# DIVERSITY AND BIOLOGICAL PROPERTIES OF SAPROBIC ASCOMYCOTA ON *CHROMOLAENA ODORATA* AND *BIDENS PILOSA*

**ZIN HNIN HTET**

**DOCTOR OF PHILOSOPHY**
**IN**
**BIOLOGICAL SCIENCE**

**SCHOOL OF SCIENCE**
**MAE FAH LUANG UNIVERSITY**
**2025**

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**THIS DISSERTATION IS A PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF DOCTOR OF PHILOSOPHY IN BIOLOGICAL SCIENCE**

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**Author:** Zin Hnin Htet

**Examination Committee:**

| | |
|---|---|
| Dhanushka Wanasinghe, Ph. D. | Chairperson |
| Assistant Professor Thilini Chethana Kandawatte Wedaralalage, Ph. D. | Member |
| Adjunct Professor Kevin David Hyde, Ph. D. | Member |
| Ishara Sandeepani Manawasinghe, Ph. D. | Member |
| Assistant Professor Mahamarakkalage Mary Ruvishika Shehali Jayawardena, Ph. D. | Member |

**Advisors:**

.....Advisor

(Assistant Professor Thilini Chethana Kandawattee Wedaralalage, Ph. D.)

.....Co-Advisor

(Adjunct Professor Kevin David Hyde, Ph. D.)

.....Co-Advisor

(Ishara Sandeepani Manawasinghe, Ph. D.)

**Dean:**

.....

(Professor Surat Laphookhieo, Ph. D.)

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| **Author** | Zin Hnin Htet |
| **Degree** | Doctor of Philosophy (Biological Science) |
| **Advisor** | Assistant Professor Thilini Chethana Kandawatte Wedaralalage, Ph. D. |
| **Co-Advisor** | Adjunct Professor Kevin David Hyde, Ph. D.<br>Ishara Sandeepani Manawasinghe, Ph. D. |

## ABSTRACT

*Bidens pilosa* and *Chromolaena odorata* are widespread weeds in the Asteraceae, recognized as invasive species in many regions worldwide. Comparative research on fungal diversity across Asteraceae weeds remains 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 fungi.

In this study, saprobic fungi collected from *Bidens pilosa* and *Chromolaena odorata* in northern Thailand comprise 54 species, distributed across 33 genera, 21 families, and seven orders within Dothideomycetes and Sordariomycetes. Among them, 23 species are identified as novel species (*Albifimbria bidentis*, *Austropleospora chromolaenae*, *Bahusandhika bidentis*, *Bartalinia bidenticola*, *Dothiorella asteracearum*, *D. chromolaenae*, *Diaporthe asteracearum*, *D. chromolaenicola*, *Forliomyces bidentis*, *Fusarium bidentis*, *F. chromolaenae*, *Kalmusia thailandica*, *Memnoniella asteracearum*, *Murichromolaenicola thailandica*, *Neoroussoella chromolaenae*, *Pseudothyridariella asteracearum*, *Ps. thailandica*, *Pseudolophiostoma chromolaenae*, *Pseudoneoconiothyrium chromolaenae*, *Pseudo. thailandicum*, *Pseudoroussoella bidenticola*, *Sarocladium bidentis*, and *Tremateia asteracearum*). In addition, 25 new host records (*Aplosporella artocarpi*, *Acrocalymma pterocarpi*, *Bahusandhika indica*, *Chromolaenicola chiangraiensis*, *C. siamensis*, *C. thailandica*, *Colletotrichum gigasporum*, *C. truncatum*, *Diaporthe biconispora*, *Dictyocheirospora nabanheensis*, *Dendryphion hydei*, *Fusarium hainanense*, *Lasiodiplodia henanica*, *L. theobromae*, *Leptospora thailandica*, *Memnoniella levispora*, *Montagnula chromolaenae*, *Neodendryphiella mali*,

*Neoroussoella entadae*, *Periconia byssoides*, *Pseudoithomyces chartarum*, *Remotididymella anthropophila*, *R. fici-microcarpae*, *Torula canangae*, and *T. mackenziei*) and six reference specimens (*Aplosporella hesperidica*, *Chromolaenicola nanensis*, *Rhytidhysteron bruguierae*, *Lophiostoma longiappendiculatum*, *Montagnula donacina*, and *Torula fici*) were documented. The species boundaries were delineated based on morphology and multi-gene phylogenetic approaches.

Furthermore, the preliminary assays revealed antibacterial activity in 31 species against *Bacillus subtilis*, *Escherichia coli*, and *Staphylococcus aureus*, highlighting their biotechnological potential. Fungal metabolites of ethyl acetate extract of *M. asteracearum* were investigated using LC-QTOF analysis. The results revealed a total of 142 compounds categorized into alkaloids, carbohydrates and derivatives, heterocyclic compounds, organic acids and carboxylic acids, lipids and fatty acids, terpenoids and steroids. The detailed morphologies, illustrations and characterized compounds of *M. asteracearum* were provided together with its chemical profiles.

A worldwide checklist documented 76 fungal taxa on *Bidens pilosa* and 145 fungal taxa on *Chromolaena odorata*, underscoring 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:** Ascomycota, Antibacterial Activity, *Bidens pilosa*, *Chromolaena odorata*, Fungal Metabolites, Phylogeny, Taxonomy, Worldwide Checklist

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# ABBREVIATIONS AND SYMBOLS

| | |
|---|---|
| cm | Centimetre |
| ESI | Electrospray Ionization source |
| et al. | and others |
| h | hour |
| *ibid.* | Ibidem |
| LC-QTOF/MS | Liquid Chromatography-quadrupole Time-of-flight Mass Spectrometry |
| m | metre |
| min | minute |
| mL | Washington |
| mm | millimetre |
| m/z | mass-to-charge ratio |
| n | number |
| nov. | novum (Latin for new thing) |
| PCR | Polymerase Chain Reaction |
| rpm | revolutions per minute |
| RT | Retention Time |
| SMs | Secondary Metabolites |
| UHPLC | Ultra-High Performance Liquid Chromatography |
| viz. | videlicet (Latin for adding precision to the information being provided) |
| $\bar{x}$ | average |
| °C | degree centigrade |
| µm | micrometer |
| % | percentage |

# CHAPTER 1

# INTRODUCTION

## 1.1 Introduction to Ascomycota

The kingdom fungi comprise of eukaryotic organisms such as lichens, molds, mushrooms, rusts, smuts and yeasts, which are important in the ecosystem as well as essential sources for industrial applications (Rossman, 1995; Seaward, 1998; Cereghino & Cregg, 1999; Stajich et al., 2009; Feldbrügge et al., 2013; Lu et al., 2020). Ascomycota is the largest phylum of fungi, currently comprising approximately 99,271 accepted species (Kirk, 2025). Members of ascomycota are remarkably diverse in their morphology, encompassing filamentous fungi, complex cup mushrooms, and single-celled yeasts.

Ascomycota is characterized by the production of sexual spores (ascospores) within a sac-like structure (asci) and includes many commonly encountered fungi. Some species of *Ascomycota* are asexual morph by forming asexual spores (conidia) without a sac-like structure (McConnaughey, 2014). Some Ascomycota can form filamentous or single-celled (like yeasts) (Payne & Cubeta, 2005). The life cycles of various species, including the model organisms *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Neurospora crassa*, *Aspergillus nidulans*, and *Podospora anserina*, have been well investigated (Bennett & Turgeon, 2016). Plant pathogens like *Fusarium graminearum* and *Cochliobolus heterostrophus*, as well as important human pathogens like *Candida albicans* and *Aspergillus fumigatus*, have also been found to exhibit sexual or parasexual cycles (Bennett &Turgeon, 2016).

Species of Ascomycota can be found in various ecological niches from both terrestrial and aquatic environments (Spatafora et al., 1998; Jones et al., 2015; Bärlocher & Boddy, 2016; Egidi et al., 2019; Li et al., 2024). Egidi et al. (2019) studied soil fungi from different collection sites and found the dominance of Ascomycota taxa from soil of 18 different countries. Moreover, Ascomycota species are good decomposers in nature with a well-known decomposition of cellulose and hemicellulose (Hudson, 1968; Lu et al., 2024). Leifheit et al., (2024) performed several *in vitro* tests for leaf and wood litter decomposition

and found that Ascomycota species are the best decomposers with the ability to decompose leaf litter effectively. Ascomycota are also important sources in industrial and biotechnological applications. The early discovery of Penicillin from *Penicillium notatum* highlighted the role Ascomycota played in the antibiotic discovery (Bennett & Chung, 2001). Their industrial use is not limited to the pharmaceutical industry; they also play a significant part in the fermentation and enzyme manufacturing processes, such as *Saccharomyces cerevisiae* in the bread and alcohol industries (Parapouli et al., 2020).

### 1.1.1 Dothideomycetes and Discovery of Secondary Metabolites

Dothideomycetes is the most diverse class of Ascomycota, which contain a diverse lifestyle of fungi such as saprobic, pathogenic, endophytic, epiphytic, fungicolous, lichenicolous, lichenized and rock-inhabiting fungi (Ruibal et al., 2009; Tan et al., 2012; Goodwin, 2013; Jiang et al., 2020; Atienza et al., 2021; Liu et al., 2024). Up to date, Dothideomycetes comprises 20,000 species classified into 50 orders, 223 families, and 1941 genera (Pem et al., 2024). Dothideomycetes species are characterized by ascolocular ascoma with bitunicate, fissitunicate asci (Pem et al., 2021, 2024). Comprehensive phylogenetic analyses and documentation of species in Dothideomycetes are given in Lumbsch and Huhndorf (2010), Hongsanan et al. (2020), Hyde et al. (2013, 2024), Pem et al. (2024). For decades, researchers have been interested in discovering natural products, often known as secondary metabolites (Croteau et al., 2000; Newman & Cragg, 2007). Fungi are one of the sources where interesting secondary metabolites (SMs) can be discovered (Zhong & Xiao, 2009; Gerke & Braus, 2014; Dasila et al., 2024) and Dothideomycetes fungi are also a source to be discovering more SMs. Many genera of Dothideomycetes have been reported in the presence of an array of SMs. For example, *Alternaria* is known to produce a diverse range of SMs, including alkaloids, cyclopeptides, miscellaneous, pyranones, phenolics, quinones, steroids, terpenoids (Lou et al., 2013). These secondary metabolites derived from *Alternaria* species are shown to have effective biological activities such as antibacterial, antitumor, antioxidant, and phytotoxic, which can be used for advanced pharmaceutical and biotechnological application (Zhao et al., 2023). Nzimande et al. (2023) studied an endophytic fungus, *Alternaria alternata* and interestingly the bioactive compounds of this fungus have the potential of being anti-HIV agents.

Moreover, *Botryosphaeria* species are also known to have secondary metabolites such as *B. dothidea* (Xiao et al., 2014), *B. fabicerciana* (Silva et al., 2022), *B. mamane*

(Triastuti et al., 2019), *B. ramosa* (Wu et al., 2019; Hu et al., 2020). Other genera in Dothideomycetes which have been reported to have SMs include *Cladosporium*, *Didymella, Lasiodiplodia*, *Pseudopalawania* (Jiang et al., 2020; Salvatore et al., 2020; Mapook et al., 2020b; Lukina et al., 2024). Some species have been shown to have phytotoxic SMs, which will be important for the development of bioherbicides in the future. For example, *Lasiodiplodia theobromae* and *L. laeliocattleyae* were reported to have mycoherbicide potential (Adetunji et al., 2018; Reveglia et al., 2019; Jampanya et al., 2025). However, several genera are supposed to have bioactive compounds based on the preliminary study of antimicrobial activity, which would be an interesting area of discovering bioactive SMs (Mapook et al., 2020a; This study).

### 1.1.2 Sordariomycetes and Discovery of Secondary Metabolites

Sordariomycetes is one of the largest classes of Ascomycota, reported from diverse hosts in different environmental habitats worldwide. They also found different lifestyles such as saprobic, pathogenic, endophytic, epiphytic, fungicolous, lichenicolous, lichenized fungi (Maharachchikumbura et al., 2016; Luo et al., 2019; Hyde et al., 2021; Zou et al., 2024). The fungi in this class are characterized by perithecial ascomata and inoperculate unitunicate asci (Maharachchikumbura et al., 2016; Luo et al., 2019; Han et al., 2024).

Sordariomycetes comprises many genera which might be interesting sources of SMs. Among the SMs reported from Sordariomycetes, many of which were discovered from Sordariales are well-known sources of SMs with potential biotechnological applications. Fungi from Chaetomiaceae, Diplogelasinosporaceae, Lasiosphaeriaceae, Naviculisporaceae, Podosporaceae, Schizotheciaceae, and Sordariaceae were discovered for SMs production (Ibrahim et al., 2021; Charria-Girón et al., 2022). These fungal taxa showed the presence of diverse compounds, which have biological significance such as antibacterial, antifungal, immunosuppressive, and phytotoxic properties (Charria-Girón et al., 2020).

## 1.2 Ecological Characteristics, Effects and Challenges of Invasive Weeds

Weed is a plant that reduces agricultural production and the environmental or aesthetic value of the land, according to Popay (2008). Merriam-Webster (2021)

defined a weed as “a plant that is not valued on where it is growing and is usually of vigorous growth”. Weeds can be categorized into three types, annuals, biennials and perennials (Tilley, 2019). Plant families with the highest number of weeds are Asteraceae, Poaceae, Fabaceae and Brassicaceae (Onen et al., 2018). Weeds require nutrients, water and sunlight for their survival and compete for space with crop plants. The more intense their competition is, the more damage is caused to the crop yield. Factors that affect weed-crop competition are the timing of weed emergence, their growth form, weed density, and characteristics of weed and crop species (Hasanuzzaman, 2015).

Weeds that can establish, persist and widely spread in natural ecosystems outside the plant’s native range are called invasive weeds (Randall, 1997). Invasive weeds also decrease the quality or cause toxicity to livestock. One of the well-known examples is fireweed. It contains pyrrolizidine alkaloids, which cause liver damage in livestock, in severe cases, increase mortality (Gardner et al., 2006). Invasive weeds also affect the natural environment. They can change the balance of ecological communities and their diversity. Weeds invade native plants by posing a threat to biodiversity (Coutts-Smith & Downey, 2006). They also destroy native habitats and ecosystems, including rivers and forests. Losses caused by invasive weeds are economically more harmful than other crop pests (Gharde et al., 2018). According to Gharde et al. (2018), weeds cause loss to the economies in many countries. For example, it was reported to cost about US$ 11 billion for ten major field crops in 18 states of India (Gharde et al., 2018).

Because of these effects, controlling invasive weeds is necessary to maintain the natural habitat. Fungi are among the most effective biocontrol agents for weeds and represent a promising tool for weed management, as they can help reduce the risks of environmental problems (Htet et al., 2020).

## 1.3 Introduction to *Bidens pilosa* (Asteraceae)

There are 230 to 240 species in *Bidens* distributed from tropical to temperate regions (Norton, 1991; Bartolome et al., 2013; Lizarazu et al., 2024). *Bidens pilosa* (L.) was introduced in 1753 by Carl Linnaeus (Karis & Ryding, 1994).

*Bidens pilosa* is an annual herbaceous plant that can grow to a height of around one to two meters (Rojas-Sandoval, 2018; Shiba et al., 2024). Leaves ovate to lanceolate, pinnate, serrate of entire margin, pilosilose to hirtellous or glabrate surface with truncate to cuneate leaf base (Figure 1.1). Inflorescences are at top of branched stalks. Ray florets are 45 broad, white florets, 5–15 mm long (Shiba et al., 2024). Disk florets tubular, yellow 3–5 mm long, exited in the center. Outer achenes are reddish brown, flat, linear to narrowly cuneate, antrorsely hispidulous margin, with a truncate at the top. Inner achenes are black, long and narrowly ribbed (Mahmoud et al., 2015; Rojas-Sandoval, 2018). It is taxonomically classified as follows:

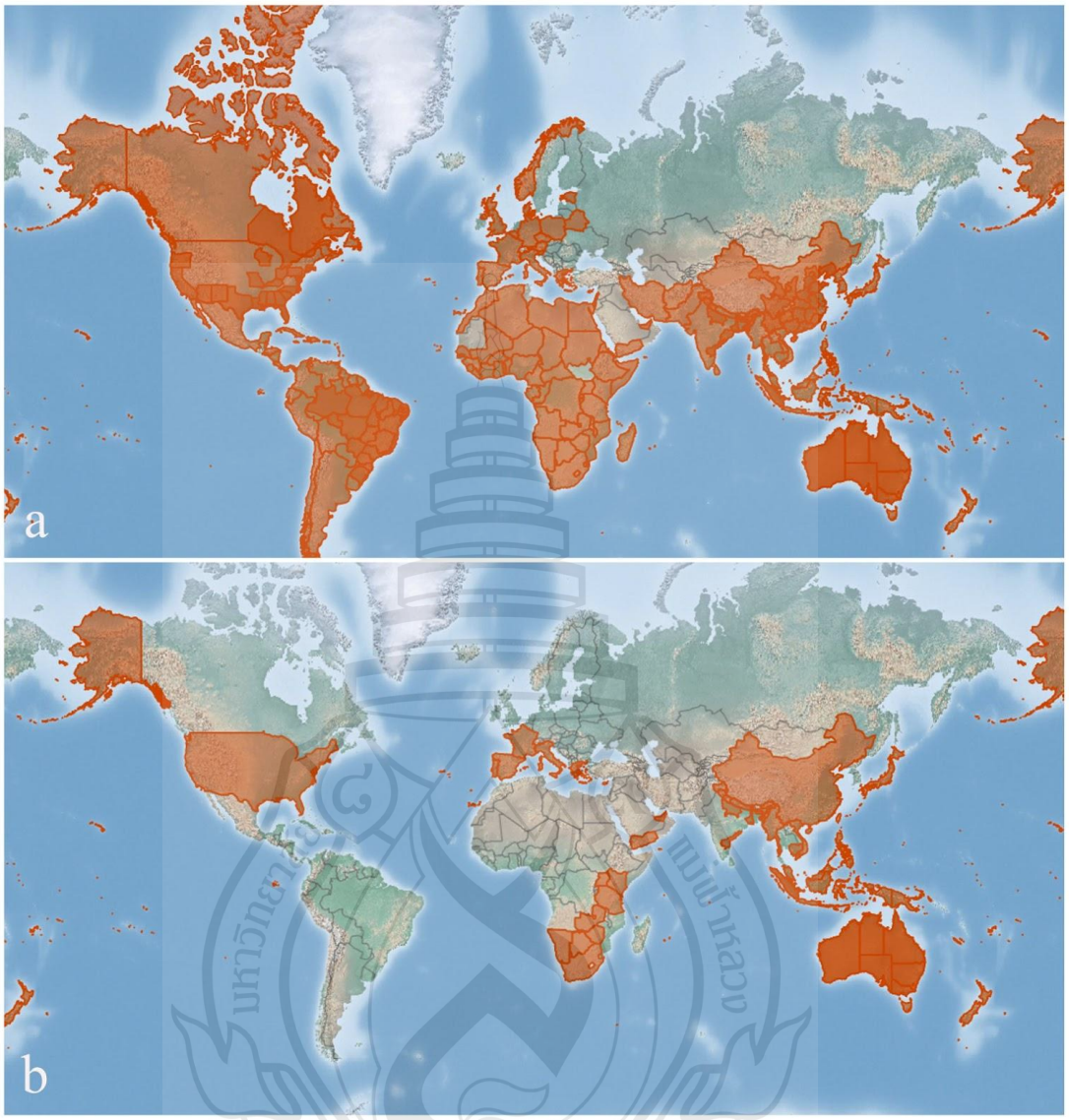
Domain: Eukaryota
Kingdom: Plantae
Phylum: Spermatophyta
Subphylum: Angiospermae
Class: Dicotyledonae
Order: Asterales
Family: Asteraceae
Genus: *Bidens*
Species: *Bidens pilosa*

*Bidens pilosa* is native to South and Central America and it became an invasive weed in many parts of the world (Mahmoud et al., 2015; Shiba et al., 2024; Fan et al., 2025). Since the 1990s, *B. pilosa* is considered as a noxious invasive weed in Latin America and eastern Africa (Mitich, 1994; Wagner et al., 1999). Nowadays, this invasiveness has become aggressive in many parts of the world, including Asia, Africa, Australia, South America and even in the Pacific islands (Shiba et al., 2024; Fan et al., 2025). According to the records of CABI compendium (retrieved

December 25, 2024, from https://doi.org/10.1079/cabicompendium.9148), *Bidens pilosa* is distributed across 160 different countries, including 48 countries in Africa, 29 countries in Asia, 17 countries in Europe, 53 countries in North America and 13 countries in South America (Figure 1.2).


**Note a** Occurrence of *Bidens pilosa* on the roadside, Mueang Chiang Rai, Thailand. **b** Appearance of ray florets and disk florets of *Bidens pilosa.* **c, f** Achenes of *Bidens pilosa.* **d** Inflorescences. **e** leaves.

**Figure 1.1** Morphology of *Bidens pilosa*




**Source** Rojas-Sandoval (2018)

**Note a** Total distribution where *Bidens pilosa* is considered native and non-native.

**b** Invasive distribution where *Bidens pilosa* is considered non-native and problematic.

**Figure 1.2** Total distribution and invasive distribution of *Bidens pilosa*

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 antibronchitis 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 purposes, in herbal remedies for childbirth (Kamatenesi-Mugisha et al., 2017). Beside medicinal applications, Poonpaiboonpipat and Poolkum (2019) discussed the use of *B. pilosa* combined with water irrigation for weed control and rice production.

## 1.4 Introduction to *Chromolaena odorata* (Asteraceae)

*Chromolaena odorata* (L.) R.M. King & H. Rob., was previously known as *Eupatorium odoratum* L. Later, King and Robinson (1970) transferred this plant to the genus *Chromolaena.*

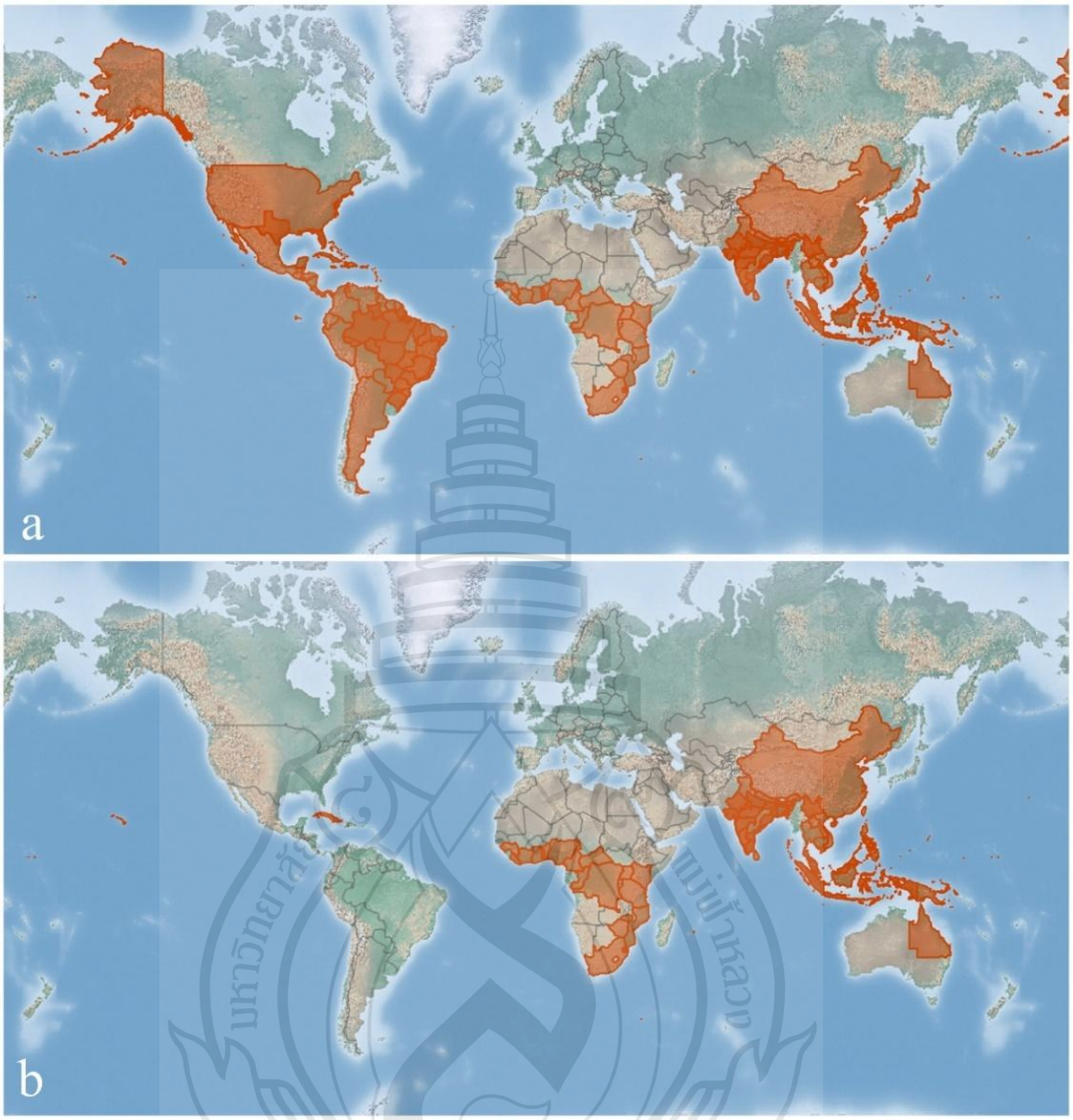
*Chromolaena odorata* is a bushy, herbaceous to woody perennial plant that grows thickly and reaches a height of approximately 2 meters or sometimes higher than 2 meters (Figure 1.3). Leaves are in the opposite arrangement, hairy, rhomboid, serrate margin with 1–2 cm petiole. Stems are erect, soft and become woody,1–3 m high. Flowers range in color from white to pale blue, purple, and lilac (Zachariades et al., 2009). Seeds are dark brown to black, with a whitish hairy tuft at the apex (Holm et al., 1977; McFadyen, 1989; Gautier, 1992; Zachariades et al., 2009). It is taxonomically classified as follows:

Domain: Eukaryota
Kingdom: Plantae
Phylum: Spermatophyta
Subphylum: Angiospermae
Class: Dicotyledonae
Order: Asterales
Family: Asteraceae
Genus: *Chromolaena*
Species: *Chromolaena odorata*

*Chromolaena odorata* is native to Americas (Zachariades et al., 2009) and is an invasive weed affecting many tropical countries, including Thailand (Goodall & Erasmus, 1996; Muniappan et al., 2005; Zachariades et al., 2010; Catarino et al., 2019). This invasive species can have many negative impacts on the environment, agriculture and wildlife (Rai & Singh, 2024). According to the records of CABI compendium (retrieved December 25, 2024, from https://doi.org/10.1079/cabicompendium.23248), *Chromolaena odorata* is distributed across 88 different countries, including 20 countries in Africa, 17 in Asia, nine in Oceania, 31 in North America and 11 in South America (Figure 1.4).


**Note** **a** Occurrence of *Chromolaena odorata* on the roadside, Mueang Chiang Rai, Thailand. **b** Appearance of leaf arrangement. **c** Leaves. **d, e** Inflorescences. **f** flowers.

**Figure 1.3** Morphology of *Chromolaena odorata*




**Source** Bakewell-Stone (2025)

**Note** **a** Total distribution where *Chromolaena odorata* is considered native and non-native. **b** Invasive distribution where *C. odorata* is considered non-native and problematic.

**Figure 1.4** Total distribution and invasive distribution of *Chromolaena odorata*

*Chromolaena odorata* has been widely used as a traditional medicine for treating wound, burns, and skin infections (Sirinthipaporn & Jiraungkoorskul, 2017). Because of the presence of several phytochemical compounds, *C. odorata* is reported to have anticancer, antidiabetic, anti-hepatotoxic, anti-inflammatory, antimicrobial, and antioxidant properties (Zahara, 2019; Ajay et al., 2021, Gaspersz

et al., 2023). Moreover, *C. odorata* is important in livestock nutrition (Aro et al., 2009). The experiment of Akintunde et al. (2021) showed that *C. odorata* leaf meal (COLM), which contains vital nutrients and phytochemicals, can be safely used as a non-toxic feed supplement for broiler chickens. *Chromolaena odorata* can be utilized as animal feed by enhancing the nutrients with bio-fermentation process (Oematan et al., 2020). Furthermore, *C. odorata* plays an interesting role in pesticidal properties (Mathur & Davou, 2007; Udebuani et al., 2015; Ezena et al., 2016; Pasaru et al., 2024). Moreover, different solvent extracts from various plant parts of *C. odorata* have demonstrated significant antimicrobial properties (Vital et al., 2009; Thophon et al., 2016; Hridhya et al., 2017; Mathew et al., 2022), highlighting its potential for biotechnological applications.

## 1.5 Research Objectives

1.5.1 To study taxonomy of the saprobic fungi on *Bidens pilosa* and *Chromolaena odorata*

1.5.2 To provide a worldwide checklist of fungi on *Bidens pilosa* and *Chromolaena odorata*

1.5.3 To provide morphological descriptions and molecular phylogeny of saprobic fungi on *Bidens pilosa* and *Chromolaena odorata*

1.5.4 To study biological activities and bioactive compounds from the selected fungal strains

## 1.6 Research Contents

The thesis is divided into six chapters.

Chapter 1 is the general introduction of my research, consisting of literature review on Ascomycota, Dothideomycetes and Sordariomycetes fungi and their importance in the production of secondary metabolites. Detailed information of two selected hosts in Asteraceae, *Bidens pilosa* and *Chromolaena odorata*, by providing their classification, distribution and utilization. The objective and content of my study are also provided.

Chapter 2 includes materials and methods to provide comprehensive information on the methodologies used in my study.

Chapter 3 includes morphological descriptions, illustrations, phylogenetic analyses of the fungal species found on *Bidens pilosa* and *Chromolaena odorata.* A preliminary investigation of the antibacterial results of fungi on *B. pilosa* and *Chromolaena odorata* are provided together with a worldwide checklist of fungi occurrence on these two weeds.

Chapter 4 provides the chemical profiling of *Memnoniella asteracearum*, along with its morphological features and detailed descriptions.

Chapter 5 is the overall conclusion, including main outcomes of the study, highlighting research advantages, future research directions and a list of publications.

# CHAPTER 2

# MATERIALS AND METHODS

## 2.1 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 (Figure 2.1). The location map (Figure 2.1) was created using DIVA-GIS (v.7.4) focusing on Thailand's provincial boundaries. All specimens were kept in plastic bags labeled with collection details and taken into the laboratory. Specimens were deposited at the Herbarium of Mae Fah Luang University (Herb. MFLU), while living cultures were maintained at the Mae Fah Luang University Culture Collection (MFLUCC). Faces of Fungi (FoF) numbers and Index Fungorum (IF) numbers were obtained as instructed by Jayasiri et al. (2019) and Index Fungorum (2025). Moreover, the species descriptions were submitted to the GMS Microfungi database (Chaiwan et al., 2021).

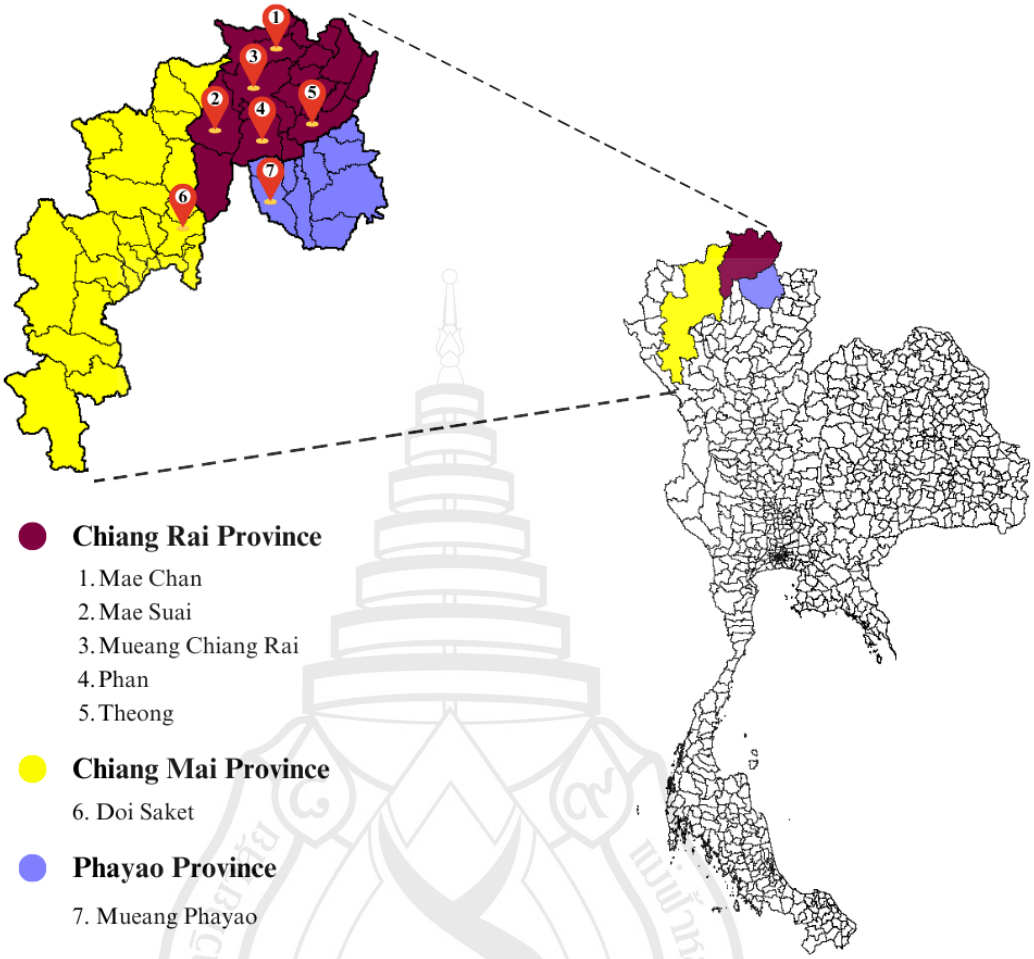



**Figure 2.1** Geographical locations where samples were collected in northern Thailand

## 2.2 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 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.

## 2.3 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 2.1). The PCR primers used in this study are shown in Table 2. 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 2.1** Primers used in this study

| Gene | Primers | | References |
|---|---|---|---|
| | Forward | Reverse | |
| Large subunit (LSU) | LR0R | LR5 | Vilgalys and 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 (*tef*1- $\alpha$) | EF1-983F | EF1-22185R | Rehner and Buckley (2005), O'Donnell et al. (1998), Carbone and Kohn (1999) |
| | EF1-728F | EF2 | |
| RNA polymerase II subunit (*rpb*2) | RPB2-5f | RPB2-7cr | Liu et al. (1999), Reeb et al. (2004) |
| Beta-tubulin (*tub*2) | Bt2a | Bt2b | |
| Glyceraldehyde-3-Phosphate Dehydrogenase (GAPDH) | GDF | GDR | Templeton et al. (1992) |
| Chitin synthase (CHS) | CHS79F | CHS345 | Carbone and Kohn (1999) |
| Actin (ACT) | ACT-512F | ACT-783R | Carbone and Kohn (1999) |

## 2.4 Sequence Alignment 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 multigene phylogenetic analyses were conducted using different gene regions (Table 2.1). 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. RAxML and Bayesian analyses were carried out on the CIPRESS Science Gateway Portal (https://www.phylo.org) using the methods described by Miller et al., (2010). Maximum likelihood analysis was performed by RAxML-HPC v.8 (Stamatakis, 2014) with rapid bootstrap analysis, followed by 1000 bootstrap replicates and the GTRGAMMA substitution model. MrBayes was used to perform BI analysis on XSEDE 3.2.7 (Ronquist et al., 20120), with tree samples taken at every 1000th generation during the 5M generation run of four concurrent Markov chains. The first 25% of the trees were removed as part of the burn-in phase, and calculations for the Posterior Probability were made for the remaining 75% of the trees (PP) (Rannala & Yang, 1996; Zhaxybayeva & Gogarten, 2002). The phylogenetic tree was displayed using Fig Tree v.1.4.0 (Rambaut, 2012) and was modified in Microsoft Office PowerPoint v. 2013.

## 2.5 Preliminary Screening of Antibacterial Activity

Preliminary screening for antimicrobial activity was carried out following the methods of Mapook et al. (2020). Antibacterial discs of Ampicillin were used as a positive control for screening (Alam et al., 2019). Preliminary antibacterial activities were tested against *Bacillus subtilis* (TISTR 1248), *Escherichia coli* (TISTR 527), and

*Staphylococcus aureus* (TISTR Y4b) using the agar plug diffusion method (Balouiri et al., 2016). Bacterial test organisms obtained from the Scientific and Technological Instrument Center; Mae Fah Luang University were grown on nutrient agar (NA) for 24 h. After 24 h of inoculation, 2–3 loops of the bacterial test organisms were transferred to the nutrient broth. Before adding microbial suspensions to the sterile mueller-hinton (MH) agar media, cell counts were performed on the suspensions ($6.7 \times 10^5$ cells/mL), as detailed by Mapook et al. (2020). Fungal mycelium plugs from my isolates were transferred to a solid medium plate and allowed to grow at room temperature for 24–48 h. Inhibition zones were measured and compared to the positive control.

## 2.6 Fermentation and Extraction

Actively growing fungal mycelia were used for fungal fermentation. Five mycelium plugs from malt extract agar (MEA) were cut and transferred to a 500 ml Erlenmeyer flask with 250 ml of yeast malt broth (YMB) by ensuring a pH of 6.3. A total 5000 ml of seed cultures and 250 ml of control Erlenmeyer flasks were incubated on an incubator shaker Innova 43/43R (Eppendorf, Germany) at 140 rpm, 23°C in dark conditions for two weeks. The extraction was carried out after 3 days of glucose depletion as monitored by the glucose strip test using Bayer Harnzuckerstreifen, (Bayer, Leverkusen, Germany). Fungal mycelium and supernatant were separated by using vacuum filtration.

The supernatant was mixed with (5000ml × 0.03 =150g) 3% Amberlite XAD-16N adsober resin (Sigma-Aldrich, Deisenhofen, Germany) and stirred for 1 h and filtered to remove the culture broth. The XAD resin was dried with an adequate amount of methanol (MeOH) and incubated in an ultrasonic bath for 30 min. Then, XAD resin was removed from methanol by filtration. Thereafter, the methanol elute was evaporated and remaining oily residue was dissolved in 200 ml of MilliQ water. This suspension was extracted with equal volume of ethyl acetate for 3 times and dried over sodium sulfate.

The extracts were evaporated using rotary evaporator (Gibthai, Thailand). The remaining residues were dissolved in 1-4 ml of methanol (MeOH) and transferred into 5 ml vials, which weight is measured before filling the extract. The extract was then dried in a vacuum chamber, with the vial lid covered in aluminum foil.

## 2.7 Chemical Profiling of Fungal Extracts

Chemical profiling of *Memnoniella asteracearum* was performed using High-Performance Liquid Chromomatography (HPLC) and Liquid Chromatography Quadrupole Time-of-Flight Mass Spectrometry (LC-QTOF). HPLC was performed using a Photodiode Array (PDA) detector from Waters, USA. Separation was carried out on a Kinetex® 5 µm EVO C18 100Å (150 × 2.1 mm) LC column, maintained at 30°C. The mobile phase consisted of water with 0.2% formic acid (A) and methanol (B). The column was eluted at a flow rate of 0.2 mL/min with the following linear gradient: 5–30% (B) from 0–8 min, 30% (B) from 8–10 min, 30–95% (B) from 10–18 min, 95% (B) from 18–22 min, 95–5% (B) from 22–25 min, and 5% (B) from 25–32 min. Samples were analyzed using HPLC with the PDA detector set at wavelengths of 256 and 425 nm. Data analysis was performed using Empower 3 software. LC-QTOF analysis was conducted using Aligent 1290 infinity II/G6545B QTOF/MS equipped with an Electrospray Ionization (ESI) source. The instrument was operated in both positive and negative ionization modes with UHPLC pressure (1,300) and Mass Range (100-10,000).

