1999)
Actin (ACT)	ACT-512F	ACT-783R	Carbone & Kohn (1999)

Sequence alignments and phylogenetic analyses

Newly generated forward and reverse sequences were assembled in the SeqMan (Swindell & Plasterer, 1997). The assembled sequences were used for BLAST searches at NCBI (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Based on recently published data and BLAST search results, taxa were selected. The sequences were downloaded from GenBank (2025) and multi-gene phylogenetic analyses were conducted using different gene regions (Table 1). Sequence alignments were processed with the MAFFT v. 7 online tool (<http://mafft.cbrc.jp/alignment/server>; 2016). Alignments were improved where necessary using MEGA v. 6.0, and composite sequence alignments were obtained (Tamura et al. 2013). Maximum likelihood (ML) and Bayesian inference (BI) analyses were conducted using the combined dataset of different gene regions. Using the techniques outlined by Miller et al. (2010), RAxML and Bayesian analyses were performed on the CIPRESS Science Gateway Portal (<https://www.phylo.org>). RAxML-HPC v.8 (Stamatakis 2014) was used to perform maximum likelihood analysis with quick bootstrap analysis, 1000 bootstrap replicates, and the GTRGAMMA substitution model. MrBayes was used to conduct BI analysis on XSEDE 3.2.7

(Ronquist et al. 2012), with tree samples collected at every 1000th generation over a 5M generation run of four concurrent Markov chains. The Posterior Probability (PP) for the remaining 75% of the trees was calculated after the first 25% of the trees were cut down during the burn-in phase (Rannala & Yang 1996, Zhaxybayeva & Gogarten 2002). Fig Tree v.1.4.0 (Rambaut 2012) was used to illustrate the phylogenetic tree, while Microsoft Office PowerPoint v. 2013 was used to make modifications.

Preliminary Screening of Antibacterial Activity

The preliminary antimicrobial activity screening was conducted following the methodology of Mapook et al. (2020). Ampicillin antibacterial discs used as a positive screening control (Alam et al. 2019). Using the agar plug diffusion method, preliminary antibacterial activity was evaluated against *Staphylococcus aureus* (TISTR Y4b), *Escherichia coli* (TISTR 527), and *Bacillus subtilis* (TISTR 1248) (Balouiri et al. 2016). Mae Fah Luang University's Scientific and Technological Instrument Center provided the bacterial test organisms, which were cultivated on nutrient agar (NA) for 24 h. Two to three loops of the bacterial test organisms were moved to the nutrient broth following a 24-hour inoculation period. According to Mapook et al. (2020), microbial suspensions were subjected to cell counts (6.7×10^5 cells/mL) prior to being added to the sterile mueller-hinton (MH) agar media. Our isolates' fungal mycelium plugs were moved to a solid medium plate and left to grow for 24 to 48 hours at room temperature. We measured the inhibition zones and contrasted them with the positive control.

RESULTS

Taxonomy

Class Dothideomycetes sensu O.E. Erikss & Winka

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Aplosporellaceae Slippers, Boissin & Crous

Aplosporellaceae was introduced by Slippers et al. (2013). Currently, two genera are accepted in Aplosporellaceae, viz., *Alanomyces* and *Aplosporella* (Hyde et al. 2024).

Aplosporella Speg. (= *Bagnisiella* Speg.)

Aplosporella was introduced by Spegazzini (1880) and typified by *A. chlorostroma*. Based on the combined LSU, SSU, ITS, *tef1-α* and *tub2* sequence data, the genus was placed in Aplosporellaceae, Botryosphaeriales. The asexual morph of *Aplosporella* is characterized by its globose to subglobose, multi-locular conidiomata with a thick, multi-layered wall, hyaline, aseptate, paraphyses, hyaline, cylindrical, blastic conidiogenous cells, and hyaline to brown, aseptate conidia (Damm et al. 2007, Ekanayaka et al. 2016, Dissanayake et al. 2021, Hyde et al. 2021, Jayawardena et al. 2022).

Aplosporella hesperidica Speg., Anal. Soc. cient. argent. 13(1): 18 (1882)

Fig. 3

Index Fungorum number: IF218239; Facesoffungi number: FoF07830

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 450–600 × 400–500 μm ($\bar{x}$ = 588 × 471 μm, n = 5), solitary, immersed to semi-immersed with 1–2 locules, globose to subglobose, black. *Ostiole* absent. *Peridium* 100–150 μm wide, multi-layered, composed of dark brown cells of *textura angularis*. *Paraphyses* 3–5 μm wide, numerous, hyaline, aseptate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–6 μm wide, holoblastic, cylindrical, hyaline, unbranched. *Conidia* 18–25 × 9–13 μm ($\bar{x}$ = 22 × 12 μm, n = 20), aseptate, hyaline to dark brown, ellipsoidal, granular appearance, thick-walled.

Material examined – Thailand, Chiang Rai Province, Mae Chan District, on dead stems of *Chromolaena odorata* (Asteraceae), 5 November 2020, Zin Hnin Htet, SW038 (MFLU 25-0272); *ibid.*, SW041 (MFLU 25-0273).

Known hosts and distribution – unidentified decaying woody host in China (Dissanayake et al. 2021); *Vigna unguiculata* (Fabaceae) in India (Deepika et al. 2020); *Eucalyptus camaldulensis* (Myrtaceae) in Ethiopia (Admasu et al. 2023); branches of *Euonymus japonicus* (Celastraceae) in China (Lin et al. 2023); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020, this study).

GenBank – MFLU 25-0273: LSU = PV992414, ITS = PV870617, *tef1-α* = PX282652, *rpb2* = PX120467; MFLU 25-0272: ITS = PV870616, *tef1-α* = PX282651, *rpb2* = PX120466.

Notes – Based on the phylogenetic analysis (Fig. 2), the specimens (MFLU 25-0272 and MFLU 25-0273) clustered together with the isolates of *Aplosporella hesperidica* with 97% ML and 0.84 BYPP bootstrap support (Fig. 2). Moreover, there is no significant difference in the morphology and base pair composition. Our collections are similar in having immersed to semi-immersed conidiomata with brown cells of *textura angularis* in the wall, and hyaline to dark brown, aseptate conidia. *Aplosporella hesperidica* was previously reported on *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020).

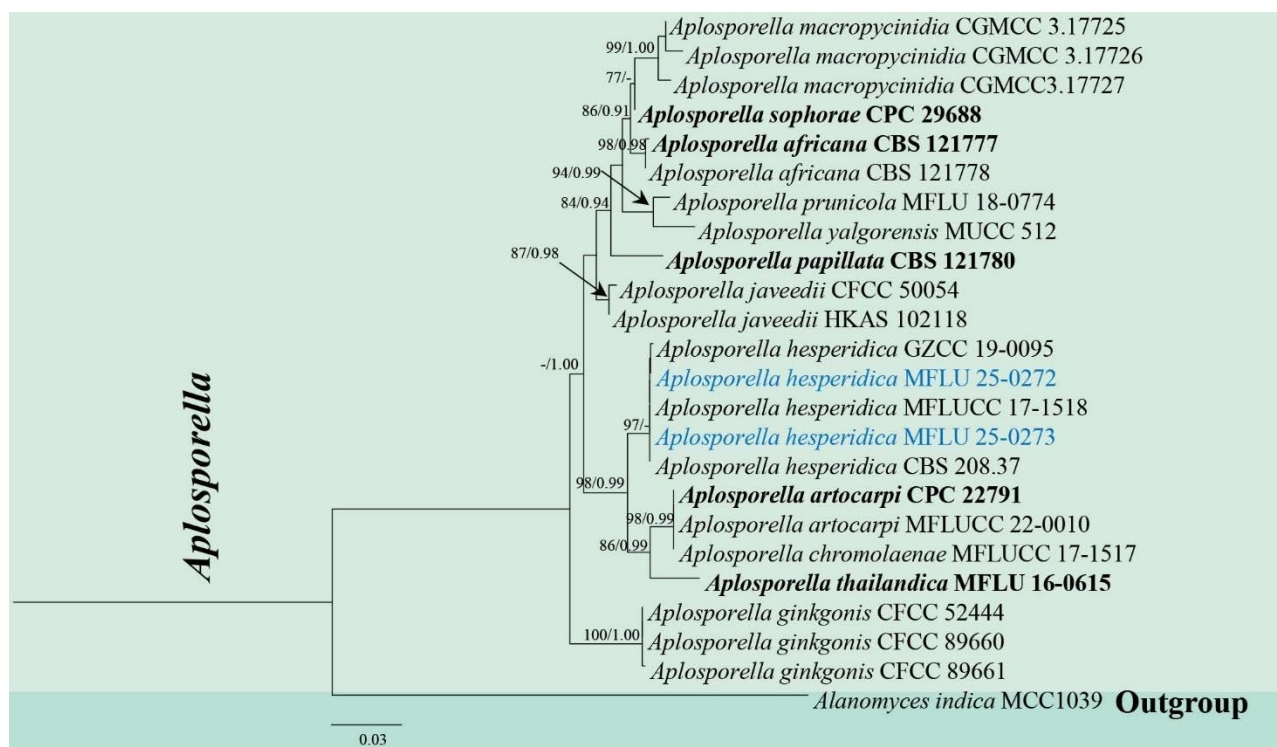


Figure 2 – Phylogram generated from ML analysis based on the combined dataset of ITS and *tef1-α* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Alanomyces indica* (MCC1039).

Botryosphaeriaceae Theiss. & H. Syd.

Botryosphaeriaceae was introduced by Theissen & Sydow (1918) to accommodate three genera, *Botryosphaeria*, *Dibotryon*, and *Phaeobotryon*. Members of Botryosphaeriaceae are found as endophytes, pathogens, and saprobes on a wide range of hosts and substrates (Slippers & Wingfield 2007, Phillips et al. 2013, Endes 2024). There are 23 genera accepted in Botryosphaeriaceae (Hyde et al. 2024).

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

Dothiorella was introduced by Saccardo (1880), and typified by *D. pyrenophora*. The sexual morph of *Dothiorella* is characterized by erumpent or superficial ascomata, and bitunicate, fissitunicate asci with 1-septate, pigmented ascospores (Phillips et al. 2005, Zhang et al. 2021, De

Farias et al. 2023). Asexual species of *Dothiorella* are characterized by immersed to erumpent conidiomata without paraphyses, and pigmented, septate ascospores (Zhang et al. 2021). Around 260 species are currently accepted in *Dothiorella* (Hyde et al. 2024). In this study, we introduce two new *Dothiorella* species, *D. asteracearum* and *D. chromolaenae*, based on morphology and the combined ITS, *tef1- α* , and *tub2* sequence data (Fig. 4).

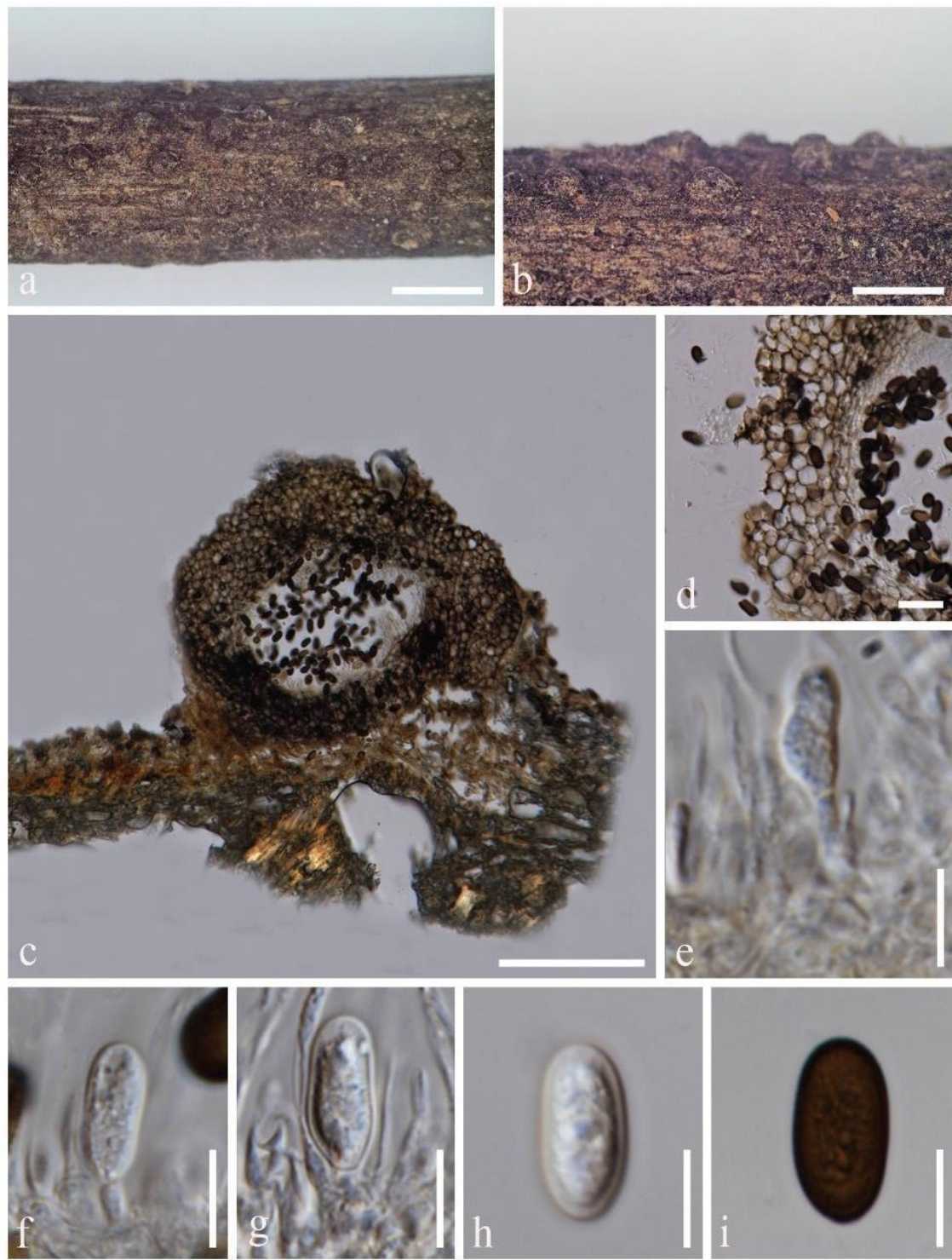


Figure 3 – *Aplosporella hesperidica* (MFLU 25-0272). a, b Appearance of conidiomata on host substrate. c Section through a conidioma. d Peridium. e–g Conidiogenous cells. h–i Conidia. Scale bars. a, b = 500 μ m, c = 300 μ m, d = 50 μ m, e, f, g, h, i = 10 μ m.

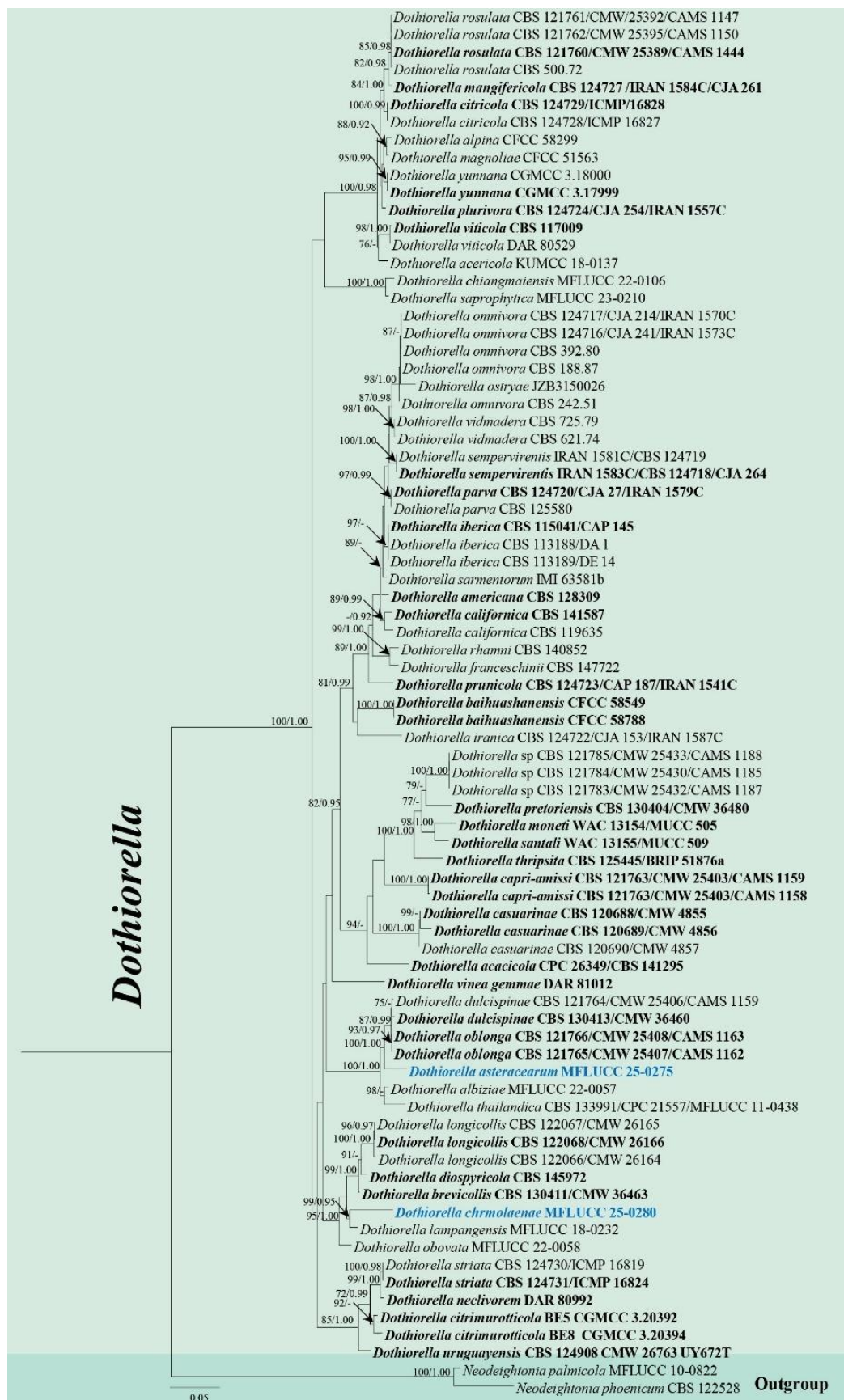


Figure 4 – Phylogram generated from ML analysis based on the combined dataset of ITS, *tef1- α* , and *tub2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Neodeightonia palmicola* (MFLUCC 10-0822) and *N. phoenicum* (CBS 122528).

Dothiorella asteracearum Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.** Fig. 5

Index Fungorum number: IF904374, Facesoffungi number: FoF18041

Etymology – Name reflects the host plant family from which this species was collected.

Holotype – MFLU 25-0274

Saprobic on dead stems of *Chromolaena odorata* (Asteraceae). **Sexual morph:** *Ascomata* 225–355 × 180–250 µm ($\bar{x}$ = 250 × 200 µm, *n* = 5), immersed to semi-immersed, solitary, appearing as small dark spots, coriaceous, globose to subglobose, brown to dark brown. *Ostiole* protruding, 20–50 µm wide. *Peridium* 30–40 µm wide, comprising multi-layered of dark brown cells of *textura angularis*. *Hamathecium* comprising 1–2 µm wide, cylindrical to filiform, septate, branching pseudoparaphyses. *Asci* 69–95 × 15–20 µm ($\bar{x}$ = 83 × 17 µm, *n* = 20), 6–8-spored, bitunicate, cylindrical, straight or slightly curved, apically rounded, pedicellate. *Ascospores* 28–41 × 12–16 µm ($\bar{x}$ = 35 × 15 µm, *n* = 20), overlapping, 1–2-seriate, reddish-brown to brown, 1-septate, oblong to ellipsoidal, constricted at the septum, straight or slightly curved, without gelatinous sheath. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 72 mm after 10 days at 27 °C, circular, filamentous, white to pale yellow, umbonate, transparent on the surface; circular, filamentous, white to pale yellow in reverse surface.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-5 (MFLU 25-0274, **holotype**); ex-type MFLUCC 25-0275.

GenBank – MFLUCC 25-0275: ITS = PV870618, *tef1-α* = PX282653.

Pre-screening for antibacterial activity – *Dothiorella asteracearum* (MFLUCC 25-0275) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on the phylogenetic analysis (Fig. 4), the strain (MFLUCC 25-0275) formed a separate clade basal to the isolates of *Dothiorella dulcispinae*, and *D. oblonga*, with 100% ML and 1.00 BYPP bootstrap support. The sexual morph of *Dothiorella* can be distinguished from other similar genera in having bitunicate, basal, clavate or oblong asci, pigmented and septate ascospores (Phillips et al. 2013). Moreover, phylogenetically related taxa, *Dothiorella albisiae*, *D. dulcispinae*, *D. oblonga* and *D. thailandica* were found as asexual morph in nature (Liu et al. 2012, Jami et al. 2013, Slippers et al. 2014, Rathnayaka et al. 2022), while our strain (MFLUCC 25-0275) was found as a sexual morph. Therefore, we could not compare morphology, and herein *D. asteracearum* is introduced as a new species based on multi-gene phylogeny. To confirm this species, more fresh specimens are necessary in the future.

Dothiorella chromolaenae Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.** Fig. 6

Index Fungorum number: IF904375, Facesoffungi number: FoF18042

Etymology – Name reflects the host plant *Chromolaena odorata*, from which this species was isolated.

Holotype – MFLU 25-0275

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 265–285 × 250–300(–380) µm ($\bar{x}$ = 270 × 285 µm, *n* = 5), pycnidial, solitary, immersed, uni-loculate, globose to subglobose, yellowish-brown to dark brown. *Ostiole* 50–90 µm wide. *Peridium* 30–80 µm wide, comprising multi-layered brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 1–2 µm ($\bar{x}$ = 6 × 1.5 µm, *n* = 5), blastic, holoblastic, acicular, hyaline. *Conidia* 15–21 × 8–10 µm ($\bar{x}$ = 19 × 8 µm, *n* = 20), ovoid, hyaline to brown, 1-septate, constricted at the septum, without guttules.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 66 mm after 10 days at 27 °C, irregular, entire, concentric, white to grey, raised, opaque on the surface; irregular, entire, white to dark green in reverse surface.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-18 (MFLU 25-0275, **holotype**); ex-type MFLUCC 25-0280.

GenBank – MFLUCC 25-0280: ITS = PV870619.

Pre-screening for antibacterial activity – *Dothiorella chromolaenae* (MFLUCC 25-0280) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

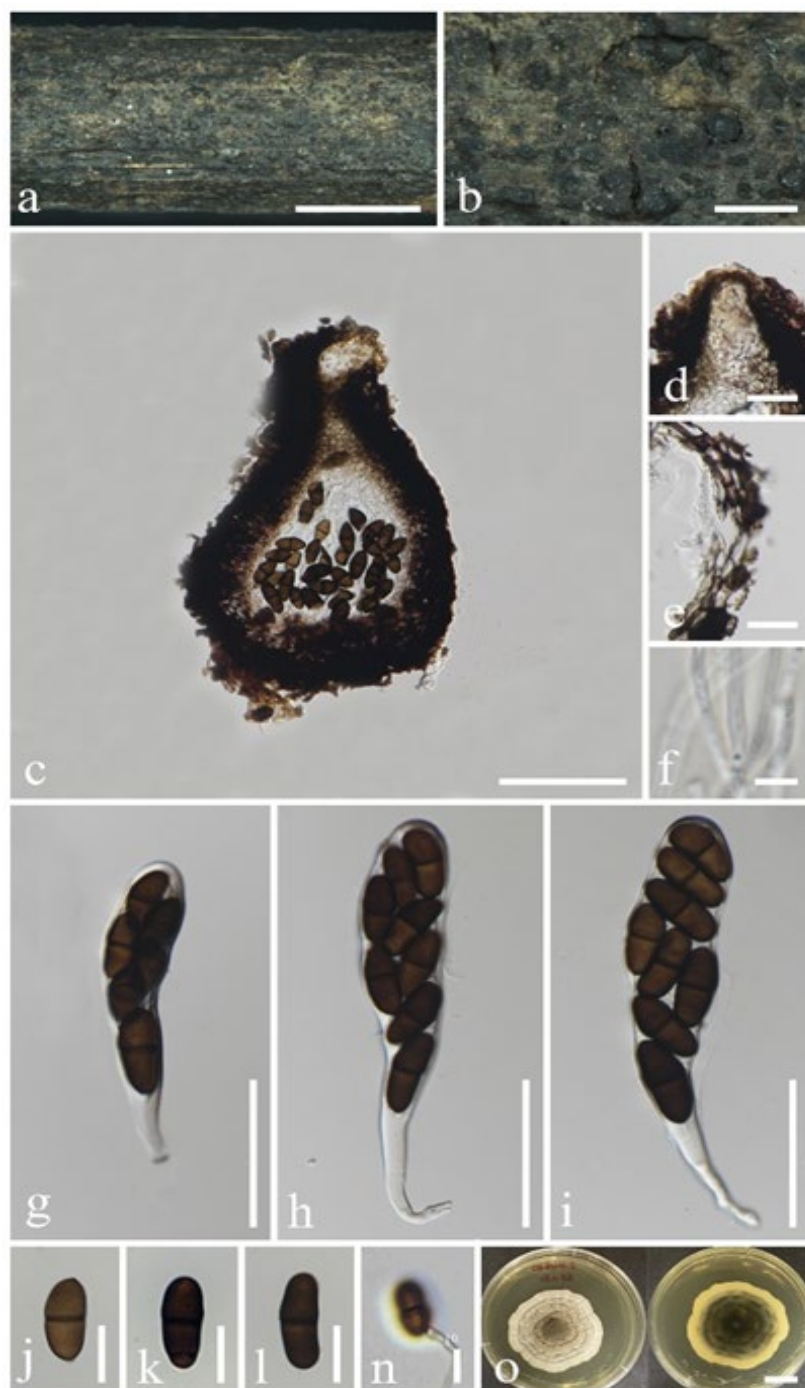


Figure 5 – *Dothiorella asteracearum* (MFLU 25-0274, holotype). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–i Asci. j–l Ascospores. n A germinating ascospore. o Culture on MEA. Scale bars: a = 1 mm, b = 500 μ m, c = 100 μ m, d, e, g, h, i = 30 μ m, f = 5 μ m, j, k, l, n = 20 μ m, o = 10 mm.

Notes – Based on the phylogenetic analysis (Fig. 4), the isolate MFLUCC 25-0280 formed a separate clade sister to *Dothiorella lampangensis* (MFLUCC 18-0232) with 99% ML and 1.00 BYPP bootstrap support. Morphologically, our collection differs from *D. lampangensis* (MFLUCC 18-0232) in having smaller conidiomata ($265\text{--}285 \times 250\text{--}300\text{--}(380)$ vs. $265\text{--}320 \mu\text{m} \times 260\text{--}380 \mu\text{m}$), acicular, shorter conidiogenous cells ($5\text{--}10 \times 1\text{--}2$ vs. $11\text{--}22 \times 3\text{--}8 \mu\text{m}$) and hyaline to brown, ovoid, larger conidia ($15\text{--}21 \times 8\text{--}10$ vs. $22\text{--}28 \times 9\text{--}11 \mu\text{m}$), while the latter has cylindrical conidiogenous cells slightly swollen at the base, initially hyaline and aseptate conidia, and becoming yellowish-brown, orange to dark brown, asymmetric, ellipsoid, obtuse at the apex, truncate at the base, 1-septate at maturity. Therefore, *D. chromolaenae* is introduced as a new species found on *Chromolaena odorata* (Asteraceae) in Thailand.

***Lasiodiplodia* Ellis & Everh**

Lasiodiplodia is typified by *L. theobromae*, and the genus includes fungi from tropical and subtropical regions worldwide. *Lasiodiplodia* species are reported as endophytes, pathogens, and saprobes on various hosts, including monocotyledons, dicotyledons, and gymnosperms (de Silva et al. 2019, Berraf-Tebbal et al. 2020, Segaran & Sathiavelu 2023). To date, *Lasiodiplodia* comprises 85 taxa (Hyde et al. 2024). In this study, we reported *Lasiodiplodia henanica* and *L. theobromae* as new records based on the combined dataset of ITS, *tef1- α* , *rpb2*, and *tub2* sequence data (Fig. 7).

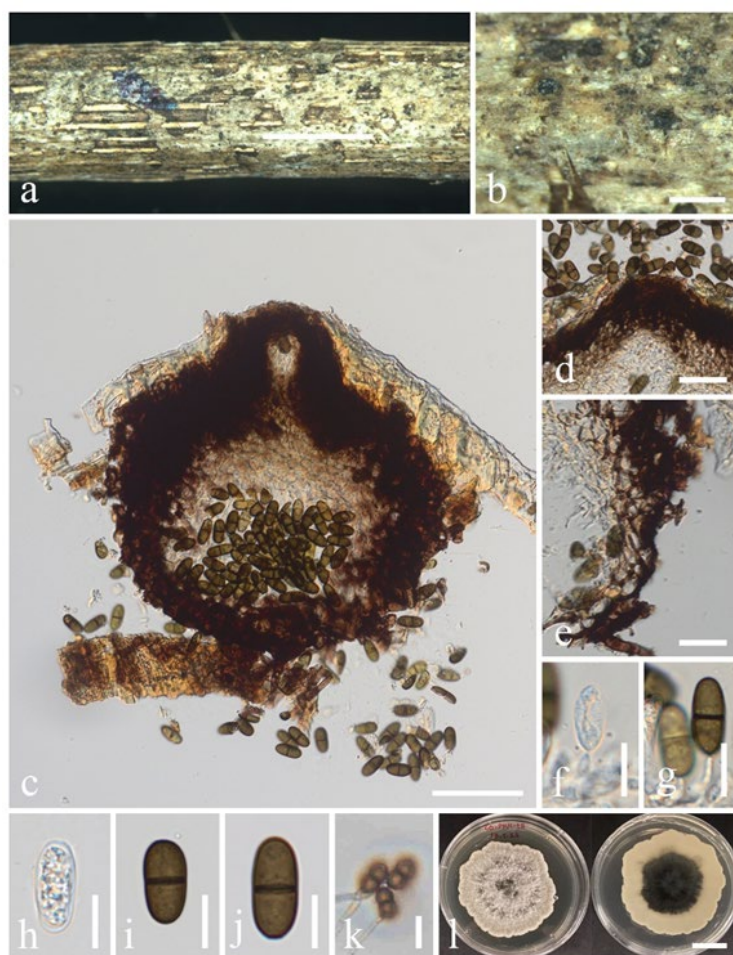


Figure 6 – *Dothiorella chromolaenae* (MFLU 25-0275, holotype). a, b Appearance of conidiomata on host substrate. c, d A section through a conidioma. d Ostiole. e Peridium. f, g Conidiogenous cells. h–j Conidia. k Germinating conidia. l Culture on MEA. Scale bars: a = 1 mm, b = 500 μm , c = 100 μm , d, e = 30 μm , f, g, h, i, j, k = 10 μm , l = 10 mm.

Lasiodiplodia

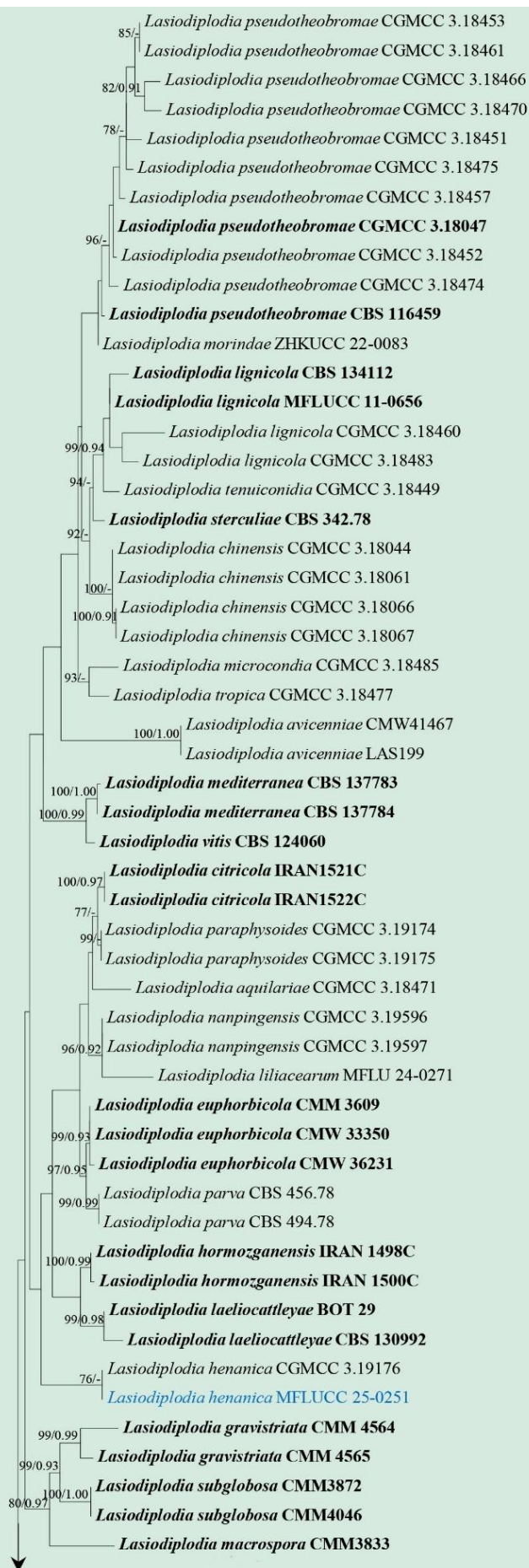


Figure 7 – Phylogram generated from ML analysis based on the combined dataset of ITS, *tef1- α* , *rpb2*, and *tub2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Diplodia cupressi* (CBS 168.87) and *D. mutila* (CBS 112553).

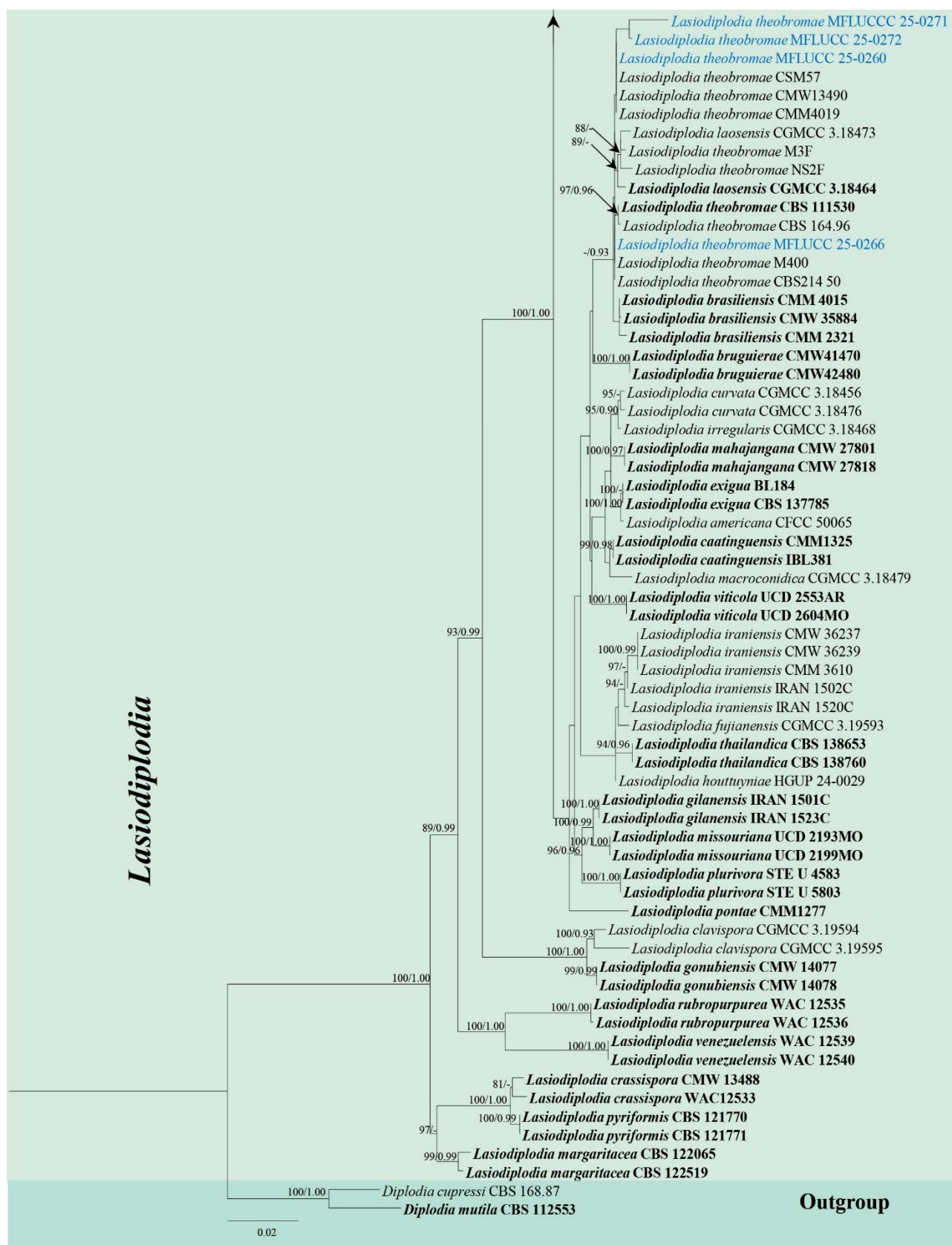


Figure 7 – Continued.

Lasiodiplodia henanica Z.P. Dou, Y. Wang & Y. Zhang ter, Life 11(7, no. 657): 6 (2021) Fig. 8

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 80–150 × 100–150 µm ($\bar{x}$ = 98.5 × 140 µm, n=5), semi-immersed to superficial, globose to subglobose, black spots on the host substrate, with an ostiole. *Ostiole* central. *Peridium* 10–20 µm wide, comprised of 2–3 layered dark brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–5 µm long, holoblastic, hyaline, unbranched. *Conidia* 20–28 × 1–2 µm ($\bar{x}$ = 25 × 1.3 µm, n=20), hyaline, ovoid to ellipsoidal, aseptate, thick-walled, with granules.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 85 mm after 10 days at 27 °C, irregular, filamentous, powdery, dark green, opaque on the surface; irregular, dark green in reverse.

Material examined – Thailand, Chiang Rai Province, Mae Suai District, on dead stems of *Chromolaena odorata* (Asteraceae), 14 March 2023, Zin Hnin Htet, Co-maesuai-1 (MFLU 25-0276, **a new host record**); living culture MFLUCC 25-0251.

GenBank – MFLUCC 25-0251: ITS = PV870620.

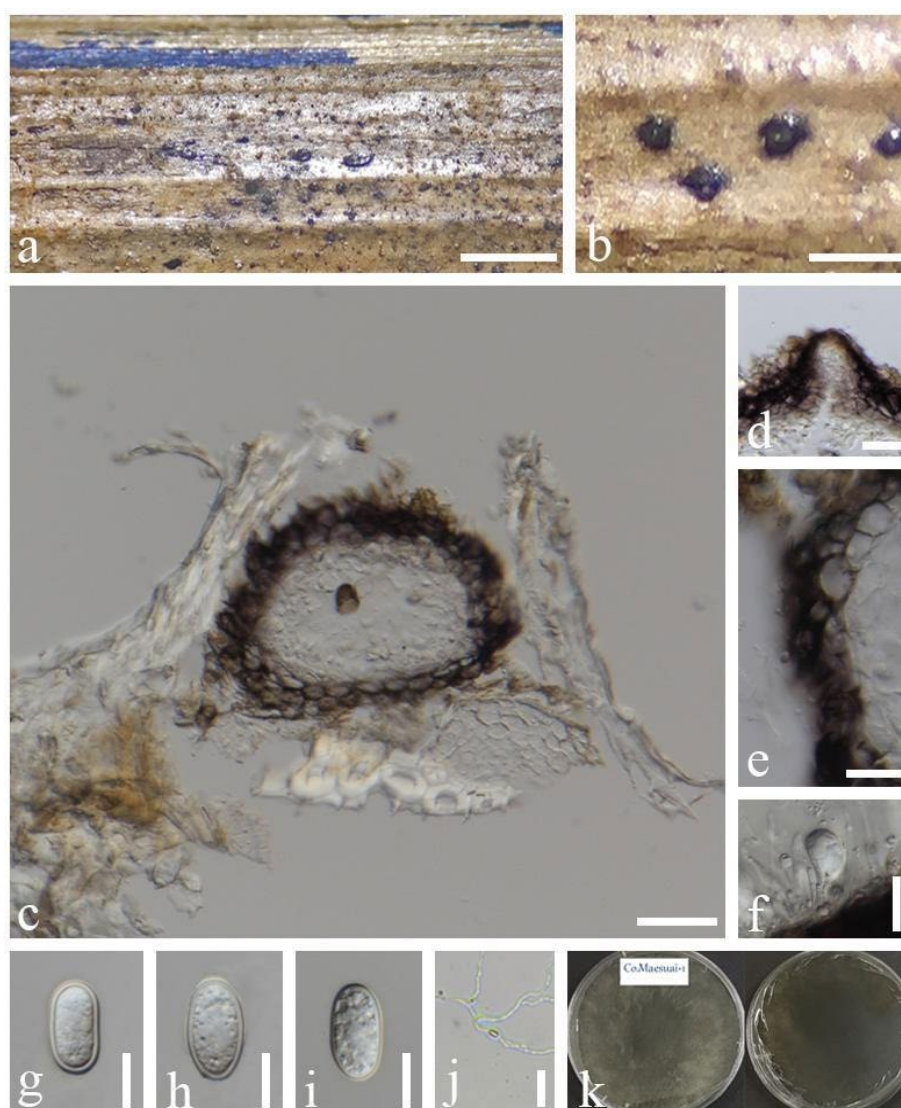


Figure 8 – *Lasiodiplodia henanica* (MFLU 25-0276, a new host record). a, b Appearance of conidiomata on host substrate. c Section through a conidioma. d Ostiole. e Peridium. f Conidiogenous cells. g–i Conidia. j A germinating conidium. k Culture on MEA. Scale bars: a, b = 1 mm, c = 50 µm, d, e, f, g, h, i, j = 10 µm.

Pre-screening for antibacterial activity – *Lasiodiplodia henanica* (MFLUCC 25-0251) showed a 16 mm partial inhibition against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm) and 17 mm inhibition zones against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm) and a 25 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm).

Known host and distribution – *Vaccinium uliginosum* (Ericaceae) in China (Wang et al. 2021); cankered stems of *Morus alba* (Moraceae) in China (Wang et al. 2021); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on the phylogenetic analysis (Fig. 7), the strain (MFLUCC 25-0251) clustered sister to *Lasiodiplodia henanica* (CGMCC 3.19176) with 76% ML and 1.00 BYPP bootstrap support. The strain (MFLUCC 25-0251) closely resembles that of *Lasiodiplodia henanica* (CGMCC 3.19176) in having stromatic, semi-immersed to superficial, globose to subglobose, dark conidiomata and in reducing conidiophores to holoblastic, hyaline, thin-walled, smooth, and unbranched conidiogenous cells. Our strain (MFLUCC 25-0251) differs from *L. henanica* in having hyaline, ovoid to ellipsoidal conidia, while *L. henanica* (CGMCC 3.19176) has hyaline, cylindrical to oblong, and aseptate conidia that become brown, 1-septate conidia at maturity (Wang et al. 2021). However, there is no significant base pair difference between them. Therefore, herein, our collection is reported as a new host record of *L. henanica* on *Chromolaena odorata* (Asteraceae) and a new geographical record in Thailand.

Lasiodiplodia theobromae (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909) Fig. 9

Index Fungorum number: IF188476, Facesoffungi number: FoF00167

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 170–215 × 145–185 µm ($\bar{x}$ = 192 × 167 µm, n = 5), globose to subglobose, semi-immersed to superficial, black, solitary, uniloculate with an ostiole. *Ostiole* central or lateral. *Paraphyses* 2–4 µm wide, hyaline, cylindrical, aseptate and rounded and wider at apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–12 × 2–5 µm ($\bar{x}$ = 7 × 3 µm, n = 5), hyaline, ovoid to cylindrical, discrete, smooth. *Conidia* 17–30 × 10–15 µm ($\bar{x}$ = 24 × 12 µm, n = 20), hyaline, aseptate, rarely become brown, 1-septate, ellipsoidal to ampulliform, with granular appearance, both ends broadly rounded, thick-walled.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 85 mm after 10 days at 27 °C, irregular, filamentous, powdery, dark green, opaque on the surface; irregular, dark green in reverse.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet, BP-NL-3 (MFLU 25-0277); living culture MFLUCC 25-0266; *ibid.*, on dead stems of *Bidens pilosa* (Asteraceae), 5 January 2023, Zin Hnin Htet, BP-5 (MFLU 25-0279); living culture MFLUCC 25-0271; *ibid.*, on dead stems of *Bidens pilosa* (Asteraceae), 5 January 2023, Zin Hnin Htet, BP-6 (MFLU 25-0280); living culture MFLUCC 25-0272. *ibid.*, on dead stems of *Chromolaena odorata* (Asteraceae), 3 August 2023, Zin Hnin Htet, CO-NL-6 (MFLU 25-0278, **a new host record**); living culture MFLUCC 25-0260.

GenBank – MFLUCC 25-0266: ITS = PV870621, *tef1-α* = PX282654, *tub2* = PX255145; MFLUCC 25-0260: ITS = PV870622, *tef1-α* = PX282655, *tub2* = PX255146; MFLUCC 25-0271: ITS = PV870623, *tef1-α* = PX282656, *tub2* = PX255147; MFLUCC 25-0272: ITS = PV870624, *tef1-α* = PX282657, *tub2* = PX282792.

Pre-screening for antibacterial activity – *Lasiodiplodia theobromae* (MFLUCC 25-0266) showed 14 mm inhibition against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm) and a 19 mm inhibition against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm). However, no inhibition was shown against *B. subtilis*.

Known host and distribution – *Lasiodiplodia theobromae* has a cosmopolitan distribution and on different host species (Salvatore et al. 2020); dead stems of *Chromolaena odorata* in Thailand (this study).

Notes – In the phylogenetic analyses (Fig. 7), the fungal collections (MFLUCC 25-0266, MFLUCC 25-0260, MFLUCC 25-0271, and MFLUCC 25-0272) clustered with the ex-neotype strain (CBS 164. 96) and other strains (CBS 111530, CBS 214.50, CSW57, CMW 13490, CMM 4019, M3F, M400, and NS2F) of *L. theobromae* and ex-type strain (CGMCC 3.18464) and other strain (CGMCC 3.18473) of *L. laosensis* with 74% ML and 0.93 BYPP bootstrap support. Moreover, the fungal collections (MFLUCC 25-0266, MFLUCC 25-0260, MFLUCC 25-0271, and MFLUCC 25-0272) exhibit morphological characteristics similar to those of *Lasiodiplodia theobromae*, possessing hyaline to brown, (0)–1-septate, ellipsoidal to ampulliform conidia. A comparison of base pair differences between these two species reveals ITS 0.69% (4/577), *tef1- α* 1.14% (6/522), *tub2* 0% (0/460), *rpb2* 0% (0/599), with gaps. *Lasiodiplodia theobromae* was previously reported on *Bidens pilosa* (Asteraceae) (Salvatore et al. 2020) and herein, *L. theobromae* is reported as a new host record on *Chromolaena odorata* (Asteraceae).

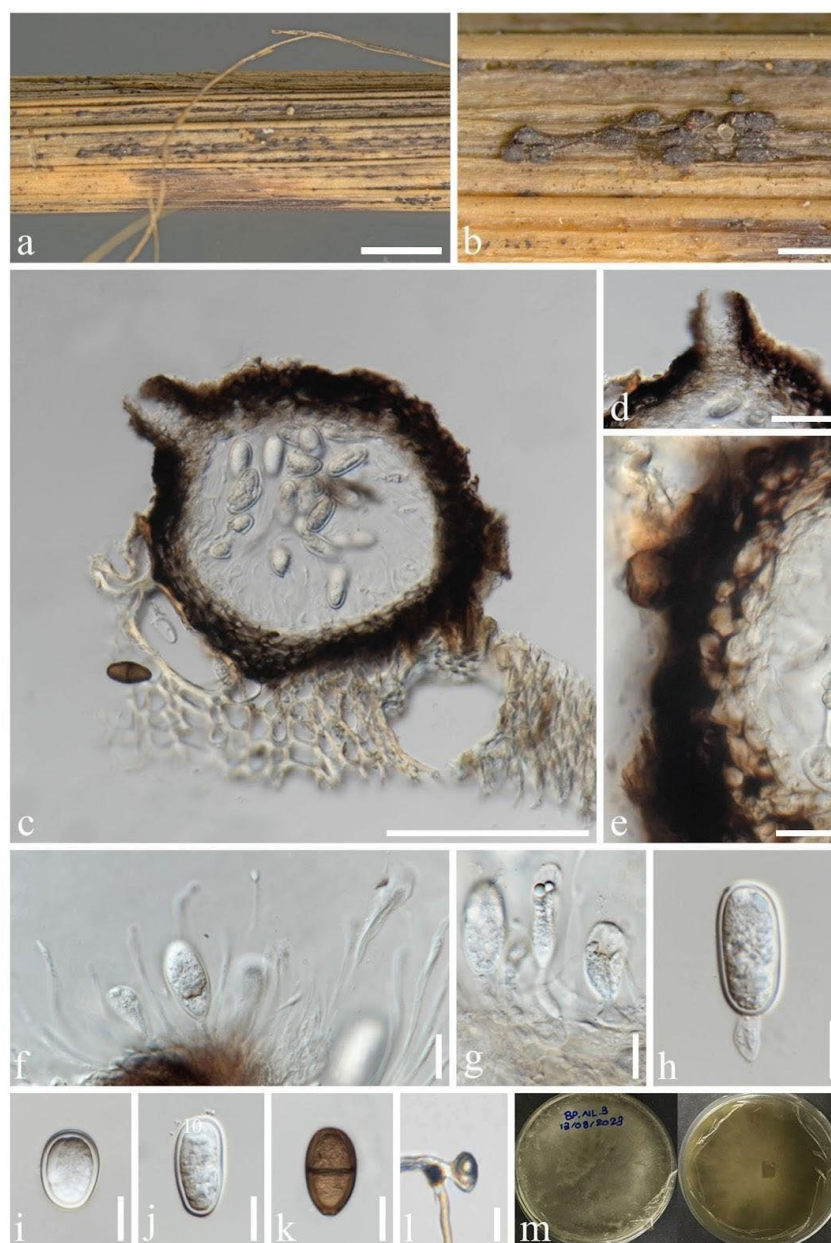


Figure 9 – *Lasiodiplodia theobromae* (MFLU 25-0277). a, b Appearance of conidiomata on host substrate. c Section through a conidioma. d Ostiole. e Peridium. f Paraphyses. g–h Conidiophores with conidiogenous cells. i–k Conidia. l A germinating conidium. m Culture on MEA. Scale bars: a = 1 mm, b = 500 μ m, c = 100 μ m, d = 20 μ m, e, f, g, h, i, j, k, l = 10 μ m.

Hysteriales Lindau

Hysteriaceae Chevall

Hysteriaceae was introduced by Chevallier (1826) with *Hysterium* as the type genus. Hysteriaceae species are characterized by the presence of carbonaceous hysterothecium, navicular, immersed to superficial with a slit or sulcus, hyaline to brown, bitunicate asci, one to multi-septate, or muriform ascospores (Boehm et al. 2009, Thambugala et al. 2016, Xu et al. 2022). Currently, there are 13 genera accepted in Hysteriaceae, viz., *Actidiographium*, *Gloniella*, *Gloniopsis*, *Hysterium*, *Hysterobrevium*, *Hysterocarina*, *Hysterodiffractum*, *Hysteroglonium*, *Oedohysterium*, *Ostreichnion*, *Pseudoscypha*, *Psiloglonium*, and *Rhytidhysterion* (Hyde et al. 2024).

Rhytidhysterion Speg

Rhytidhysterion was introduced by Spegazzini (1881). *Rhytidhysterion brasiliense* was designated as the type species (Clements & Shear 1931). *Rhytidhysterion* species are mainly found as saprobes, and few are reported as endophytes and pathogens on a wide range of hosts from a variety of geographical distributions (Soto-Medina & Lücking 2017, De Silva et al. 2020, Wanasinghe et al. 2021).

Rhytidhysterion bruguierae Dayarathne, Mycosphere 11(1): 20 (2020)

Fig. 11

= *Rhytidhysterion erioi* Ekanayaka & K.D. Hyde, in Hyde et al., *Fungal Diversity* 100: 21 (2020)

Index Fungorum number: IF556574, Facesoffungi number: FoF 06154

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 205–300 × 500–600 µm ($\bar{x}$ = 256 × 550 µm, n = 5), hysterothecial, superficial, carbonaceous, scattered, closed at first and opening at maturity, elongate, dark brown to black with red at the center, without ostiole. *Peridium* 30–70 µm wide, comprising multi-layered, brown to dark brown cells of *textura angularis*. *Hamathecium* comprises 3–5 µm wide, cylindrical to filiform, septate, branching pseudoparaphyses, swollen apex with red to pinkish epithecium above the asci. *Asci* 120–150 × 10–15 µm ($\bar{x}$ = 135 × 12.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical, straight or slightly curved, short pedicellate, apically rounded with an ocular chamber. *Ascospores* 15–25 × 5–10 µm ($\bar{x}$ = 12.9 × 7.1 µm, n = 20), uniseriate, overlapping in the ascus, hyaline to brown, broadly fusiform, with upper part or second cell slightly wider, 1–3-septate slightly constricted at the septum, straight or slightly curved, guttulate. **Asexual morph:** Undetermined.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, Rhy4 (MFLU 25-0233).

GenBank – MFLU 25-0233: SSU = PV996952, ITS = PV870577, *tef1-α* = PX255031, *rpb2* = PX120441.

Known host and distribution – decaying wood of *Bruguiera* sp. (Rhizophoraceae) in Thailand (Dayarathne et al. 2020); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020); dead twigs of *Murraya paniculata* in Thailand (Senwanna et al. 2023); decaying wood of *Alnus nepalensis* (Betulaceae) in China (Du et al. 2023); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analysis (Fig. 10), this strain (MFLU 25-0233) grouped within *Rhytidhysterion bruguierae* clade, sister to MFLUCC 17-1502 with 98% ML and 0.94 BYPP bootstrap support. This strain (MFLU 25-0233) is similar in morphology to the type strain of *R. bruguierae* (MFLUCC 18-0398) in having superficial, boat-shaped, hysterothecial ascomata, branching septate, pseudoparaphyses with pinkish to reddish swollen apex, cylindric-clavate, bitunicate asci, hyaline to reddish-brown, ellipsoidal to fusiform, 1–3-septate ascospores. Moreover, there is no significant base pair difference between our collection and phylogenetically related strain. *Rhytidhysterion bruguierae* was previously reported on the same host (*Chromolaena odorata*) within the same locality, Thailand (Mapook et al. 2020). However, *R. erioi* (the sequences obtained from Hyde et al. 2020) clustered together with *R. bruguierae* strains with 100 % ML and 1.00 BYPP. The morphology of this collection resembles the other collections of *R. bruguierae*. Thus, we synonymize

R. erioi (MFLU 16-0584) under *Rhytidhysterium bruguierae* (Du et al. 2023). Recently, there are 43 species listed in the Index Fungorum (2025).

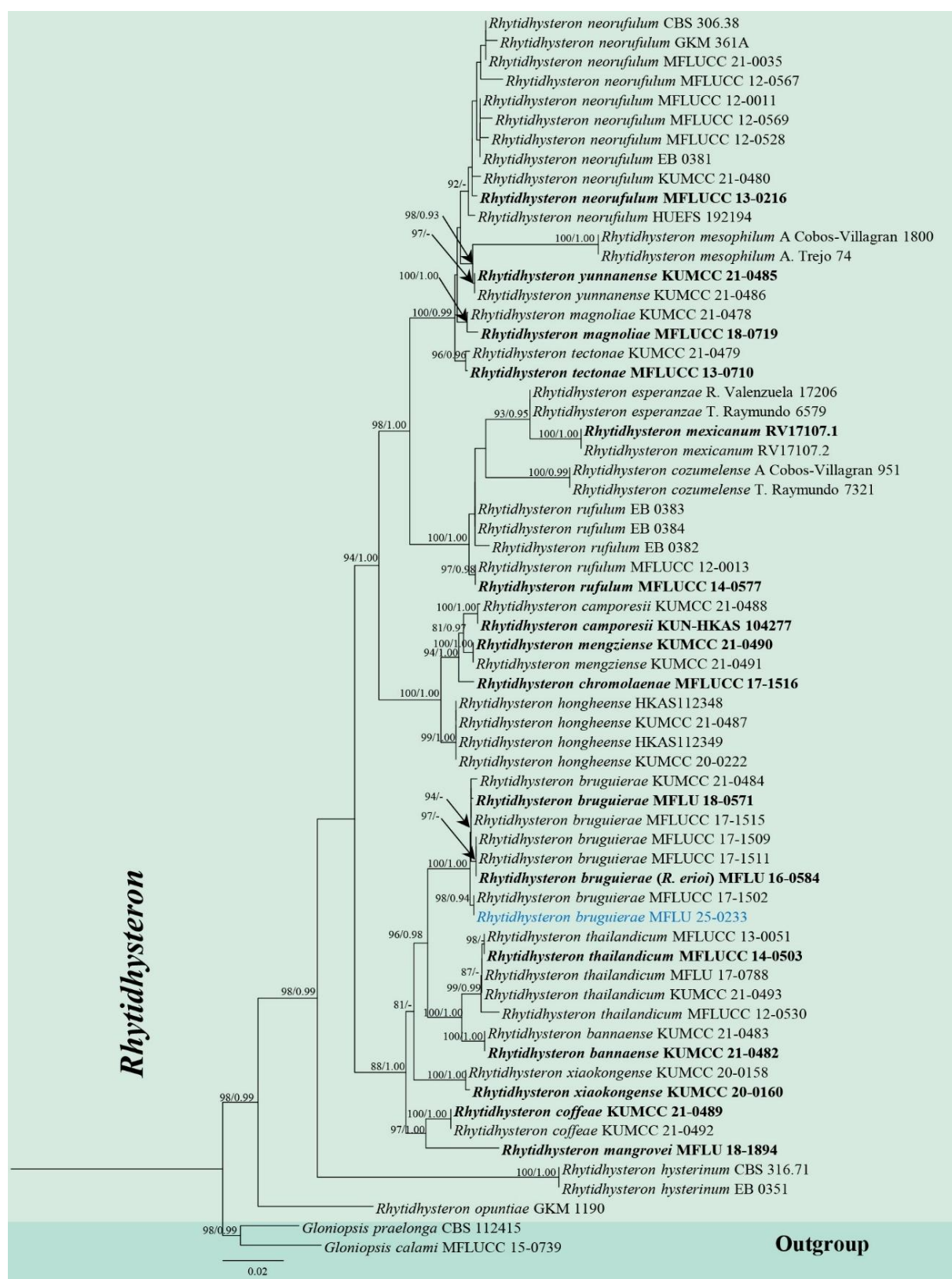


Figure 10 – Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, and *tefl-α* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Glioniopsis praelonga* (CBS 112415) and *G. calami* (MFLUCC 15-0739).



Figure 11 – *Rhytidhysterium bruguierae* (MFLU 25-0233). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Peridium. e, f Pseudoparaphyses. g–j Asci. k–p Ascospores. Scale bars: a = 1 mm, b = 500 μ m, c = 100 μ m, d = 20 μ m, e, f = 5 μ m, g, h, i, j = 30 μ m, k, l, m, n, o, p = 10 μ m.

Pleosporales Luttr. ex M.E. Barr
Acrocalymmaceae Crous & Trakun

Acrocalymmaceae was introduced by Trakunyingcharoen et al. (2014) to accommodate a monotypic genus *Acrocalymma*. Currently, there is only one accepted genus in Acrocalymmaceae (Hyde et al. 2024).

Acrocalymma Alcorn & J.A.G. Irwin

Acrocalymma was introduced by Alcorn & Irwin (1987), typified by *A. medicaginis*. The asexual morph of *Acrocalymma* is characterized by immersed to semi-erumpent, globose, pycnidial conidiomata, hyaline, cylindrical to subcylindrical, annellidic conidiogenous cells, hyaline, cylindrical conidia with or without appendages (Alcorn & Irwin 1987, Zhang et al. 2012, Jayasiri et al. 2019, Mortimer et al. 2021). The sexual morph of *Acrocalymma* is characterized by immersed, globose to subglobose ascomata with an ostiole, septate, branched pseudoparaphyses, bitunicate, cylindric-clavate asci, hyaline, fusiform ascospores with or without sheaths (Shoemaker et al. 1991, Mortimer et al. 2021). *Acrocalymma* species can be found in both terrestrial and aquatic habitats (Mortimer et al. 2021, Liu & Zheng 2022, Calabon et al. 2023). Currently, there are 19 species listed in Index Fungorum (2025). In this study, *Acrocalymma pterocarpi* is reported as a new record based on a combined LSU, SSU, ITS, and *tef1-α* sequence data (Fig. 12).

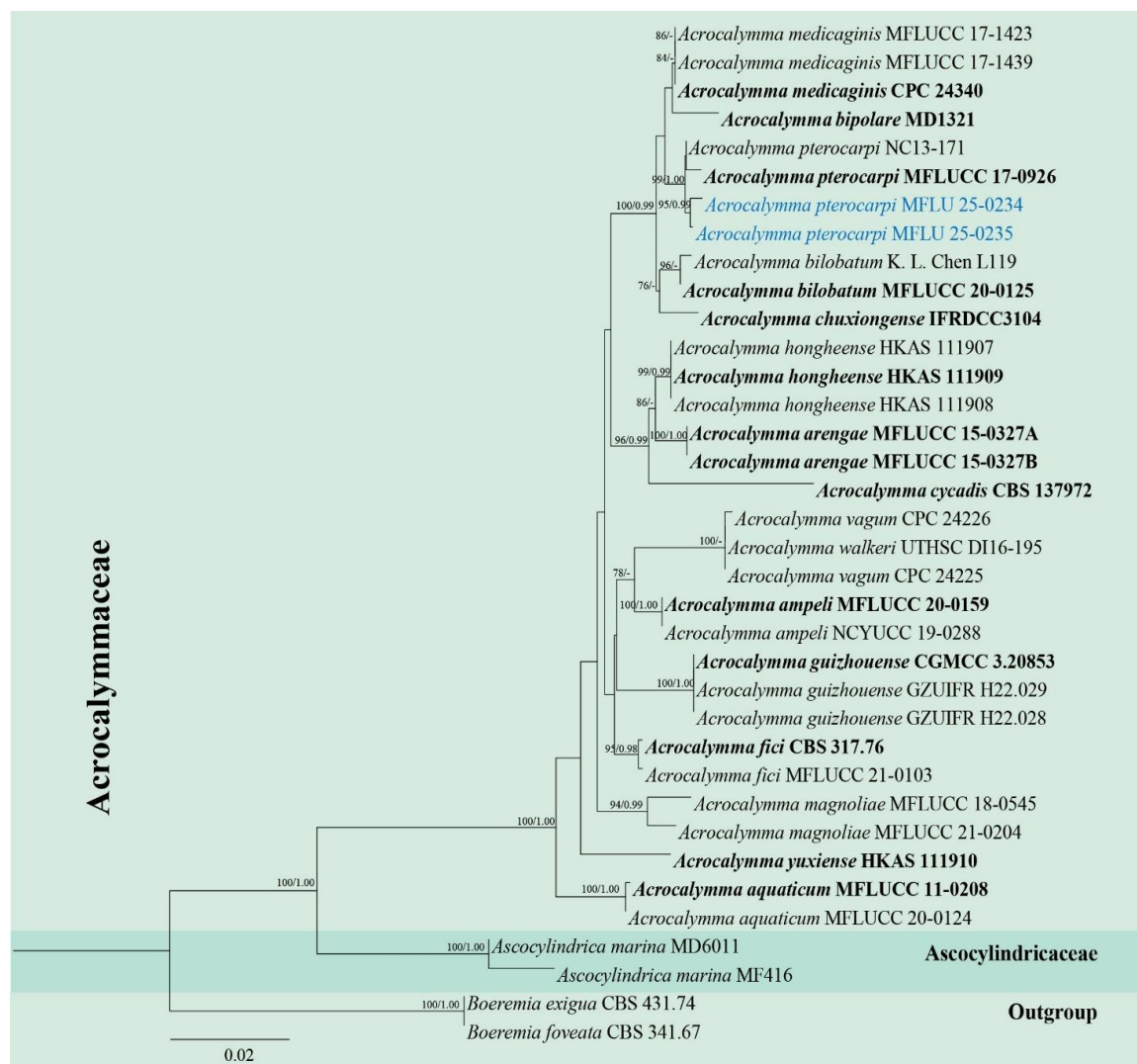


Figure 12 – Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, and *tef1-α* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the

nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Boeremia foveata* (CBS 341.67) and *B. exigua* (CBS 431.74).

Acrocalymma pterocarpi Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 20 (2019) Fig 13
Index Fungorum number: IF555528, Facesoffungi number: FoF05228

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 100–150 × 110–140 µm ($\bar{x}$ = 123.5 × 131.4 µm, n = 5), immersed to semi-immersed, globose to subglobose, with an ostiole. *Ostiole* central, papillate. *Peridium* 10–20 µm wide, composed of two to three layers of brown cells of *textura angularis*. *Hamathecium* comprises of 1–2 µm wide, filiform, branched, septate, pseudoparaphyses. *Asci* 50–100 × 6–10 µm ($\bar{x}$ = 80.1 × 7.5 µm, n = 10), 8-spored, bitunicate, fissitunicate, hyaline, cylindric-clavate, short pedicellate, straight to flexuous, rounded at the apex. *Ascospores* 16–22 × 5–8 µm ($\bar{x}$ = 18 × 5.8 µm, n = 20), overlapping biseriate, hyaline, fusiform, 1-septate, guttulate, constricted at the septum. **Asexual morph:** Undetermined.

Material examined – Thailand, Chiang Rai Province, Phan District, on dead stems of *Chromolaena odorata* (Asteraceae), 14 March 2023, Zin Hnin Htet, CO-DP-8 (MFLU 25-0235, **a new host record**); *ibid.*, CO-DP-6 (MFLU 25-0234).

GenBank – MFLU 25-0234: LSU = PV992403, SSU = PV996953, ITS = PV870578, *tef1-α*: PX255032; MFLU 25-0235: LSU = PV992404, SSU = PV996954, ITS = PV870579, *tef1-α* = PX255033.

Known host and distribution – fallen pod of *Pterocarpus indicus* (Fabaceae) in Thailand (Jayasiri et al. 2019); dead twigs attached to the *Magnolia* sp. (Magnoliaceae) in China (de Silva et al. 2022); dead twigs of *Bidens* sp. (Asteraceae) in Thailand (Chethana et al. 2023); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analysis (Fig. 12), our strains MFLU 25-0234 and MFLU 25-0235 grouped together with the isolates of *Acrocalymma pterocarpi* with 99% ML and 1.00 BYPP bootstrap support. Our strains are morphologically similar to *A. pterocarpi* in having globose to subglobose ascomata with a central ostiole, 1–2 µm wide, branched, septate pseudoparaphyses, bitunicate, fissitunicate asci, hyaline, filiform, septate ascospores. Moreover, there is no significant base pairs difference between our collections and *A. pterocarpi* (NC 13-171) and (MFLUCC 17-0326). Therefore, these collections are reported as new host records of *A. pterocarpi* on *Chromolaena odorata* (Asteraceae) in Thailand and a second record on Asteraceae plants from Thailand.

Dictyosporiaceae Boonmee & K.D. Hyde

Dictyosporiaceae was introduced by Boonmee et al. (2016), to accommodate a holomorphic group of saprobic fungi which are characterized asexually by cheiросporous, digitate, and/or dictyosporous, pale brown or brown conidia and sexually by the presence of globose to subglobose, dark brown to black ascomata, bitunicate, asci, and septate, hyaline, with or without sheathed ascospores (Boonmee et al. 2016, Liu et al. 2023). Dictyosporiaceae species can be found as saprobes in both terrestrial and aquatic habitats (Boonmee et al. 2016, Yang et al. 2018, Tennakoon et al. 2023). Currently, there are 21 genera accepted in Dictyosporiaceae (Hyde et al. 2024). In this study, we reported *Dictyocheiросpora nabanheensis* and *Neodendryphiella mali* as new records based on combined sequence data of LSU, SSU, ITS, and *tef1-α* (Fig. 14).

Dictyocheiросpora M.J. D'souza, Boonmee & K.D. Hyde

Boonmee et al. (2016) introduced *Dictyocheiросpora* to accommodate three other cheiroid genera, *Dictyopalmispora*, *Jalapriya*, and *Vikalpa* in Dictyosporiaceae. Dictyosporiaceae was typified by *Dictyocheiросpora rotunda*, and characterized by pale brown, complanate or non-complanate, and euseptate or distoseptate conidia. Currently, there are 29 species accepted in *Dictyocheiросpora* (Shu et al. 2024, Index Fungorum 2025). In this study, we report *Dictyocheiросpora nabanheensis* as a new host record based on the combined dataset of LSU, SSU, ITS, and *tef1-α* sequence data.

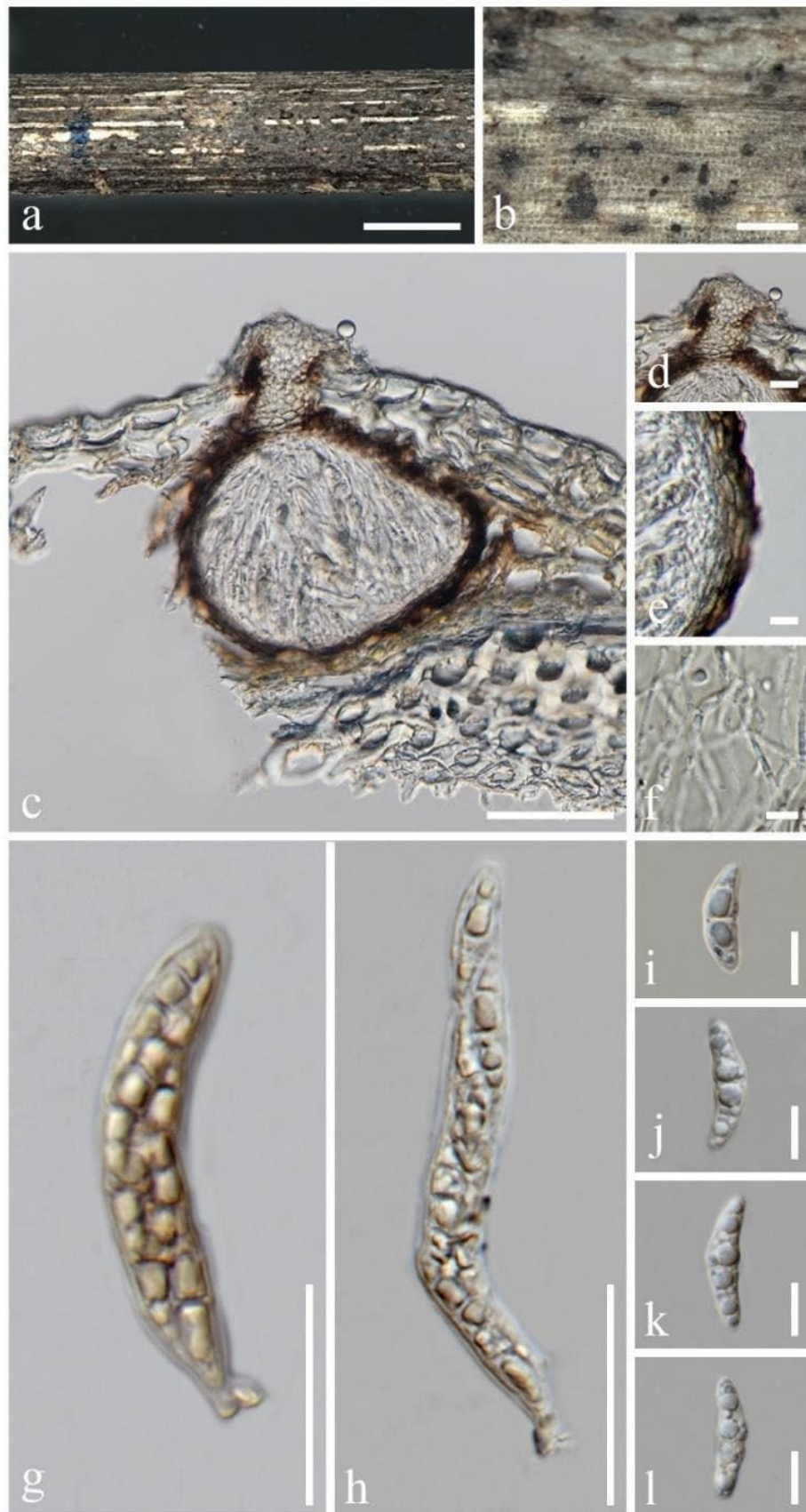


Figure 13 – *Acrocalymma pterocarpi* (MFLU 25-0234, a new host record). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–h Asci. i–l Ascospores. Scale bars: a = 1 mm, b = 200 μ m, c = 50 μ m, d, f = 5 μ m, g, h = 30 μ m, e, i, j, k, l = 10 μ m.

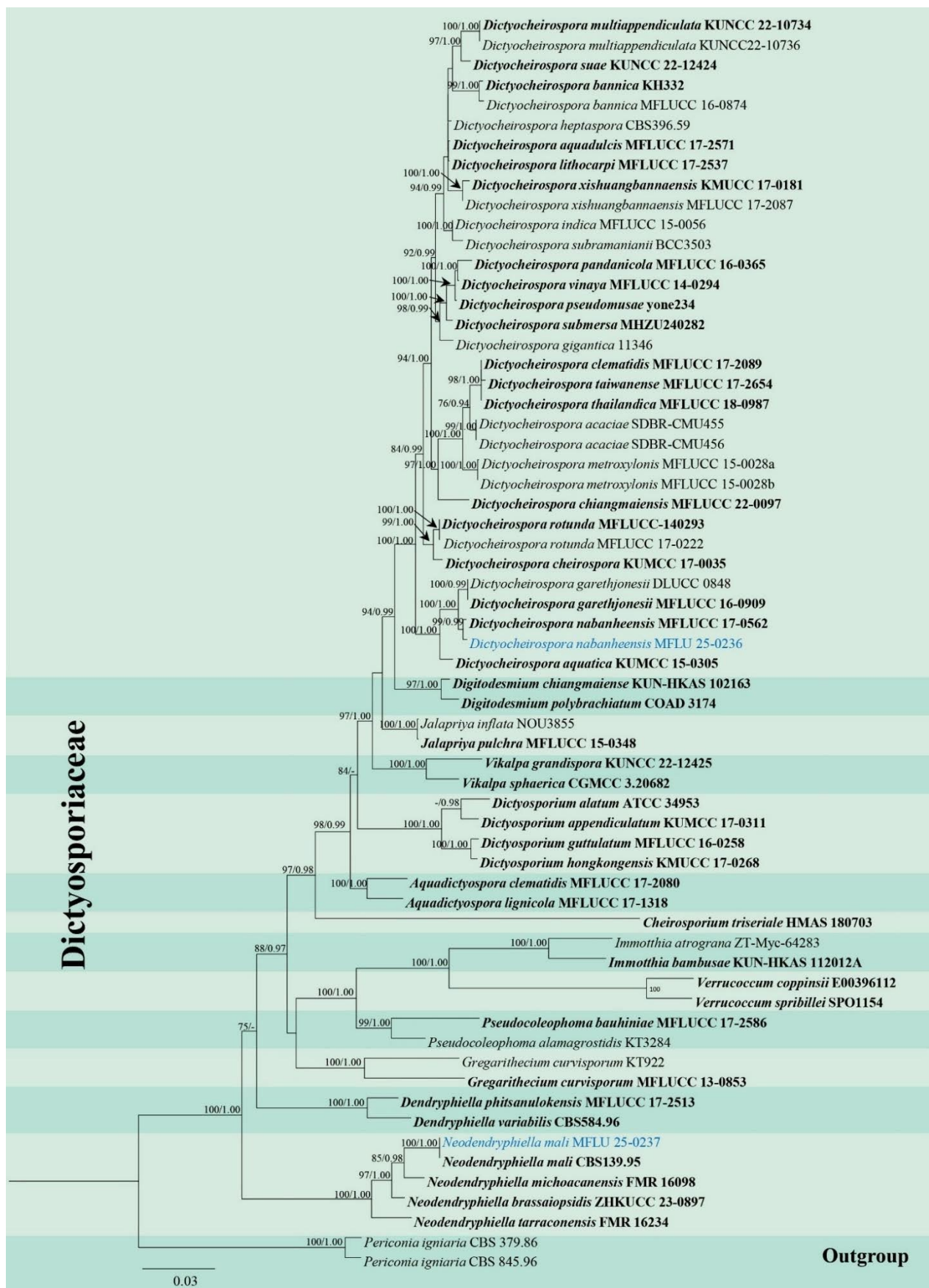


Figure 14 – Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, and *tef1- α* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Periconia igniaria* (CBS 379.86 and CBS 845.96).

Index Fungorum number: IF554474, Facesoffungi number: FoF04483

Saprobic on dead stem of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* on natural substrate forming sporodochial conidiomata, superficial, gregarious, scattered, punctiform, brown, velvety, with abundant sporulation. *Mycelium* immersed, composed of brown, smooth, thin-walled, septate hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* $4\text{--}6 \times 2.5\text{--}4\text{ }\mu\text{m}$ ($\bar{x} = 5 \times 3.34\text{ }\mu\text{m}$, $n = 10$), holoblastic, monoblastic, integrated, terminal, determinate, hyaline, smooth-walled. *Conidia* $33\text{--}45 \times 12\text{--}20\text{ }\mu\text{m}$ ($\bar{x} = 36.2 \times 16.6\text{ }\mu\text{m}$, $n = 20$), solitary, oval to ellipsoidal, acrogenous, cheiroid, with a basal connecting cell, pale brown to brown, consisting of 6–7 rows, individual rows discoid. *Conidial arm* $28\text{--}40 \times 4\text{--}6\text{ }\mu\text{m}$ ($\bar{x} = 31.8 \times 5\text{ }\mu\text{m}$, $n = 20$), digitate, cylindrical, straight or slightly curved, arising from a basal cell, 6–9-distoseptate, slightly constricted at the septa, with guttules.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 17 mm after 10 days at 27 °C, irregular, filamentous, white to brown, umbonate, opaque on the surface; irregular, filamentous, white to pale yellow in reverse.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet BP-NL-1 (MFLU 25-0236, **a new host record**); living culture MFLUCC 25-0265.

GenBank – MFLUCC 25-0265: ITS = PV870580, *tef1-α* = PX255034.

Pre-screening for antibacterial activity – *Dictyocheiropora nabanheensis* (MFLUCC 25-0265) showed a 9 mm inhibition zone against *B. subtilis*, observable as a complete inhibition, when compared with the positive control (15 mm), and no inhibition zone against *E. coli* and *S. aureus*.

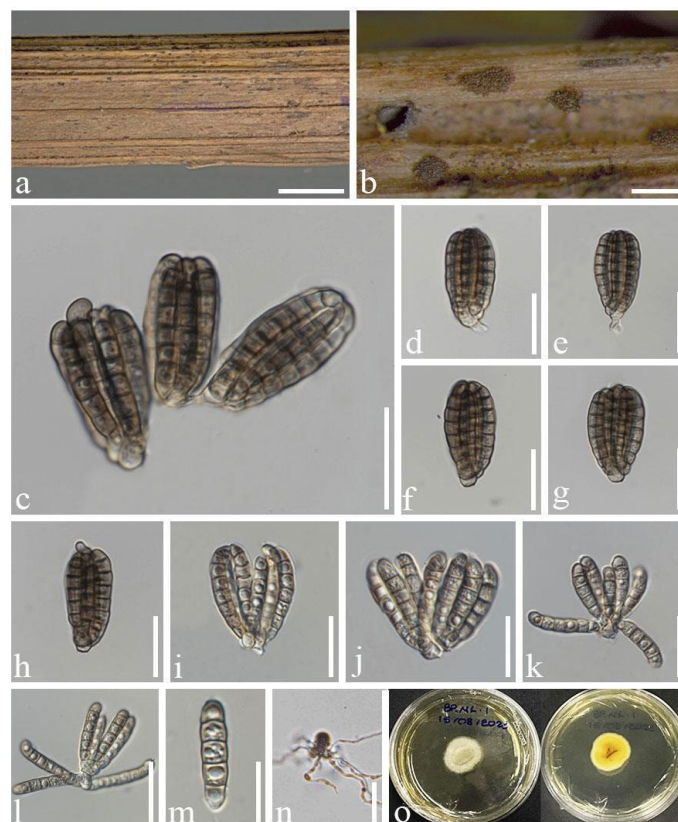


Figure 15 – *Dictyocheiropora nabanheensis* (MFLU 25-0236, a new host record). a, b Appearance of colonies on host substrate. c–e Conidia and conidiogenous cells. f–h Conidia. i–m Conidia arms. n A germinating conidium. o Culture on MEA. Scale bars: a = 1 mm, b = 200 μm , c, d, e, f, g, h, i, j, k, l, m, n = 20 μm .

Known host and distribution – *Pandanus* sp. (Pandanaceae) in China (Tibpromma et al. 2018); decaying pod of *Leucaena* sp. (Fabaceae) in Thailand (Jayasiri et al. 2019); *Borassus flabellifer* (Arecaceae) in India (Rajeshkumar et al. 2021); *Coffea arabica* (Rubiaceae) in China (Lu et al. 2025); *Cocos nucifera* (Arecaceae) in Thailand (Tian et al. 2024); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analysis (Fig. 14), our strain (MFLUCC 25-0265) is grouped sister to *Dictyocheiropora nabanheensis* (MFLUCC 17-0562) with 99% ML and 1.00 BYPP bootstrap support. Our new collection is morphologically similar to *Dictyo. nabanheensis* (MFLUCC 17-0562) in having oval to ellipsoid, pale brown to brown, cheiroid conidia ($33\text{--}45 \times 12\text{--}20$ vs. $35\text{--}40 \times 18\text{--}21$ μm) with 6–7 rows of cells with 5–10 septa. However, our new collection has smaller conidiogenous cells ($4\text{--}6 \times 2.5\text{--}4$ vs. $9\text{--}20 \times 5\text{--}7$ μm) and conidia without rounded apical appendages compared to *Dictyo. nabanheensis* (MFLUCC 17-0562). Moreover, there is no significant base pair difference between our strain (MFLUCC 25-0265) and *Dictyo. nabanheensis* (MFLUCC 17-0562). *Dictyocheiropora nabanheensis* has mainly been reported on Arecaceae, Fabaceae, Pandanaceae, and Rubiaceae from China and Thailand (Tibpromma et al. 2018, Jayasiri et al. 2019, Rajeshkumar et al. 2021, Tian et al. 2024). In our study, we isolated *Dictyo. nabanheensis* for the first time from Asteraceae and reported our new collection as a new host record on *Bidens pilosa* in northern Thailand.

Neodendryphiella

Iturrieta-González et al. (2018) introduced *Neodendryphiella* in Dictyosporiaceae, with *N. terraconensis* designated as the type species. *Neodendryphiella* is characterized by macronematous, mononematous, straight or flexuous, subhyaline to brown conidiophores, terminal or intercalary conidiogenous cells, ellipsoidal, aseptate or septate, and yellowish-brown to brown conidia (Iturrieta-González et al. 2018). Currently, four species are listed in *Neodendryphiella*, viz., *N. brassaiopsidis*, *N. mali*, *N. michoacanensis*, and *N. tarraconensis* (Index Fungorum 2025). In this study, we reported *Neodendryphiella mali* as a new record on *Chromolaena odorata*.

Neodendryphiella mali Iturr.-Gonz., Gené & Dania García, MycoKeys 37: 25 (2018) Fig. 16

Index Fungorum number: IF824665, Facesoffungi number: FoF18030

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* on the host substrate, superficial, scattered, yellow. *Mycelium* immersed to superficial, septate, branched, pale brown. *Conidiophores* $115\text{--}200 \times 4\text{--}10$ μm ($\bar{x} = 171.4 \times 6.4$ μm , $n = 5$), macronematous, mononematous, straight or slightly curved, branched, septate, pale brown at the apex and dark brown at the base. *Conidiogenous cells* terminal or intercalary, cylindrical. *Ramoconidia* $7\text{--}15 \times 4\text{--}6$ μm ($\bar{x} = 10.82 \times 5.62$ μm , $n = 5$), pale brown, ampuliform to cylindrical, smooth to verruculose. *Conidia* $8\text{--}12 \times 4\text{--}6$ μm ($\bar{x} = 9.6 \times 5$ μm , $n = 20$), (0–)1-septate, pale brown, ovoid to ellipsoidal, or cylindrical, verruculose to verrucose.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 12 May 2023, Zin Hnin Htet, CO-HMS-7 (MFLU 25-0237, **a new host record**).

GenBank – MFLU 25-0237: ITS = PV870581.

Known host and distribution – leaf of *Malus domestica* (Rosaceae) in Italy (Iturrieta-González et al. 2018); herbivore dung in Spain (Iturrieta-González et al. 2018); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analysis (Fig. 14), the strain (MFLU25-0237) grouped with *Neodendryphiella mali* (CBS 139.95) with 100% ML and 1.00 BYPP bootstrap support. Our collection differs from *N. mali* (type; CBS 139.95) in having larger conidia ($8\text{--}12 \times 4\text{--}6$ μm vs. $4\text{--}15 \times 3\text{--}5$ μm). However, there is no significant base pair difference between two strains. In this study, we isolated *N. mali* for the first time from Asteraceae and reported our collection as the new host record on *Chromolaena odorata* (Asteraceae) in northern Thailand.

Didymellaceae Gruyter, Aveskamp & Verkley

Didymellaceae was established by De Gruyter et al. (2009) to include genera such as *Ascochyta*, *Didymella*, *Phoma*, and other *phoma*-like groups. Aveskamp et al. (2010) investigated morphological characters together with LSU, ITS, and *tub2* sequence data to resolve the generic limits of taxa currently placed in the Didymellaceae. They also introduced *Boeremia* to the family and identified two sexual genera in the family: *Leptosphaerulina* and *Macroventuria* (Aveskamp et al. 2010). Based on both morphology and phylogenetic analyses, 13 genera were placed in Didymellaceae (Hyde et al. 2013). Chen et al. (2015) recognized 17 well-supported monophyletic clades as distinct genera and refined the definitions of *Ascochyta*, *Didymella*, *Epicoccum*, and *Phoma* to better reflect their evolutionary relationships based on ITS, LSU, *rpb2* and *tub2* sequence data. Subsequently, several genera have been added to Didymellaceae, such as *Heracleicola* and *Neodidymella* (Ariyawansa et al. 2015), *Didymellocamarosporium* (Wijayawardene et al. 2016), *Briansuttonomyces* (Crous & Groenewald 2016), and *Neomicrosphaeropsis* (Thambugala et al. 2017). Valenzuela-Lopez et al. (2018) introduced six new genera, viz., *Cumuliphoma*, *Ectophoma*, *Juxtiphoma*, *Remotididymella*, *Similiphoma*, and *Vacuiphoma* based on LSU, ITS, *tub2* and *rpb2* sequence data. Hou et al. (2020) added *Vandijkomycella* to Didymellaceae. Currently, there are 50 genera accepted in Didymellaceae (Hyde et al. 2024). In this study, we recorded two *Remotididymella* species based on morphology and the combined dataset of LSU, ITS, *tef1-α*, and *rpb2* sequence data (Fig. 17).



Figure 16 – *Neodendryphiella mali* (MFLU 25-0237, a new host record). a, b Colonies on host substrate. c, d Conidiophores. e, f Conidiophores and conidiogenous cells. g–k Conidia. Scale bars: a = 1000 μ m, b = 500 μ m, c, d = 50 μ m, e, f = 5 μ m, g, h, i, j, k, l = 10 μ m.

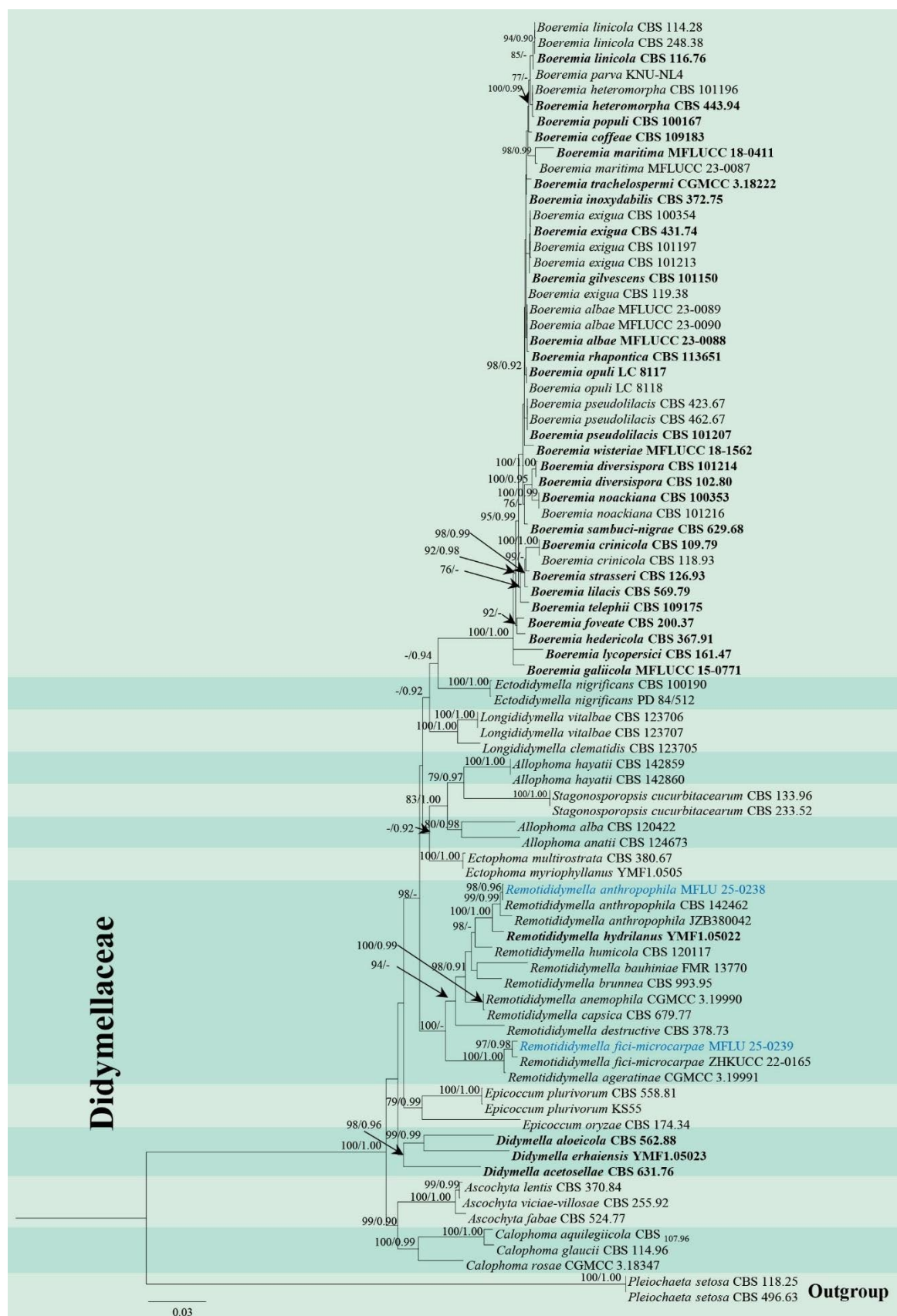


Figure 17 – Phylogram generated from the ML analysis of a combined dataset of LSU, ITS, *tef1-α*, and *rpb2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Pleiochaeta setosa* (CBS 118.25 and CBS 496.63).

***Remotididymella* Valenz. -Lopez**

Remotididymella was introduced by Valenzuela-Lopez et al. (2018), typified by *R. destructiva*. The asexual morph of *Remotididymella* is characterized by aseptate, hyaline, smooth- and thin-walled, allantoid or cylindrical, guttulate conidia (Valenzuela-Lopez et al. 2018, Hou et al. 2020, Yang et al. 2021, Chen et al. 2023), while the sexual morph is distinguished by immersed or superficial, globose, conical globose to lenticular ascomata, septate, branching and hyaline, cellular pseudoparaphyses, bitunicate, fissitunicate, clavate to cylindrical, short-pedicellate asci and hyaline, fusiform, 1–3-septate, ascospores with gelatinous sheaths (Jayasiri et al. 2019). Eleven species are accepted in *Remotididymella* (Chen et al. 2023, Hyde et al. 2024, Index Fungorum 2025). Many *Remotididymella* species were reported with their asexual morph (Valenzuela-Lopez et al. 2018, Hou et al. 2020, Yang et al. 2021, Chen et al. 2023), while *R. bauhiniae* was found as a sexual morph in Jayasiri et al. (2019).

***Remotididymella anthropophila* Valenz. Lopez, Cano, Guarro & Stchigel, Studies in Mycology 90: 35 (2017)** Fig. 18

Index Fungorum number: IF819991, Facesoffungi number: FoF06579

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 40–80 × 50–100 µm ($\bar{x}$ = 60 × 75.2 µm, n = 5), pycnidial, solitary, immersed to semi-immersed, uniloculate, globose, yellowish-brown to brown, without ostioles. *Peridium* 10–20 µm wide, comprising 1–2 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–3 × 2–3 µm ($\bar{x}$ = 2.4 × 2.7 µm, n = 5) phialidic, hyaline, ampuliform to cylindrical. *Conidia* 4–5.5 × 1.5–2.5 µm ($\bar{x}$ = 4.7 × 1.8 µm, n = 20), cylindrical, hyaline, aseptate, smooth, guttulate.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 80 mm after 10 days at 27 °C, irregular, filamentous, pale to dark green, flat, opaque on the surface; irregular, filamentous, concentric, dark green in reverse.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 June 2023, Zin Hnin Htet, BP-HMS-16 (MFLU 25-0238, **a new host record**); living culture MFLUCC 25-0259.

GenBank – MFLUCC 25-0259: ITS = PV870582, *rpb2* = PX120442, *tub2* = PX246144.

Pre-screening for antibacterial activity – *Remotididymella anthropophila* (MFLUCC 25-0259) showed a 12 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared with the positive control (15 mm), a 14 mm inhibition zone against *E. coli*, observable as a complete inhibition, when compared with the positive control (30 mm), and a 15 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared with the positive control (25 mm).

Known host and distribution – a pathogen on an unidentified host in China (Valenzuela-Lopez et al. 2018); human bronchial secretion in the USA (Valenzuela-Lopez et al. 2018); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analysis (Fig. 17), our strain (MFLUCC 25-0259) forms a clade with *Remotididymella anthropophila* (strains CBS14246 and JZB380042) with 99% ML and 0.99 BYPP bootstrap support. Our collection is morphologically similar to *R. anthropophila* (CBS14246) in having pycnidial conidiomata, hyaline, phialidic conidiogenous cells, cylindrical, hyaline, aseptate conidia, but it differs in having smaller conidiomata (40–80 × 50–100 vs. 300–400 × 250–400 µm), wider conidiogenous cells (2–3 vs. 5–6 µm) and smaller conidia (4–5.5 × 1.5–2.5 vs. 5.5–7.5 × 1.5–2.5 µm). However, there are no significant base pair differences between our strain and *R. anthropophila* (CBS14246). *Remotididymella anthropophila* (CBS14246) was discovered as a pathogen from human bronchial secretion in the USA and *R. anthropophila* (JZB380042) was found as a pathogen on an unidentified plant in China (Valenzuela-Lopez et al. 2018). Herein, our collection is reported as a new host record of *R. anthropophila* on *Bidens pilosa* (Asteraceae) and a new geographical record in Thailand.

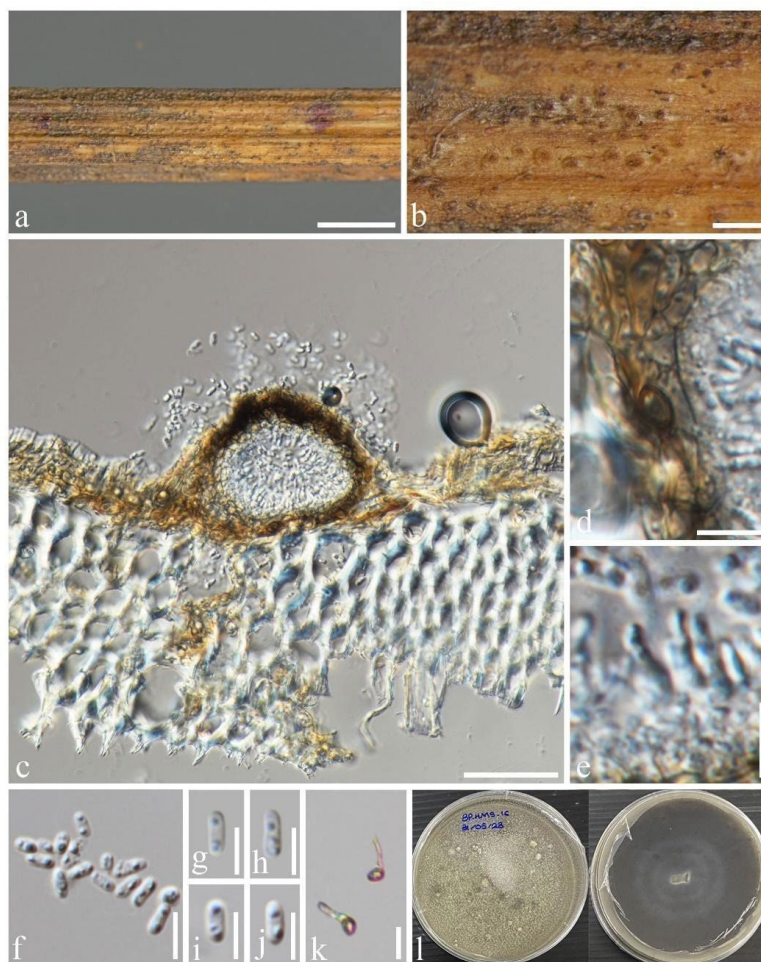


Figure 18 – *Remotididymella anthropophila* (MFLU 25-0238, a new host record). a, b Appearance of conidiomata on host substrate. c Section through a conidioma. d Peridium. e Conidia on conidiogenous cells. f–j Conidia. k Germinating conidia. l Culture on MEA. Scale bars: a = 1 mm, b = 200 μ m, c = 50 μ m, d = 20 μ m, e, f, g, h, i, j, k = 5 μ m

Remotididymella fici-microcarpae Kular, Journal of Fungi 9 (182): 14 (2023)

Fig. 19

Index Fungorum number: IF900161, Facesoffungi number: FoF18031

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** *Ascomata* 150–250 $\times$ 140–160 μ m ($\bar{x}$ = 181 $\times$ 144 μ m, n = 5), immersed to semi-immersed, solitary or scattered, appearing as raised small dark spots, globose to subglobose, brown to dark brown. *Ostiole* central, protruding. *Peridium* 10–20 μ m wide, comprising 3–4 layered dark brown cells of *textura angularis*. *Hamathecium* comprises 2–3 μ m wide, cylindrical to filiform, aseptate, branching pseudoparaphyses. *Asci* 50–75 $\times$ 8–10 μ m ($\bar{x}$ = 65.2 $\times$ 9.2 μ m, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, short-pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 15–22 $\times$ 3–5 μ m ($\bar{x}$ = 18.9 $\times$ 4.4 μ m, n = 20), slightly overlapping, biseriate, hyaline, fusiform, 1-septate, constricted at the central septum, straight or slightly curved. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 31 mm after 10 days at 27 $^{\circ}$ C, irregular, filamentous, round with scalloped margin, white to pale yellow, flat, opaque on the surface; irregular, filamentous, concentric, pale brown in the middle and white margin in reverse.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Bidens pilosa* (Asteraceae), 16 December 2023, Zin Hnin Htet, BP-MY-4 (MFLU 25-0239, **a new host record**); living culture MFLUCC 25-0273.

GenBank – MFLUCC 25-0273: ITS = PV870583, *rpb2* = PX120443.

Pre-screening for antibacterial activity – *Remotididymella fici-microcarpae* (MFLUCC 25-0273) showed no antibacterial activity against *B. subtilis*, *E. coli* and *S. aureus*.

Known host and distribution – stems of *Ficus microcarpa* (Moraceae) in China (Kularathnage et al. 2023); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analysis (Fig. 17), the strain (MFLUCC 25-0273) formed sister lineage to *Remotididymella fici-microcarpae* (ZHKUCC 22-0165) with 97% ML and 0.98 BYPP bootstrap support. *Remotididymella fici-microcarpae* (ZHKUCC 22-0165) is found as an asexual morph on a Moraceae host from China in nature (Kularathnage et al. 2023), while our species is found only with its sexual morph on Asteraceae hosts in Thailand. Furthermore, there is no significant base pair difference between our strain and *R. fici-microcarpae* (ZHKUCC 22-0165). Therefore, this collection is reported as the first sexual morph record of *R. fici-microcarpae*, marking both a new host record on *Bidens pilosa* (Asteraceae) and a new geographical record in Thailand.

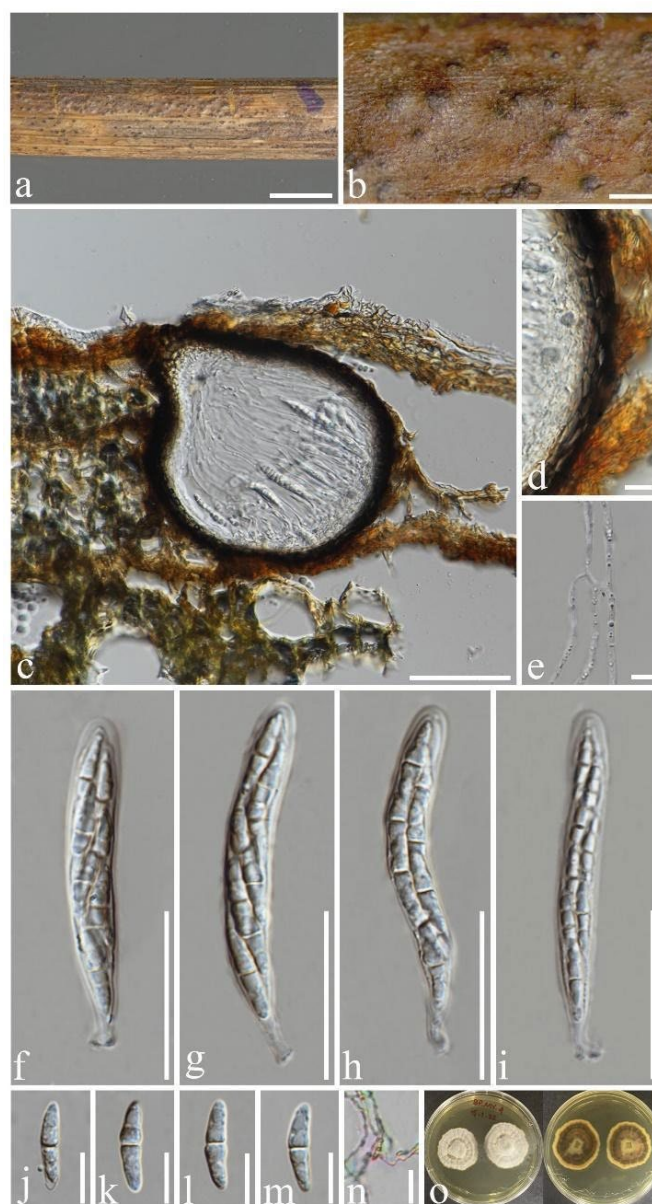


Figure 19 – *Remotididymella fici-microcarpae* (MFLU 25-0239, a new host record and a new geographical record). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. n Germinating ascospore. o Culture on MEA. Scale bars: a = 1 mm, b = 200 μ m, c = 100 μ m, d, j, k, l, m, n = 10 μ m, e = 5 μ m, f, g, h, i = 30 μ m.

Didymosphaeriaceae Munk

Didymosphaeriaceae was introduced by Munk (1953), and currently the family comprises 39 genera (Hyde et al. 2024). Members of this family can be found as endophytes, pathogens, and saprobes in the soil as well as various host plants from both aquatic and terrestrial habitats (Mapook et al. 2020, Yuan et al. 2020, Zhang et al. 2024). In this study, we introduce *Austropleospora chromolaenae*, and *Kalmusia thailandica* as new species and *Chromolaenicola nanensis*, *Montagnula chromolaenae*, *M. donacina*, and *Pseudopithomyces chartarum* as new records based on a combined dataset of LSU, SSU, ITS, *tefl-α*, and *rpb2* sequence data (Fig. 20).

Austropleospora chromolaenae Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.** Fig. 21
Index Fungorum number: IF904364, Facesoffungi number: FoF18032

Etymology – Name reflects the host plant *Chromolaena odorata*, from which this species was isolated.

Holotype – MFLU 25-0240

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 180–210 × 200–230 μm ($\bar{x}$ = 202.3 × 215.5 μm, n = 5), immersed to semi-immersed, solitary, appearing as small dark spots on the substrate, globose to subglobose, brown to dark brown, without ostiole. *Peridium* 10–25 μm wide, consisting of 2–3 layers of yellowish-brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–5 × 3–7 μm ($\bar{x}$ = 4.3 × 5.6 μm, n = 5), phialidic, hyaline ampulliform to lageniform, aseptate, unbranched. *Conidia* 5–8 × 3–5 μm ($\bar{x}$ = 6.1 × 4.8 μm, n = 20), ovoid or obovate to ellipsoidal, initially hyaline and aseptate, becoming pale brown to brown and 1-septate at maturity, thick-walled, verrucose.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 22 mm after 10 days at 27 °C, irregular, filamentous, concentric, white to pale yellow, convex; irregular, concentric, yellow to pale brown in reverse surface.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-10 (MFLU 25-0240, **holotype**); ex-type MFLUCC 25-0277.

GenBank – MFLUCC 25-0277: ITS = PV870584.

Pre-screening for antibacterial activity – *Austropleospora chromolaenae* (MFLUCC 25-0277) showed no antibacterial activity against *B. subtilis*, *E. coli* and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on phylogenetic analysis (Fig. 20), our strain (MFLUCC 25-0277) formed a distinct lineage from *Austropleospora* species with 94% ML and 0.83 BYPP bootstrap support. Our strain is found as an asexual morph in nature and differs from the type species of the genus, *Austropleospora osteospermi* in having larger conidiomata (180–210 × 200–230 μm vs. 75–110 × 100–130 μm), shorter conidiogenous cells (10–12 × 2.5–3.5 μm vs. 4–5 × 3–7 μm), and ovoid or obovate to ellipsoidal, 1-septate, smaller conidia (5–8 × 3–5 μm vs. 14–18 × 4.8–6.5 μm), compared to the cylindrical to narrowly ellipsoidal, 1–3-septate conidia of the latter. A comparison of base pair differences between our collection and *Austropleospora osteospermi* (LM 2009a) reveals a 3.5% (23/647) difference in ITS, without gaps. Due to the unavailability of other gene sequences, we cannot compare base pairs. Therefore, we introduce *Austropleospora chromolaenae* as a new species from *Chromolaena odorata* (Asteraceae) in Thailand, based on morphology and multi-gene phylogeny.

Chromolaenicola Mapook & K.D. Hyde

Chromolaenicola was introduced by Mapook et al. (2020), and there are seven accepted species in the genus (Index Fungorum 2025), viz., *Chromolaenicola chiangraiensis*, *C. clematidis*, *C. lampangensis*, *C. nanensis*, *C. sapinda*, *C. siamensis* and *C. thailandensis*. They have been reported as saprobes in terrestrial habitats on different plant families (Asteraceae, Bromeliaceae,

Fabaceae, Ranunculaceae, and Sapindaceae) in China and Thailand (Jayasiri et al. 2019, Mapook et al. 2020, Phukhamsakda et al. 2020, Ren et al. 2022, Tian et al. 2024, Wanasinghe et al. 2025).

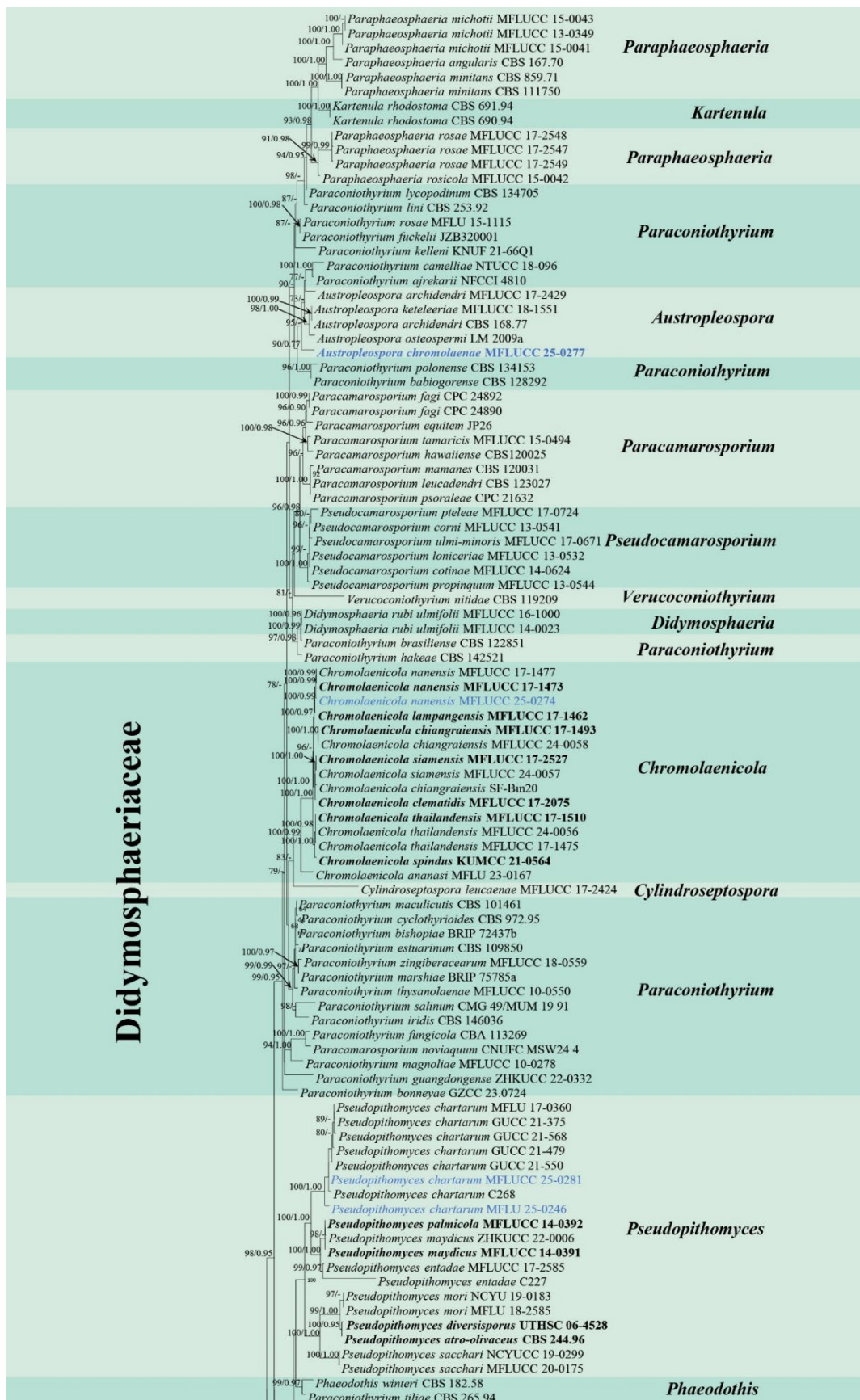


Figure 20 – Continued.

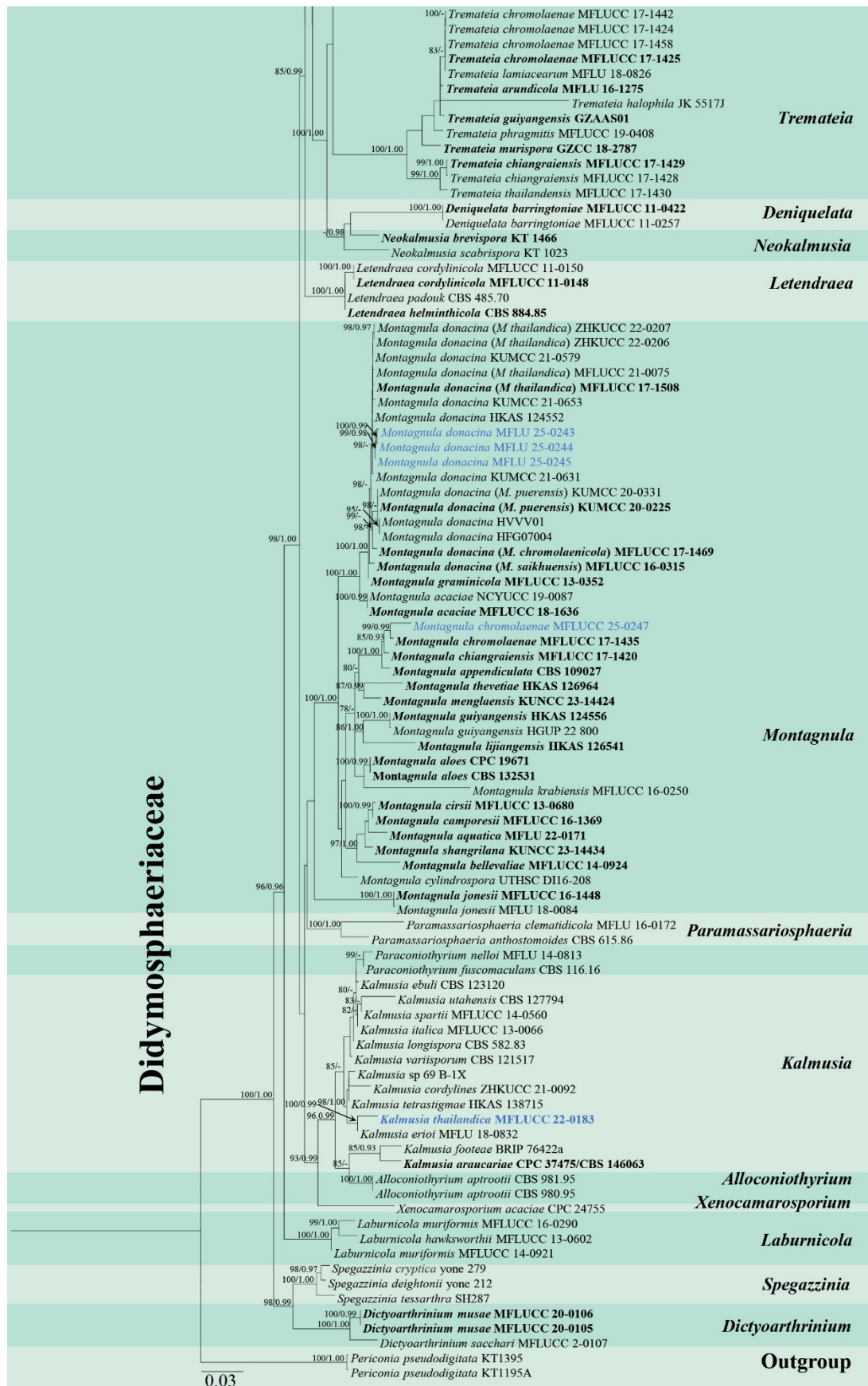


Figure 20 – Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, *tef1- α* , and *rpb2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Periconia pseudodigitata* (KT1395 and KT1395A).

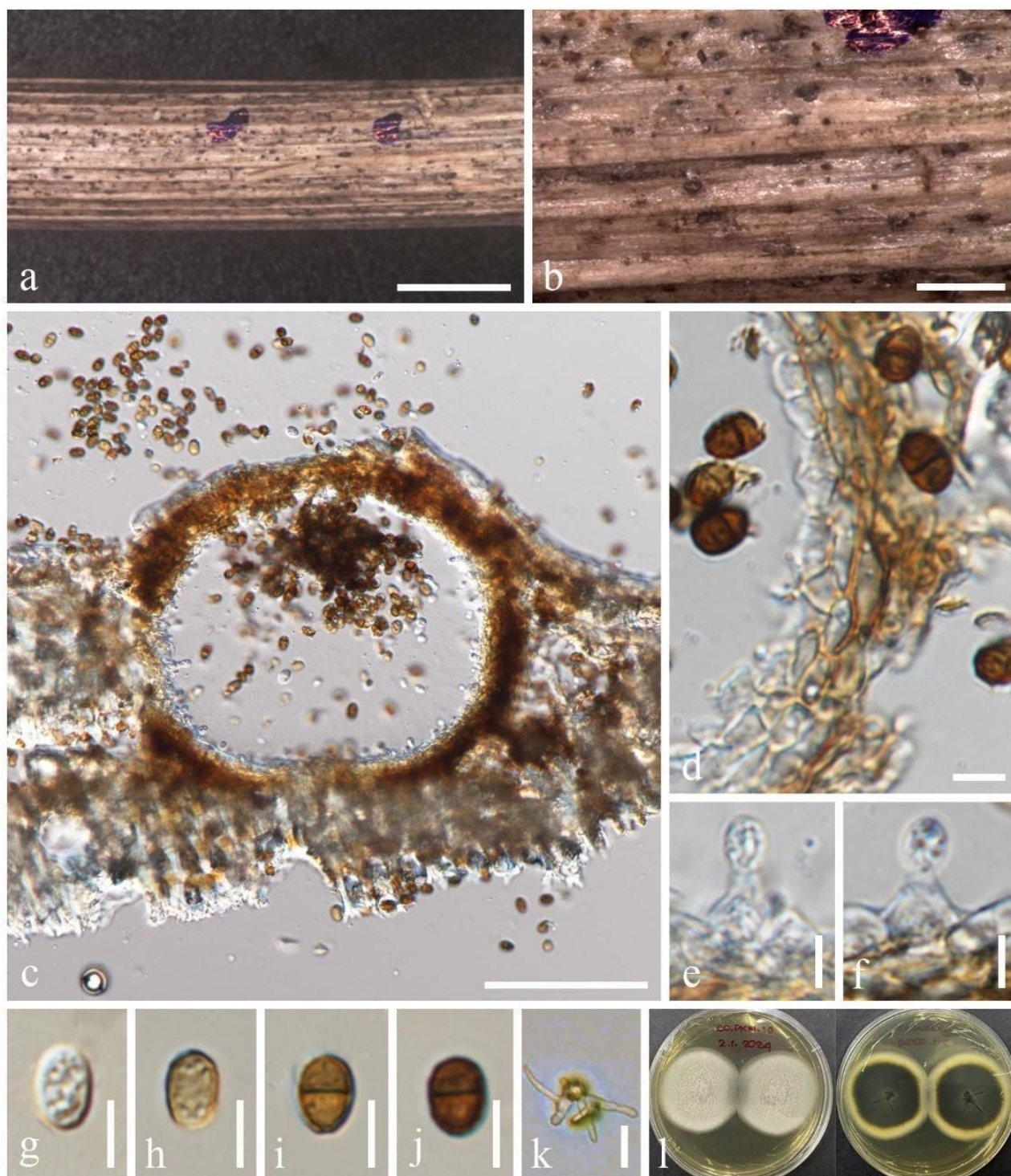


Figure 21 – *Austropleospora chromolaenae* (MFLU 25-0240, holotype). a, b Conidiomata on host substrate. c Section through a conidioma. d Peridium. e, f Conidiogenous cells. g–j Conidia. k A germinating conidium. l Culture on MEA. Scale bars: a = 1000 μ m, b = 500 μ m, c, d = 50 μ m, e, f = 5 μ m, g, h, i, j, k, l = 10 μ m.