# CHAPTER 3

# TAXONOMY, BIOLOGICAL PROPERTIES AND WORLDWIDE CHECKLIST OF SAPROBIC ASCOMYCOTA ON *BIDENS PILOSA* AND *CHROMOLAENA ODORATA*

## 3.1 Introduction

As a major driver of biodiversity loss, invasive plant species threaten the natural environment and human health globally (Hooper et al., 2005; Hejda et al., 2009; Pyšek et al., 2012; Blackburn et al., 2014; Jeschke et al., 2014; Kumschick et al., 2015; Weidlich et al.; 2020). Invasive plant species disrupt natural community assembly but and act as one of the most significant impediments to restoring native ecosystems (D'Antonio & Meyerson, 2002; Weidlich et al.; 2020).

*Bidens pilosa* is a widespread weed in tropical, subtropical and warm temperate regions (Arthur et al., 2012). This weed is a diverse annual herb native to tropical and Central America (Arthur et al., 2012) and is considered an invasive weed in Thailand (Zungsontiporn, 2007). Even though several studies have been conducted on fungi associated with *Bidens pilosa* (Guatimosim et al., 2015; Zhang et al., 2018; Li et al., 2020), the comprehensive fungal diversity of *Bidens pilosa* is still yet to be understood. Fungi associated with *Bidens pilosa* have been observed in some studies, and the reported species belong to the families Albuginaceae, Apiosporaceae, Botryosphaeriaceae, Ceratobasidiaceae, Cladosporiaceae, Diaporthaceae, Erysiphaceae, Glomerellaceae, Mycosphaerellaceae, Nectriaceae, Periconiaceae, Peronosporaceae, Phyllostictaceae, Sclerotiniaceae, Stachybotryaceae, Tetraplosphaeriaceae, and Torulaceae (Abdou et al., 2010; Guatimosim et al., 2015; Zhang et al., 2018; Li et al., 2020).

*Chromolaena odorata* (Asteraceae) is also an invasive weed affecting many tropical countries, including Thailand (Goodall & Erasmus, 1996; Muniappan et al., 2005; Zachariades et al., 2010; Catarino et al., 2019). The invasiveness of this weed has led to many negative impacts on natural biodiversity and the economy (Hu et al., 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 et al., 2009; Thophon et al., 2016; Hridhya et al., 2017; Mathew et al., 2022), highlighting its potential for biotechnological applications.

## 3.2 Taxonomy

**Class Dothideomycetes** sensu O.E. Erikss & Winka

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

**Pleosporales** Luttr. ex M.E. Barr

### 3.2.1 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*, *Hysterodifractum*, *Hysteroglonium*, *Oedohysterium*, *Ostreichnion*, *Pseudoscypha*, *Psiloglonium*, and *Rhytidhysteron* (Hyde et al., 2024).

***Rhytidhysteron*** Speg

*Rhytidhysteron* was introduced by Spegazzini (1881) with *R. brasiliense* designated as the type species (Clements & Shear, 1931). *Rhytidhysteron* 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 (De Silva et al., 2020; Thambugala et al., 2016; Soto-Medina & Lücking, 2017; Wanasinghe et al., 2021; Ren et al., 2022; Du et al., 2023). Recently, there are 43 species listed in the Index Fungorum (2025). In this study, *Rhytidhysteron bruguierae* was reported as a reference specimen, based on a combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data (Figure 3.1).

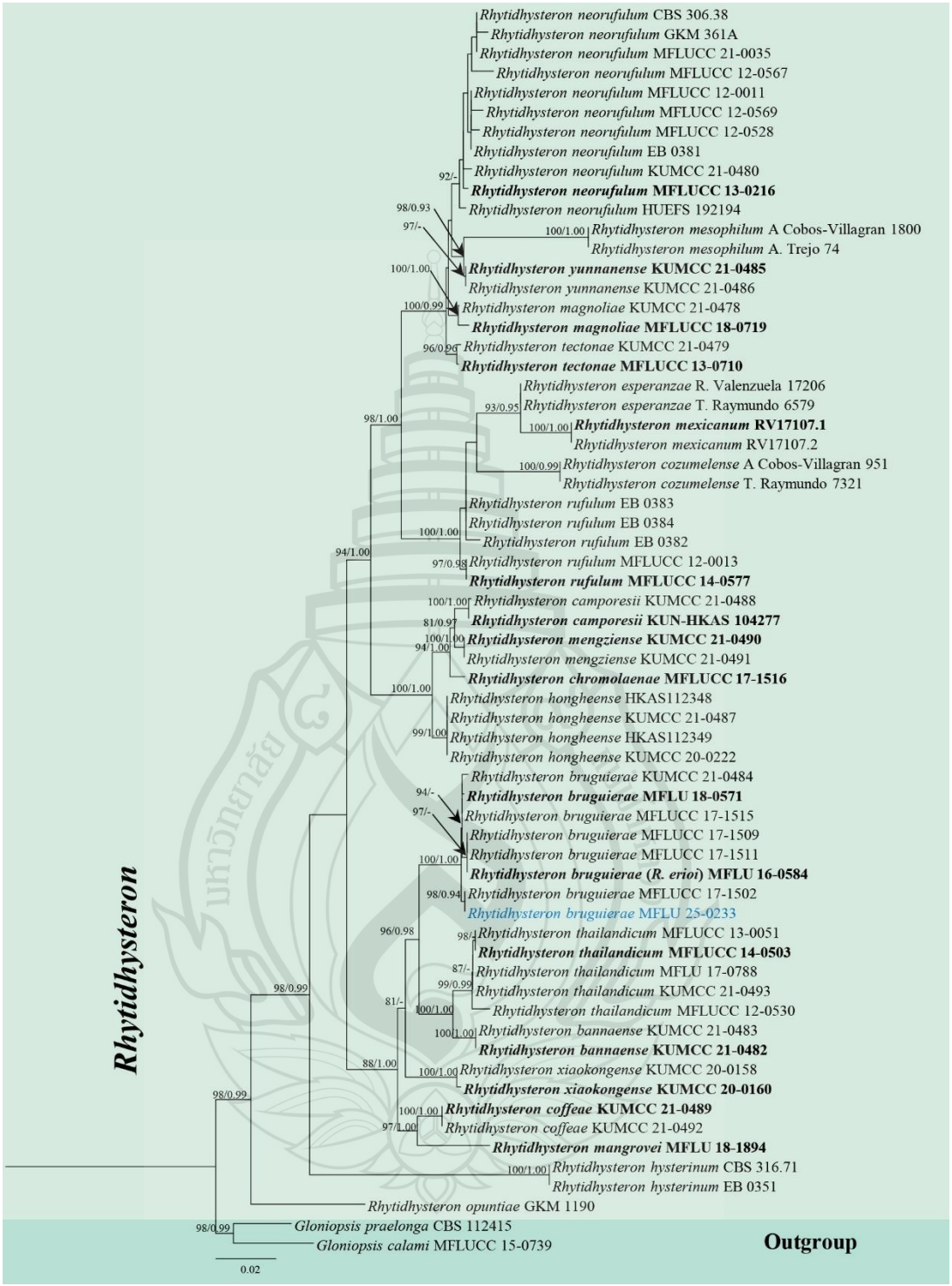



**Figure 3.1** Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Gloniopsis praelonga* (CBS 112415) and *G. calami* (MFLUCC 15-073).

***Rhytidhysteron bruguierae*** Dayarathne, Mycosphere 11(1): 20 (2020)

*Index Fungorum number*: IF556574*, Facesoffungi number*: FoF 06154*,* Figure 3.2

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph**: *Ascomata* 205–300 × 500–600 µm ($\overline{x}$ = 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 ($\overline{x}$ = 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 ($\overline{x}$ = 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, **a reference specimen**).

*GenBank*: **SSU**: PV996952; **ITS**: PV870577; ***tef*1-*α***: PX255031; ***rpb*2**: 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 (Figure 3.1), my strain (MFLU 25-0233) grouped within *Rhytidhysteron bruguierae* clade, sister to MFLUCC 17-1502 with 98% ML and 0.94 BYPP bootstrap support. My collection is similar in morphology to the type strain, *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 my collection and phylogenetically related species. *Rhytidhysteron bruguierae* was previously reported on the same host (*Chromolaena odorata*) within the same locality,

Thailand (Mapook et al., 2020). Therefore, this collection is designated as a reference specimen for *R. bruguierae* and the second record on *Chromolaena odorata* from northern Thailand.


**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d** Peridium. **e, i** Pseudoparaphyses. **g–j** Asci. **k–p** Ascospores. Scale bars: a = 1 mm, b=500 µm, c=100 µm, d=20 µm, e, f=5, g–j=30 µm, k–p=10 µm.

**Figure 3.2** *Rhytidhysteron bruguierae* (MFLU 25-0233, a reference specimen)

### 3.2.2 Acrocalymmaceae Crous & Trakun

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

***Acrocalymma*** Alcorn & J.A.G. Irwin

*Acrocalymma* was introduced by Alcorn and 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 accepted in Index Fungorum (2025). In this study, *Acrocalymma pterocarpi* was reported as a new record based on a combined LSU, SSU, ITS, and *tef*1-*α* sequence data (Figure 3.3).

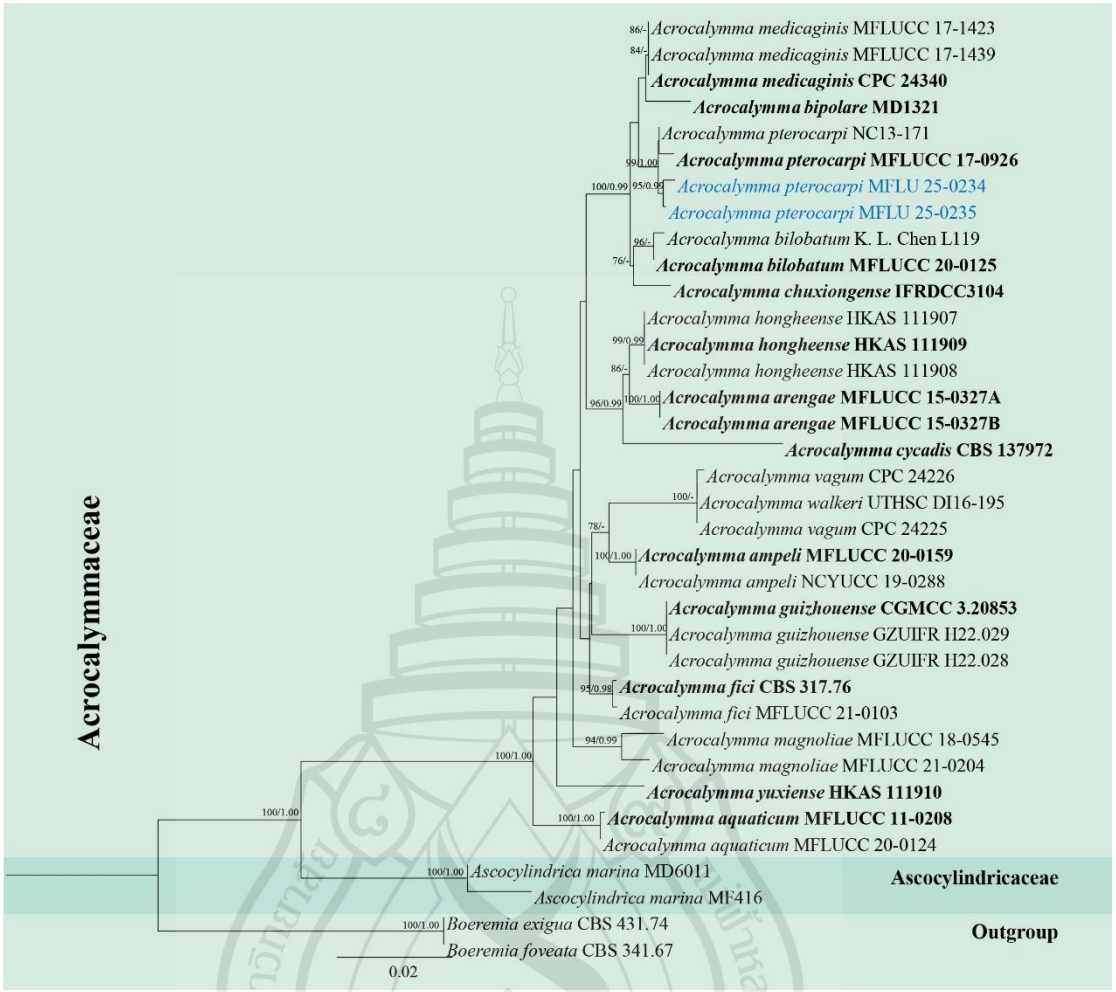



**Figure 3.3** Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Boeremia 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)

*Index Fungorum number*: IF555528, *Facesoffungi number*: FoF05228, Figure 3.4

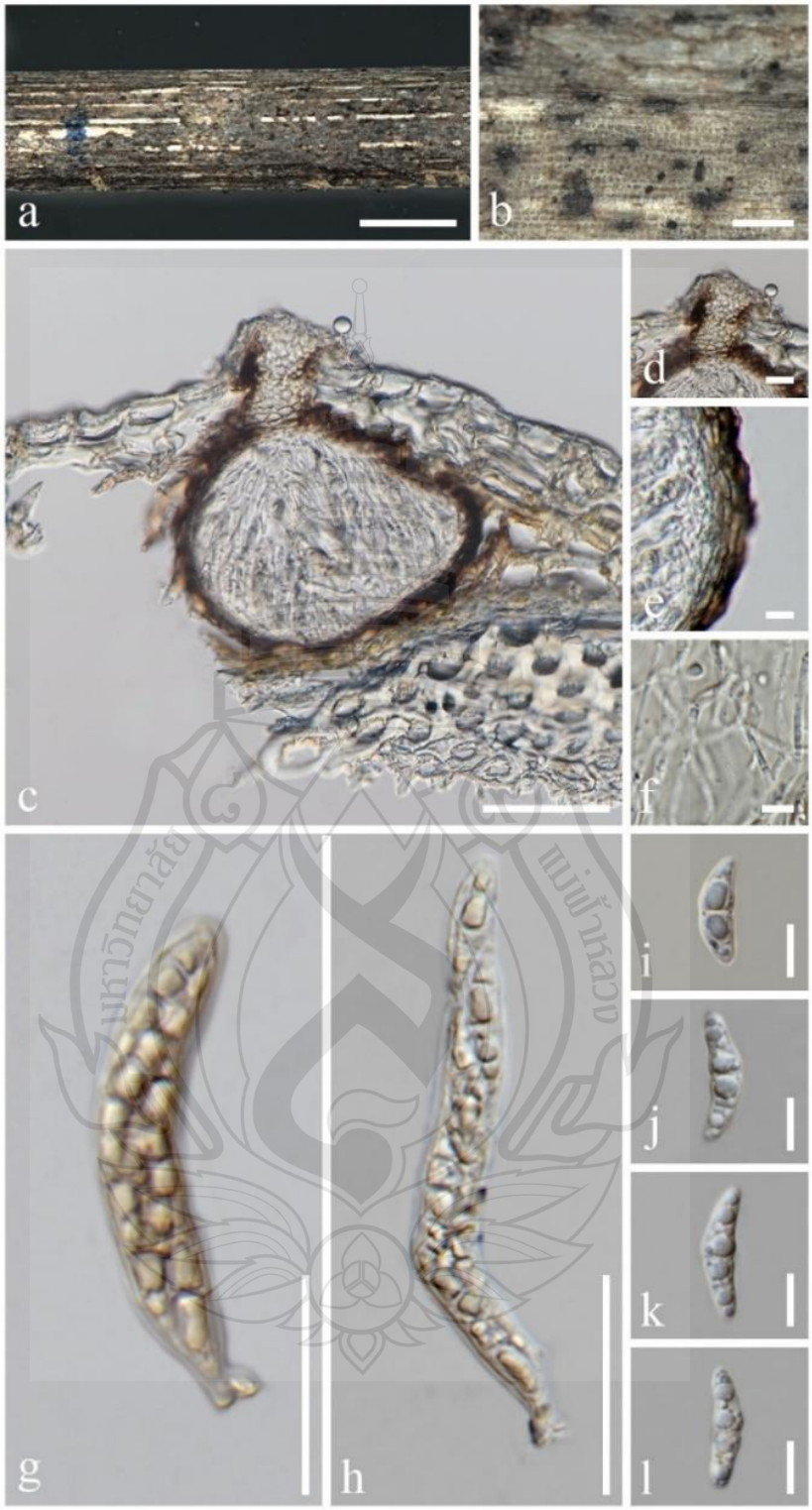
*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 100–150 × 110–140 µm ($\bar{x}$ = 123.5 × 131.4 µm, n = 5), immersed to semi-immersed, globose to subglobose, with an ostiole. *Ostiole* central, papillate. *Peridium* 10–20 µm wide, composed of two to three layers of brown cells of *textura angularis*. *Hamathecium* comprises of 1–2 µm wide, filliform, 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*., on dead stems of *Chromolaena odorata* (Asteraceae), 14 March 2023, Zin Hnin Htet (CO-DP-6, MFLU 25-0234, **a reference specimen**)

*GenBank*: **LSU**: PV992403, PV992404; **SSU**: PV996953, PV996954; **ITS**: PV870578, PV870579; ***tef*1-*α***: PX255032, 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).

*Note*: In the phylogenetic analysis (Figure 3.3), my 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. My 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 my 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.




**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d** Ostiole. **e** Peridium. **f** Pseudoparaphyses. **g–h** Asci. **i–l** Ascospores. Scale bars: a = 1 mm, b=200 µm, c=50 µm, d, f=5, g, h =30 µm, e, i, j, k, l=10 µm

**Figure 3.4** *Acrocalymma pterocarpi* (MFLU 25-0234, a new host record)

### 3.2.3 Dictyosporiaceae Boonmee & K.D. Hyde

Dictyosporiaceae was introduced by Boonmee et al. (2016), to accommodate holomorphic group saprobic fungi which are characterized asexually by cheirosporous, 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 (Kodsueb et al., 2007; Boonmee et al., 2016; Li et al., 2017; Tibpromma et al., 2018; Yang et al., 2018; Wijayawardene et al., 2020; Atienza et al., 2021; Jiang et al., 2021; Tian et al., 2022; Shen et al., 2022). There are 21 genera accepted in Dictyosporiaceae (Hyde et al., 2024). In this study, I reported *Dictyocheirospora nabanheensis* and *Neodendryphiella mali* as new records based on combined sequence data of LSU, SSU, ITS, and *tef*1-*α* (Figure 3.5).

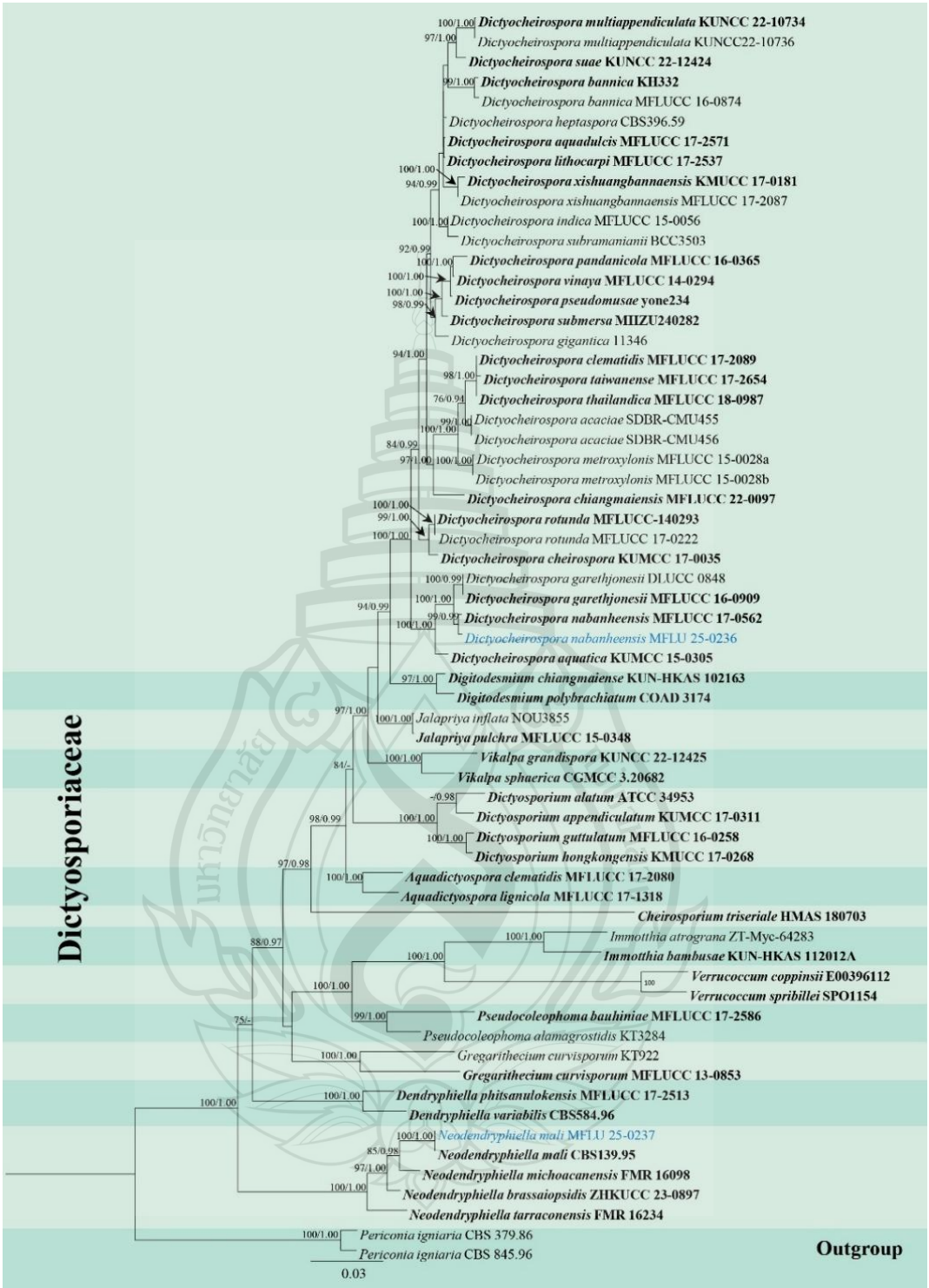



**Figure 3.5** Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Periconia igniaria* (CBS 379.86 and CBS 845.96)

***Dictyocheirospora*** M.J. D'souza, Boonmee & K.D. Hyde

Boonmee et al. (2016) introduced *Dictyocheirospora* to accommodate three other cheiroid genera, *Dictyopalmispora*, *Jalapriya*, and *Vikalpa* in Dictyosporiaceae. Dictyosporiaceae was typified by *Dictyocheirospora rotunda*, and characterized by pale brown, complanate or non-complanate, and euseptate or distoseptate conidia. Currently, there are 29 species accepted in *Dictyocheirospora* (Shu et al., 2024, Index Fungorum 2025). In this study, I reported *Dictyocheirospora nabanheensis* as a new host record based on the combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data.

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

*Index Fungorum number*: IF554474, *Facesoffungi number*: FoF04483, Figure 3.6

*Saprobic* on the 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* 4–6 × 2.5–4 µm ($\overline{x}$ = 5 × 3.34 µm, n = 10), holoblastic, monoblastic, integrated, terminal, determinate, hyaline, smooth-walled. *Conidia* 33–45 × 12–20 µm ($\overline{x}$ = 36.2 × 16.6 µm, 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* 28–40 × 4–6 µm ($\overline{x}$ = 31.8 × 5 µm, n = 20), digitate, cylindrical, straight or slightly curved, arising from a basal cell, 6–9 distosepta, 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.

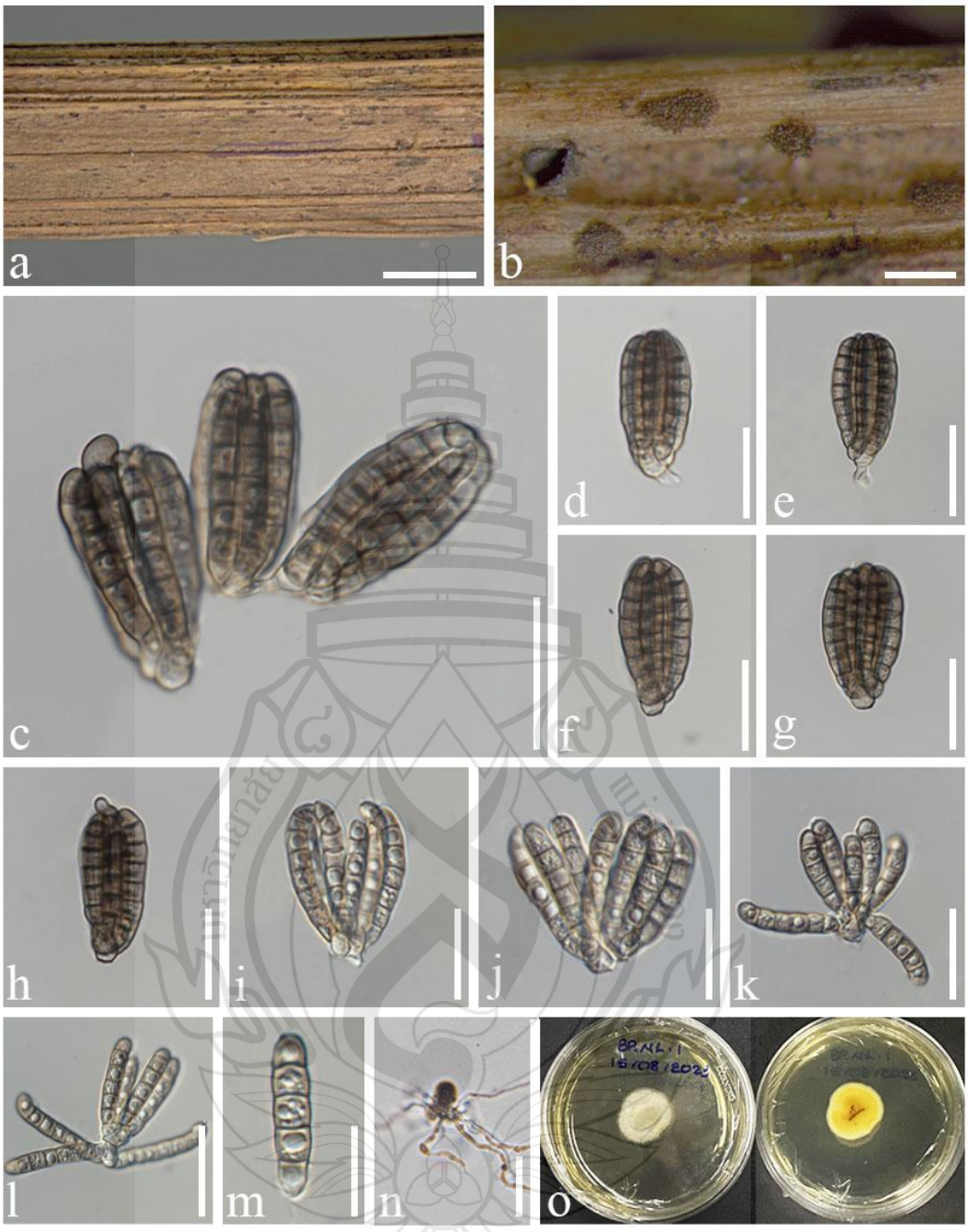
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet (BP-NL-1, MFLU 25-0236, **a new host record**); living culture MFLUCC 25-0265.

*GenBank*: **ITS**: PV870580; ***tef*1-*α***: PX255034.

*Pre-screening for antibacterial activity*: *Dictyocheirospora 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*.

*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); coffee plants in China (Lu et al., 2024); *Cocos nucifera* (Arecaceae) in Thailand (Tian et al., 2024); dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

*Notes:* In the phylogenetic analysis (Figure 3.5), my strain (MFLU 25-0236) is grouped sister to *Dictyocheirospora nabanheensis* (MFLUCC 17-0562) with 99% ML and 1.00 BYPP bootstrap support. My new collection is morphologically similar to *Dictyo. nabanheensis* (MFLUCC 17-0562) in having oval to ellipsoid, pale brown to brown, cheiroid conidia (33–45 × 12–20 vs. 35–40 × 18–21 μm) with 6–7 rows of cells with 5–10 septa. However, my new collection has smaller conidiogenous cells (4–6 × 2.5–4 vs. 9–20 × 5–7 μm) and conidia without rounded apical appendages compared to *Dictyo. nabanheensis* (MFLUCC 17-0562). There is no base pair difference between my strain (MFLU 25-0236) and *Dictyo. nabanheensis* (MFLUCC 17-0562). *Dictyocheirospora nabanheensis* was mainly 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 my study, I isolated *Dictyo. nabanheensis* for the first time from Asteraceae and reported my new collection as a new host record on *Bidens pilosa* in northern Thailand.




**Note a, b** Appearance of colonies on host substrate. **c–e** Conidia and conidiogenous cells. **f–h** Conidia. **i–m** Conidia arms. **m** 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.

**Figure 3.6** *Dictyocheirospora nabanheensis* (MFLU 25-0236, a new host record)

***Neodendryphiella*** Iturrieta-González, Dania García & Gené

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 flexeous, 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, I reported *Neodendryphiella mali* as a new record on *Chromolaena odorata*.

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

*Index Fungorum number*: IF824665, *Facesoffungi number*: FoF18030*,* Figure 3.7

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

*Note*: In the phylogenetic analysis (Figure 3.5), my strain (MFLU25-0237) is grouped to *Neodendryphiella mali* (CBS 139.95) with 100% ML and 1.00 BYPP bootstrap support. my collection differs from *N. mali* (type; CBS 139.95) in having larger conidia (8–12 × 4–6 µm vs. 4–15 × 3–5 µm). However, there is no significant

base pair difference between two strains. In this study, *N. mali* was isolated for the first time from Asteraceae and reported the current collection as the new host record on *Chromolaena odorata* (Asteraceae) in northern Thailand.


**Note** **a, b** Colonies on host substrate. **c, d** Conidiophores. **e, f** Conidiophores and conidiogenous cells. **g–k** Conidia. Scale bars: a = 1000 μm, b=500 μm, c, d=50 μm, e, f=5 μm, g–l=10 μm.

**Figure 3.7** *Neodendryphiella mali* (MFLU 25-0237, a new host record)

### 3.2.4 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 *tub*2 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). Hyde et al. (2013) accepted 13 genera in the family based on both morphology and phylogenetic analyses. 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, *rpb*2 and *tub*2 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). Later, Valenzuela-Lopez et al. (2018) introduced six new genera, viz., *Cumuliphoma*, *Ectophoma*, *Juxtiphoma*, *Remotididymella*, *Similiphoma*, and *Vacuiphoma* based on LSU, ITS, *tub*2 and *rpb2* sequence data. Hou et al. (2020) added *Vandijckomycella* to Diymellaceae. Currently, there are 50 genera accepted in Didymellaceae (Hyde et al., 2024). In this study, I recorded two *Remotididymella* species based on morphology and the combined dataset of LSU, ITS, *tef*1-*α*, and *rpb*2 sequence data (Figure 3.8).


**Figure 3.8** Phylogram generated from the ML analysis of a combined dataset of LSU, ITS, *tef*1-*α*, and *rpb*2 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 *Pleiochaeta setosa* (CBS 118.25 and CBS 496)

***Remotididymella*** Valenz. -Lopez

*Remotididymell*a 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, ascospore with gelatinous sheath (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)

*Index Fungorum number*: IF819991, *Facesoffungi number*: FoF06579*,* Figure 3.9

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 40–80 × 50–100 µm ($\overline{x}$ = 60 × 75.2 µm, n = 5), pycnidial, solitary, immersed to semi-immersed, uniloculate, globose, yellowish brown to brown, without ostiole. *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 ($\overline{x}$ = 2.4 × 2.7 µm, n = 5) phialidic, hyaline, ampuliform to cylindrical. *Conidia* 4–5.5 × 1.5–2.5 µm ($\overline{x}$ = 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.

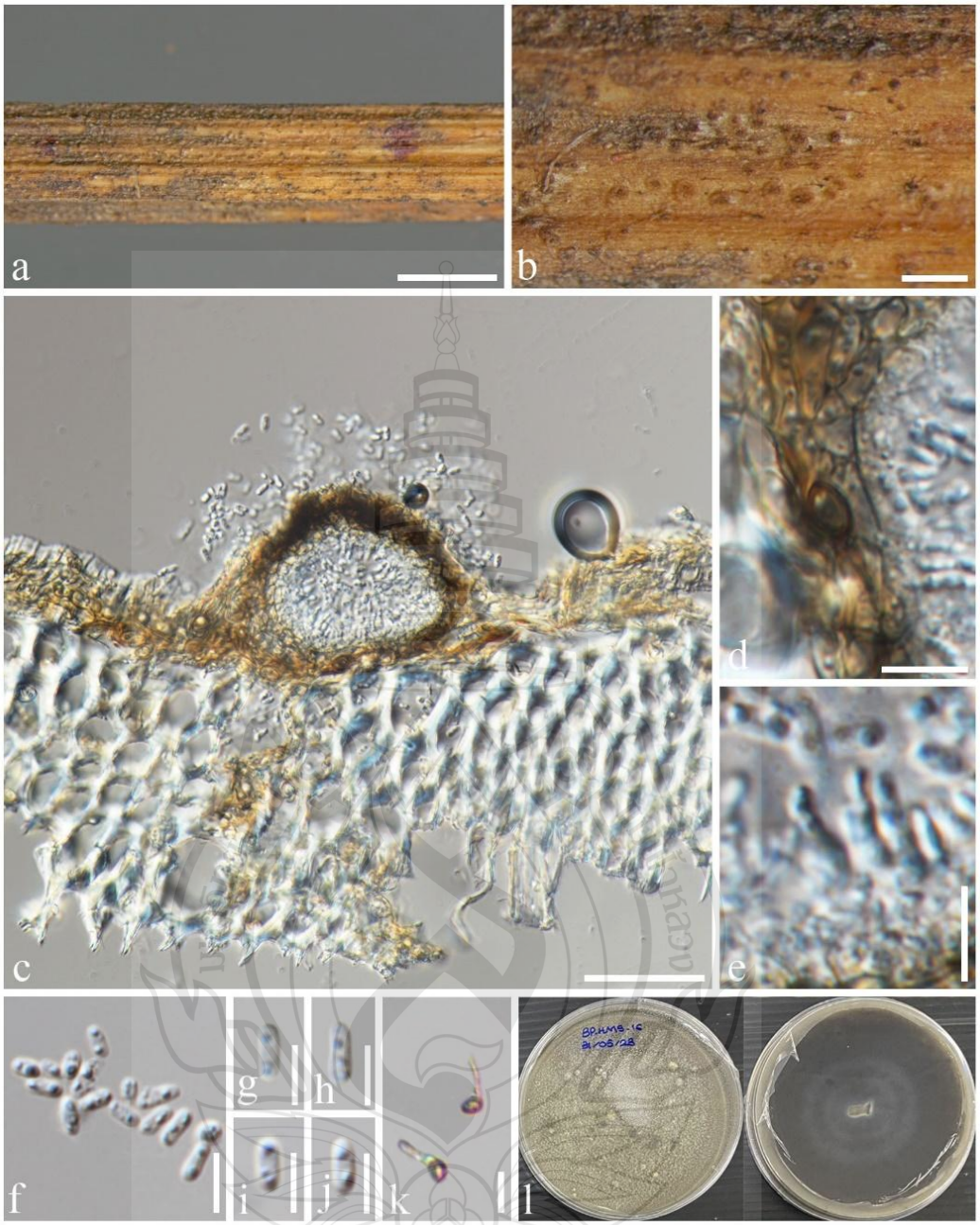
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 June 2023, Zin Hnin Htet (BP-HMS-16, MFLU 25-0238, **a new host record**); living culture MFLUCC 25-0259.

*GenBank:* **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 15mm 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 unknown 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 (Figure 3.8), my strain (MFLU 25-0238) forms a clade with *Remotididymella anthropophila* strains (CBS14246 and JZB380042) with 99% ML and 0.99 BYPP bootstrap support. My collection is morphologically similar to *R. anthropophila* (CBS14246) in having pycnidial conidiomata, hyaline, phialidic conidiogenous cells, cylindrical, hyaline, aseptate conidia, but 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 is no base pair difference between my strain (MFLU 25-0238) and *R. anthropophila* (CBS14246). *Remotididymella anthropophila* (CBS14246) was discovered as a pathogenfrom human bronchial secretion in the USA and *R. anthropophila* (JZB380042) was found as a pathogen on an unknown plant in China (Valenzuela-Lopez et al., 2018). Herein, this collection is reported as a new host record of *R. anthropophila* on *Bidens pilosa* (Asteraceae) and a new geographical record in Thailand.




**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through 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 µm, c = 50 µm, d = 20 µm, e, f, g, h, i, j, k = 5 µm.

**Figure 3.9** *Remotididymella anthropophila* (MFLU 25-0238, a new host record)

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

*Index Fungorum number*: IF900161, *Facesoffungi number*: FoF18031, Figure 3.10

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

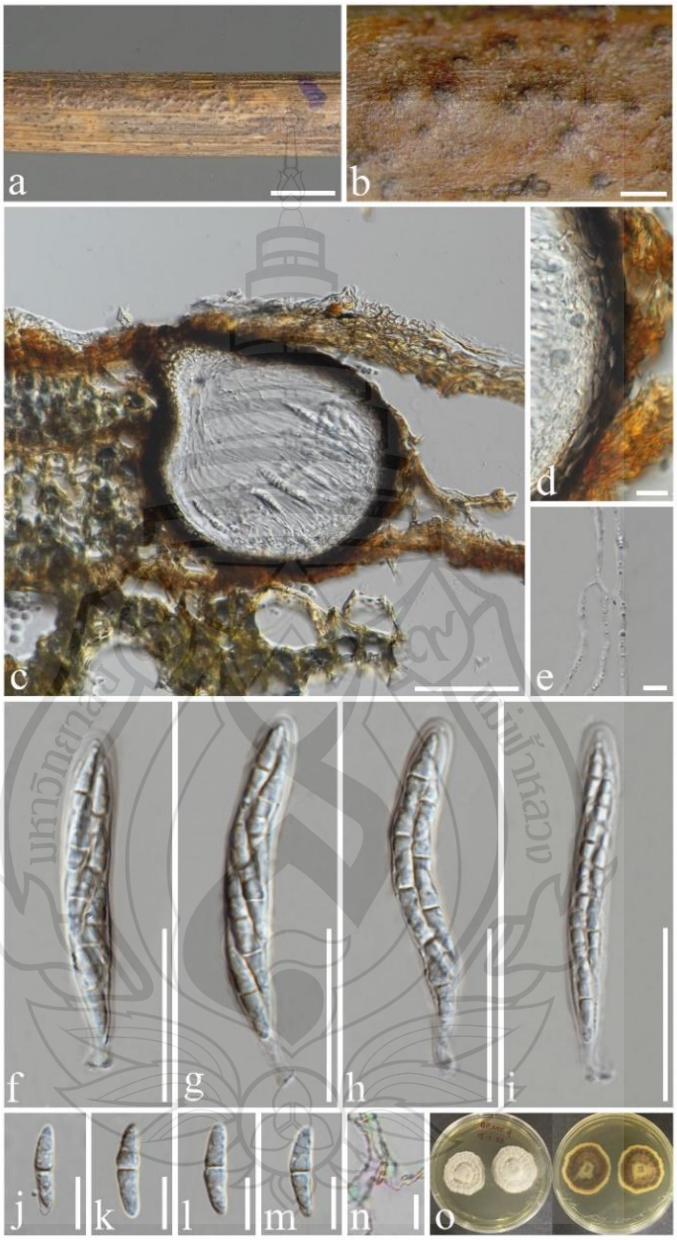
*GenBank:* **ITS**: PV870583; ***rpb2***: PX120443

*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 (Figure 3.8), 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 the new species is found only with its sexual morph on Asteraceae hosts in Thailand. Furthermore, there is no base pair difference between my strain (MFLU 25-

0239) 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.




**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d** Peridium. **e** Pseudoparaphyses. **f–i** Asci. **j–m** Ascospores. **n** A germinating ascospore. **o** Culture on MEA. Scale bars: a = 1 mm, b = 200 µm, c = 100 µm, d, j, k, l, m, n = 10 µm, e = 5 µm, f, g, h, i = 30 µm.

**Figure 3.10** *Remotididymella fici-microcarpae* (MFLU 25-0239, a new host record and a new geographical record)

### 3.2.5 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; Samarakoon, Wanasinghe et al., 2020; Samarakoon et al., 2020; Yuan et al., 2020; Dissanayake et al., 2021; Wong et al., 2021; Suwannarach et al., 2021; Sun et al., 2023; Zhang et al., 2024). In this study, I introduced *Austropleospora chromolaenae*, *Kalmusia thailandica*, and *Tremateia asteracearum* as new species and *Chromolaenicola nanensis*, *Montagnula chromolaenae*, *M. donacina*, and *Pseudoithomyces chartarum* as new records based on a combined dataset of LSU, SSU, ITS, *tef*1-*α*, and *rpb*2 sequence data (Figure 3.11).

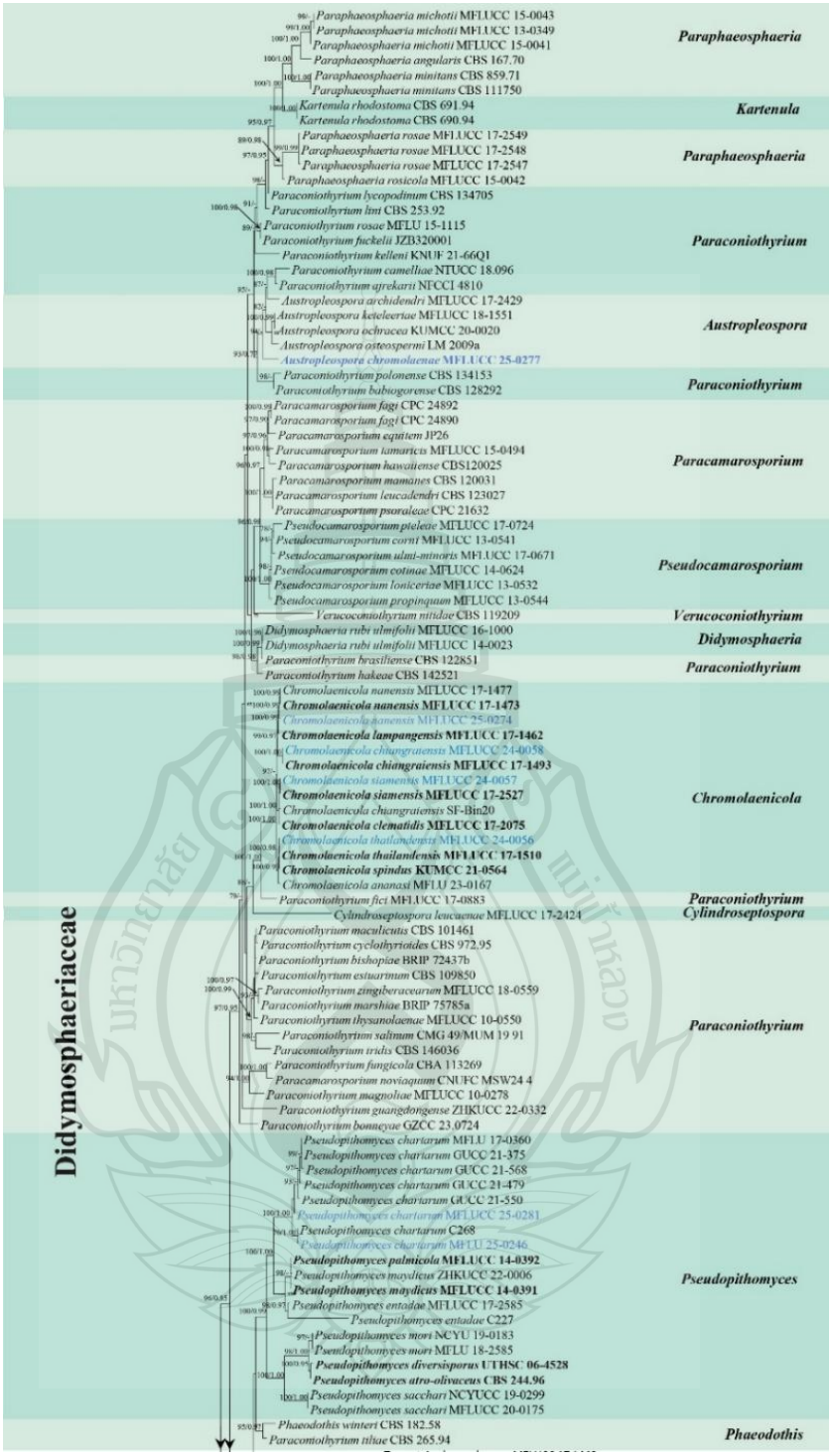



**Figure 3.11** Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, *tef*1-*α*, and *rpb*2 sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Periconia pseudodigitata* (KT1395 and KT1395A)

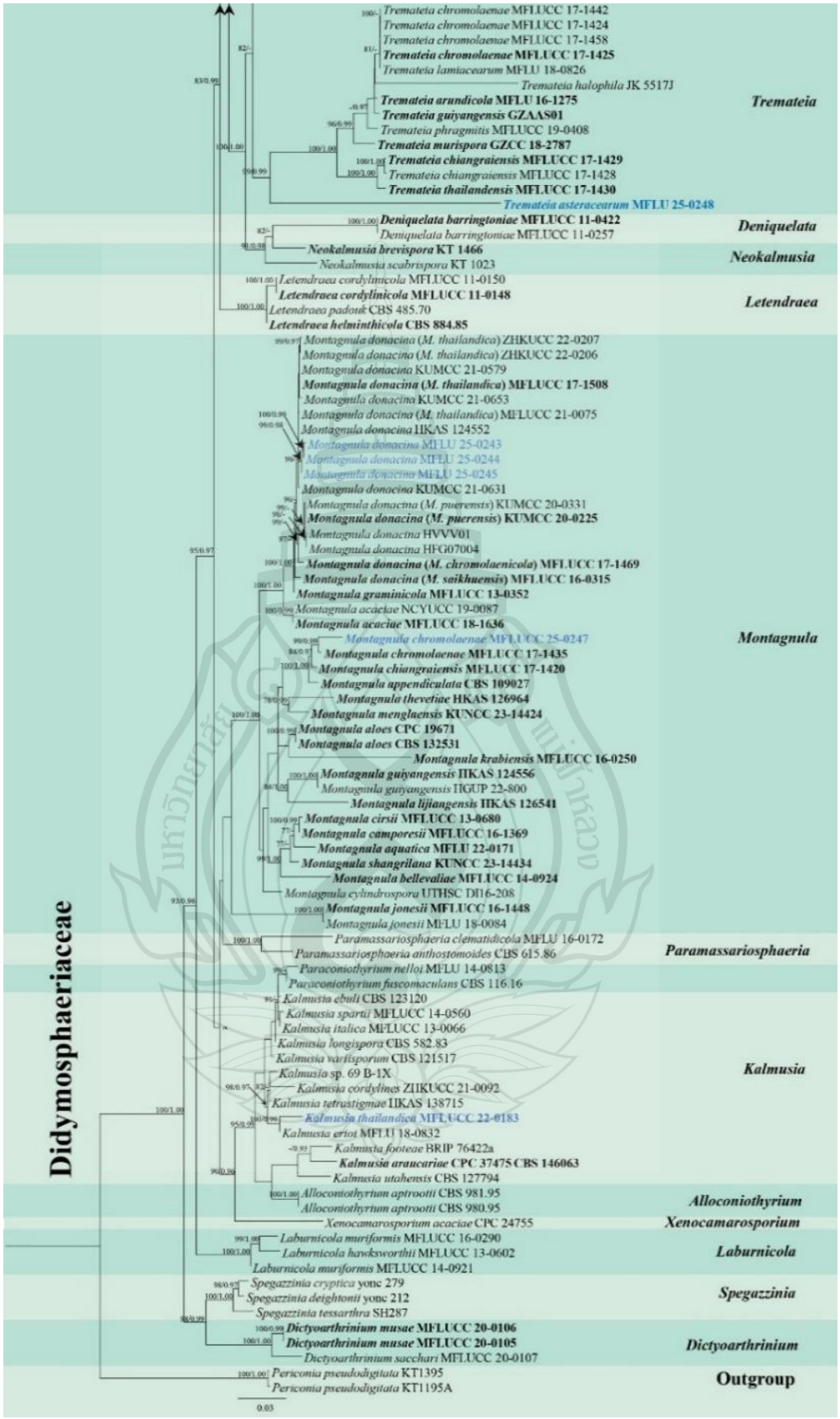



**Figure 3.11** (continued)

***Austropleospora*** R.G. Shivas & L. Morin

*Austropleospora* was introduced by Shivas and Morin (2010), typified by *A. osteospermi.* The sexual species of *Austropleospora* are characterised by subglobose ascomata, bitunicate, cylindric-clavate asci, and ellipsoidal ascospores. The asexual morph is characterised by pycnidial, globose conidiomata, annellidic, cylindrical conidiogenous cells, and cylindrical to narrowly ellipsoidal conidia. The genus is currently comprised of four species viz. *Austropleospora* archidendri, *A. keteleeriae*, *A. ochracea* and *A. osteospermi* (Index Fungorum 2024; Hyde et al., 2024).

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

*Index Fungorum number*: IF904364*, Facesoffungi number*: FoF18032*,* Figure 3.12

*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**: *Conidiomata* 180–210 × 200–230 µm ($\overline{x}$ = 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-layered, yellowish-brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–5 × 3–7 µm ($\overline{x}$ = 4.3 × 5.6 µm, n = 5), phialidic, hyaline ampulliform to lageniform, aseptate, unbranched. *Conidia* 5–8 × 3–5 µm ($\overline{x}$ = 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.

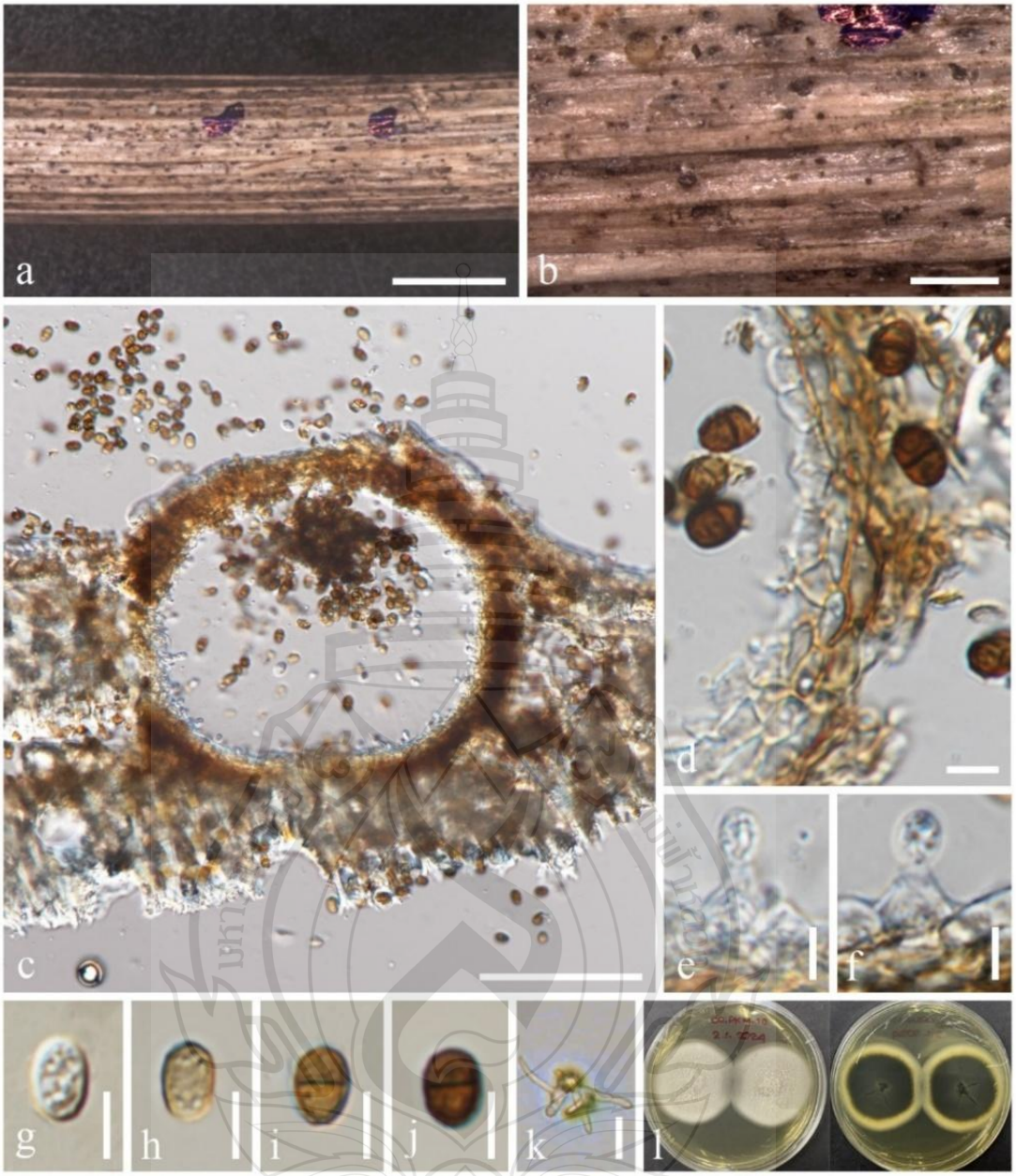
*Material examined*: Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-10, MFLU 25-0240**, holotype**); ex-type living culture MFLUCC 25-0277.

*GenBank*: **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 (Figure 3.11), my strain (MFLUCC 25-0277) formed a distinct lineage from *Austropleospora* species with 94% ML and 0.83 BYPP bootstrap support. My 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 the cylindrical, to narrowly ellipsoidal, 1–3-septate conidia of the latter. A comparison of base pair differences between my 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, base pairs cannot be compared. Therefore, *Austropleospora chromolaenae* is introduced as a new species from *Chromolaena odorata* (Asteraceae) in Thailand, based on morphology and multigene phylogeny.




**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e, f** Conidiogenous cells. **g–j** Conidia. **k** A germinating conidium. Scale bars: a = 1000 µm, b = 500 µm, c, d = 50 µm, e, f = 5 µm, g, h, i, j, k, l = 10 µm.

**Figure 3.12** *Austropleospora chromolaenae* (MFLU 25-0240, holotype)

***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), including four asexual morphs (*Chromolaenicola chiangraiensis*, *C. clematidis*, *C. lampangensis*, and *C. siamensis*) and three sexual morph taxa (*C. nanensis*, *C. sapinda* and *C. thailandensis*) (Mapook et al., 2020; Ren et al., 2022). *Chromolaenicola* species have been reported as saprobes in terrestrial habitats in China and Thailand (Jayasiri et al., 2019; Mapook et al., 2020; Phukhamsakda et al., 2020; Ren et al., 2022). They were found on different plant families, viz., Asteraceae, Bromeliaceae, Fabaceae, Ranunculaceae, and Sapindaceae (Jayasiri et al., 2019; Mapook et al., 2020; Phukhamsakda et al., 2020; Ren et al., 2022; Tian et al., 2024).

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

*Index fungorum number*: IF557280, *Faces of fungi* number: FoF07784, Figure 3.13

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: appearing as Colonies on the host substrate, superficial, scattered, gregarious, black. Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* 2–4 × 1–2 µm ($\overline{x}$=2.5 × 1.6 µm, n = 10), holoblastic, hyaline, smooth, ovoid to filiform. Conidia 9–13 × 6–10 µm ($\overline{x}$=10.1 × 6.9 µm, n = 30), oval to slightly ellipsoidal, aseptate when immature, 1-septate when mature, thick-walled, reddish brown, verruculose.

*Culture characteristics*: Conidia germinating on MEA within 24 hours, reaching 20 mm after 10 days at room temperature, irregular, undulate, curled margin, yellow to pale brown on the surface and wrinkle and brown in reverse.

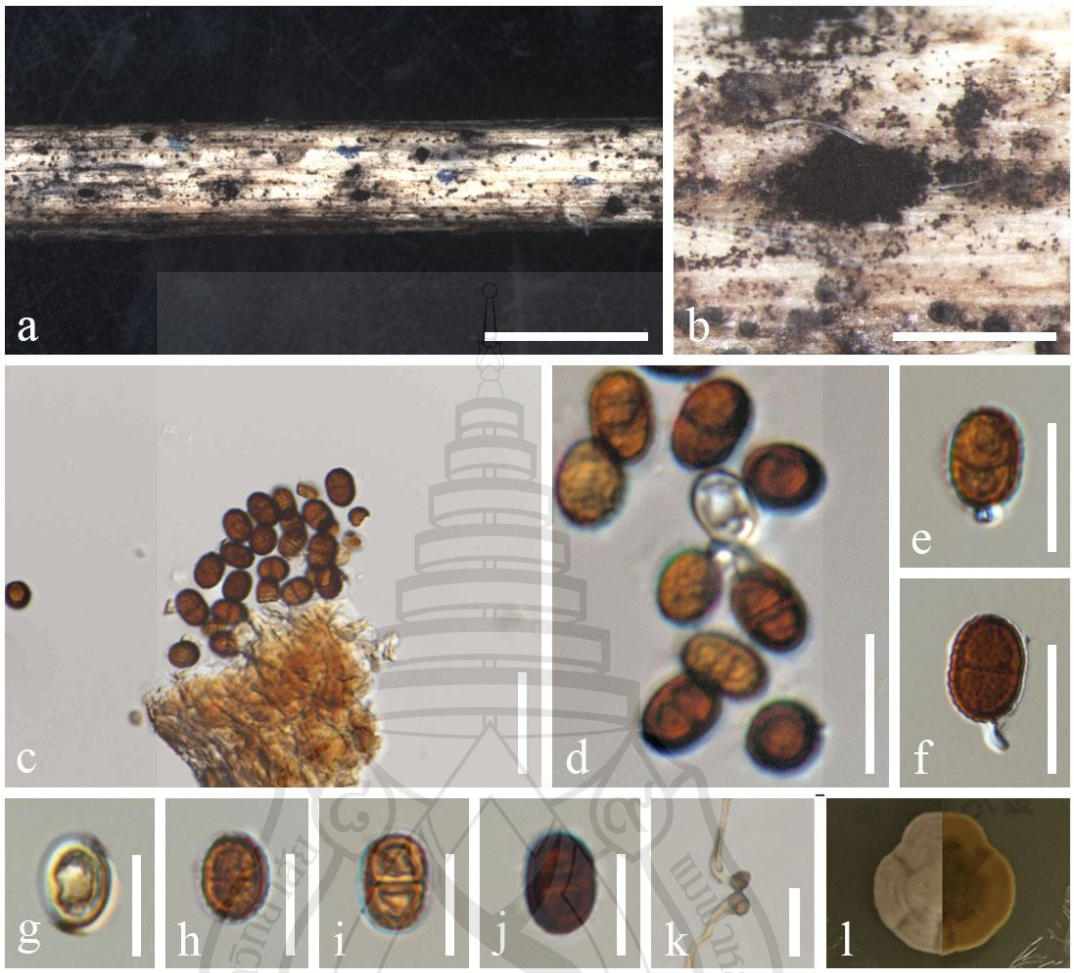
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet (BP-DP-10, MFLU 24-0030, **new host**); living culture MFLUCC 24-0058.

*GenBank:* **LSU**: PP464125; **SSU**: PP464129; **ITS**: PP464138; ***tef*1-*α***: PP474193; ***rpb*2**: PP474190.

*Pre-screening for antibacterial activity*: *Chromolaenicola chiangraiensis* (MFLUCC 24-0058) showed a 18 mm inhibition zone against *B. subtilis*, and no inhibition zone against *E. coli* and *S. aureus*.

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

*Notes*: Morphologically, my species, *Chromolaenicola chiangraiensis* (MFLUCC 24-0058) is similar to *C. chiangraiensis* (MFLUCC 17-1493) in having superficial, scattered, dark brown to black colonies, holoblastic, hyaline conidiogenous cells, oval to ellipsoidal, aseptate to 1-septate, reddish brown, verruculose conidia but differ in having shorter conidiogenous cells (2–4 vs 3.5–6.5 µm). A comparison of the *tef*1-*α* gene region of *Chromolaenicola chiangraiensis* (MFLUCC 24-0058) and *C. chiangraiensis* (MFLUCC 17-1493) reveals 13 base pair differences (1.48%) across 876 nucleotides. Therefore, the strain MFLUCC 24-0058 is described as a new host record of *Chromolaenicola chiangraiensis* from *Bidens pilosa* (Asteraceae), which was previously recorded from *Chromolaena odorata* (Asteraceae) in Chiang Rai Province, Thailand (Mapook et al., 2020).




**Source** Htet et al. (2024)

**Note** **a, b** Appearance of colonies on host substrate. **c–f** Conidia and conidiogenous cells. **g–j** Conidia. **k** Germinating conidia. **l** Culture on MEA. Scale bars: a, b = 500 µm, c = 30 µm, d, e, f, g, h, i, j =10 µm, k = 20 µm.

**Figure 3.13** *Chromolaenicola chaingraiensis* (MFLU 24-0030, a new host record)

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

*Index Fungorum number*: IF557282*, Facesoffungi number*: FoF07786*,* Figure 3.14

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph**: *Ascomata* 190–275 × 205–230 µm ($\bar{x}$ = 220.3 × 217.3 µm, 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 µm wide, multilayered, comprising dark brown cells of *textura angularis*. *Hamathecium* comprises 1–2 µm wide,

cylindrical to filiform, septate, branching pseudoparaphyses. *Asci* 97–140 × 10–16 µm ($\overline{x}$ = 124 × 12.8 µm, n = 20), 6–8-spored, bitunicate, cylindrical, straight or slightly curved, apically rounded, short pedicellate with an ocular chamber. *Ascospores* 14–24 × 5–10 µm ($\overline{x}$ = 20 × 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.

*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.

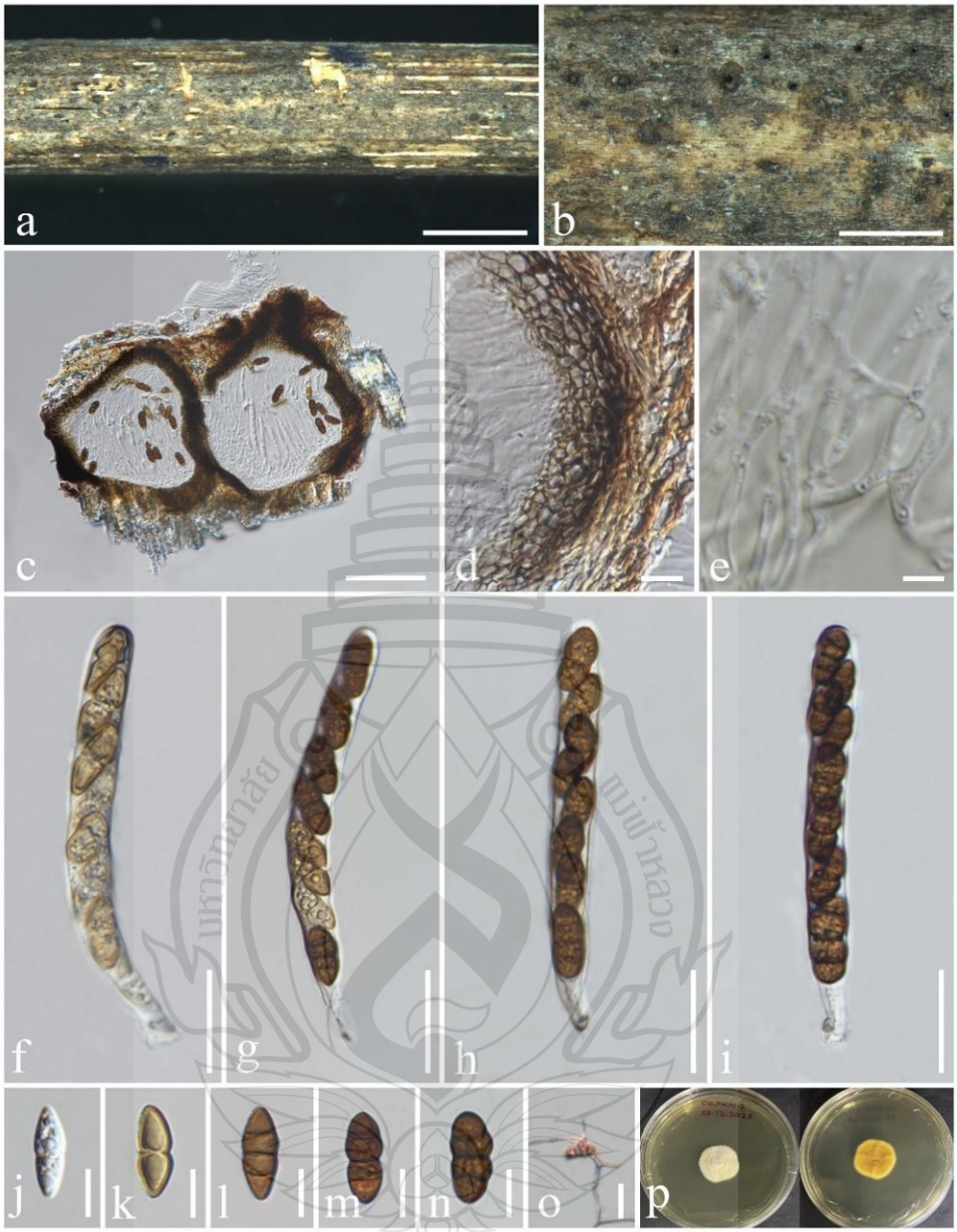
*Material examined*: Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-2, MFLU 25-0241, **a reference specimen**); living culture MFLUCC 25-0274.

*GenBank*: **ITS**: PV870585; **SSU**: PV996955; ***tef*1-*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 (Figure 3.11), my strain (MFLUCC 25-0274) formed a sister clade with the isolates of *Chromolanicola nanensis* (MFLUCC 17-1473 and MFLUCC 17-1477) strains with 100 % ML and 1.00 BYPP bootstrap support. This new collection is morphologically similar to *C. nanensis* in having immersed to semi-immersed, solitary or scattered ascomata, bitunicate asci (97–140 × 10–16 µm vs. 110–145 × 10–12.5 µm), uniseriate, hyaline to reddish brown, septate, muriform ascospores but differs in having larger conidiomata (190–275 × 205–230 µm vs. 210–230 × 200–220 µm), larger ascospores (14–24 × 5–10 µm vs. 16–20 × 7.5–9 µm). However, there is no significant base pair difference between this collection and *C. nanensis*. *Chromolaenicola nanensis* was previously reported on *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al., 2020). Therefore, this collection is designated as a reference specimen for *C. nanensis* and the second record on *Chromolaena odorata* from northern Thailand.




**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through 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 µm, c = 100 µm, d = 20 µm, e = 5 µm, f, g, h, i = 30 µm, j, k, l, m, n, o = 10µm.

**Figure 3.14** *Chromolaenicola nanensis* (MFLU 25-0241, a reference specimen)

***Chromolaenicola siamensis*** (Jayasiri, E.B.G. Jones & K.D. Hyde) Mapook & K.D. Hyde, Fungal Diversity 101: 28 (2020)

*Index fungorum number*: IF557283, *Faces of fungi number*: FoF07787, Figure 3.15

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 130–235 × 170–230 µm ($\overline{x}$ =150.6 × 225.5 µm, n = 5), pycnidial, solitary, immersed to semi-immersed, uniloculate, globose, yellowish brown to brown, without ostiole. *Peridium* 15–20 µm wide, comprising 2–3 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–2.5 × 2–4 µm ($\overline{x}$=2 × 2.5 µm, n = 30), phialidic, hyaline. *Conidia* 7–15 × 5–10 µm ($\overline{x}$ =10.4 × 6.7 µm, n = 30), globose to subglobose, 1-septate, thick-walled, reddish brown to dark brown, verruculose.

*Culture characteristics*: Conidia germinating on MEA after 24 hours, 22 mm after 10 days at room temperature, irregular, entire, curled margin, yellow to pale brown on the surface, wrinkled and brown in reverse.

*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa*, 14 March 2023, Zin Hnin Htet (BP-DP-7, MFLU 24-0029, **new host**); living culture MFLUCC 24-0057.

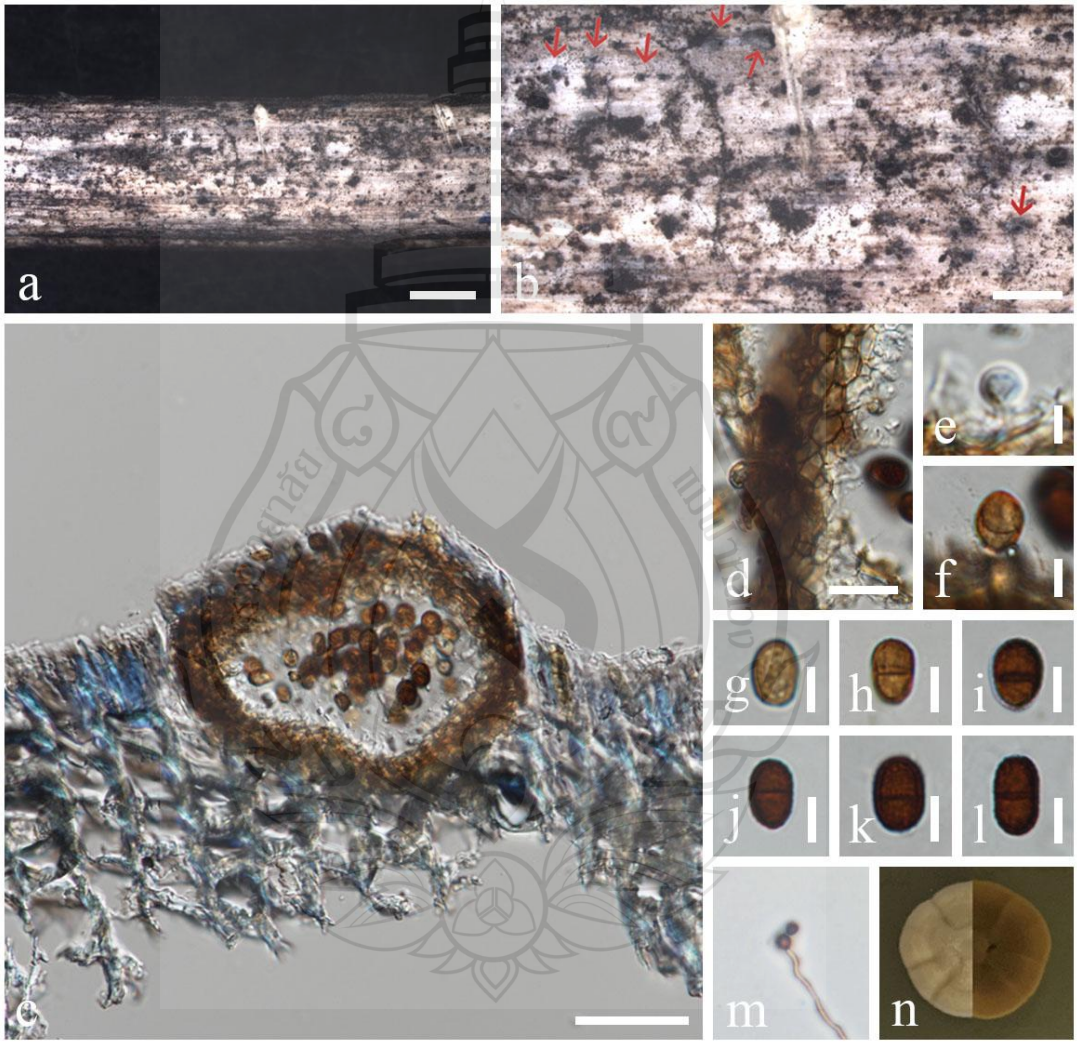
*GenBank:* **LSU**: PP464124; **SSU**: PP464128; **ITS**: PP464137; ***tef*1-*α***: PP474192; ***rpb*2**: PP474189

*Pre-screening for antibacterial activity*: *Chromolaenicola siamensis* (MFLUCC 24-0057) showed a 18 mm inhibition zone against *B. subtilis*, and no inhibition zone against *E. coli* and *S. aureus*.

*Known host and distribution*: on decaying pod of *Leucaena sp.* (Fabaceae) in Thailand (Jayasiri et al., 2019); on dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al., 2020); on dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

*Notes*: In the phylogenetic study (Figure 3.11), the strain (MFLUCC 24-0057) is sistered to *Chromolaenicola siamensis* (MFLUCC 17-1527) with 89% ML and 0.80 BYPP. When compared the morphology, the strain (MFLUCC 24-0057) is similar to *Chromolaenicola siamensis* (MFLUCC 17-1527) in having pycnidial, solitary, immersed, globose to obpyriform, unilocular conidiomata, phialidic, hyaline conidiogenous cells, and hyaline to dark brown, globose to subglobose, aseptate to 1-septate conidia with similar

size (7–15 × 5–10 µm vs 7.2–9.4 × 5.4–6.5 µm). Strain (MFLUCC 24-0057) differs from *C. siamensis* (MFLUCC 17-1527) in having thinner peridium (15–20 µm vs 15–38 µm) and shorter conidiogenous cells (1–2.5 × 2–4 µm vs 6.5–7.4 × 3.2–4.7 µm). However, the comparison of base pair differences revealed no or insignificant results LSU 0% (0/851), ITS 0.2% (1/459), *tef1-α* 0.3% (2/740), *rpb2* 0.1% (1/914), which indicates that they are conspecific. Therefore, *C. siamensis* is reported as a new host record from *Bidens Pilosa* (Asteraceae).




**Source** Htet et al. (2024)

**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e, f** Conidiogenous cells. **g–l** Conidia. **m** Germinating conidia. **n** Culture on MEA. Scale bars: a, b = 500 µm, c = 50 µm, d =20 µm, e –m = 5 µm.

**Figure 3.15** *Chromolaenicola siamensis* (MFLU 24-0029, a new host record)

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

*Index Fungorum number:* IF557284, *Facesoffungi number:* FoF07788, Figure 3.16

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 100–150 × 110–150 µm ($\overline{x}$ = 111 × 130 µm, n = 5), pycnidial, solitary, immersed to semi-immersed, uniloculate, globose, yellowish brown to brown, ostiolate. *Peridium* 13–20 µm wide, comprising 1–2 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–2 × 3–4 µm ($\overline{x}$ = 1.4 × 3.6 µm, n = 5) phialidic, hyaline. *Conidia* 5–11 × 4–10 µm ($\overline{x}$=12.8 × 6.1 µm, n = 20), ovoid to obpyriform, yellowish brown to brown, aseptate when immature, becoming brown and 1-septate at maturity, thick-walled, verruculose.

*Culture characteristics*: Conidia germinating on MEA within 24 hours, reaching 21 mm after 10 days at room temperature, irregular, entire margin, smooth, wrinkled, pale yellow on the surface, curled and brown in reverse.

*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet (BP-DP-2, MFLU 24-0028, **new asexual morph**); living culture MFLUCC 24-0056.

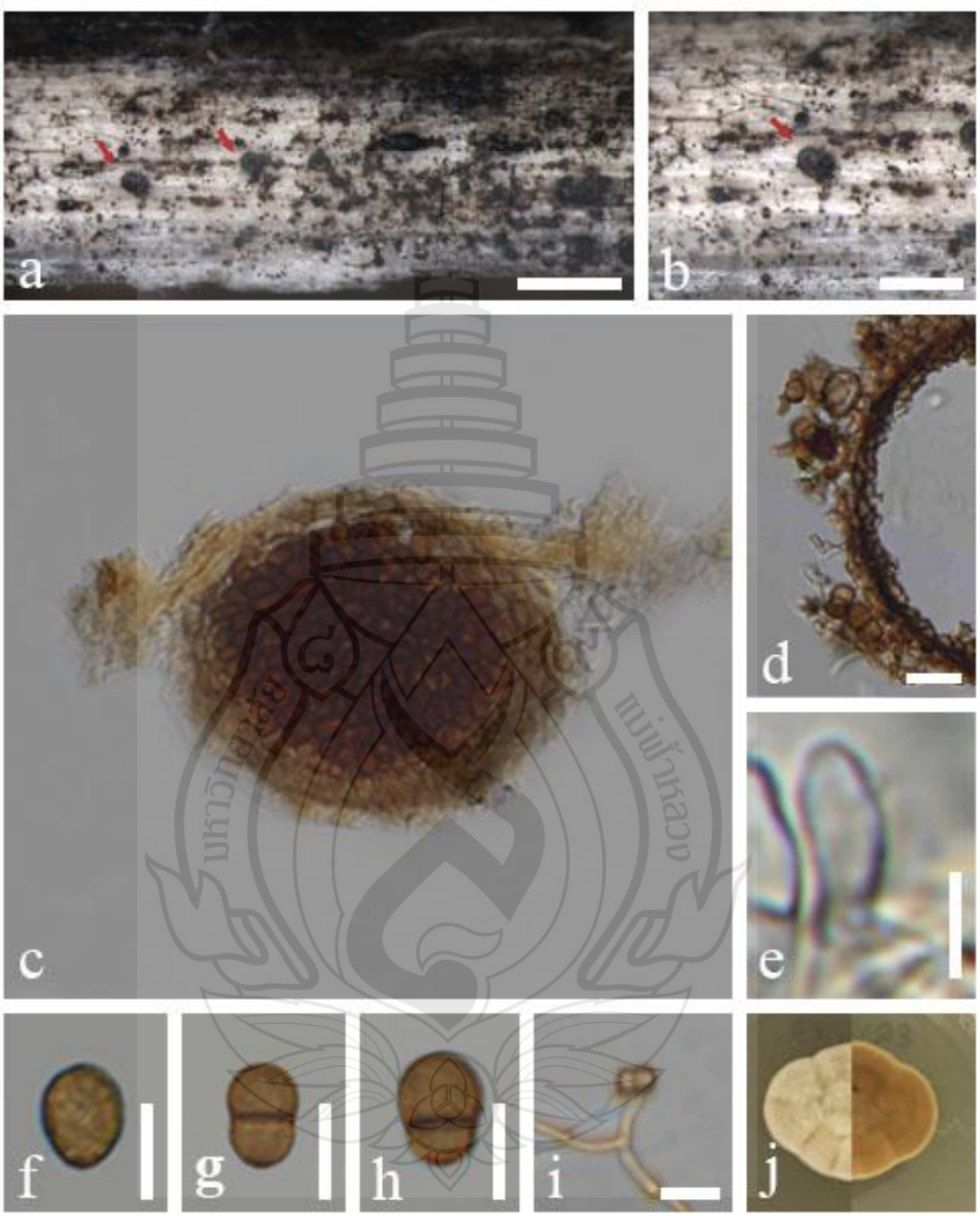
*GenBank:* **LSU**: PP464123; **SSU**: PP464127; **ITS**: PP464136; ***tef*1-*α***: PP474191; ***rpb*2**: PP474188

*Pre-screening for antinacterial activity*: *Chromolaenicola thailandensis* (MFLUCC 24-0056) showed a 17 mm inhibition zone against *B. subtilis*, and no inhibition zone against *E. coli* and *S. aureus*.

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

*Notes*: *Chromolaenicola thailandensis* (MFLUCC 17-1510, MFLUCC 17-1475) was found in its sexual morph in nature (Mapook et al., 2020). Current study collected an asexual morph of *C. thailandensis* (MFLUCC 24-0056) on dead stems of *Bidens pilosa*. However, its sexual morph is not obtained in culture; hence failed to compare its morphology with *C. thailandensis* (MFLUCC 17-1510, MFLUCC 17-1475). There are no base pair differences in all five gene regions between my strain (MFLUCC 24-0056) and *C. thailandensis* (MFLUCC 17-1510). Therefore, these strains are reported as the new asexual morph of *C. thailandensis* and also the new host record from *Bidens pilosa*

(Asteraceae) while previous strains of *C. thailandensis* was recorded on *Chromolaena odorata* (Asteraceae) in Chiang Rai Province, Thailand (Mapook et al., 2020).




**Source** Htet et al. (2024)

**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e** Conidiogenous cells. **f–h** Conidia. **i** A germinating conidium. **j** Culture on MEA. Scale bars: a, b = 200 µm, c = 50 µm, d–i = 10 µm.

**Figure 3.16** *Chromolaenicola thailandensis* (MFLU 24-0028, a new asexual morph)

***Kalmusia*** Niessl

Niessl (1872) introduced *Kalmusia* and *K. ebuli* is the type species. In the past, *Kalmusia* has been assigned to a wide variety of 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 combined SSU, LSU, RPB2 and *tef*1-*α* sequences and placed *Kalmusia* in the Didymosphaeriaceae. There are 56 epithets of *Kalmusia* listed in Index Fungorum (2022). The sexual morph of *Kalmusia* is distinguished by pedicellate asci with septate pseudoparaphyses, brown, 3-septate inequilateral ascospores, immersed, globose ascomata with a central, stout papilla, surrounded by hyphae in the substrate while asexual morph of *Kalmusia* has solitary pycnidia 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.