Chromolaenicola nanensis Mapook & K.D. Hyde, Fungal Diversity 101: 28 (2020)

Fig. 22

Index Fungorum number: IF557282, Facesoffungi number: FoF07786

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 190–275 $\times$ 205–230 μ m ($\bar{x}$ = 220 $\times$ 217 μ m, n = 5), immersed to semi-immersed, solitary or scattered, appearing as small dark spots on the substrate, coriaceous, globose to subglobose, brown to dark brown. *Ostiole* protruding. *Peridium* 20–50 μ m wide, multi-layered, comprising dark brown cells of *textura*

angularis. *Hamathecium* comprises 1–2 μm wide, cylindrical to filiform, septate, branching pseudoparaphyses. *Asci* 97–140 $\times$ 10–16 μm ($\bar{x}$ = 124 $\times$ 13 μm , n = 20), 6–8-spored, bitunicate, cylindrical, straight or slightly curved, apically rounded, short pedicellate with an ocular chamber. *Ascospores* 14–24 $\times$ 5–10 μm ($\bar{x}$ = 20 $\times$ 8 μm , n = 20), slightly overlapping, uni-seriate, initially hyaline, 1-septate when immature, becoming reddish-brown to brown at maturity, ellipsoid to broadly fusiform, muriform, and 3-transversely septate, with 1-vertical septum when mature, constricted at the central septum, straight or slightly curved, without gelatinous sheath. **Asexual morph:** Undetermined.



Figure 22 – *Chromolaenicola nanensis* (MFLU 25-0241). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–n Ascospores.

o A germinating ascospore. p Culture on MEA. Scale bars: a = 1 mm, b = 500 μ m, c = 100 μ m, d = 20 μ m, e = 5 μ m, f, g, h, i = 30 μ m, j, k, l, m, n, o = 10 μ m.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 22 mm after 10 days at 27 °C, irregular, filamentous, concentric, white to pale yellow, convex; irregular, concentric, yellow to pale brown in reverse surface.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-2 (MFLU 25-0241); living culture MFLUCC 25-0274.

GenBank – MFLUCC 25-0274: ITS = PV870585, SSU = PV996955, *tef1- α* = PX255035.

Pre-screening for antibacterial activity – *Chromolaenicola nanensis* (MFLUCC 25-0274) showed no antibacterial activity against *E. coli*, *B. subtilis* and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020, this study).

Notes – Based on the phylogenetic analysis (Fig. 20), the strain (MFLUCC 25-0274) formed a sister clade with the isolates of *Chromolanicola nanensis* (strains MFLUCC 17-1473 and MFLUCC 17-1477) with 100% ML and 1.00 BYPP bootstrap support. Our collection is morphologically similar to *C. nanensis* in having immersed to semi-immersed, solitary or scattered ascomata, bitunicate asci (97–140 $\times$ 10–16 μ m vs. 110–145 $\times$ 10–12.5 μ m), uniseriate, hyaline to reddish-brown, septate, muriform ascospores but differs in having larger conidiomata (190–275 $\times$ 205–230 μ m vs. 210–230 $\times$ 200–220 μ m), larger ascospores (14–24 $\times$ 5–10 μ m vs. 16–20 $\times$ 7.5–9 μ m). However, there is no significant base pair difference between our collection and *C. nanensis*. *Chromolaenicola nanensis* was previously reported on *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020).

***Kalmusia* Niessl**

Niessl (1872) introduced *Kalmusia*, and *K. ebuli* is the type species. In the past, *Kalmusia* has been transferred to various families (Arx & Müller 1975, Barr 1992, Hyde et al. 2013, Zhang et al. 2014). Ariyawansa et al. (2014) confirmed the phylogenetic placement of *Kalmusia* based on phylogenetic analysis of the combined SSU, LSU, *rpb2* and *tef1- α* sequences, and placed *Kalmusia* in Didymosphaeriaceae. There are 56 epithets of *Kalmusia* listed in the Index Fungorum (2025). The sexual morph of *Kalmusia* is characterized by immersed, globose ascomata with a central, stout papilla, surrounded by hyphae in the substrate, pedicellate asci, septate pseudoparaphyses, brown, 3-septate inequilateral ascospores, while its asexual morph has solitary pycnidia, peridium with *textura angularis* cells, small, hyaline, oblong to slightly ellipsoidal conidia with holoblastic conidiogenous cells.

Kalmusia thailandica Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 23

Index Fungorum number: IF904365; Facesoffungi number: FoF14037

Etymology – Name reflects the country from which this species was collected.

Holotype – MFLU 22-0259

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 90–150 $\times$ 125–145 μ m ($\bar{x}$ = 111 $\times$ 130 μ m, n = 5), appearing as black spots on the host surface, unilocular, solitary, scattered, erumpent, ostiolate. *Peridium* 10–20 μ m wide, comprising 3–5-layers of hyaline to pale yellow cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–3 $\times$ 1.5–2 μ m ($\bar{x}$ = 1.2 $\times$ 1.7 μ m, n = 5), holoblastic, cylindrical to ampulliform, hyaline, aseptate. *Conidia* 3–4.5 $\times$ 1–2 μ m ($\bar{x}$ = 3.6 $\times$ 1.7 μ m, n = 20), cylindrical to ellipsoidal, hyaline, aseptate, smooth-walled.

Culture characteristics – Conidia germinating on PDA, reaching 30 mm diam. within 10 days at 27 °C, circular, flat, wavy margin, curled, circular zonate with aerial mycelia, both surface and reverse white.

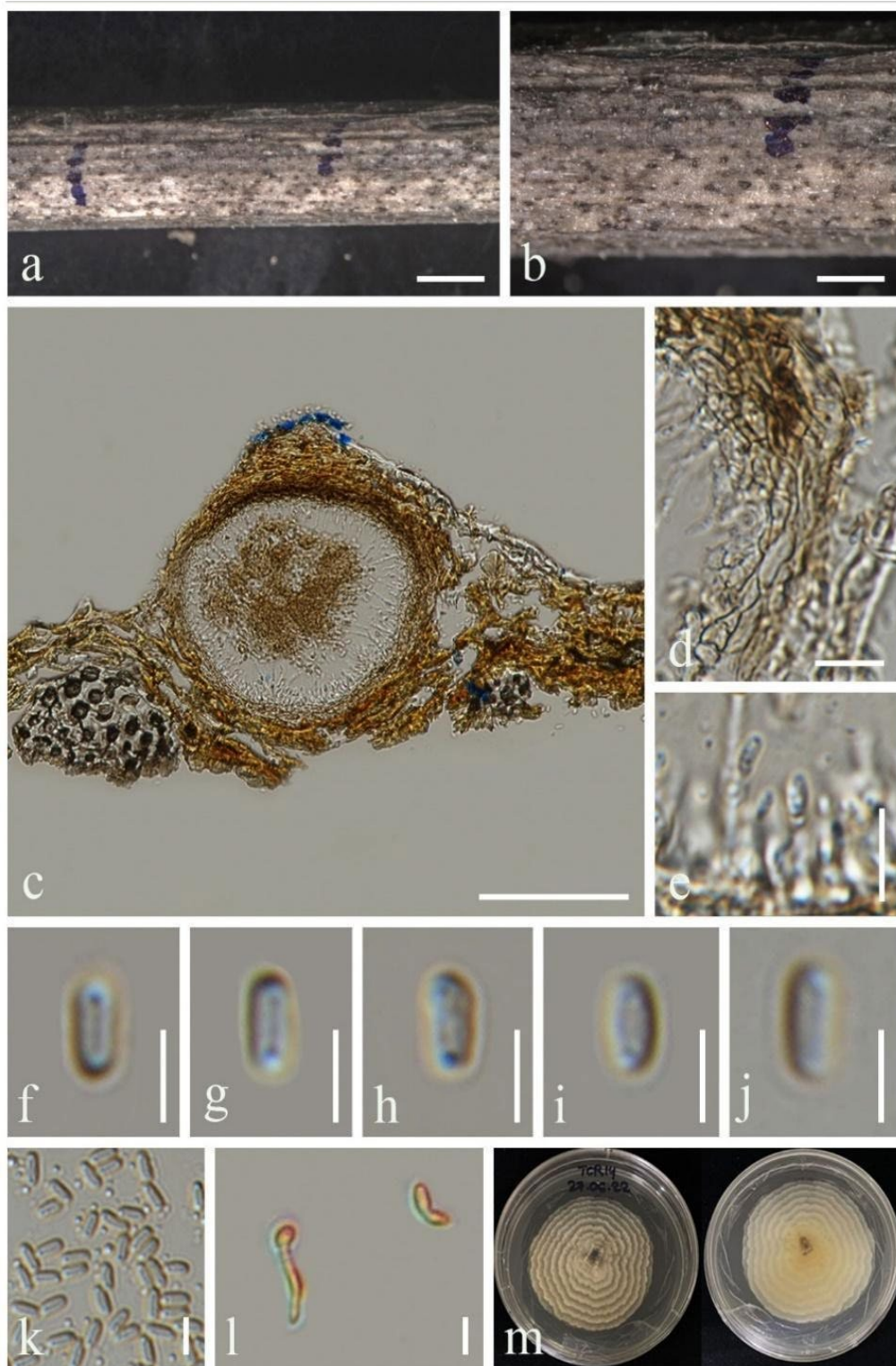


Figure 23 – *Kalmusia thailandica* (MFLU 22-0259, holotype). a, b Appearance of conidiomata on host substrate. c Section through a conidioma. d Peridium. e Conidia attached to conidiogenous cells. f–k Conidia. l Germinating conidia. m Culture on PDA. Scale bar: a, b = 500 μ m, c = 100 μ m, d = 20 μ m, e–l = 5 μ m.

Material examined – Thailand, Chiang Rai Province, Theong District, on dead stems of *Chromolaena odorata* (Asteraceae), 24 January 2022, Ausana Mapook, TCR14 (MFLU 22-0259, **holotype**), ex-type MFLUCC 22-0183.

GenBank – MFLUCC 22-0183: ITS = PV870586, LSU = PV992405, SSU = PV996956, *tef1- α* = PX282665.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analysis (Fig. 20), our strain (MFLUCC 22-0183) grouped within *Kalmusia* and formed a sister lineage with *K. erioi* (MFLU 18-0832) with 100 % ML and 1.00 BYPP bootstrap support. However, *Kalmusia erioi* has been described only from its sexual morph and the culture was not sporulated. Thus, we are unable to compare the morphology of our collection with *K. erioi*. Morphologically, our strain (MFLUCC 22-0183) is similar to *K. italica* (MFLUCC 13-0066) and *K. spartii* (MFLUCC 14-0560) in having aseptate, hyaline conidia with cylindrical, holoblastic conidiogenous cells, but differs in having cylindrical to ampulliform conidia in contrast to the conidia of *K. italica* and *K. spartii*. A base pair comparison between our strain and *Kalmusia erioi* (MFLU 18-0238) reveals 3.5% (20/560) base pair difference in the ITS, without gaps. Due to the unavailability of other gene sequences, we cannot compare base pairs. Therefore, *Kalmusia thailandica* is introduced as a new species found on *Chromolaena odorata* (Asteraceae) in Thailand, based on morphology and multi-gene phylogeny.

Montagnula Berl.

Montagnula was introduced by Berlese (1896), with *M. infernalis* designated as the type species. The genus is characterized by immersed to semi-immersed, globose to subglobose ascomata, septate pseudoparaphyses, bitunicate, fissitunicate, usually cylindric-clavate to clavate, with long pedicellate asci, and oblong to narrowly oblong, sometimes fusiform ascospores (Tennakoon et al. 2016, Mapook et al. 2020, Sun et al. 2023). *Montagnula* species have been reported in terrestrial habitats with a wide geographic and host distribution (Wanasinghe et al. 2024). Currently, there are 33 species listed in *Montagnula* (Wijayawardene et al. 2022, Index Fungorum 2025).

Montagnula chromolaenae Mapook & K.D. Hyde, *Fungal Diversity* 101, 1–175 (2020) Fig. 24

Index Fungorum number: IF557297, Facesoffungi number: FoF07790

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Ascomata 145–250 × 220–300 μ m ($\bar{x}$ = 150 × 250 μ m, n = 5), immersed to erumpent, solitary, globose to subglobose, appearing as small dark spots on the substrate, with an ostiole. Ostiole central, papillate. Peridium 13–20 μ m wide, comprising 2–3 layers of yellowish-brown to brown cells of *textura angularis*. Hamathecium comprises 2–3 μ m wide, cylindrical to filiform, aseptate, branching pseudoparaphyses. Asci 60–100 × 9–15 μ m ($\bar{x}$ = 71.5 × 12.1 μ m, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, short-pedicellate. Ascospores 13–17 × 4–7 μ m ($\bar{x}$ = 12.2 × 5.1 μ m, n = 20), overlapping in the ascus, biseriate, yellowish-brown to brown, 1-septate, fusiform to ovoid, constricted at the central septum, straight or slightly curved, with a gelatinous sheath covering both ends of ascospores, straight or slightly curved. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 18 mm after 10 days at 27 °C, irregular, undulate, flat, white to grey, wrinkle, opaque, back: dark grey, irregular, undulate in reverse surface.

Material examined – Thailand, Chiang Rai Province, Phan District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet, BP-DP-9 (MFLU 25-0242, **a new host record**); living culture MFLUCC 25-0247.

GenBank – MFLUCC 25-0247: ITS = PV870587, LSU = PV992406, SSU = PV996957

Pre-screening for antibacterial activity – *Montagnula chromolaenae* (MFLUCC 25-0247) showed antibacterial activity against *E. coli* with a 9 mm inhibition zone, observable as a complete inhibition, when compared with a positive control (30 mm), but no inhibition against *B. subtilis* and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analysis (Fig. 20), the strain (MFLUCC 25-0247) grouped within *Montagnula* species, sister to *Montagnula chromolaenae* (MFLUCC 17-1435) with 99% ML and 0.99 BYPP bootstrap support. Our strain is morphologically similar to *M. chromolaenae* (MFLUCC 17-1435) in having immersed, globose to subglobose ascomata with a yellowish-brown to brown peridium, hyaline, cylindrical to filiform, septate, branching pseudoparaphyses, bitunicate asci, and yellowish-brown to brown, 1-septate, fusiform to ovoid ascospores ($13\text{--}17 \times 4\text{--}7$ vs. $15\text{--}16.5 \times 5\text{--}6$ μm) covered with a gelatinous sheath. However, our strain (MFLUCC 25-0247) differs slightly from *M. chromolaenae* (MFLUCC 17-1435) in having wider ascomata ($145\text{--}250 \times 220\text{--}300$ μm vs. $170\text{--}175(230) \times (140\text{--})170\text{--}190$ μm) and shorter asci ($60\text{--}100 \times 9\text{--}15$ μm vs. $85\text{--}105 \times 9\text{--}15$ μm). The nucleotide comparison of the ITS region of our strain (MFLUCC 25-0247) and *M. chromolaenae* reveals 2.6% (14/533) nucleotide differences. Therefore, *M. chromolaenae* is reported as a new host record on *Bidens pilosa* and the second occurrence on Asteraceae in northern Thailand.

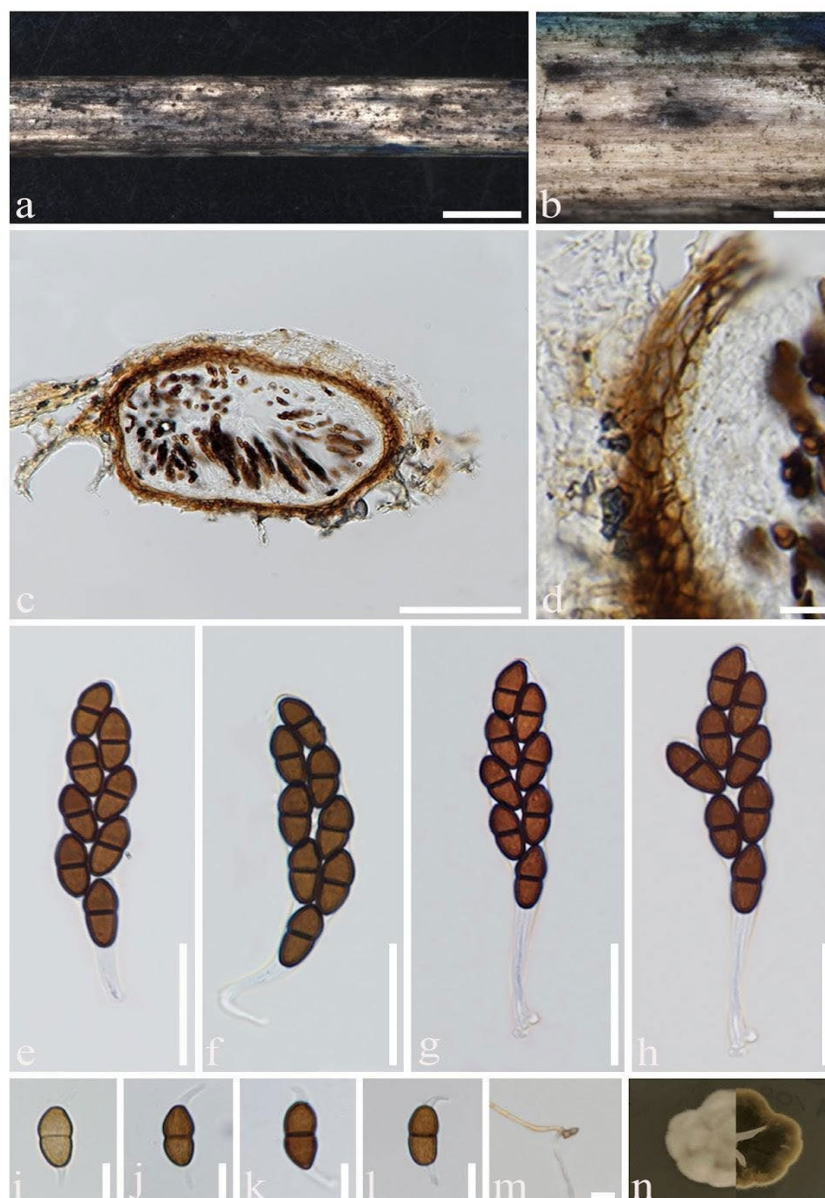


Figure 24 – *Montagnula chromolaenae* (MFLU 25-0242, a new host record). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Peridium. e–h Asci. i–l Ascospores. m A germinating ascospore. n Culture on MEA. Scale bar: a = 1 mm, b = 500 μm , c = 100 μm , e, f, g, h = 30, i, j, k, l, m = 10 μm

Montagnula donacina (Niessl) Wanas., E.B.G. Jones & K.D. Hyde, Index Fungorum 319: 1 (2017)
Fig. 25

Index Fungorum number: IF552762, Facesoffungi number: FoF04638

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 200–300(–410) × 220–300(–370) µm ($\bar{x}$ = 265.2 × 157.8 µm, n = 5) immersed to erumpent, solitary, scattered, globose to subglobose, ostiolate. *Ostiole* 50–70 µm wide, central, papillate. *Peridium* (20–)40–80 µm wide, comprising 2–3 layers of yellowish-brown cells of *textura angularis*. *Hamathecium* comprises 1–2 µm wide, cylindrical to filiform, aseptate, branching pseudoparaphyses. *Asci* 75–105 × 9–15 µm ($\bar{x}$ = 93.7 × 13.1 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, long-pedicellate with rounded to furcate base. *Ascospores* 10–16 × 5–8 µm ($\bar{x}$ = 13.9 × 6 µm, n = 20), uniseriate, overlapping in the ascus, yellowish-brown to brown, 1-septate, fusiform, constricted at the central septum, straight or slightly curved, acute end cells, without gelatinous sheath. **Asexual morph:** Undetermined.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-13 (MFLU 25-0243).

GenBank – MFLU 25-0243: ITS = PV870588, *tef1-α* = PX255037, *rpb2* = PX120445.

Known host and distribution – *Acer* sp. (Sapindaceae) in China (Du et al. 2021); *Acacia reficiens* (Fabaceae) in Namibia (Aptroot 1995); *Acacia* sp. (Fabaceae) in India (Aptroot 1995); *Adhatoda vasica* (Acanthaceae) in India (Aptroot 1995); *Ailanthus altissima* (Simaroubaceae) in India (Aptroot 1995); *Althaea rosea* (Malvaceae) in China (Aptroot 1995); *Annona squamosa* (Annonaceae) in India (Aptroot 1995); *Arundo donax* (Poaceae) in Portugal (Aptroot 1995); *Bambusoideae* (Poaceae) in Brazil and Papua New Guinea (Aptroot 1995); *Cajanus cajan* (Fabaceae) in India (Aptroot 1995); *Calamus australis* (Arecaceae) in Australia (Aptroot 1995); *Careya arborea* (Lecythidaceae) in India (Aptroot 1995); *Citrus aurantiifolia* (Rutaceae) in India (Aptroot 1995); *Clerodendrum infortunatum* (Lamiaceae) in India (Aptroot 1995); *Clerodendrum multiflorum* (Lamiaceae) in India (Aptroot 1995); *Coffea arabica* (Rubiaceae) in Paraguay (Aptroot 1995); *Coffea robusta* (Rubiaceae) in Central African Republic (Aptroot 1995); *Craterellus odoratus* (Cantharellaceae) in China (Zhao et al. 2018); dead stem of *Citrus* sp. (Rutaceae) in Thailand (Wanasinghe et al. 2016); *Duranta repens* (Verbenaceae) in India (Aptroot 1995); *Ficus glomerata* (Moraceae) in India (Aptroot 1995); *Funtumia africana* (Apocynaceae) in Sierra Leone (Aptroot 1995); *Hibiscus* sp. (Malvaceae) in India (Aptroot 1995); *Ipomoea carnea* (Convolvulaceae) in India (Aptroot 1995); *Mallotus philippinensis* (Euphorbiaceae) in India (Aptroot 1995); *Morus alba* (Moraceae) in India (Aptroot 1995); *Litchi litchi* (Sapindaceae) in Myanmar (Thaung 2008); *Nerium odorum* (Apocynaceae) in India (Aptroot 1995); *Paeonia suffruticosa* (Paeoniaceae) in China (Li et al. 2023); *Phyllostachys bambusoides* (Poaceae) in Japan (Wang et al. 2004); *Pistacia* sp. (Anacardiaceae) in India (Aptroot 1995); *Platanus* sp. (Platanaceae) in USA (Wang et al. 2004); *Premna cumingiana* (Lamiaceae) in Philippines (Aptroot 1995); *Pseudosasa japonica* (Poaceae) in France (Aptroot 1995); *Saccharum officinarum* (Poaceae) in Brazil (Aptroot 1995); *Tectona grandis* (Lamiaceae) in India (Aptroot 1995); *Terminalia tomentosa* (Combretaceae) in India (Aptroot 1995); *Trachycarpus fortunei* (Arecaceae) in China (Hyde et al. 1999); *Vitis vinifera* (Vitaceae) in Australia (Pitt et al. 2014); *Wikstroemia* sp. (Thymelaeaceae) in USA (Aptroot 1995); *Zea mays* (Poaceae) in Georgia (Aptroot 1995); *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020, this study).

Notes – In the phylogenetic analyses (Fig. 20), the new collections (MFLU 25-0243, MFLU 25-0244, and MFLU 25-0245) grouped in the same clade with the isolates of *Montagnula donacina* with 99% ML and 0.98 BYPP bootstrap support. Morphologically, our collections are similar to *M. donacina* in having immersed to erumpent, solitary, globose to subglobose ascomata, bitunicate, fissitunicate, clavate to cylindrical, long-pedicellate asci, and yellowish-brown to brown, 1-septate, fusiform ascospores (Sun et al. 2023). Moreover, there are no significant base pair differences between our collections and phylogenetically related isolates of *M. donacina*. Previously, *M. donacina* was found on *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020).

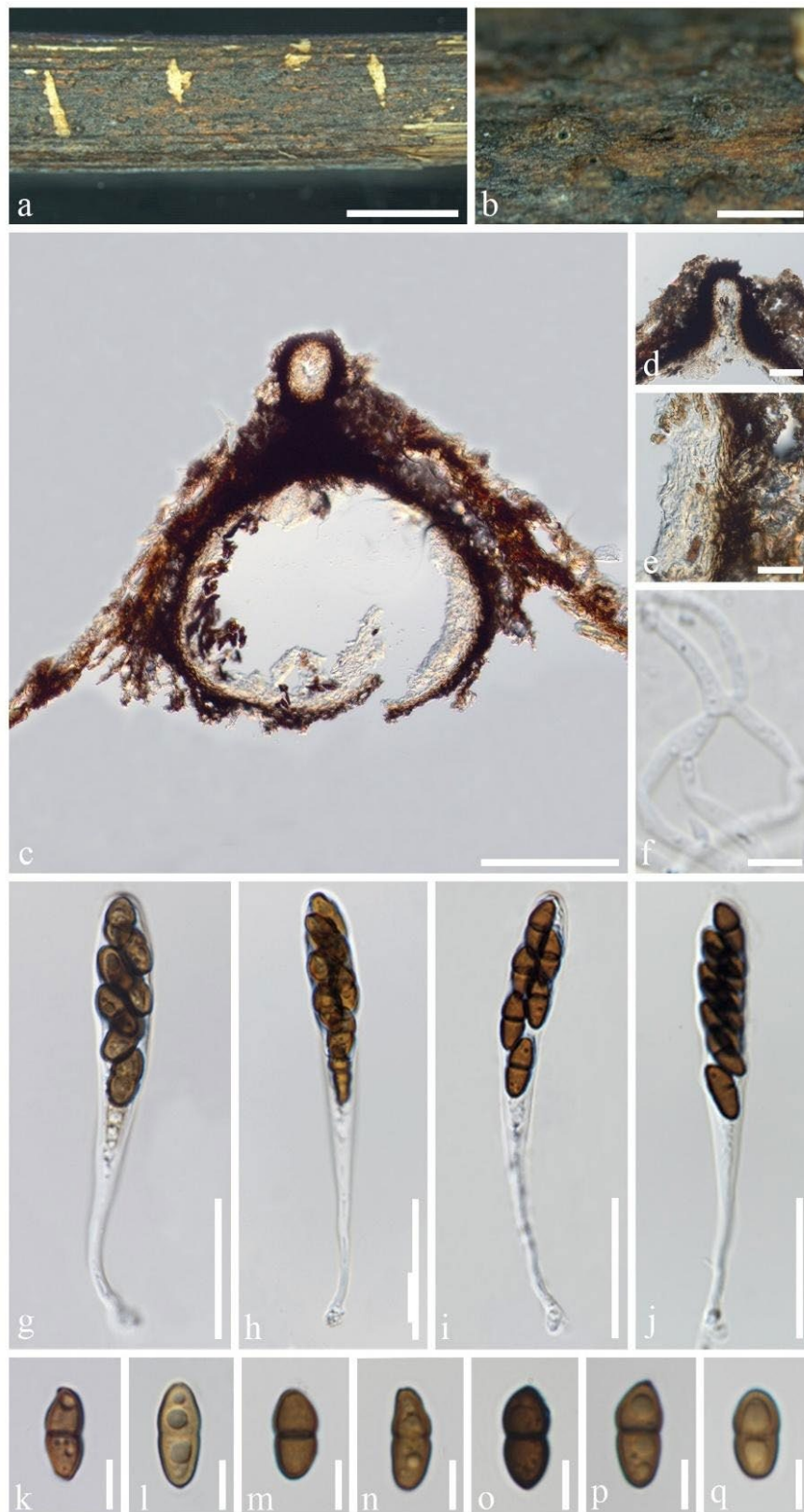


Figure 25 – *Montagnula donacina* (MFLU 25-0243). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–j Asci. k–q Ascospores. Scale bar: a = 1 mm, b = 500 μ m, c = 100 μ m, d = 50 μ m, e = 20 μ m, f = 5 μ m, g, h, i, j = 30 μ m, k, l, m, n, o, p, q = 10 μ m

Pseudopithomyces Ariyaw. & K.D. Hyde

Ariyawansa et al. (2015) introduced *Pseudopithomyces* in Didymosphaeriaceae, typified by *Ps. chartarum*. *Pseudopithomyces* species are pathogens or saprobes on a variety of hosts (Wanasinghe et al. 2018, Jayasiri et al. 2019, Wu et al. 2023). These species are distinguished by micronematous, semi-macronematous, or mononematous, unbranched, flexuous, hyaline to subhyaline conidiophores, monoblastic or blastic, globose or subglobose conidiogenous cells, acrogenous, fusiform or subglobose conidia with single to multiple septation. (Ariyawansa et al. 2015, Crous et al. 2016). Currently, there are 13 species listed in *Pseudopithomyces* (Index Fungorum, 2025).

Pseudopithomyces chartarum (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, Fungal Diversity 75: 27–274 (2015). Fig. 26

Index Fungorum number: IF551393, Facesoffungi number: FoF00938

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* scattered, powdery, effuse, appearing as small dark circles with white at the middle. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–10 × 3–5 µm ($\bar{x}$ = 7.5 × 4.2 µm, n = 10), terminal, hyaline, unbranched, globose to subglobose or cylindrical. *Conidia* 15–20 × 8–10 µm ($\bar{x}$ = 16.2 × 8.9 µm, n = 20), subglobose to cylindrical, light brown to brown, muriform, 2–3 transverse septa, 1–2 longitudinal septa, verruculose, thick-walled.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 45 mm after 10 days at 27 °C, circular, filamentous, light olive-green, powdery, flat, opaque; circular, filamentous, concentric, white to light olive-green.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 5 January 2023, Zin Hnin Htet, BP-2 (MFLU 25-0246, **a new host record**); Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-20 (MFLU 25-0247, **a new host record**); living culture MFLUCC 25-0281.

GenBank – MFLU 25-0246: LSU = PV992407, SSU = PV996960, ITS: PV870591, *tef1-α*: PX255040; *rpb2*: PX120448; MFLUCC 25-0281: ITS = PV870592, *rpb2* = PX120449.

Pre-screening for antibacterial activity – *Pseudopithomyces chartarum* (MFLUCC 25-0281) showed an 11 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm), but showed no inhibition against *B. subtilis* and *E. coli*.

Known host and distribution – *Musa* sp. (Musaceae) in Thailand (Photita et al. 2003, Ariyawansa et al. 2015, Chethana et al. 2023); *Triticum aestivum* (Poaceae) in Argentina (Perelló et al. 2017); decaying pod of *Radermachera sinica* (Bignoniaceae) in Thailand (Jayasiri et al. 2019); decaying pod of *Bauhinia* sp. (Fabaceae) (Jayasiri et al. 2019); decaying pod of *Leucaena* sp. (Fabaceae) in Thailand (Jayasiri et al. 2019); decaying cone of *Magnolia grandiflora* (Magnoliaceae) in China (Jayasiri et al. 2019); dead leaves of *Macaranga tanarius* (Euphorbiaceae) in Taiwan region (Tennakoon et al. 2021); *Prunus spinosa* (Rosaceae) in Iran (Khalilabad & Fotouhifar 2022); *Tetrapanax papyrifer* (Araliaceae) in China (Wu et al. 2023); *Zanthoxylum bungeanum* (Rutaceae) in China (Zeng et al. 2024); *Lonicera caerulea* (Caprifoliaceae) in China (Yan et al. 2024); dead stems of *Bidens pilosa* and *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analyses (Fig. 20), our strains (MFLUCC 25-0281 and MFLU 25-0246) grouped in the same clade with *Pseudopithomyces chartarum* isolates (MFLUCC 17-2567, GUCC 21-375, GUCC 21-568, GUCC 21-479, GUCC 21-550 and C268) with 100% ML and 1.00 BYPP bootstrap support. Morphologically, our collection has smaller conidia (15–20 × 8–10 µm vs 18–25 × 10–15 µm) with 2–3 transverse septa, 1–2 longitudinal septa, while *Ps. chartarum* (MFLUCC 17-2567) has conidia with 3–4 transverse septa and 1–3 longitudinal septa. However, there are no significant base pair differences between our collection and phylogenetically related species. The nucleotide comparison of the ITS region of our strain (MFLUCC 25-0281) and *Ps. chartarum* reveals only 0.4% (2/503) nucleotide differences. Therefore, herein, two new host records of *Pseudopithomyces chartarum* are reported on the *Bidens pilosa* and *Chromolaena odorata* (Asteraceae) in northern Thailand.

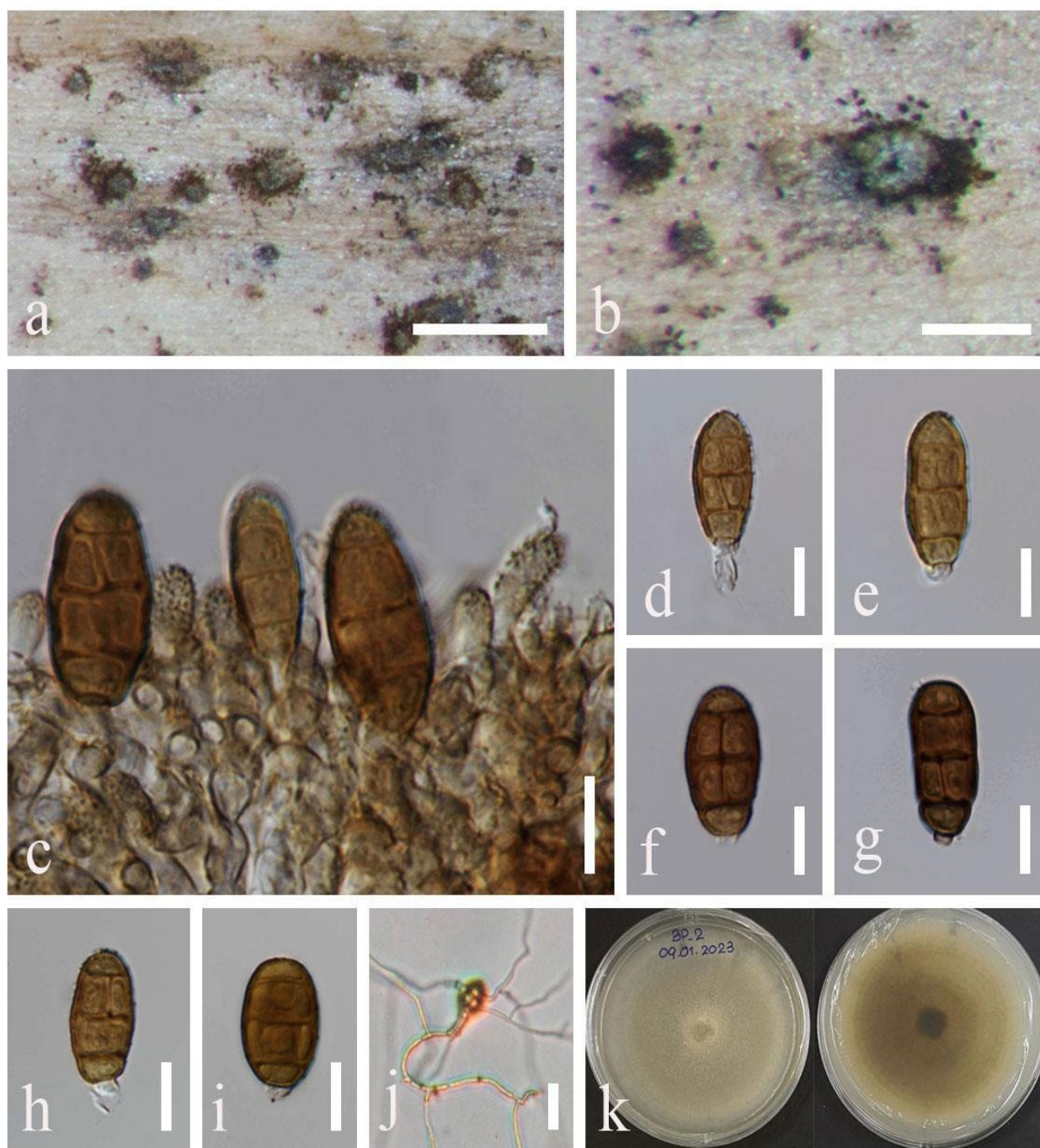


Figure 26 – *Pseudopithomyces chartarum* (MFLU 25-0246, a new host record). a, b Appearance of colonies on the host substrate. c–i Conidia and conidiogenous cells. j A germinating conidium. k Culture on the MEA. Scale bars: a = 500 μ m, b = 200 μ m, c, d, e, f, g, h, i, j = 10 μ m.

Lentimurisporaceae N.G. Liu, J.K Liu & K.D. Hyde

Lentimurisporaceae was introduced by Liu et al. (2018) to accommodate *Lentimurispora* and two other hyphomycetous genera, viz., *Bahusandhika* and *Berkleasmium*. Lentimurisporaceae is characterized by micronematous conidiophores, monoblastic conidiogenous cells, and muriform to lenticular conidia (Liu et al. 2018). Currently, there are two genera in this family, viz., *Lentimurispora* and *Bahusandhika* (Hyde et al. 2024, Pem et al. 2024). In this study, we introduce *Bahusandhika bidentis* as a new species and *B. indica* as a new host and geographic record based on the combined phylogeny of LSU, SSU, ITS, and *tef1- α* sequence data and morphology (Fig. 27).

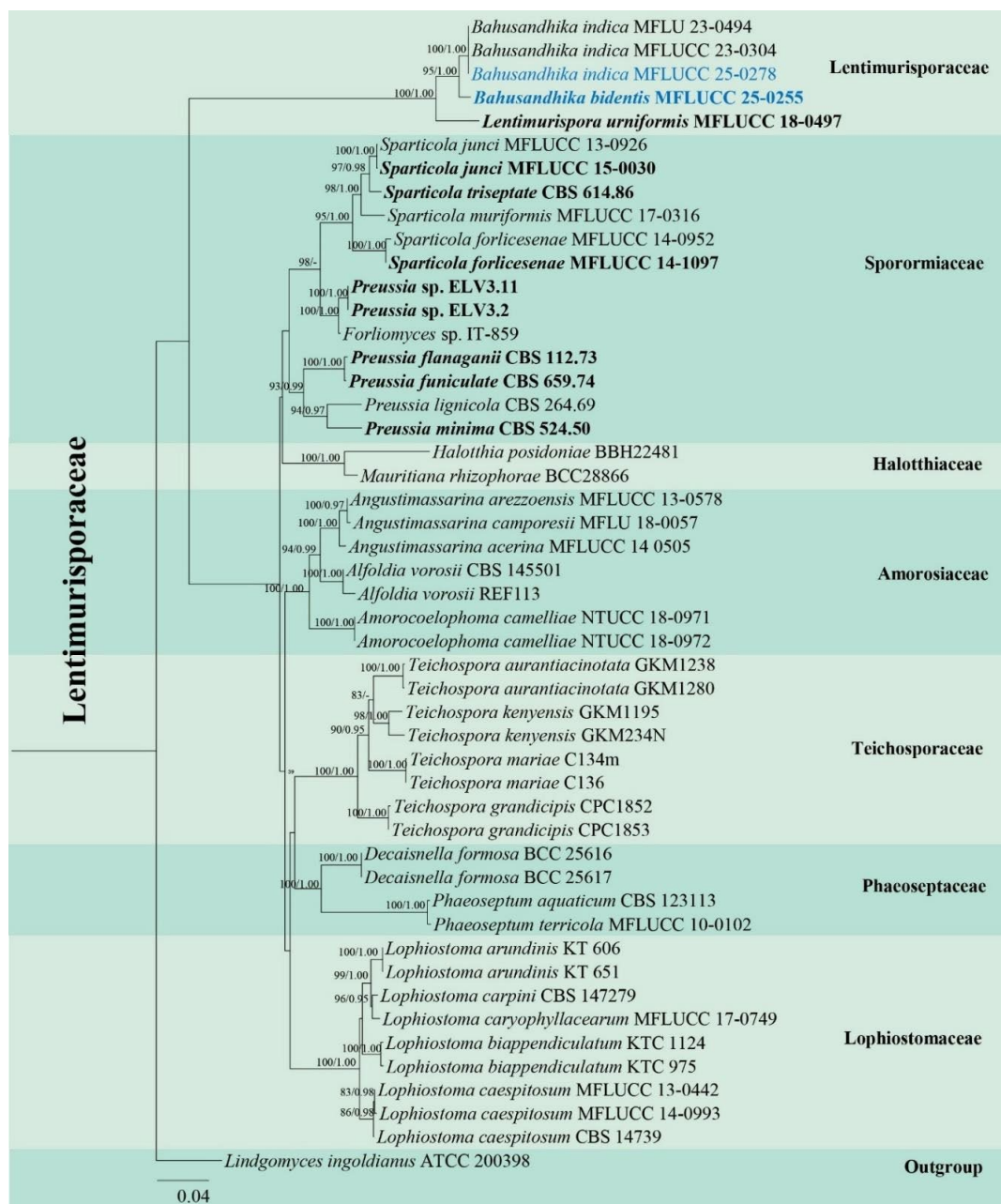


Figure 27 – Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, and *tef1-α* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Lindgomyces ingoldianus* (ATCC 200398).

***Bahusandhika* Subram.**

Bahusandhika was introduced by Subramanian (1956) and typified by *B. indica*. The genus has *torula*-like characters with blastic, sphaerical, ovoid, ampulliform conidiogenous cells and catenate, fusiform, cylindrical or rhomboidal, phragmoseptate conidia (Crane & Miller 2016). The taxonomic position of *Bahusandhika* was unstable due to the limited molecular data (Pratibha et al. 2014, Crane & Miller 2016, McKenzie et al. 2016). Liu et al. (2018) placed *Bahusandhika* in Lentimurisporeaceae based on the combined phylogeny of LSU, SSU and *tef1-α* sequence data. Hyde et al. (2024) accepted seven species in *Bahusandhika*, viz., *B. compacta*, *B. grootfonteinensis*, *B. hughesii*, *B. indica*, *B. rhombica*, *B. sundara*, and *B. terrestris*. The sequence data for *B. indica* are

available in GenBank, while the other species are identified based on the morphological characters (Crane & Miller 2016).

Bahusandhika bidentis Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.** Fig. 28

Index Fungorum number: IF904367, Faces of fungi number: FOF18034

Etymology – Name reflects the host plant *Bidens pilosa*, from which this species was isolated.

Holotype – MFLU 25-0249

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* effuse, pulverulent or velvety, black. *Mycelium* composed of septate, brown, branched hyphae. *Conidiophores* septate, brown, constricted at the septa. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 × 3–5 µm ($\bar{x}$ = 2.5 × 2.3 µm, n = 10), monoblastic, yellowish-brown, ampulliform to ovoid or rounded, formed singly or in groups of 2–3 chains. *Conidia* 11–20 × 7–15 µm ($\bar{x}$ = 16.1 × 11.3 µm, n=20), muriform, simple or branched, ovoid or obovoid to slightly ellipsoidal, rough, thick-walled, unevenly dictyoseptate, yellowish-brown to brown, verrucose.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 20 mm after 10 days at 27 °C, irregular, entire, grey, flat, opaque and slightly cracked; white to grey, irregular, dark grey in reverse surface.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 June 2023, Zin Hnin Htet, BP-HMS-5 (MFLU 25-0249, **holotype**); ex-type MFLUCC 25-0255.

GenBank – MFLUCC 25-0255: LSU = PV992408, SSU = PV996961, ITS = PV870593, *tefl*- α = PX255042.

Pre-screening for antibacterial activity – *Bahusandhika bidentis* (MFLUCC 25-0255) showed a 15 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), and a 14 mm inhibition zone against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm) and a 15 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm).

Known host and distribution – dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analyses (Fig. 27), our new fungal strain (MFLUCC 25-0255) grouped within *Bahusandhika* by forming a separate lineage, sister to *Bahusandhika indica* (strains MFLU 23-0494, MFLUCC 23-0304, and MFLUCC 25-0278) with 95% ML and 1.00 BYPP statistical support. Base pair difference between our strain and *B. indica* (MFLUCC 23-0304) revealed 4% (19/473) difference in the ITS, and 2.6% (20/777) difference in *tefl*- α .

Among the known *Bahusandhika* species, the new strain (MFLUCC 25-0255) is morphologically mostly resembles to *B. indica*, both sharing short, septate brown hyphae and small, brown conidia formed in acropetal chains. However, our collection exhibits conidiogenous cells in singly or in groups of 2–3 in a chain and muriform, simple or branched, unevenly dictyoseptate conidia, while *B. indica* has monotretic, integrated or discrete, terminal conidiogenous cells formed on conidia, which are formed as catenate in long, branched chains, with 1–3 septa (Pratibha et al. 2014).

In considering a detailed morphological comparison, *B. rhombica* produces fusiform to rhomboidal conidia (33–46 µm long, 4–7-septate) with reddish-brown central cells, whereas *B. terrestris* has obovate to cylindrical conidia (14.5–36 µm long, 1–5-septate) with euseptation rather than muriform septation (Crane & Miller 2016). In contrast, our collection bears shorter, muriform conidia (< 20 µm) that are thick-walled and irregularly septate. Further, *B. grootfonteinensis* and *B. hughesii* can be distinguished by their long, acropetal chains of conidia, cylindrical to fusiform moniliform conidia, and *B. hughesii* is characterized by multiple transverse septa (6–25), reaching up to 200 µm in length (Crane & Miller 2016). The absence of such conidial chains and the presence of muriform conidia readily differentiate our collection from these species. Also, *B. grootfonteinensis* possesses spiny-warted conidia with a cupulate apical cell (Crous et al. 2015), a feature not observed

in *B. bidentis*. *Bahusandhika sundara* is morphologically close to *B. intercalaris*, but differs in having greenish-black colonies, wider hyphae, and longer conidiophores. It is worth noting that *Bahusandhika compata* has been reclassified as a synonym of *Torula compacta* (Sacc.) S. Hughes, following the taxonomic reassessment of *Bahusandhika* and *Torula* by Crane & Miller (2016).

Thus, based on the distinctive conidial ornamentation and septation pattern, combined with the multi-gene phylogenetic analyses, *Bahusandhika bidentis* is recognized here as a new species, found on *Bidens pilosa* (Asteraceae) in northern Thailand. At present, *B. indica* is the only species of the genus with available molecular data, and thus comparison between the species is limited to morphology.

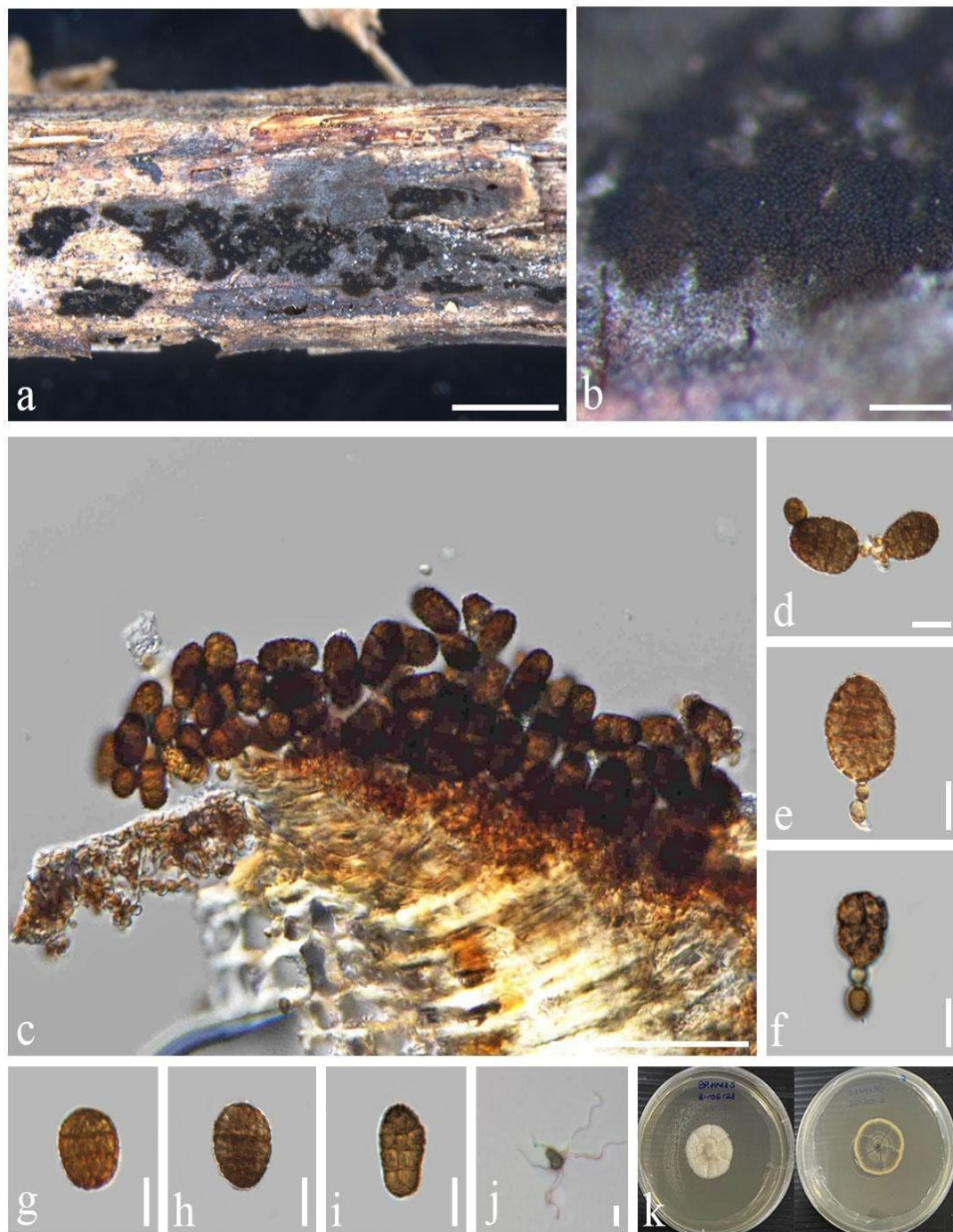


Figure 28 – *Bahusandhika bidentis* (MFLU 25-0249, holotype) a, b Appearance of colonies on host substrate. d–f Conidia and conidiogenous cells. g–i Conidia. j A germinating conidium. k Culture on MEA. Scale bars: a = 1 mm, b = 200 μ m, c = 100 μ m, d, e, f, g, h, i, j = 10 μ m.

Bahusandhika indica (Subram.) Subram, J. Indian bot. Soc. 35: 469 (1956)

Fig. 29

Index Fungorum number: IF293586, Facesoffungi number: FoF09666

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* discrete, effuse, pulverulent, brown and velvety in appearance on the surface. *Mycelium* composed of septate, brown, branched hyphae. *Conidiophores* septate, brown, constricted at the septa. *Conidiogenous cells* 2–5 × 2–5 µm ($\bar{x}$ = 3.54 × 3.28 µm, n = 5), monoblastic, uniformly light brown, ovoid to obovoid, formed either separately or in groups at the apex of the conidium. *Conidia* 10–20 × 5–10 µm ($\bar{x}$ = 14.5 × 6.7 µm, n = 20) brown to dark brown, ovoid to oblong, sometimes cylindrical, 1–3-septate, slightly constricted at septa, catenate formed in branched, with acropetal chains.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 22 mm after 10 days at 27 °C, irregular, entire, white to grey, raised, opaque; white to grey irregular, entire on reverse surface.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-15 (MFLU 25-0250, **a new host record**); living culture MFLUCC 25-0278.

GenBank – MFLUCC 25-0278: ITS = PV870594.

Pre-screening for antibacterial activity – *Bahusandhika indica* (MFLUCC 25-0278) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Known host and distribution – unidentified host in the Himalaya region (Prasher & Verma 2012); floral litter of *Cocos nucifera* (Arecaceae) in India (Pratibha et al. 2014); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analyses (Fig. 27), the strain (MFLUCC 25-0278) formed in the same clade with the isolates of *Bahusandhika indica* (MFLU 23-0494 and MFLUCC 23-0304) with 100% ML and 1.00 BYPP bootstrap support. Our collection is morphologically similar to *B. indica* in having monoblastic conidiogenous cells, which are uniformly light brown, ovoid to obovoid, formed either separately or in groups, at the apex of the conidia (Pratibha et al. 2014). Moreover, there are no significant base pair differences between ITS gene regions of our collection and phylogenetically related species. Therefore, a new host record of *B. indica* is reported on *Chromolaena odorata* (Asteraceae), and a new geographic record for Thailand.

Lophiostomataceae Sacc.

Lophiostomataceae was introduced by Saccardo (1883), and *Lophiostoma* is the type genus. Lophiostomataceae comprises 32 genera (Hyde et al. 2024), and its species are found mainly as saprobes in the terrestrial and aquatic habitats (Bao et al. 2019, Aluthmuhandiram et al. 2022). The characteristics of ascomata, peridium, pseudoparaphyses, and ascospores vary greatly throughout Lophiostomataceae species. Therefore, species identification based only on morphology is challenging (Thambugala et al. 2015, Bao et al. 2019). Molecular markers LSU, SSU, ITS, *tef1-α* and *rpb2* are available for species identification in Lophiostomataceae. In this study, we introduce a new species, *Pseudolophiostoma chromolaenae*.

Pseudocapulatispora Mapook & K.D. Hyde

Pseudocapulatispora was introduced by Mapook et al. (2020). The genus is characterized by by immersed, coriaceous ascomata with a crest-like, laterally compressed ostiole, and by broadly fusiform, uniseptate ascospores surrounded by a sheath that is drawn out to form distinct polar appendages. *Pseudocapulatispora* species are mainly found as saprobes on various host plants (Mapook et al. 2020, Phukamsadakra et al. 2020). There are three species in *Pseudocapulatispora* (Index fungorum, 2025).

Pseudocapulatispora longiappendiculata Mapook & K.D. Hyde, Fungal Diversity 101: 48 (2020)

Fig. 31

Index Fungorum number: IF838988, Facesoffungi number: FoF07797



Figure 29 – *Bahusandhika indica* (MFLU 25-0250, new host and geographical records). a, b Appearance of colonies on the host substrate. c–m Conidia and conidiogenous cells. n A germinating conidium. o Culture on the MEA. Scale bars: a = 1 mm, b = 200 μ m, h, i, j = 20 μ m, c, d, e, f, g, k, l, m, n = 10 μ m

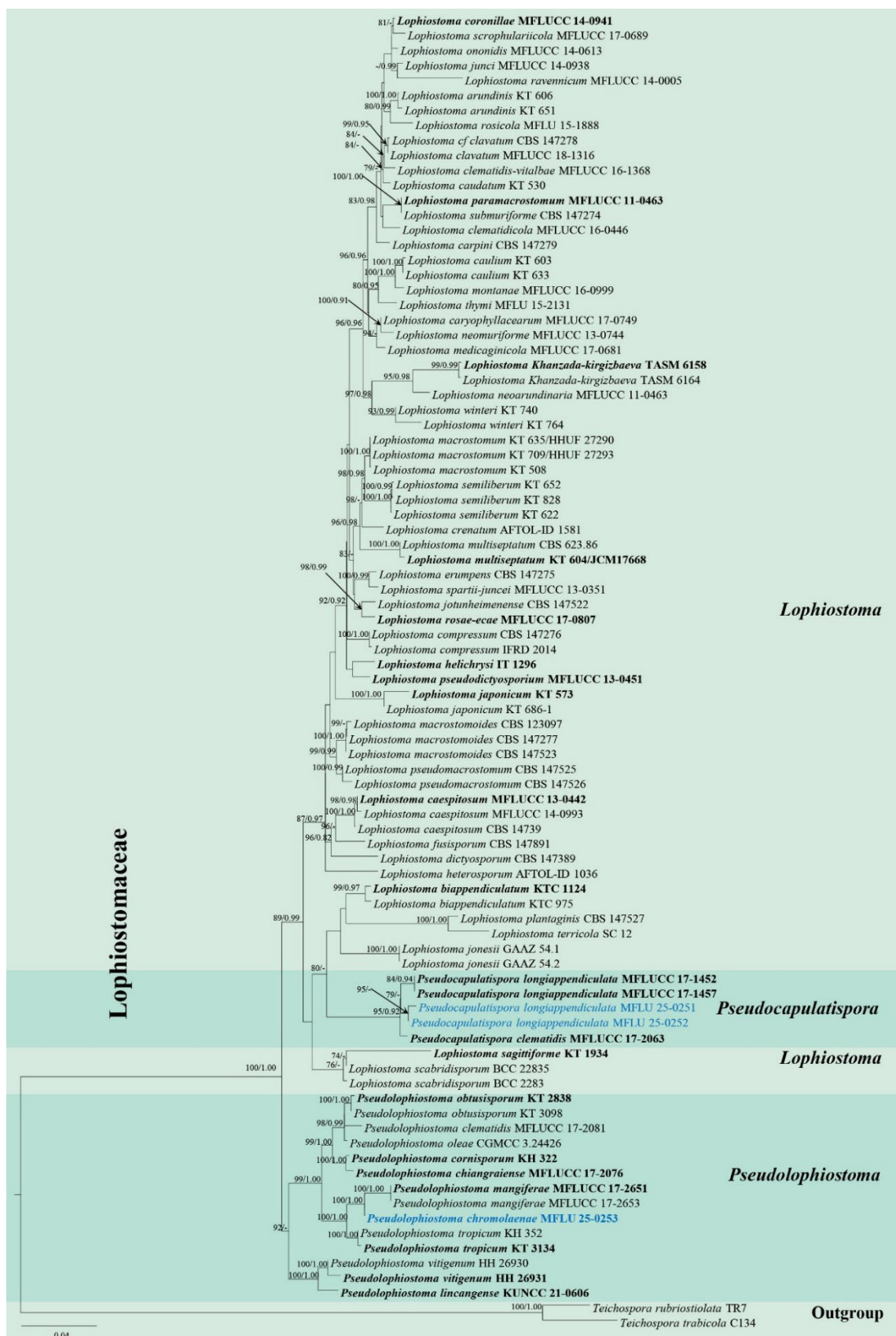


Figure 30 – Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, *tef1-α* and *rpb2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Teichospora rubriostiolata* (TR7) and *T. trabricola* (C134).

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 190–285 × 180–265 µm ($\bar{x}$ = 200 × 197 µm, n = 5), immersed, dark brown to black, globose to subglobose, ostiolate. *Ostioles* 115–130 µm wide, single, central. *Peridium* 20–50 µm wide, comprising several layers of hyaline to brown cells of *textura angularis*. *Hamathecium* comprises 1–2 µm wide, aseptate, branched pseudoparaphyses between and above the asci. *Asci* 65–125 × 14–18 µm ($\bar{x}$ = 93 × 15 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short-pedicellate, rounded at the apex, with an ocular chamber. *Ascospores* 24–30 × 5–10 µm ($\bar{x}$ = 25 × 8 µm, n = 20), uniseriate, overlapping in the ascus, hyaline, broadly fusiform, 1-septate, straight or slightly curved, widest at the region above or below the central septum, guttulate, constricted at the septum, with a narrow sheath; sheath drawn out to form polar appendages 25–35 × 5–7 µm ($\bar{x}$ = 30 × 6 µm, n = 5), from the apex of the ascospores terminating in a droplet at their apices. **Asexual morph:** Undetermined.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-1 (MFLU 25-0251); CO-PKN-4 (MFLU 25-0252).