*Index Fungorum number*: IF904365*; Facesoffungi number*: FoF14037, Figure 3.17

*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**: *Conidiomata* 90–150 × 125–145 µm ($\overline{x}$ = 111 × 130 µm, n = 5), appearing as black spots on the host surface, unilocular, solitary, scattered, erumpent, ostiolate. *Peridium* 10–20 µm wide, comprising 3–5-layered, hyaline to pale yellow cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–3 × 1.5–2 µm ($\overline{x}$ = 1.2 × 1.7 µm, n = 5), holoblastic, cylindrical to ampulliform, hyaline, aseptate. *Conidia* 3–4.5 × 1–2 µm ($\overline{x}$ = 3.6 × 1.7 µm, n = 20), cylindrical to ellipsoidal, hyaline, aseptate, smooth-walled.

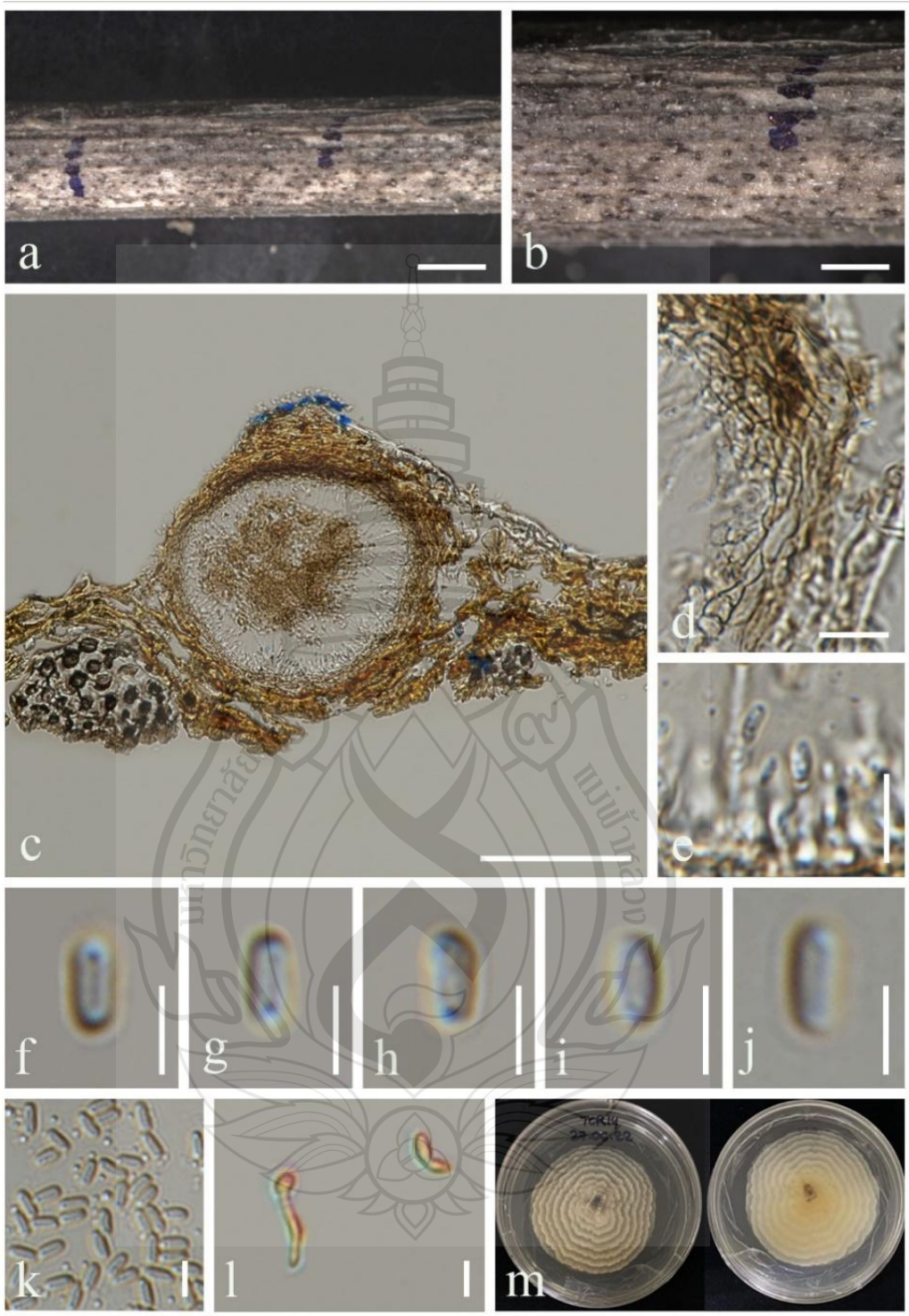
*Culture characteristics*: Conidia germinating on PDA, reaching 30 mm diam. within 10 days at 27°C, circular, flat, wavy margin, curled, circular zonate with aerial mycelia, both surface and reverse white.

*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*: **ITS**: PV870586, **LSU**: PV992405, **SSU**: PV996956, ***tef*1-*α***: PX282665.

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

*Notes*: In the phylogenetic analysis (Figure 3.11), my strain (MFLUCC 22-0183) grouped within *Kalmusia* and formed a sister lineage with *K. eriori* (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, I am unable to compare the morphology of my collection with *K. erioi.* Morphologically, my strain (MFLUCC 22-0183) is similar to *K. italica* (MFLUCC 13-0066) and *K. spartii* (MFLUCC 14-0560) by 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 my 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, I cannot compare base pairs. Therefore, I introduced *Kalmusia thailandica* as a new species found on *Chromolaena odorata* (Asteraceae) in Thailand, based on morphology and multi-gene phylogeny.




**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e** Conidia attached to conidiogenous cells. **F–k** Conidia. **l** Germinating conidia. **m** Culture on PDA. **Scale bar:** a, b = 500 µm, c = 100 µm, d = 20 µm, e–l= 5 µm.

**Figure 3.17** *Kalmusia thailandica* (MFLU 22-0259, holotype)

***Montagnula*** Berl.

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

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

*Index Fungorum number*: IF557297, *Facesoffungi number*: FoF07790*,* Figure 3.18

*Saprobic* on dead stems of *Bidens pilosa*. S**exual morph**: *Ascomata* 150–250 × 220–300 µm ($\bar{x}$ = 175.5 × 244.8 µm, n = 5), immersed to eruptment, solitary, globose to subglobose, appearing as small dark spots on the substrate, with an ostiole. *Ostiole* central, papillate. *Peridium* 13–20 µm wide, comprising 2–3 layered yellowish brown to brown cells of *textura angularis*. *Hamathecium* comprises 2–3 µm wide, cylindrical to filiform, aseptate, branching pseudoparaphyses. *Asci* 60–100 × 9–15 µm ($\bar{x}$ = 71.5 × 12.1 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, short-pedicellate. *Ascospores* 13–17 × 4–7 µm ($\bar{x}$ =12.2 × 5.1 µm, 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, gelatinous sheath covering from 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.

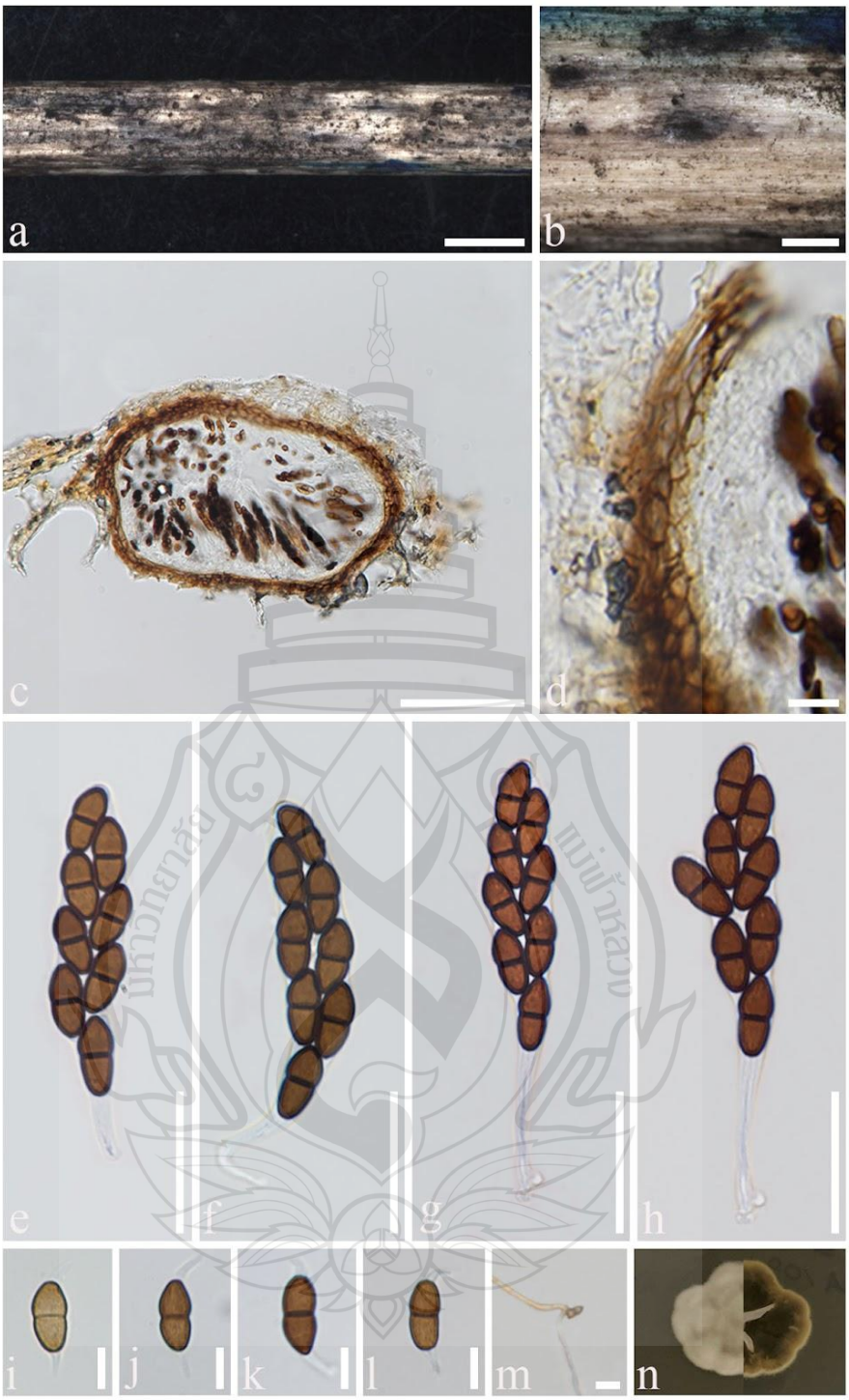
*Material examined*: Thailand, Chiang Rai Province, Phan District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet (BP-DP-9, MFLU 25-0242, **a new host record**); living culture MFLUCC 25-0247.

*GenBank*: **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).

*Note*: In phylogenetic analysis (Figure 3.11), the strain (MFLUCC 25-0247) is grouped within *Montagnula* species, sister to *Montagnula chromolaenae* (MFLUCC 17-1435) with 99% ML and 0.99 BYPP bootstrap support. The new strain is morphologically similar to *M. chromolaenae* (MFLUCC 17-1435) in having immersed, globose to subglobose ascomata with yellowish brown to brown peridium, hyaline, cylindrical to filiform, septate, branching pseudoparaphyses, bitunicate asci, yellowish brown to brown, 1-septate, fusiform to ovoid ascospores (13–17 × 4–7 vs. 15–16.5 × 5–6 µm) covering with a gelatinous sheath. However, the strain (MFLUCC 25-0247) slightly differs from *M. chromolaenae* (MFLUCC 17-1435) in having wider ascomata (145–250 × 220–300 µm vs. 170–175(–230) × (140–)170–190 µm) and shorter asci (60–100 × 9–15 µm vs. 85–105 × 9–15 µm). The nucleotide comparison of the ITS region of this 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 second occurrence on Asteraceae in northern Thailand, based on phylogeny and morphology.




**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through 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.

**Figure 3.18** *Montagnula chromolaenae* (MFLU 25-0242, a new host record)

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

*Index Fungorum number:* IF552762*, Facesoffungi number:* FOF04638*,* Figure 3.19

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

*Culture characteristics*: Ascospores germinating on MEA within 24 hours, reaching 79 mm after 10 days at room temperature, circular, filamentous, white, flat, opaque; white to grey, circular, filamentous in reverse surface.

*Material examined*: Thailand, Phayao Province, Phakretnark Waterfall, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-13, MFLU 25-0243, **reference specimen**); Thailand, Phayao Province, Phakretnark Waterfall, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-16, MFLU 25-0244, **reference specimen**); Thailand, Phayao Province, Phakretnark Waterfall, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-22, MFLU 25-0245, **reference specimen**).

*GenBank*: **SSU**: PV996958, PV996959; **ITS**: PV870588, PV870589, PV870590; ***tef*1-*α***: PX255037, PX255038, PX255039; ***rpb*2**: PX120445, PX120446, PX120447.

*Known host and distribution*: on *Acer* sp. (Sapindaceae) in China (Du et al., 2021); on *Acacia reficiens* (Fabaceae) in Nambia (Aptroot, 1995); on *Acacia* sp. (Fabaceae) in India (Aptroot, 1995); on *Adhatoda vasica* (Acanthaceae) in India (Aptroot, 1995); on *Ailanthus altissima* (Simaroubaceae) in India (Aptroot, 1995); on *Althaea rosea* (Malvaceae) in China (Aptroot, 1995); on *Annona squamosa* (Annonaceae) in India (Aptroot, 1995); *on Arundo donax* (Poaceae) in Portugal (Aptroot, 1995); on *Bambusoideae* (Poaceae) in Brazil and Papua New Guinea (Aptroot, 1995); on *Cajanus*

*cajan* (Fabaceae) in India (Aptroot, 1995); on *Calamus australis* (Arecaceae) in Australia (Aptroot, 1995); on Careya arborea (Lecythidaceae) in India (Aptroot, 1995); on *Citrus aurantiifolia* (Rutaceae) in India (Aptroot, 1995); on *Clerodendrum infortunatum* (Lamiaceae) in India (Aptroot, 1995); on *Clerodendrum multiflorum* (Lamiaceae) in India (Aptroot, 1995); on *Coffea arabica* (Rubiaceae) in Paraguay (Aptroot, 1995); on *Coffea robusta* (Rubiaceae) in Central African Republic (Aptroot, 1995); on *Craterellus odoratus* (Cantharellaceae) in China (Zhao et al., 2018); on dead stem of *Citrus* sp. (Rutaceae) in Thailand (Wanasinghe et al., 2016); on *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al., 2020; this study); on *Duranta repens* (Verbenaceae) in India (Aptroot, 1995); on *Ficus glomerata* (Moraceae) in India (Aptroot, 1995); on *Funtumia africana* (Apocynaceae) in Sierra Leone (Aptroot, 1995); on *Hibiscus* sp. (Malvaceae) in India (Aptroot, 1995); on *Ipomoea carnea* (Convolvulaceae) in India (Aptroot, 1995); on *Mallotus philippinensis* (Euphorbiaceae) in India (Aptroot, 1995); on *Morus alba* (Moraceae) in India (Aptroot, 1995); on *Litchi litchi* (Sapindaceae) in Myanmar (Thaung, 2008); on *Nerium odorum* (Apocynaceae) in India (Aptroot, 1995); on *Paeonia suffruticosa* (Paeoniaceae) in China (Li et al., 2023); on *Phyllostachys bambusoides* (Poaceae) in Japan (Wang et al., 2004); on *Pistacia* sp. (Anacardiaceae) in India (Aptroot, 1995); on *Platanus* sp. (Platanaceae) in USA (Wang et al., 2004); on *Premna cumingiana* (Lamiaceae) in Phillippines (Aptroot, 1995); on *Pseudosasa japonica* (Poaceae) in France (Aptroot, 1995); on *Saccharum officinarum* (Poaceae) in Brazil (Aptroot, 1995); on *Tectona grandis* (Lamiaceae) in India (Aptroot, 1995); on *Terminalia tomentosa* (Combretaceae) in India (Aptroot, 1995); on *Trachycarpus fortune* (Arecaceae) in China (Hyde et al., 1999); on *Vitis vinifera* (Vitaceae) in Australia (Pitt et al., 2014); on *Wikstroemia* sp. (Thymelaeaceae) in USA (Aptroot, 1995); on Zea mays (Poaceae) in Georgia (Aptroot, 1995).

*Note*: In the phylogenetic analysis (Figure 3.11), 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 100% ML and 0.87 BYPP. Morphologically, these collections are similar to *M. donacina* in having immersed to eruptment, solitary, globose to subglobose ascomata, bitunicate, fissitunicate, clavate to cylindrical, long-pedicellate asci, yellowish brown to brown, 1-septate, fusiform ascospore. There is no base pairs difference between the current collctions and phylogenetically related isolates of *M. donacina.*

Previously, *M. donacina* was found on *Chromolaena odora* (Asteraceae) in Thailand (Mapook et al., 2020). Therefore, herein the reference specimen of *M. donacina* on *Chromolaena odorata* (Asteraceae) is reported.


**Note** **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 bar: a = 1 mm, b = 500 µm, c = 100 µm, d = 50 µm, e = 20 µm, f = 5 µm, g, h, i, j = 30 µm, k, l, m, n = 10 µm.

**Figure 3.19** *Montagnula donacina* (MFLU 25-0243, a reference specimen)

***Pseudopithomyces*** Ariyaw. & K.D. Hyde

Ariyawansa et al. (2015) introduced *Pseudopithomyces* in Didymosphaeriaceae, typified by *Ps. chartarum*. *Pseudopithomyces* species are found as pathogens or saprobes on a variety of hosts (Ariyawansa et al., 2015; Crous et al., 2016; Wanasinghe et al., 2018; Jayasiri et al., 2019; Mapook et al., 2020; Tennakoon et al., 2021; Wu et al., 2023).These species are distinguished by micronematous, semi-macronematous, or mononemous, 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).

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

*Index Fungorum number*: IF551393, *Facesoffungi number*: FoF00938, Figure 3.20

*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 ($\overline{x}$ = 7.5 × 4.2 µm, n = 10), terminal, hyaline, unbranched, globose to subglobose or cylindrical. *Conidia* 15–20 × 8–10 µm ($\overline{x}$ = 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.

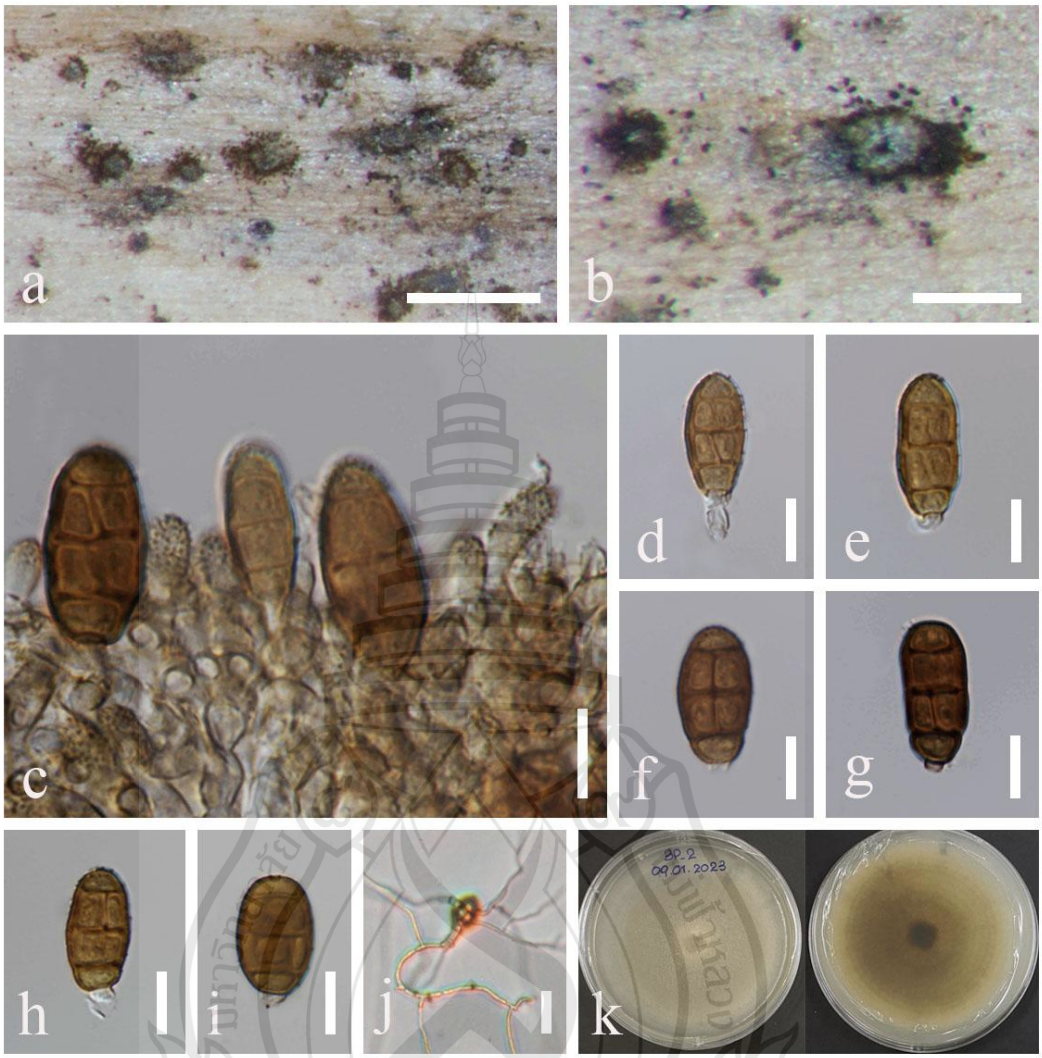
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 5 January 2023, Zin Hnin Htet (BP-2, MFLU 25-0246, **a new host record**); *ibid.*, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae),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

*GenBank*: **LSU**: PV992407; **SSU**: PV996960; **ITS**: PV870591, PV870592; ***tef*1-*α***: PX255040; ***rpb*2**: PX120448, 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 (China) (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 (Figure 3.11), the new strain (MFLUCC 25-0281) grouped in the same clade with *Pseudopithomyces chartarum* isolates (MFLUCC 17-2560, GUCC 21-375, GUCC 21-568, GUCC 21-479, GUCC 21-550) with 74% ML and 0.67 BYPP bootstrap support. Morphologically, this 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 is no base pairs differences between this collection and phylogenetically related species. The nucleotide comparison of the ITS region of the strain (MFLUCC 25-0281) and *Ps. chartarum* reveals only 0.4% (2/503) nucleotide differences. Therefore, herein, new host records of *Pseudopithomyces chartarum* on the *Bidens pilosa* and *Chromolaena odorata* (Asteraceae) in northern Thailand are reported.




**Note** **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 µm, b = 200 µm, c, d, e, f, g, h, i, j = 10 µm.

**Figure 3.20** *Pseudopithomyces chartarum* (MFLU 25-0246, a new host record)

***Trematеia asteracearum*** Htet, A. Mapook, K.WT. Chethana & K.D. Hyde, **sp. nov.**

*Index Fungorum number*: IF904366, *Facesoffungi number*: FoF18033, Figure 3.21

*Etymology*: Name reflects the host plant family Asteraceae, from which this species was isolated.

*Holotype*: MFLU 25-0248

*Saprobic* on dead stems of *Chromolaena odorata*. S**exual morph**: *Ascomata* 180–280 × 200–305 µm ($\overline{x}$ = 219.3 × 251.8 µm, n = 5), immersed, solitary, scattered, appearing as black spots on the host surface, globose to subglobose, ostiolate. *Ostiole* 47 µm wide, single, central, with a papillate. *Peridium* 17–25 µm wide, comprising 2–3 layered yellowish-brown cells of *textura angularis*. *Hamathecium* comprises 1–2 µm wide, cylindrical to filiform, aseptate, branching pseudoparaphyses. *Asci* 100–125 × 15–30 µm ($\overline{x}$ = 116.5 × 21.8 µm, n = 20), 8-spored, bitunicate, fissitunicate, clavate to cylindrical, short-pedicellate, rounded at the apex. *Ascospores* 20–30 × 10–15 µm ($\overline{x}$ = 24.6 × 11.6 µm, n = 20), overlapping 1-seriate to 2-seriate, oval to ellipsoidal, muriform, 3–4-transverse septa, with 1–2 vertical septa, wider at the middle, constricted at each septum, guttulate, without a gelatinous sheath. **Asexual morph**: Undetermined.

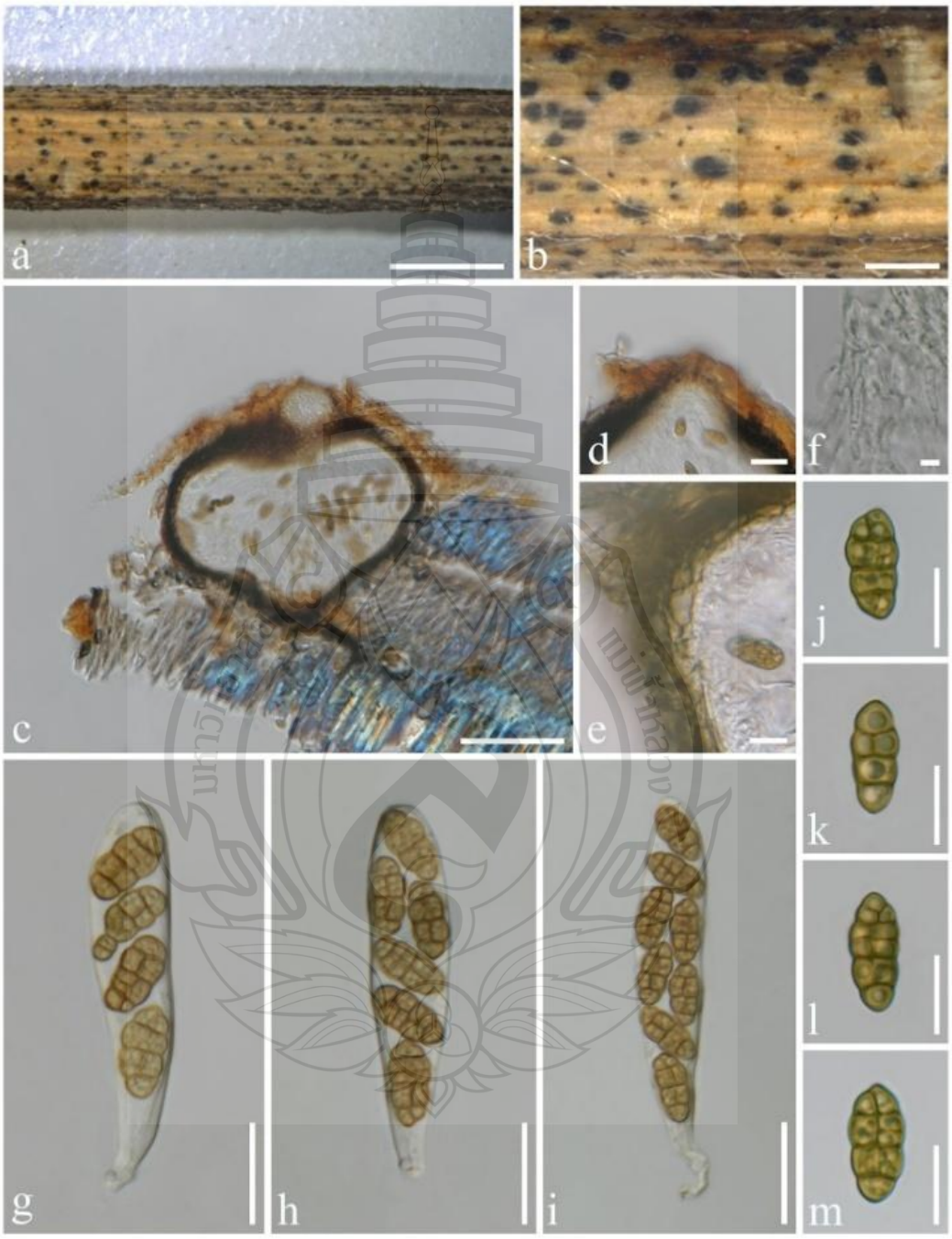
*Material examined*: Thailand, Chiang Rai Province, Mae Chan District, on dead stems of *Chromolaena odorata* (Asteraceae), 5 November 2020, Zin Hnin Htet (SW020, MFLU 25-0248, **holotype**).

*GenBank*: ***tef*1-*α***: PX255041

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

*Note*: In the phylogenetic analyses (Figure 3.11), the strain (MFLU 25-0248) formed a clade basal to the isolates of *Trematеia* with 99% ML and 0.99 BYPP bootstrap support. This collection is morphologically similar to *Trematеia* species in having immersed, globose to subglobose ascomata with a small, central ostiole, 8-spored, bitunicate, fissitunicate, cylindric-clavate asci, and oval to ellipsoidal, muriform ascospores. This collection differs from the type specimen of *T. halophila* in having smaller ascomata (180–280 × 200–305 µm vs. 225–320 × 330−410 µm), smaller asci (100–125 × 15–30 vs. 120–170× 24−30 µm) and smaller ascospores (20–30 × 10–15 vs. 25–42 × 12−20 µm) with lesser number of septa (3–4-transverse septa, 1–2 vertical

septa vs. 3–5-transverse septa, 1–2 vertical septa) compared to the latter. Therefore, based on these differences in morphology and phylogeny, *T. asteracearum* is introduced as a new species from *Chromolaena odorata* (Asteraceae) in Thailand.




**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d** Ostiole. **e** Peridium. **f** Pseudoparaphyses. **g–i** Asci. **j–m** Ascospores. Scale bar: a=1 mm, b=500 µm, c=100 µm, d, e=20 µm, f=5 µm, g, h, i=30 µm, j, k, l, m=10 µm.

**Figure 3.21** *Trematei asteracearum* (MFLU 25-0248, holotype)

### 3.2.6 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, I introduced *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 *tef*1-*α* sequence data and morphology (Figure 3.22).

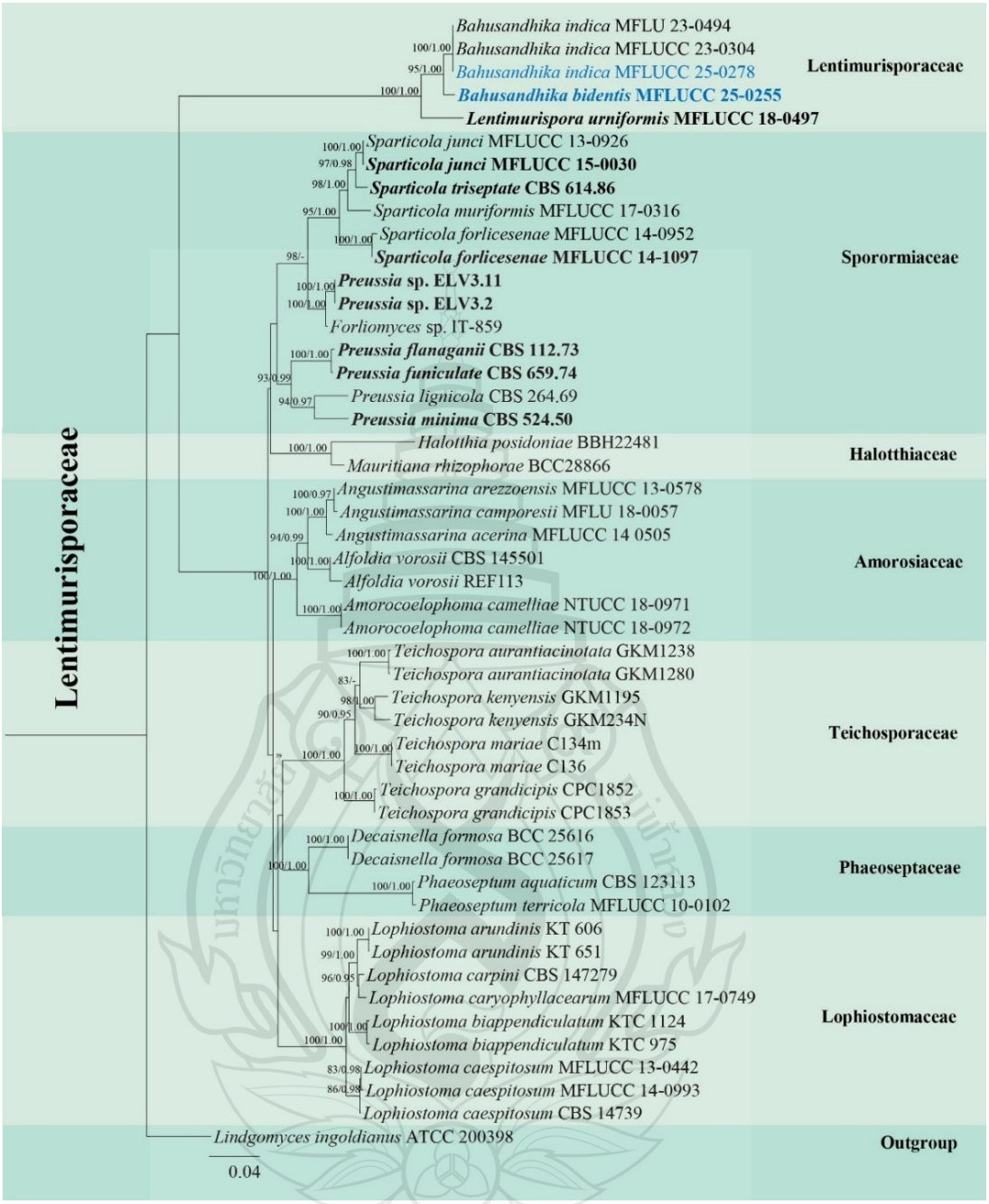



**Figure 3.22** Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Lindgomyces ingoldianus* (ATCC 200398)

***Bahusandhika*** Subram.

*Bahusandhika* was introduced by Subramanian (1956) and typified by *B. indica*. The genus has a 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). Later, Liu et al. (2018) placed *Bahusandhika* in Lentimurisporaceae based on the combined phylogeny of LSU, SSU and *tef*1-*α* sequence data. Recently, 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* is 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.**

*Index Fungorum number*: IF904367, *Facesoffungi* number: FOF18034, Figure 3.23

*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**: *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 ($\overline{x}$ = 2.5 × 4.3 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 ($\overline{x}$ = 16.1 × 11.3µm, 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.

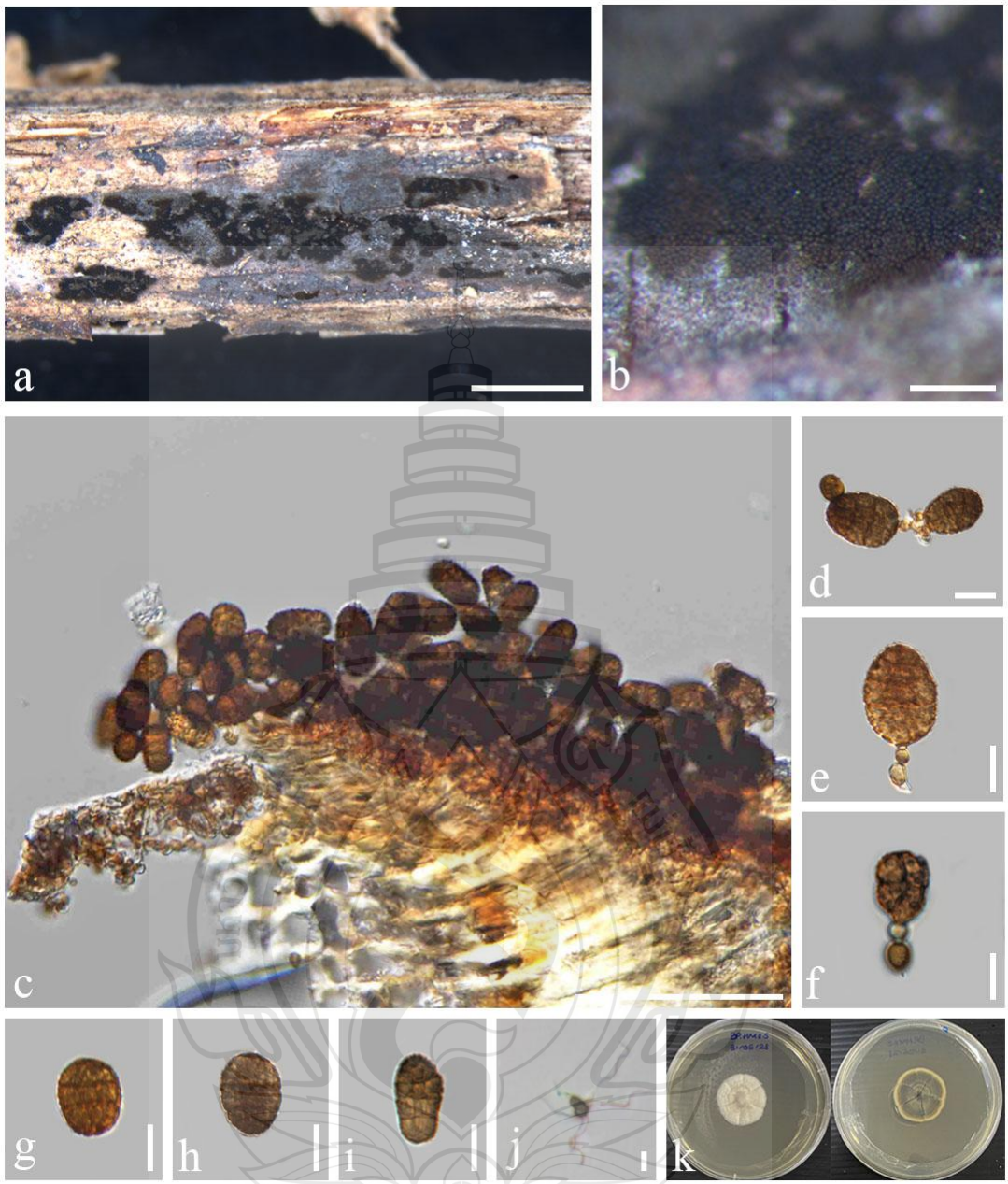
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 June 2023, Zin Hnin Htet (BP-HMS-5, MFLU 25-0249, **holotype**); ex-type MFLUCC 25-0255.

*GenBank*: **LSU**: PV992408; **SSU**: PV996961; **ITS:** PV870593; ***tef*1-*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 (Figure 3.22), the strain (MFLUCC 25-0255) grouped with *Bahusandhika* by forming a separate lineage to *Bahusandhika indica* (MFLU 23-0494, MFLUCC 23-0304, MFLUCC 25-0278) with 95% ML and 1.00 BYPP bootstrap support. Morphologically, the strain (MFLUCC 25-0255) 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). The base pair difference between this strain and *B. indica* (MFLUCC 23-0304) revealed 4% (19/473) difference in the ITS, 0.4% (3/821) difference in LSU, 0.1% (1/808) difference in SSU, and 2.6% (20/777) difference in *tef*1-*α*. Therefore, based on morphology and multi-gene phylogeny, *Bahusandhika bidentis* is introduced as a new species found on *Bidens pilosa* (Asteraceae) in northern Thailand.




**Note** **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 µm, c = 100 µm, d, e, f, g, h, i, j = 10 µm.

**Figure 3.23** *Bahusandhika bidentis* (MFLU 25-0249, holotype)

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

*Index Fungorum number*: IF293586*, Facesoffungi number*: FoF09666, Figure 3.24

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** *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 ($\overline{x}$ = 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 ($\overline{x}$ = 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.