GenBank – MFLU 25-0251: ITS = PV870595, MFLU 25-0252: ITS = PV870596.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020; this study)

Notes – In the phylogenetic analyses (Fig. 30), two strains (MFLU 25-0251 and MFLU 25-0252) formed a clade sister to *Pseudocapulatispora longiappendiculata* (MFLUCC 17-1452 and MFLUCC 17-1457) and *Pseudocapulatispora clematidis* (MFLUCC 17-2063) with 95% ML and 0.54 BYPP. The strain (MFLU 25-0251) is morphologically similar to *Pseudocapulatispora longiappendiculata* and *Pseudocapulatispora clematidis* in having solitary, immersed, ostiolate ascomata, 8-spored, unitunicate, fissitunicate, oblong to cylindrical-clavate, short pedicellate asci and straight or slightly curved, guttulate ascospores with polar appendages (Mapook et al. 2020, Phukhamsakda et al. 2020). The strain (MFLU 25-0251) slightly differs from *Pseudocapulatispora longiappendiculata* in having larger ascomata (190–285 × 180–265 vs. 250–265 µm), longer asci (65–125 × 14–18 vs. 75–120 × 14–20 µm) and longer polar appendages (25–35 × 5–7 µm vs. 10–40 × 3–5 µm). Moreover, the base pair comparison between the strain (MFLU 25-0251) and *Pseudocapulatispora longiappendiculata* (MFLUCC 171457) reveals 1.2 % (6/507) difference in the ITS, without gaps. Due to the unavailability of other gene sequences, we cannot compare base pairs. *Pseudocapulatispora longiappendiculata* was previously found on *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020). Therefore, our collections are the second record on *Chromolaena odorata* from northern Thailand. Although Andreasen et al. (2021) treated this taxon within *Lophiostoma* based primarily on phylogenetic evidence, we prefer to retain the original genus *Pseudocapulatispora* here, as it exhibits clear morphological distinctions that are best interpreted under a polyphasic taxonomic framework.

Pseudolophiostoma

Thambugala et al. (2015) introduced *Pseudolophiostoma* based on the combined LSU, SSU, ITS and *tefl-α* sequence data. *Pseudolophiostoma* species are mainly found as saprobes (Hashimoto et al. 2018, Phukhamsakda et al. 2020, Ren et al. 2024). *Pseudolophiostoma* is characterized by immersed, globose to subglobose ascomata, with an ostiolar neck, 8-spored, cylindrical-clavate, pedicellate asci, and fusiform, hyaline, septate ascospores, with a gelatinous sheath (Ren et al. 2024). There are eight species accepted in *Pseudolophiostoma* (Ren et al. 2024, Index Fungorum 2025).

Pseudolophiostoma chromolaenae Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 32

Index Fungorum number: IF904368, Facesoffungi number: FoF18035

Etymology – Name reflects the host plant *Chromolaena odorata*, from which this species was isolated.

Holotype – MFLU 25-0253

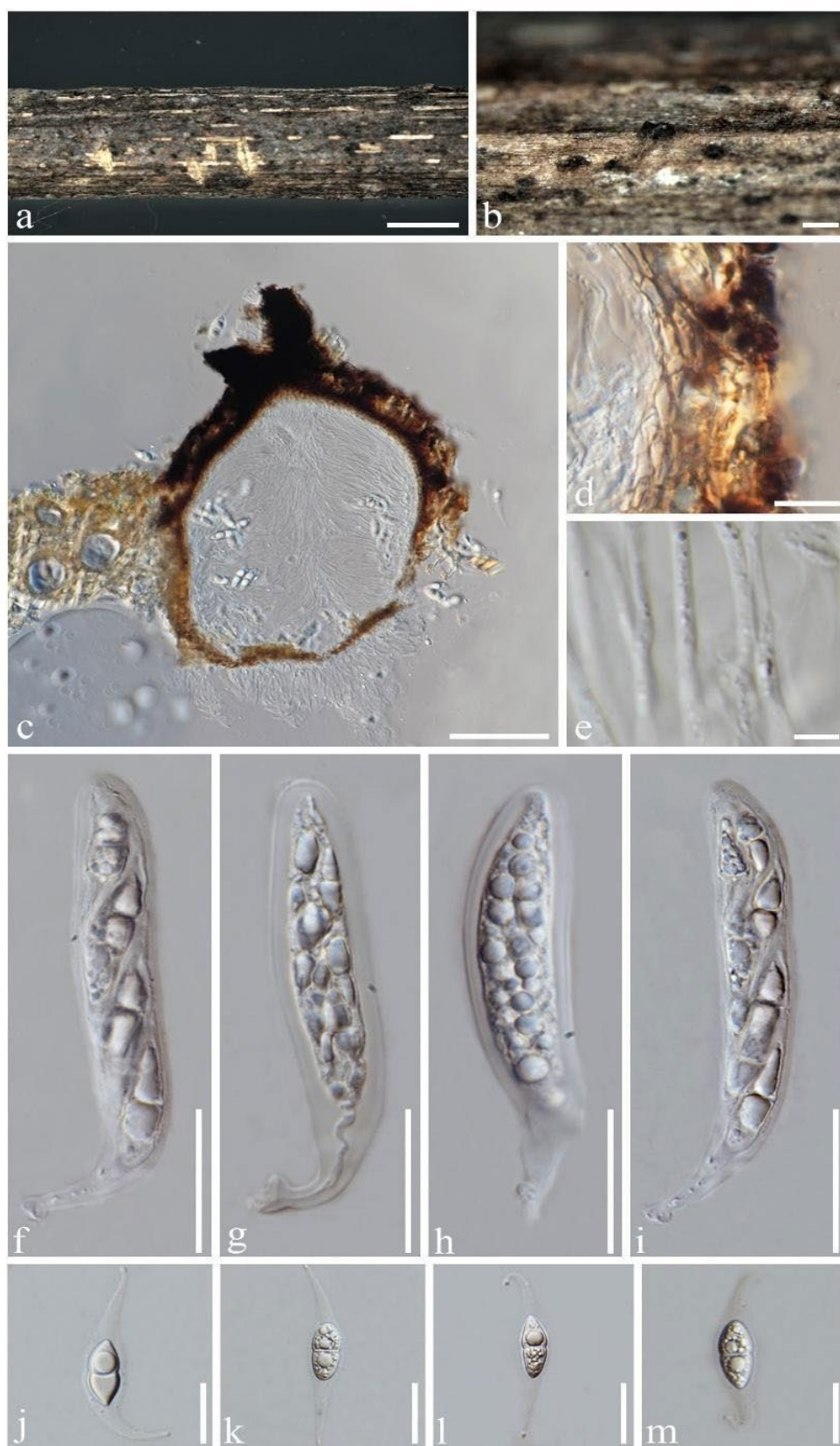


Figure 31 – *Pseudocapulatispora longiappendiculata* (MFLU 25-0251). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–m Ascospores. Scale bars: a = 1 mm, b = 500 µm, c = 100 µm, d = 20 µm, e = 5 µm, f, g, h, i = 30 µm, j, k, l, m = 20 µm.

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 230–270 × 185–225 µm ($\bar{x}$ = 250 × 210 µm, n = 5), immersed to erumpent, dark brown to black, globose to subglobose, ostiolate. *Ostioles* central, 80–110 µm wide, single, central, papillate. *Peridium* 80–120 µm wide, comprising several layers of hyaline to brown cells of *textura angularis*. *Hamathecium* 2–4 µm wide, comprises septate, branched pseudoparaphyses between and above the asci. *Asci* 55–80 × 8–12 µm ($\bar{x}$ = 67.7 × 10 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, short-pedicellate, with rounded ends and an ocular chamber at the apex. *Ascospores* (18–)20–30 × 4–8 µm ($\bar{x}$ = 24.5 × 5.2 µm, n = 20), 1–2-seriate, overlapping in the ascus, hyaline, broadly fusiform, 1-septate, straight or slightly curved, widest at the region above or below the central septum, guttulate, constricted at the septum, surrounded by a narrow gelatinous sheath; sheath drawn out to form polar appendages. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 40 mm after 10 days at 27 °C, irregular, filamentous, white to olive green, slightly raised, opaque, rough and bearing green liquid after 7 days on the surface; olive to dark green with white margin in reverse surface.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-26 (MFLU 25-0253, **holotype**).

GenBank – MFLU 25-0253: SSU = PV996962, ITS = PV870597, *tefl-α* = PX255043, *rpb2* = PX120450.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on the phylogenetic analyses (Fig. 30), the strain (MFLU 25-0253) grouped separately from the isolates of *Ps. mangiferae* (MFLUCC 17-2653 and MFLUCC 17-2651) with 100% ML and 1.00 BYPP bootstrap support. Our strain (MFLU 25-0253) differs from *Ps. magniferae* in having immersed ascomata, shorter asci (55–80 × 8–12 µm vs. 75–100 × 10–14 µm), broadly fusiform, 1-septate, hyaline, guttulate ascospores, while *Ps. magniferae* has scattered, semi-immersed ascomata, 1-septate with 2 euseptate, fusiform, hyaline ascospores without guttules (Tennakoon et al. 2018). Therefore, *Pseudolophiostoma chromolaenae* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand.

Periconiaceae Nann

Periconiaceae was introduced by Nannizzi (1934), with *Periconia* as the type genus. Hyde et al. (2024) included two genera in Periconiaceae, viz., *Flavomyces* and *Periconia*. Members of Periconiaceae can be found mainly as saprobic hyphomycetes (Yang et al. 2022, Su et al. 2023), and some are reported as endophytes and pathogens (Knapp et al. 2015, Sarkar et al. 2019, Samarakoon et al. 2019).

Periconia Tode

Periconia was introduced by Tode (1791), typified by *P. lichenoides*. *Periconia* are characterized asexually by macronematous, mononematous, branched or unbranched, and pale to dark brown conidiophores, mono-polyblastic, discrete conidiogenous cells on the terminal or intercalary of the stipe, globose to ellipsoidal, catenate or solitary, smooth or verruculose, and pale brown to brown conidia (Su et al. 2023). To date, there are over 170 species accepted in *Periconia* (Hyde et al. 2024). In this study, we recorded *Periconia byssoides* as a new record based on the combined phylogeny of LSU, SSU, ITS, *tefl-α*, and *rpb2* sequence data (Fig. 33).

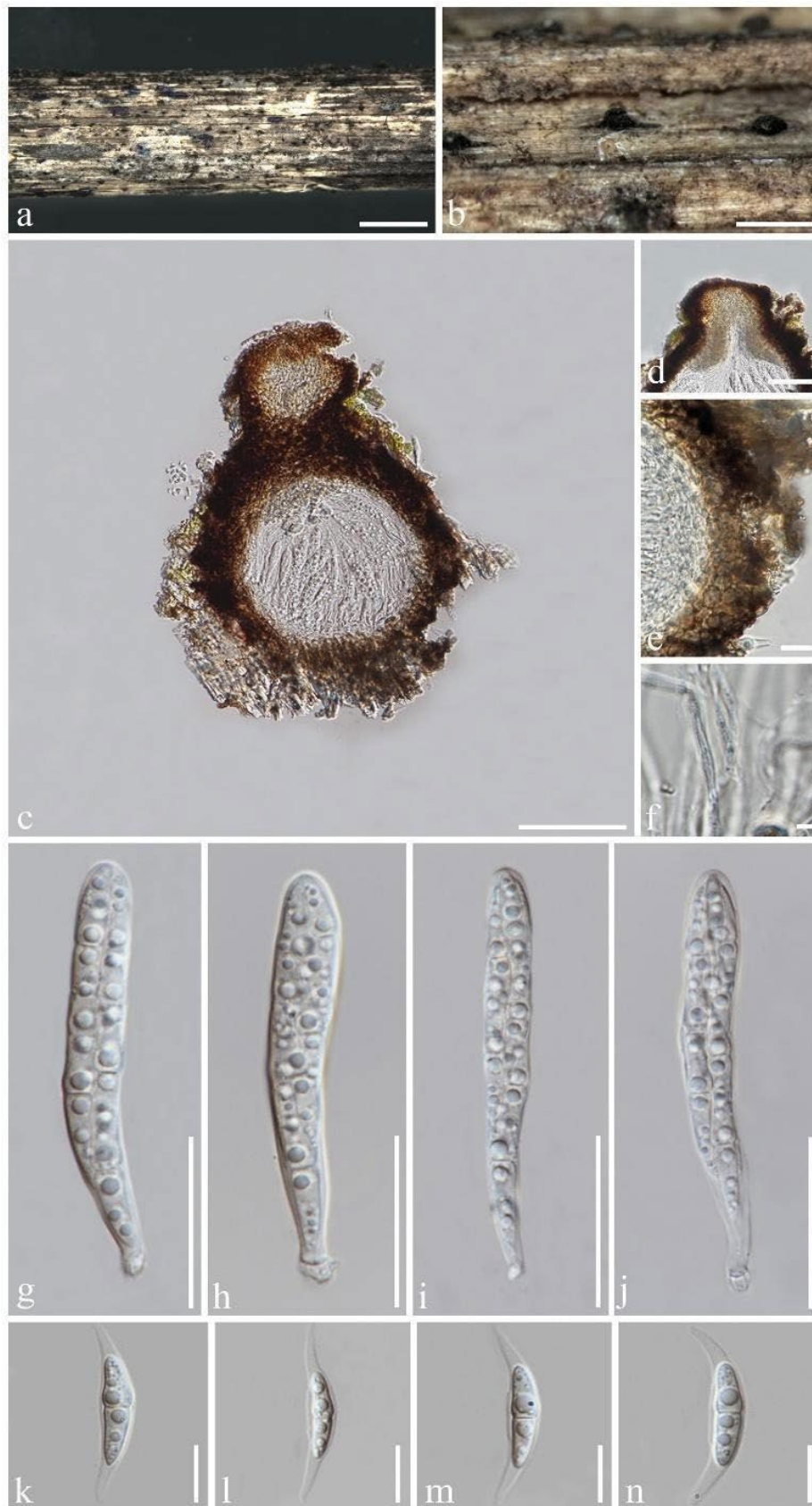


Figure 32 – *Pseudolophiostoma chromolaenae* (MFLU 25-0253, holotype). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–j Asci. k–n Ascospores. Scale bars: a = 1 mm, b = 500 μ m, c = 100 μ m, d = 50 μ m, e = 20 μ m, f = 5 μ m, g, h, i, j = 30 μ m, k, l, m, n = 10 μ m.

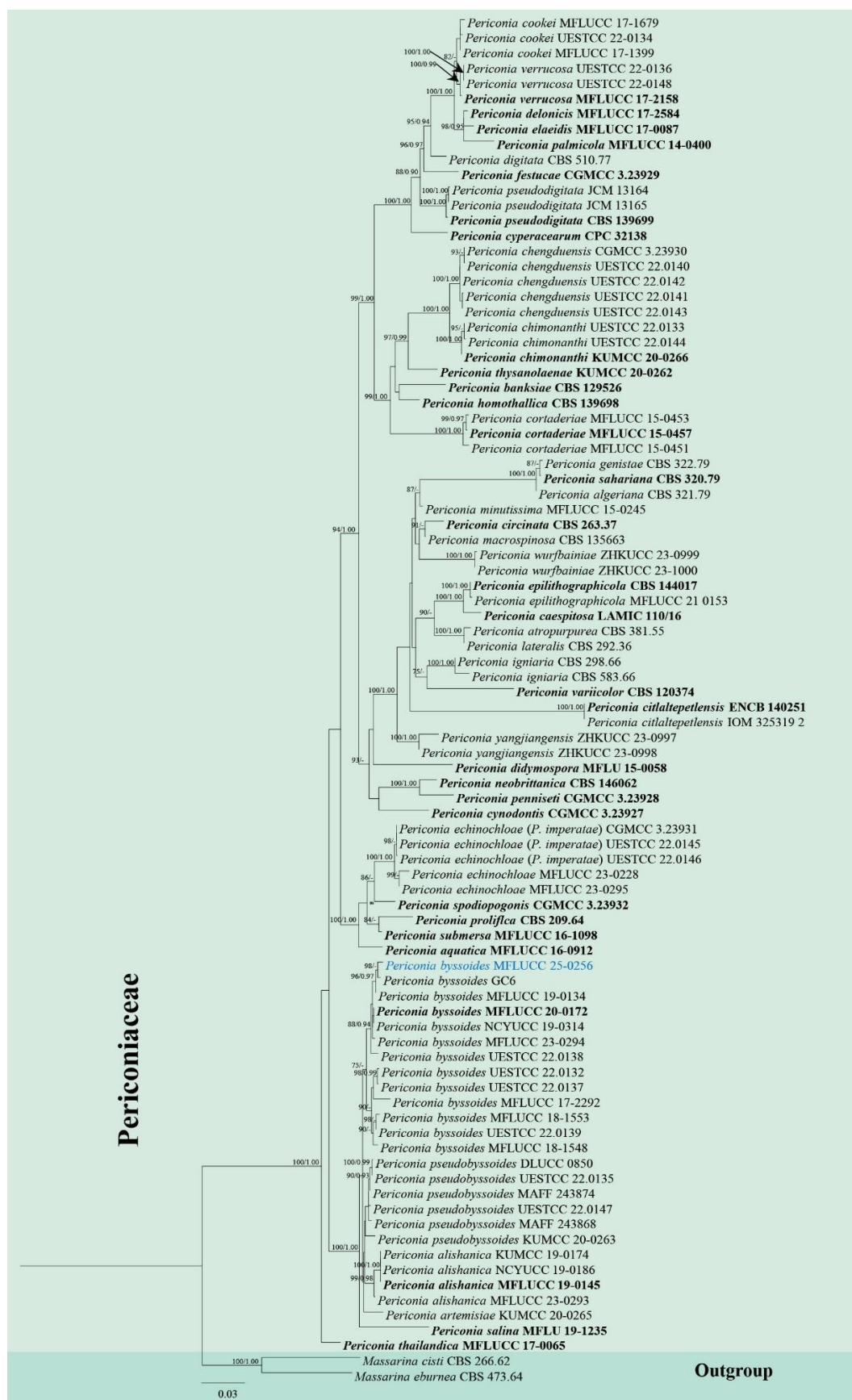


Figure 33 – Phylogram generated from ML analysis based on the combined sequence data of LSU, SSU, ITS, *tef1-α*, and *rpb2*. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Massarina cisti* (CBS 266.62) and *M. eburnea* (CBS 473.64).

Periconia byssoides Pers., Syn. meth. fung. (Göttingen) 2: 686 (1801)

Fig. 34

Index Fungorum number: IF144538, Facesoffungi number: FoF09319

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies effuse, powdery, gregarious, black. *Conidiophores* 390–450 × 13–15 µm ($\bar{x}$ = 414 × 14.7 µm, n = 10), macronematous, mononematous, single or grouped, brown in the upper part and dark brown towards the base, erect, or flexuous, septate, constricted at the septa, smooth, thick-walled. *Conidiogenous cells* blastic, polyblastic, pale brown to brown, globose to subglobose, smooth or verruculose, discrete on stipe. *Conidia* 8–15 × 7–14 µm ($\bar{x}$ = 12 × 11 µm, n = 20), catenate, pale brown, globose, one-celled, verruculose, thick-walled.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 40 mm after 10 days at 27 °C, circular, filamentous, white to grey, powdery, flat, opaque; circular, filamentous, yellowish brown.



Figure 34 – *Periconia byssoides* (MFLU 25-0254, a new host record). a, b Appearance of colonies on the host substrate. c Conidiophore. d Conidia and conidiogenous cells. e–g Conidia. h A germinating conidium. i Culture on MEA. Scale bars: a = 500 µm, b, c = 200 µm, d = 20 µm, e, f, g, h = 10 µm.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 June 2023, Zin Hnin Htet, BP-HMS-8 (MFLU 25-0254, **a new host record**); living culture MFLUCC 25-0256.

GenBank – MFLUCC 25-0256: LSU = PV992409, SSU = PV996963, ITS = PV870598, *tef1- α* = PX255044, *rpb2* = PX120451.

Pre-screening for antibacterial activity – *Periconia byssoides* (MFLUCC 25-0256) showed a 15 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), and a 13 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm), but no inhibition against *E. coli*.

Known host and distribution – stalk of *Conium maculatum* (Apiaceae) in Lithuania (Markovskaja & Kacergius 2014); dead stalks of *Heracleum sosnowskyi* (Apiaceae) in Lithuania (Markovskaja & Kacergius 2014); stalk of *Angelica sylvestris* (Apiaceae) in Lithuania (Markovskaja & Kacergius 2014); decaying cone of *Magnolia grandiflora* (Magnoliaceae) in China (Jayasiri et al. 2019); dead leaves of *Macaranga tanarius* (Euphorbiaceae) in Taiwan region (Tennakoon et al. 2021); decaying pod of *Peltophorum* sp. (Fabaceae) in Thailand; dead stems of *Prunus armeniaca* (Rosaceae) in China (Yang et al. 2022); dead culms of *Imperata cylindrica* (Poaceae) in China (Su et al. 2023); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analyses (Fig. 33), the strain (MFLUCC 25-0256) clustered with other strains of *Periconia byssoides* (GC6 and MFLUCC 19-0134) with 98% ML and 0.89 BYPP bootstrap support. Morphologically, our collection is similar to other *P. byssoides* strains in having macronematous, erect or flexuous conidiophores, globose, polyblastic conidiogenous cells, pale brown, catenate, globose, one-celled, verruculose conidia (Su et al. 2023). There are also no significant base pair differences between ITS, LSU, SSU, *tef1- α* , and *rpb2* sequences of the isolates of *P. byssoides* (MFLUCC 20-0172) and our strain (MFLUCC 25-0256). Therefore, a new host record of *P. byssoides* is reported on *Bidens pilosa* (Asteraceae) in northern Thailand.

Phaeosphaeriaceae M.E. Barr

Phaeosphaeriaceae was typified by *Phaeosphaeria oryzae* (Miyake 1909, Barr 1979). Morphological characters of the species in this family are similar to Didymosphaeriaceae and Leptosphaeriaceae, and can be difficult to distinguish between species (Zhang et al. 2009, Phookamsak et al. 2014, Yang et al. 2019). Currently, there are 88 accepted genera in Phaeosphaeriaceae (Hyde et al. 2024). In this study, we record *Leptospora thailandica* as a new host record.

Leptospora thailandica Phukhams. & K.D. Hyde, Fungal Diversity 80: 100 (2016) Fig. 36

Index Fungorum number: IF552239, Facesoffungi number: FoF02381

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** *Ascomata* 200–270 $\times$ 140–200 μ m ($\bar{x}$ = 227 $\times$ 168 μ m, n = 5), solitary, immersed to semi-immersed, erumpent, globose to subglobose, scattered, black, ostiolate. *Ostiole* central, ostiolar neck composed of hyaline to brown cells, reddish at the apex. *Peridium* 17–30 μ m wide, comprising 3–4 layers of brown cells of *textura angularis*. *Hamathecium* 1.5–3 μ m wide, comprises branched, septate, hyaline pseudoparaphyses. *Asci* 55–75 $\times$ 7–12 μ m ($\bar{x}$ = 67 $\times$ 9 μ m, n = 10), 8-spored, bitunicate, fissitunicate, cylindrical, rounded at the apex, straight or slightly flexuous, short pedicellate, with a minute ocular chamber. *Ascospores* 40–60 $\times$ 2–3 μ m ($\bar{x}$ = 50 $\times$ 2.4 μ m, n = 20), spiral arrangement in the ascus, hyaline to pale brown, filiform, septate, tapering at both ends, with granular appearance, straight or flexuous, thick-walled, smooth-walled. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 24 mm after 10 days at 27 °C, irregular, filamentous, opaque, flat, white to pale yellow on the surface; irregular, yellowish to pale brown in reverse.

Material examined – Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet, BP-NL-5 (MFLU 25-0255, **a new host record**); living culture MFLUCC 25-0267.

GenBank – MFLUCC 25-0267: SSU = PV996964, ITS = PV870599, *tef1- α* = PX255045.

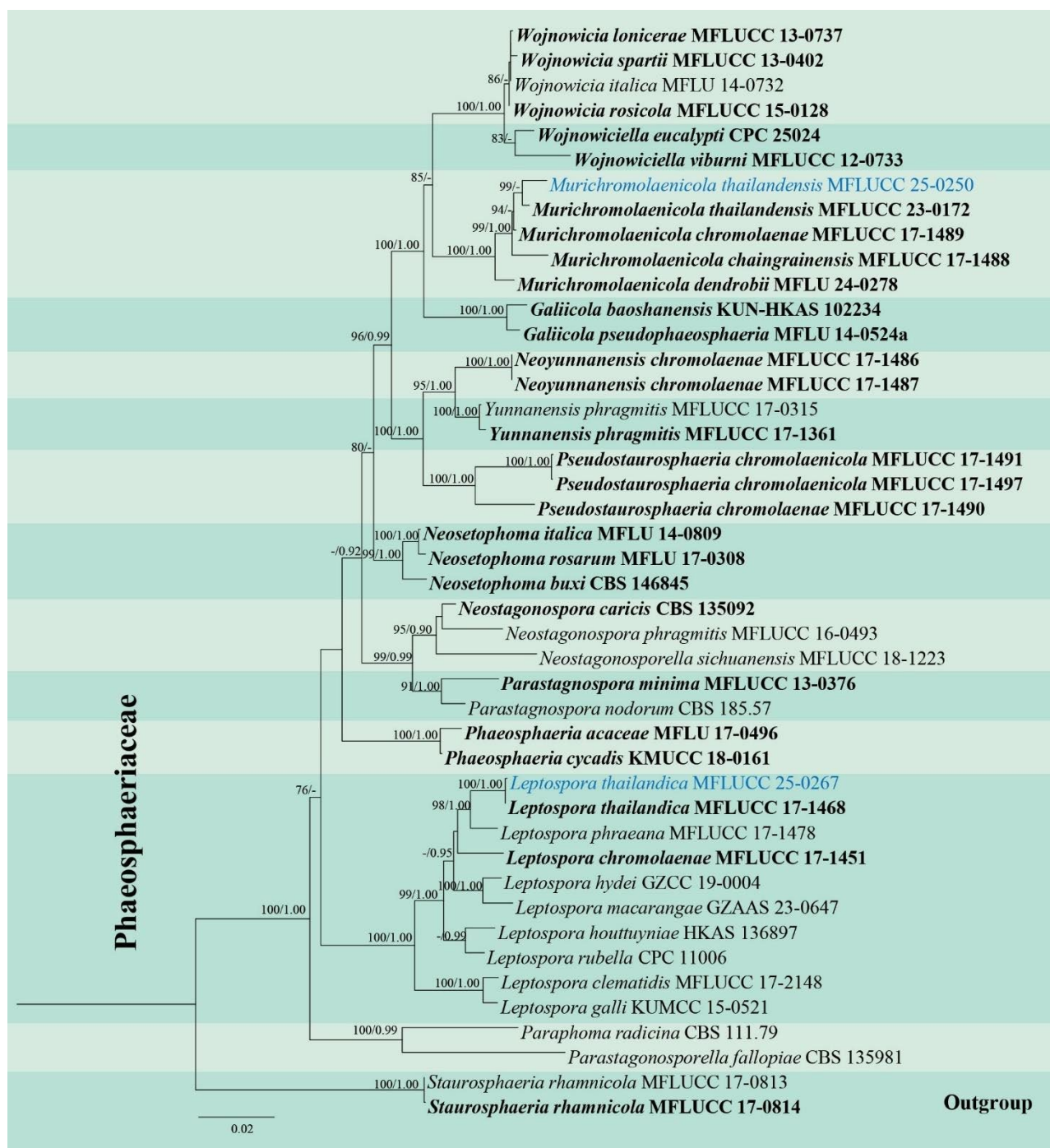


Figure 35 – Phylogram generated from the ML analysis of the combined data of LSU, SSU, ITS, and *tef1- α* sequences. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Staurosphaeria rhamnica* (MFLUCC 17-0813 and MFLUCC 17-0814).

Pre-screening for antibacterial activity – *Leptospora thailandica* (MFLUCC 25-0267) showed a 15 mm inhibition against *B. subtilis*, observable as partial inhibition, compared to positive control (15 mm), but showed no inhibition against *E. coli* and *S. aureus*.

Known host and distribution – dead branches of *Duranta* sp. (Verbenaceae) in Thailand (Hyde et al. 2016); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al. 2020); dead branch of *Clematis subumbellata* (Ranunculaceae) in Thailand (Phukhamsakda et al. 2020); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In the phylogenetic analyses (Fig. 35), our strain (MFLUCC 25-0267) clustered sister to *Leptospora thailandica* (MFLUCC 17-1468) with 100% ML and 1.00 BYPP bootstrap support. Our collection is morphologically similar to *L. thailandica* (MFLUCC 17-1468) in having immersed, erumpent ascomata, a central ostiole with reddish pigmentation, branched, septate, hyaline pseudoparaphyses, 8-spored, bitunicate asci, and hyaline, filiform ascospores (Phukhamsakda et al. 2020). But our collection differs from *L. thailandica* (MFLUCC 17-1468) in having larger ascomata ($200\text{--}270 \times 140\text{--}200\text{ }\mu\text{m}$ vs. $188\text{--}207 \times 112\text{--}170\text{ }\mu\text{m}$), shorter asci ($55\text{--}75\text{ }\mu\text{m}$ vs. $68\text{--}114\text{ }\mu\text{m}$), and shorter ascospores ($40\text{--}60\text{ }\mu\text{m}$ vs. $63\text{--}89\text{ }\mu\text{m}$). There is also no significant base pair difference between the ITS sequence of our collection and *L. thailandica* (MFLUCC 17-1468). *Leptospora thailandica* was previously reported on Ranunculaceae and Verbenaceae (Hyde et al. 2016, Phukhamsakda et al. 2020). Therefore, we report our collection as a new host record of *L. thailandica* on *Bidens pilosa* (Asteraceae) in northern Thailand, which is also the second record in Thailand.

***Murichromolaenicola* Mapook & K.D. Hyde**

Murichromolaenicola was introduced by Mapook et al. (2020) with two species in Phaeosphaeriaceae, viz., *M. chromolaenae* (type) and *M. chiangraiensis*. Currently, there are four species accepted in *Murichromolaenicola*, viz., *M. chaingraiensis*, *M. chromolaenae*, *M. dendrobii* and *M. thailandensis* (Index Fungorum 2025).

Murichromolaenicola thailandensis Htet, Mapook & K.D. Hyde, Phytotaxa 618 (2): 120–130 (2023) Fig. 37

Index Fungorum number: IF849500, Facesoffungi number: FoF14609

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* $130\text{--}150 \times 140\text{--}160\text{ }\mu\text{m}$ ($\bar{x} = 140 \times 155\text{ }\mu\text{m}$, $n = 5$), pycnidial, solitary, immersed, unilocular, globose to subglobose, black, ostiole opening through host surface, with small papilla. *Peridium* $15\text{--}25\text{ }\mu\text{m}$ wide, comprising two to three layers of yellowish-brown cells arranged in *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* $3\text{--}5 \times 3\text{--}5\text{ }\mu\text{m}$ ($\bar{x} = 4 \times 3.5\text{ }\mu\text{m}$, $n = 5$), enteroblastic, phialidic, hyaline, globose to subglobose. *Conidia* $10\text{--}20 \times 5\text{--}10\text{ }\mu\text{m}$ ($\bar{x} = 16 \times 8$, $n = 20$), yellowish-brown to dark brown, oblong or oval to obovoid, round at both ends, $3\text{--}5$ transverse with $1\text{--}2$ longitudinal septa, not constricted at the septa, with a gelatinous cap observed clearly when mounted in Indian ink.

Culture characteristics – Conidia germinating on MEA, reaching 25 mm diam. within 7 days at $27\text{ }^{\circ}\text{C}$, circular, entire, concentric, flat, opaque, grey on the surface; concentric, pale brown in the middle and white at the margin of the reverse surface.

Material examined – Thailand, Chiang Rai Province, Phan District, on dead stems of *Chromolaena odorata* (Asteraceae), 14 March 2023, Zin Hnin Htet, CO-DP-7 (MFLU 25-0256); living culture MFLUCC 25-0250.

GenBank – MFLUCC 25-0250: LSU = OR343207, SSU = OR343209, ITS = OR343208, *tef1- α* = OR420087, *rpb2* = OR420088.

Pre-screening for antibacterial activity – *Murichromolaenicola thailandensis* (MFLUCC 25-0250) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Htet et al. 2023, this study).

Notes – In the phylogenetic analyses (Fig. 35), our strain (MFLUCC 25-0250) clustered sister to *Murichromolaenicola thailandensis* (MFLUCC 23-0172) with 99% ML and 0.89 BYPP bootstrap support. Our collection is morphologically similar to *M. thailandensis* (MFLUCC 23-0172) in having immersed, unilocular, globose to subglobose conidiomata, phialidic, hyaline conidiogenous cells, hyaline to brown, muriform conidia with a gelatinous cap in Indian Ink (Htet et al. 2023). Moreover, there are no significant base pair differences in the ITS gene sequences between our collection and *M. thailandensis* (MFLUCC 23-0172). *Murichromolaenicola thailandensis* was previously recorded on *Chromolaena odorata* in Thailand (Htet et al. 2023).



Figure 36 – *Leptospora thailandica* (MFLU 25-0255, a new host record). a, b Appearance of ascomata on the host substrate. c Section through an ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–i Asci. j–k Ascospores. l A germinating ascospore. m Culture on MEA. Scale bars: a = 500 μm , b = 200 μm , c = 100 μm , d = 40 μm , f = 5 μm , e, g, h, i, j, k, l = 10 μm .

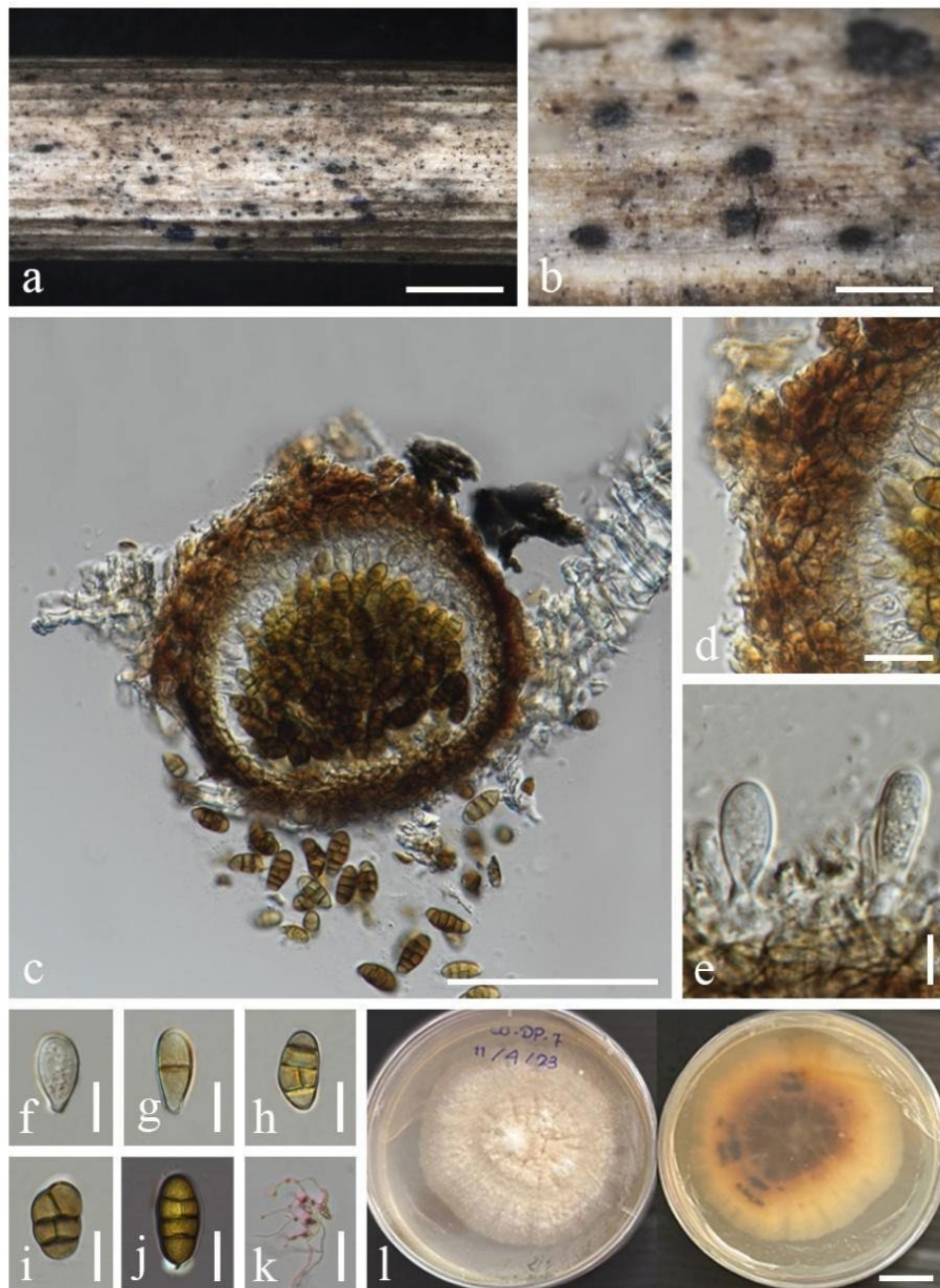


Figure 37 – *Murichromolaenicola thailandica* (MFLU 25-0256). a, b Appearance of conidiomata on the host substrate. c Section through a conidioma. d Peridium. e Conidiogenous cells. f–i Conidia. j Conidia stained in Indian Ink. k A germinating conidium. l Culture on MEA. Scale bars a, b = 500 μ m, c = 100 μ m, d = 20 μ m, e = 5 μ m, f, g, h, i, j, k, = 10 μ m, l = 10 mm.

Roussoellaceae Jian K. Liu, Phook., D.Q. Dai & K.D. Hyde

Liu et al. (2014) introduced Roussoellaceae based on morphology and data from the LSU, ITS, *tef1*- α , and *rpb2* sequences. Roussoellaceae species are reported as human pathogens and saprobes (Ahmed et al. 2014, Liu et al. 2014, Wu et al. 2023). Currently, 12 genera are accepted in Roussoellaceae (Hyde et al. 2024). In this study, we recorded *Pseudoneoconiothyrium chromolaenae* and *Ps. thailandicum* as new species.

Neorousssoella Jian K. Liu, Phook. & K.D. Hyde

Liu et al. (2014) introduced the genus *Neorousssoella* to accommodate a saprobic *Roussoella*-like taxon, with *N. bambusae* designated as the type species. The sexual morphology of *Neorousssoella* is defined by immersed ascostromata that appear as flattened ovoid, dome-shaped, or

black formations on the host surface behind a clypeus or epidermis. The ascospores are dark to yellowish-brown, ellipsoidal to fusiform, two-celled, and encased in a mucilaginous sheath, whereas the asci are bitunicate and cylindrical (Liu et al. 2014). The asexual morphology of *Neorousoella* is characterized by superficial or immersed pycnidia with annellidic, ampulliform, cylindrical conidiogenous cells that produce hyaline, pale brown, oblong to ellipsoidal conidia with two guttules (Jayasiri et al. 2019, Htet et al. 2024a). Currently, there are 15 epithets listed (Index Fungorum 2025, Htet et al. 2024a)

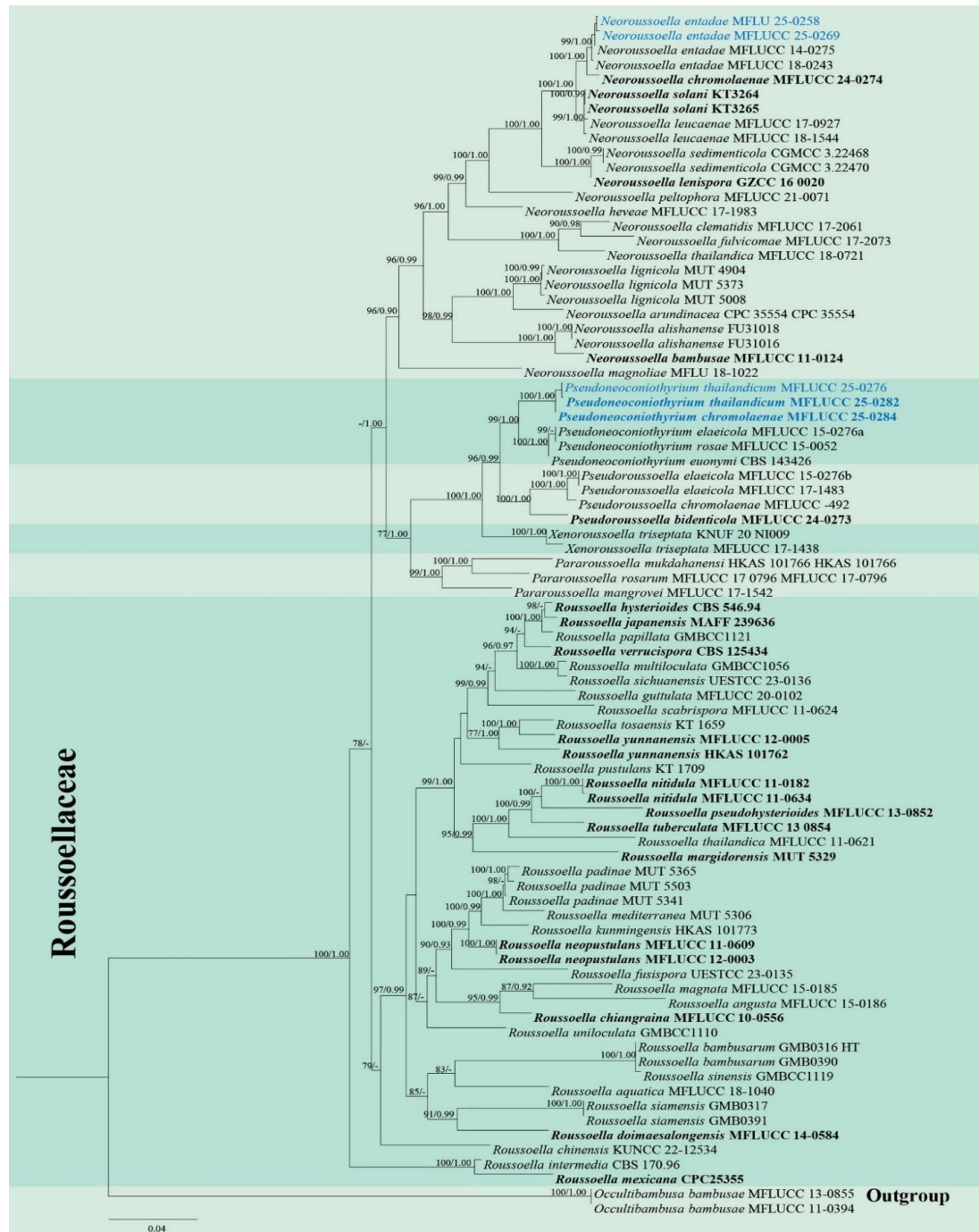


Figure 38 – Phylogram generated from the ML analysis based on the combined LSU, SSU, ITS, and *tef1-α* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Occultibambusa bambusae* (MFLUCC 13-0855 and MFLUCC 11-0394).

Neorousoella entadae Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 105 (2019) Fig. 39
Index Fungorum number: IF555568, Facesoffungi number: FoF05275

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 100–150 × 100–170 µm ($\bar{x}$ = 138 × 120 µm, n = 5), pycnidial, solitary, immersed to semi-immersed, uni-loculate, brown, globose to subglobose, dark fruiting bodies on the host substrate, without an ostiole. *Peridium* 10–20 µm wide, comprising 2–3 layers of yellowish-brown to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–3.4 µm long, phialidic, short, globose to subglobose, hyaline and unbranched. *Conidia* 3–5 × 2–3 µm ($\bar{x}$ = 4.3 × 2.2 µm, n = 20), globose to subglobose, hyaline to pale brown, aseptate, thick-walled, with a guttule.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 25 mm after 10 days at 27 °C, round with scalloped margin, white to pale yellow, raised, opaque; circular, entire, pale brown in reverse.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet, BP-NL-8 (MFLU 25-0257, **a new host record**); living culture MFLUCC 25-0269; Phayao Province, Mueang Phayao District, on dead stems of *Bidens pilosa* (Asteraceae), 16 December 2023, Zin Hnin Htet, BP-MY-5 (MFLU 25-0258).

GenBank – MFLUCC 25-0269: SSU = PV996966, ITS = PV870601, *tef1-α* = PX255047, *rpb2* = PX120453; MFLU 25-0258: ITS = PV870602, *tef1-α* = PX255048, *rpb2* = PX120454.

Pre-screening for antibacterial activity – *Neorousoella entadae* (MFLU 25-0257) showed no antibacterial activity against *B. subtilis*, *E. coli* and *S. aureus*.

Known host and distribution – decaying pods of *Entada phaseoloides* (Fabaceae) in Thailand (Jayasiri et al. 2019), decaying pod of *Leucaena* sp. (Fabaceae) in Thailand (Jayasiri et al. 2019); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Htet et al. 2024); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – Based on the multi-locus phylogeny (Fig. 38), the isolates (MFLU 25-0257 and MFLU 25-0258) clustered with the isolates of *Neorousoella entadae* (MFLUCC 18-0243 and MFLUCC 14-0275) with 99% ML and 1.00 BYPP bootstrap support. When comparing base pair differences between our isolates and *N. entadae* (MFLUCC 18-0243), there were no significant variations obtained among the respective ITS, *tef1-α* and *rpb2* gene regions. Our collection is similar to *N. entadae* in having globose to subglobose, pycnidial conidiomata, hyaline, phialidic conidiogenous cells, and hyaline to pale brown, aseptate conidia (Jayasiri et al. 2019). Therefore, these collections are reported as new host records of *N. entadae* on *Bidens pilosa* (Asteraceae).

Pseudoneoconiothyrium Wanas., Phukhams., Camporesi & K.D. Hyde

Pseudoneoconiothyrium was introduced by Wanasinghe et al. (2018). The genus was placed in Roussoellaceae based on LSU, SSU, ITS, *tef1-α* and *rpb2* sequence data (Phookamsak et al. 2019). To date, there are two accepted species in this genus (Hyde et al. 2024, Index Fungorum 2025).

Pseudoneoconiothyrium chromolaenae Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**
Fig. 40

Index Fungorum number: IF904369, Facesoffungi number: FoF18036

Etymology – Name reflects the host plant *Chromolaena odorata* from which this species was isolated.

Holotype – MFLU 25-0259

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 235–320 × 170–210 µm ($\bar{x}$ = 276 × 192 µm, n = 5), immersed, solitary, appearing as dark spots on the surface. *Ostiole* 25–30 µm wide, central. *Peridium* 20–60 µm wide, 2–3 layered, comprising hyaline to dark brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 × 4–6 ($\bar{x}$ = 4.1 × 4.8) annellidic, ovoid to

obovoid, or ampulliform, hyaline and unbranched. *Conidia* $4\text{--}7 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} = 5.7 \times 3.7 \mu\text{m}$, $n = 20$), ovoid to ellipsoidal, hyaline to brown, aseptate, thick-walled with guttules.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 22 mm after 10 days at 27 °C, irregular, entire, white, flat, opaque; irregular, entire, cracked, creamy-brown in reverse surface.

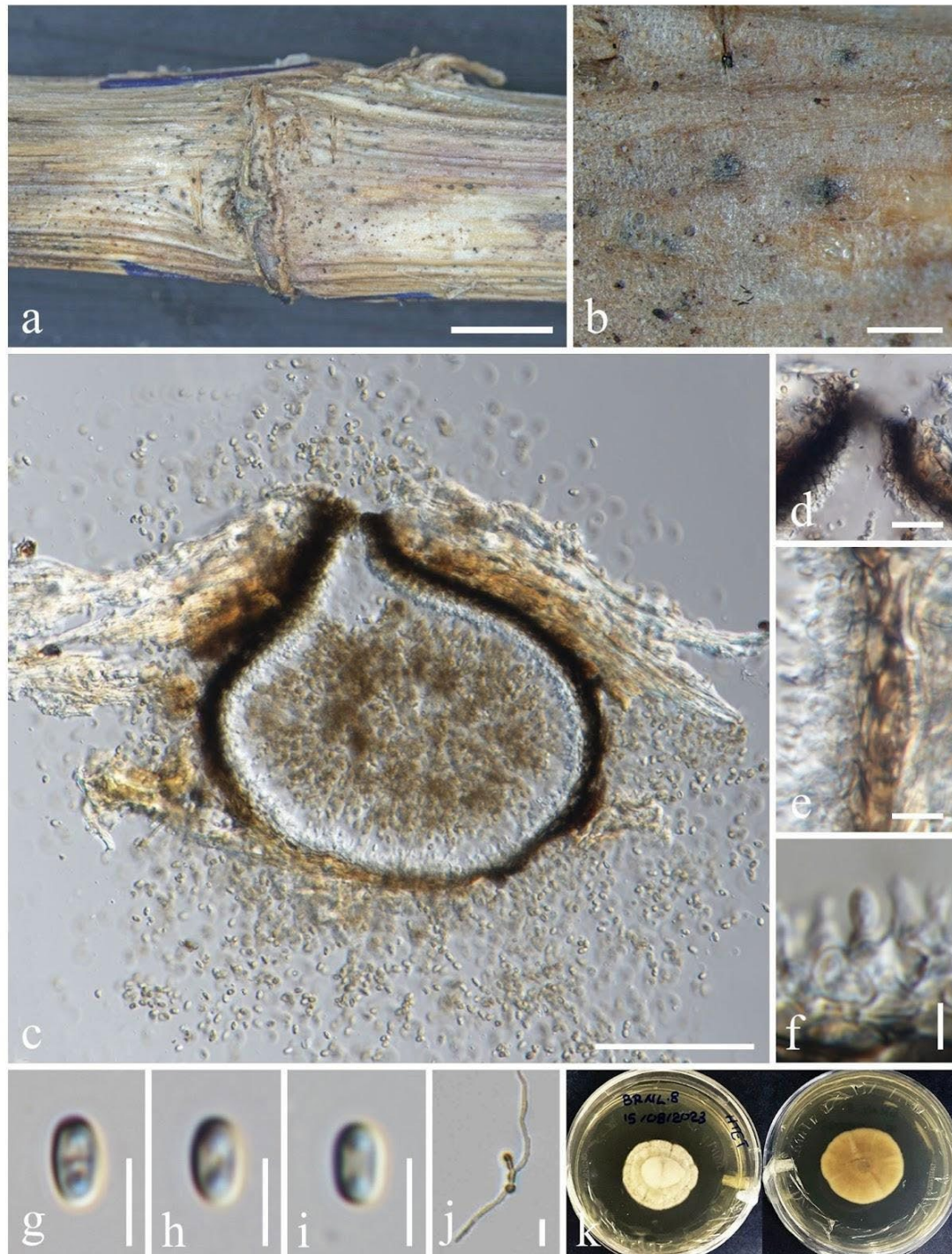


Figure 39 – *Neorousoella entadae* (MFLU 25-0257, a new host record). a, b Appearance of conidiomata on the host substrate. c Section through a conidioma. d Ostiole. e Peridium. f Conidia and conidiogenous cells. g–i Conidia. j A germinating conidium. k Culture on MEA. Scale bars: a = 500 μm , b = 200 μm , c = 50 μm , d, e, j = 10 μm , f–i = 5 μm



Figure 40 – *Pseudoneoconiothyrium chromolaenae* (MFLU 25-0259, holotype). a, b Appearance of conidiomata on the host substrate. c Section through a conidioma. d Ostiole e Peridium. f–h Conidiogenous cells. i–k Conidia. l A germinating conidium. m Culture on MEA. Scale bars: a = 500 μ m, b = 200 μ m, c = 100 μ m, d, e = 20 μ m, f, g, h, i, j, k, l = 5 μ m.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-31 (MFLU 25-0259, **holotype**), ex-type MFLUCC 25-0284.

GenBank – MFLUCC 25-0284: ITS = PV870603.

Pre-screening for antibacterial activity – *Pseudoneoconiothyrium chromolaenae* (MFLUCC 25-0284) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Our strain (MFLUCC 25-0284) is found as an asexual morph in nature, and is morphologically similar to *Ps. rosae* (MFLUCC 15-0052) in having hyaline, annellidic, ovoid to obovoid conidiogenous cells, hyaline to brown conidia with guttules (Wanasinghe et al. 2018). Based on the phylogenetic analysis (Fig. 38), the strain (MFLUCC 25-0284) formed a clade basal to *Pseudoneoconiothyrium thailandicum* (MFLUCC 25-0276 and MFLUCC 25-0282) with 100% ML and 1.00 BYPP bootstrap support. A comparison of base pair difference between our strain (MFLUCC 25-0284) differs from *Ps. thailandicum* (MFLUCC 25-0282) reveals 1.8% (9/542) in ITS. Our strain (MFLUCC 25-0284) differs from *Ps. thailandicum* (MFLUCC 25-0282) in having larger conidiomata (235–320 × 170–210 µm vs. 155–255 × 195–245 µm), and ovoid to ellipsoidal, aseptate conidia, in contrast to the ovoid, (0–)1-septate conidia of the latter. Therefore, *Ps. chromolaenae* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand.

Pseudoneoconiothyrium thailandicum Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.** Fig. 41

Index Fungorum number: IF904370, Facesoffungi number: FoF18037

Etymology – Name reflects the country from which this species was collected.

Holotype – MFLU 25-0260

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 200–250 × 170–255 µm ($\bar{x}$ = 228 × 213 µm, n = 5), immersed, solitary, scattered, appearing as dark spots on the surface. *Ostiole* 65–80 µm wide. *Peridium* 20–30 µm wide, 3–4 layered, comprising hyaline to light brown cells of *textura angularis*. *Hamathecium* comprising 1–3 µm wide, cylindrical to filiform, septate, branched, trabeculate pseudoparaphyses. *Asci* 75–115 × 7–12 µm ($\bar{x}$ = 90 × 10 µm, n = 10), 8-spored, bitunicate, cylindrical to clavate, straight or slightly flexuous, apically rounded, short pedicellate with a small ocular chamber. *Ascospores* 10–15 × 3–7 µm ($\bar{x}$ = 11 × 6 µm, n = 20), uniseriate, hyaline to pale brown when young, becoming yellowish-brown at maturity, ovoid to ellipsoidal, 1-septate, constricted at the septum, with guttules. **Asexual morph:** Coelomycetous. *Conidiomata* 155–255 × 195–245 µm ($\bar{x}$ = 175 × 220 µm, n = 5), immersed to semi-immersed, solitary, appearing as raised, dark spots on the surface. *Ostiole* protruding. *Conidiomatal wall* 20–40 µm wide, 3–4 layered, comprising hyaline to light brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–4 × 4–5 ($\bar{x}$ = 3.2 × 4.4), annellidic, ampulliform, hyaline and unbranched. *Conidia* 5–7 × 3–8 µm ($\bar{x}$ = 6.4 × 4.3 µm, n = 20), ovoid, hyaline to brown, (0–)1-septate, thick-walled with guttules.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 29 mm after 10 days at 27 °C, irregular, filamentous, white, powdery, raised, opaque; irregular, filamentous, creamy-brown in reverse surface.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-9 (MFLU 25-0260, **holotype**), ex-type MFLUCC 25-0276; *ibid.*, CO-PKN-27 (MFLU 25-0261, **a new asexual morph record**), living culture MFLUCC 25-0282.

GenBank – MFLUCC 25-0276: ITS = PV870604, *tef1-α* = PX255049; MFLUCC 25-0282 ITS = PV870605, SSU = PV996967, *tef1-α* = PX282642.

Pre-screening for antibacterial activity – *Pseudoneoconiothyrium thailandicum* (MFLUCC 25-0276) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Refer to the remarks provided under *Pseudoneoconiothyrium chromolaenae* for comparative discussion. Here, we provide the new species, *Pseudoneoconiothyrium thailandicum*

found on *Chromolaena odorata* (Asteraceae), and first sexual-asexual linkage of the species by expanding its taxonomic framework comprehensively.

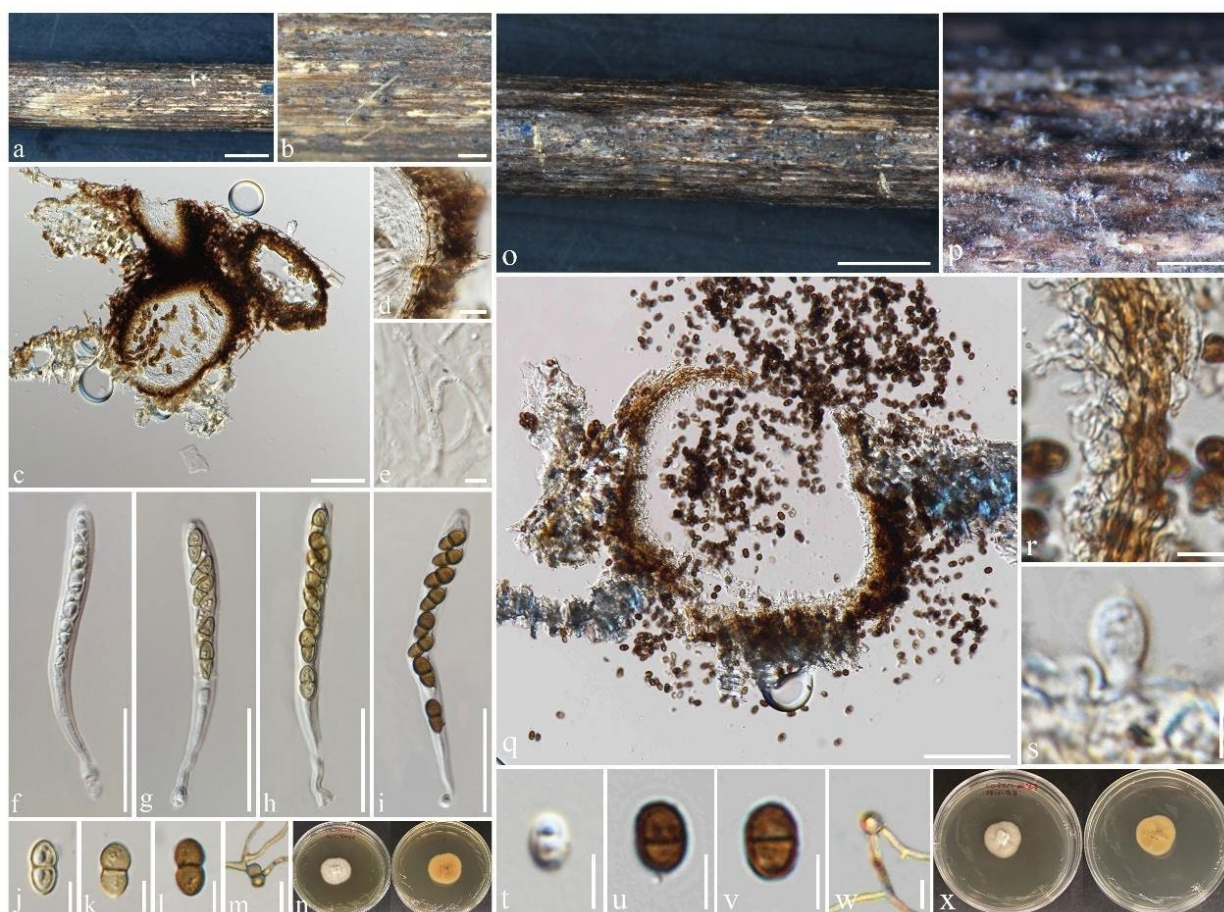


Figure 41 – *Pseudoneoconiothyrium thailandicum* (MFLU 25-0260, holotype) a, b Appearance of ascomata on the host substrate. c Sections through ascoma. d Peridium. e Pseudoparaphyses. f–i Asci. j–l Ascospores. m A germinating ascospore. n Culture on MEA. o, p Appearance of conidiomata on the host substrate. q A section through a conidioma r Conidiomatal wall. s Conidiogenous cells. t–v Conidia. w A germinating conidium. x Culture on MEA. Scale bars: a, o = 500 μ m, b, p = 200 μ m, c, q = 100 μ m, d, r = 20 μ m, e, j, k, l, m, s, t, u, v, w = 5 μ m, f, g, h, i = 30 μ m.

Sporormiaceae Munk

Sporormiaceae species are widespread worldwide (Kirk et al. 2008). They are commonly recorded as saprobes on a variety of substrates, but they can also be found as endophytes (Arenal et al. 2004, Su et al. 2016, Lytvynenko et al. 2022). The taxonomic positions of several taxa were uncertain due to the lack of sequence data (Chang & Wang 2009) and similar morphology between taxa. Kruys & Wedin (2009) resolved this issue by providing molecular data and confirmed the position of *Sporormia*, *Preussia* and *Westerdykella* in Sporormiaceae. Zhang et al. (2009) also confirmed the taxonomic position of Sporormiaceae in Pleosporales. Phukhamsakda et al. (2016) introduced two genera, *Sporormia* and *Forliomyces*, based on LSU, SSU, ITS, *tef1- α* and *rpb2* sequence data. Crous et al. (2020) added *Xenomonodictys* as a monotypic genus to Sporormiaceae. Currently, there are eleven genera in Sporormiaceae (Hyde et al. 2024).

Forliomyces Phukhams., Camporesi & K.D. Hyde

Forliomyces was introduced by Phukhamsakda et al. (2016), typified by *F. uniseptata*. *Forliomyces* species are characterized by brown, pyriform, 1-septate conidia with phialidic conidiogenous cells. Only one species is accepted in this genus (Index Fungorum 2025), which was

only reported as an asexual morph (Phukhamsakda et al. 2016, Hyde et al. 2024). In this study, we introduce *Forliomyces bidentis* as a new species based on the combined LSU, SSU, ITS, and *tef1-α* sequence data (Fig. 42).

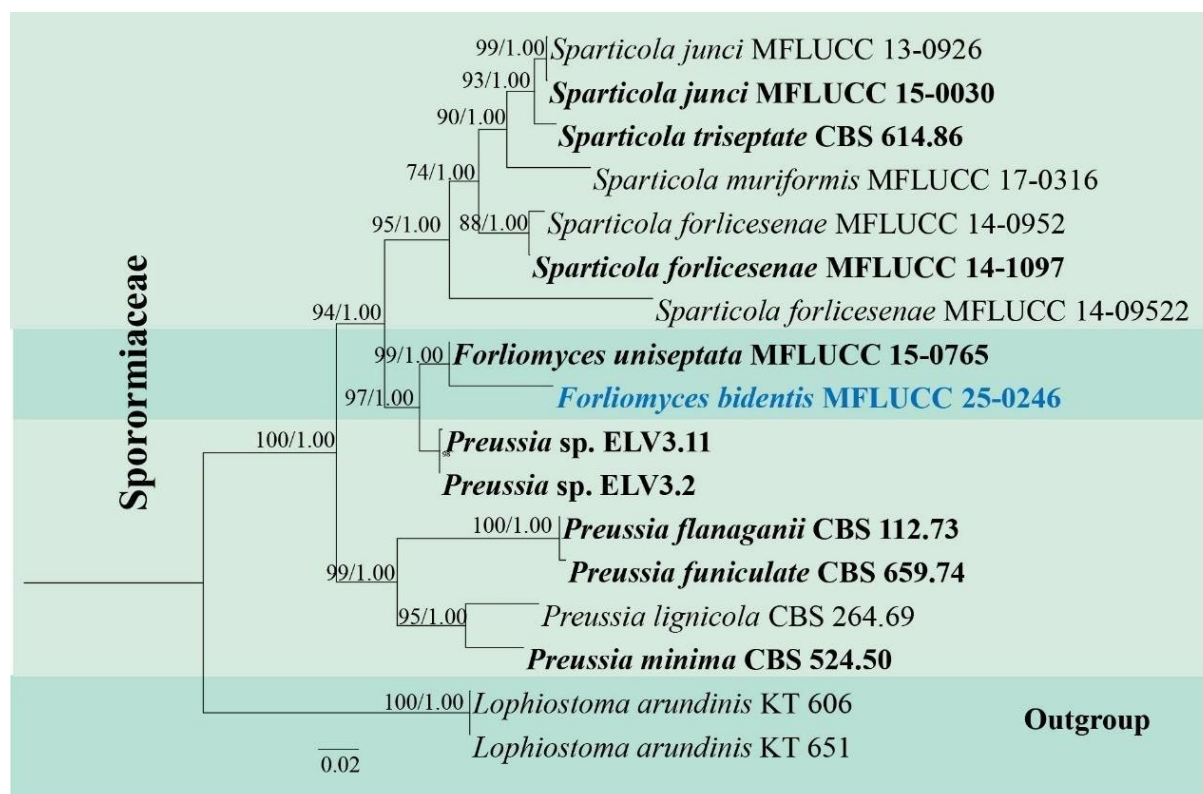


Figure 42 – Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, and *tef1-α* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Lophiostoma aurundinis* (KT 606 and KT 651).

Forliomyces bidentis Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 43

Index Fungorum number: IF904371, Facesoffungi number: FoF18038

Etymology – Name reflects the host plant *Bidens pilosa*, from which this species was isolated.

Holotype – MFLU 25-0262

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 180–200 $\times$ 210–250 μm ($\bar{x}$ = 126 $\times$ 173 μm , n = 5), pycnidial, solitary, immersed, uni-loculate, yellowish-brown, globose to subglobose, dark fruiting bodies on the host substrate, without an ostiole. *Peridium* 20–40 μm wide, comprising 2–3 layers of pale-yellow cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–2 μm long, phialidic, short, globose to subglobose, hyaline and unbranched. *Conidia* 7–15 $\times$ 6–10 μm ($\bar{x}$ = 11 $\times$ 8 μm , n = 20), globose to subglobose, hyaline to reddish-brown, aseptate when young and become 1-septate when mature, thick-walled, without guttules.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 21 mm after 10 days at 27 °C, irregular, entire, powdery, grey, opaque on the surface; concentric, entire, dark grey from reverse.

Material examined – Thailand, Chiang Rai Province, Phan District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet, BP-DP-3 (MFLU 25-0262, **holotype**); ex-type MFLUCC 25-0246.

GenBank – MFLUCC 25-0246: ITS = PV870606, LSU = PX494320.

Pre-screening for antibacterial activity – *Forliomyces bidentis* (MFLUCC 25-0246) showed a 19 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to

positive control (15 mm), a 10 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm), but no inhibition against *E. coli*.

Known host and distribution – dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – Based on the multi-locus phylogeny (Fig. 42), our strain (MFLUCC 25-0246) clustered separately from *Forliomyces uniseptata* (MFLUCC 15-0765) with 99% ML and 1.00 BYPP bootstrap support. Our strain (MFLUCC 25-0246) is morphologically similar to *Forliomyces uniseptata* in having immersed, globose to subglobose, uniloculate pycnidial conidiomata, phialidic conidiogenous cells, and hyaline to reddish-brown, aseptate to 1-septate conidia. However, our strain (MFLUCC 25-0246) differs from *F. uniseptata* (MFLUCC 15-0765) in having smaller conidiomata ($180\text{--}200 \times 210\text{--}250\text{ }\mu\text{m}$ vs. $155\text{--}190 \times 185\text{--}320\text{ }\mu\text{m}$), smaller conidiogenous cells ($1\text{--}2\text{ }\mu\text{m}$ vs. $2\text{--}14\text{ }\mu\text{m}$), and slightly smaller, wider, oval-shaped conidia ($7\text{--}15 \times 6\text{--}10\text{ }\mu\text{m}$ vs. $10\text{--}15 \times 5\text{--}8\text{ }\mu\text{m}$), compared to the oblong to clavate conidiogenous cells and oblong, subovoid conidia of the *F. uniseptata* (Phukhamsakda et al. 2016). When comparing the base pair differences between our isolate and *Forliomyces uniseptata* (MFLUCC 15-0765), no differences were observed in the ITS, while 5.9% (52/880) differences were observed in the LSU without gaps. Therefore, *Forliomyces bidentis* is introduced as a new species, which is also the first occurrence of *Forliomyces* species on *Bidens pilosa* (Asteraceae).

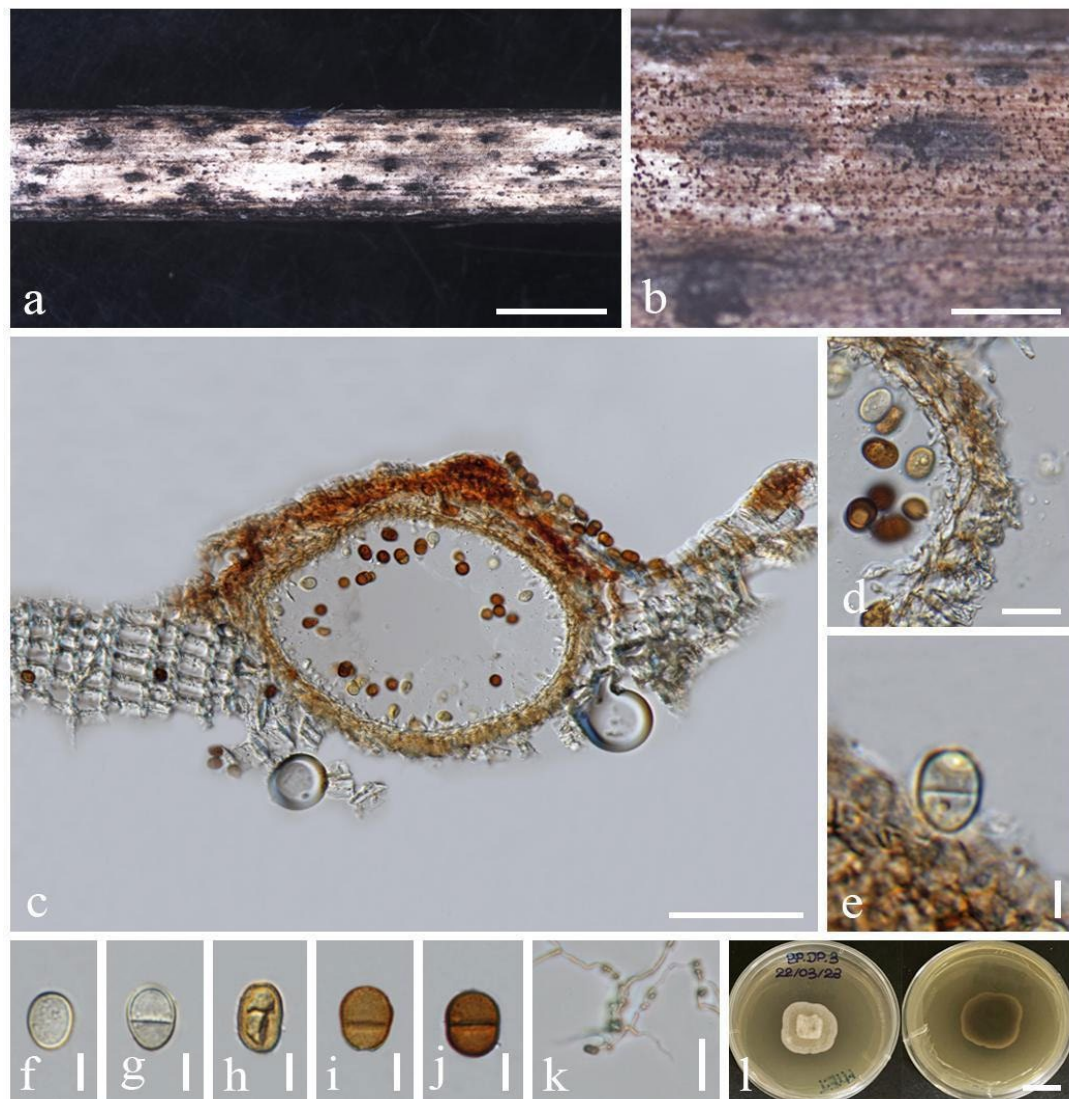


Figure 43 – *Forliomyces bidentis* (MFLU 25-0262, holotype). a, b Appearance of conidiomata on host substrate. c A section through a conidioma. d Conidiomatal wall. e Conidia and conidiogenous

cells. f–j Conidia. k A germinating conidium. l Culture on MEA. Scale bars: a = 500 μm , b = 200 μm , c = 100 μm , d = 20 μm , e–j = 5 μm , k = 10 μm .

***Thyridariaceae* Q. Tian & K.D. Hyde**

Thyridariaceae was introduced by Hyde et al. (2013) to accommodate *Thyridaria*. Subsequently, many taxa were added to this family (Jaklitsch & Voglmayr 2016, Mapook et al. 2020, Tian et al. 2024). Currently, nine genera are accepted in *Thyridariaceae*, viz., *Chromolaenomyces*, *Cycasicola*, *Liua*, *Parathyridaria*, *Parathyridariella*, *Pseudothyridariella*, *Thyridaria*, *Thyridariella*, and *Vaginospora* (Tian et al. 2024, Index Fungorum 2025).

***Pseudothyridariella* Mapook & K.D. Hyde**

Pseudothyridariella was introduced by Mapook et al. (2020) based on LSU, ITS, *tef1- α* , *rpb2* and SSU sequence data, with *Ps. chromolaenae* as a type species. Li et al. (2023) introduced *Ps. idesiae*, which is also the first asexual morph in *Pseudothyridariella*. *Pseudothyridariella* species are reported as saprobes in terrestrial habitats from China and Thailand (Mapook et al. 2020, Li et al. 2023). There are six species listed in Wijayawardene et al. (2022) and Index Fungorum (2025). In this study, we introduce *Pseudothyridariella asteracearum* and *Ps. thailandica* based on the combined LSU, SSU, ITS, *tef1- α* and *rpb2* sequence data (Fig. 44).

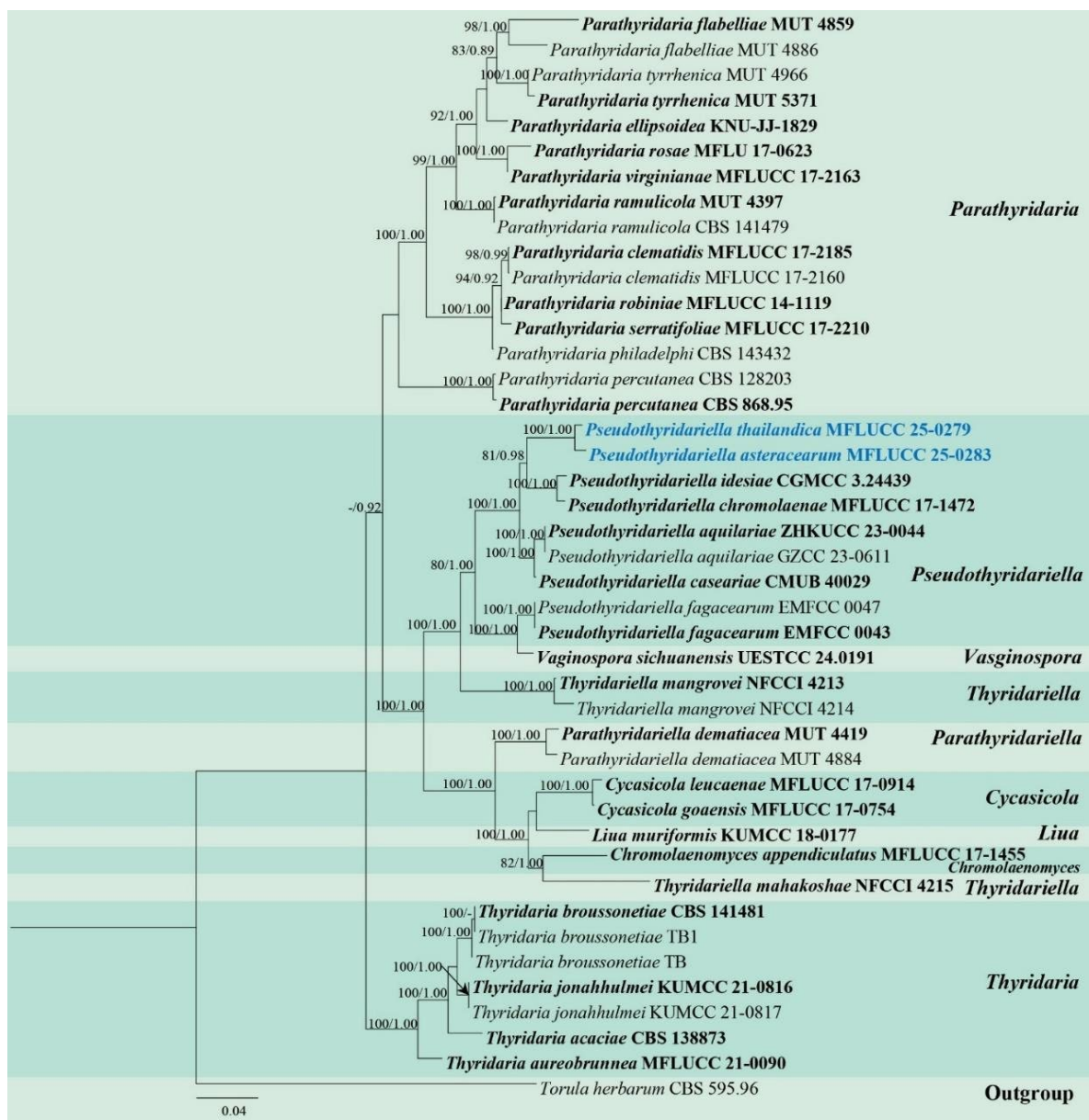


Figure 44 – Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, *tef1-α* and *rpb2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Torula herbarum* (CBS 595.96).

Pseudothyridariella asteracearum Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 45

Index Fungorum number: IF904372, Facesoffungi number: FoF18039

Etymology – Name reflects the host plant family Asteraceae from which this species was collected

Holotype – MFLU 25-0263

Saprobic on dead stems of *Chromolaena odorata* (Asteraceae). **Sexual morph:** *Ascomata* 155–215 × 165–255 μm ($\bar{x}$ = 194 × 219 μm, n = 5), immersed, dark brown to black, globose to subglobose, ostiolate. *Ostioles* central, 50–100 μm wide. *Peridium* 12–25 μm wide, comprising several layers of hyaline to brown cells of *textura angularis*. *Hamathecium* comprising 1–2 μm wide, septate, branched pseudoparaphyses between and above the asci. *Asci* 115–155 × 15–20 μm ($\bar{x}$ = 128 × 18 μm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, pedicellate, rounded at the apex. *Ascospores* 20–30 × 8–10 μm ($\bar{x}$ = 25 × 9 μm, n = 20), overlapping, 1–2 seriate, initially hyaline when young and dark brown at maturity, ellipsoid to broadly fusiform, muriform, with 5–8-transverse septa, and 1 or more vertical septum, slightly constricted at the central septum, straight or curved. **Asexual morph:** Undetermined.

Culture characteristics – Ascospores germinating on MEA within 24 hours, reaching 16 mm after 10 days at 27 °C, irregular, entire, white to olive green, convex, opaque, white to grey on the surface; pale brown, concentric in reverse.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-29 (MFLU 25-0263, **holotype**); ex-type MFLUCC 25-0283.

GenBank – MFLUCC 25-0283: ITS = PV870614, SSU = PV996973, *tef1-α* = PX282650, *rpb2* = PX120464.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Pre-screening for antibacterial activity – *Pseudothyridariella asteracearum* (MFLUCC 25-0283) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Notes – Our strain (MFLUCC 25-0283) is morphologically similar to *Ps. chromolaenae* (MFLUCC 17-1472) in having bitunicate, fissitunicate, cylindric-clavate, pedicellate asci and ellipsoid to broadly fusiform, muriform ascospores (Mapook et al. 2020), but differs in having globose, smaller ascomata (155–215 × 165–255 μm vs. 170–345 × 95–220 μm), and longer asci (115–155 × 15–20 μm vs. 80–105(–135) × (14–)17–22 μm). In the phylogenetic analysis (Fig. 44), our strain (MFLUCC 25-0283) clustered with *Ps. thailandica* (MFLUCC 25-0279) with 100% ML and 1.00 BYPP bootstrap support. Moreover, the genus *Vaginospora* was placed as a sister group to *Pseudothyridariella fagacearum* with high bootstrap support, indicating a close phylogenetic relationship between these two genera. Morphologically, species of *Pseudothyridariella* can be distinguished from *Thyridariella* and *Vaginospora* by the nature of their ascospores. *Pseudothyridariella* produces ascospores slightly constricted only at the central septum, whereas *Thyridariella* and *Vaginospora* have ascospores constricted at every septum. A comparison of base pairs between our strain (MFLUCC 25-0283) and *Ps. thailandica* (MFLUCC 25-0279) reveals 1.6% (18/1068) difference in *rpb2* without gaps. Due to the unavailability of other gene sequences, we cannot compare base pairs. Moreover, our strain (MFLUCC 25-0283) was found as a sexual morph in nature, while *Ps. thailandica* (MFLUCC 25-0279) was found as an asexual morph in nature. Therefore, we could not compare the morphology between species. Herein, we introduce *Ps. asteracearum* as a new species based on multi-gene phylogeny.

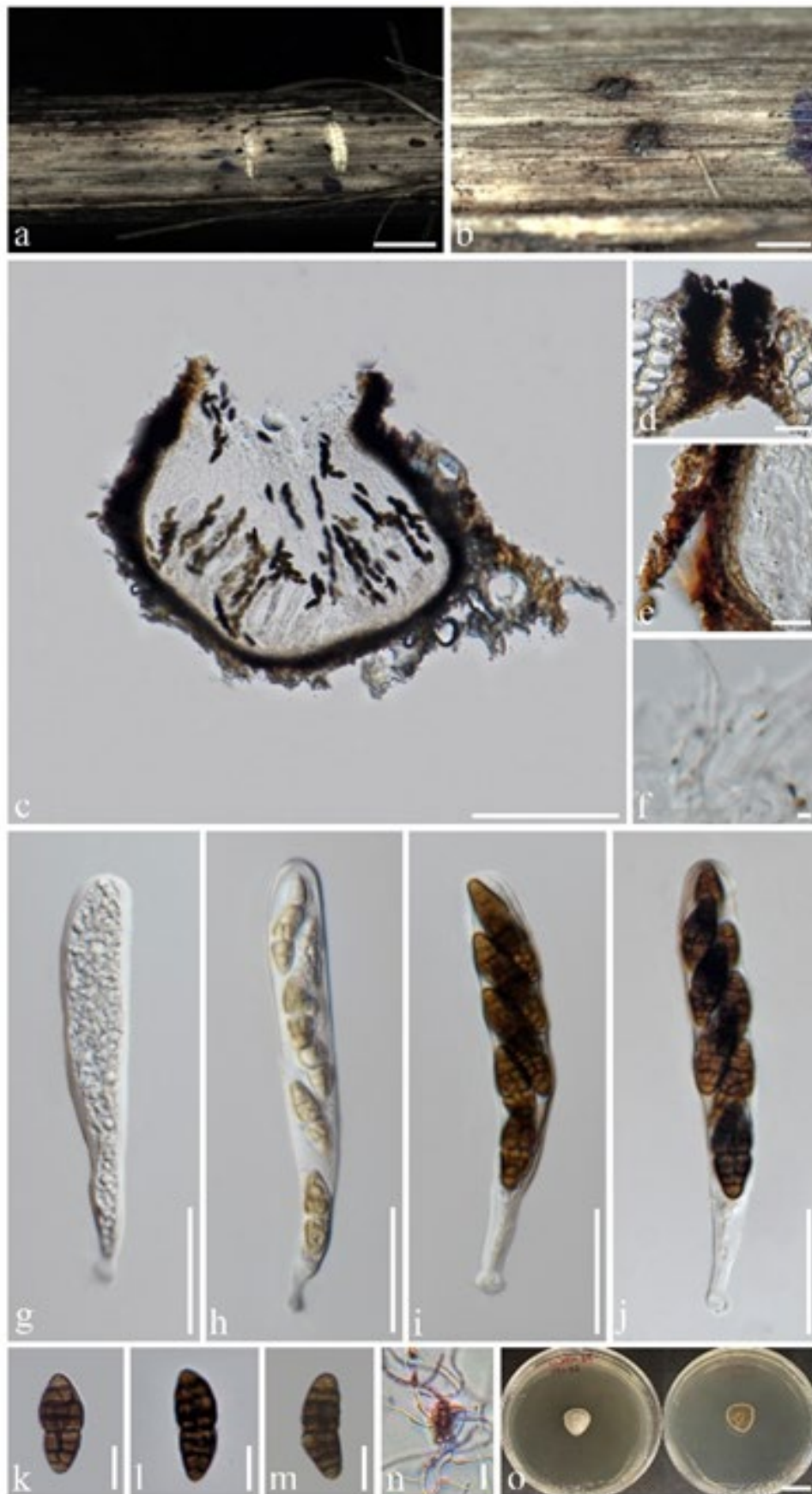


Figure 45 – *Pseudothyridariella asteracearum* (MFLU 25-0263, holotype). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Ostiole. e Peridium. f Pseudoparaphyses. g–j Asci. k–m Ascospores. n A germinating ascospore. o Culture on MEA. Scale bars: a = 500 μm , b = 200 μm , c = 100 μm , d, e = 20 μm , f = 5 μm , g, h, i, j = 30 μm , k, l, m, n = 10 μm , o = 10 mm.

Pseudothyridariella thailandica Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.** Fig. 46

Index Fungorum number: IF904373, Facesoffungi number: FoF18040

Etymology – Name reflects the country from which this species was collected.

Holotype – MFLU 25-0264

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 145–200 × 216–230 µm ($\bar{x}$ = 170 × 223 µm, n = 5), pycnidial, solitary, immersed, uni-loculate, globose to subglobose, yellowish-brown to brown, without ostiole. *Conidiomatal wall* 15–25 µm wide, comprising 2–3 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. Conidiogenous cells 5–11 µm wide, blastic, holoblastic, hyaline. *Conidia* 10–15 × 4–7 µm ($\bar{x}$ = 13 × 6 µm, n = 20), ovoid to oblong, yellowish-brown to brown, aseptate when young and becoming 3-septate when mature, thick-walled, without guttules.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 21 mm after 10 days at 27 °C, irregular, entire, white, umbonate, opaque, white on the surface; irregular, pale brown in reverse.

Material examined – Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet, CO-PKN-17 (MFLU 25-0264, **holotype**); ex-type MFLUCC 25-0279.

GenBank – MFLUCC 25-0279: ITS = PV870615, *rpb2* = PX120465.

Pre-screening for antibacterial activity – *Pseudothyridariella thailandica* (MFLUCC 25-0279) showed no antibacterial activity against *B. subtilis*, *E. coli*, and *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (This study).

Notes – Refer to the remarks provided under *Pseudothyridariella asteracearum* for comparative discussion.

Torulaceae Corda

Torulaceae is characterized by its effuse, powdery colony, immersed mycelia, erect, micronematous or macronematous conidiophores, verruculose, monoblastic to polyblastic conidiogenous cells with phragmosporous, acrogenous brown conidia (Tian et al. 2024). Crous et al. (2015) conducted the phylogenetic revision of Torulaceae based on the combined ITS and LSU sequence data, in which *Dendryphon* is included in Torulaceae. Several studies were conducted on Torulaceae and introduced novel genera such as *Sporidesmioides* (Li et al. 2016), *Rostriconidium* (Su et al. 2018), *Rutola* (Crous et al. 2020), and *Cylindrotorula* (Boonmee et al. 2021). To date, there are seven genera accepted in Torulaceae (Hyde et al. 2024), viz., *Cylindrotorula*, *Dendryphon*, *Neotorula*, *Rostriconidium*, *Rotorula*, *Sporidesmioides* and *Torula*. In this study, we reported *Dendryphon hydei*, *Torula canangae*, *T. fici* and *T. mackenziei* as new records, based on the combined dataset of LSU, SSU, ITS, and *tef1-α* sequences (Fig. 47).

Dendryphon Wallr

Dendryphon was introduced by Wallroth (1833) and typified with *D. comosum*. *Dendryphon* species can be found as saprobic on various host substrates. This genus is characterized by erect, solitary, branched, polytretic conidiophores, forming septate, brown to dark brown, thick-walled, a finely roughened stipe, distinct conidiogenous cells, and dark, catenate, simple or branched chains of brown, septate conidia (Crous et al. 2014, Su et al. 2018, Li et al. 2020). Hyde et al. (2024) listed around 50 species in *Dendryphon*, and only seven species have DNA sequence data (Li et al. 2020).

Dendryphon hydei J.F. Li, Phookamsak & Jeewon, PLoS ONE 15(2): e0228067, 6 (2020) Fig. 48

Index Fungorum number: IF556746, Facesoffungi number: FoF556746

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* on the substratum superficial, effuse, gregarious, hairy, brown to dark brown. *Mycelium* composed of branched, septate, pale brown to brown hyphae. *Conidiophores* 250–

370 × 10–13 µm ($\bar{x}$ = 277 × 11 µm, n = 5), macronematous, mononematous, septate, verrucose, thick-walled, branching simple or penicillate at the apex of primary branches, brown, flexuous. *Conidiogenous cells* 5–10 × 4–5 µm ($\bar{x}$ = 7.5 × 4.5 µm, n = 20), terminal, integrated, pale brown, polytretic. *Conidia* (13–)15–30 × 4–7 µm ($\bar{x}$ = 20 × 5.5 µm, n = 20) single, yellowish-brown to brown, slightly paler at the end cells, dry, verrucose, monilioid, aseptate when young, 1–5-septate when mature, constricted at the septa. Conidial secession schizolytic.

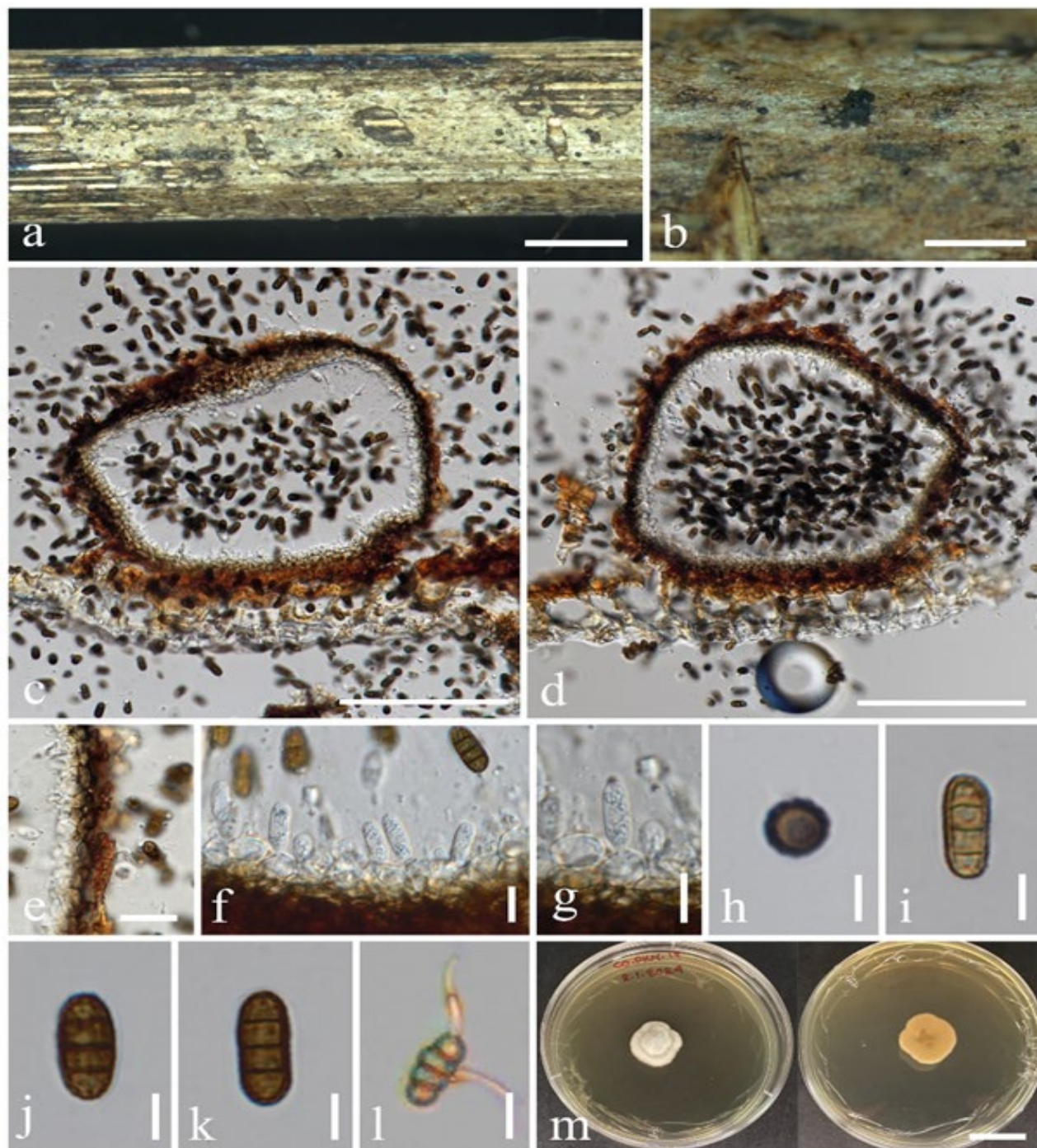


Figure 46 – *Pseudothyridariella thailandica* (MFLU 25-0264, holotype). a, b Appearance of conidiomata on host substrate. c, d A section through a conidioma. e Conidioma wall. f, g Conidiogenous cells. h–k Conidia. l A germinating conidium. m Culture on MEA. Scale bars: a, b = 500 µm, c, d = 100 µm, e = 20 µm, f, g, l = 10 µm, h, i, j, k = 5 µm, m = 10 mm.

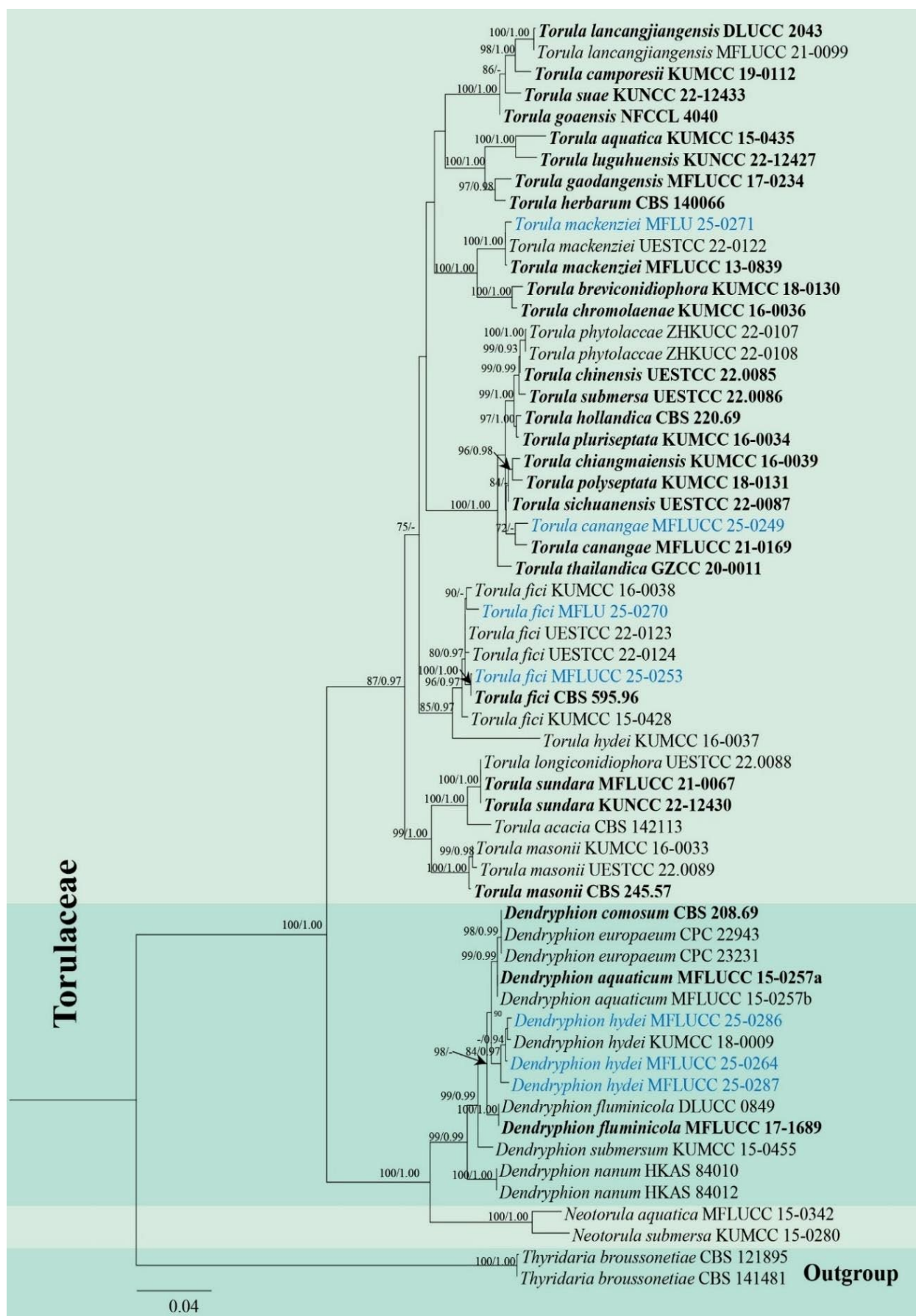


Figure 47 – Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, and *tef1-α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given

at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Thyridaria broussonetiae* (CBS 121895 and CBS 141481).

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 22 mm after 10 days at 27 °C, circular, filamentous, raised, powdery, grey to dark grey, opaque on the surface; circular, filamentous, dark grey in reverse.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 3 August 2023, Zin Hnin Htet, CO-NL-11 (MFLU 25-0265, **a new host record**); living culture MFLUCC 25-0264; *ibid.*, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet, BP-NL-12 (MFLU 25-0266); living culture MFLUCC 25-0287; Phan District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet, BP-DP-22 (MFLU 25-0267); living culture MFLUCC 25-0286.

GenBank – MFLUCC 25-0264: SSU = PV996968, ITS = PV870607, *tef1-α* = PX282643, *rpb2* = PX120457; MFLUCC 25-0287: SSU = PV996969, ITS = PV870608, *tef1-α* = PX282644, *rpb2* = PX120458; MFLUCC 25-0286: SSU = PV996970; ITS = PV870609; *tef1-α* = PX282645; *rpb2* = PX120459.

Pre-screening for antibacterial activity – *Dendryphion hydei* (MFLUCC 25-0286) showed a 14 mm inhibition against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm), and a 20 mm inhibition against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm), but showed no inhibition against *B. subtilis*.

Known host and distribution – dead stems of *Bidens pilosa* (Asteraceae) in Thailand (Li et al. 2020, this study); unidentified plant in China (Wang et al. 2024); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analysis (Fig. 47), the strains (MFLUCC 25-0286, MFLUCC 25-0287 and MFLUCC 25-0264) clustered in a clade with the isolates of *Dendryphion hydei* (KUMCC 18-009) with 84% ML and 0.97 BYPP bootstrap support. Our collection is morphologically similar to *D. hydei* (KUMCC 18-009) in having macronematous, erect or flexuous, brown to dark brown conidiophores, terminal, pale brown, polytretic conidiogenous cells, and pale brown, septate conidia, but no significant difference was observed. The morphological characteristics exhibited no considerable difference between our strain and *D. hydei*. Moreover, there is no significant base pair difference between the strains of *D. hydei* (KUMCC 18-009, MFLUCC 25-0286, MFLUCC 25-0287 and MFLUCC 25-0264). *Dendryphion hydei* was previously reported on *Bidens pilosa* (Asteraceae) (Li et al. 2020).

***Torula* Pers.**

Torula was introduced by Persoon (1794) and typified by *T. monilis*. *Torula* species can be distinguished by terminal or lateral, monoblastic or polyblastic conidiogenous cells, with a basally thicker, strongly melanized wall, and a thin-walled apex that frequently collapses and becomes coronate (Tian et al. 2023). Currently, over 50 species are accepted in *Torula* (Hyde et al. 2024).

Torula canangae N.I. de Silva, Lumyong & K.D. Hyde, Mycosphere 13(1): 1012 (2022) Fig. 49
Index Fungorum number: IF559523, Facesoffungi number: FoF10720

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* effuse on the host, black, powdery. *Mycelium* partly immersed to superficial on the substrate, composed of septate, branched, smooth, hyaline hyphae. *Conidiophores* 7–13 × 3–5 μm ($\bar{x}$ = 8 × 4 μm, n = 10), macronematous, mononematous, solitary, pale brown to brown, smooth. *Conidiogenous cells* 3–6 × 4.5–6.5 μm ($\bar{x}$ = 3.3 × 5 μm, n = 10), mono- to polyblastic, doliiiform to subglobose, dark brown to black, paler at apex, smooth, thick-walled. *Conidia* (13–)20–40(–54) × 5–8 μm ($\bar{x}$ = 15 × 6 μm, n = 20), light brown to dark brown, subcylindrical, catenate, acrogenous, phragmosporous, smooth to distinctly verrucose, 3–9-septate, rounded and yellowish-brown at apex, slightly constricted at some septa.

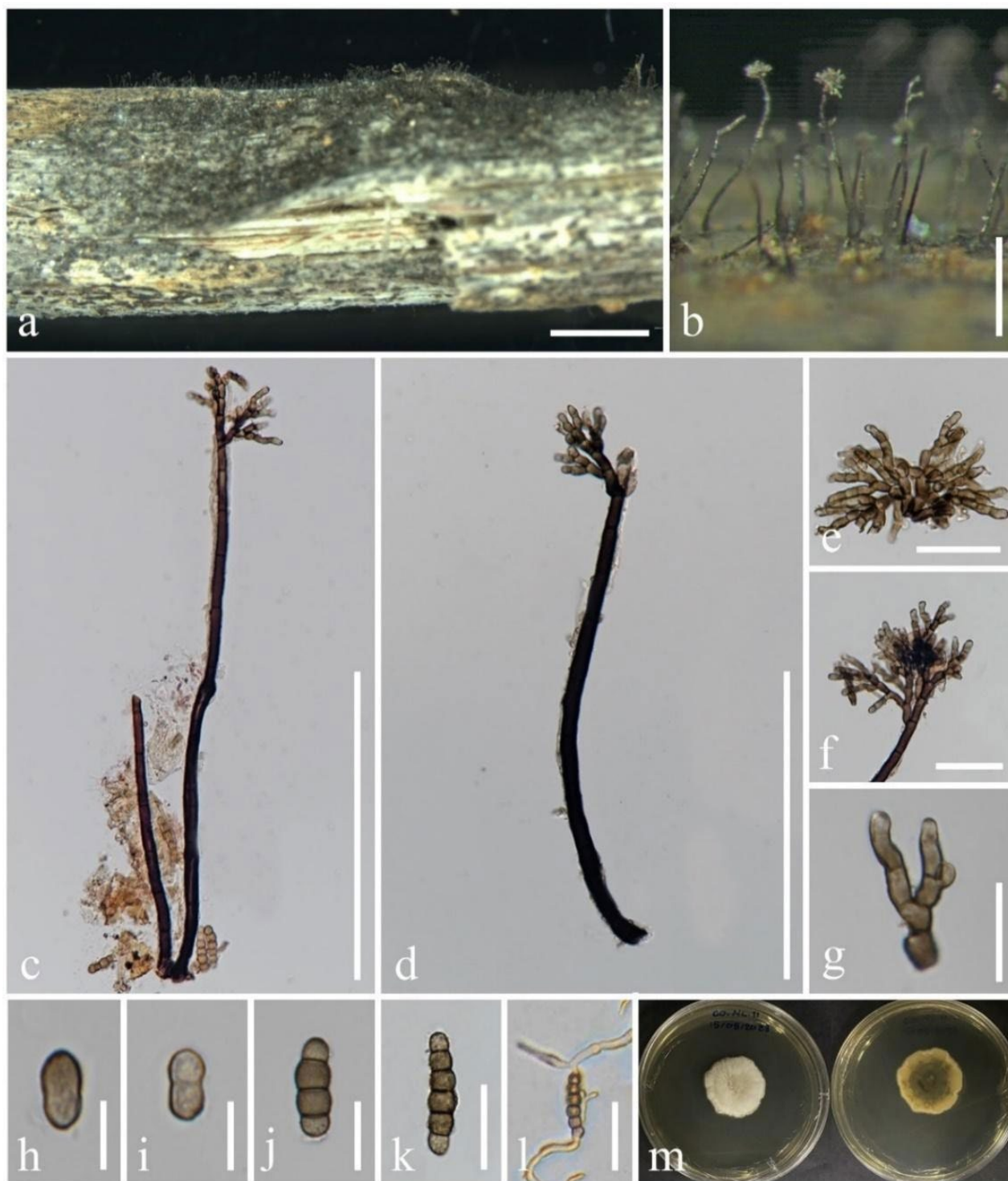


Figure 48 – *Dendryphion hydei* (MFLU 25-0267, a new host record). a, b Colonies on host substrate. c–g Conidiophores and conidiogenous cells. h–k Conidia. l A germinating conidium. m Culture on MEA. Scale bars: a = 500 μ m, b, c, d = 200 μ m, e = 40 μ m, f, g, h, i, j, k, l = 20 μ m.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 30 mm after 10 days at 27 °C, irregular, entire, concentric, pale brown, powdery, flat, opaque on the surface; irregular, entire, concentric, pale brown to brown in reverse.

Material examined – Thailand, Chiang Rai Province, Phan District, on dead stems of *Chromolaena odorata* (Asteraceae), 14 March 2023, Zin Hnin Htet, CO-DP-4 (MFLU 25-0268, **a new host record**); living culture MFLUCC 25-0249.

GenBank – MFLUCC 25-0249: LSU = PV992412, SSU = PV996971, ITS = PV870610, *tef1- α* = PX282646, *rpb2* = PX120460.

Pre-screening for antibacterial activity – *Torula canangae* (MFLUCC 25-0249) showed a 18 mm inhibition against *B. subtilis*, observable as a partial inhibition when compared to positive control (15 mm), a 10 mm inhibition against *E. coli* is observable as a complete inhibition, when compared to positive control (30 mm), and a 21 mm inhibition against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm).

Known host and distribution – dead twigs of *Cananga odorata* (Annonaceae) in Thailand (De Silva et al. 2022); submerged decaying wood in China (Wang et al. 2023); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on phylogenetic analysis (Fig. 47), our collection (MFLUCC 25-0249) clustered sister to *T. canangae* (MFLUCC 21-0169) with 72% ML and 0.74 BYPP bootstrap support. Moreover, there is no significant base pair difference between our collections and *T. canangae* (MFLUCC 21-0169). Morphologically, *Torula canangae* (MFLUCC 21-0169) differs in having longer acrogenous conidia ((28–)78–113 (–142) $\times$ 6–9 μ m), compared to the ((13–)20–40(–54) $\times$ 5–8 μ m) sized conidia of our collection (MFLUCC 25-0249). Therefore, based on multi-gene phylogeny, this collection is reported as a new host record of *T. canangae* on *Chromolaena odorata* (Asteraceae) in Thailand.

Torula fici Crous, IMA Fungus 6(1): 192 (2015)

Fig. 50

Index Fungorum number: IF816154, Facesoffungi number: FoF02712

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* effuse on the host, dark brown to black, powdery. *Mycelium* partly immersed to superficial on the host surface, comprising septate, smooth, and pale brown to light brown hyphae. *Conidiophores* 5–12 $\times$ 2–4 μ m ($\bar{x}$ = 7 $\times$ 3 μ m, n = 10), macronematous, mononematous, solitary, pale brown to brown, smooth. *Conidiogenous cells* 3–6 $\times$ 4.5–6.5 μ m ($\bar{x}$ = 3.3 $\times$ 5 μ m, n = 10), mono- to polyblastic, doliiform to subglobose, dark brown to black, paler at apex, smooth, thick-walled. *Conidia* (5–)10–20 $\times$ 4–6 μ m ($\bar{x}$ = 15 $\times$ 5.5 μ m, n = 20), solitary to catenate, acrogenous, simple, phragmosporous, brown to dark brown, minutely verruculose, 2–3-septate, rounded at both ends, composed of subglobose cells, slightly constricted with dark bands at the septa, rounded at the apex.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 30 mm after 10 days at 27 °C, irregular, filamentous, powdery, brown, flat, opaque on the surface; irregular, filamentous, dark green to grey in reverse.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 12 June 2023, Zin Hnin Htet, CO-HMS-5 (MFLU 25-0269); living culture MFLUCC 25-0253; Theong District, on dead stems of *Chromolaena odorata* (Asteraceae), 24 Jan 2022, A. Mapook, TCR 2 (MFLU 25-0270).

GenBank – MFLU 25-0270: LSU = PV992413, ITS = PV870612, *tef1- α* = PX282648, *rpb2* = PX120462; MFLUCC 25-0253: ITS = PV870611, *tef1- α* = PX282647, *rpb2* = PX120461,

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Li et al. 2017, Mapook et al. 2020, this study); dead leaves of *Ficus septica* (Moraceae) in Taiwan region (Jayawardena et al. 2022); *Ficus religiosa* in Cuba (Crous et al. 2015a); decaying fruit pericarp of *Garcinia* sp. (Clusiaceae) in Thailand (Jayasiri et al. 2019); decaying cone of *Magnolia grandiflora* (Magnoliaceae) in China (Jayasiri et al. 2019); decaying wood of an unidentified plant in China (Su et al. 2018); *Musa* sp. (Musaceae) in China (Samarakoon et al. 2021); *Ficus ampelas* (Moraceae) in Taiwan region (Tennakoon et al. 2021); *Ficus septica* (Moraceae) in Taiwan region (Tennakoon et al. 2021).

Notes – Based on the phylogenetic analysis (Fig. 47), the collections (MFLUCC 25-0253 and MFLU 25-0270) grouped in the same clade with the isolates of *Torula fici* (KUMCC 16-0038, UESTCC 22-0123, UESTCC 22-0124, CBS 595.96, KUMCC 15-0428) with 96% ML and 0.97

BYPP bootstrap support. Moreover, there are no significant base pair differences between our collection and the strains of *T. fici*. *Torula fici* has been collected from the same host, *Chromolaena odorata* and from the same country (Li et al. 2017, Mapook et al. 2020).

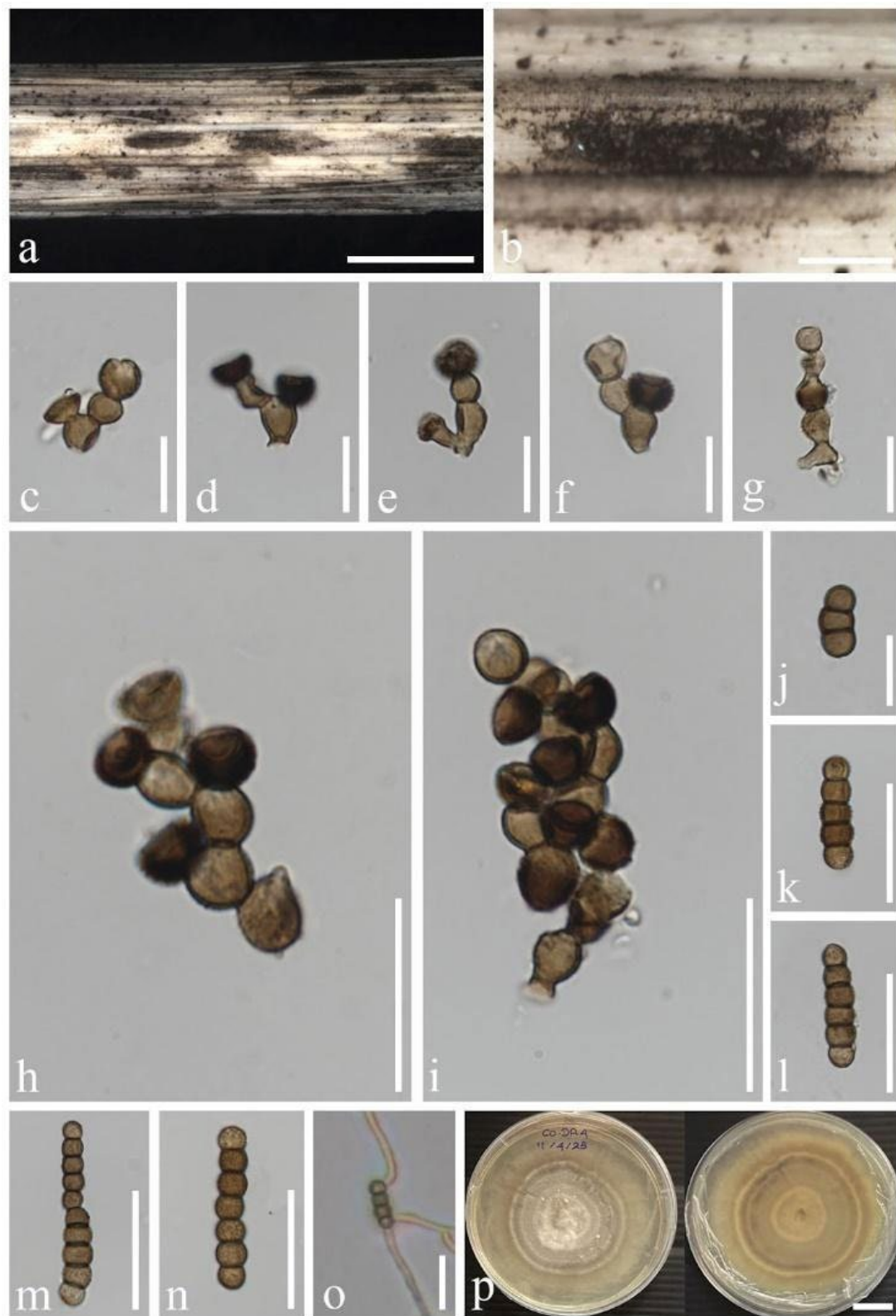


Figure 49 – *Torula canangae* (MFLU 25-0268, a new host record). a, b Colonies on host substrate. c–i Conidiophores and conidiogenous cells. j–n Conidia. o A germinating conidium. p Culture on MEA. Scale bars: a = 500 μ m, b = 200 μ m, c, d, e, f, g, j = 20 μ m, h, i, k, l, m, n = 30 μ m, p = 10 mm.

Torula mackenziei Jun F. Li, Phook. & K.D. Hyde, Mycol. Progr. 16(4): 455 (2017)

Fig. 51

Index Fungorum number: IF819537, Facesoffungi number: FoF02714

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* effuse on the host, black, powdery. *Mycelium* partly immersed to superficial on the substrate, composed of septate, branched, smooth, hyaline hyphae. *Conidiophores* $7\text{--}13 \times 3\text{--}5 \text{ }\mu\text{m}$ ($\bar{x} = 8 \times 4 \text{ }\mu\text{m}$, $n = 10$), macronematous, mononematous, solitary, pale brown to brown, smooth. *Conidiogenous cells* $3\text{--}6 \times 4.5\text{--}6.5 \text{ }\mu\text{m}$ ($\bar{x} = 3.3 \times 5 \text{ }\mu\text{m}$, $n = 10$), mono- to polyblastic, doliform to subglobose, dark brown to black, paler at apex, smooth, thick-walled. *Conidia* $(13\text{--})20\text{--}40(\text{--}54) \times 5\text{--}8 \text{ }\mu\text{m}$ ($\bar{x} = 15 \times 5.5 \text{ }\mu\text{m}$, $n = 20$), light brown to dark brown, subcylindrical, catenate, acrogenous, phragmosporous, smooth to distinctly verrucose, 3–9-septate, rounded and yellowish brown at apex, slightly constricted at some septa.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 3 August 2023, Zin Hnin Htet, CO-NL-1 (MFLU 25-0271, **a new host record**).

GenBank – MFLU 25-0271: SSU = PV996972, ITS = PV870613, *tef1*- α = PX282649, *rpb2* = PX120463.

Known host and distribution – dead branch of *Bidens pilosa* (Asteraceae) in Thailand (Li et al. 2017); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on the phylogenetic analysis (Fig. 47), the collection (MFLU 25-0271) clustered sister to the isolates of *Torula mackenziei* (UESTCC 22-0122 and MFLUCC 13-0839) with 100% ML and 1.00 BYPP bootstrap support. Morphologically, our collection is similar to *T. mackenziei* (MFLU 16-2820), however, it differs in conidial size [$(13\text{--})20\text{--}40(\text{--}54) \times 5\text{--}8 \text{ }\mu\text{m}$ vs. $9.4\text{--}18.5 \times (3.8\text{--})4.4\text{--}4.7 \text{ }\mu\text{m}$]. Therefore, based on multi-gene phylogeny, our collection is reported as new host records of *T. mackenziei* on *Chromolaena odorata* (Asteraceae) in Thailand.

Class Sordariomycetes O.E. Erikss. & Winka

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

Diaporthales Nannf.

Diaporthaceae Höhn. ex Wehm

Diaporthaceae was introduced by von Höhnelt (1917) to accommodate diaporthoid taxa. Members of Diaporthaceae were found in a variety of hosts as endophytes, pathogens and saprobes (Udayanga et al. 2011, 2012, Dissanayake et al. 2024). Eighteen genera are accepted in Diaporthaceae (Hyde et al. 2024).

Diaporthe

Diaporthe was introduced by Nitschke (1870), typified by *D. eres*. The genus is comprised of endophytes, saprobes, and pathogens on a variety of hosts in temperate and tropical climates around the world (Udayanga et al. 2014, Blagojević et al. 2023). *Diaporthe* species has previously been identified by based on morphology and host-specificity. For an accurate identification of *Diaporthe*, several studies have revisited the phylogeny of valid *Diaporthe* species with molecular data (Udayanga et al. 2012, Dissanayake et al. 2017, Norphanphoun et al. 2022, Dissanayake et al. 2024). The most used gene regions for phylogenetic analysis of *Diaporthe* species are ITS, *tub2*, *tef1*- α , histone, and calmodulin (Norphanphoun et al. 2022, Dissanayake et al. 2024). Hyde et al. (2024) mentioned that around 300 species are included in *Diaporthe*. In our study, we reported new species and new records of *Diaporthe* from *D. biconispora* and *D. longicolla* complexes (Figs 52 and 53).

Diaporthe asteracearum Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 54

Index Fungorum number: IF904376, Facesoffungi number: FoF18044

Etymology – Name reflects the host plant family Asteraceae, from which this species was collected.

Holotype – MFLU 25-0281

Saprobic on dead stems of *Chromolaena odorata*. *Ascomata* 150–300 × 235–280 μm ($\bar{x}$ = 160 × 273 μm , n = 5), globose to subglobose, solitary to gregarious, immersed, with long necks. *Peridium* 10–30 μm , comprised of 1–2 layers of pale brown cells of *textura angularis*. *Hamathecium* filamentous, septate, branched pseudoparaphyses. *Asci* 30–45 × 6–10 μm ($\bar{x}$ = 37 × 7 μm , n = 10), unitunicate, 8-spored, obclavate, flat at the apex, with an ocular chamber. *Ascospores* 5–10 × 2–3 μm ($\bar{x}$ = 8 × 2.6 μm , n = 20), hyaline, biserial, overlapping in the ascus, fusiform to ellipsoidal, 1-septate, constricted at the septum, guttulate.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 85 mm after 10 days at 27°C, circular, filamentous, powdery, white, flat, transparent on the surface; circular, filamentous, concentric, white to pale yellow in reverse surface.



Figure 50 – *Torula fici* (MFLU 25-0269). a, b Colonies on host substrate. c–j Conidiophores and conidiogenous cells. k–q Conidia. r A germinating conidium. s Culture on MEA. Scale bars: a = 500 μm , b = 200 μm , c, d, e, f, g, k, l, m, n, o = 10 μm , h, i = 30 μm , j, p, q, r = 20 μm , s = 10 mm.