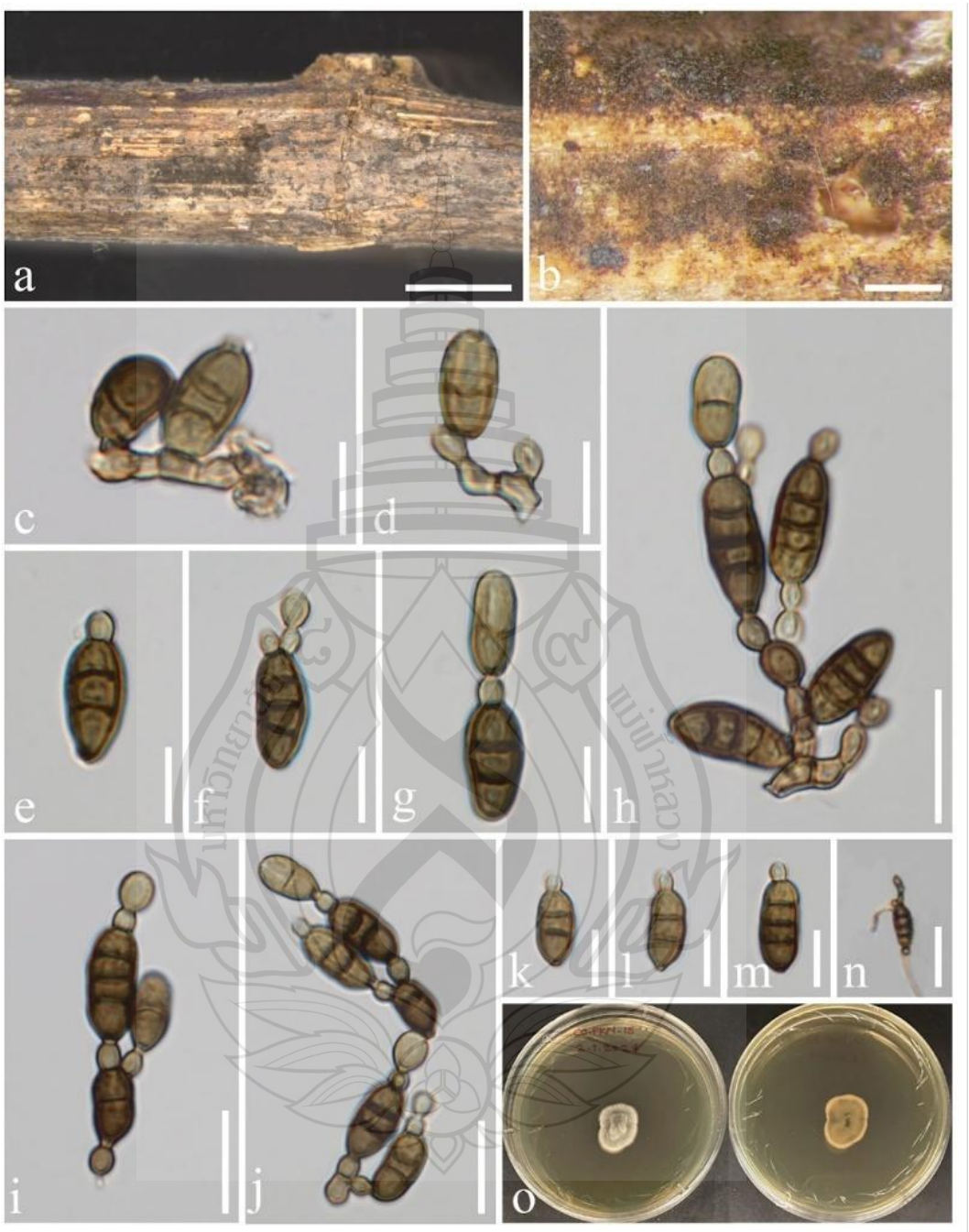
*GenBank*: **ITS**: PV870594.

*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*: unknown 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).

*Note*: In the phylogenetic analyses (Figure 3.22), 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. This new 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 base pair differences between ITS gene regions of the current collection and phylogenetically related species. Therefore, based on the morphology and multi-gene

phylogeny, a new host record of *B. indica* is reported on *Chromolaena odorata* (Asteraceae), and a new geographic record for Thailand.




**Note 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 µm, h, I, h= 20 µm, c, d, e, f, g, k, l, m, n= 10 µm.

**Figure 3.24** *Bahusandhika indica* (MFLU 25-0250, new host and geographical records)

### 3.2.7 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 the morphology is challenging (Thambugala et al., 2015; Bao et al., 2019). Therefore, molecular markers LSU, SSU, ITS, *tef*1-*α* and *rpb*2 are available for species identification in Lophiostomataceae. In this study, a new species, *Pseudolophiostoma chromolaenae* and *Lophiostoma chromolaenae* as a reference specimen were introduced, based on morphology and the combined phylogeny of LSU, SSU, ITS, and *tef*1-*α* sequence data (Figure 3.25).

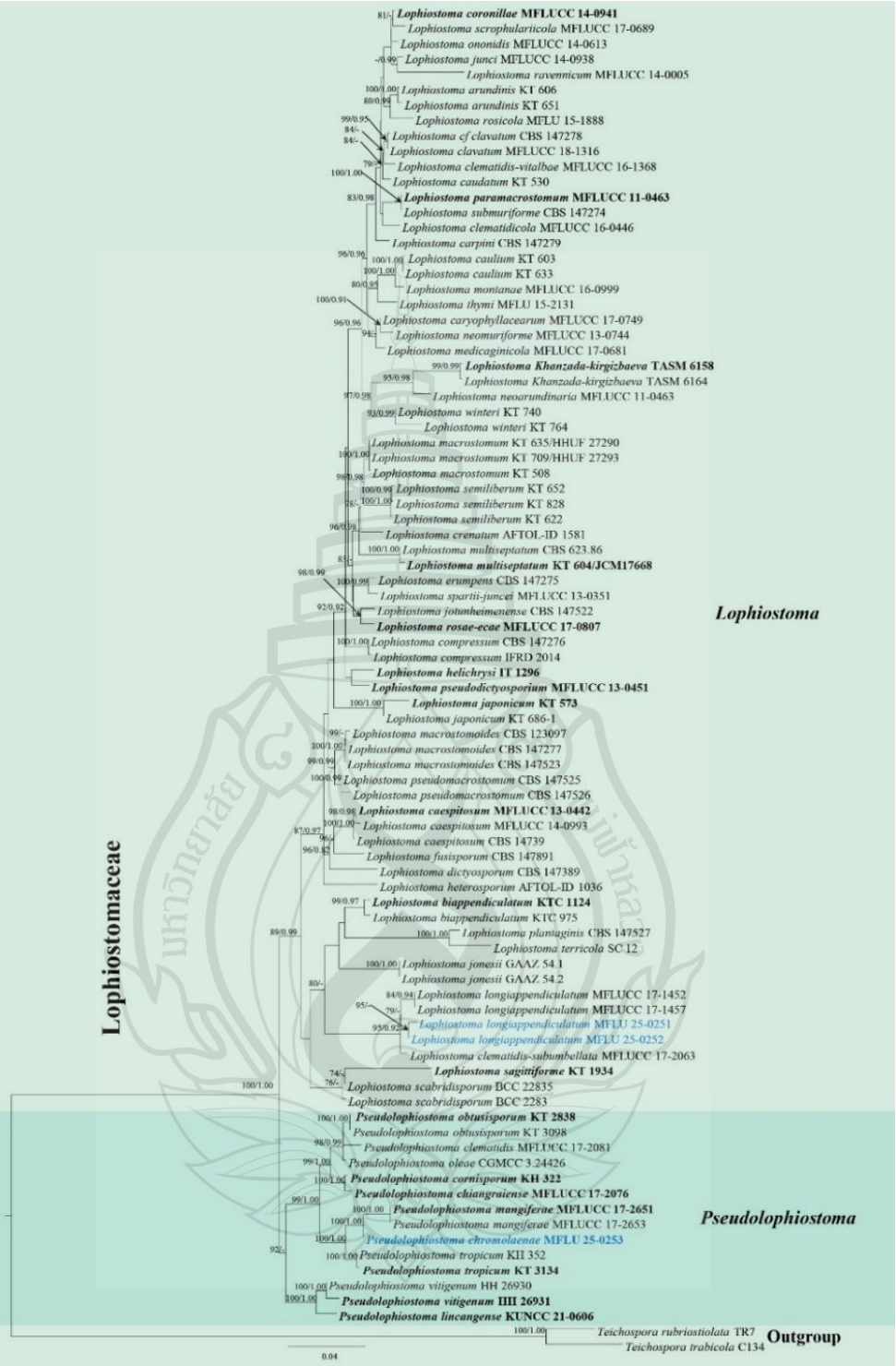



**Figure 3.25** Phylogram generated from the ML analysis of a combined dataset of LSU, SSU, ITS, *tef*1-*α* and *rpb*2 sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Teichospora rubriostiolata* (TR7) and *T. trabicola* (C134)

***Lophiostoma*** Ces. & De Not.

*Lophiostoma* was introduced by Cesati and de Notaris (1863). The genus is characterized by immersed to semi-immersed, globose to subglobose ascomata, with an ostiole, bitunicate, fissitunicate, pedicellate asci, and hyaline to brown, septate ascospores, with or without appendages. *Lophiostoma* species are mainly found as saprobes on various host plants (Andreasen et al., 2021). *Lophiostoma*, currently, comprises around 50 taxa (Hyde et al., 2024).

***Lophiostoma longiappendiculatum*** (Mapook & K.D. Hyde) Andreasen, Jaklitsch & Voglmayr, Persoonia 46: 240–271 (2021)

*Index Fungorum number*: IF838988*, Facesoffungi number*: FoF07797*,* Figure 3.26

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 190–285 × 180–265 µm ($\overline{x}$ = 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 ($\overline{x}$ = 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 ($\overline{x}$ = 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 ($\overline{x}$ = 30 × 6 µm, n = 5), from apex of the ascospores terminating in a droplet at their tips. **Asexual morph:** Undetermined.

*Culture characteristics*: Ascospores germinating on MEA within 24 hours, reaching 29 mm after 10 days at 27°C, irregular, entire, petallate, grey, flat, opaque, slightly wrinkled on the surface, changing the MEA media to yellow; petallate, dark green with white margin in the 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-1, MFLU 25-0251, **a reference specimen**); *ibid*., on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-4, MFLU 25-0252, **a reference specimen)**.

*GenBank*: **ITS**: PV870595, PV870596

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

*Notes*: In the phylogenetic analyses (Figure 3.25), these strains (MFLU 25-0251 and MFLU 25-0252) formed a clade sister to *Lophiostoma longiappendiculatum* (MFLUCC 17-1452 and MFLUCC 17-1457) and *L. clematidis-subumbellatae* (MFLUCC 17-2063) with 95% ML and 0.54 BYPP. The strain (MFLU 25-0251) is morphologically similar to *L. longiappendiculatum* and *L. clematidis-subumbellatae* 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 (Andreasen et al., 2021). The strain (MFLU 25-0251) slightly differs from *L. longiappendiculatum* 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 *L. longiappendiculatum* (MFLUCC 17-1457) reveals 1.2 % (6/507) difference in the ITS, without gaps. Due to the unavailability of other gene sequences, base pairs cannot be compared. *Lophiostoma longiappendiculatum* was previously found on *Chromolaena odorata* (Asteraceae) in Thailand (Mapook et al., 2020). Therefore, my collections are designated as a reference specimen for *L. longiappendiculatum* and the second record on *Chromolaena odorata* from northern Thailand.


**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d** Peridium. **e** Pseudoparaphyses. **f–i** Asci. **j–l** 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 = 20 µm.

**Figure 3.26** *Lophiostoma longiappendiculatum* (MFLU 25-0251, a reference specimen)

***Pseudolophiostoma***

Thambugala et al. (2015) introduced *Pseudolophiostoma* based on the combined LSU, SSU, ITS and *tef*1-*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, s**p. nov.**

*Index Fungorum number*: IF904368*, Facesoffungi number*: FoF18035, Figure 3.27

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

*Holotype*: MFLU 25-0253

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph:** *Ascomata* 230–270 × 185–225 µm ($\overline{x}$ = 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 ($\overline{x}$ = 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 ($\overline{x}$ = 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.

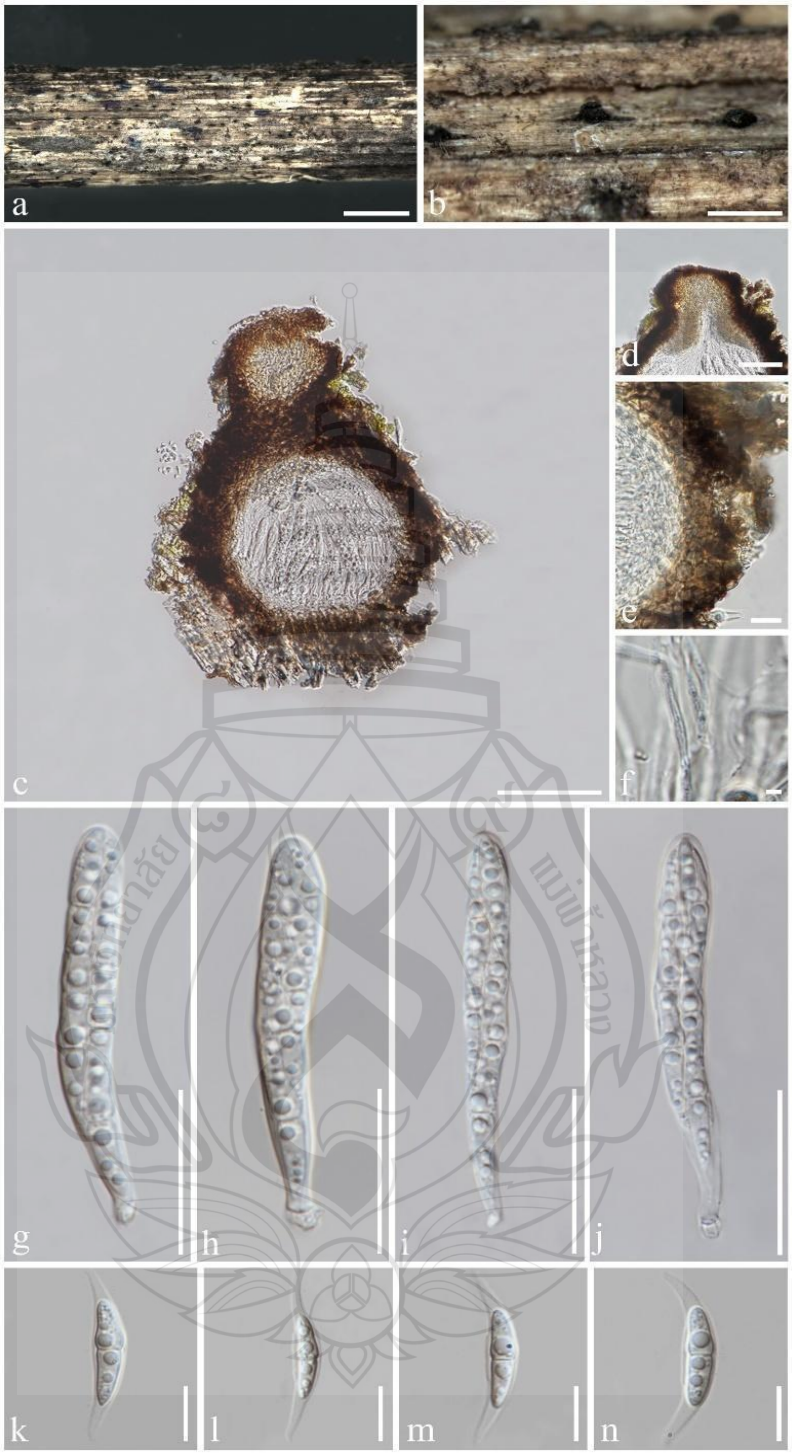
*Culture characteristics*: Ascospores germinating on MEA within 24 hours, reaching 40 mm after 10 days at 27°C, irregular, filamentous, white to olive green, slightly raised, opaque, rough and bearing green liquid after 7 days on the surface; olive to dark green with white margin in reverse surface.

*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*: **SSU**: PV996962; **ITS**: PV870597; ***tef*1-*α***: PX255043; ***rpb*2**: PX120450.

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

*Notes*: Based on the phylogenetic analyses (Figure 4.25), 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. The 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* have scattered, semi-immersed ascomata, 1-septate with 2 euseptate, fusiform, hyaline ascospores without guttules (Tennakoon et al., 2018). Therefore, based on morphology and multi-gene phylogeny, *Pseudolophiostoma chromolaenae* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand.




**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through ascoma. **d** Ostiole. **e** Peridium. **f** Pseudoparaphyses. **g–j** Asci. **k–n** Ascospores. Scale bars: a = 1 mm, b = 500 µm, c = 100 µm, d = 50 µm, e = 20 µm, f = 5 µm, g, h, i, j = 30 µm, k, l, m = 10µm.

**Figure 3.27** *Pseudolophiostoma chromolaenae* (MFLU 25-0253, holotype)

### 3.2.8 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). This study recorded *Periconia byssoides* as a new record based on the combined phylogeny of LSU, SSU, ITS, *tef*1-*α*, and *rpb*2 sequence data (Figure 3.28).

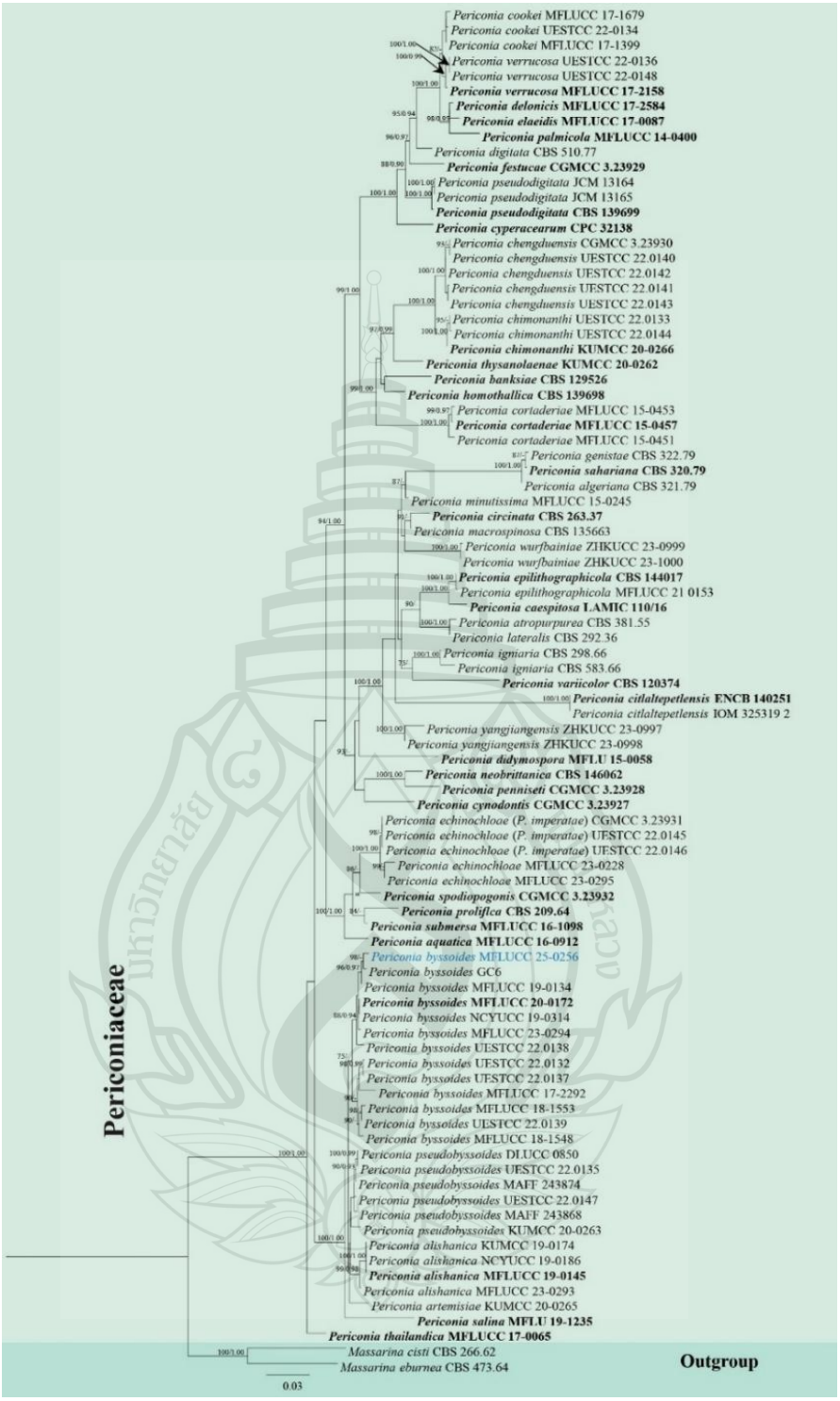



**Figure 3.28** Phylogram generated from ML analysis based on the combined sequence data of LSU, SSU, ITS, *tef*1-*α*, and *rpb*2. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Massarina cisti* (CBS 266.62) and*M. eburnean* (CBS 473.64)

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

*Index Fungorum number*: IF144538, *Facesoffungi number*: FoF09319, Figure 3.29

*Saprobic* on dead stems of *Bidens pilosa.* **Sexual morph:** Undetermined. **Asexual morph:** Hyphomycetous. *Colonies* effuse, powdery, gregarious, black. *Conidiophores* 390–450 × 13–15 μm ($\overline{x}$ = 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 ($\overline{x}$ = 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.

*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.

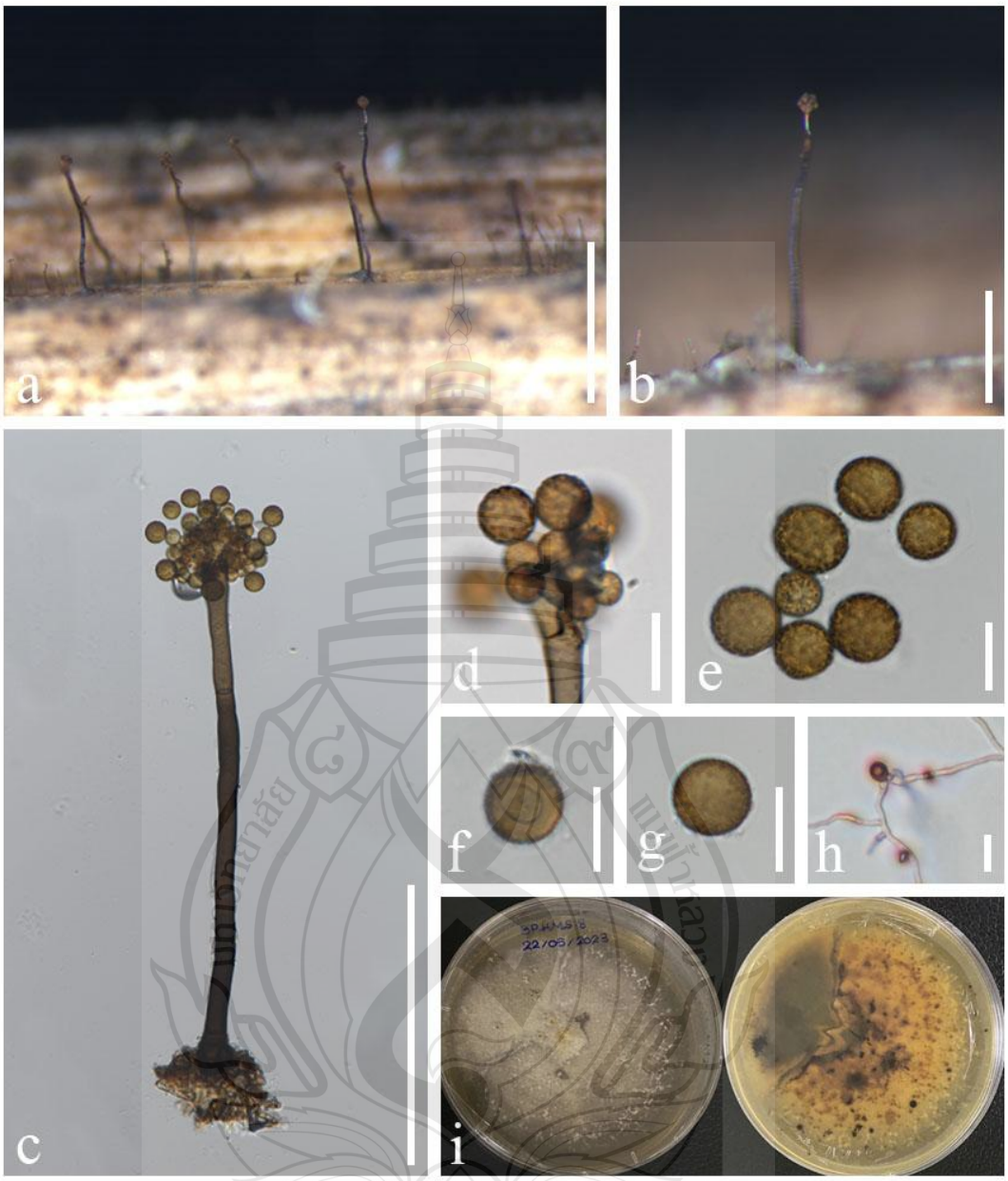
*GenBank*: **LSU**: PV992409; **SSU**: PV996963; **ITS**: PV870598; ***tef*1-*α***: PX255044; ***rpb*2**: PX120451.

*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 in hibition, 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 (China) (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); the dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study);

*Notes*: In the phylogenetic analyses (Figure 3.28), 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, this 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. There are also no base pair differences between ITS, LSU, SSU, *tef*1-*α*, and *rpb*2 sequences of the isolates of *P. byssoides* (MFLUCC 20-0172) and the strain (MFLUCC 25-0256). Therefore, a new host record of *P. byssoides* on *Bidens pilosa* (Asteraceae) is reported in northern Thailand.




**Note** **a, b** Appearance of colonies on the host substrate. **d** 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.

**Figure 3.29** *Periconia byssoides* (MFLU 25-0254, a new host record)

### 3.2.9 **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 delineate 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). This study records *Leptospora thailandica* as a new host record and *Murichromolaenicola thailandensis* as a reference specimen based on the combined data of LSU, SSU, ITS, and *tef*1-*α* sequences (Figure 3.30).

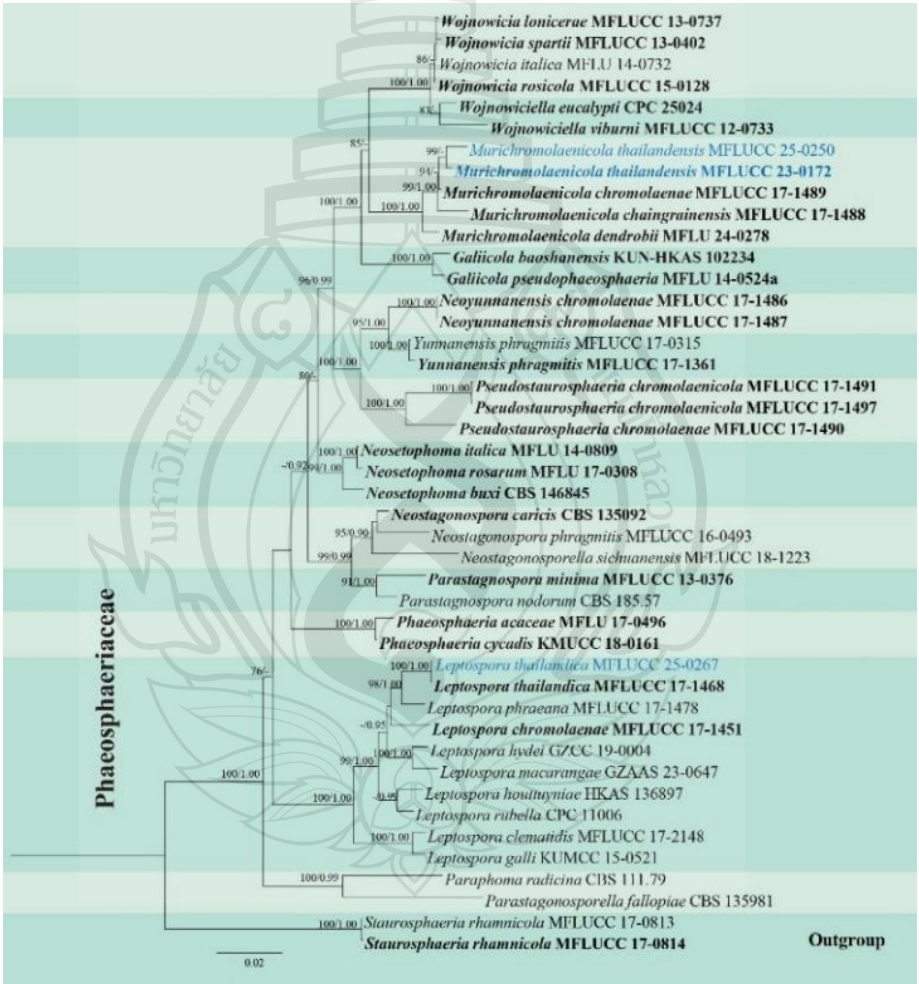



**Figure 3.30** Phylogram generated from the ML analysis of the combined data of LSU, SSU, ITS, and *tef*1-*α* sequences. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Staurosphaeria rhamnicola* (MFLUCC 17-0813 and MFLUCC 17-0814)

***Leptospora*** Rabenh.

*Leptospora* is firstly accommodated to *Sphaeria rubella* (Persoon, 1801). Later, the genus was transferred to Dothideomycetes (Rabenhorst, 1858). The type species is *Leptospora rubella.* Currently, the genus is accepted in Phaeosphaeriaceae based on combined sequence data of ITS, LSU and SSU. *Leptospora* species have been reported from both terrestrial and aquatic habitats (Hyde et al., 2016; Sun et al., 2025). *Leptospora* is characterized by scattered, solitary ascomata visible as black spots or red to purple stains on the surface, with a red colour at the apex of ostiolar neck, cylindrical to subcylindric-clavate asci and hyaline to pale brown, filiform ascospores. (Hyde et al., 2016; Sun et al., 2025). To date, *Leptospora* is comprised of around 25 taxa (Hyde et al., 2024).

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

*Index Fungorum number*: IF552239, *Facesoffungi number*: FoF02381, Figure 3.31

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: *Ascomata* 200–270 × 140–200 µm ($\overline{x}$ = 227 × 168 µm, 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 µm wide, comprising 3–4 layers of brown cells of *textura angularis*. *Hamathecium* 1.5–3 µm wide, comprises branched, septate, hyaline pseudoparaphyses. *Asci* 55–75 × 7–12 µm ($\overline{x}$ = 67 × 9 µm, 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 × 2–3 µm ($\overline{x}$ = 50 × 2.4 µm, 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*: **SSU**: PV996964; **ITS**: PV870599; ***tef*1- *α***: PX255045

*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 (Figure 3.30), the strain (MFLUCC 25-0267) is clustered sister to *Leptospora thailandica* (MFLUCC 17-1468) with 100% ML and 1.00 BYPP bootstrap support. This collection is morphologically similar to *L. thailandica* (MFLUCC 17-1468) in having immersed, eruptment ascomata, central ostiole with reddish pigmentation, branched, septate, hyaline pseudoparaphyses, 8-spored, bitunicate asci, and hyaline, filiform, ascospores (Phukhamsakda et al., 2020). But my collection differs from *L. thailandica* (MFLUCC 17-1468) in having larger ascomata (200–270 × 140–200 µm vs. 188–207 × 112–170 µm), shorter asci (55–75 µm vs. 68–114 µm), and shorter ascospores (40–60 µm vs. 63–89 µm). There is also no base pair difference between the ITS sequence of this 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, my collection is reported as a new host record of *L. thailandica* on *Bidens pilosa* (Asteraceae) in northern Thailand, which is also the second record in Thailand.


**Note** **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 3.31** *Leptospora thailandica* (MFLU 25-0255, a new host record)

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

*Murichromolaenicola* was introduced by Mapook et al. (2020) with two species in Phaeosphaeriaceae (Pleosporales), viz., *M. chromolaenae* (type) and *M. chiangraiensis*. The sexual morph of *Murichromolaenicola* is characterized by semi-immersed to superficial, globose to obpyriform, ostiolate ascomata, bitunicate, cylindric-clavate, pedicellate asci with hyaline to brown, ellipsoid to broadly fusiform, muriform ascospores, with a gelatinous sheath. The asexual morph is characterized by immersed to semi-immersed, globose, pycnidial conidiomata, phialidic, ampulliform to cylindrical, hyaline, unbranched conidiogenous cells, and ellipsoid to broadly fusiform, yellowish brown to brown, muriform conidia, with 5–7 transverse septa and 1–2 vertical septa, and polar appendages (Mapook et al., 2020). 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)

*Index Fungorum number:* IF849500*, Facesoffungi number:* FoF14609*,* Figure 3.32

*Etymology*: Named after the country where the specimen is collected, Thailand.

*Holotype*: MFLU 23-0324

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

*Culture characteristics*: Conidia germinating on PDA, reaching 25 mm diam within 7 days at room temperature, circular, entire, concentric, flat, opaque, grey on the surface; concentric, pale brown in middle and white at the margin of the reverse surface.

*Material examined*: Thailand, Chiang Rai Province, Theong District, on dead stems of *Chromolaena odorata* (Asteraceae), 24 Jan 2022, A. Mapook, TCR 12 (MFLU 23-0324, **holotype**); ex-type MFLUCC 23-0172; Thailand, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 14 March 2023, Zin Hnin Htet (CO-DP-7, MFLU 25-0256, **reference specimen**); living culture MFLUCC 25-0250.

*GenBank:* **LSU**: OR343207, **SSU**: OR343209, **ITS**: OR343208, ***tef*1-*α***: OR420087, ***rpb*2**: OR420088

*Pre-screening for antimicrobial activity*: *Murichromolaenicola thailandensis* (MFLUCC 23-0172) showed no inhibition against all test organisms, *B. subtilis*, *E. coli*, and *S. aureus.*

*Known host and distribution*: on dead stems of *Chromolaena odorata* (this study).

*Notes*: In the blast search of NCBI, the closest match to the ITS and *tef*1-*α* sequences of *Murichromolaenicola thailandensis* (MFLUCC 23-0172) is *M. chromolaena*e (MFLUCC 17-1489) with 99.21% (NR_168850) and 98.90% (MN998164) similarities, respectively. The closest match to the LSU sequence was *Neostagonosporella sichuanensis* (isolates SAUFP201604001, MH368079), with 98.86% similarity. The closest match for the SSU sequence was *Parastagonospora nodurum* (CBS 185.57, KY090706), with 99.71% similarity. The closest match for *rpb2* was *Wojnowicia italica* (MFLU 14-0732, KX430004), with 90.43% similarity. In the present phylogenetic analyses (Figure 3.30), the strain from the current study clusters with *M. chromolaenae* (MFLUCC 17-1489) with 99% Ml bootstrap support. Based on the morphological comparison, *M. thailandensis* resembles *M. chromolaenae* (MFLUCC 17-1489) by its immersed conidiomata, yellowish brown to brown cells of *textura angularis* and yellowish brown to brown ascospores with transverse and longitudinal septa. However, the current strain differs from *M. chromolaenae* in having comparatively smaller conidiomata (130–150 × 140–160 µm vs 200–235 × 195–230 µm) and smaller conidia with a gelatinous cap (10–20 × 5–10 µm vs 14–25 × 6.5–11 µm). Furthermore, the conidia of *M. chromolaenae* have ellipsoid to broadly fusiform, 5–7 transverse septa with polar appendages from both ends, while my strain has oblong or oval to obovoid conidia, rounded at both ends, 3–5 transverse septa and a gelatinous cap at one end. Moreover, *M. thailandensis* and *M. chromolaenae* differ in their culture

characteristics on malt extract agar (MEA). *Murichromolaenicola chromolaenae* has crateriform, undulate, white cultures with greyish center at the surface and reverse colony from olivaceous center to creamy-white at the margin, while *M. thailandensis* has circular, entire, concentric, flat, opaque, grey at the surface and wrinkled, pale brown at the reverse surface. In addition, the nucleotide comparison of the ITS gene region of this strain and *M. chromolaenae* reveals 1.56% (8/512) nucleotide differences. Therefore, this strain is introduced as a new species, based on phylogeny and morphological comparison, in accordance with Chethana et al. (2021).


**Source** Htet et al. (2023)

**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e** Conidiogenous cells. **f–i** Conidia. **j–k** Conidia stained in Indian Ink. **l** A germinating conidium. **m** Culture on MEA. **n** Culture on PDA. Scale bars a, b = 500 µm, c = 100 µm, d = 20 µm, e = 5 µm, f–l = 10 µm.

**Figure 3.32** *Murichromolaenicola thailandica* (MFLU 23-0324, holotype)

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

Roussoellaceae was introduced by Liu et al. (2014) based on morphology and LSU, ITS, *tef*1-*α* and *rpb*2 sequence data. Members of Roussoellaceae can be found as saprobes and human pathogens (Ahmed et al., 2014; Liu et al., 2014; Mapook et al., 2020; Hyde et al., 2023; Wu et al. 2023). Currently, there are 12 genera in Roussoellaceae, viz., *Appendispora*, *Cytoplea*, *Elongatopedicellata*, *Immorrhia*, *Neoroussoella*, *Pararoussoella*, *Pseudoneoconiothyrium*, *Pseudoroussoella*, *Roussoella*, *Roussoellopsis*, *Setoarthopyrenia*, and *Xenoroussoella* (Hyde et al., 2024). This study recorded *Pseudoneoconiothyrium chromolaenae* and *Ps. thailandicum* as new species and *Neorousseolla entadae* as a reference specimen based on the combined LSU, SSU, ITS, and *tef*1-*α* sequence data (Figure 3.33).

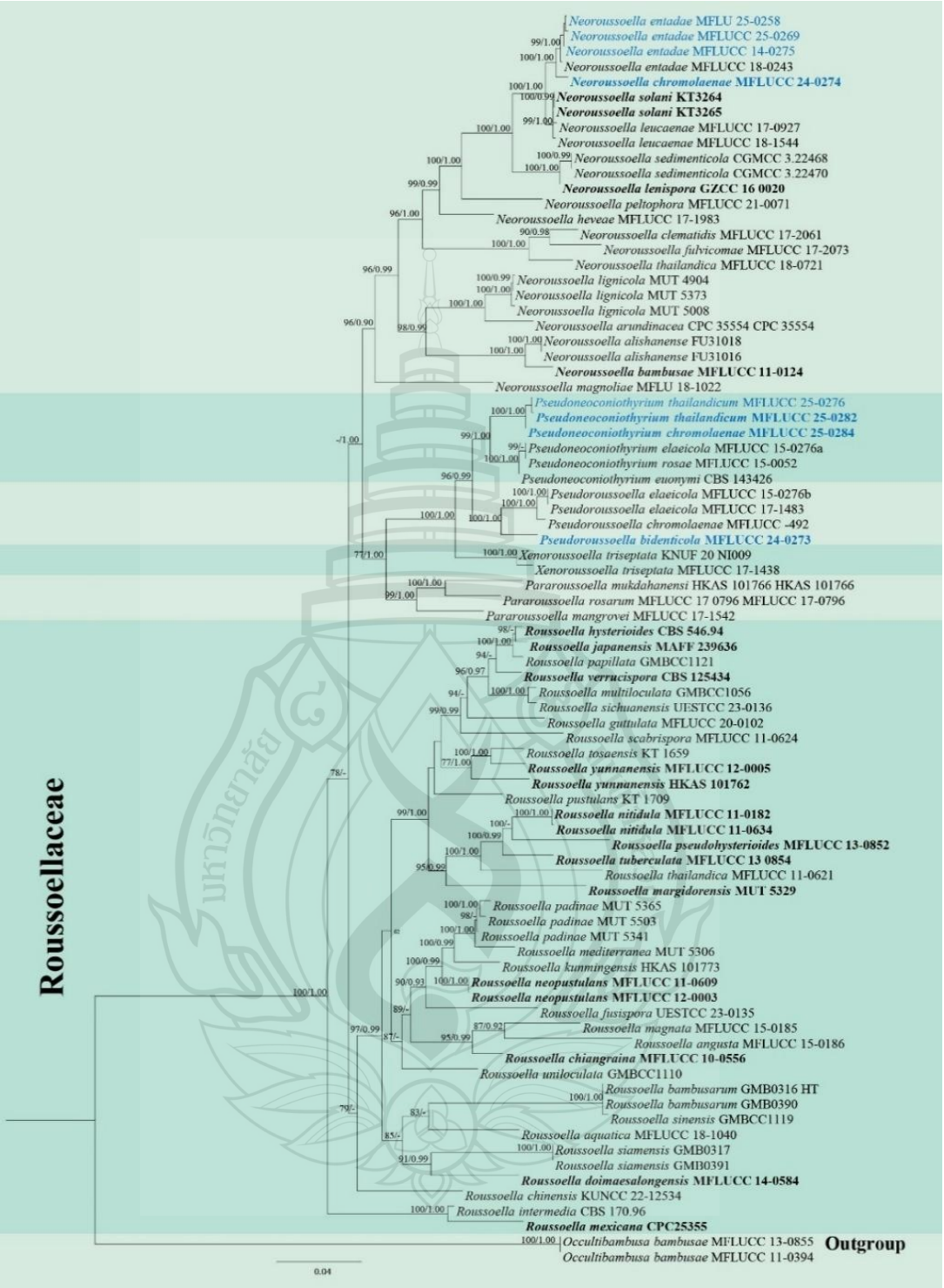



**Figure 3.33** Phylogram generated from the ML analysis based on the combined LSU, SSU, ITS, and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Occultibambusa bambusae* (MFLUCC 13-0855 and MFLUCC 11-0394)

***Neoroussoella*** Jian K. Liu, Phook. & K.D. Hyde

*Neoroussoella* was introduced by Liu et al. (2014) to accommodate a saprobic roussoella-like taxon with the type species, *N. bambusae*. The sexual morphology of *Neoroussoella* is defined by immersed ascostromata beneath a clypeus or epidermis, appearing as black, dome-shaped, or flattened ovoid structures on the host surface. The asci are bitunicate and cylindrical, while the ascospores are brown or yellowish-brown, ellipsoidal to fusiform, and 2-celled, surrounded by a mucilaginous sheath (Liu et al., 2014). The asexual morphology of *Neoroussoella* is characterized by superficial or immersed pycnidia with annellidic, ampulliform, cylindrical conidiogenous cells, producing hyaline, pale brown, oblong to ellipsoidal conidia, each with two guttules (Liu et al., 2014; Jayasiri et al., 2019). Currently, there are 15 epithets listed in the Index Fungorum (2025), viz., *Neoroussoella alishanensis*, *N. bambusae*, *N. clematidis*, *N. chiangmaiensis*, *N. entadae*, *N. fulvicomae*, *N. heveae*, *N. lenispora*, *N. leucaenae*, *N. lignicola*, *N. magnoliae*, *N. peltophora*, *N. sedimenticola*, *N. solani*, and *N. thailandica*.