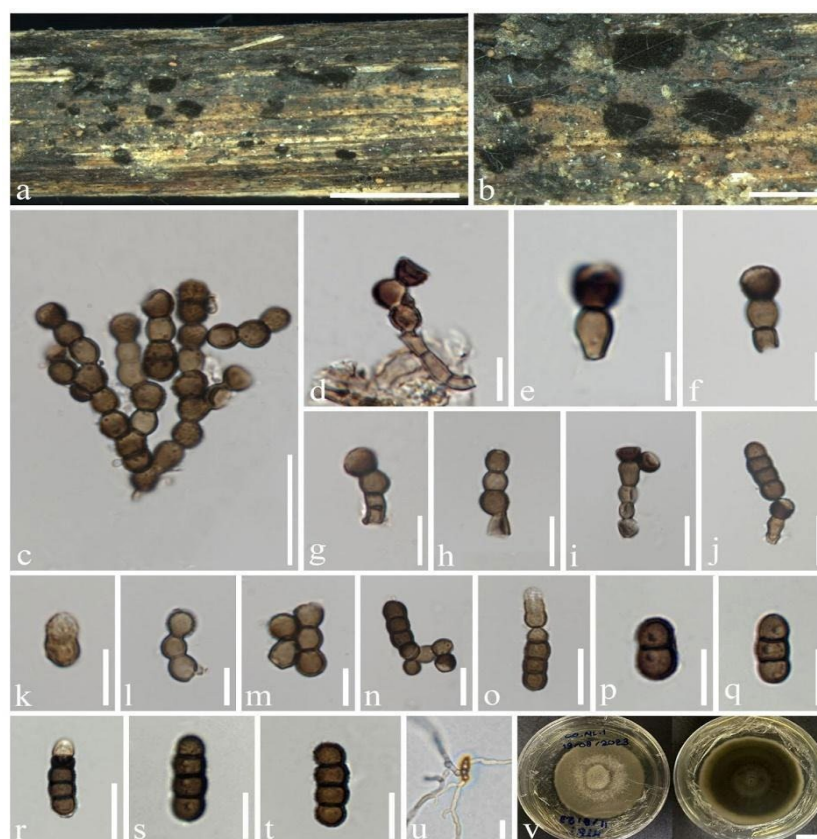


Figure 51 – *Torula mackenziei* (MFLU 25-0271, a new host record). a, b Colonies on host substrate. c–j Conidiophores and conidiogenous cells. k–t Conidia. u A germinating conidium. v Culture on MEA. Scale bars: a = 500 μ m, b = 200 μ m, c = 20, d, e, f, g, k, l, m, n, o, p, q, r, s, t, u = 10 μ m, v = 10 mm.

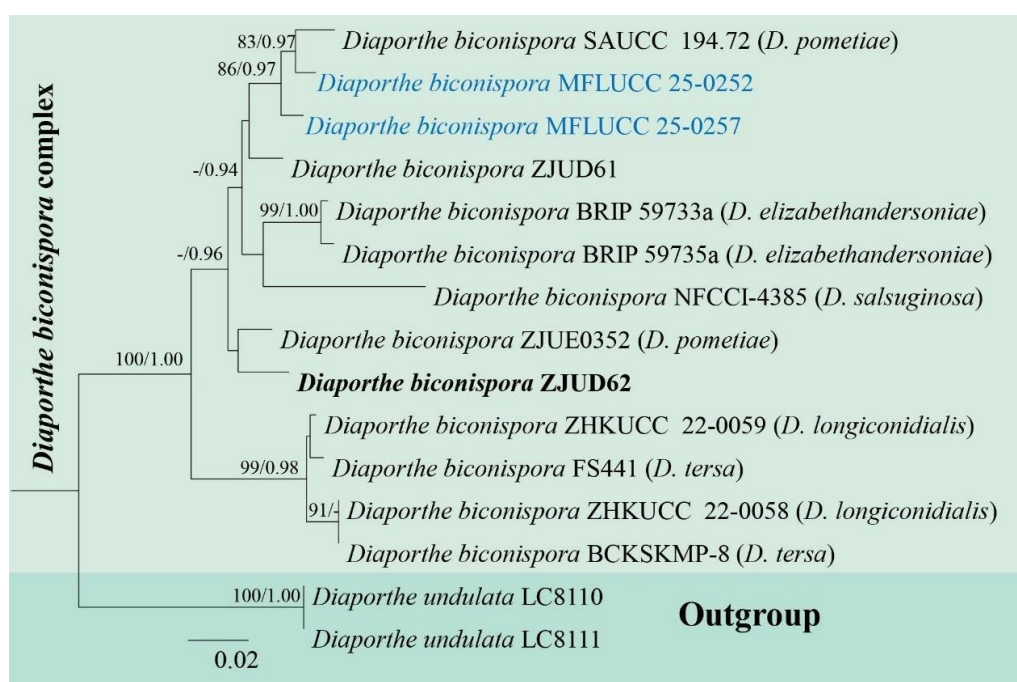


Figure 52 – Phylogram generated from ML analysis of a combined dataset of ITS, *tef1- α* , and *tub2* sequence data. Bootstrap support values for ML $\geq$ 75% and BYPP $\geq$ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Diaporthe undulata* (LC1180 and LC1181).

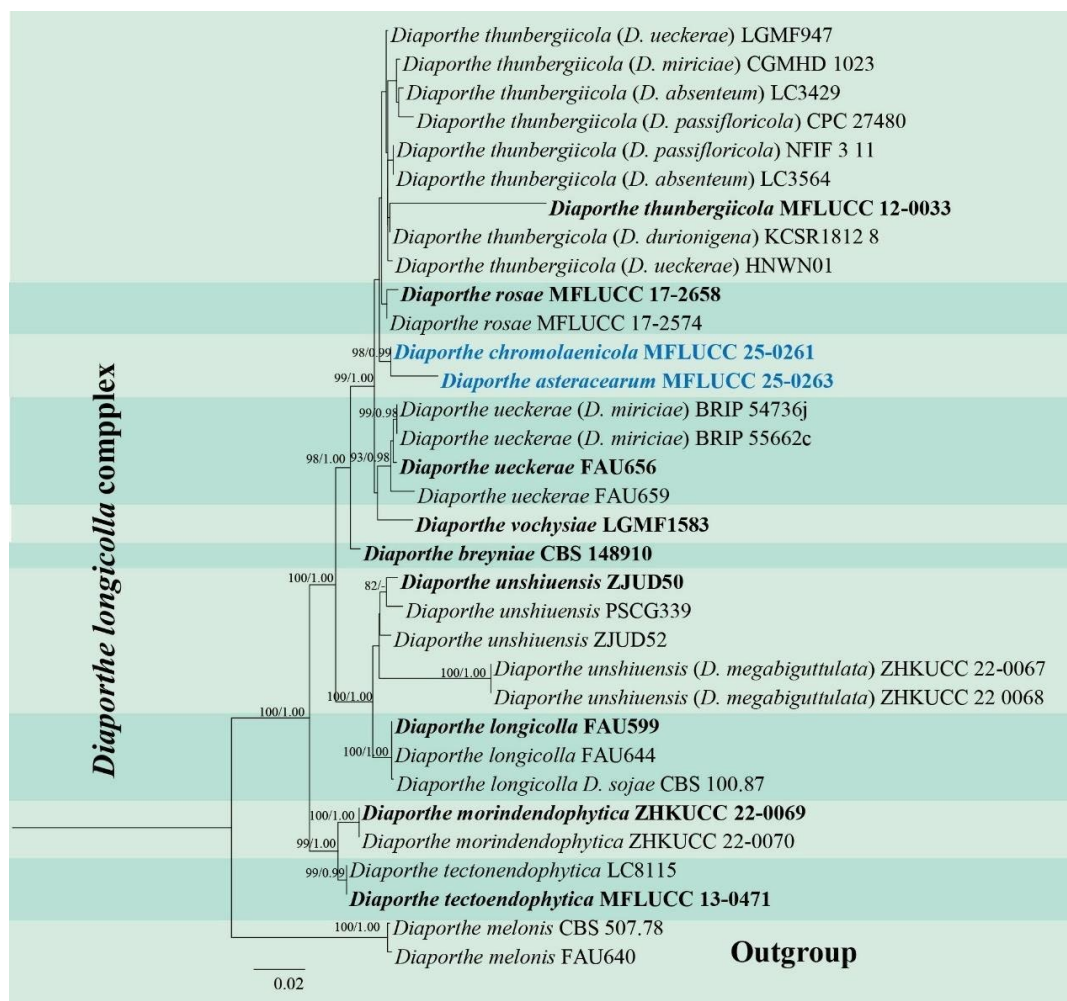


Figure 53 – Phylogram generated from ML analysis based on the combined dataset of ITS, *tef1- α* , and *tub2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Diaporthe melonis* (CBS 507.78 and FAU640).

Material examined – Thailand, Chiang Rai Province, Nang Lae District, on dead stems of *Chromolaena odorata* (Asteraceae), 3 August 2023, Zin Hnin Htet, CO-NL-10 (MFLU 25-0281, **holotype**); ex-type MFLUCC 25-0263.

GenBank – MFLUCC 25-0263: ITS = PV870625, *tef1- α* = PX282658, *tub2* = PX255052.

Pre-screening for antibacterial activity – *Diaporthe asteracearum* (MFLUCC 25-0263) showed a 10 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), a 9 mm inhibition against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm) and no inhibition zone against *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on the phylogenetic analysis (Fig. 53), our strain (MFLUCC 25-0263) formed a distinct clade with *D. chromolaenicola* (MFLUCC 25-0261), supported by 98% ML and 0.99 BYPP, and branching from a clade containing the isolates of *D. thunbergiicola* and *D. rosae* (50% ML, 0.65 BYPP). Morphologically, our isolate (MFLUCC 25-0263) is characterized by having unitunicate, 8-spored, obclavate asci and fusiform to ellipsoidal, 1-septate, guttulate ascospores, which are similar to the sexual morph of other *Diaporthe* species such as *D. juglandicola*, *D. rudis* (Yang et al. 2017, Wanasinghe et al. 2018). Our isolate (MFLUCC 25-0263) is found as a sexual morph in nature, and its phylogenetically related species, *D. chromolaenicola*, *D. rosae* and *D.*

thunbergiicola, are found as asexual morphs (Hongsanant et al. 2023). Therefore, we could not compare the morphology between them. A comparison of base pairs difference between our strain (MFLUCC 25-0263) and *D. rosae* (MFLUCC 17-2574) reveals ITS 0.5% (3/573), *tef1-α* 2.7 % (10/372) and *tub2* 2.7% (13/489), while a comparison between our strain (MFLUCC 25-0263) and *D. chromolaenicola* (MFLUCC 25-0261) reveals ITS 0% (0/573), *tef1-α* 0% (0/372) and *tub2* 4% (20/489), respectively. Therefore, *Diaporthe asteracearum* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand, based on phylogeny.



Figure 54 – *Diaporthe asteracearum* (MFLU 25-0281, holotype). a, b Appearance of ascomata on host substrate. c Section through an ascoma. d Ostiole. e Peridium. f Paraphyses. g–i Asci. j Asci stained with Melzer's Reagent. k–n Ascospores. o A germinating ascospore. p Culture on MEA. Scale bars: a = 1 mm, b = 300 μ m, c = 100 μ m, d, e = 20 μ m, f, k, l, m, n, o = 5 μ m, g, h, i, j = 10 μ m

Diaporthe biconispora F. Huang, K.D. Hyde & Hong Y. Li, Fungal Biology 119: 338 (2015)

Fig. 55

Index Fungorum number: IF810578, Faces of fungi number: FoF08406

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 80–150 $\times$ 100–150 μ m ($\bar{x}$ = 98 $\times$ 123 μ m, n = 5), pycnidial, solitary, immersed, uni-loculate, brown, globose to subglobose, dark fruiting bodies on the host substrate,

without an ostiole. *Peridium* 12–35 µm wide, comprising several layers of yellowish-brown to brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2–4 × 2–4 µm ($\bar{x}$ = 3 × 3 µm, n = 5), holoblastic, phialidic, globose to subglobose, or ampulliform, terminal. *Alpha conidia* 5–10 × 1.5–3 µm ($\bar{x}$ = 7.5 × 2 µm, n = 20), hyaline, aseptate, fusoid to ovoid, hyaline, aseptate, tapering at both ends, with 2–4-guttules. *Beta conidia* 20–25 × 1–2 µm ($\bar{x}$ = 22 × 1.5 µm, n = 10), hyaline, aseptate, filiform, straight or curved, granular appearance, wider at the middle and tapering towards both ends.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 42 mm after 10 days at 27 °C, circular, filamentous, concentric, opaque, flat, pale yellow on the surface; circular, concentric, yellow in reverse.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District on dead stems of *Bidens pilosa* (Asteraceae), 12 June 2023, Zin Hnin Htet, BP-HMS-11 (MFLU 25-0282, **a new host record**); living culture MFLUCC 25-0257; *ibid.*, on dead stems of *Chromolaena odorata* (Asteraceae), 12 June 2023, Zin Hnin Htet, CO-HMS-4 (MFLU 25-0283, **a new host record**); living culture MFLUCC 25-0252.

GenBank – MFLUCC 25-0257: ITS = PV870626, *tef1*- α = PX282659, *tub2* = PX255053; MFLUCC 25-0252: ITS = PX494321, *tef1*- α = PX578844, *tub2* = PX578845

Pre-screening for antibacterial activity – *Diaporthe biconispora* (MFLUCC 25-0252) showed a 15 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), a 12mm inhibition zone against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm) and a 18 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm).

Known host and distribution – *Avicennia marina* (Acanthaceae) in China (Vrijmoed et al. 1994); *Citrus grandis* (Rutaceae) in China (Huang et al. 2015); deep-sea sediments in China (Rossmann et al. 2016); *Pometia pinnata* (Sapindaceae) in China (Huang et al. 2021); *Sapindus mukorossi* (Sapindaceae) in China (Si et al. 2021); *Morinda officinalis* (Rubiaceae) in China (Luo et al. 2022); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – While Norphanphoun et al. (2022) studied the taxonomic position of *Diaporthe* complex, there were two species accepted in the *D. biconispora* species complex, viz., *D. biconispora* and *D. salsuginosa*. Dissanayake et al. (2024) revisited the species complex in *Diaporthe* and synonymized *D. longiconidialis*, *D. pometiae*, *D. salsuginosa*, and *D. tersa* under *D. biconispora*. In the phylogenetic analyses (Fig. 52), our isolate (MFLUCC 25-0252) clustered within *D. biconispora* complex with 100% ML and 1.00 BYPP bootstrap support. Moreover, there are no significant base pair differences between species. Therefore, our collections are reported as new host records of *D. biconispora* on *Bidens pilosa* and *Chromolaena odorata* (Asteraceae) and a new geographical record in Thailand.

Diaporthe chromolaenicola Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.** Fig. 56

Index Fungorum number: IF904377, Facesoffungi number: FoF18045

Etymology – Name reflects the host plant *Chromolaena odorata*, from which this species was isolated.

Holotype – MFLU 25-0284

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** Coelomycetous. *Conidiomata* 130–150 × 90–120 µm ($\bar{x}$ = 146 × 106 µm, n = 5), pycnidial, solitary, immersed, uni-loculate, rarely with one locule, globose to subglobose, dark fruiting bodies on the host substrate, with an ostiole with a small papilla in the centre. *Peridium* 20–25 µm wide, comprising 2–3 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–10 × 2–3 µm ($\bar{x}$ = 5.5 × 2 µm, n = 5), phialidic, ampulliform, terminal. *Alpha conidia* 5–10 × 1–3 µm ($\bar{x}$ = 7 × 2.4 µm, n = 20), hyaline, aseptate, fusoid to ovoid, tapering at both ends, 2-guttules. *Beta conidia* 20–28 × 1–2 µm ($\bar{x}$ = 25 × 1.3 µm, n = 20), hyaline, aseptate, filiform, curved, granular appearance, wider at the middle and tapering towards both ends.

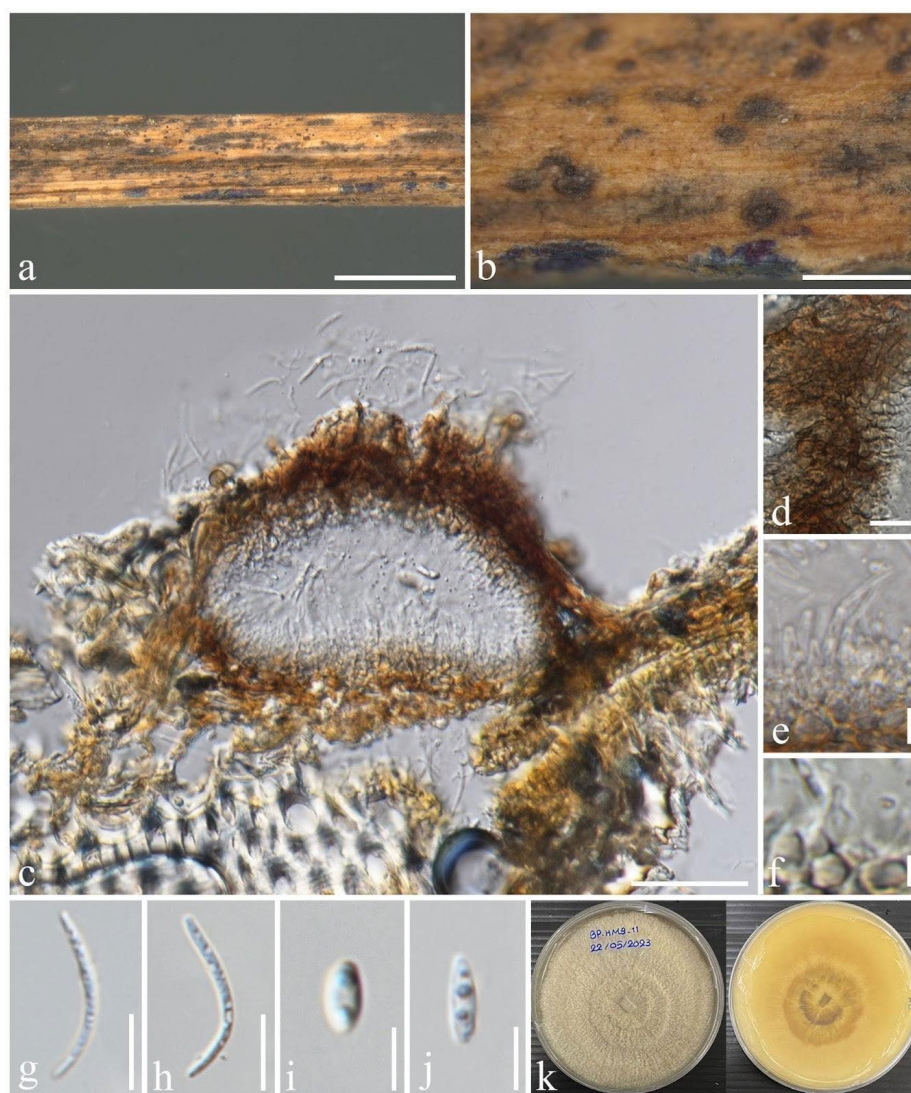


Figure 55 – *Diaporthe biconispora* (MFLU 25-0282, a new host record). a, b Appearance of conidiomata on host substrate. c A section through a conidioma. d Peridium. e–f Conidiogenous cells. g–j Alpha and beta conidia. k Culture on MEA. Scale bars: a = 1 mm, b = 200 μ m, c = 50 μ m, d, g, h = 10 μ m, e, f, i, j = 5 μ m.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 85 mm after 10 days at 27 °C, circular, filamentous, powdery, white, flat, transparent on the surface; circular, filamentous, concentric, white to pale yellow in reverse surface.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 3 August 2023, Zin Hnin Htet, CO-NL-7 (MFLU 25-0284, **holotype**); ex-type MFLUCC 25-0261.

GenBank – MFLUCC 25-0261: ITS = PV870627, *tef1*- α = PX282660, *tub2* = PX246147.

Pre-screening for antibacterial activity – *Diaporthe chromolaenicola* (MFLUCC 25-0261) showed a 14 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), a 12 mm inhibition against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm) and no inhibition zone against *S. aureus*.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on phylogenetic analysis (Fig. 53), the strain (MFLUCC 25-0261) clustered sister to *D. asteracearum* (MFLUCC 25-0263), with 98% ML and 0.99 BYPP bootstrap support. The strain (MFLUCC 25-0261) was found as an asexual morph in nature, and *D. asteracearum* (MFLUCC 25-0263) is found as a sexual morph. Therefore, we could not compare the morphology

between them. Furthermore, our strain (MFLUCC 25-0261) and *D. asteracearum* clustered separately from the isolates of *D. thunbergiicola* and *D. rosae* (Fig. 53). Morphologically, our strain (MFLUCC 25-0261) is similar to *D. rosae* (MFLUCC 17-2658) in having globose to subglobose, pycnidial conidiomata, phialidic, ampulliform conidiogenous cells, hyaline, aseptate beta conidia and guttulate alpha conidia (Wanasinghe et al. 2018), but differs in having shorter conidiogenous cells ($8\text{--}10 \times 2\text{--}3 \mu\text{m}$ vs. $13 \times 1\text{--}2.5 \mu\text{m}$), and longer alpha conidia ($5\text{--}10 \times 1\text{--}3 \mu\text{m}$ vs. $5.5\text{--}7.5 \times 2\text{--}3 \mu\text{m}$) and longer beta conidia ($20\text{--}28 \times 1\text{--}2 \mu\text{m}$ vs. $12.5\text{--}18 \times 1\text{--}2 \mu\text{m}$). When we compared the base pair differences between this strain (MFLUCC 25-0261) and *D. asteracearum* (MFLUCC 25-0263), the result reveals ITS 0% (0/573), *tef1- α* 0% (0/372) and *tub2* 4% (20/489), respectively. Therefore, we introduce *Diaporthe chromolaenicola* as a new species on *Chromolaena odorata* (Asteraceae) in Thailand.

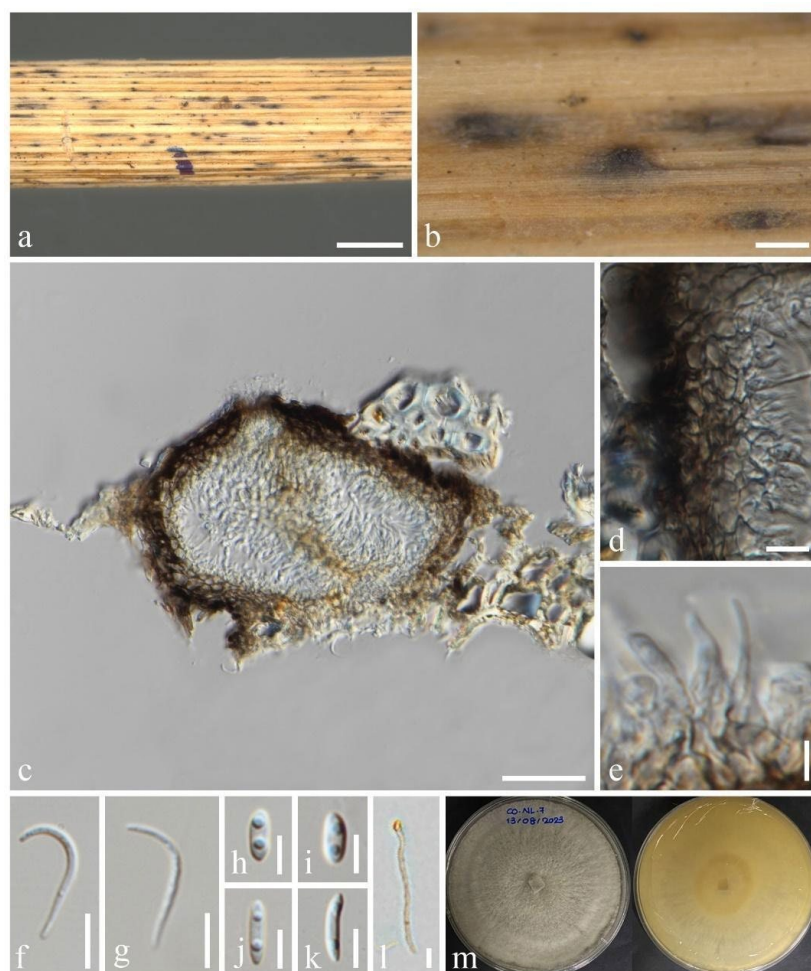


Figure 56 – *Diaporthe chromolaenicola* (MFLU 25-0284, holotype). a, b Appearance of conidiomata on host substrate. c A section through a conidioma. d Peridium. e Conidiogenous cells with conidia. f–k Alpha and beta conidia. l A germinating conidium. m Culture on MEA. Scale bars: a = 1 mm, b = 200 μm , c = 50 μm , d = 10 μm , e, h, i, j, k = 5 μm , f, g = 10 μm .

Subclass Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadeff. ex R  blov  , W. Gams & Seifert

Glomerellaceae Locq. ex Seifert & W. Gams

Glomerellaceae is a monotypic family, including *Colletotrichum* species. Members of Glomerellaceae are found as endophytes, pathogens and saprobes worldwide (Hyde et al. 2009, Zapata & Palfner 2022, Liu et al. 2023, Zhang et al. 2024).

Colletotrichum Corda

Colletotrichum was introduced by Corda (1831), and typified by *C. lineola*. Due to the similar morphology between species, the accurate species identification of this genus was challenging. Hyde et al. (2009) recommended the use of both combined gene analyses and the morphological characters to study *Colletotrichum* complexes. Currently, several gene regions are used for the identification of *Colletotrichum* species, such as *ACT*, *tub2*, *CHS*, *Apn2*, *GAPDH*, *GS*, *HIS*, *ITS*, *SOD2*, *Mat1* and *Ap/Mat*. (Than et al. 2008, Bhunjun et al. 2021, Liu et al. 2022, Zhang et al. 2024). In our study, we introduce two new records in *Colletotrichum gigasporum* and *C. truncatum* complexes (Figs 57 and 58).

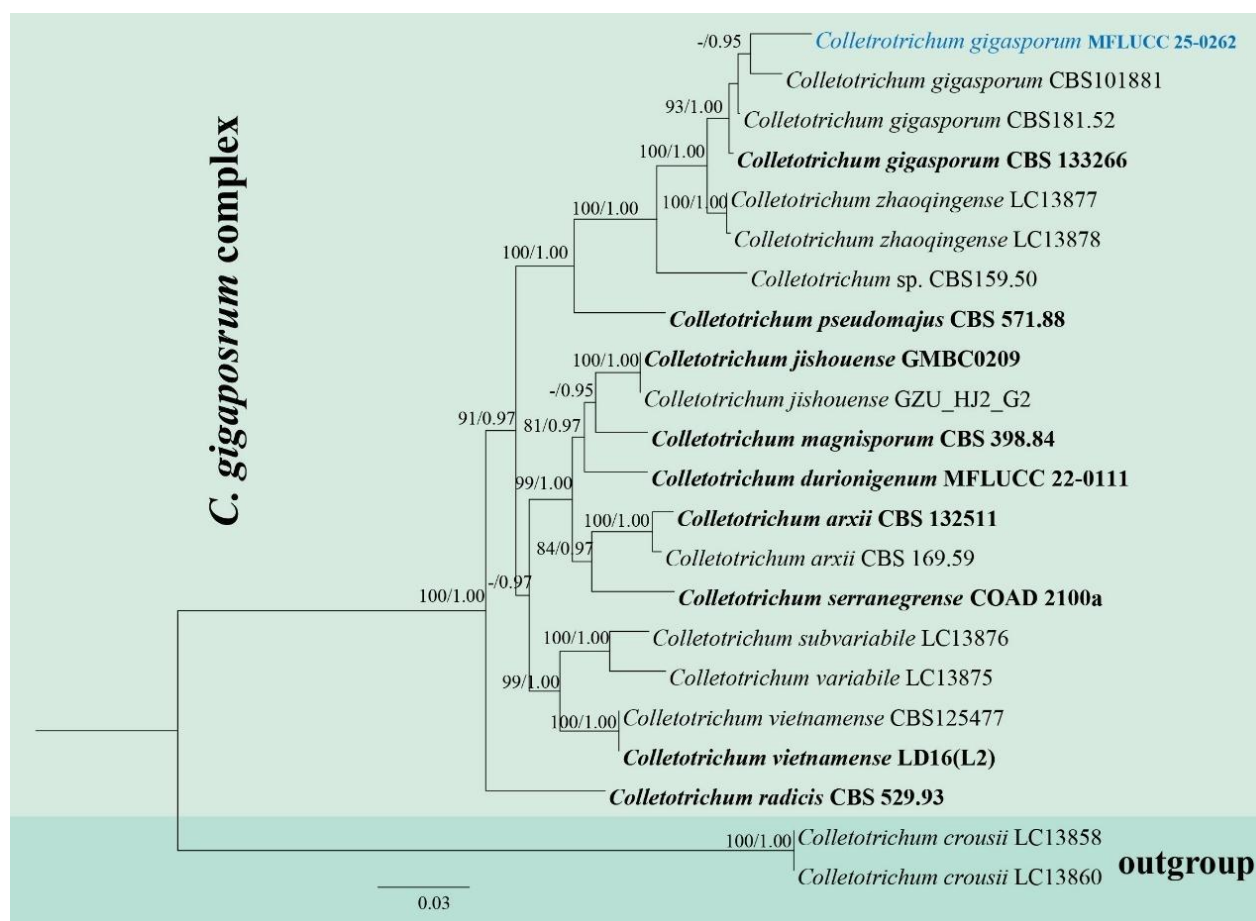


Figure 57 – Phylogram generated from ML analysis based on the combined dataset of ITS, *ACT*, *CHS*, *GAPDH*, and *tub2* sequence data of *Colletotrichum gigasporum* complex. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Colletotrichum crousii* (LC13858 and LC13860).

Colletotrichum gigasporum Rakotonir. & Munaut, Mycological Progress 12(2): 407 (2012) Fig. 59
Index Fungorum number: IF800175, Facesoffungi number: FoF10777

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* acervular, conidiophores and setae formed from the base. *Setae* 50–150 μm long, dark brown, aseptate, tapering at the apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 μm long, phialidic, hyaline, ovoid to cylindrical, smooth, unbranched. *Conidia* 17–22 $\times$ 7–9 μm ($\bar{x}$ = 20 $\times$ 8 μm , n = 20), hyaline, aseptate, verruculose, cylindrical, rounded at both ends.

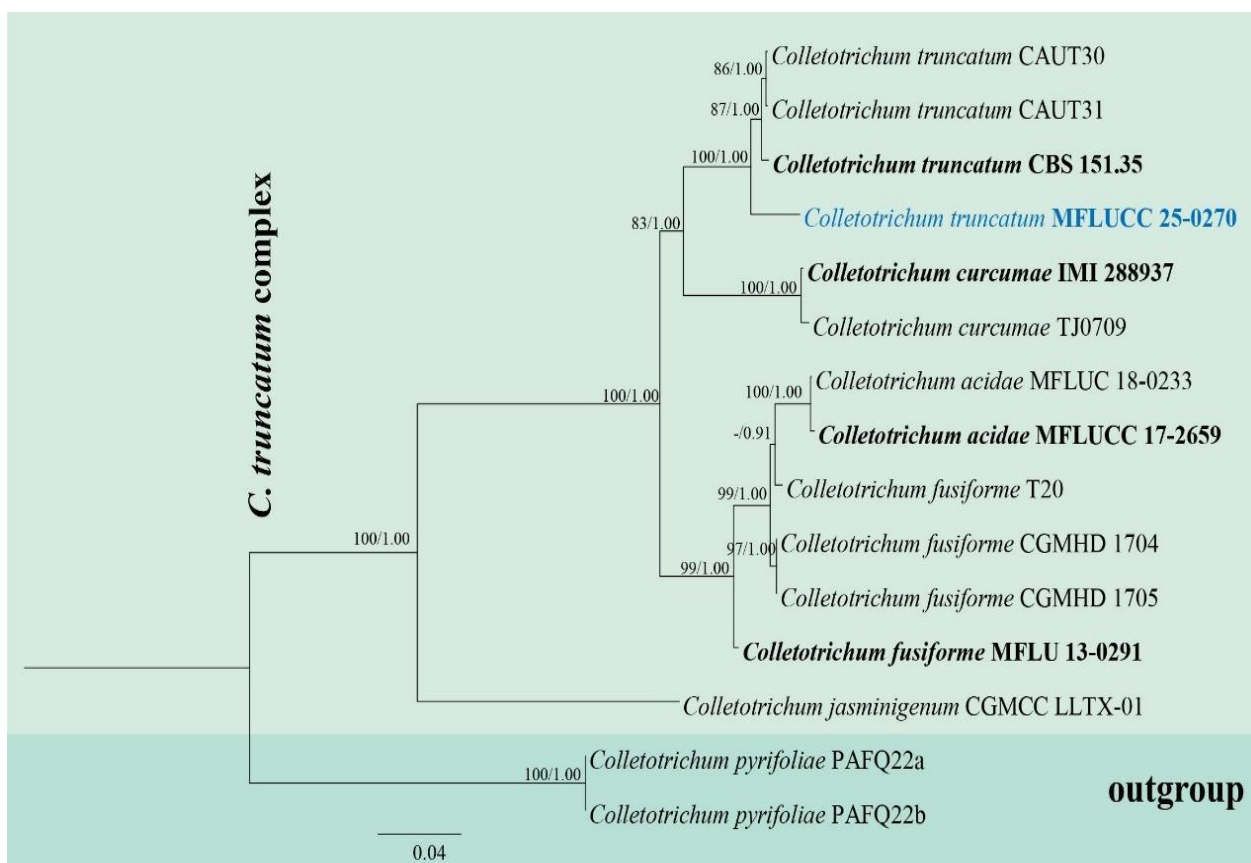


Figure 58 – Phylogram generated from maximum parsimony analysis of a combined dataset of ITS, *ACT*, *CHS*, *GAPDH*, and *tub2* sequence data of *Colletotrichum truncatum* complex. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Colletotrichum pyriforme* (PAFQ22a and PAFQ22b).

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 66 mm after 10 days at 27 °C, circular, entire, concentric, powdery, white to greenish grey, raised, opaque on the surface; circular, filamentous, concentric, white to pale yellow in reverse surface.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 3 August 2023, Zin Hnin Htet, CO-NL-8 (MFLU 25-0285, **a new host record**); living culture MFLUCC 25-0262.

GenBank – MFLUCC 25-0262: ITS = PV870628, *ACT* = PX120436, *GAPDH* = PX120434, *CHS* = PX120439.

Pre-screening for antibacterial activity – *Colletotrichum gigasporum* (MFLUCC 25-0262) showed a 14 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), but no inhibition zone against *E. coli*, and *S. aureus*.

Known host and distribution – *Centella asiatica* (Apiaceae) in Madagascar (Rakotoniriana et al. 2013); *Stylosanthes guianensis* (Fabaceae) in Mexico (Rakotoniriana et al. 2013); *Coffea arabica* (Rubiaceae) in Colombia (Rakotoniriana et al. 2013); *Diospyros kaki* (Ebenaceae) in Japan (Liu et al. 2014); *Solanum betaceum* (Solanaceae) in New Zealand (Liu et al. 2014); *Homo sapiens* (Homonidae) in Brazil (Liu et al. 2014); *Theobroma cacao* (Malvaceae) in Panama and East Africa (Liu et al. 2014); *Persea americana* (Lauraceae) in Sri Lanka (Liu et al. 2014); *Virola surinamensis* (Myristicaceae) in Panama (Liu et al. 2014); *Coffea* sp. (Rubiaceae) in Vietnam (Liu et al. 2014);

Trichilia tuberculata (Meliaceae) in Panama (Liu et al. 2014); *Acacia auriculiformis* (Fabaceae) in Thailand (Liu et al. 2014); *Musa* sp. (Musaceae) in Mexico (Liu et al. 2014); *Centella asiatica* (Apiaceae) in Madagascar (Liu et al. 2014); durian fruit (Malvaceae) in Thailand (Hunupolagama et al. 2015); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – In *Colletotrichum*, species delimitation based only on morphology is nearly impossible due to the overlapping morphological characters. Morphologically, our isolate (MFLUCC 25-0262) is similar to other *Colletotrichum* species in having dark brown, aseptate setae, phialidic, hyaline, ovoid to cylindrical, unbranched conidiogenous cells, and hyaline, aseptate, verruculose, cylindrical conidia (Jayawardena et al. 2021). Based on phylogenetic analysis (Fig 57), our strain (MFLUCC 25-0262) formed a sister clade to *Colletotrichum gigasporum* (CBS 101881) with 73% ML and 0.95 BYPP bootstrap support. Thus, based on morphology and phylogenetic analysis, we conclude our collection is *C. gigasporum* and it reports as a new host record on *Chromolaena odorata* (Asteraceae) in Thailand.

Colletotrichum truncatum (Schwein.) Andrus & W. D. Moore, Phytopathology 25: 121 (1935)

Fig. 60

Index Fungorum number: IF280780, Facesoffungi number: FoF03827

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* acervular, conidiophores and setae formed from the base. *Setae* 100–200 µm long, dark brown, aseptate, tapering at the apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 µm long, hyaline, cylindrical to ellipsoidal, smooth, unbranched. *Conidia* 20–28 × 2–4 µm ($\bar{x}$ = 25 × 3 µm, n = 20), hyaline, aseptate, verruculose, falcate, tapering at both ends.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 46 mm after 10 days at 27 °C, irregular, filamentous, concentric, scalloped, white to pale yellow, flat, opaque in the middle, transparent at the margin; irregular, filamentous, concentric, yellow in reverse surface.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet, BP-NL-9 (MFLU25-0286, **a new host record**); living culture MFLUCC 25-0270.

GenBank – MFLUCC 25-0270: ITS = PV870629, *ACT* = PX120437, *GAPDH* = PX120435, *CHS* = PX120440.

Pre-screening for antibacterial activity – *Colletotrichum truncatum* (MFLUCC 25-0270) showed a 19 mm inhibition zone against *B. subtilis*, a 12 mm inhibition zone against *E. coli*, and a 18 mm inhibition zone against *S. aureus*.

Known host and distribution – *Colletotrichum truncatum* has a cosmopolitan distribution and on different host species (Talhinhas et al. 2021, Wang et al. 2024); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – Based on the phylogenetic analysis of *Colletotrichum truncatum* species complex, the strain (MFLUCC 25-0270) formed a separate branch from the clade of *C. truncatum* (CAUT30, CAUT31, CBS 151.35), with 100% ML and 1.00 BYPP bootstrap support (Fig. 58). Morphologically, the collection is similar to *C. truncatum* (MFLUCC 22-0110) in having hyaline, aseptate, falcate conidia but differs in having shorter conidiogenous cells (3–5 µm vs. 18–30 µm) and conidia size (20–28 × 2–4 µm vs. 27.5–31 × 3.3–4.4 µm) (Armand et al. 2023). Thus, based on morphology and phylogenetic analysis, we conclude our collection is *C. truncatum* and it reports a new host record on *Bidens pilosa* (Asteraceae) in northern Thailand.



Figure 59 – *Colletotrichum gigasporum* (MFLU 25-0285, a new host record). a, b Appearance of conidiomata acervular on host substrate. c Acervuli. d Basal part of a setae. e Conidiogenous cells and developing conidia. f–i Conidia. j A germinating conidium. k Culture on MEA. Scale bars: a = 1 mm, b = 500 µm, c = 100 µm, d = 20 µm, e, f, g, h, i, j = 10 µm.

Hypocreales Lindau

Nectriaceae Tul. & C. Tul

Nectriaceae is a family that includes fungal species with uniloculate, white, yellow, orange-red, or purple ascomata, typified by *Nectria* (Fr.). The asexual morph of Nectriaceae species has phialidic conidiogenesis, which produces amerosporous to phragmosporous conidia (Lombard et al. 2015). Nectriaceae species are found as saprobes, pathogens, fungicolous or entopathogenic

(Lombard et al. 2015, Torbati et al. 2021, Zheng et al. 2024). To date, there are 83 genera accepted in Nectriaceae (Hyde et al. 2024).

***Fusarium* Link**

Fusarium was introduced by Link (1809), and typified by *F. sambucinum* Fuckel (= *Fusarium roseum* Link). *Fusarium* species are the most common and widespread pathogens in the world involved in both plant and human diseases (Nelson et al. 1981, Ma et al. 2013, Wang et al. 2024). They are also found as endophytic and saprobic fungi on a wide range of habitats and hosts (Mandeel 2006, Summerell & Leslie 2011, Navarro et al. 2014, Rashmi et al. 2019). According to Hyde et al. (2024), there are around 400 species in this genus. Molecular markers available for *Fusarium* are ITS, *tef1- α* , *rpb2*, *tub2*, and *CaM* (Han et al. 2023). Following the species concept of Crous et al. (2021), we conducted phylogenetic analysis and introduce two new species, *F. bidenticola*, and *F. chromolaenae* with *F. hainanense* as a new record in the *Fusarium incarnatum-equiseti* complex, based on the combined dataset of ITS, *tef1- α* , *rpb2*, *tub2*, and *CaM* sequence data (Fig. 61).



Figure 60 – *Colletotrichum truncatum* (MFLU 25-0286, a new host record). a, b Appearance of conidiomata acervular on host substrate. c, d Acervuli. e Setae basal parts and conidiogenous cells

developing conidia. f–h Conidia. i A germinating conidium. j Culture on MEA. Scale bars: a = 1 mm, b = 500 μ m, c, d = 100 μ m, e, f, g, h, i = 10 μ m.

Fusarium bidentis Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 62

Index Fungorum number: IF904378, Facesoffungi number: FoF18046

Etymology – Name reflects the host plant *Bidens pilosa*, from which this species was isolated.

Holotype – MFLU 25-0290

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* superficial, scattered, white to pale yellow. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* phialidic, monophialides, hyaline, obpyriform to lageniform, smooth, thin-walled. *Macroconidia* 31–45 $\times$ 3–4 μ m ($\bar{x}$ = 38.4 $\times$ 3.6 μ m, n = 20), hyaline, aseptate, filiform to falcate, tapering at both ends, with curved apical cells, rough surface with guttules. *Chlamydospores* hyaline, globose, and form in groups. *Microconidia* not observed.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 80 mm after 10 days at 27 °C, irregular, filamentous, white to pale yellow, flat, opaque on the surface; irregular, filamentous, pale yellow in reverse surface.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 May 2023, Zin Hnin Htet, BP-HMS-15 (MFLU 25-0290, **holotype**); ex-type MFLUCC 25-0258.

GenBank – MFLUCC 25-0258: ITS = PV870630, *tef1- α* = PX282661, *rpb2* = PX120468.

Pre-screening for antibacterial activity – *Fusarium bidentis* (MFLUCC 25-0258) showed a 13 mm inhibition against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), a 15 mm inhibition against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm), and a 17 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm).

Known host and distribution – dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – Based on the phylogenetic analysis of *F. incarnatum-equiseti* species complex, the strain (MFLUCC 25-0258) formed a clade sister to *F. mianyangense* (LC15879) with 98% ML and 1.00 BYPP bootstrap support (Fig. 61). *Fusarium mianyangense* (LC15879) has hyaline, falcate, smooth- and thin-walled, 3(–5)-septate conidia (Han et al. 2023), while our collection has hyaline, filiform to falcate, aseptate and longer conidia than *F. mianyangense* (31–45 $\times$ 3–4 μ m vs. 29.5–36.6 $\times$ 3–4.9 μ m). A comparison of base pair difference reveals 0% (0/524) in *tef1- α* region and 1.6% (11/696) in *rpb2* region. Therefore, we introduce our collection as a new species mainly based on multi-gene phylogenetic analyses and morphological differences with *F. mianyangense* (LC15879) (Han et al. 2023).

Fusarium chromolaenae Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 63

Index Fungorum number: IF904379, Facesoffungi number: FoF18047

Etymology – Name reflects the host plant *Chromolaena odorata*, from which this species was isolated.

Holotype – MFLU 25-0288

Saprobic on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 205–350 $\times$ 240–300 ($\bar{x}$ = 290 $\times$ 288 μ m, n = 5), superficial, globose to subglobose, dark blue to black on the host surface, with or without ostiole. *Peridium* 20–40 μ m wide, comprising 3–4 layered of dark blue cells

of *textura angularis*. *Asci* 95–120 × 11–15 ($\bar{x}$ = 107 × 14 μ m, n = 20), 8-spored, unitunicate, hyaline, cylindric-clavate, with a short pedicel. *Ascospores* 25–35(–40) × 5–8 μ m ($\bar{x}$ = 30 × 6 μ m, n = 20), hyaline, multi-seriate, overlapping in the ascus, lanceolate, broader at the base, aseptate and granular appearance when young and becoming 3–4 septate, straight or flexuous, without appendages. **Asexual morph:** Undetermined.

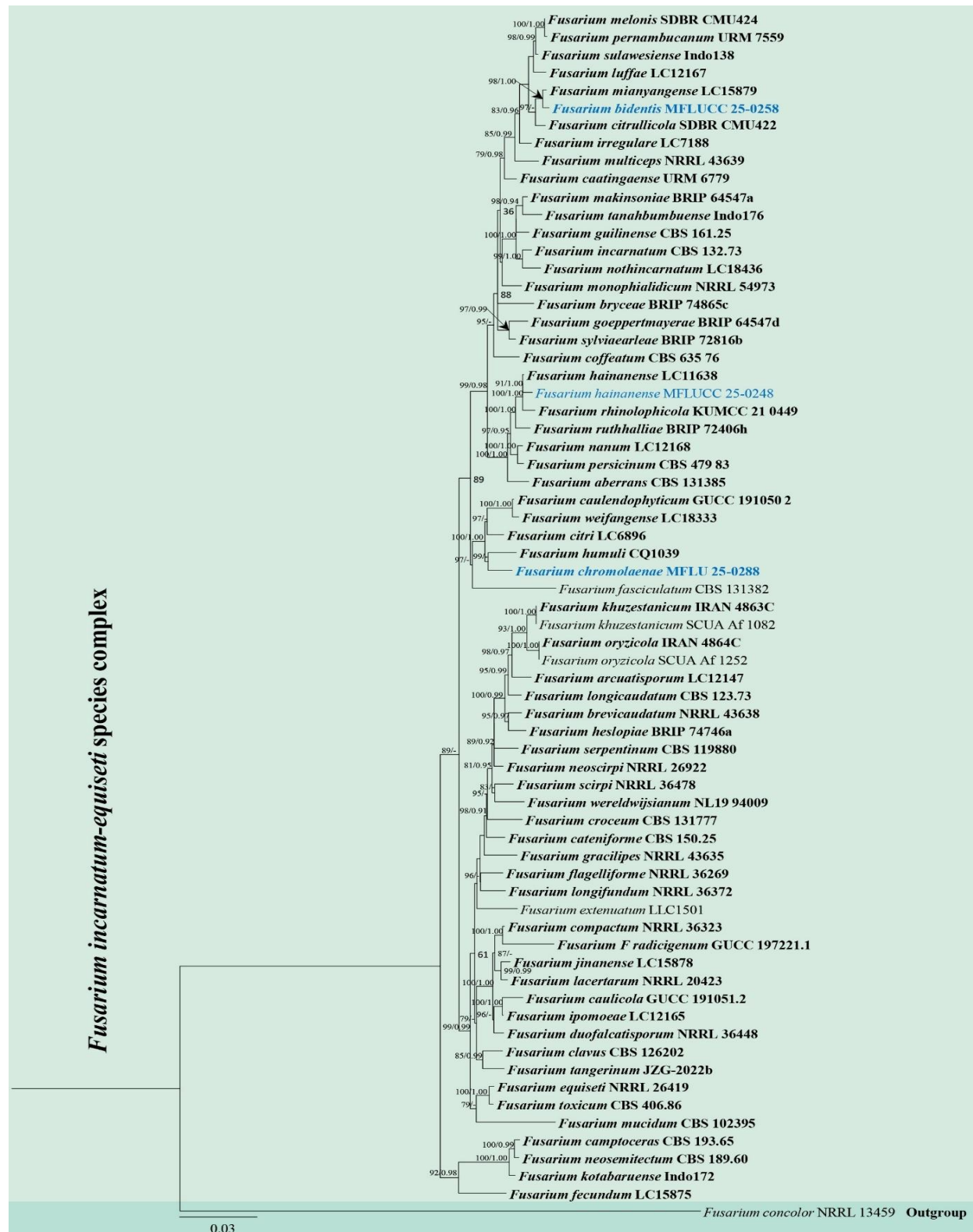


Figure 61 – Phylogram generated from ML analysis of a combined dataset of ITS, *tef1- α* , *rpb2*, *tub2*, and *CaM* sequence data of *Fusarium incarnatum-equiseti* complex. Bootstrap support values for ML

$\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Fusarium concolor* (NRRL 13459).

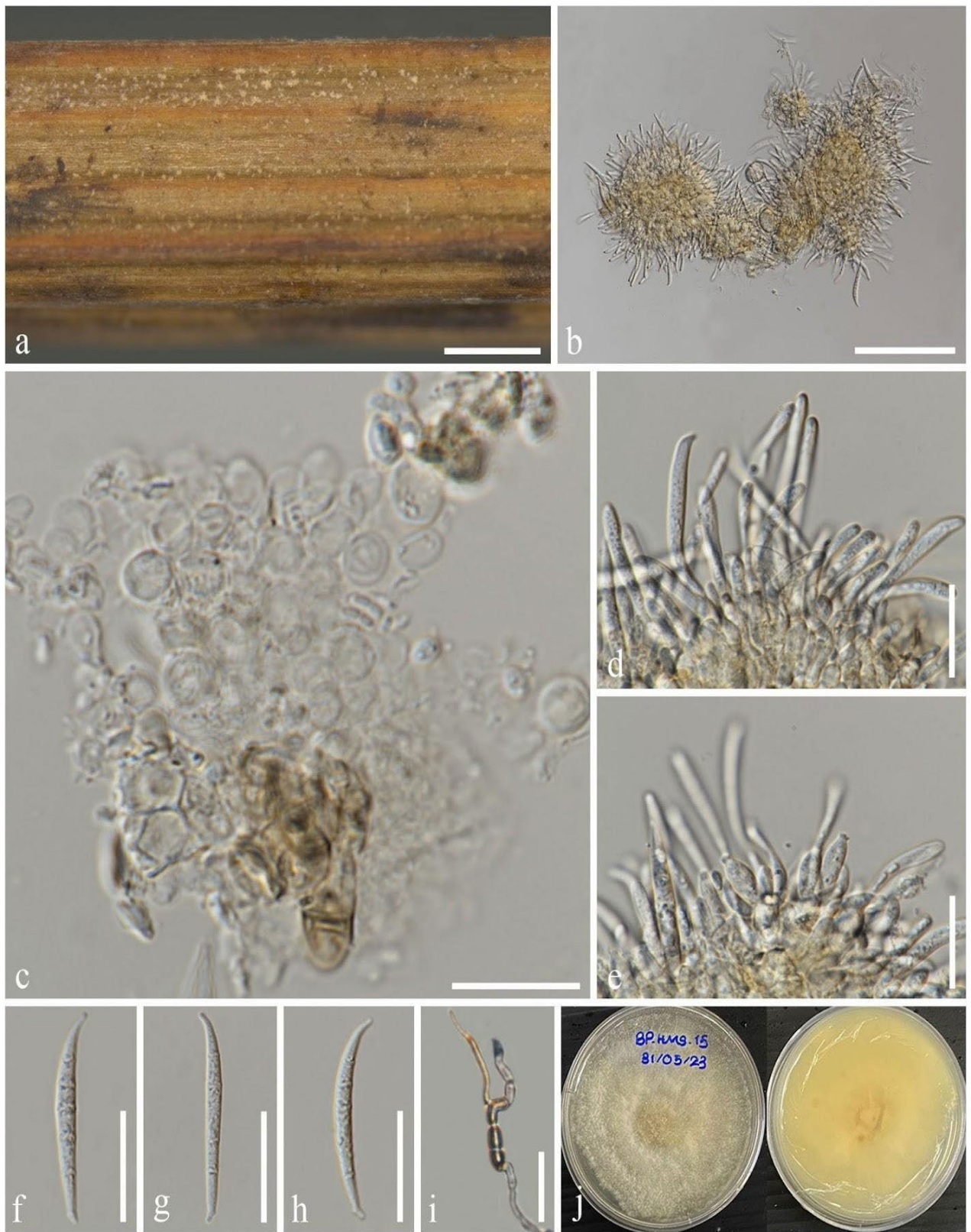


Figure 62 – *Fusarium bidentis* (MFLU 25-0290, holotype). a, b Colonies on host substrate. c–e Conidiophores and conidiogenous cells. f–h Conidia. i A germinating conidium. j Culture on MEA. Scale bars: a = 1 mm, b = 100 µm, c = 30 µm, d, e, f, g, h, i = 20 µm.

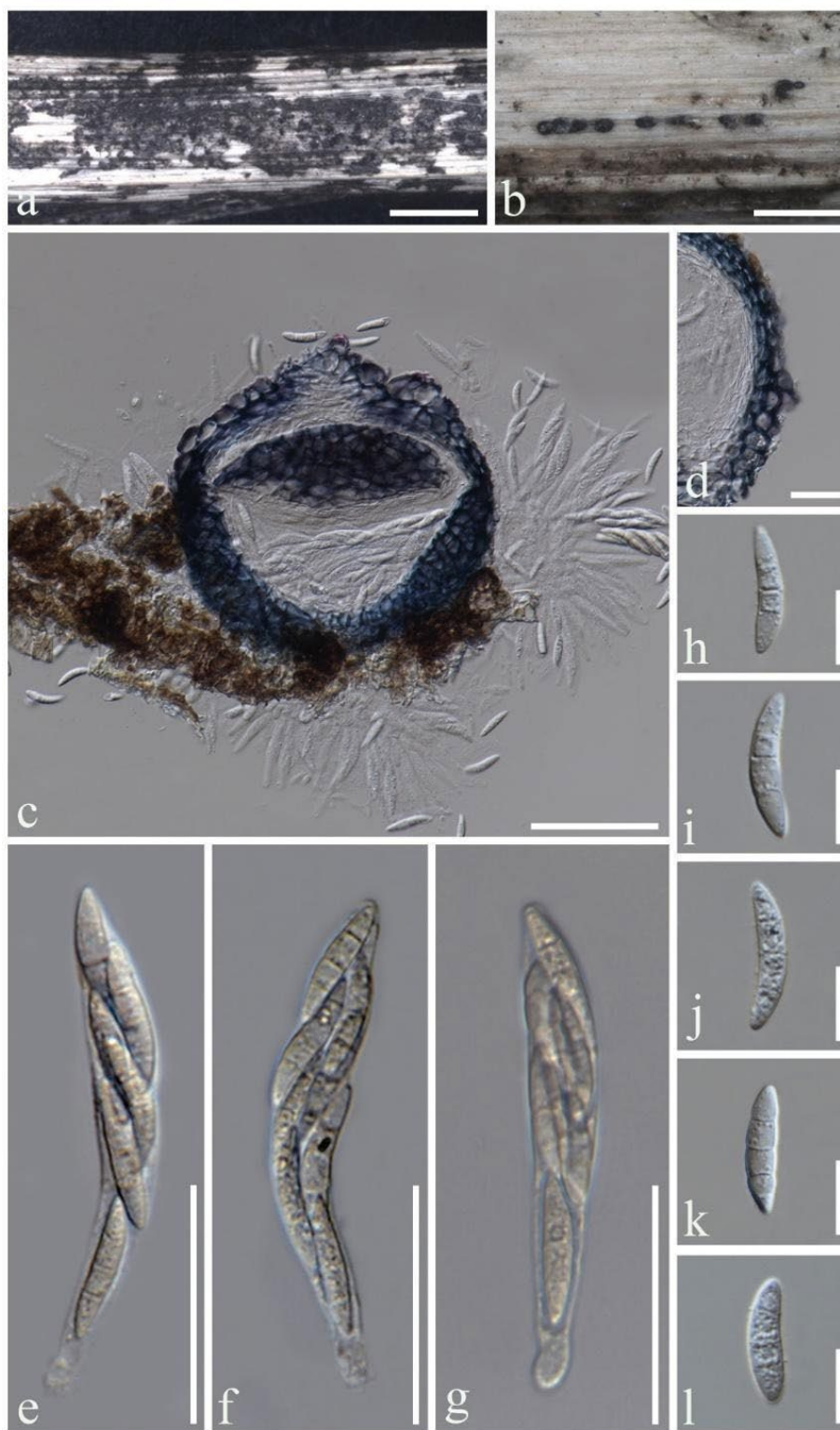


Figure 63 – *Fusarium chromolaenae* (MFLU 25-0288, a new host record). a, b Appearance of ascomata on host substrate. c A Section through an ascoma. d Peridium. e–g Asci. h–l Ascospores. Scale bars: a, b = 500 μm, c = 100 μm, d = 20 μm, e, f, g = 40 μm, h, i, j, k, l = 10 μm.

Material examined – Thailand, Chiang Mai Province, Doi Saket District, on dead stems of *Chromolaena odorata* (Asteraceae), 6 July 2022, Santhiti Vadthananarat, SVC4 (MFLU 25-0288, **holotype**).

GenBank – MFLU 25-0288: ITS = PV870631, *tef1-α* = PX282662, *rpb2* = PX120469.

Known host and distribution – dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

Notes – Based on phylogenetic analysis (Fig. 61), the collection (MFLU 25-0288) clustered sister to *Fusarium humuli* (CQ1039) with 99% ML and 0.83 BYPP bootstrap support. *Fusarium humuli* (CQ1039) was found as an asexual morph in nature, with falcate, slender, straight to slightly curved, 3–5-septate conidia (Wang et al. 2019). Our collection is found as a sexual morph in nature; therefore, we could not compare the morphology. A comparison of base pair differences of *tef1-α* and *rpb2* between our collection and *Fusarium humuli* (CQ1039) reveals 3.5% (23/654) and 1.4% (13/875) differences, respectively. Therefore, *Fusarium chromolaenae* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand based on multi-gene phylogeny.

Fusarium hainanense M.M. Wang, Qian Chen & L. Cai, Persoonia 43: 82 (2019)

Fig. 64

Index Fungorum number: IF829536, Facesoffungi number: FoF14335

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. Colonies superficial, scattered, white to pale yellow. Conidiophores branched, irregularly branched, bearing terminal or lateral phialides, often reduced to single phialides. Conidiogenous cells phialidic, mono- and polyphialidic, hyaline, subulate to subcylindrical. Macroconidia 40–55(–69) × 5–8 μm ($\bar{x}$ = 52 × 7 μm, n = 20), hyaline, 5–8-septate, falcate, tapering at both ends, or broader at the middle or base, rough surface. Microconidia not observed. Chlamydospores not observed.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 48 mm after 10 days at 27 °C, irregular, filamentous, concentric, yellow in the middle, white at the margin, raised, opaque on the surface; irregular, filamentous, cracked, pale yellow in reverse surface.

Material examined – Thailand, Chiang Rai Province, Phan District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet, BP-DP-15 (MFLU 25-0289, **a new host record**); living culture MFLUCC 25-0248.

GenBank – MFLUCC 25-0248: ITS = PV870632, *tef1-α* = PX282663, *rpb2* = PX120470.

Pre-screening for antibacterial activity – *Fusarium hainanense* (MFLUCC 25-0248) showed a 19 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), a 12 mm inhibition zone against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm) and a 18 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm).

Known host and distribution – stem of *Oryza* sp. (Poaceae) in China (Wang et al. 2019); leaf of *Musa nana* (Musaceae) in China (Wang et al. 2019); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analysis of the *F. incarnatum-equiseti* species complex, our strain (MFLUCC 25-0248) clustered sister to *F. hainanense* (LC11638) with 91 % ML and 1.00 BYPP bootstrap support (Fig. 61). Previously, the isolates of *F. hainanense* were found as endophytes from different hosts in China (Wang et al. 2019). *Fusarium hainanense* (LC11638) has hyaline, falcate, fusiform, straight to slightly curved, macroconidia with 1–3 septa (18–33 × 2–5 μm), while our collection is found as saprobes in nature and has hyaline, 5–8-septate, falcate, conidia tapering at both ends or broader at the middle or base, with a rough surface (40–55(–69) × 5–8 μm). When we compare the base pair differences of ITS and *tef1-α*, there are no significant base pair differences between the strain (MFLUCC 25-0248) and *F. hainanense* (LC11638). Therefore, our collection is reported as a new host record of *F. hainanense* on *Bidens pilosa* (Asteraceae) and a new geographical record in Thailand.