***Neoroussoella chromolaenae*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, *MycoKeys* 111: 139 (2024)

*Index fungorum number*: IF902613; *Facesoffungi number*: FoF16402; Figure 3.34

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

*Holotype*: MFLU 24-0264

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph**: undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* 70–150 × 120–150 µm ($\bar{x}$=85 × 138 µm, n = 5), pycnidial, solitary, uniloculate, immersed, ostiolate. *Ostiole* papillate. *Peridium* 10–20 µm wide, comprising 2–3 layers of brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–5 × 2–3.5 µm ($\bar{x}$=3 × 3 µm, n = 10), phialidic, ampulliform to cylindrical, hyaline. *Conidia* 3–6 × 2–4 µm ($\bar{x}$=4.4 × 3.1 µm, n = 20), hyaline, oblong to slightly ellipsoid, aseptate, with small guttules.

*Culture characteristics*: Conidia germinating on MEA within 24 hours, reaching 22 mm after 10 days at 27°C, irregular, curled margin, brown in the middle and

becoming pale brown on the outer parts of the culture, wrinkled on the surface; wrinkle, pale brown to brown in reverse.

*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 14 March 2023, Zin Hnin Htet (CO-DP-3, MFLU 24-0264, **holotype**); ex-type MFLUCC 24-0274.

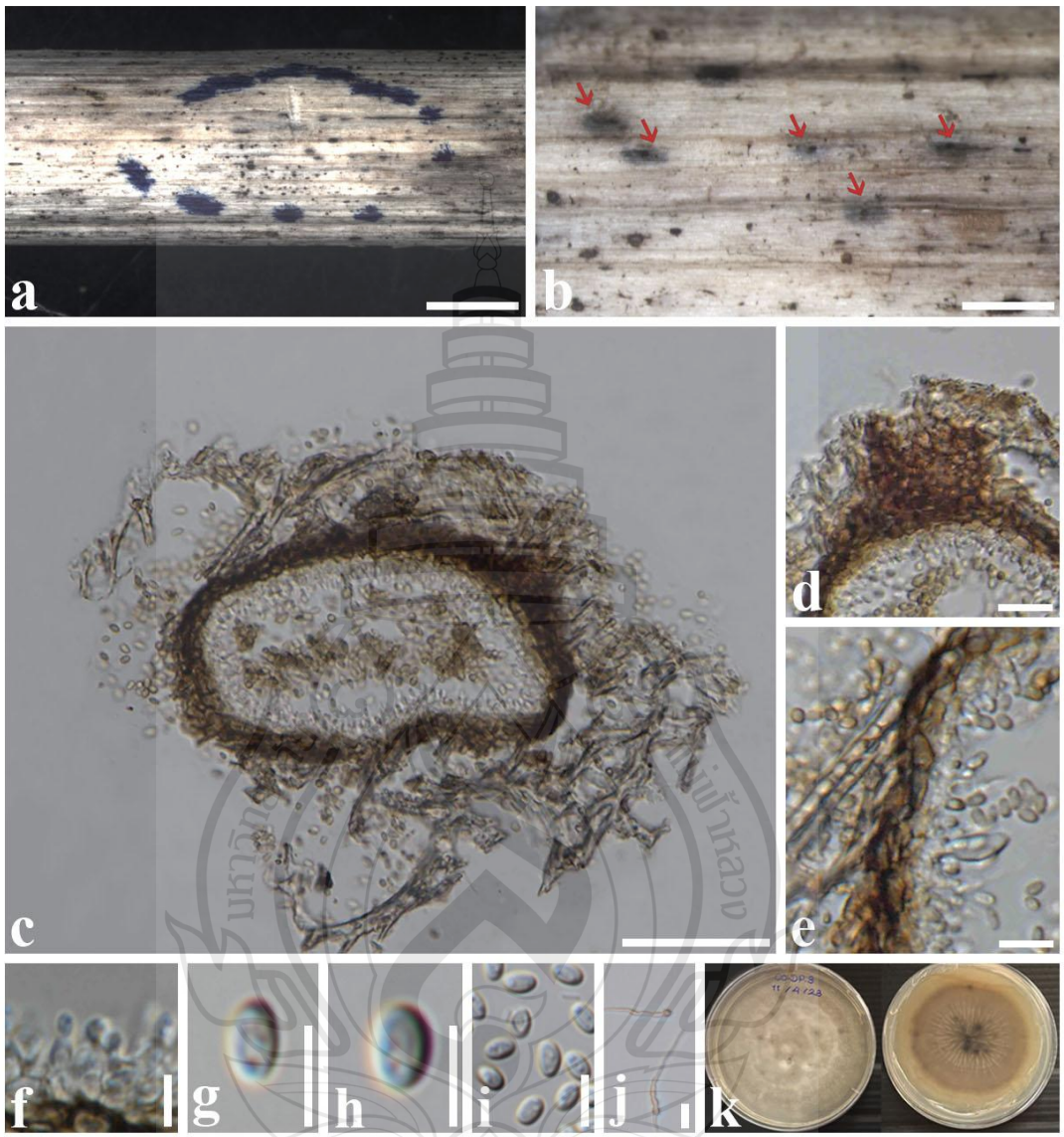
*GenBank*: **LSU**: PQ226193; **SSU**: PQ226196; **ITS**: PQ226190; ***tef*1-*α***: PQ240621; ***rpb*2**: PQ240623

*Pre-screening for antimicrobial activity*: ***Neoroussoella chromolaenae*** (MFLUCC 24-0274) showed a 16 mm inhibition against *B. subtilis*, a 11 mm inhibition against *E. coli* and a 20 mm inhibition against *S. aureus*.

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

*Note*: In a megablast search of GenBank, the closest match for the ITS sequence of my isolate was fungal sp. isolate NFC-3 (MG189955) with 99.47% similarity. The closest match for the LSU region was *N. solani* CBS 141288 (MH878207) with 100% similarity, and the closest match for the SSU region was *N. bambusae* strain GMB1295 (OM764650) with 93.99% similarity. Additionally, the closet matches for the *tef*1-*α* and *rpb*2 gene regions were *Neoroussoella entadae* strain MFLUCC 18-0243 (MK360065) and *N. entadae* strain MFLUCC 17-0920 (MK434898) with 99.45% and 99.77% similarities, respectively. Based on the multi-locus phylogeny (Figure 3.33), my isolate (MFLUCC 24-0274) formed a separate branch from the isolates of *N. entadae* with 100% ML and 1.00 BYPP. A comparative analysis of base pair differences between *Neoroussoella chromolaenae* (MFLUCC 24-0274) and *N. entadae* (MFLUCC 18-0243) revealed variations in ITS (0.6% - 3/476), LSU (0.1% - 1/838), SSU (1.9% - 14/717), *tef*1-*α* (0.5% - 5/902), and *rpb*2 (2.0% - 18/885) without gaps, respectively. Morphologically, this collection is similar to *N. entadae* (MFLUCC 17–0920) in having solitary, unilocular, ostiolate, phialidic, ampulliform to cylindrical, hyaline conidiogenous cells, and oblong to ellipsoidal, hyaline conidia (Jayasiri et al., 2019). However, this species differs from *N. entadae* (MFLUCC 17–0920) in having smaller conidiomata (70–150 × 120–150 µm vs. 127–192 × 161–190 µm), slightly wider conidiogenous cells (2–3.5 µm vs. 0.7–1.8 µm) and larger conidia size (3–6 × 2–

4 µm vs. 3–4 × 1.7–1.9 µm). Therefore, *N. chromolaenae* is described here as a new species based on phylogeny and morphological evidence.




**Source** Htet et al. (2024)

**Note** **a**, **b** Appearance of conidiomata on the substrate. **c** A section through conidioma. **d** Ostiole. **e** Peridium. **f** Conidia and conidiogenous cells. **g**–**i** Conidia. **j** Germinating conidia. **k** Culture on the MEA. Scale bars: a, b = 500 µm, c = 100 µm, d, e = 20 µm, e–j = 10 µm.

**Figure 3.34** *Neoroussoella chromolaenae* (MFLU 24-0264, holotype)

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

*Index Fungorum number*: IF555568, *Facesoffungi* number: FoF05275, Figure 3.35

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* 100–150 × 100–170 µm ($\overline{x}$ = 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 ($\overline{x}$ = 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.

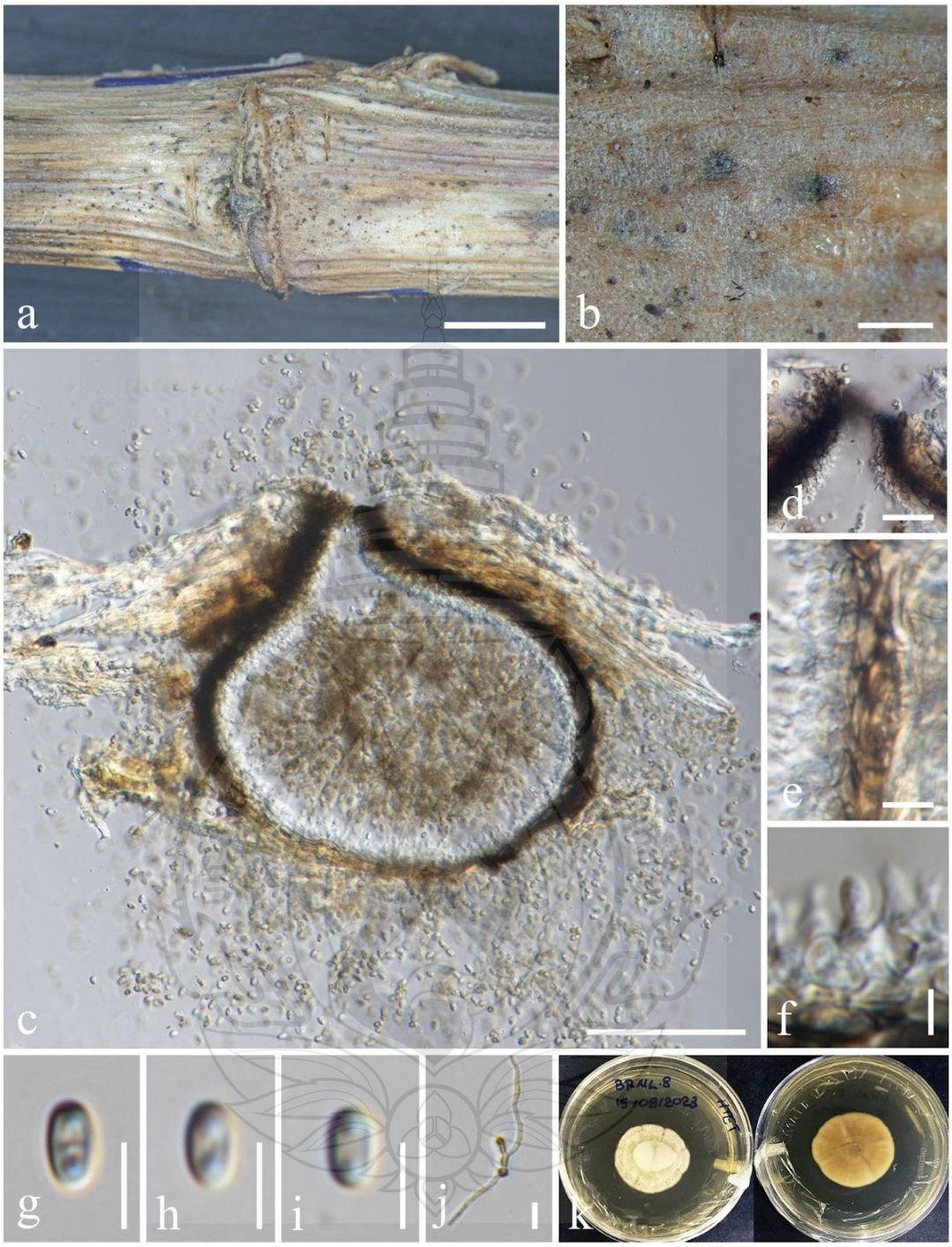
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet (BP-NL-8, MFLU 25-0257, **a new host record**); living culture MFLUCC 25-0269; *ibid.,* Phayao Province, Mueang Phayao District, on dead stems of *Bidens pilosa* (Asteraceae), 16 December 2023, Zin Hnin Htet (BP-MY-5, MFLU 25-0258, **a reference specimen**); *ibid.,* Chiang Rai Province, Thoeng district, on dead stems of *Chromolaena odorata* (Asteraceae), 24 Jan 2022, A. Mapook (TCR18, MFLU 24-0265, new host record); living culture MFLUCC 24-0275.

*GenBank*: **SSU**: PV996966; **ITS**: PV870601, PV870602; ***tef*1-*α***: PX255047, PX255048; ***rpb*2**: PX120453, PX120454

*Pre-screening for antibacterial activity*: *Neoroussoella entadae* (MFLUCC 25-0269) 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); the dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Htet et al., 2024); the dead stems of *Bidens pilosa* (Asteraceae) in Thailand (this study).

*Notes*: Based on the multi-locus phylogeny (Figure 3.33), these isolates (MFLUCC 25-0269 and MFLU 25-0258) clustered with the isolates of *Neoroussoella entadae* (MFLUCC 18-0243 and MFLUCC 14-0275) with 99% ML and 1.00 BYPP bootstrap support. When comparing base pair differences between these isolates and *N. entadae* (MFLU 18-0243), there were no variations among the respective ITS, *tef*1-*α* and *rpb*2 gene regions. This 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 introduced as a new host record of *N. entadae* on *Bidens pilosa* (Asteraceae) based on morphology and multi-gene phylogeny.




**Note** **a, b** Appearance of conidiomata on the host substrate. **c** Section through 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 3.35** *Neoroussoella entadae* (MFLU 25-0257, a new host record)

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

*Pseudoneoconiothyrium* was introduced by Wanasinghe et al. (2018). Later, the genus was placed in Roussoellaceae based on LSU, SSU, ITS, *tef*1-*α* and *rpb*2 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.**

*Index Fungorum number*: IF904369*, Facesoffungi number*: FoF18036*,* Figure 3.36

*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**: *Conidiomata* 235–320 × 170–210 µm ($\overline{x}$ = 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 ($\overline{x}$ = 4.1 × 4.8) annellidic, ovoid to obovoid, or ampulliform, hyaline and unbranched. *Conidia* 4–7 × 3–5 µm ($\overline{x}$ = 5.7 × 3.7 µm, 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, reddish brown in reverse surface.

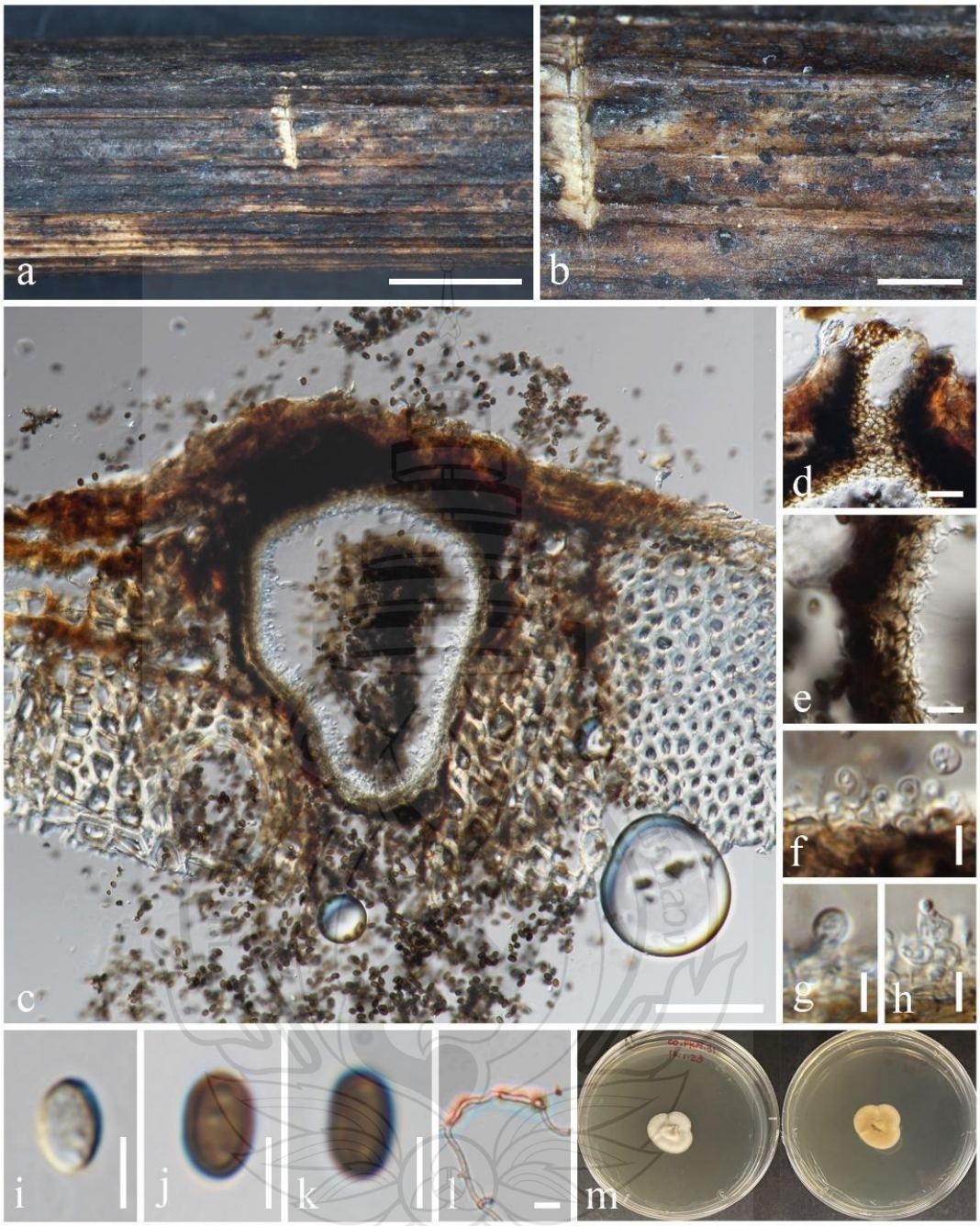
*Material examined*: Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-31, MFLU 25-0259, **holotype**), ex-type MFLUCC 25-0284.

*GenBank*: **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).

*Note*: Based on the phylogenetic analysis (Figure 3.33), 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. My strain (MFLUCC 25-0284) is found as an asexual morph in nature, and 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). The strain (MFLUCC 25-0284) differs from *Ps. thailandicum* (MFLUCC 25-0282) in having larger conidioma (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.




**Note** **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 = 500µm, b = 200 µm, c = 100 µm, d, e = 20 µm, f, g, h, i, j, k, l = 5 µm, m = 10mm.

**Figure 3.36** *Pseudoneoconiothyrium chromolaenae* (MFLU 25-0259, holotype)

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

*Index Fungorum number*: IF904370*, Facesoffungi number*: FoF18037*,* Figure 3.37

*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**: *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, reddish brown in reverse surface.

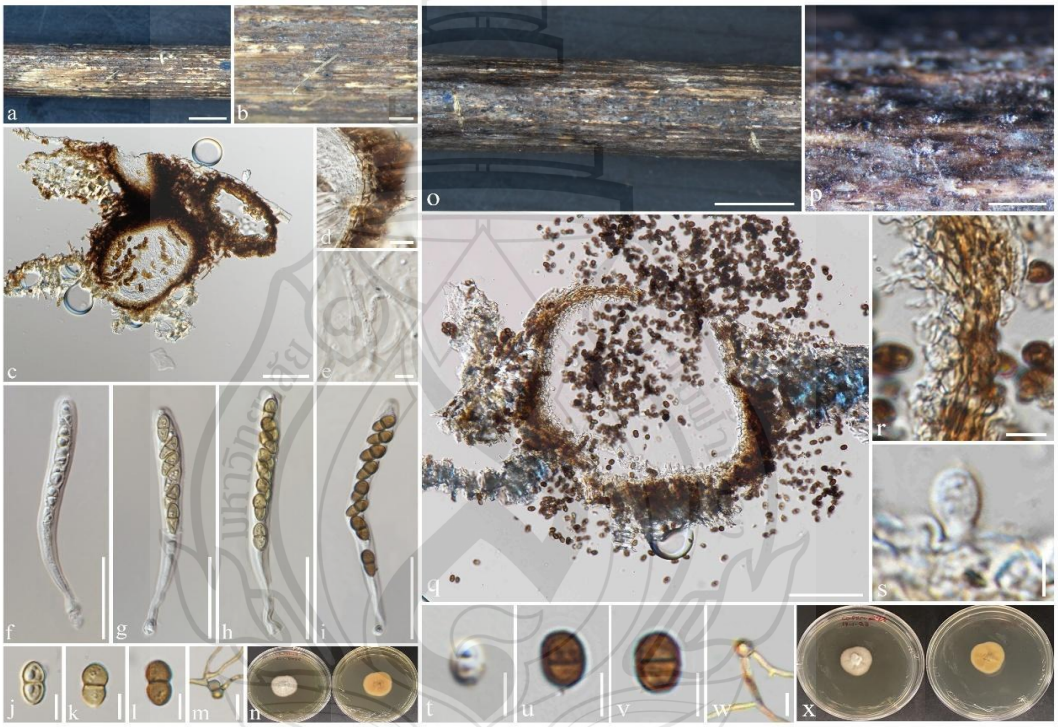
*Material examined*: Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-9, MFLU 25-0260, **holotype**), ex-type MFLUCC 25-0276; *ibid*., on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023,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

*GenBank*: **ITS**: PV870604, PV870605; **SSU**: PV996967; ***tef*1-*α***: PX255049, 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).

*Note*: Refer to the remarks provided under *Pseudoconiothyrium chromolaenae* for comparative discussion. Here, *Ps. thailandicum* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand, based on morphology and multigene phylogeny.



**Note** **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 µm, b, p =200 µm, c, q = 100 µm, d, r = 20 µm, e, j, k, l, m, s, t, u, v, w =5 µm, f, g, h, i = 30 µm.

**Figure 3.37** *Pseudoneoconiothyrium thailandicum* (MFLU 25-0260, holotype)

***Pseudoroussoella*** Mapook & K.D. Hyde

*Pseudoroussoella* was introduced by Mapook et al. (2020) based on morphology and LSU, SSU, ITS, *tef*1-*α* and *rpb2* sequence data. The sexual morph of *Pseudoroussoella* species is characterized by globose to subglobose, dark brown to black ascomata with an ostiole, comprised of *textura epidermoidea* to *textura angularis* or *textura intricata* cells, with septate, trabeculate pseudoparaphyses, 8-spored, bitunicate, fissitunicate, cylindrical to clavate asci with a pedicel, and uniseriate, hyaline to pale brown, oval to ellipsoid, 1-septate ascospores bearing a gelatinous sheath (Mapook et al., 2020). Asexual morphs of *Pseudoroussoella* species are distinguished by solitary, superficial, uni-loculate, globose to obpyriform, pycnidial conidiomata with an ostiole, comprised of *textura angularis* cells, annellidic, ampulliform to oblong, hyaline and unbranched conidiogenous cells and pale brown to reddish brown, aseptate conidia with guttules (Mapook et al., 2020). Currently, two species are listed in the Index Fungorum (2024).

***Pseudoroussoella bidenticola*** Htet, A. Mapook & K.D. Hyde, *MycoKeys* 111: 139 (2024)

*Index fungorum number*: IF902614, *Faces of fungi* number: FOF16403, Figure 3.38

*Holotype*: MFLU 24-0266

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

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: Coelomycetous. *Conidiomata* 120–150 × 150–180 µm ($\bar{x}$=126 × 173 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* 1–2 µm long, holoblastic, short, globose to subglobose, hyaline and unbranched. *Conidia* 5–7.5 × 4–5.5 µm ($\bar{x}$=6 × 4.8 µm, n = 20), globose to subglobose, brown to reddish brown, aseptate, thick-walled with a guttule.

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

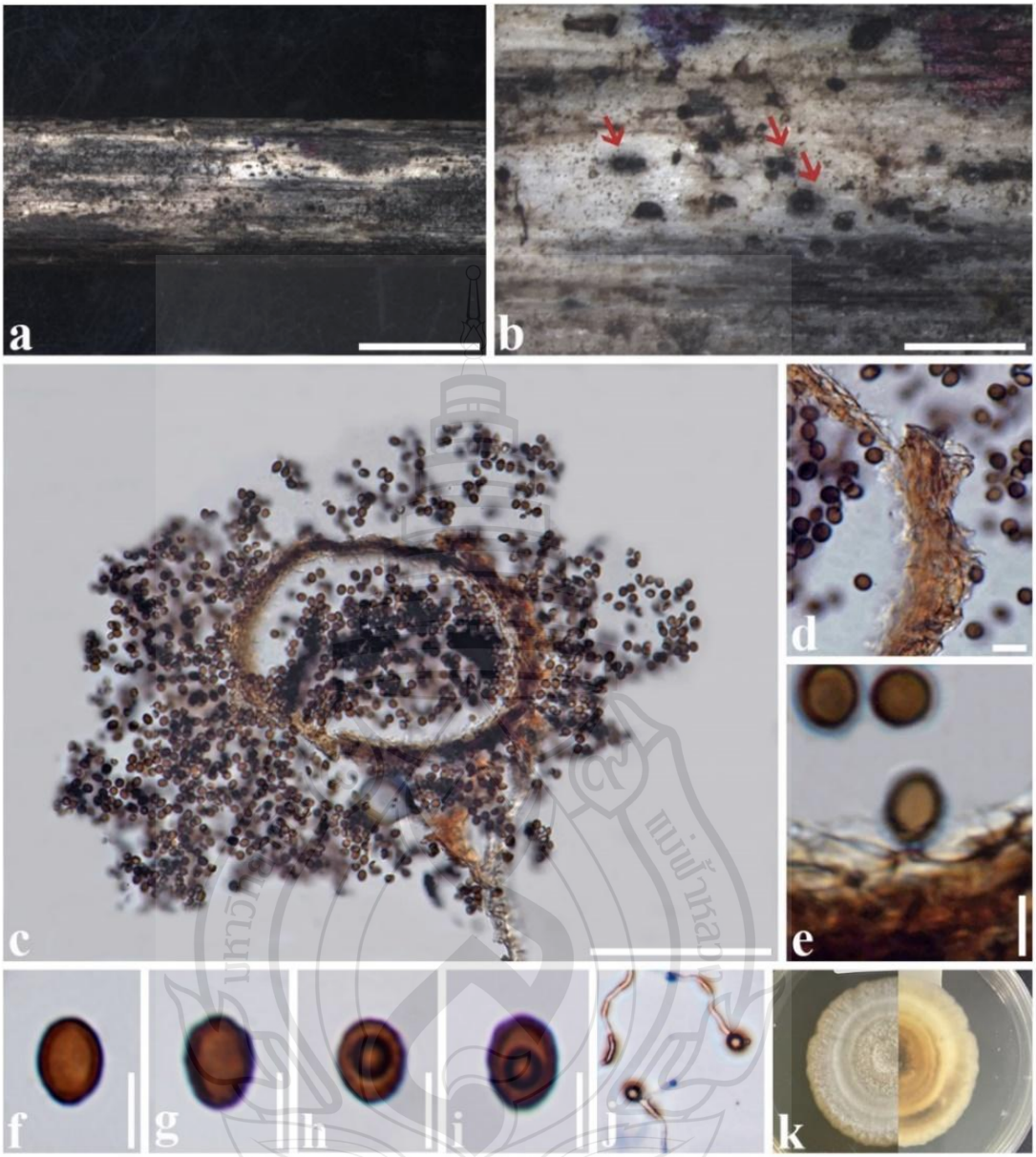
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023, Zin Hnin Htet (BP-DP-11, MFLU 24-0266, **holotype**); ex-type MFLUCC 24-0273.

*GenBank:* **LSU**: PQ226195; **SSU:** PQ226198; **ITS**: PQ226192; ***tef*1-*α***: PQ240622; ***rpb2***: PQ240625

*Pre-screening for antibacterial activity*: *Pseudoroussoella bidenticola* (MFLUCC 24-0273) showed a 18 mm inhibition zone against *B. subtilis*, and a 12mm inhibition zone against *E. coli* and a 13 mm inhibition zone against *S. aureus*.

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

*Notes*: Based on the multi-locus phylogeny (Figure 3.33), the isolate (MFLUCC 24-0273) formed a separate branch related to *Pseudoroussoella* species with 100% ML and 1.00 BYPP. *Pseudoroussoella elaeicola* (MFLUCC 17-1483 and MFLUCC 17–2086) was found as a sexual morph in nature (Phookamsak et al., 2019; Mapook et al., 2020); hence, their morphology cannot be directly compared with the isolate. However, based on comparing the morphology of *Pseudorousoella bidenticola* (MFLUCC 24-0273) and *Ps. chromolaenae* (MFLUCC 17-1492), the species differs from *Ps. chromolaenae* (MFLUCC 17-1492) in having immersed to semi-immersed, globose to subglobose, brown, conidiomata without ostiole, smaller-sized (120–150 × 150–180 µm vs 130–175 (–230) × 160–230 µm), holoblastic, globose to subglobose conidiogenous cells, and brown to reddish brown, globose to subglobose conidia with guttules, while *Ps. chromolaenae* (MFLUCC 17-1492) displays superficial, globose to obpyriform, yellowish brown to brown conidiomata with a central ostiole, annellidic, ampulliform to oblong conidiogenous cells, and oblong to oval, conidia that are pale brown to light brown when immature, becoming yellowish brown to reddish brown when mature. When comparing base pair differences between *Ps. bidenticola* (MFLUCC 24-0273) and *Ps. chromolaenae* (MFLUCC 17-1492), variations were observed in ITS (3.6% - 23/469), LSU (0.6% - 5/799), SSU (0.6% - 4/630), *tef*1-*α* (2.6% - 24/891), without gaps. Therefore, this collection (MFLUCC 24-0273) is introduced as a new species based on morphology and multigene phylogeny. Moreover, this is also the first record of *Pseudoroussoella* species from *Bidens pilosa* (Asteraceae).




**Source** Htet et al. (2024)

**Note** **a, b** Appearance of conidioma on host substrate. **c** Section through conidiomata. **d** Peridium. **e** Conidia and conidiogenous cells. **f–i** Conidia. **j** Germinating conidia. **k** Culture on MEA. Scale bars: a, b = 500 µm, c = 100 µm, d =10 µm, e–i = 5 µm.

**Figure 3.38** *Pseudoroussoella bidenticola* (MFLU 24-0266, holotype)

### 3.2.11 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 and 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, *tef*1-*α* and *rpb*2 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*, a monotypic genus, was introduced by Phukhamsakda et al. (2016), typified by *F. uniseptata. Forliomyces* species are characterized by brown, pyriform, 1-septate conidia. 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). This study introduced *Forliomyces bidentis* as a new species based on the combined LSU, SSU, ITS, and *tef*1-*α* sequence data (Figure 3.39).

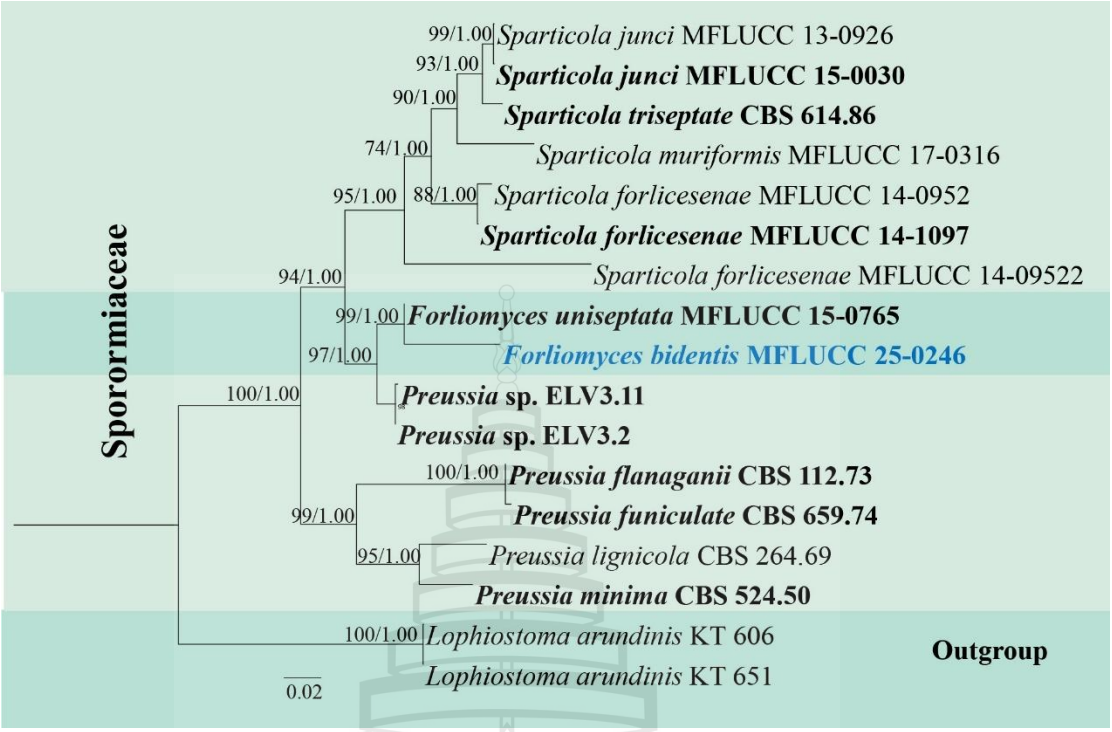



**Figure 3.39** Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Lophiostoma aurundinis* (KT606 and KT651)

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

*Index Fungorum number*: IF904371, *Facesoffungi* number: FoF18038, Figure 3.40

*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 × 210–250 µm ($\overline{x}$ = 176 × 234.5 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 × 6–10 µm ($\bar{x}$ = 11×8 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 in 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.

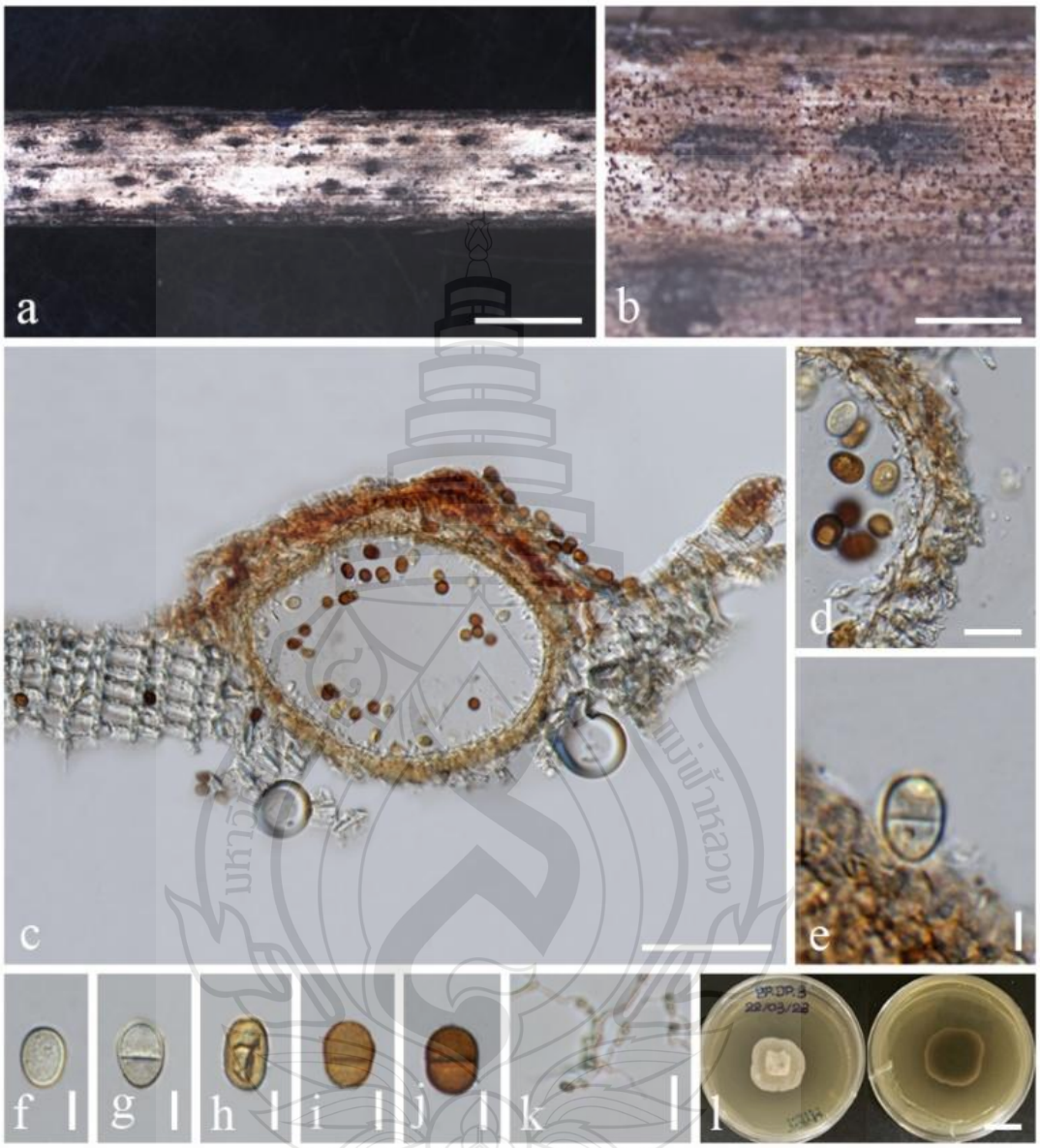
*GenBank:* **ITS**: PV870606.

*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 (Figure 3.21), the strain (MFLUCC 25-0246) clustered separately from *Forliomyces uniseptata* (MFLUCC 15-0765) with 99% ML and 1.00 BYPP bootstrap support. The new strain (MFLUCC 25-0246) is morphologically similar to *Forliomyces uniseptata* in having immersed, globose to subglobose, uniloculate pycnidial conidiomata, hyaline, phialidic conidiogenous cells, hyaline to reddish brown, aseptate to 1-septate conidia. However, the strain (MFLUCC 25-0246) differs from *F. uniseptata* (MFLUCC 15-0765) in having smaller conidiomata (180–200 × 210–250 µm vs. 155–190 × 185–320 µm), smaller conidiogenous cells (1–2 µm vs. 2–14 µm), slightly smaller, wider, oval-shaped conidia (7–15 × 6–10 µm vs. 10–15 × 5–8µm), 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 the new 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, based on morphology and multi-gene

phylogeny, *Forliomyces bidentis* is introduced as a new species, which is also the first occurrence of *Forliomyces* species on *Bidens pilosa* (Asteraceae).




**Note** **a, b** Appearance of conidiomata on host substrate. **c** A section through a conidioma. **d** Conidiomatal wall 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.