Sarocladiaceae L. Lombard

Sarocladiaceae was introduced by Crous et al. (2018) to accommodate two genera, *Parasarocladium* and *Sarocladium*. Sarocladiaceae is characterized by hyaline to pale brown vegetative hyphae, erect, arising directly from vegetative hyphae, simple or branched, straight to flexuous conidiophores, phialidic conidiogenous cells, and hyaline to subhyaline, ellipsoidal to

fusiform, smooth-walled, aseptate conidia (Crous et al. 2018, Phukhamsakda et al. 2020, Hou et al. 2023). To date, there are four genera accepted in Hyde et al. (2024), viz., *Chlamydocillium*, *Parasarocladium*, *Polyphialocladium* and *Sarocladium*.

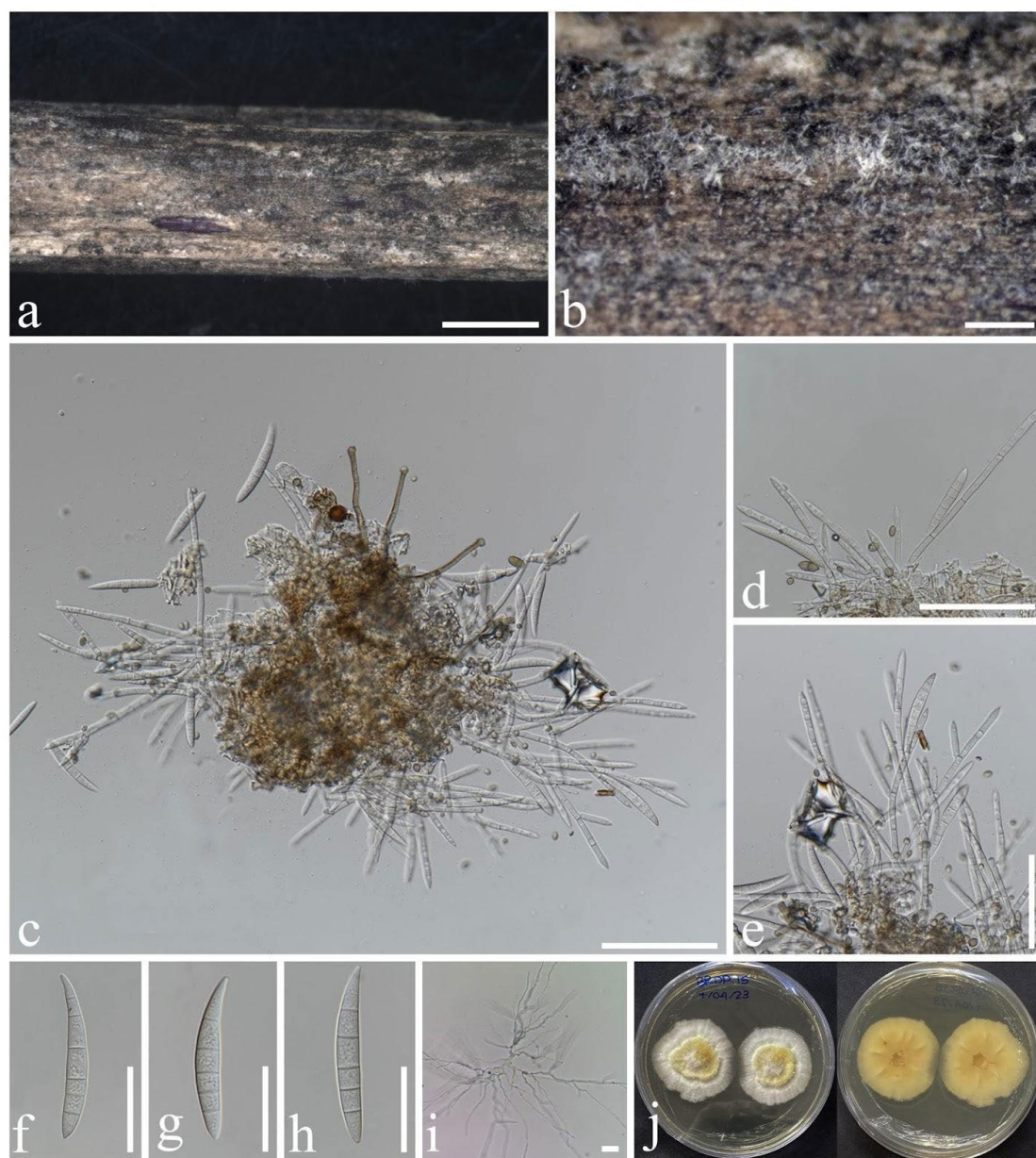


Figure 64 – *Fusarium hainanense* (MFLU 25-0289, a new host record and a new geographical record). a, b Colonies on host substrate. c–e Conidiophores and conidiogenous cells. f–h Conidia. i A germinating conidium. j Culture on MEA. Scale bars: a = 1 mm, b = 500 μ m, c, d, e = 100 μ m, f, g, h = 30 μ m, i = 10 μ m.

Sarocladium W. Gams & D. Hawksw.

The taxonomic position of *Sarocladium* species was confirmed by Crous et al. (2018) and placed in Sarocladiaceae with the type species, *S. oryzae*. *Sarocladium* is characterized by the presence of elongate phialides forming on vegetative hyphae or conidiophores with hyaline to subhyaline, aseptate conidia (Crous et al. 2018, Hou et al. 2023). *Sarocladium* species are reported as endophytes, pathogens, saprobes (Giraldo et al. 2015, Yeh et al. 2014, Anjos et al. 2020, Phukhamsakda et al. 2020, Unartngam et al. 2024, Ochieng et al. 2024). Currently, there are 30 species in this genus (Hyde et al. 2024), while 36 epithets are listed in the Index Fungorum (2025).

In this study, *Sarocladium bidentis* is introduced as a new species based on ITS, LSU, and *ACT* sequence data (Fig. 65).

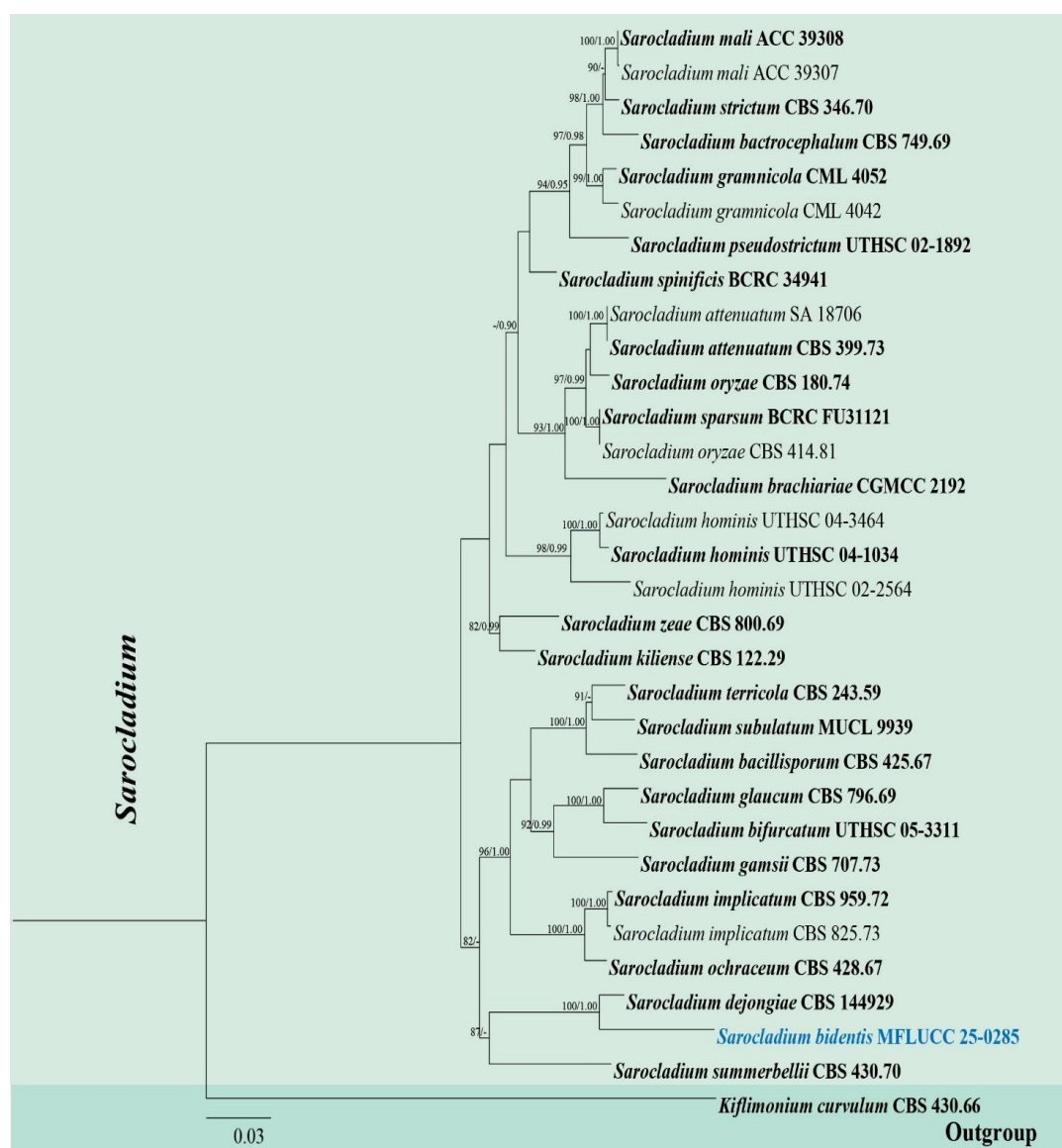


Figure 65 – Phylogram generated from ML analysis of a combined dataset of ITS, LSU, and *ACT* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Kifimonium curvulum* (CBS 430.66).

Sarocladium bidentis Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 66

Index Fungorum number: IF904380, Facesoffungi number: FoF18048

Etymology – Name reflects the host plant *Bidens pilosa*, from which this species was isolated.

Holotype – MFLU 25-0290

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:**

Hyphomycetous. *Colonies* effuse on the natural substrate, scattered, hairy, pale brown. *Mycelium* partially immersed, composed of pale brown hyphae. *Conidiophores* 250–300 × 5–7 µm ($\bar{x}$ = 265 × 6 µm, n = 10), macronematous, synnematous, tree-like, parallel and unbranched in the stipe, yellow to pale brown, gregarious, or scattered, erect, straight or slightly flexuous. *Conidiogenous cells* 3–5 × 3–4 µm ($\bar{x}$ = 4 × 3.4 µm, n = 10), polyphialidic, integrated or terminal, pale yellow, cylindrical, straight to slightly curved, slightly narrowing at apex, acropetally proliferating, hyaline to pale brown.

verrucose. *Conidia* $5\text{--}7 \times 2\text{--}5 \text{ }\mu\text{m}$ ($\bar{x} = 5.6 \times 2.2 \text{ }\mu\text{m}$, $n = 20$), unicellular, aseptate, cylindrical, rounded at both ends, thick-walled, hyaline to pale yellow, verrucose.

Culture characteristics – *Conidia* germinating on MEA within 24 hours, reaching 23 mm after 10 days at 27 °C, irregular, entire, white to pale orange, flat, transparent on the surface; irregular, entire, pale orange on reverse surface.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 May 2023, Zin Hnin Htet, BP-HMS-1 (MFLU 25-0290, **holotype**); ex-type MFLUCC 25-0285.

GenBank – MFLUCC 25-0285: LSU = PV992415, ITS = PV870633, *tub2* = PX255054, *ACT* = PX120438.

Pre-screening for antibacterial activity – *Sarocladium bidentis* (MFLUCC 25-0285) showed a 20 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), a 14 mm inhibition zone against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm), and a 16 mm inhibition zone against *S. aureus*, observable as a complete inhibition, when compared to positive control (25 mm).

Known host and distribution – dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analysis (Fig. 65), the strain (MFLUCC 25-0285) clustered with *Sarocladium dejongiae* (CBS 144929) with 100% ML and 1.00 BYPP bootstrap support. Morphologically, our collection differs from *S. dejongiae* (CBS 144929) in having macronematous, synnematus, tree-like conidiophores ($250\text{--}300 \times 5\text{--}7 \text{ }\mu\text{m}$), polyphialidic, integrated or terminal, pale yellow, cylindrical, straight to slightly curved conidiogenous cells ($3\text{--}5 \times 3\text{--}4 \text{ }\mu\text{m}$), unicellular, aseptate, cylindrical conidia ($5\text{--}7 \times 2\text{--}5 \text{ }\mu\text{m}$), whereas *S. dejongiae* has $1\text{--}2.5 \text{ }\mu\text{m}$ wide, septate, hyaline, vegetative hyphae, conidiophores (up to $35 \text{ }\mu\text{m}$ long) arising directly from vegetative hyphae or from ropes of hyphae, simple or rarely branched, subcylindrical, phialidic conidiogenous cells ($17\text{--}24 \times 1\text{--}2 \text{ }\mu\text{m}$) and aseptate, cylindrical, ellipsoidal, ovoid to irregular conidia ($3\text{--}5 \times 1\text{--}2 \text{ }\mu\text{m}$) formed in slimy heads. A comparison of base pair differences between our collection and *S. dejongiae* (CBS 144929) reveals ITS 6.7% (39/578), and LSU 1.49% (13/870) (without gaps), respectively. Therefore, *Sarocladium bidentis* is introduced as a new species on *Bidens pilosa* (Asteraceae) in northern Thailand.

Stachybotryaceae L. Lombard & Crous

Stachybotryaceae was introduced by Crous et al. (2014) to accommodate three genera, viz., *Myrothecium*, *Peethambara* and *Stachybotrys* as the type genus. Stachybotryaceae is characterized by mononematous or sporodochial to synnematus conidiomata, phialidic conidiogenous cells, 0–1-septate, hyaline to olive green conidia forming black slimy or dry masses on the host surface (Lombard et al. 2016). Stachybotryaceae species can be found as endophytes, saprobes and pathogens on a variety of host substrates (Lombard et al. 2016, Li et al. 2020, Yasanthika et al. 2020, Samarakoon et al. 2021, Yeh et al. 2023). Currently, there are 41 genera in Stachybotryaceae (Hyde et al. 2024).

Albifimbria L. Lombard & Crous

Albifimbria was introduced by Lombard et al. (2016) based on LSU, ITS, *rpb2*, *tef1- α* , *tub2* and CaM sequence data, providing a distant clade to the *Myrothecium* in Stachybotryaceae. *Albifimbria* is characterized by sporodochial, discoid conidiomata surrounded by a white setose fringe, hyaline to olive green conidiogenous cells, and hyaline to olive green, broadly fusiform conidia (Lombard et al. 2016, Li et al. 2020). Currently, there are four species listed in *Albifimbria*, viz., *A. lateralis*, *A. terrestris*, *A. verrucaria*, *A. viridis* (Index Fungorum 2025). In our study, *Albifimbria bidentis* is introduced as a new species based on combined ITS, *rpb2*, and *tub2* sequence data (Fig. 67).

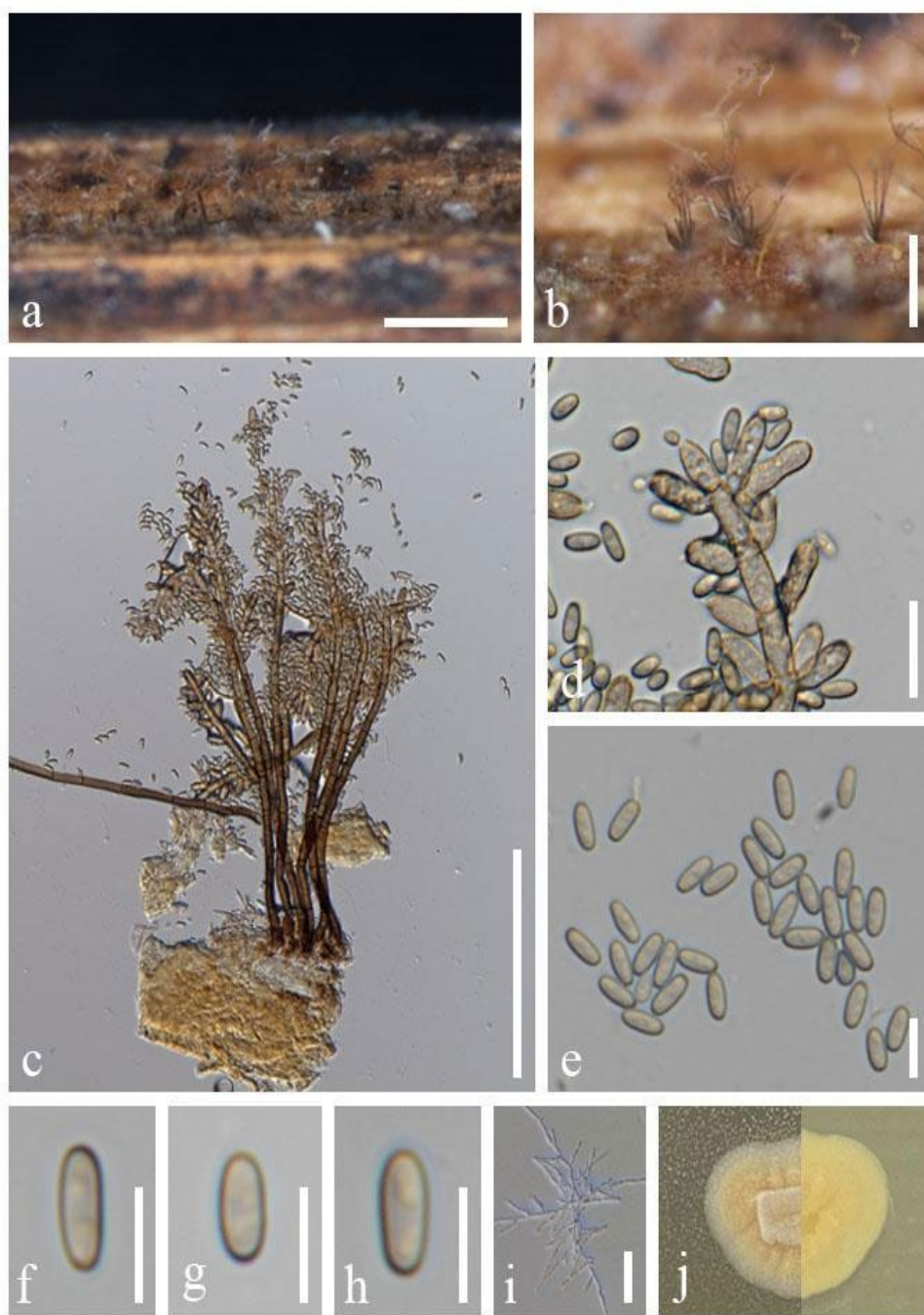


Figure 66 – *Sarocladium bidentis* (MFLU 25-0290, holotype). a, b Appearance of colonies on host substrate. c, d Conidiophores and conidiogenous cells. e–h Conidia. i A germinating conidium. j Culture on MEA. Scale bars: a = 1 mm, b = 200 μ m, c = 100 μ m, d = 10 μ m, e, f, g, h = 5 μ m, i = 10 μ m

Albifimbria bidentis Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, **sp. nov.**

Fig. 68

Index Fungorum number: IF904381, Faces of fungi number: FoF18049

Etymology – Name reflects the host plant *Bidens pilosa*, from which this species was isolated.

Holotype – MFLU 25-0291

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph:** Undetermined. **Asexual morph:** *Sporodochia* superficial, stromatic, discoid, gregarious, irregular, with a dark green conidia mass surrounded by a white setose fringe. *Conidiophores* 30–50 $\times$ 2–3 ($\bar{x}$ = 46 $\times$ 2.5 μ m, n=20) arising from the basal stroma, branched, hyaline to olive green, smooth. *Conidiogenous cells* 10–15 $\times$ 1–3 μ m ($\bar{x}$ = 13 $\times$ 2 μ m, n=30) phialidic, cylindrical, hyaline to olive green, smooth. *Conidia* 7–8 $\times$ 2–3

µm ($\bar{x} = 7.7 \times 2.8$ µm, n=20), unicellular, aseptate, smooth, hyaline to olive green, broadly fusiform, tapering at both ends, smooth.

Culture characteristics – Conidia germinating on MEA within 24 hours, reaching 42 mm after 10 days at 27 °C, circular, filamentous, white, appearing green droplets in the middle, raised, opaque, powdery on the surface; circular, filamentous, pale yellow in reverse surface.

Material examined – Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet, BP-NL-6 (MFLU 25-0291, **holotype**); ex-type MFLUCC 25-0268.

GenBank – MFLUCC 25-0268: ITS = PV870634, *tef1*-α = PX282664, *tub2* = PX246148, *rpb2* = PX120471.

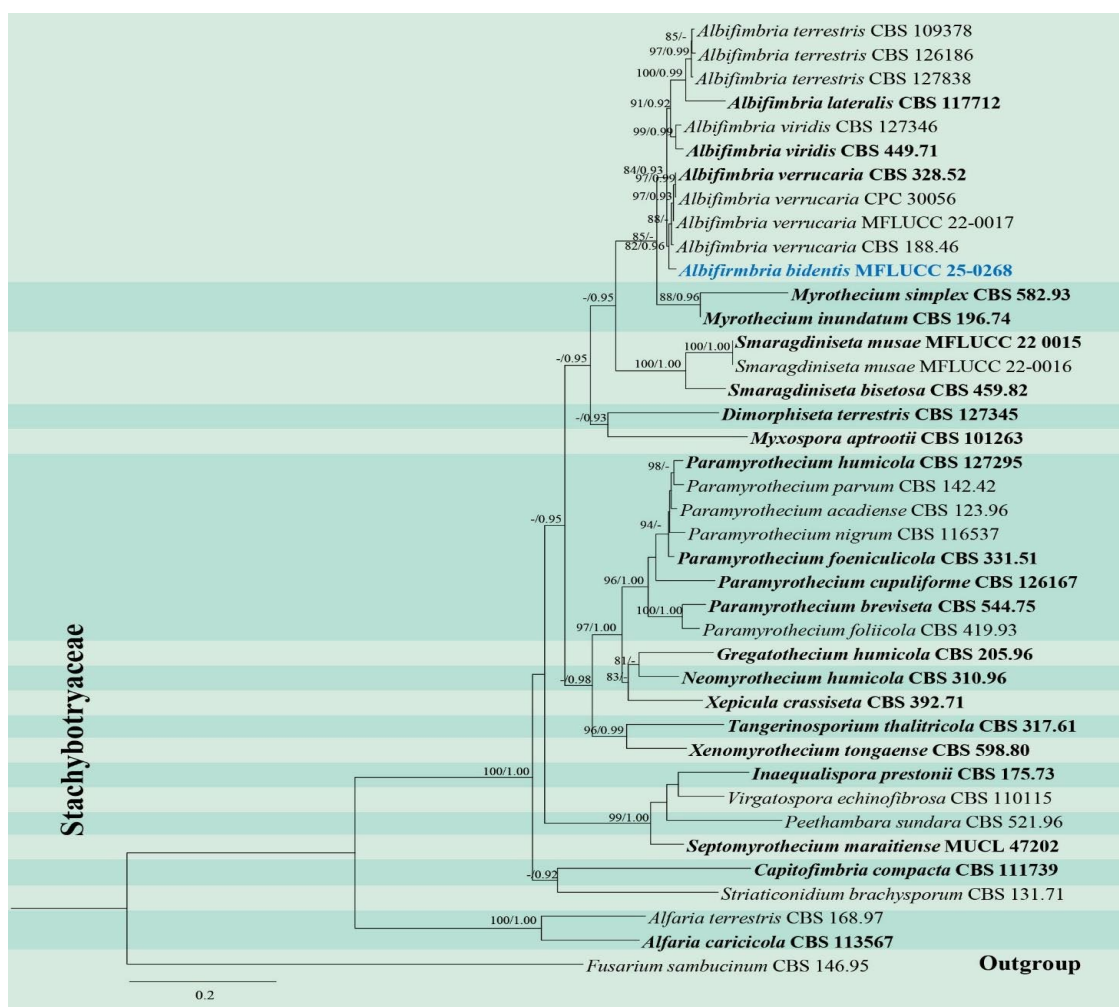


Figure 67 – Phylogram generated from ML analysis of a combined dataset of ITS, *rpb2*, and *tub2* sequence data. Bootstrap support values for ML $\geq 75\%$ and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Fusarium sambucinum* (CBS 146.95).

Pre-screening for antibacterial activity – *Albifimbria bidentis* (MFLUCC 25-0268) showed a 13 mm inhibition zone against *B. subtilis*, observable as a partial inhibition, when compared to positive control (15 mm), a 11 mm inhibition zone against *E. coli*, observable as a complete inhibition, when compared to positive control (30 mm), but showed no inhibition against *S. aureus*.

Known host and distribution – dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

Notes – In phylogenetic analysis (Fig. 67), the strain (MFLUCC 25-0268) formed a separate branch from *Albifimbria verrucaria* isolates (CBS 328.52, CPC 30056, CBS 188.46, and MFLUCC

22-0017) with 82% ML and 0.96 BYPP bootstrap support. The strain (MFLUCC 25-0268) is morphologically similar to *A. verrucaria* (CBS. 328.52 and MFLUCC 22-0017) in having sporodochial, superficial, stromatic, discoid conidiomata, with broadly fusiform, aseptate conidia (Lombard et al. 2016, Samarakoon et al. 2022), but our strain differs from *A. verrucaria* (MFLUCC 22-0017) in having unbranched conidiophores, hyaline to olive green, smooth, shorter conidiogenous cells ($10\text{--}15 \times 1\text{--}3 \mu\text{m}$ vs. $30\text{--}48 \times 1\text{--}2 \mu\text{m}$), hyaline to olive green conidia (Samarakoon et al. 2022). A comparison of base pair differences between these two species reveals *rpb2* 2.4% (9/372), without gaps. Therefore, *A. bidentis* is introduced as a new species found on *Bidens pilosa* (Asteraceae) in northern Thailand

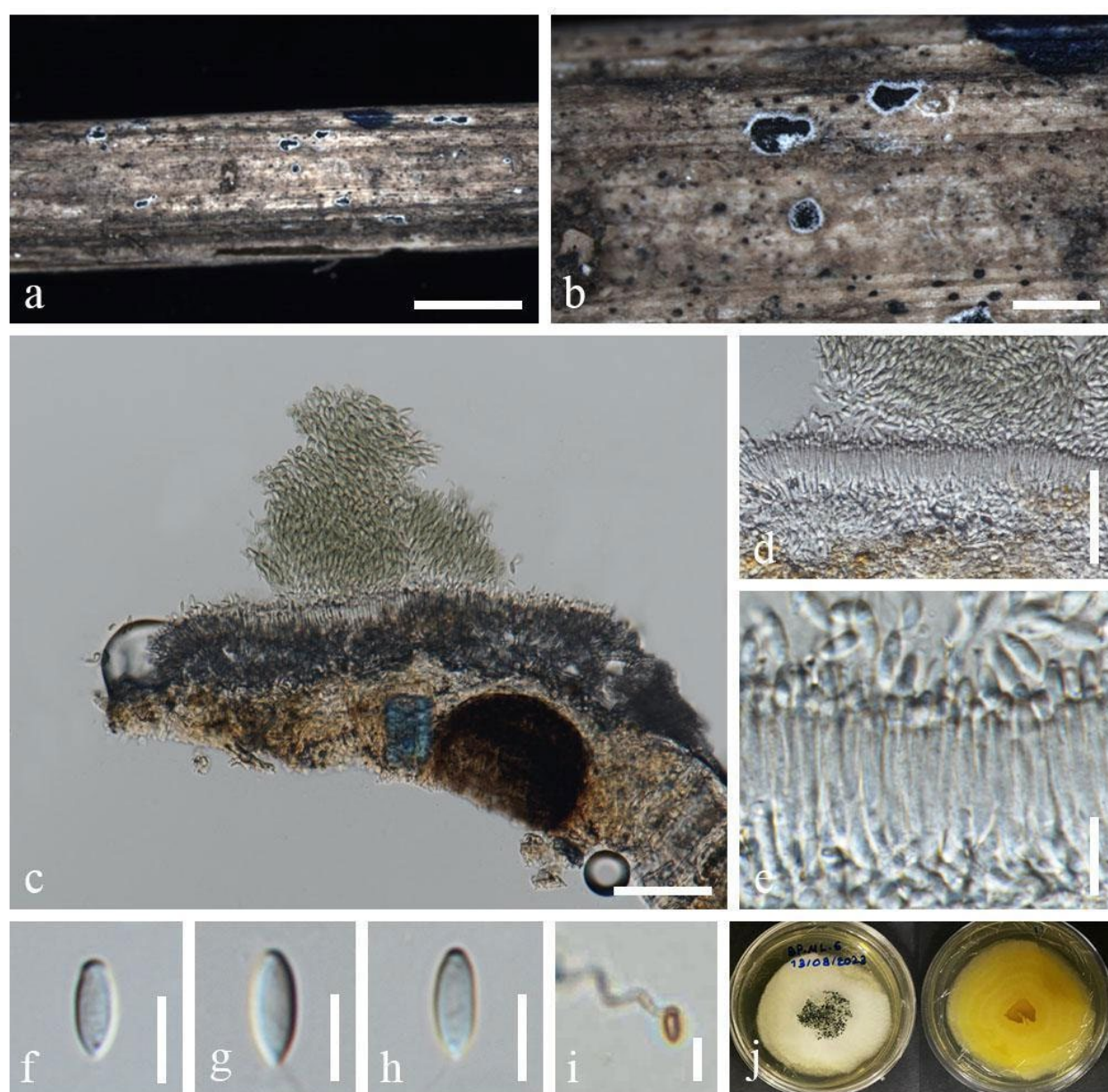


Figure 68 – *Albifimbria bidentis* (MFLU 25-0291, holotype) a, b Appearance of sporodochia on host substrate. d, e Conidiophores with conidiogenous cells. f–h Conidia. i A germinating conidium. j Culture on MEA. Scale bars: a = 1 mm, b = 200 μm , c = 50 μm , d = 20 μm , e–i = 10 μm .

Checklist of fungi associated with *Bidens pilosa*

The USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman 2025), relevant publications, and the author's research were used to prepare the worldwide checklist of fungi on *Bidens pilosa*. The current fungal names and classifications have been updated

following Index Fungorum (2025), the Outline of Fungi and fungus-like taxa (Hyde et al. 2024) and other recent publications (Pem et al. 2024, Thiyagaraja et al. 2025).

Phylum Ascomycota Caval.-Sm.

Subphylum Pezizomycotina O.E. Erikss. & Winka

Class Dothideomycetes sensu O.E. Erikss. & Winka

Subclass Pleosporomycetidae C.L. Schoch, Spatafora, Crous & Shoemaker

Pleosporales Luttr. ex M.E. Barr

Dictyosporiaceae Boonmee & K.D. Hyde

1. *Dictyocheiросpora nabanheensis* Tibpromma & K.D. Hyde, *Fungal Diversity* 93: 1–160 (2018).

Thailand (This study)

Didymellaceae Gruyter, Aveskamp & Verkley

2. *Ascochyta* sp.

Australia (Simmonds 1966)

3. *Remotididymella fici-microcarpae* Kular, *Journal of Fungi* 9 (182): 14 (2023)

Thailand (This study)

4. *Remotididymella anthropophila* Valenz. Lopez, Cano, Guarro & Stchigel, *Studies in Mycology* 90: 35 (2017)

Thailand (This study)

Didymosphaeriaceae Munk

5. *Chromolaenicola Chiangraiensis* Mapook & K.D. Hyde *Fungal Diversity* 101: 1–175 (2020).

Thailand (Htet et al. 2024)

6. *Chromolaenicola siamensis* (Jayasiri, E.B.G. Jones & K.D. Hyde) Mapook & K.D. Hyde *Fungal Diversity* 101: 1–175 (2020)

Thailand (Htet et al. 2024)

7. *Chromolaenicola thailandensis* Mapook & K.D. Hyde *Fungal Diversity* 101, 1–175 (2020)

Thailand (Htet et al. 2024)

8. *Pseudopithomyces chartarum* (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, *Fungal Diversity* 75: 27–274 (2015).

Thailand (This study)

Lentimurisporaceae N.G. Liu, J.K. Liu & K.D. Hyde

9. *Bahusandhika bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (This study)

Periconiaceae Nann

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

Thailand (This study)

Phaeosphaeriaceae M.E. Barr

11. *Leptospora thailandica* Phukhams. & K.D. Hyde, *Fungal Diversity* 80: 100 (2016)

Thailand (This study)

Pleosporaceae Nitschke

12. *Alternaria* sp.

Brazil (Mendes et al. 1998), Venezuela (Urtiaga 2004)

13. *Alternaria zinniae* M.B. Ellis, *Mycol. Pap.* 131: 22 (1972)

Kenya (Natrass, 1961)

Roussoellaceae Jian K. Liu, Phook., D.Q. Dai & K.D. Hyde

14. *Neoroussoella entadae* Jayasiri, E.B.G. Jones & K.D. Hyde, *Mycosphere* 10(1): 105 (2019)

Thailand (this study)

15. *Pseudorousoella bidenticola* Htet, A. Mapook & K.D. Hyde, MycoKeys 111: 139 (2024)
Thailand (Htet et al. 2024)
- Sporormiaceae** Munk
16. *Forliomyces bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (This study)
- Tetraplophaeriaceae** Kaz. Tanaka & K. Hiray
17. *Tetraploa aristata* Berk. & Broome, Ann. Mag. nat. Hist., Ser. 2 5: 459 (1850)
Cuba (Mercado Sierra 1984)
- Torulaceae** Corda
18. *Dendryphion hydei* J.F. Li, Phookamsak & Jeewon, PLoS ONE 15(2): e0228067, 6 (2020)
Thailand (Li et al. 2020, This study)
- Subclass Dothideomycetidae** P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker
- Mycosphaerellales** P.F. Cannon
- Mycosphaerellaceae** Lindau
19. *Cercospora bidentis* Tharp, Mycologia 9(2): 108 (1917)
Brazil (Mendes et al. 1988, Guatimosim et al. 2015), China (Tai 1979), Cuba (Mercado Sierra 1984), Democratic Republic of the Congo (Kinshasa) (Pollack 1987), Ghana (Hughes 1952), Guinea (Kranz 1963), India (Vasudeva 1963), Kenya (Natrass 1961), Malaysia (Turner 1971), Mauritius (Wiehe 1948), Papua New Guinea (Shaw 1984), Samoa (McKenzie 1996), South Africa (Crous & Braun 1996), Taiwan region (Hsieh & Goh 1990), Thailand (Nakashima et al. 2007, Phengsintham et al. 2010, Phengsintham et al. 2013), Tonga (Dingley et al. 1981), Trinidad and Tobago (Baker & Dale 1951, Dennis 1970), United States (Alfieri et al. 1984), Venezuela (Dennis 1970, Urtiaga 1986), Zambia (Riley 1956)
20. *Cercospora megalopotamica* (Speg.) U. Braun, Schlechtendalia 5: 66 (2000)
China (Tai 1979, Zhuang 2001), Colombia (Chardon & Toro 1930, Dennis 1970), United States (Raabe et al. 1981).
21. *Cercospora maculicola* Thirum. & Govindu, Sydowia 8(1-6): 344 (1954)
Brazil (Guatimosim et al. 2015), India (Thirumalachar & Govindu 1954, Vasudeva 1963, Kamal 2010)
22. *Cercospora bidentis-pilosae* Sawada, Rep. Govt Res. Inst. Dep. Agric., Formosa 85: 98 (1943)
Taiwan region (Chupp 1954)
23. *Mycosphaerella* sp.
Cuba (Urtiaga 1986), Venezuela (Urtiaga 1986)
24. *Pseudocercospora vitis* (Lév.) Speg., Anal. Mus. nac. B. Aires, Ser. 3 13: 438 (1910) [1911]
Brazil (Pereira et al. 2019)
25. *Ramularia concomitans* Ellis & Holw., in Ellis & Everhart, J. Mycol. 4(1): 2 (1888)
China (Zhang et al. 2003, Zhang 2006)
26. *Septoria balansae* Speg., Anal. Soc. cient. argent. 22(4): 196 (1886)
Colombia (Dennis 1970)
- Myriangiales** Starbäck
- Elsinoaceae** Höhn. ex Sacc. & Trotter
27. *Elsinoe bidentis* (Bitanc. & Jenkins) X.L. Fan & Crous, in Fan, Barreto, Groenewald, Bezerra, Pereira, Cheewangkoon, Tian & Crous, Stud. Mycol. 87: 14 (2017)
Brazil (Fan et al. 2017)
28. *Sphaceloma* sp. (=Elsinoe sp.)

Zimbabwe (Whiteside 1966)

29. ***Sphaceloma bidentis*** (Bitanc. & Jenkins) X.L. Fan & Crous, Stud. Mycol. 87: 14 (2017)
Brazil (Mendes et al. 1998)

Dothideomycetes orders *incertae sedis*

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Botryosphaeriaceae Theiss. & Syd.

30. ***Lasiodiplodia theobromae*** (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909)
Cuba (Urtiaga 2004); Thailand (this study)

Phyllostictaceae Fr.

31. ***Phyllosticta* sp.**
Brazil (Mendes et al. 1998), Cuba (Urtiaga 1986)

Dothideomycetes families *incertae sedis*

Englerulaceae Henn

32. ***Sarcinella pulchra*** (Sacc.) Seifert, in Rossman et al., IMA Fungus 7(2): 303 (2016) (= *Schiffnerula pulchra*)
Cuba (Mercado Sierra 1984)

Kirschsteiniotheliales genera *incertae sedis*

33. ***Brachysporiella dennisii*** J.L. Crane & Dumont, Can. J. Bot. 56(20): 2613 (1978)
Cuba (Mercado Sierra 1984)

Class Sordariomycetes O.E. Erikss. & Winka

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

Diaporthales Nannf.

Diaporthaceae Höhn. ex Wehm

34. ***Diaporthe biconispora*** F. Huang, K.D. Hyde & Hong Y. Li, Fungal Biology 119: 338 (2015)
Thailand (This study)
35. ***Diaporthe phaseolorum*** (Cooke & Ellis) Sacc., Syll. fung. (Abellini) 1: 692 (1882) (= *Diaporthe phaseolorum* f. sp. *meridionalis*)
Brazil (Mendes et al. 1998)

Subclass Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadeff. ex Réblová, W. Gams & Seifert

Glomerellaceae Locq. ex Seifert & W. Gams

36. ***Colletotrichum* sp.**
United States (Alfieri et al. 1984)
37. ***Colletotrichum truncatum*** (Schwein.) Andrus & W.D. Moore, Phytopathology 25: 121 (1935)
Thailand (This study)
38. ***Colletotrichum bidentis*** Damm, Guatim. & B.S. Vieira, in Damm, Cannon, Liu, Barreto, Guatimosim & Crous, Fungal Diversity 61: 34 (2013)
Brazil (Guatimosim et al. 2015)
39. ***Colletotrichum dematium*** (Pers.) Grove, J. Bot., Lond. 56: 341 (1918)
Cuba (Urtiaga 1986, Jayawardena et al. 2016), Venezuela (Urtiaga 1986, Jayawardena et al. 2016)
40. ***Colletotrichum gloeosporioides*** (Penz.) Penz. & Sacc., Atti Inst. Veneto Sci. lett., ed Arti, Sér. 6 2(5): 670 (1884) (= *Glomerella cingulata*)
Venezuela (Urtiaga 1986)

Hypocreales Lindau

Clavicipitaceae Rogerson

41. *Aschersonia cubensis* Berk. & M.A. Curtis, J. Linn. Soc., Bot. 10(46): 351 (1869)
Puerto Rico (U.S.A.) (Stevenson 1975)

Nectriaceae Tul. & C. Tul.

42. *Fusarium bidentis* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (This study)
43. *Fusarium hainanense* M.M. Wang, Qian Chen & L. Cai, Persoonia 43: 82 (2019)
Thailand (This study)

Subclass Xylariomycetidae O.E. Erikss. & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss.

Apiosporaceae K.D. Hyde, J. Fröhl., Joanne E. Taylor & M.E. Barr

44. *Nigrospora oryzae* (Berk. & Broome) Petch, J. Indian bot. Soc. 4: 24 (1924)
Brazil (Mendes et al. 1998)

Bartaliniaceae Wijayaw., Maharachch. & K.D. Hyde

45. *Bartalinia bidenticola* Htet, Mapook & K.D. Hyde, in Jayawardena et al., Fungal Diversity 117: 147 (2022)
Thailand (Jayawardena et al. 2022)

Class Leotiomycetes O.E. Erikss. & Winka

Subclass Leotiomycetidae P.M. Kirk, P. Cannon, Minter & Stalpers

Helotiales Nannf

Erysiphaceae Tul. & C. Tul.

46. *Erysiphe galeopsidis* (DC.) U. Braun, Schlechtendalia 3: 50 (1999)
Cuba (Amano, 1986)
47. *Golovinomyces ambrosiae* (Schwein.) U. Braun & R.T.A. Cook, Mycol. Res. 113(5): 628 (2009)
China (Mukhtar et al. 2022)
48. *Neoerysiphe cumminsiana* (U. Braun) U. Braun, Schlechtendalia 3: 50 (1999)
Argentina (Braun et al. 2001), Brazil (Cook et al. 2006, Guatimosim et al. 2015)
49. *Oidium* sp.
China (Zheng & Yu 1987), Cuba (Braun 1982), India (Amano 1986; Paul & Thakur 2006), Jamaica (Amano 1986), Malawi (Wiehe 1953), Sudan (Amano 1986), Venezuela (Amano 1986; Urtiaga 1986), Zambia (Amano 1986)
50. *Podosphaera fuliginea* (Schltdl.) U. Braun & S. Takam., Schlechtendalia 4: 29 (2000)
(=*Sphaerotheca fuliginea*)
China (Tai 1979), India (Pande 2008), South Africa (Gorter 1981)
51. *Podosphaera fusca* (Fr.) U. Braun & Shishkoff, in Braun & Takamatsu, Schlechtendalia 4: 29 (2000) (=*Sphaerotheca fuliginea*=*Podosphaera xanthii*)
China (Zheng & Yu 1987), India (Bappammal et al. 1995, Paul & Thakur 2006), Korea (Cho et al. 2013), Thailand (Meeboon et al. 2016)
52. *Podosphaera macularis* (Wallr.) U. Braun & S. Takam., Schlechtendalia 4: 30 (2000)
(=*Sphaerotheca macularis*)
Puerto Rico (U.S.A.) (Stevenson 1975), United States (Alfieri 1984)
- #### **Sclerotiniaceae Whetzel**
53. *Botrytis cinerea* Pers., Syn. meth. fung. (Göttingen) 2: 690 (1801)
China (Zhang 2006)
54. *Sclerotinia sclerotiorum* (Lib.) de Bary, Vergl. Morph. Biol. Pilze (Leipzig): 56 (1884)
Brazil (Mendes 1998), China (Tai 1979), South Africa (Crous et al. 2000)

Phylum Basidiomycota R.T. Moore
Subphylum Agaricomycotina Doweld
Class Agaricomycetes Doweld
Agaricales Underw.
Typhulaceae Jülich

55. *Agroathelia rolfsii* (Sacc.) Redhead & Mullineux, Index Fungorum 554: 1 (2023)
(=*Sclerotium rolfsii*)

Zimbabwe (Whiteside 1966)

Cantharellales Gäum.

Ceratobasidiaceae G.W. Martin

56. *Rhizoctonia solani* J.G. Kühn, Ann. Sper. agr., N.S.: 224 (1858) (= *Thanatephorus cucumeris*)

Brazil (Mendes et al. 1998)

Subphylum Ustilaginomycotina Doweld

Class Exobasidiomycetes Begerow, M. Stoll & R. Bauer

Entylomatales R. Bauer & Oberw

Entylomataceae R. Bauer & Oberw

57. *Entyloma guaraniticum* Speg., Anal. Soc. cient. argent. 17(3): 128 (1884)

Argentina (Zundel 1953), Australia (Simmonds 1966), China (Wang 1946, Tai 1979, Vanky & Guo 1986, Zhuang 2001, Lin 2011), Cuba (Piepenbring & Hernandez 1998, Piepenbring 1999), Dominican Republic (Zundel 1953, Ciferri 1961), Hong Kong (Benjamin & Slot 1969), Kenya (Zambettakis 1971), Madagascar (Zambettakis 1971), Papua New Guinea (Shivas et al. 2001), Paraguay (Piepenbring 1999), Puerto Rico (U.S.A.) (Zundel 1953, Stevenson 1975), Sudan (Zambettakis 1971), Taiwan region (Piepenbring 1999), Uganda (Zambettakis 1971), United States (Zundel 1953, Piepenbring 1999), Zambia (Vanky & Vanky 2002), Zimbabwe (Zambettakis 1971).

58. *Entyloma compositarum* Farl. ex G.P. Clinton, J. Mycol. 8(3): 152 (1902)

Brazil (Guatimosim et al. 2015), Ecuador (Zundel 1953), United States (Raabe et al. 1981, Alfieri et al. 1984), Venezuela (Zundel 1953).

59. *Entyloma spegazzinii* Sacc. & P. Syd., Syll. fung. (Abellini) 16: 376 (1902)
(=*Entyloma bidentis*)

Australia (Vanky & Shivas 2008), Bolivia (Vanky et al. 2009), Brazil (Zundel 1953, Guatimosim et al. 2015), Colombia (Piepenbring 2002), Costa Rica (Piepenbring 1996), India (Zundel 1953, Gandhe 2011), Kenya (Nattrass 1961), Malawi (Wiehe 1953, Peregrine & Siddiqi 1972), Malaysia (Johnston 1960), Mauritius (Wiehe 1948, Zundel 1953, Orieux & Felix 1968, Zambettakis 1971), Panama (Piepenbring 2001, Piepenbring 2006), Papua New Guinea (Shaw 1984, Shivas et al. 2001), South Africa (Zundel 1953, Zambettakis 1971, Gorter 1981, Crous 2000), Tanzania (Zundel 1953, Riley 1960, Zambettakis 1971, Vanky 2003), Taiwan region (Anonymous 1979), Thailand (Shivas et al. 2007), Zambia (Riley 1956), Zimbabwe (Whiteside 1966, Vanky & Vanky 2002)

60. *Entyloma incertum* Cif., Annls mycol. 26(1/2): 38 (1928)

Ecuador (Dennis 1970), Venezuela (Dennis 1970, Chardon & Toro 1934)

61. *Entyloma polysporum* (Peck) Farl., Bot. Gaz. 8: 275 (1883)

United States (Fischer 1953), Venezuela (Dennis 1970)

Subphylum Pucciniomycotina R. Bauer, Begerow, J.P. Samp., M. Weiss & Oberw

Class Pucciniomycetes R. Bauer, Begerow, J.P. Samp., M. Weiss & Oberw

Pucciniales Caruel

Pucciniaceae Chevall

62. *Uredo* sp.

Cuba (Urtiaga 1986)

63. *Uredo bidentis* Henn., Hedwigia 35(5): 251 (1896)

Australia (McAlpine 1906)

64. ***Uromyces* sp.**

Colombia (Salazar-Yepes et al. 2002)

65. ***Uromyces bidenticola*** (Henn.) Arthur, *Mycologia* 9(2): 71 (1917)

Argentina (Lindquist 1982), Australia (Simmonds 1966), Barbados (Simmonds 1966), Bolivia (Jackson 1932), Brazil (Jackson 1932, Guatimosim et al. 2015), Canary Islands (Spain) (Jorstad 1958), Cape Verde (Gjaerum 1984, Gjaerum & Sunding 1986), Chile (Mujica & Vergara 1945), China (Tai 1979), Colombia (Chardon & Toro 1930, Kern et al. 1933, Pardo Cardona 1994, Buritica et al. 1996, Pardo Cardona 1998, Salazar-Yepes et al. 2002), Cook Islands (Dingley et al. 1981), Costa Rica (Berndt 2004), Cuba (Arthur & Johnston 1917, Arnold 1986, Uriaga 1986, Urban 1990), Dominica (Baker & Dale 1948), Dominican Republic (Kern et al. 1933), Grenada (Hughes 1952), Guatemala (Arthur 1918), Haiti (Benjamin & Slot 1969), Indonesia (Boedijn 1959, Jorstad 1959), Jamaica (Dale 1955), Japan (Hiratsuka et al. 1992), Kenya (Nattrass 1961), Madagascar (Bouriquet & Bassino 1965), Malawi (Bisby & Wiehe 1953, Wiehe 1953, Peregrine & Siddiqi 1972), Malaysia (Johnston 1960), Mauritius (Orieux & Felix 1968), New Zealand (McKenzie 1992, McKenzie 1998), Nigeria (Eboh 1981), Panama (Perdomo-Sanchez & Piepenbring 2008), Papua New Guinea (Shaw 1984), Philippines (Arthur & Cummins 1936, Teodoro 1937), Puerto Rico (U.S.A.) (Arthur 1917, Roure 1963, Stevenson 1975), Rwanda (Majewski & Nowak 1982), Samoa (Dingley et al. 1981), Sri Lanka (Gjaerum 1995), Taiwan region (Anonymous 1979, Guo & Wang 1986), Trinidad and Tobago (Arthur 1922, Baker & Dale 1951), Uganda (Wakefield & Hansford 1948), United States (Raabe et al. 1981, Alfieri et al. 1984, French 1989), Uruguay (Lindquist & Garcia Zorrón de Rosengurtt 1967), Venezuela (Chardon & Toro 1934, Kern et al. 1934, Uriaga 1986), Vietnam (Kaneko et al. 2007), Yemen (Gjaerum 1987), Zimbabwe (Whiteside 1966)

66. ***Uromyces bidentis*** Lagerh., in Patouillard & Lagerheim, *Bull. Soc. mycol. Fr.* 11(4): 213 (1895)

Brazil (Jackson 1932, Hennen et al. 1982, Mendes et al. 1998, Hennen et al. 2005), Canary Islands (Spain) (Urries 1957), Colombia (Chardon & Toro 1930, Kern et al. 1933, Dennis 1970, Pardo Cardona 1994, Buritica & Pardo Cardona 1996, Pardo Cardona 1998, Salazar-Yepes et al. 2002), Cook Islands (Dingley et al. 1981), Dominican Republic (Kern 1933, Kern et al. 1934, Ciferri 1961), India (Ragunathan & Ramakrishnan 1972, Hosagoudar 1988), New Zealand (Pennycook 1989, McKenzie 1998), Philippines (Teodoro 1937), Puerto Rico (U.S.A.) (Arthur 1916, Arthur 1917, Roure 1963, Stevenson 1975), South Africa (Gorter 1981, Crous et al. 2000), Taiwan region (Sawada 1943), United States (Blasdale 1919), Venezuela (Dennis 1970, Chardon & Toro 1934, Kern et al. 1934).

67. ***Uromyces bidentis*** Lagerh., in Patouillard & Lagerheim, *Bull. Soc. mycol. Fr.* 11(4): 213 (1895)

Brazil (Jackson 1932, Hennen et al. 1982, Mendes et al. 1988, Hennen et al. 2005), Canary Islands (Spain) (Urries 1957), Colombia (Chardon & Toro 1930, Kern et al. 1933, Dennis 1970, Pardo Cardona 1994, Buritica & Pardo Cardona 1996, Pardo Cardona 1998, Salazar-Yepes et al. 2002), Cook Islands (Dingley et al. 1981), Dominican Republic (Kern 1930, Kern et al. 1933, Ciferri 1961), India (Ragunathan & Ramakrishnan 1972, Hosagoudar 1988), New Zealand (Pennycook 1989, McKenzie 1998), Philippines (Teodoro 1937), Puerto Rico (U.S.A.) (Arthur 1916, Arthur 1917, Roure 1963, Stevenson 1975), South Africa (Gorter 1981, Crous et al. 2000), Taiwan region (Sawada 1943), United States (Blasdale 1919), Venezuela (Dennis 1970, Chardon & Toro 1934, Kern et al. 1934).

Class Ustilaginomycetes R. Bauer, Oberw. & Vánky

Urocystidales R. Bauer & Oberw.

Glomosporiaceae Cif.

68. ***Thecaphora denticulata*** Durán, *Can. J. Bot.* 60(8): 1517 (1982)

Mexico (Duran 1987, Huguenin 1966, Mouchacca & Horak 1998)

69. ***Thecaphora pustulata*** G.P. Clinton, *Revista Agric. Puerto Rico* 64: 23 (1921)

Colombia (Zundel 1953, Piepenbring 2002), Costa Rica (Piepenbring 1996), Puerto Rico (U.S.A.) (Zundel 1953, Stevenson 1975, Vanky 1985, Vanky 1994, Kruse et al. 2018)

Phylum GLOMEROMYCOTA C. Walker & A. Schüssler

Class Glomeromycetes Caval.-Sm.

Glomerales J.B. Morton & Benny

Glomeraceae Piroz. & Dalpé

70. ***Dominikia iranica*** (Błaszk., Kovács & Balázs) Błaszk., Chwat & Kovács, in Błaszkowski, Chwat, Góralska & Ryszka, Kovács, Nova Hedwigia 100(1-2): 230 (2014) [2015] (= *Rhizophagus iranicus*)

China (Zhang et al. 2018)

71. ***Microkamienskia perpusilla*** (Błaszk. & Kovács) Corazon-Guivin, G.A. Silva & Oehl, in Corazon-Guivin, Mendoza, Guerrero-Abad, Vallejos-Tapullima, Carballar-Hernández, Silva & Oehl, Nova Hedwigia 109(3-4): 361 (2019) (= *Glomus perpusillum*)

China (Zhang et al. 2018)

72. ***Septoglomus constrictum*** (Trappe) Sieverd., G.A. Silva & Oehl, in Oehl, Silva, Goto & Sieverding, Mycotaxon 116: 105 (2011)

China (Zhang et al. 2018)

73. ***Septoglomus viscosum*** (T.H. Nicolson) C. Walker, D. Redecker, Stille & A. Schüßler, in Redecker, Schüßler, Stockinger, Stürmer, Morton & Walker, Mycorrhiza 23(7): 524 (2013)

China (Zhang et al. 2018)

74. ***Rhizophagus intraradices*** (N.C. Schenck & G.S. Sm.) Sieverd., G.A. Silva & Oehl, Mycotaxon 129(2): 378 (2015) [2014]

China (Zhang et al. 2018)

Phylum Oomycota Arx

Class Peronosporomycetes M. W. Dick

Albuginales Thines

Albuginaceae Schroet.

75. ***Albugo* sp.**

Venezuela (Urtiaga 2004)

Peronosporales A. N. Bektov

Peronosporaceae de Bary

76. ***Plasmopara halstedii*** (Farl.) Berl. & De Toni, in Berlese, De Toni & Fischer, Syll. fung. (Abellini) 7(1): 242 (1888)

Brazil (Guatimosim et al. 2015, Campbell 1932), United States (Alfieri et al. 1984)

Checklist of fungi associated with *Chromolaena odorata*

The USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2025), relevant publications, and the author's own research were used to prepare the worldwide checklist of fungi on *Chromolaena odorata*. The current fungal names and classifications have been updated following Index Fungorum (2025), the Outline of Fungi and Fungus-like taxa (Hyde et al. 2024), and other recent publications (Pem et al. 2024, Thiagaraja et al. 2025).

Phylum Ascomycota Caval.-Sm.