**Figure 3.40** *Forliomyces bidentis* (MFLU 25-0262, holotype)

### 3.2.12 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; Wanasinghe et al., 2018; Devadatha et al., 2018; Mapook et al., 2020; Tian et al., 2024). Currently, nine genera are accepted in Thyridariacae, viz., *Chromolaenomyces*, *Cycasicola*, *Liua*, *Parathyridaria*, *Parathyridariella*, *Pseudothyridariella*, *Thyridaria*, *Thyridariella,* and *Vaginospora,* with morphology and molecular data (Tian et al., 2024; Index Fungorum 2025).

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

*Pseudothyridariella* was introduced by Mapook et al. (2020) based on LSU, ITS, *tef*1-*α*, *rpb*2 and SSU sequence data, with *Ps. chromolaenae* as a type species. Later, 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). This study introduced *Pseudothyridariella asteracearum* and *Ps. thailandica* based on the combined LSU, SSU, ITS, *tef*1-*α* and *rpb*2 sequence data (Figure 3.41).

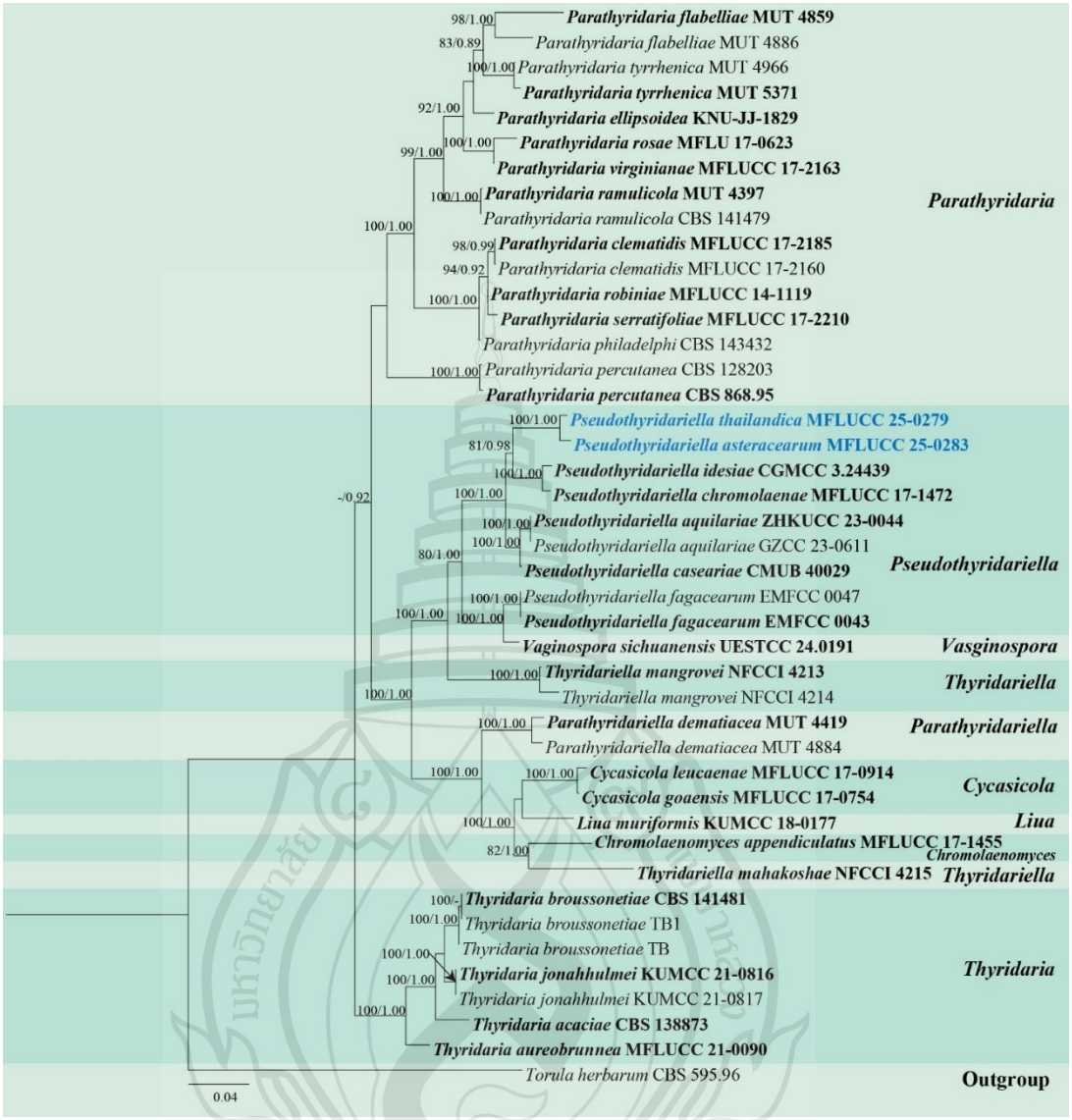



**Figure 3.41** Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, *tef*1-*α* and *rpb*2 sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Torula herbarum* (CBS 595.96)

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

*Index Fungorum number*: IF904372, *Facesoffungi number*: FoF18039, Figure 3.42

*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 ($\overline{x}$ = 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 ($\overline{x}$ = 128 × 18 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindric-clavate, pedicellate, rounded at the apex. *Ascospores* 20–30 × 8–10µm ($\overline{x}$ = 25 × 9 µm, n = 20), overlapping, 1–2 seriate, initially hyaline at young and dark brown at maturity, ellipsoid to broadly fusiform, muriform, with 5–8-transverse septa, and 1 or more vertical septa, 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*: **ITS**: PV870614; **SSU**: PV996973; ***tef*1-*α***: PX282650; ***rpb*2**: 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.*

*Note*: The 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 (Figure 3.41), the strain (MFLUCC 25-0283) clustered with *Ps. thailandica* (MFLUCC 25-0279) with 100% ML and 1.00 BYPP bootstrap support. A comparison of base pairs between this strain (MFLUCC 25-0283) and *Ps. thailandica* (MFLUCC 25-0279) reveals 1.6% (18/1068) difference in *rpb*2 without gaps. Due to the unavailability of other gene sequences, base pairs cannot be compared. Moreover, the 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, I the morphology could not be compared between species. Herein, *Ps. asteracearum* is introduced as a new species based on multi-gene phylogeny.


**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through 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 = 10µm, o = 10mm.

**Figure 3.42** *Pseudothyridariella asteracearum* (MFLU 25-0263, holotype)

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

*Index Fungorum number*: IF904373*, Facesoffungi number*: FoF18040, Figure 3.43

*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:** *Conidiomata* 145–200 × 216–230 µm ($\overline{x}$ = 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 ($\overline{x}$ = 13 × 6 µm, n = 20), ovoid to oblong, yellowish brown to brown, aseptate when young and becoming 3-septate when mature, thick-walled, without guttule.

*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.

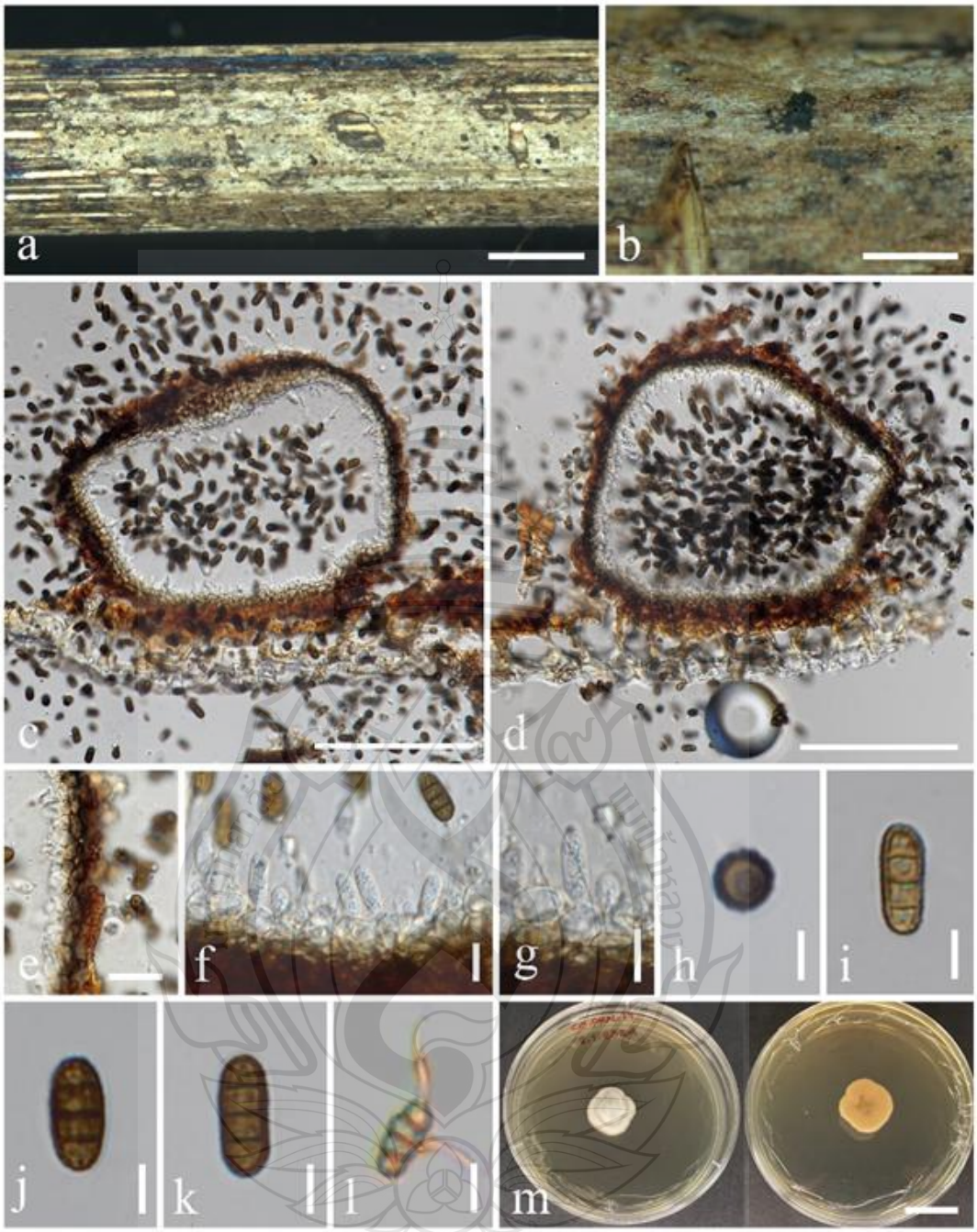
*Material examined*: Thailand, Phayao Province, Mueang Phayao District, on dead stems of *Chromolaena odorata* (Asteraceae), 16 December 2023, Zin Hnin Htet (CO-PKN-17, MFLU 25-0264, **holotype**); ex-type MFLUCC 25-0279.

*GenBank*: **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. Here, *Ps. thailandica* is introduced as a new species on *Chromolaena odorata* based on multi-gene phylogeny.




**Note** **a, b** Appearance of conidiomata on host substrate. **c, d** A section through a conidioma. **e** Conidiomatal 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 = 10mm.

**Figure 3.43** *Pseudothyridariella thailandica* (MFLU 25-0264, holotype)

### 3.2.12 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 *Dendryphion* is included in Torulaceae. Later, 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*, *Dendryphion*, *Neotorula*, *Rostriconidium*, *Rotorula*, *Sporidesmioides* and *Torula*. This study reported *Dendryphion hydei*, *Torula canangae*, *T. fici* and *T. mackenziei* as new records and reference specimens, based on the combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequences (Figure 3.44).

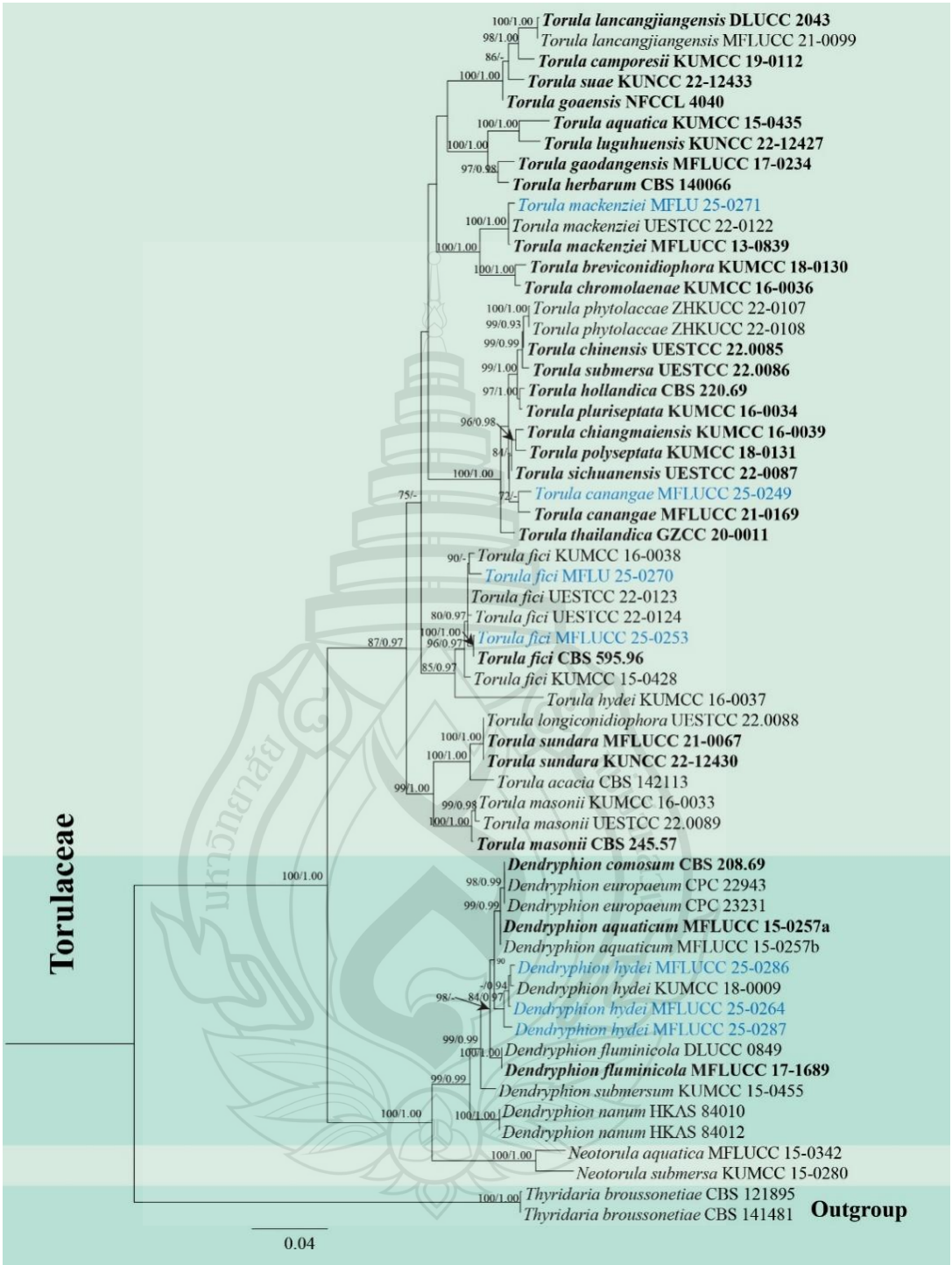



**Figure 3.44** Phylogram generated from ML analysis based on the combined dataset of LSU, SSU, ITS, and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Thyridaria broussonetiae* (CBS 121895 and CBS 141481)

***Dendryphion*** Wallr

*Dendryphion* was introduced by Wallroth (1833) and typified with *D. comosum*. *Dendryphion* 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 *Dendryphion,* and only seven species have DNA sequence data (Li et al. 2020).

***Dendryphion hydei*** J.F. Li, Phookamsak & Jeewon, PLoS ONE 15(2): e0228067, 6 (2020)

*Index Fungorum number*: IF556746, *Facesoffungi* number: FoF556746, Figure 3.45

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: *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 ($\overline{x}$ = 277 × 11 μm, n = 5), macronematous, mononematous, septate, verrucose, thick-walled, branching simple or penicillate at the tip of primary branches, brown, flexuous. *Conidiogenous cells* 5–10 × 4–5 μm ($\overline{x}$ = 7.5 × 4.5 μm, n = 20), terminal, integrated, pale brown, polytretic. *Conidia* (13–)15–30 × 4–7 μm ($\overline{x}$ = 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.

*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, **a reference specimen**); living culture MFLUCC 25-0287; *ibid*., Phan District, on dead stems of *Bidens pilosa* (Asteraceae), 14 March 2023,

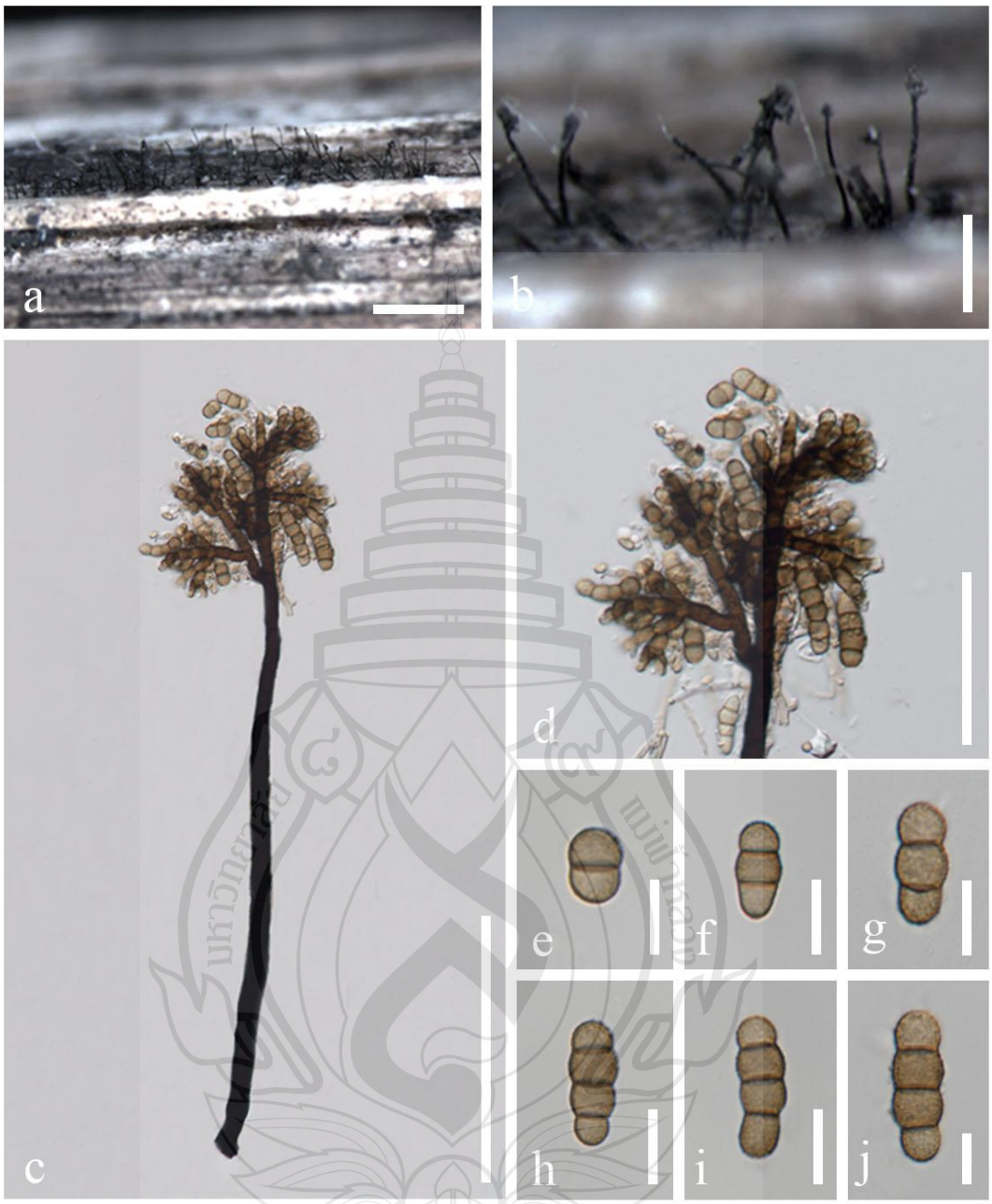
Zin Hnin Htet (BP-DP-22, MFLU 25-0267, **a reference specimen**); living culture MFLUCC 25-0286.

*GenBank*: **SSU**: PV996968; PV996969, PV996970; **ITS**: PV870607, PV870608, PV870609; ***tef*1-*α***: PX282643, PX282644, PX282645; rpb**2**: PX120457, PX120458, 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); unknown plant in China (Wang et al., 2024); dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (this study).

*Notes*: In phylogenetic analysis (Figure 3.44), 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. The 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 difference was observed. The morphological characteristics exhibited no considerable difference between my strain and *D. hydei.* There is no base pairs 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). Therefore, these collections are reported as reference specimens for *Dendryphion hydei.*




**Note** **a, b** Colonies on host substrate. **c–d** Conidiophores and conidiogenous cells. **e–j** Conidia. Scale bars: a = 500 µm, c, d = 200 µm, e, f, g, h, i, j = 20 µm.

**Figure 3.45** *Dendryphion hydei* (MFLU 25-0267, a new host record)

***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)

*Index Fungorum number*: IF559523, *Facesoffungi number*: FoF10720, Figure 3.46

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph:** Undetermined. **Asexual morph:** *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 ($\overline{x}$ = 8 × 4 µm, n = 10), macronematous, mononematous, solitary, pale brown to brown, smooth. *Conidiogenous cells* 3–6 × 4.5–6.5 µm ($\overline{x}$ = 3.3 × 5 µm, n = 10), mono- to polyblastic, doliiform to subglobose, dark brown to black, paler at apex, smooth, thick-walled. *Conidia* (13–)20–40(54–) × 5–8 µm ($\overline{x}$ = 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.

*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.

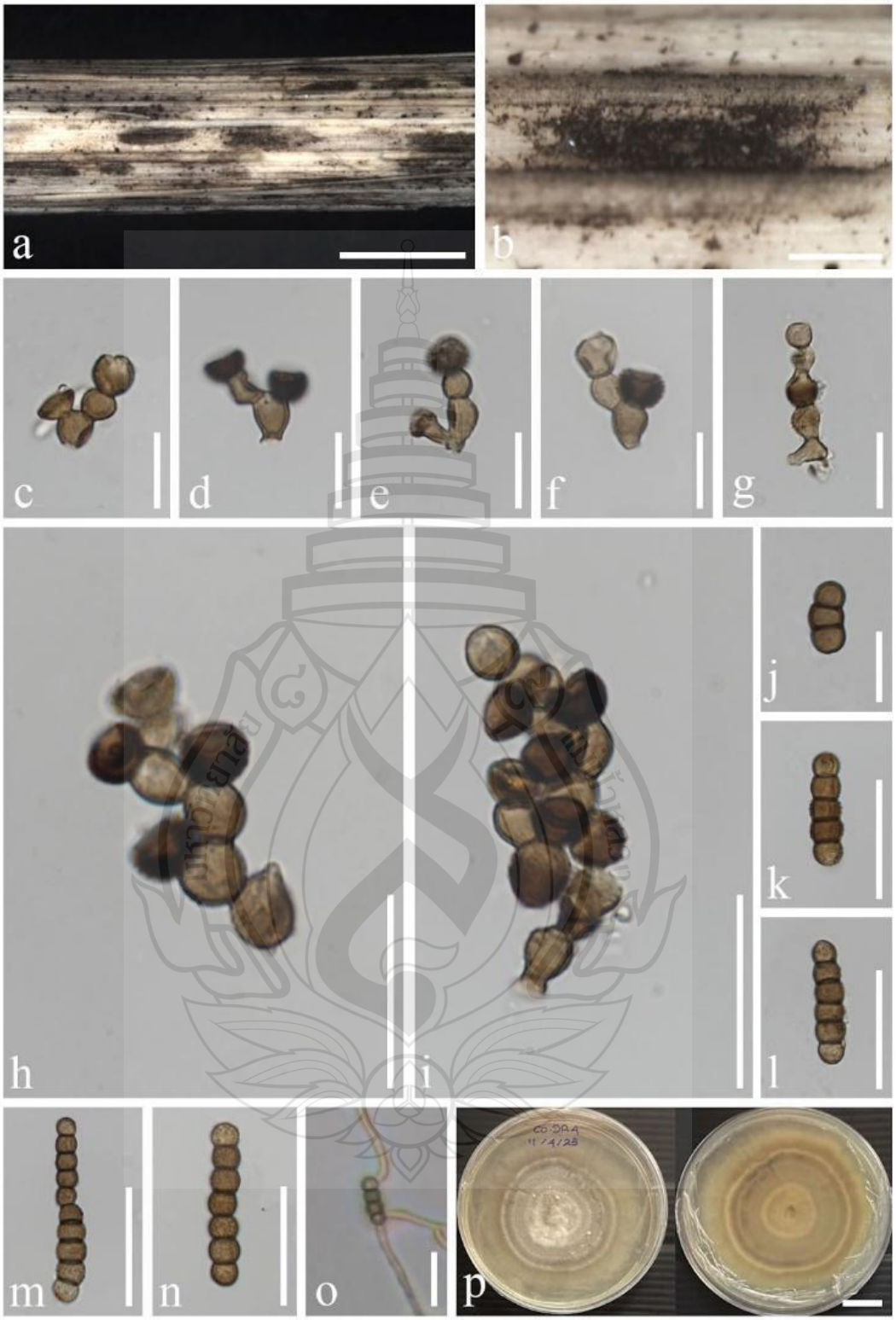
*GenBank:* **LSU**: PV992412; **SSU**: PV996971; **ITS**: PV870610; ***tef*1-*α***: PX282646; ***rpb*2**: PX120460

*Pre-screening for antibacterial activity*: *Torula canangae* (MFLUCC 25-0249) showed a 18mm 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).

*Note*: Based on phylogenetic analysis (Figure 3.44), the 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 base pair difference between this collection and *T. canangae* (MFLUCC 21-0169). Morphologically, *Torula canangae* (MFLUCC 21-0169) differs in having longer acrogenous conidia ((28–)78–113 (–142) × 6–9 µm), compared to the ((13–)20–40(54–) × 5–8 µm sized conidia of this collection). Therefore, based on multi-gene phylogeny, this collection is reported as a new host record of *T. canangae* on *Chromolaena odorata* (Asteraceae) in Thailand.




**Note** **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 µm, b = 200 µm, c, d, e, f, g, j = 20 µm, h, i, k, l, m, n = 30 µm, p = 10mm.

**Figure 3.46** *Torula canangae* (MFLU 25-0268, a new host record)

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

*Index Fungorum number*: IF816154, *Facesoffungi number*: FoF02712, Figure 3.47

*Saprobic* on dead stems of *Chromolaena odorata.* **Sexual morph:** Undetermined. **Asexual morph:** *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 × 2–4 µm ($\overline{x}$ = 7 × 3 µm, n = 10), macronematous, mononematous, solitary, pale brown to brown, smooth. *Conidiogenous cells* 3–6 × 4.5–6.5 µm ($\overline{x}$ = 3.3 × 5 µm, n = 10), mono- to polyblastic, doliiform to subglobose, dark brown to black, paler at apex, smooth, thick-walled. *Conidia* (5–)10–20 × 4–6 µm ($\overline{x}$ = 15 × 5.5 µm, 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, **a reference specimen**); living culture MFLUCC 25-0253; *ibid.*, Theong District, on dead stems of *Chromolaena odorata* (Asteraceae), 24 Jan 2022, A. Mapook, TCR 2 (MFLU 25-0270, **a reference specimen**)

*GenBank*: **LSU**: PV992413; **ITS**: PV870611, PV870612; ***tef*1-*α***: PX282647, PX282648; ***rpb*2**: PX120461, PX120462.

*Known host and distribution*: dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Li et al., 1017; Mapook et al., 2020; this study); dead leaves of *Ficus septica* (Moraceae) in Taiwan region (China) (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); deacaying wood of unknown plant in China (Su et al., 2018); *Musa* sp. (Musaceae) in China (Samarakoon et al., 2021); *Ficus ampelas* (Moraceae) in Taiwan region (China) (Tennakoon et al., 2021); *Ficus septica* (Moraceae) (Moraceae) in Taiwan region (China) (Tennakoon et al., 2021).

*Note*: Based on the phylogenetic analysis (Figure 3.44), 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 is no base pair differences between this 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). Therefore, herein, these collections are reported as a reference specimen of *T. fici*.


**Note** **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 = 10mm.

**Figure 3.47** *Torula fici* (MFLU 25-0269, a reference specimen)

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

*Index Fungorum number*: IF819537, *Facesoffungi number*: FoF02714, Figure 3.48

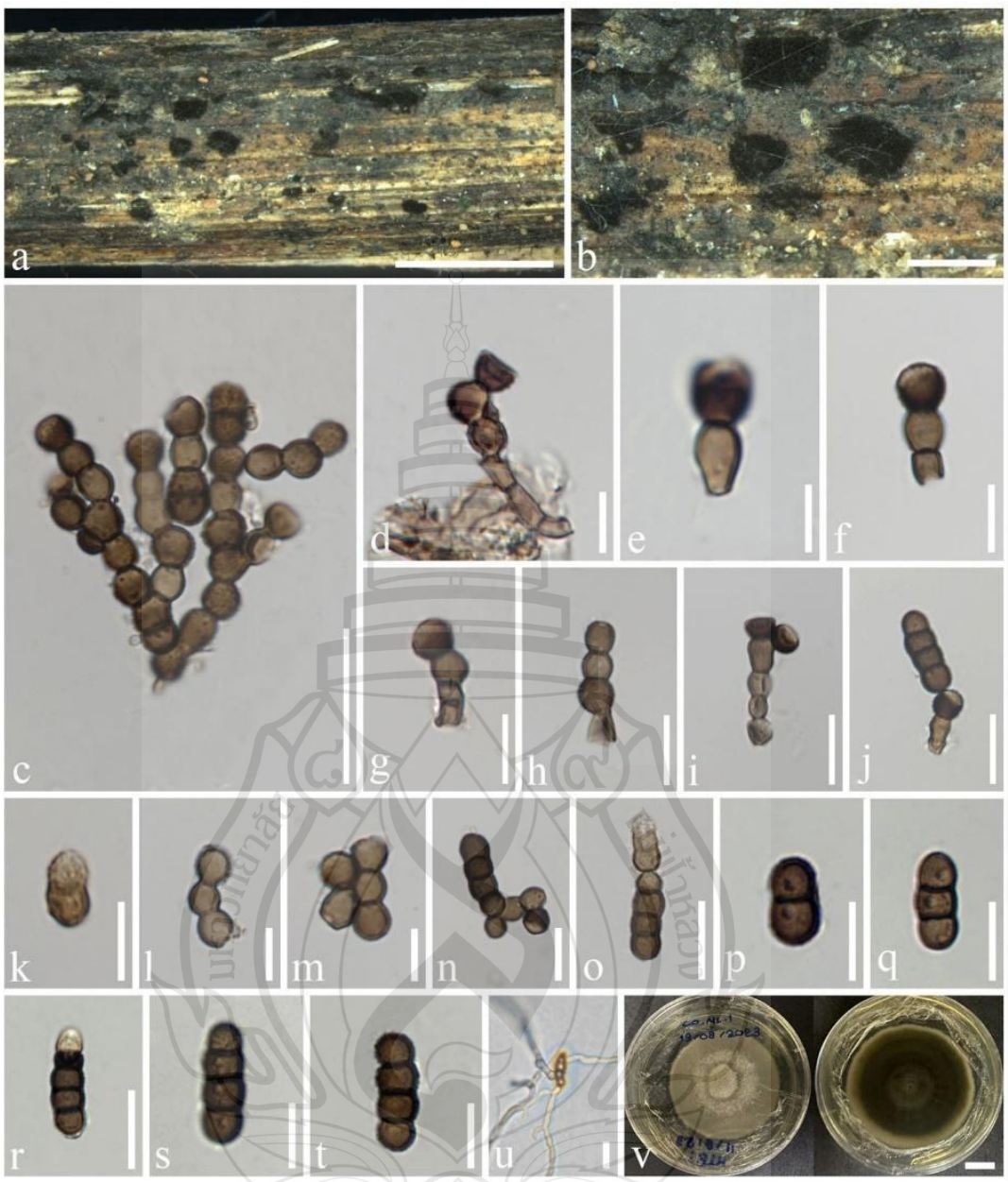
*Saprobic* on dead stems of *Chromolaena odorata.* **Sexual morph:** Undetermined. **Asexual morph:** *Colonies* effuse on the host, black, powdery. *Mycelium* partly immersed to superficial on the substrate, composed of septate, branched, smooth, hyaline hyphae. *Conidiophores* 7–13 × 3–5 µm ($\overline{x}$ = 8 × 4 µm, n = 10), macronematous, mononematous, solitary, pale brown to brown, smooth. *Conidiogenous cells* 3–6 × 4.5–6.5 µm ($\overline{x}$ = 3.3 × 5 µm, n = 10), mono- to polyblastic, doliiform to subglobose, dark brown to black, paler at apex, smooth, thick-walled. *Conidia* (13–)20–40(54–) × 5–8 µm ($\overline{x}$ = 15 × 5.5 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.

*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*: **SSU**: PV996972; **ITS**: PV870613; ***tef*1-*α***: PX282649; ***rpb*2**: 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).

*Note*: Based on the phylogenetic analysis (Figure 3.44), this 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, this collection is similar to *T. mackenziei* (MFLU 16–2820), however, differs in conidial size ((13–)20–40(54–) × 5–8 µm vs. 9.4–18.5 × (3.8–) 4.4–4.7 µm). Therefore, based on multi-gene phylogeny, these collections are reported as a new host record of *T. mackenziei* on *Chromolaena odorata* (Asteraceae) in Thailand.




**Note** **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 µm, b = 200 µm, c = 20, d, e, f, g, k, l, m, n, o, p, q, r, s, t, u = 10 µm, v = 10 mm.

**Figure 3.48** *Torula mackenziei* (MFLU 25-0271, a new host record)

**Dothideomycetes orders *incertae sedis***

**Botryosphaeriales** C.L. Schoch, Crous & Shoemaker

### 3.2.13 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, *tef*1-*α* and *tub*2 sequence data, the genus was placed in Aplosporellaceae, Botryosphaeriales. The asexual morph of *Aplosporella* is characterized by its globose to subglobose, muti-locular conidiomata with a thick, multilayered 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., 2021a, b; Hyde et al., 2021, Jayawardena et al., 2022). In this study, *Aplosporella hesperidica* was reported as a reference specimen based on the combined ITS and *tef*1-*α* sequence data (Figure 3.49).

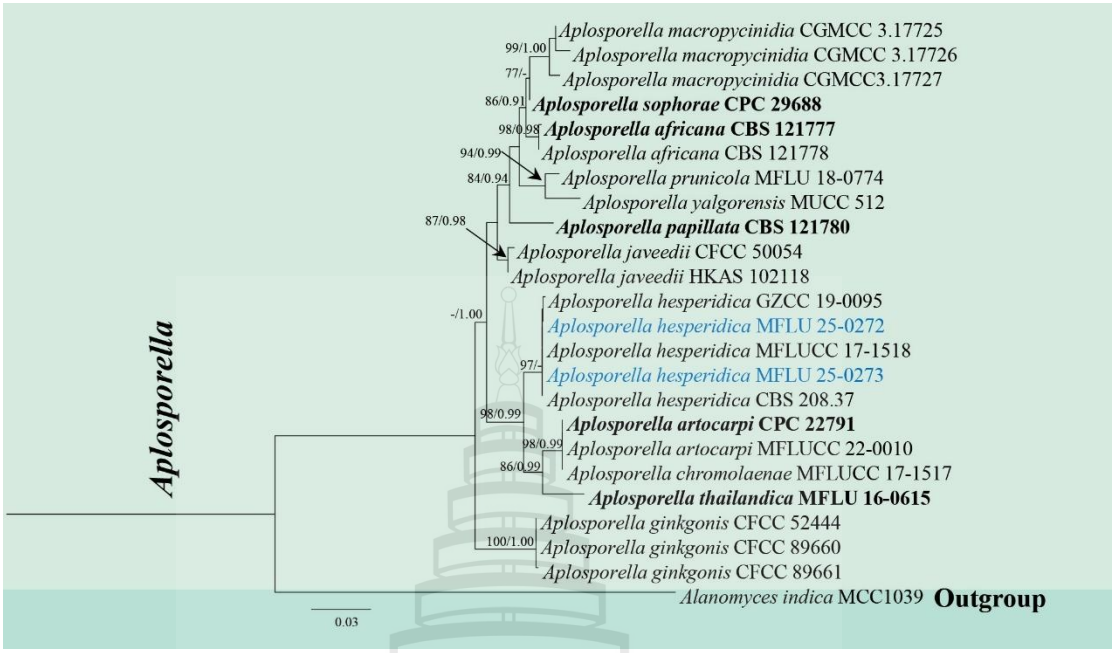



**Figure 3.49** Phylogram generated from ML analysis based on the combined dataset of ITS and *tef*1-*α* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Alanomyces indica* (MCC1039)

***Aplosporella artocarpi*** Trakun., L. Lombard & Crous, in Trakunyingcharoen et al., Persoonia 34: 91 (2014)

*Index Fungorum number*: IF810167; *Facesoffungi number*: FoF10747, Figure 3.50

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* (280–) 300–350 × 370–450 (–500) µm ($\bar{x}$ = 300 × 415 µm, n = 5), solitary, immersed to semi-immersed with 2–3 locules, globose to subglobose, black. *Ostiole* absent. *Peridium* 45–50 (–60) µm wide, multi-layered, comprised of dark brown cells of *textura angularis*. *Hamanthecium* 3–5 µm wide, numerous, hyaline, aseptate, paraphyses. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1–2 µm wide, holoblastic, cylindrical, hyaline. *Conidia* 15–20 × 5–10 µm ($\bar{x}$ = 17 × 7 µm, n = 15), aseptate, rough-walled, granular appearance, hyaline to dark brown, ellipsoidal, without appendages.

*Culture characteristics*: Conidia germinating on PDA within 24 h, reaching 85 mm after 7 days at room temperature, concentric, flat, irregular, rough surface, greenish-grey.

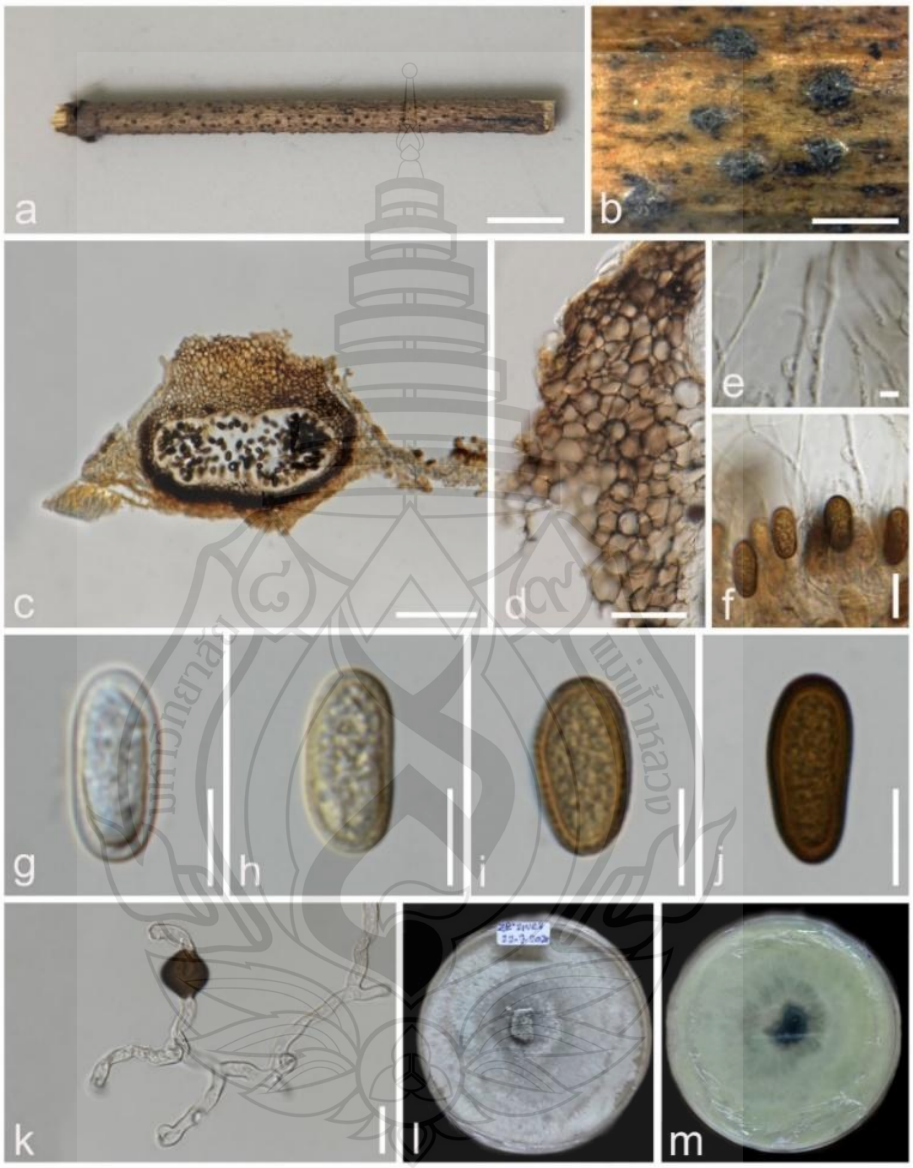
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 10 July 2020, Zin Hnin Htet, SW23 (MFLU 22–0108), living culture MFLUCC 22-0010.