Class Dothideomycetes sensu O.E. Erikss & Winka

Subclass Dothideomycetidae P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker

Capnodiales Woron

Capnodiaceae (Sacc.) Höhn. ex Theiss

1. ***Capnodium* sp.**

Venezuela (Urtiaga 1986)

Cladosporiales Abdollahz. & Crous

Cladosporiaceae Chalm. & R.G. Archibald

2. ***Cladosporium* sp.**

West Indies (Minter et al. 2001)

3. ***Cladosporium eupatorii*** Cif., Sydowia 8(1-6): 251 (1954) (= *Hormodendrum eupatorii*)

Dominican Republic (Ciferri 1961, Barreto & Evans 1994)

Mycosphaerellales P.F. Cannon 2001

Mycosphaerellaceae Lindau

4. ***Cercospora* sp.**

Cambodia (Litzenberger et al. 1994), Malaysia (Johnston 1960, Williams & Liu 1976), Nepal (Barreto & Evans 1994), Thailand (Puckdeedindan 1966, Nguanhom et al. 2015), Venezuela (Urtiaga 2004)

5. ***Micronematomyces caribensis*** (Crous & den Breeÿen) U. Braun, C. Nakash., Videira & Crous, in Videira et al., Stud. Mycol. 87: 337 (2017)

Cuba, Jamaica (den Breeÿen et al. 2006, Videira et al. 2017)

6. ***Micronematomyces chromolaenae*** (Crous & den Breeÿen) U. Braun, C. Nakash., Videira & Crous, in Videira et al., Stud. Mycol. 87: 337 (2017)

Mexico (den Breeÿen et al. 2006, Videira et al. 2017)

7. ***Passalora* sp.**

Jamaica, USA (den Breeÿen et al. 2006)

8. ***Passalora capsicola*** (Vassiljevsky) U. Braun & F.O. Freire, Cryptog. Mycol. 23(4): 299 (2003) [2002]

= *Phaeoramularia capsicola* (Vassiljevsky) Deighton, in Ellis, Trans. Br. mycol. Soc. 67(1): 140 (1976)

Jamaica, USA (Videira et al. 2017)

9. ***Phloeospora* sp.**

Venezuela (Urtiaga 1986, Barreto & Evans 1994)

10. ***Pseudocercospora* sp.**

Guatemala (Videira et al. 2017), Mexico (den Breeÿen et al. 2006)

11. ***Pseudocercospora aciculina*** (Chupp) U. Braun & Crous, in Crous & Braun, CBS Diversity Ser. (Utrecht) 1: 42 (2003)

= *Cercospora aciculina* Chupp, Monograph of Cercospora: 118 (1954)

Cambodia (Litzenberger et al. 1962), Nigeria (Fajola 1978, Barreto & Evans 1994)

12. ***Pseudocercospora ageratoides*** (Ellis & Everh.) Y.L. Guo, Acta Mycol. Sin. 12(4): 271 (1993)

= *Cercospora ageratoides* Ellis & Everh., J. Mycol. 5(2): 71 (1889)

Cote d'Ivoire (Yen 1974)

13. ***Pseudocercospora convoluta*** (Crous & den Breeÿen) U. Braun, C. Nakash., Videira & Crous, in Videira et al., Stud. Mycol. 87: 312 (2017)

= *Passalora convoluta* Crous & den Breeÿen, in Breeÿen, Groenewald, Verkley & Crous, Fungal Diversity. 23: 96 (2006)

Costa Rica (den Breeÿen et al. 2006, Videira et al. 2017)

14. ***Pseudocercospora eupatoriella*** Crous & den Breeÿen, in Breeÿen, Groenewald, Verkley & Crous, Fungal Diversity. 23: 101 (2006)

Jamaica (den Breeÿen et al. 2006, Guatimosim et al. 2016), USA (den Breeÿen et al. 2006)

15. ***Pseudocercospora eupatorii*** (Peck) U. Braun & R.F. Castañeda, Cryptog. Bot. 2(2-3): 293 (1991)

= *Cercospora eupatorii* Peck, Ann. Rep. N.Y. St. Mus. nat. Hist. 33: 29 (1883) [1880]

Cambodia, Cote d'Ivoire, Cuba, Hawaii, India, Nepal, North America (Govindu et al. 1970, Yen 1974, Urtiaga 1986, Barreto & Evans 1994), Andaman Islands (Hosagoudar & Mathew 2000), India (Kamal 2010), Thailand (Meeboon et al. 2007)

16. *Pseudocercospora eupatorii-formosani* U. Braun & Bagyan., Sydowia 51(1): 8 (1999)
Bangladesh (Barreto & Evans 1994), Brunei Darussalam (Peregrine & Ahmad 1982, Barreto & Evans 1994, Braun & Sivapalan 1999), China (Roux et al. 1997, Liu & Guo 1998, Guo 1999a, Guo 1999b, Zhuang et al. 2001), India (Barreto & Evans 1994), Laos (Phengsintham et al. 2010), Malaysia (Barreto & Evans 1994), Myanmar (Thaung 1984, Barreto & Evans 1994), Taiwan region (Kirschner & Chen 2007), Thailand (Barreto & Evans 1994, Phengsintham et al. 2013), Venezuela (Urtiaga & Braun 2013)
 17. *Ragnhildiana perfoliati* (Ellis & Everh.) U. Braun, C. Nakash., Videira & Crous, in Videira, Groenewald, Nakashima, Braun, Barreto, de Wit & Crous, Studies in Mycology 87: 345 (2017)
= *Mycovellosiella perfoliati* (Ellis & Everh.) U. Braun, C. Nakash., Videira & Crous 1960
= *Passalora perfoliati* (Ellis & Everh.) U. Braun & Crous, in Crous & Braun, CBS Diversity Ser. (Utrecht) 1: 314 (2003)
Brazil (Barreto & Evans 1994), Laos (Videira et al. 2017), West Indies (Minter et al. 2001), Jamaica (den Breeyen et al. 2006), Taiwan region (Kirschner & Chen 2007)
 18. *Ramularia eupatorii* J.M. Yen, Cahiers Pacif. 13: 272 (1969) (= *Mycosphaerella eupatorii*)
Malaysia (Yen 1969, Barreto & Evans 1994)
 19. *Ramularia tungurahuana* Petr., Sydowia 4(1-6): 507 (1950) (= *Mycosphaerella tungurahuana*)
Malaysia (Yen 1969)
 20. *Septoria chromolaenae* Crous & den Breeÿen, in Breeÿen et al., Fungal Divers 23: 102 (2006)
Cuba (Verkley et al. 2013), Jamaica (den Breeyen et al. 2006)
 21. *Septoria ekmaniana* Petr. & Cif., Annls mycol. 30(3/4): 300 (1932)
Dominican Republic (Ciferri 1961, Barreto & Evans 1994), Mexico (den Breeyen et al. 2006), West Indies (Minter et al. 2001)
 22. *Septoria eupatorii* Roberge ex Desm., Annls Sci. Nat., Bot., sér. 3 20: 90 (1853)
Venezuela (Urtiaga 1986, Barreto & Evans 1994)
 23. *Septoria* sp.
Guam (Russo 1985, Barreto & Evans 1994)
- Myriangiales** Starbäck
Myriangiaceae Nyl.
24. *Anhellia nigra* (Viégas) Arx, Persoonia 2(4): 434 (1963)
= *Tubercularia nigra* F. Stevens, Annls mycol. 28(5/6): 371 (1930)
Brazil (Barreto & Evans 1994), West Indies (Minter et al. 2001)
- Subclass Pleosporomycetidae** C.L. Schoch et al.,
Hysteriales Lindau
Hysteriaceae Chevall.
25. *Rhytidhysterium bruguierae* Dayarathne, in Dayarathne et al., Mycosphere 11(1): 20 (2020)
Thailand (Dayarathne et al. 2020, Mapook et al. 2020, this study)
 26. *Rhytidhysterium chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Pleosporales** Luttrell ex M.E. Barr
Acrocalymmaceae Crous & Trakun.
27. *Acrocalymma medicaginis* Alcorn & J.A.G. Irwin, Trans. Br. mycol. Soc. 88(2): 163 (1987)
Thailand (Mapook et al. 2020)

28. *Acrocalymma pterocarpi* Jayasiri, E.B.G. Jones & K.D. Hyde, *Mycosphere* 10(1): 20 (2019)
Thailand (this study)
- Corynesporascaceae** Sivan.
 29. *Corynespora cassicola* (Berk. & M.A. Curtis) C.T. Wei, *Mycol. Pap.* 34: 5 (1950)
Palau (Dixon et al. 2009)
- Dictyosporiaceae** Boonmee & K.D. Hyde
 30. *Neodendryphiella mali* Iturr.-Gonz., Gené & Dania García, *MycoKeys* 37: 25 (2018)
Thailand (this study)
- Didymellaceae** Gruyter et al.,
 31. *Didymella chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 32. *Nothophoma chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Didymosphaeriaceae** Munk
 33. *Austropleospora chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
 34. *Chromolaenicola Chiangraiensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 35. *Chromolaenicola lampangensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 36. *Chromolaenicola nanensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020, this study)
 37. *Chromolaenicola thailandensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 38. *Didymosphaeria* sp.
India (Barreto & Evans, 1994)
 39. *Kalmusia thailandica* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
 40. *Montagnula Chiangraiensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 41. *Montagnula chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020, this study)
 42. *Montagnula chromolaenicola* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 43. *Montagnula donacina* (Niessl) Wanas., E.B.G. Jones & K.D. Hyde, *Index Fungorum* 319: 1 (2017)
Thailand (this study)
 44. *Montagnula thailandica* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 45. *Pseudopithomyces chartarum* (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, *Fungal Diversity* 75: 27–274 (2015)
Thailand (this study)
 46. *Pseudopithomyces palmicola* J.F. Li, Ariyaw. & K.D. Hyde, in Ariyawansa et al., *Fungal Diversity*. 75: 41 (2015)
Thailand (Mapook et al. 2020)
 47. *Tremateia Chiangraiensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 48. *Tremateia chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
 49. *Tremateia thailandensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)

Hermatomycetaceae Locq.

50. *Hermatomyces chromolaenae* Jun F. Li, Mapook & K.D. Hyde, in Tibpromma et al., Fungal Divers 83: 47 (2017)
Thailand (Tibpromma et al. 2017)

Lophiostomataceae Sacc.

51. *Flabellascoma minimum* A. Hashim., K. Hiray. & Kaz. Tanaka, in Hashimoto et al., Studies in Mycology 90: 169 (2018)
Thailand (Mapook et al. 2020)
52. *Pseudocapulatispora longiappendiculata* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020, this study)
53. *Pseudolophiostoma chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)

Lentimurisporaceae N.G. Liu, J.K. Liu & K.D. Hyde

54. *Bahusandhika indica* (Subram.) Subram., J. Indian bot. Soc. 35: 469 (1956)
Thailand (this study)

Melanommataceae G. Winter (= *Pseudodidymellaceae* A. Hashim. & Kaz. Tanaka)

55. *Byssosphaeria schiedermayeriana* (Fuckel) M.E. Barr, Mycotaxon 20(1): 34 (1984)
= *Herpotrichia schiedermayeriana* Fuckel, Jb. nassau. Ver. Naturk. 27- 28: 27 (1874) [1873-74]
Brazil (Barreto & Evans 1994)

Nigrogranaceae Jaklitsch & Voglmayr

56. *Nigrograna chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)

Neomassarinae Mapook & K.D. Hyde

57. *Neomassarina chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
58. *Neomassarina thailandica* Phook., Jayasiri & K.D. Hyde, in Hyde et al., Fungal Diversity. 80: 138 (2016)
Thailand (Mapook et al. 2020)

Neopyrenochaetaceae Valenzuela-Lopez et al.,

59. *Neopyrenochaeta chiangraiensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
60. *Neopyrenochaeta chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
61. *Neopyrenochaeta thailandica* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
62. *Neopyrenochaeta triseptatispora* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)

Phaeosphaeriaceae M.E. Barr

63. *Leptospora chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
64. *Leptospora phraeana* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
65. *Leptospora thailandica* Phukhams. & K.D. Hyde, in Hyde et al., Fungal Diversity. 80: 100 (2016)
Thailand (Mapook et al. 2020)
66. *Murichromolaenicola chiangraiensis* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
67. *Murichromolaenicola chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
68. *Murichromolaenicola thailandensis* Htet, Mapook & K.D. Hyde, Phytotaxa 618 (2): 120–130 (2023)

- Thailand (Htet et al. 2023, this study)
69. *Neophiobolus chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
70. *Ophiobolus ipohensis* J.M. Yen, Cahiers Pacif. 13: 277 (1969)
Malaysia (Yen 1969, Barreto & Evans 1994)
71. *Ophiosphaerella eupatorii* J.M. Yen, Cahiers Pacif. 13: 278 (1969)
Malaysia (Yen 1969, Barreto & Evans 1994)
72. *Paraleptospora chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
73. *Paraleptospora chromolaenicola* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
74. *Phaeosphaeria eupatoriicola* J.M. Yen, Cahiers Pacif. 13: 279 (1969)
Malaysia (Yen 1969, Barreto & Evans 1994)
75. *Pseudoophiosphaerella huishuiensis* J.F. Zhang, J.K. Liu & Z.Y. Liu, in Zhang, Liu, Jeewon, Wanasinghe & Liu, Mycosphere 8(1): 207 (2019)
Thailand (Mapook et al. 2020)
76. *Pseudostaurosphaeria chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
77. *Pseudostaurosphaeria chromolaenicola* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
78. *Setophoma chromolaenae* Quaedvl., Verkley, R.W. Barreto & Crous, Studies in Mycology 75: 373 (2013)
Brazil (Quaedvlieg et al. 2013)
79. *Yunnanensis chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Pleosporaceae** Nitschke
80. *Alternaria zinniae* M.B. Ellis, Mycol. Pap. 131: 22 (1972)
Brazil (Barreto & Evans 1994)
- Pyrenochaetopsidaceae** Valenzuela-Lopez et al.,
81. *Pyrenochaetopsis chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Roussoellaceae** J.K. Liu et al.,
82. *Neorousoella chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (Htet et al. 2024)
83. *Neorousoella entadae* Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 105 (2019)
Thailand (Htet et al. 2024, this study)
84. *Pseudoneoconiothyrium chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
85. *Pseudoneoconiothyrium thailandicum* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
86. *Pseudorousoella chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
87. *Pseudorousoella elaeicola* (Konta & K.D. Hyde) Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
88. *Setoarthopyrenia chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
89. *Xenorousoella triseptata* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Thyridariaceae** Q. Tian & K.D. Hyde

90. *Chromolaenomyces appendiculatus* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
91. *Pseudothyridariella asteracearum* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
92. *Pseudothyridariella chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
93. *Pseudothyridariella thailandica* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)

Torulaceae Corda

94. *Dendryphion hydei* J.F. Li, Phookamsak & Jeewon, PLoS ONE 15(2): e0228067, 6
(2020)
Thailand (this study)
95. *Torula canangae* N.I. de Silva, Lumyong & K.D. Hyde, Mycosphere 13(1): 1012
(2022)
Thailand (this study)
96. *Torula chromolaenae* J.F. Li, Phook., Mapook & K.D. Hyde, in Li et al., Mycol.
Progr. 16(4): 454 (2017)
Thailand (Li et al. 2017, Mapook et al. 2020)
97. *Torula fici* Crous, in Crous et al., IMA Fungus 6(1): 192 (2015)
Thailand (Li et al. 2017, Mapook et al. 2020, this study)
98. *Torula hydei* J.F. Li, Phookamsak & Jeewon, in Li, Jeewon, Mortimer, Doilom,
Phookamsak & Prompt, PLoS ONE 15(2): e0228067, 8 (2020)
Thailand (Li et al. 2020)
99. *Torula mackenziei* Jun F. Li, Phook. & K.D. Hyde, Mycol. Progr. 16(4): 455 (2017)
Thailand (this study)
100. *Torula polyseptata* C.G. Lin & K.D. Hyde, in Hyde et al., Fungal Diversity. 96: 71
(2019)
Thailand (Hyde et al. 2019a; Mapook et al. 2020)

Pleosporales genera *incertae sedis*

101. *Scolecobasidium eupatorii* Y.L. Guo, Acta Mycol. Sin. 12(4): 271 (1993)
China (Zhuang et al. 2001)

Dothideomycetes orders *incertae sedis*

Botryosphaeriales C.L. Schoch et al.,

Aplosporellaceae Slippers et al.,

102. *Aplosporella chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
103. *Aplosporella hesperidica* Speg., Anal. Soc. cient. argent. 13(1): 18 (1882)
Thailand (Mapook et al. 2020, this study)
104. *Aplosporella artocarpi* Trakun., L. Lombard & Crous, in Trakunyingcharoen,
Lombard, Groenewald, Toanun & Crous, Persoonia 34: 91 (2014)
Thailand (Jayawardena et al. 2022)

Botryosphaeriaceae Theiss. & P. Syd., Annales Mycologici 16 (1-2): 16 (1918)

105. *Dothiorella asteracearum* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
106. *Dothiorella chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
107. *Dothiorella oblonga* F.J.J. Van der Walt, Slippers & G.J. Marais, in Slippers et al.,
Persoonia 33: 163 (2014)
Thailand (Mapook et al. 2020)

108. *Lasiodiplodia theobromae* (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909)
Thailand (this study)
109. *Sphaeropsis chromolaenicola* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Phyllostictaceae** Fr.
110. *Asteromella eupatoriicola* (Kabát & Bubák) H. Ruppr. 1958
= *Phyllosticta eupatoriicola* Kabát & Bubák, Hedwigia 46: 288 (1907)
Malaysia, South America (Barreto & Evans 1994), Puerto Rico (Stevenson 1975), Virgin Islands (Stevenson 1975), West Indies (Minter et al. 2001)
111. *Phyllosticta eupatorii* Punith., Mycol. Pap. 136: 21 (1974)
Sri Lanka (Barreto & Evans 1994)
- Dyfoliomyces** K.L. Pang et al.,
- Pleurotremataceae** Walt. Watson (=Dyfoliomyces K.D. Hyde et al.,)*
112. *Dyfoliomyces chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Muyocoprionales** Mapook et al.,
- Muyocoprionaceae** K.D. Hyde
113. *Muyocoprion chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
114. *Muyocoprion chromolaenicola* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
115. *Muyocoprion lithocarpi* Mapook, Boonmee & K.D. Hyde, Phytotaxa 265(3): 235 (2016), new host record
Thailand (Mapook et al. 2020)
116. *Neocochlearomyces chromolaenae* Pinruan, Sommai, Suetrong, J.Z. Groenew. & Crous, in Crous et al., Persoonia 41: 381 (2018)
Thailand (Crous et al. 2018)
- Patellariales** D. Hawksw. & O.E. Erikss.
- Patellariaceae** Corda
117. *Patellaria chromolaenae* Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
- Dothideomycetes** families *incertae sedis*
- Dysrhynchiscae** Boonmee & K.D. Hyde*
118. *Dysrhynchis citricola* Bat. & Peres, Nova Hedwigia 2(4): 469 (1960)
Dominican Republic (Ciferri 1961, Barreto & Evans 1994)
- Dothideomycetes** genera *incertae sedis*
119. *Ampullifera* sp.
West Indies (Minter et al. 2001)
120. *Melioliphila melioloides* (Speg.) Piroz., Kew Bull. 31(3): 596 (1977)
West Indies (Minter et al. 2001)
121. *Phaeoramularia eupatorii-odorati* (J.M. Yen) X.J. Liu & Y.L. Guo, Acta phytopath. sin. 12(no. 4): 7 (1982)
= *Mycovellosiella eupatorii-odorati* (J.M. Yen) J.M. Yen, Bull. trimest. Soc. mycol. Fr. 97(3): 131 (1981)
China (Liu & Guo 1988, Morgan-Jones 1997, Roux et al. 1997, Zhuang et al. 2001, Guo & Liu 2003), Malaysia (Yen 1968, Barreto & Evans 1994)
- Class Eurotiomycetes** Tehler ex O.E. Eriksson & K. Winka
- Subclass Chaetothyriomycetidae** Doweld
- Chaetothyriales** M.E. Barr
- Chaetothyriaceae** Hansf. ex M.E. Barr

122. ***Chaetothyrium dominicanum*** Cif., Sydowia 10(1-6): 133 (1957) [1956]
= *Sphaerochaetia dominicana* (Cif.) Bat. & Cif., Beih. Sydowia 3: 27 (1962)
Dominican Republic (Ciferri 1961, Batista & Ciferri 1962, Barreto & Evans 1994), on living
leaf of *C. odorata* (= *E. odoratum*)

Class Leotiomycetes O.E. Erikss. & Winka

Helotiales Nannf

Ploettnerulaceae Kirschst

123. ***Pyrenopeziza* sp.** (= *Cylindrosporium* sp.)
Cambodia (Barreto & Evans 1994)

Class Sordariomycetes O.E. Erikss. & Winka

Subclass Diaporthomycetidae Senan. et al.,

Diaporthales Nannf

Diaporthaceae Höhn. ex Wehm

124. ***Diaporthe asteracearum*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
125. ***Diaporthe chromolaenae*** Mapook & K.D. Hyde
Thailand (Mapook et al. 2020)
126. ***Diaporthe chromolaenicola*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde
Thailand (this study)
127. ***Diaporthe eupatoriicola*** Petr., Annls mycol. 20(3/4): 147 (1922)
Sri Lanka (Barreto & Evans 1994)

Diaporthomycetidae families *incertae sedis*

Sporidesmiaceae Fr.

128. ***Sporidesmium* sp.**
West Indies (Minter et al. 2001)

Subclass Hypocreomycetidae O.E. Erikss. & Winka

Glomerellales Chadeff. ex Réblová et al.,

Glomerellaceae Locq. ex Seifert & W. Gams

129. ***Colletotrichum* sp.**
Cambodia (Barreto & Evans 1994), Venezuela (Urtiaga 2004)
130. ***Colletotrichum gigasporum*** Rakotonir & Munaut in Rakotoniriana, Scauflaire,
Rabemanantsoa, Uryeg-Ratsimamanga, Corbisier, Quetin-Leclercq, Declerck & Munaut, Mycol.
Progr. 12 (2): 407 (2012) [2013]
Thailand (this study)
131. ***Colletotrichum gloeosporioides*** (Penz.) Penz. & Sacc., Atti Inst. Veneto Sci. lett., ed
Arti, Sér. 6 2: 670 (1884)
Cuba (Urtiaga 1986, Barreto & Evans 1994), Sri Lanka (Barreto & Evans 1994), Venezuela
(Urtiaga 2004)

Hypocreales Lindau

Bionectriaceae

132. ***Clonostachys byssicola*** Schroers, Stud. Mycol. 46: 80 (2001)
Thailand (Chethana et al. 2021)
133. ***Clonostachys eriocamporesiana*** R.H. Perera & K.D. Hyde, in Hyde et al., Fungal
Diversity 100: 197 (2020)
Thailand (Hyde et al. 2020)

Cordycipitaceae Kreisel ex G.M. Sung et al.,

134. ***Akanthomyces lecanii*** (Zimm.) Spatafora, Kepler & B. Shrestha, in Kepler et al.,
2017
= *Verticillium lecanii* (Zimm.) Viégas, Revista Inst. Café São Paulo 14: 754 (1939)

West Indies (Minter et al. 2001)

Hypocreaceae De Not.

135. *Acrostalagmus albus* Preuss, Linnaea 24: 126 (1851)

South America (Viegas 1961)

136. *Acrostalagmus aphidum* Oudem., Beih. Botan. Centralbl., Abt. B 11: 537 (1902)

Puerto Rico, Virgin Islands (Stevenson 1975), West Indies (Minter et al. 2001)

137. *Trichoderma guizhouense* Q.R. Li, McKenzie & Yong Wang bis, in Li et al., Mycol.

Progr. 12(2): 170 (2012) [2013]

Thailand (Mapook et al. 2020)

Nectriaceae Tul. & C. Tul.

138. *Fusarium chromolaenae* Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

139. *Fusarium culmorum* (Wm.G. Sm.) Sacc., Syll. fung. (Abellini) 10: 726 (1892)

140. *Fusarium fujikuroi* Nirenberg, Mitt. biol. BundAnst. Ld- u. Forstw. 169: 32 (1976)

= *Fusarium moniliforme* J. Sheld., Nebraska Agric. Exp. Stat. Rep. 17: 23 (1904)

Nigeria (Richardson 1990)

141. *Fusarium pallidroseum* (Cooke) Sacc., Syll. fung. (Abellini) 4: 720 (1886)

Nigeria (Richardson 1990)

142. *Fusarium solani* (Mart.) Sacc., Michelia 2(no. 7): 296 (1881)

Nigeria (Richardson, 1990)

Stachybotryaceae Lombard & Crous

143. *Memnoniella asteracearum* Htet, A. Mapook & K.W.T. Chethana

Thailand (Htet et al., in press)

144. *Memnoniella levispora* Subram., J. Indian Bot. Soc. 33: 40 (1954)

= *Memnoniella chromolaenae* Mapook & K.D. Hyde

Thailand (Mapook et al. 2020, Htet et al., in press)

Subclass Sordariomycetidae O.E. Erikss & Winka

Meliolales Gäum. ex D. Hawksw. & O.E. Erikss.

Meliolaceae G.W. Martin ex Hansf.

145. *Appendiculella sororcula* (Speg.) Hansf., Beih. Sydowia 2: 615 (1961)

= *Irene sororcula* (Speg.) F. Stevens, Annls mycol. 25(5/6): 423 (1927)

Dominican Republic (Ciferri 1961), Puerto Rico, Venezuela (Hansford 1949), Trinidad and Tobago (Baker & Dale 1951)

146. *Meliola* sp.

India (Barreto & Evans 1994)

147. *Ophiociliomyces bauhiniae* Bat. & I.H. Lima, Anais Soc. Biol. Pernambuco 13(2): 30 (1955)

Brazil (Barreto & Evans 1994), Cambodia (Litzenberger et al. 1994)

Subclass Xylariomycetidae O.E. Erikss & Winka

Amphisphaeriales D. Hawksw. & O.E. Erikss

Apiosporaceae K.D. Hyde et al.,

148. *Arthrinium chromolaenae* Mapook & K.D. Hyde

Thailand (Mapook et al. 2020)

Xylariales Nannf.

Cainiaceae J.C. Krug

149. *Longiappendispora chromolaenae* Mapook & K.D. Hyde

Thailand (Mapook et al. 2020)

Sordariomycetes genera *incertae sedis*

150. *Pleurophragmium capense* (Thüm.) S. Hughes, Can. J. Bot. 36: 796 (1958)

= *Spiropes capensis* (Thüm.) M.B. Ellis, Mycol. Pap. 114: 5 (1968)

West Indies (Minter et al. 2001)

Ascomycota genera *incertae sedis*

151. *Alysidiopsis yunnanensis* Y.L. Guo & X.J. Liu, Acta Mycol. Sin. 11(3): 213 (1992)
China (Zhuang et al. 2001)

152. *Hansfordia pulvinata* (Berk. & M.A. Curtis) S. Hughes 1958
= *Dicyma pulvinata* (Berk. & M.A. Curtis) Arx 1981

West Indies (Minter et al. 2001)

153. *Redbia trichomambusta* R.W. Barreto, in Barreto & Evans, Mycol. Res. 98(10): 1111
(1994)

Brazil (Barreto & Evans 1994)

154. *Redbia* sp.

West Indies (Minter et al. 2001)

Phylum Basidiomycota R.T. Moore

Class Agaricomycetes Doweld

Cantharellales Gäum.

Ceratobasidiaceae G.W. Martin

155. *Rhizoctonia solani* J.G. Kühn, Ann. Sper. agr., N.S.: 224 (1858)
= *Thanatephorus cucumeris* (A.B. Frank) Donk, Reinwardtia 3: 376 (1956)
Taiwan region (Sawada 1931)

Sebacinales M. Weiss, Selosse, Rexer, A. Urb. & Oberw

Sebacinaceae K. Wells & Oberw.

156. *Chaetospermum camelliae* Agnihothr., Mycopath. Mycol. appl. 16: 115 (1962)
Thailand (Luangharn et al., in press)

Class Pucciniomycetes Bauer et al.,

Pucciniales Clem. & Shear

Coleosporiaceae Dietel

157. *Coleosporium eupatorii* Arthur, Bull. Torrey bot. Club 33: 31 (1906)
China (Tai 1979, Barreto & Evans 1994, Zhuang et al. 2005)

158. *Coleosporium steviae* Arthur, Bot. Gaz. 40: 197 (1905)
China (Barreto & Evans 1994), Mexico (Gallegos & Cummins 1981)

Cronartiaceae Dietel

159. *Cronartium praelongum* G. Winter, Hedwigia 26: 24 (1887)
Colombia (Chardon & Toro 1930, Kern et al. 1933), Venezuela (Chardon & Toro 1934, Kern et al. 1934)

Pucciniales genera *incertae sedis*

160. *Uredo bullula* F. Kern, Mycologia 20(2): 77 (1928)

Dominican Republic (Kern 1930, Kern et al. 1933, Ciferri 1961, Barreto & Evans 1994),
West Indies (Minter et al. 2001)

Puccinosiraceae Cummins & Y. Hirats.

161. *Cionothrix praelonga* (G. Winter) Arthur, N. Amer. Fl. (New York) 7(2): 124 (1907)
= *Cronartium praelongum* G. Winter, Hedwigia 26: 24 (1887)

Dominican Republic, Mexico, Trinidad and Tobago, Venezuela (Arthur 1922, Baker & Dale 1951, Barreto & Evans 1994), Colombia (Buritica & Pardo 1996, Pardo Cardona, 1998), Costa Rica (Arthur 1918a, Berndt 2004) Guatemala (Arthur 1918b), Mexico (Gallegos & Cummins 1981), Panama (Piepenbring 2006), West Indies (Minter et al. 2001)

DISCUSSION

Comparative fungal diversity and host association of invasive Asteraceae weeds

In this study, 45 saprobic fungi were described found on dead stems of *Bidens pilosa* and *Chromolaena odorata* in Thailand. This study highlights the underexplored fungal diversity harbored

by invasive weed species. The results of Mapook et al. (2020) are expanded upon in this study by using a second weed host that was collected from the same geographical region as *Chromolaena odorata*.

Dendryphon hydei, *Diaporthe biconispora*, *Lasiodiplodia theobromae*, *Leptospora thailandica*, *Neoroussioella entadae*, *Pseudopithomyces chartarum*, and *Torula mackenziei* were found on both plants among the 54 species identified in this study (Li et al. 2017, Mapook et al. 2020).

Chromolaenicola, *Murichromolaenicola*, *Pseudoroussioella*, and *Pseudothyridariella* are among the taxa that Mapook et al. (2020) established. These genera were initially reported from *Chromolaena odorata*, demonstrating the fungal originality associated with *Chromolaena odorata*. Combined with the results of this study, it is obvious that the number of fungal species from these genera is increasing. The majority of species within these genera have so far been recorded predominantly from hosts in the family Asteraceae.

Notably, some species identified in this study, such as *Lasiodiplodia theobromae*, *Diaporthe biconispora*, and *Fusarium henanica*, have previously been reported in other ecological roles, including as endophytes or plant pathogens (Huang et al. 2015, Wang et al. 2019, Salvatore et al. 2020). Their presence on *Bidens pilosa* and *Chromolaena odorata* suggests potential ecological plasticity and highlights the dynamic interactions between fungi and their hosts, which may vary depending on environmental conditions or host physiology.

It is interesting to note that two fungal species (*Remotididymella anthropophila* and *Colletotrichum gigasporum*) were discovered in Asteraceae weeds that were previously identified from human sources (Valenzuela-Lopez et al. 2018, Liu et al. 2014). This finding raises concerns about their ecological adaptation and opportunistic behavior. More research is needed to discover whether these species have features that allow for occasional human connection.

Host preference and possible host-specificity

Based on the checklist, the species found in this study contributed significantly to expanding the known diversity of fungi associated with invasive Asteraceae hosts.

In contrast, five species were found exclusively on *Bidens pilosa*, viz., *Albifimbria bidentis*, *Bahusandhika bidentis*, *Forliomyces bidentis*, *Fusarium bidentis*, and *Sarocladium bidentis*. Fifteen species occurred exclusively on *Chromolaena odorata*, viz., *Austropleospora chromolaenae*, *Dothiorella asteracearum*, *Dothiorella chromolaenae*, *Diaporthe asteracearum*, *Diaporthe chromolaenicola*, *Fusarium chromolaenae*, *Kalmusia thailandica*, *Pseudocapulatispora longiappendiculata*, *Murichromolaenicola thailandensis*, *Pseudothyridariella asteracearum*, *Pseudothyridariella thailandica*, *Pseudolophiostoma chromolaenae*, *Pseudoneoconiothyrium chromolaenae*, and *Pseudoneoconiothyrium thailandicum*. Moreover, more research is necessary to verify the possible host-specificity of recently discovered species within understudied genera like *Forliomyces* and *Bahusandhika*. Currently, it is difficult to clearly determine their host range because of the small number of collections and the absence of thorough genetic data (Pratibha et al. 2014, Phukhamsakda et al. 2016, Crane & Miller 2016). Multi-gene phylogenetic analyses and more specimens from various hosts and ecosystems are required to determine whether these fungi truly demonstrate host-specificity or more ecological flexibility (Zhou & Hyde 2001).

Proportion of novel taxa and the unexplored mycobiota in invasive weeds

This study introduces a total of 17 new fungal species, many of which also represent new host records, significantly enriching our understanding of the mycobiota associated with invasive weeds. These taxa include morphologically and phylogenetically complex groups within Sordariomycetes, such as *Diaporthe*, *Colletotrichum*, and *Fusarium*, which are known for their taxonomic challenges and ecological diversity (Han et al. 2023, Dissanayake et al. 2024, Zhang et al. 2024). Overall, the newly recorded species are distributed across 30 genera, 20 families, and six orders within the classes Dothideomycetes and Sordariomycetes (Fig. 69). Notably, Dothideomycetes emerged as the dominant class in the present study (Fig. 69), with Pleosporales being the most frequently

encountered order (Fig. 70). Within this order, the family Didymosphaeriaceae was particularly well represented (Fig. 71), underscoring its ecological prominence on asteraceous weed hosts. This finding is consistent with the results of Mapook et al. (2020), in which Pleosporales was also recognized as the dominant order, with the highest diversity in the families Didymosphaeriaceae and Phaeosphaeriaceae. Both studies collectively indicate that asteraceous weeds, particularly *C. odorata*, harbor a high diversity of fungi within Dothideomycetes, supporting previous observations by Schoch et al. (2009), Hyde et al. (2013), and Jayasiri et al. (2019) regarding the ecological abundance and taxonomic significance of this class.

The taxonomic novelties and new host records in this study revealed unexplored fungal diversity associated with invasive plant species such as *Bidens pilosa* and *Chromolaena odorata*. These findings focus on weed species, which were often overlooked in mycological surveys, and can serve as important reservoirs of taxonomic and functional novelty. This study highlights the importance of additional sampling on Asteraceae weeds in the future to know the ecological role of weed-associated fungi.

Comparative antimicrobial spectrum and test organisms on *Chromolaena odorata* and *Bidens pilosa*

Previous studies on fungi associated with *Chromolaena odorata* have explored their antimicrobial potential against a range of bacterial and fungal test organisms. The study by Mapook et al. (2020) reported preliminary screening of numerous isolates against *Bacillus subtilis*, *Escherichia coli*, and *Mucor plumbeus*, revealing that several species exhibited measurable zones of inhibition. The inclusion of *M. plumbeus*, a fungal test organism, provided a broad-spectrum assessment of both antibacterial and antifungal activity, highlighting the metabolic versatility of *C. odorata* associated fungi.

In contrast, the present study focused exclusively on antibacterial activity, employing *B. subtilis*, *E. coli*, and *Staphylococcus aureus* as test organisms. The replacement of *M. plumbeus* with *S. aureus* represents a methodological refinement aimed at assessing clinical relevance, given that *S. aureus* is a medically important gram-positive bacterium associated with human infections (Pal et al. 2021).

However, no comprehensive antimicrobial investigations have been conducted comparable to our findings related to *B. pilosa*. The present study therefore, provides the first substantial screening of *B. pilosa*-derived fungi for antibacterial activity.

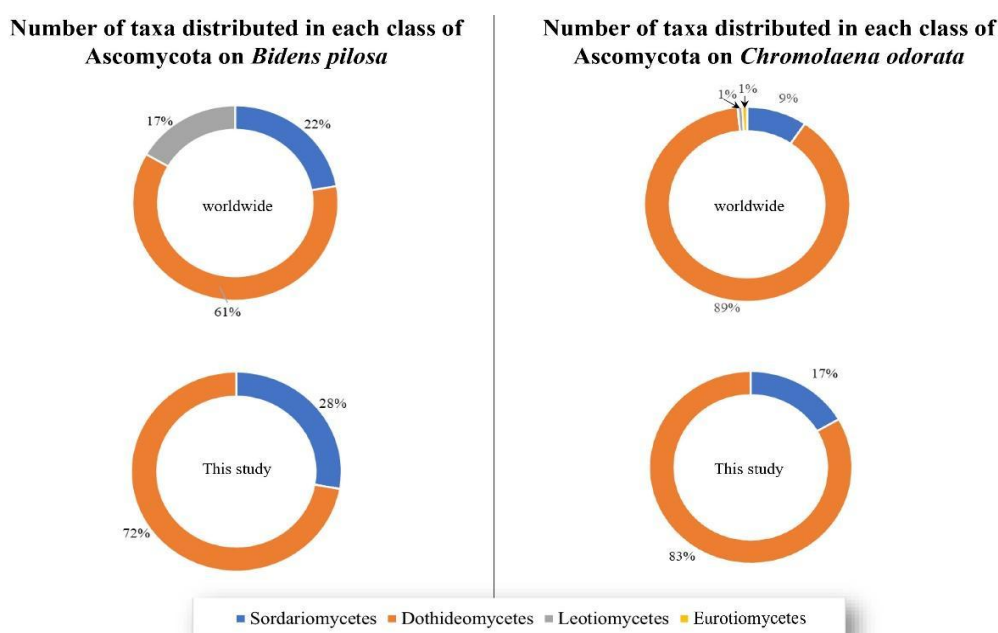


Figure 69 – Numbers of taxa distributed in each class of Ascomycota

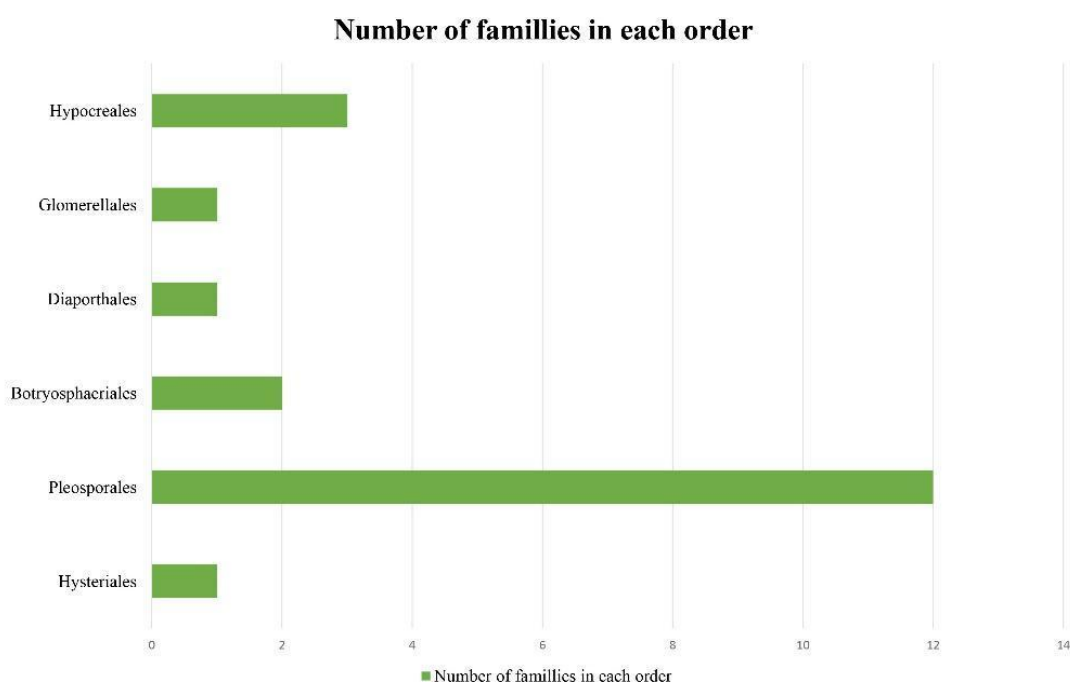


Figure 70 – Numbers of families in each order of Dothideomycetes and Sordariomycetes found in this study

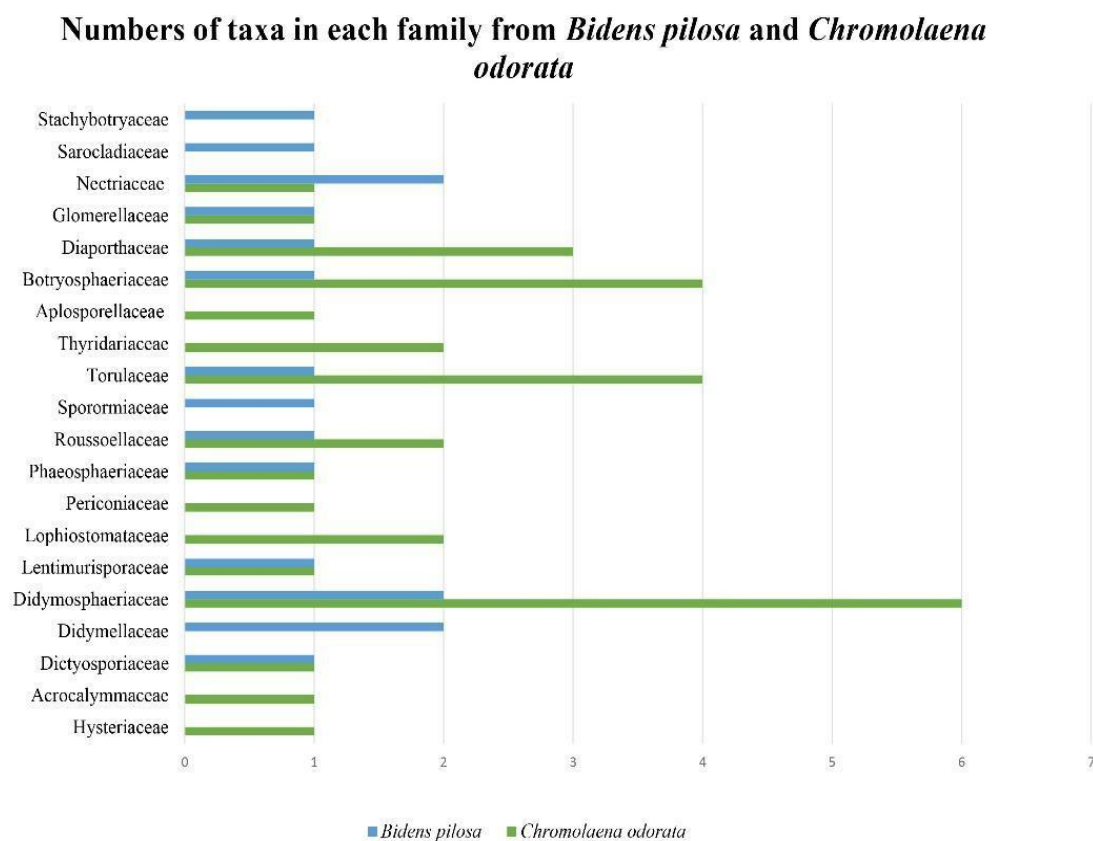


Figure 71 – Numbers of taxa in each family from *Bidens pilosa* and *Chromolaena odorata* found in this study

Antibacterial activity of fungi on *Bidens pilosa* and *Chromolaena odorata*

The antibacterial activity of fungi associated with *B. pilosa* and *C. odorata* is provided in Tables 2 and 3 respectively. The bacteria *Bacillus subtilis* (gram-positive), *Escherichia coli* (gram-negative), and *Staphylococcus aureus* (gram-positive) were all susceptible to the antibacterial action of fungal taxa isolated from *Bidens pilosa* and *Chromolaena odorata*.

Among 17 fungal species identified on *Bidens pilosa*, 11 species inhibited the growth of *B. subtilis*, 11 species were effective against *S. aureus*, and 10 species inhibited *E. coli*. Two species, *Neorousoella entadae* and *Remotididymella fici-microcarpae* showed no inhibition zone against all three test organisms (Fig. 72). *Periconia byssoides*, and *Forliomyces bidentis* were shown to have activity against only Gram-positive bacteria, *B. subtilis* and *S. aureus*. Six species had broad-spectrum antibacterial activity, which can inhibit the growth of both gram-positive and gram-negative bacteria (Table 2).

Among the 29 species identified on *Chromolaena odorata*, 10 species were not subjected to antibacterial screening due to the lack of viable cultures. The findings show that eight fungal species inhibited the growth of *B. subtilis*, three species were effective against *S. aureus*, and eight species inhibited *E. coli*. Ten species, viz., *Austropleospora chromolaenae*, *Bahusandhika indica*, *Chromolaenicola nanensis*, *Dothiorella asteracearum*, *Dothiorella chromolaenae*, *Murichromolaenicola thailandensis*, *Pseudoneoconiothyrium chromolaenae*, *Pseudoneoconiothyrium thailandicum*, *Pseudothyridariella asteracearum*, *Pseudothyridariella thailandica*, showed no inhibitory activity against any of the tested bacterial strains (Fig. 73). Certain species, including *Diaporthe biconispora*, *Lasiodiplodia henanica*, and *Torula canangae* showed antibacterial activity against both gram-positive and gram-negative bacteria. Notably, *Pseudopithomyces chartarum* inhibit only gram-negative bacteria, *E. coli* (Table 3).

The antibacterial activity of fungi associated with both *Bidens pilosa* and *Chromolaena odorata* were evaluated against both Gram-positive (*Bacillus subtilis* and *Staphylococcus aureus*) and Gram-negative (*Escherichia coli*) bacteria, as shown in Fig 74. Several isolates from both hosts exhibited varying inhibition zones, indicating that fungi from invasive weeds possess diverse antibacterial properties.

Table 2 – Preliminary screening of fungi on *Bidens pilosa* for antibacterial properties

Number	Species name	<i>B. subtilis</i> (+)	<i>E. coli</i> (-)	<i>S. aureus</i> (+)
1.	<i>Albifimbria bidentis</i> (MFLUCC 25-0268)	13 mm	11 mm	no inhibition
2.	<i>Bahusandhika bidentis</i> (MFLUCC 25-0255)	15 mm	14 mm	15 mm
3.	<i>Colletotrichum truncatum</i> (MFLUCC 25-0270)	19 mm	12 mm	18 mm
4.	<i>Dendryphion hydei</i> (MFLUCC 25-0286)	no inhibition	14 mm	20 mm
5.	<i>Diaporthe biconispora</i> (MFLUCC 25-0252)	15 mm	12 mm	18 mm
6.	<i>Dictyocheiropora nabanheensis</i> (MFLUCC 25-0265)	9 mm	no inhibition	no inhibition
7.	<i>Forliomyces bidentis</i> (MFLUCC 25-0246)	19 mm	no inhibition	10 mm

Number	Species name	<i>B. subtilis</i> (+)	<i>E. coli</i> (-)	<i>S. aureus</i> (+)
8.	<i>Fusarium bidentis</i> (MFLUCC 25-0258)	13 mm	15 mm	17 mm
9.	<i>Lasiodiplodia theobromae</i> (MFLUCC 25-0266)	no inhibition	13 mm	19 mm
10.	<i>Leptospora thailandica</i> (MFLUCC 25-0267)	15 mm	no inhibition	no inhibition
11.	<i>Montagnula chromolaenae</i> (MFLUCC 25-0247)	no inhibition	9 mm	no inhibition
12.	<i>Neorousoella entadae</i> (MFLU 25-0257)	no inhibition	no inhibition	no inhibition
13.	<i>Periconia byssoides</i> (MFLUCC 25-0256)	15 mm	no inhibition	13 mm
14.	<i>Pseudopithomyces chartarum</i> (MFLUCC 25-0281)	no inhibition	no inhibition	11 mm
15.	<i>Remotididymella anthropophila</i> (MFLUCC 25-0259)	12 mm	14 mm	15 mm
16.	<i>Remotididymella fici-microcarpae</i> (MFLUCC 25-0273)	no inhibition	no inhibition	no inhibition
17.	<i>Sarocladium bidentis</i> (MFLUCC 25-0285)	19 mm	16 mm	22 mm

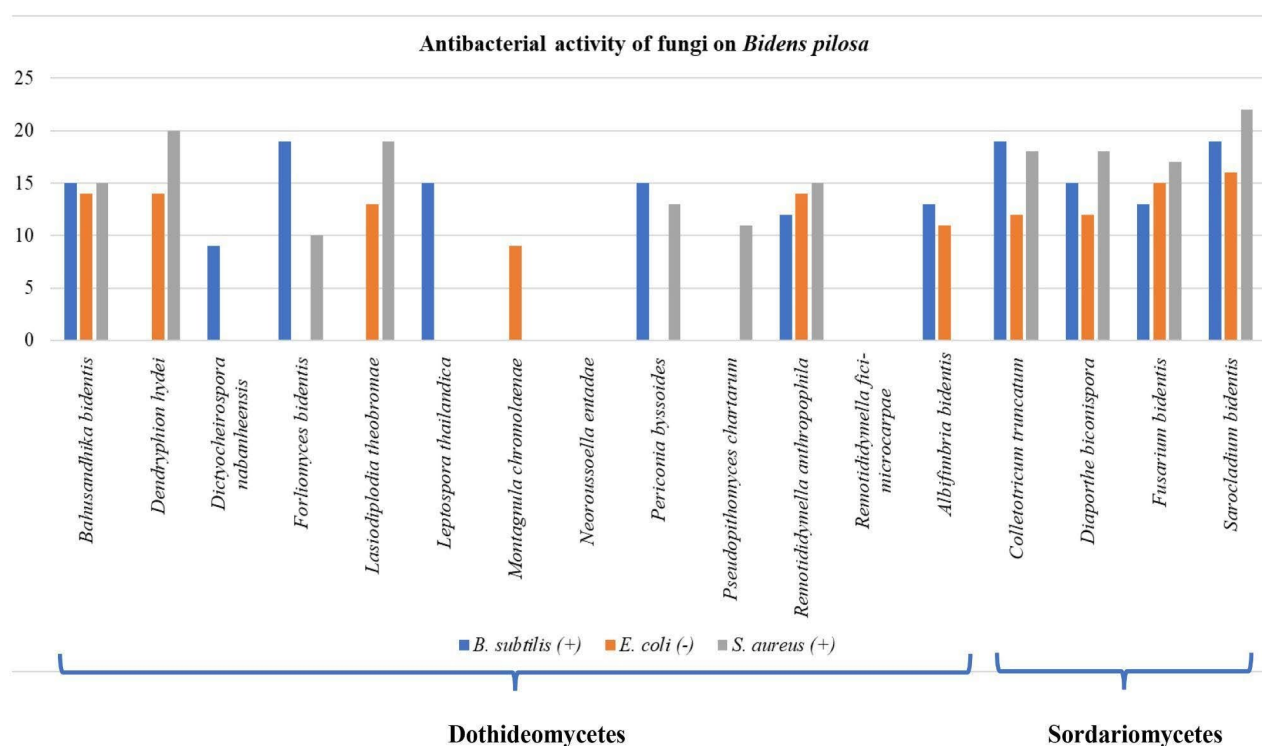


Figure 72 – Antibacterial activity of fungi on *Bidens pilosa* in this study

Table 3 – Preliminary screening of fungi on *Chromolaena odorata* for antibacterial properties

Number	Species name	<i>B. subtilis</i> (+)	<i>E. coli</i> (-)	<i>S. aureus</i> (+)
1.	<i>Aplosporella hesperidica</i> (MFLU 25-0272)	Not studied		
2.	<i>Austropleospora chromolaenae</i> (MFLUCC 25-0277)	no inhibition	no inhibition	no inhibition
3.	<i>Bahusandhika indica</i> (MFLUCC 25-0278)	no inhibition	no inhibition	no inhibition
4.	<i>Chromolaenicola nanensis</i> (MFLUCC 25-0274)	no inhibition	no inhibition	no inhibition
5.	<i>Colletotrichum gigasporum</i> (MFLUCC 25-0262)	14 mm	no inhibition	no inhibition
6.	<i>Dendryphion hydei</i> (MFLUCC 25-0287)	14 mm	11 mm	no inhibition
7.	<i>Diaporthe asteracearum</i> (MFLUCC 25-0263)	10 mm	9 mm	no inhibition
8.	<i>Diaporthe biconispora</i> (MFLUCC 25-0252)	17 mm	18 mm	21 mm
9.	<i>Diaporthe chromolaenicola</i> (MFLUCC 25-0261)	14 mm	12 mm	no inhibition
10.	<i>Dothiorella asteracearum</i> (MFLUCC 25-0275)	no inhibition	no inhibition	no inhibition
11.	<i>Dothiorella chromolaenae</i> (MFLUCC 25-0280)	no inhibition	no inhibition	no inhibition
12.	<i>Fusarium chromolaenae</i> (MFLU 25-0288)	Not studied		
13.	<i>Kalmusia thailandica</i> (MFLU 22-0259)	Not studied		
14.	<i>Lasiodiplodia henanica</i> (MFLUCC 25-0251)	16 mm	17 mm	25 mm
15.	<i>Lasiodiplodia theobromae</i> (MFLUCC 25-0266)	11 mm	no inhibition	no inhibition
16.	<i>Pseudocapulatispora longiappendiculata</i> (MFLU 25-0252)	Not studied		
17.	<i>Montagnula donacina</i> (MFLU 25-0243)	Not studied		
18.	<i>Murichromolaenicola thailandensis</i> (MFLUCC 23-0172)	no inhibition	no inhibition	no inhibition
19.	<i>Neodendryphiella mali</i> (MFLU 25-0237)	Not studied		
20.	<i>Pseudopithomyces chartarum</i> (MFLUCC 25-0281)	no inhibition	10 mm	no inhibition
21.	<i>Pseudolophiostoma chromolaenae</i> (MFLU 25-0253)	Not studied		
22.	<i>Pseudoneoconiothyrium chromolaenae</i> (MFLUCC 25-0284)	no inhibition	no inhibition	no inhibition
23.	<i>Pseudoneoconiothyrium thailandicum</i> (MFLUCC 25-0276)	no inhibition	no inhibition	no inhibition
24.	<i>Pseudothyridariella asteracearum</i> (MFLUCC 25-0283)	no inhibition	no inhibition	no inhibition
25.	<i>Pseudothyridariella thailandica</i> (MFLUCC 25-0279)	no inhibition	no inhibition	no inhibition
26.	<i>Rhytidhysterium bruguierae</i> (MFLU 25-0233)	Not studied		
27.	<i>Torula canangae</i> (MFLUCC 25-0249)	18 mm	10 mm	21 mm
28.	<i>Torula fici</i> (MFLU 25-0269)	Not studied		
29.	<i>Torula mackenzie</i> (MFLU 25-0271)	Not studied		

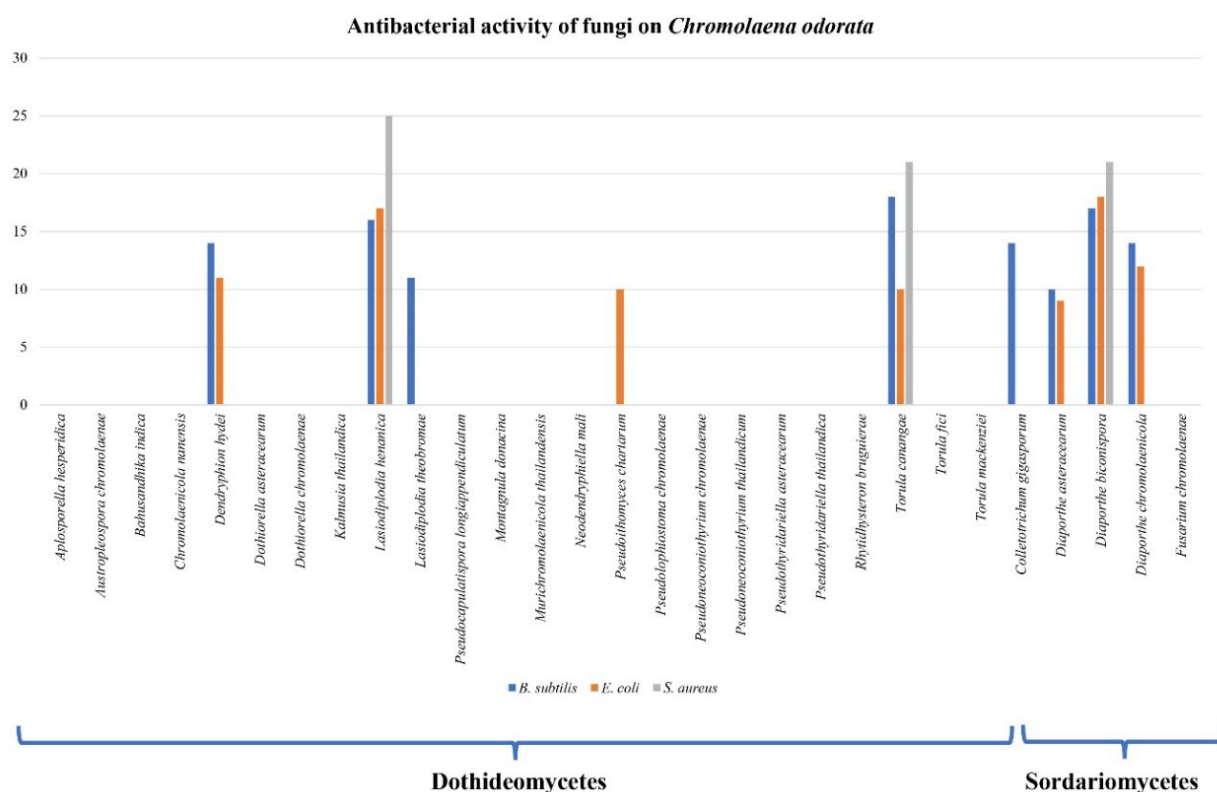


Figure 73 – Antibacterial activity of fungi on *Chromolaena odorata* in this study

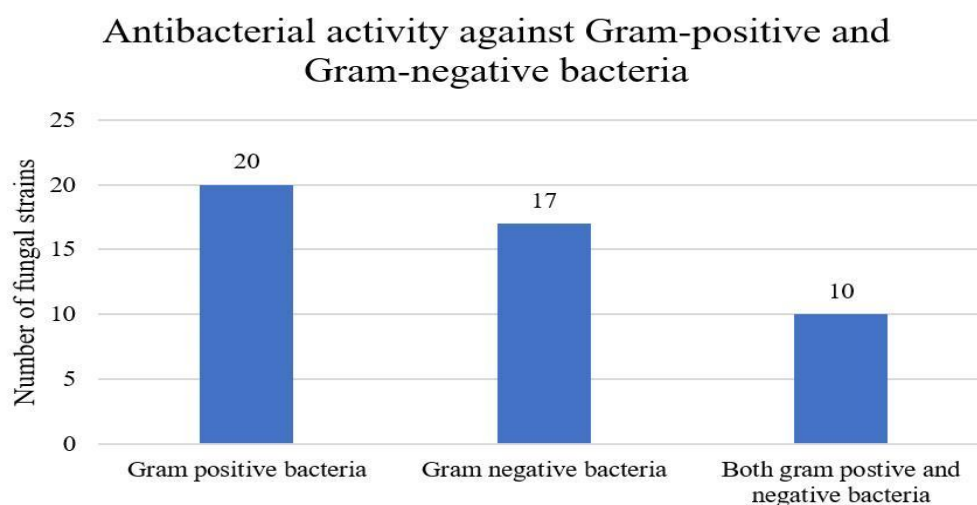


Figure 74 – Antibacterial activity of fungi on *Bidens pilosa* and *Chromolaena odorata* against the Gram-positive and Gram-negative bacteria in this study

Checklist of fungi on *Bidens Pilosa* and *Chromolaena odorata*

A total of 76 fungal taxa has been documented on *Bidens pilosa*, which includes ten unclassified species and the new isolates identified in this research. From this total, we have observed and reported 22 distinct species. According to the USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2025) and pertinent literature, 54 species have been previously recorded. These species are distributed in 18 orders, 33 families, and 44 genera, representing the phyla Ascomycota, Basidiomycota, Glomeromycota, and Oomycota. The phylum Ascomycota is the most dominant, comprising 32 genera across 23 families. Our research contributes to the understanding of the diversity of saprobic fungi included in this checklist (Fig. 75).

In comparison, a total of 161 fungal taxa has been documented on *Chromolaena odorata*, which includes 14 unclassified species and the new isolates identified in this research. From this total, we have observed and reported 35 fungal species. According to the USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2025) and pertinent literature, 109 species have been previously recorded. These species are distributed across 21 orders, 48 families, and 95 genera, representing two phyla; Ascomycota and Basidiomycota. Ascomycota is the most dominant on *Chromolaena odorata* with 89 genera across 43 families. This research contributes to the understanding of the diversity of saprobic fungi included in this checklist (Fig. 76).

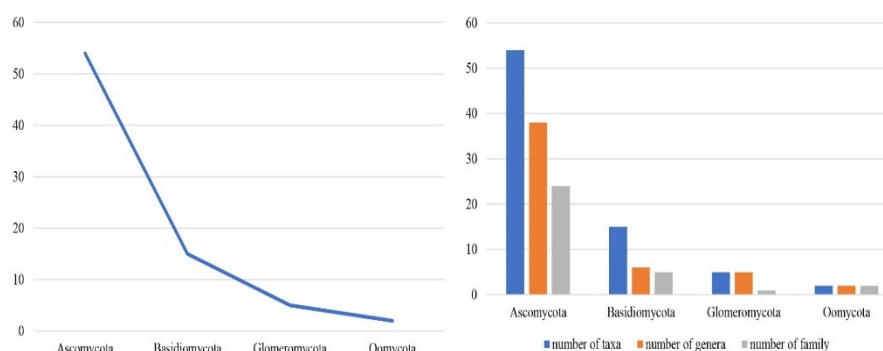


Figure 75 – Worldwide checklist of fungi on *Bidens pilosa*

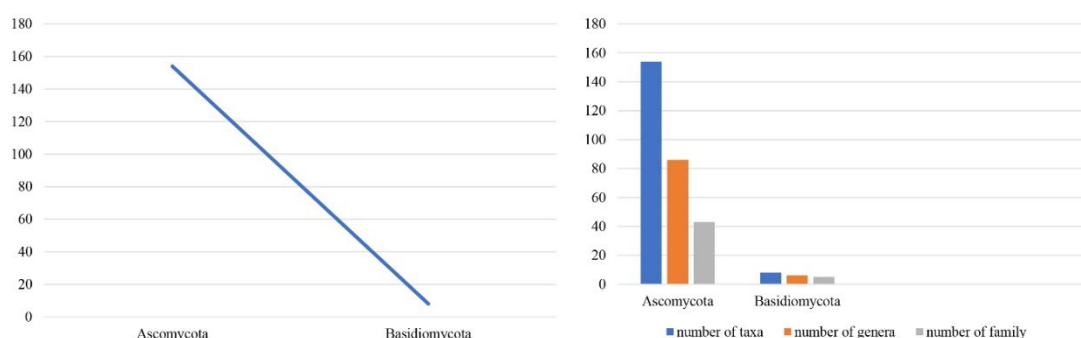


Figure 76 – Worldwide checklist of fungi on *Chromolaena odora*

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DECLARATION ON CONFLICT OF INTEREST

The authors have declared that no competing interests exist.

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