*Known hosts*: On asymptomatic twig of *Artocarpus heterophyllus* (Moraceae) in Thailand (Trakunyingcharoen et al., 2015); on asymptomatic leaves of *Stoechospermum marginatum* (Dictyotaceae) and *Caulerpa taxifolia* (Caulerpaceae) in India (Sahoo et al., 2021); on dead branches of *Mangifera indica* (Anacardiaceae) in China (Yang et al., 2022); on dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Jayawardena et al., 2022).

*GenBank*: **LSU**: ON834371; **ITS**: ON823183

Notes: In the phylogenetic analysis, *Aplosporella artocarpi* (MFLUCC 22-0010) is closely related to *Aplosporella artocarpi* (CPC 22.791) with 98% ML, 0.99 BYPP (Figure 3.49). Furthermore, comparisons of ITS region between my taxon, *Aplosporella artocarpi* (MFLUCC 22-0010) and ex-type strain of *A. artocarpi* (CPC 22791) show one base pair difference (0.18%) across 531 nucleotides. *Aplosporella* species can be found on a wide range of hosts such as Anacardiaceae, Asteraceae, Caulerpaceae, Cupressaceae, Dictyotaceae, Fabaceae, Ging koaceae, Moraceae,

Myrtaceae, Proteaceae, and Rosaceae (Du et al., 2017; Mapook et al., 2020; Sahoo et al., 2021; Yang et al., 2021). *Aplosporella artocarpi* (MFLU 22-0108) is collected from Thailand and reported here as a new host record associated with *Chromolaena odorata* (Asteraceae) in Thailand.




**Source** Jayawardena et al. (2022)

**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e** Pseudoparaphyses. **f** Conidia on the conidiogenous cells. **g-j** Conidia. **k** A germinating conidium. **l–m** Culture on PDA from surface and reverse. Scale bars. a = 1000 µm, b = 500 µm, c = 100 µm, d = 30 µm, e = 5 µm, f, l, m = 20 µm, g, h, i, j, k = 10 µm

**Figure 3.50** *Aplosporella artocarpi* (MFLU 22–0108, new host record)

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

*Index Fungorum number*: IF218239; *Facesoffungi number*: FoF07830, Figure 3.51

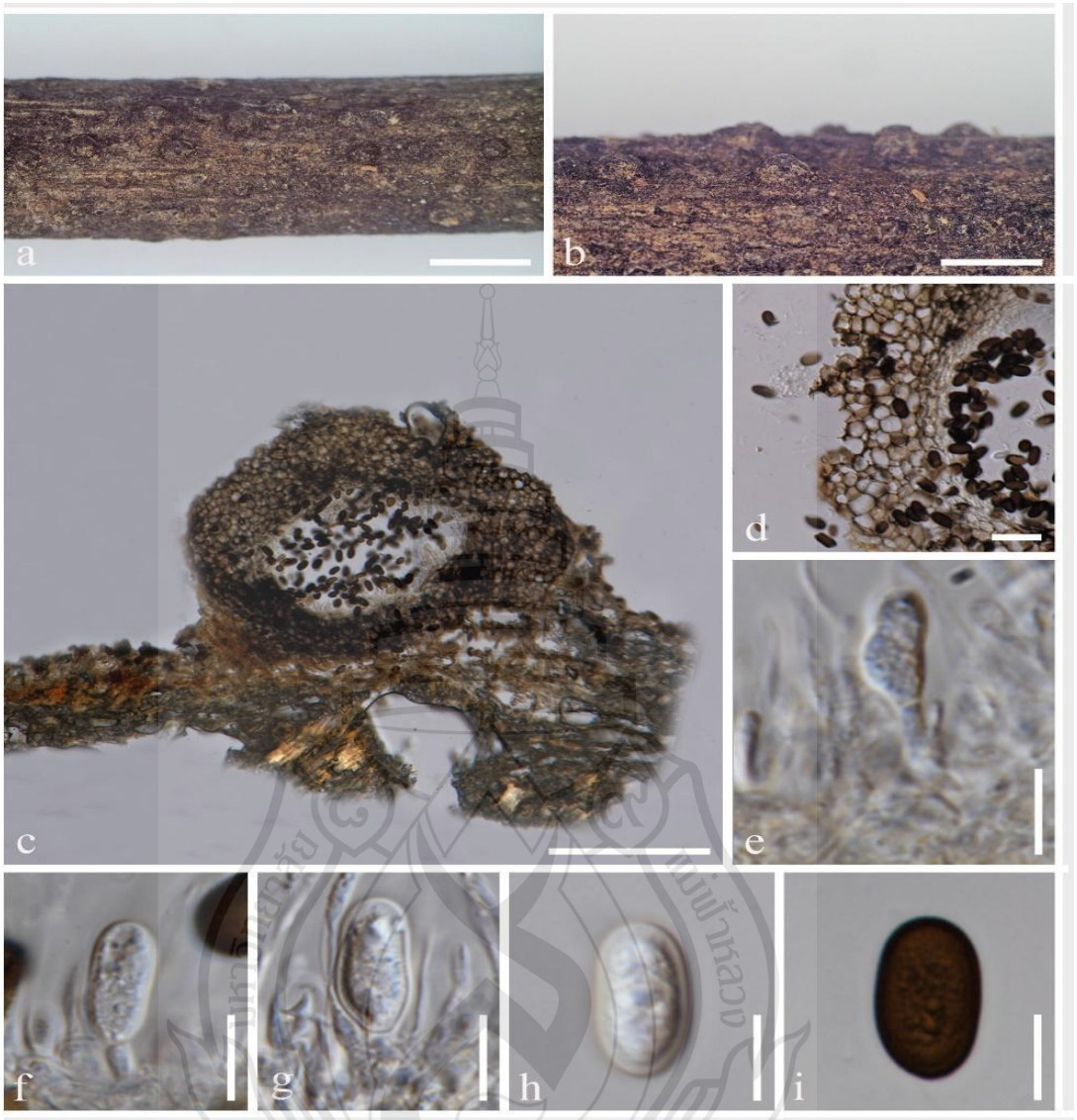
*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 450–600 × 400–500 µm ($\bar{x}$ = 588 × 471 µm, n = 5), solitary, immersed to semi-immersed with 1–2 locules, globose to subglobose, black. *Ostiole* absent. *Peridium* 100–150 µm wide, multi-layered, composed of dark brown cells of *textura angularis*. *Hamanthecium* 3–5 µm wide, numerous, hyaline, aseptate, paraphyses. *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, **a reference specimen**); *ibid*., on dead stems of *Chromolaena odorata* (Asteraceae), 5 November 2020, Zin Hnin Htet, SW041 (MFLU 25-0273, **a reference specimen**)

*Known hosts and distribution*: unknown decaying woody host in China (Dissanayake et al., 2021); *Vigna unguiculatea* (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*: **LSU**: PV992414; **ITS**: PV870616, PV870617; ***tef*1-*α***: PX282651, PX282652; ***rpb*2**: PX120467

*Notes*: Based on the phylogenetic analysis (Figure 3.49), 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 (Figure 3.49). Moreover, there is no difference in the morphology and base pair composition. My 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). Therefore, herein, these collections are described as the reference specimens of *A. hesperica* on *C. odorata* (Asteraceae) from Thailand.




**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e–g** Conidiogenous cells. **h–i** Conidia. Scale bars. a, b = 500 µm, c = 300 µm, d = 50 µm, e, f, g, h, i = 10 µm.

**Figure 3.51** *Aplosporella hesperidica* (MFLU 25-0272, a reference specimen)

### 3.2.14 Botryosphaeriaceae Theiss. & H. Syd.

Botryosphaeriaceae was introduced by Theissen and 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, pigmented, septate ascospores (Zhang et al., 2021). Around 260 species are currently accepted in *Dothiorella* (Hyde et al., 2024). This study introduced two new *Dothiorella* species, *D. asteracearum* and *D. chromolaenae,* based on morphology and the combined ITS, *tef*1-*α*, and *tub*2 sequence data (Figure 3.52).

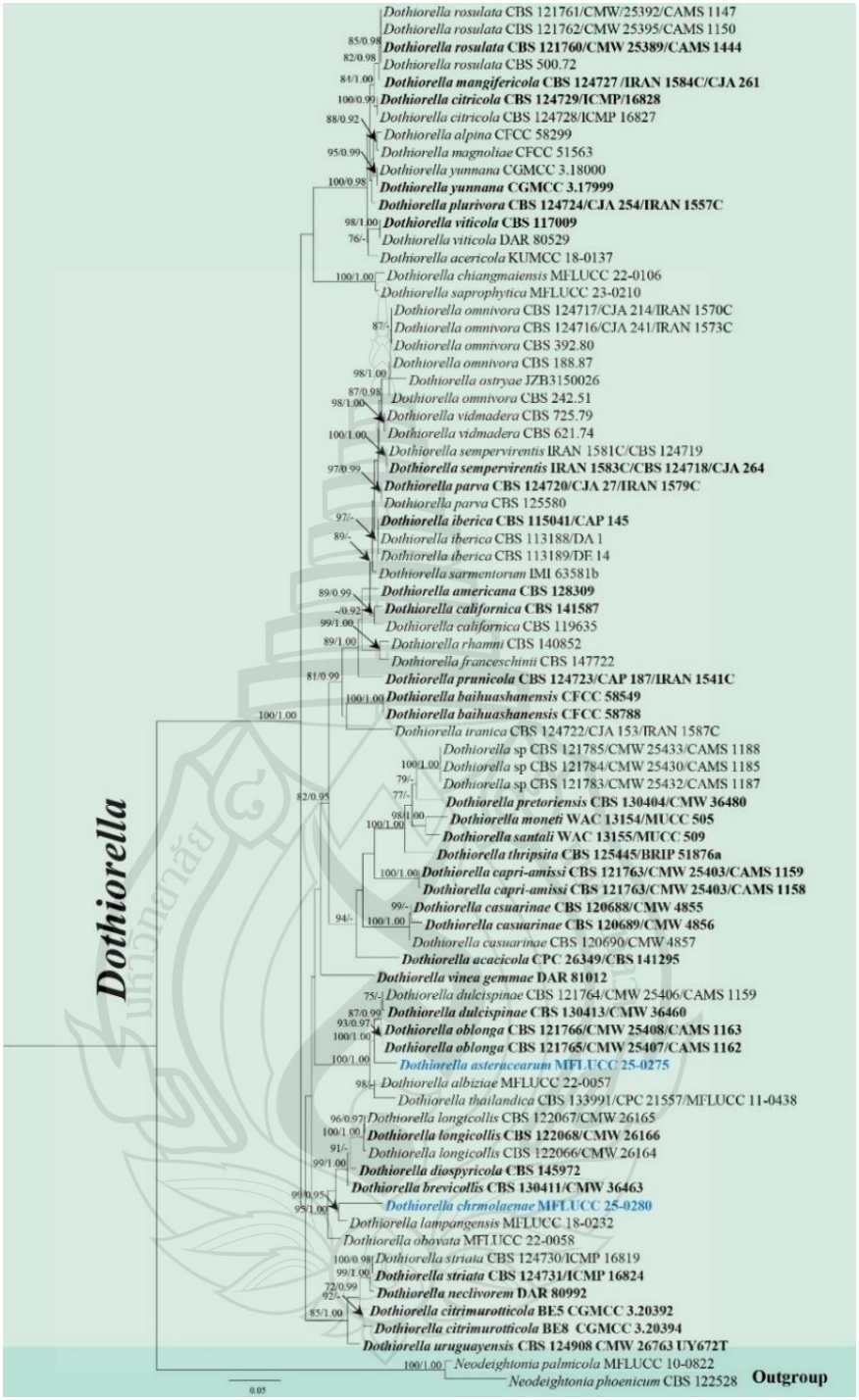



**Figure 3.52** Phylogram generated from maximum likelihood analysis based on the combined dataset of ITS, *tef1-α*, and *tub2* sequence data. Bootstrap support values for ML equal to or greater than 75% and BYPP equal to or greater than 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted with *Neodeightonia palmicola* (MLFUCC 10-0822) and *N. phoenicum* (CBS 122528)

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

*Index Fungorum number*: IF904374*, Facesoffungi number*: FoF18041*,* Figure 3.53

*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 ($\overline{x}$ = 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 multilayered 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 ($\overline{x}$ = 83 × 17 µm, n = 20), 6–8-spored, bitunicate, cylindrical, straight or slightly curved, apically rounded, pedicellate. *Ascospores* 28–41 × 12–16 µm ($\overline{x}$ = 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*: **ITS**: PV870618; ***tef*1-*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 (Figure 3.52), the isolate (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 albiziae*, *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 the strain (MFLUCC 25-0275) found as a sexual morph. Therefore, morphology could not be compared, 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.


**Note** **a, b** Appearance of ascoma on host substrate. **c** Section through 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 µm, c = 100 µm, d, e, g, h, i = 30 µm, f = 5 µm, j, k, l, n = 20 µm, o = 10mm.

**Figure 3.53** *Dothiorella asteracearum* (MFLU 25-0274, holotype)

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

*Index Fungorum number*: IF904375, *Facesoffungi number*: FoF18042, Figure 3.54

*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**: *Conidiomata* 265–285 × 250–300(–380) µm ($\overline{x}$ = 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 ($\overline{x}$ = 6 × 1.5 µm, n = 5), blastic, holoblastic, acicular, hyaline. *Conidia* 15–21 × 8–10 µm ($\overline{x}$ = 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.

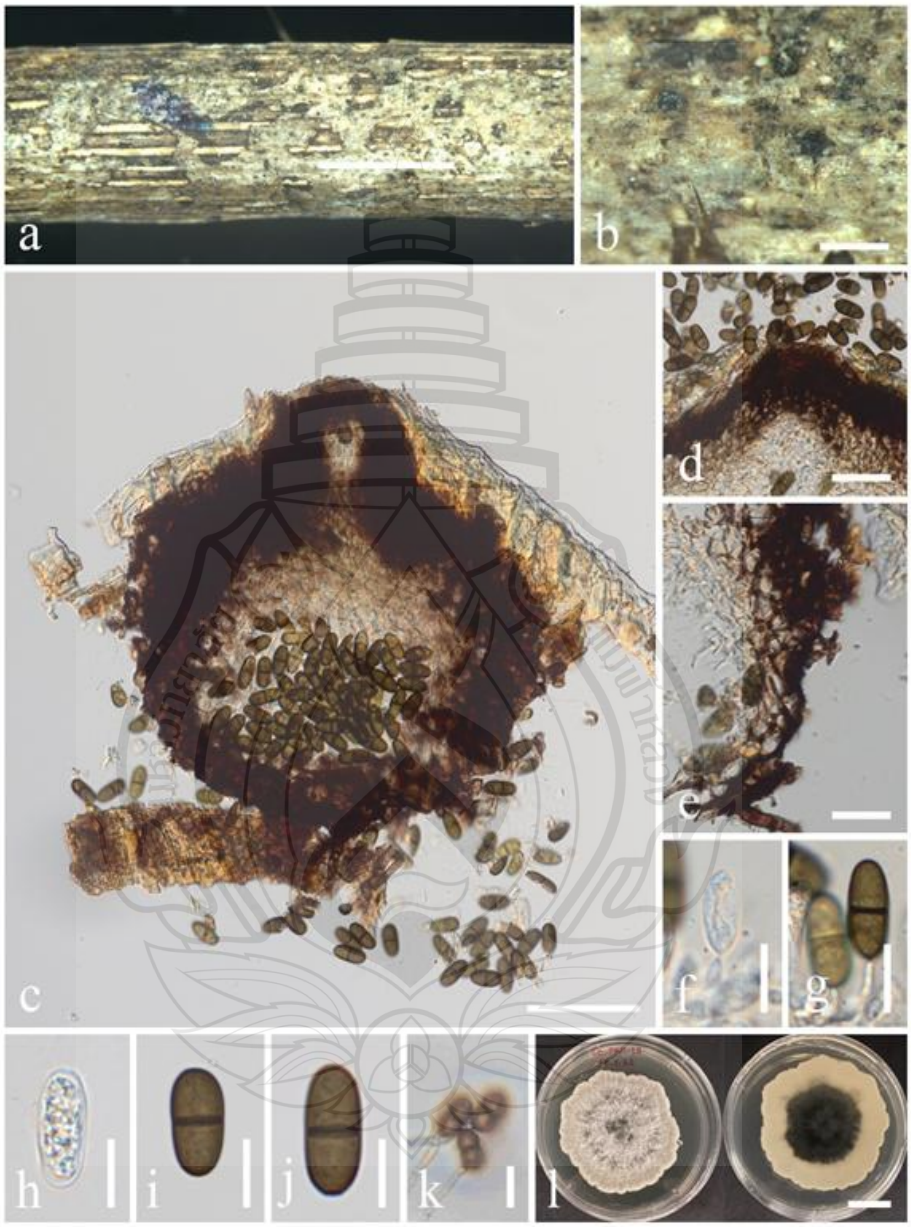
*GenBank*: **ITS**: PV870619

*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).

*Notes*: Based on the phylogenetic analysis (Figure 3.52), 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, the collection differs from *D. lampangensis* (MFLUCC 18-0232) in having smaller conidiomata (265–285 × 250–300(–380) vs. 265–320 µm × 260–380 µm), acicular, shorter conidiogenous cells (5–10 × 1–2 vs. 11–22 × 3–8 µm) and hyaline to brown, ovoid, larger conidia (15–21 × 8–10 vs. 22–28 × 9–11 µm), 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 apex, truncate at base, 1-septate at maturity. Therefore, *Dothiorella chromolaenae* is introduced as a new species found on *Chromolaena odorata* (Asteraceae) in Thailand.




**Note** **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 = 10mm.

**Figure 3.54** *Dothiorella chromolaenae* (MFLU 25-0275, holotype)

***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 gymnosperm plants (de Silva et al., 2019; Berraf-Tebbal et al., 2020; Segaran & Sathiavelu, 2023). To date, *Lasiodiplodia* comprises 85 taxa (Hyde et al., 2024). This study reported *Lasiodiplodia henanica* and *L. theobromae* as new records based on the combined dataset of ITS, *tef*1-*α*, *rpb*2, and *tub*2 sequence data (Figure 3.55).

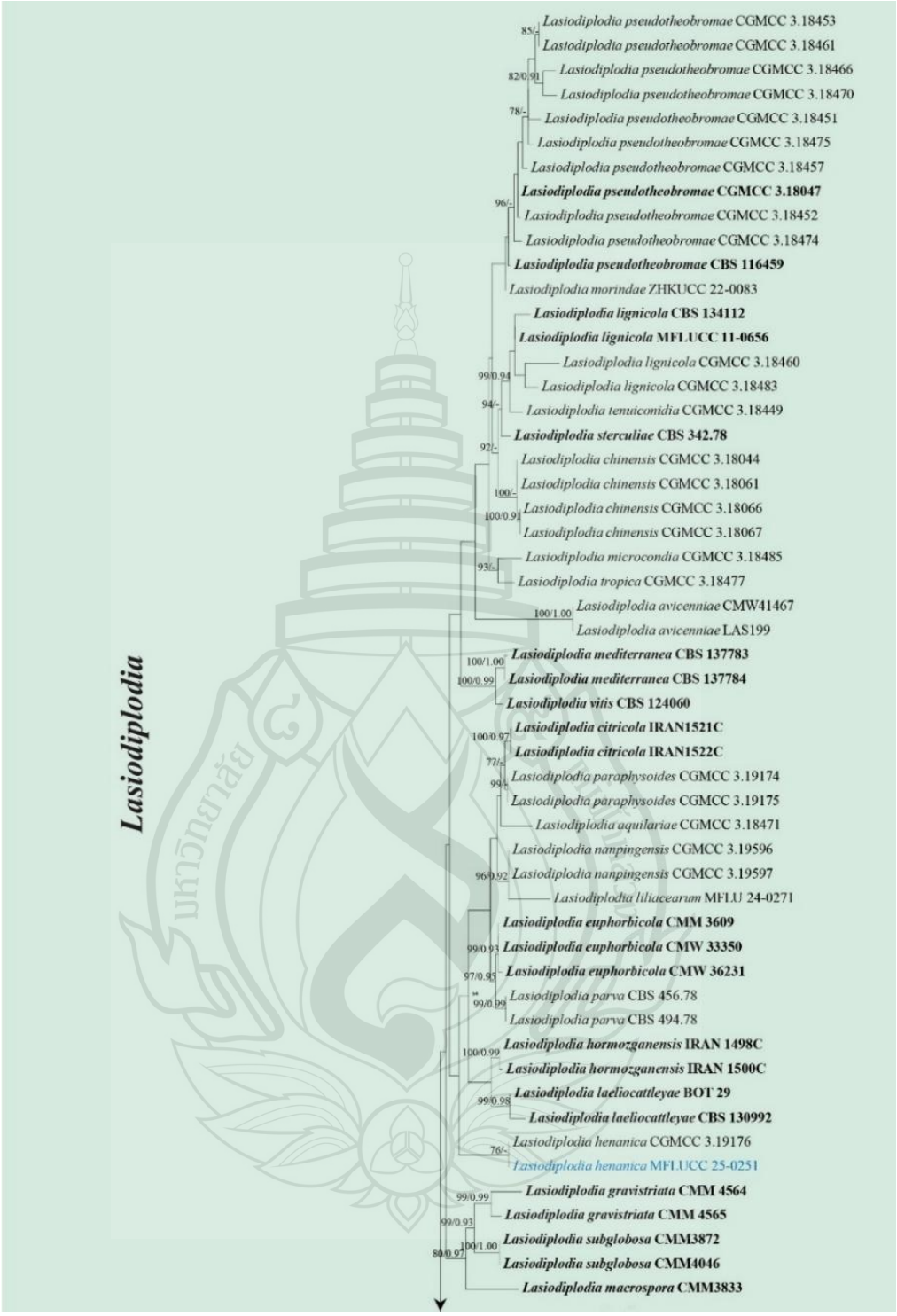



**Figure 3.55** Phylogram generated from ML analysis based on the combined dataset of ITS, *tef*1-*α*, *rpb*2, and *tub*2 sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Diplodia cupressi* (CBS 168.87) and *D. mutila* (CBS 112553)

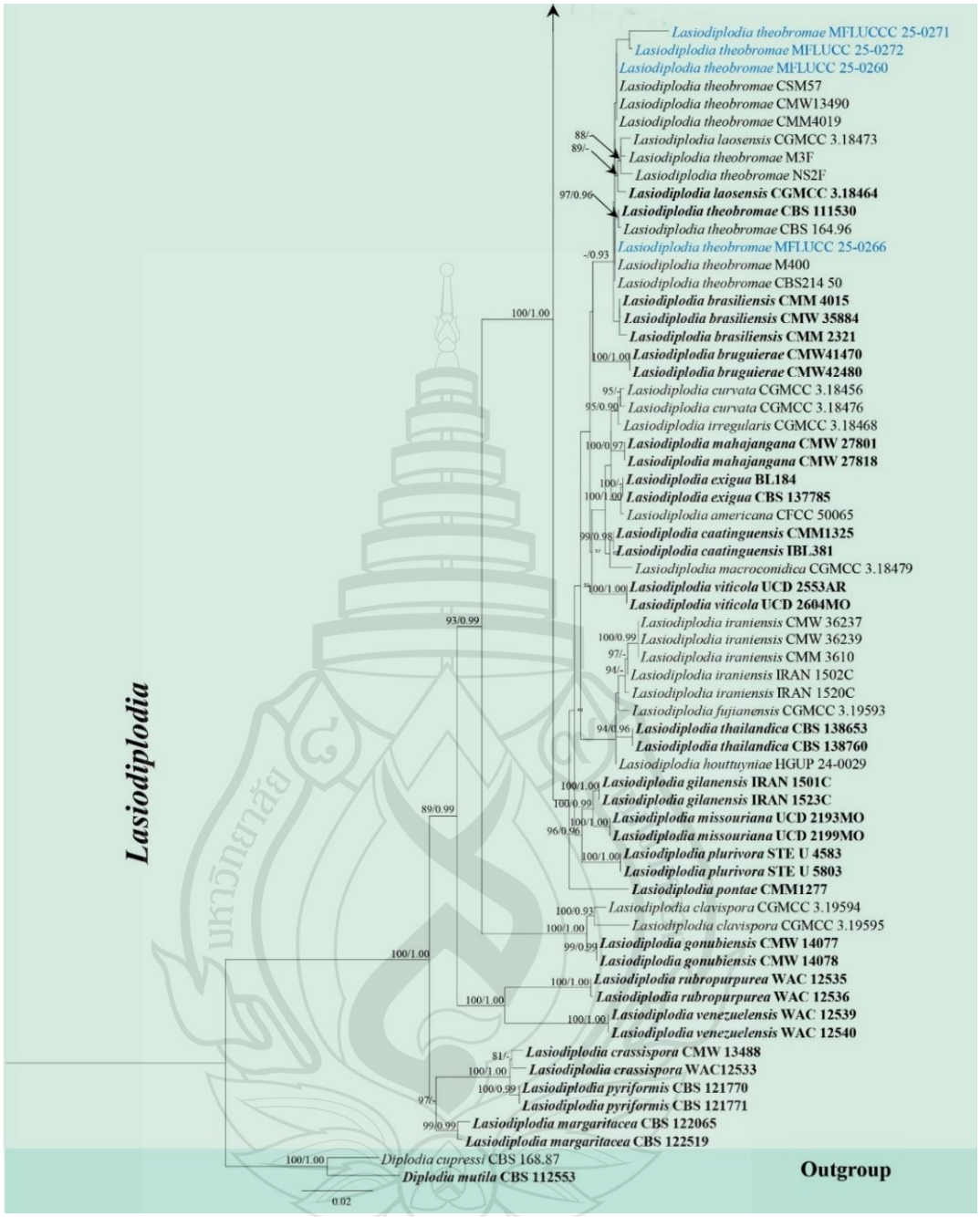



**Figure 3.55** (continued)

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

*Index Fungorum number*: IF817650, *Facesoffungi number*: FoF18043, Figure 3.56

*Saprobic* on dead stems of *Chromolaena odorata.* **Sexual morph:** Undetermined. **Asexual morph:** *Conidiomata* 80–150 × 100–150 µm ($\overline{x}$ = 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 ($\overline{x}$ = 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.

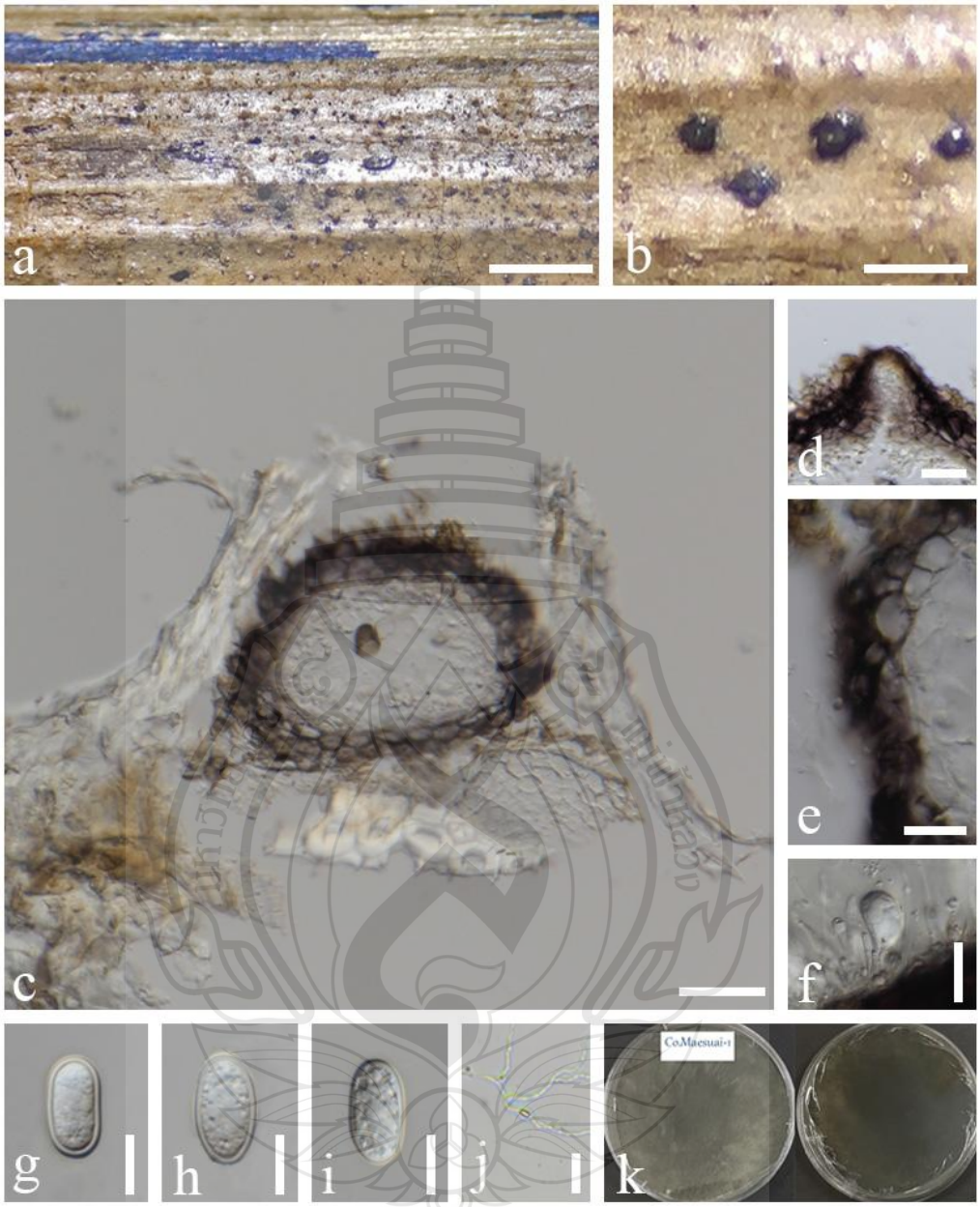
*GenBank*: **ITS**: PV870620.

*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).

*Note*: Based on the phylogenetic analysis (Figure 3.55), the strain (MFLUCC 25-0251) is clustered sister to *Lasiodiplodia henanica* (CGMCC 3.19176) with 76% ML and 1.00 BYPP bootstrap support. Morphologically, the new strain differs from *L. henanica* in only having hyaline, ovoid to ellipsoidal conidia, while *L. henanica* has hyaline and aseptate conidia that becomes brown, 1-septate conidia at maturity (Wang et al., 2021). However, there is no base pair difference between them. Therefore, herein, this collection

is reported as a new host record of *L. henanica* on *Chromolaena odorata* (Asteraceae) and a new geographical record in Thailand.




**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through 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.

**Figure 3.56** *Lasiodiplodia.henanica* (MFLU 25-0276, a new host record)

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

*Index Fungorum number*: IF188476, *Facesoffungi number*: FoF00167, Figure 3.57

*Saprobic* on dead stems of *Bidens pilosa.* **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 170–215 × 145–185 µm ($\overline{x}$= 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 ($\overline{x}$ = 7 × 3 µm, n= 5), hyaline, ovoid to cylindrical, discrete, smooth. *Conidia* 17–30 × 10–15 µm ($\overline{x}$ = 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.

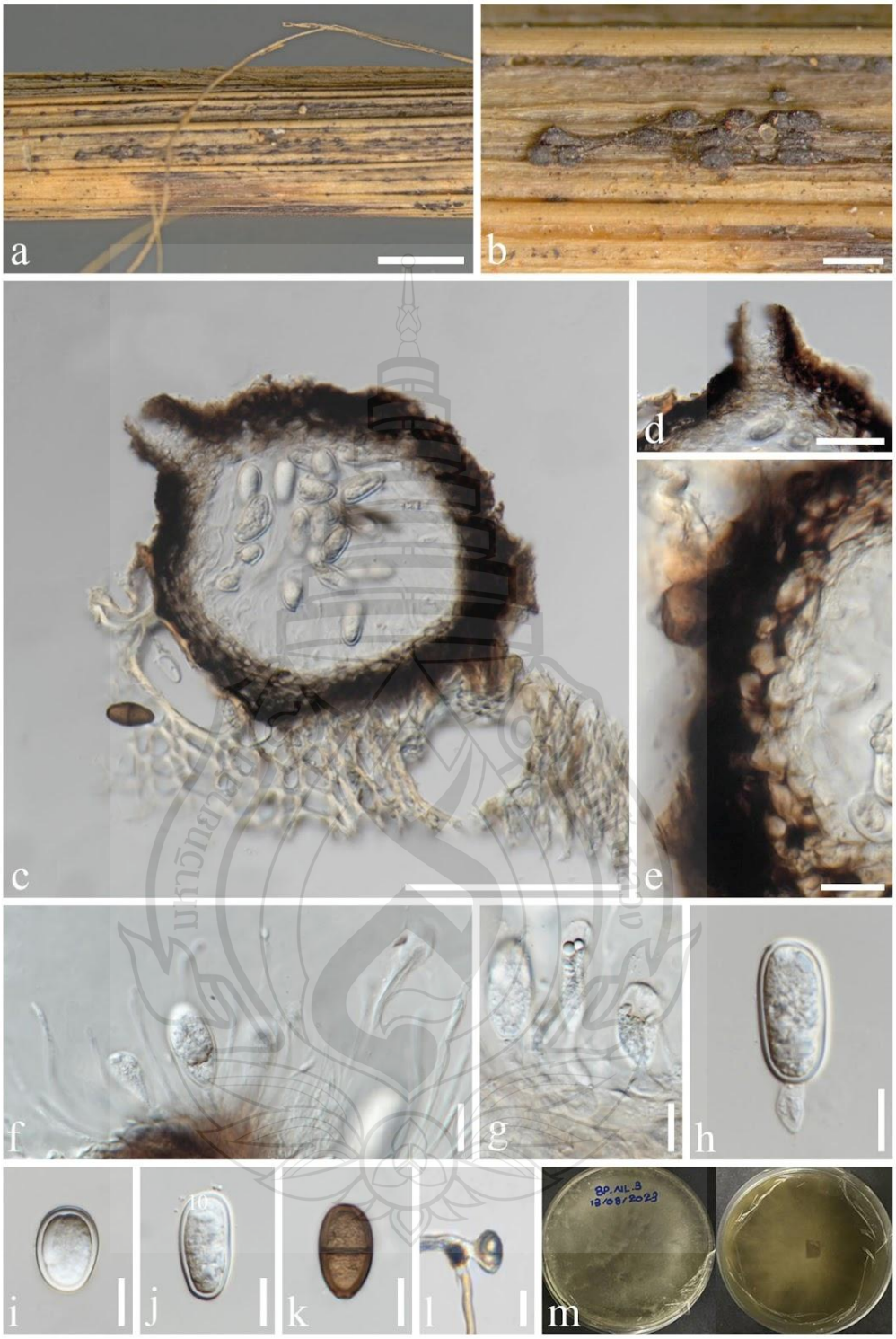
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet (BP-NL-3, MFLU 25-0277, **a new host record)**; living culture MFLUCC 25-0266; *ibid*., on dead stems of *Chromolaena odorata* (Asteraceae), 3 August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

*GenBank*: **ITS**: PV870621, PV870622, PV870623, PV870624; ***tef*1-*α***: PX282654, PX282655, PX282656, PX282657; ***tub*2**: PX255145, PX255146, PX255147, 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 (Figure 3.55), 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, both of these *Lasiodiplodia* species share similar morphological characters such as hyaline to brown, (0)–1-septate, ellipsoidal to ampulliform conidia (Wang et al., 2019). A comparison of base pair difference between these two species reveals ITS 0.69% (4/577), *tef*1-*α* 1.14% (6/522), *tub*2 0% (0/ 460), *rpb*2 0% (0/599), with gaps. *Lasiodiplodia theobromae* was previously reported on *Bidens pilosa* (Asteraceae) (Mullen, 1991), and the new collection is reported as a reference specimen of *L. theobromae.*




**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through 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 µm, c = 100 µm, d = 20 µm, e, f, g, h, i, j, k, l = 10 µm.

**Figure 3.57** *Lasiodiplodia theobromae* (MFLU 25-0277, a new host record)

**Class Sordariomycetes O.E.** Erikss. & Winka

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

**Diaporthales** Nannf.

### 3.2.15 Diaporthaceae Höhn. ex Wehm

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

***Diaporthe* Nitschke.**

*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 identified on morphology and host-specificity. To get 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, *tub*2, *tef*1-*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.* This study reported new species and new records of *Diaporthe* from *D. biconispora* and *D. longicolla* complexes (Figures 3.58 and 3.59).

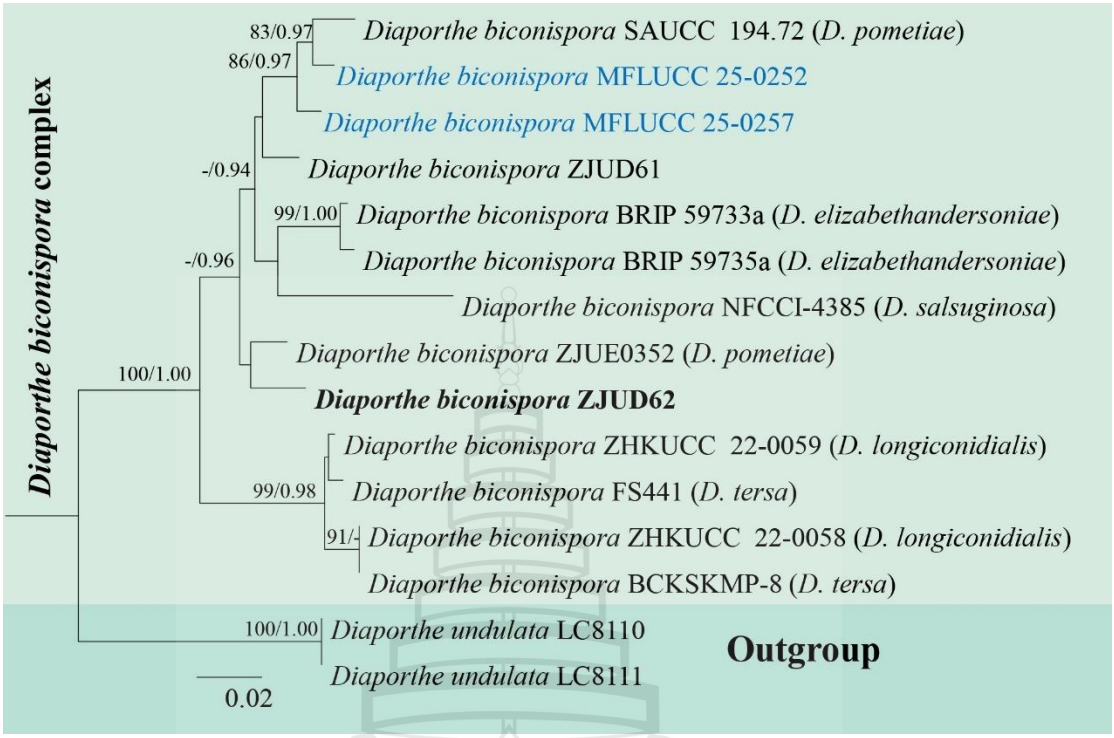



**Figure 3.58** Phylogram generated from ML analysis of a combined dataset of ITS, *tef*1-*α*, and *tub*2 sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Diaporthe undulata* (LC1180 and LC1181)

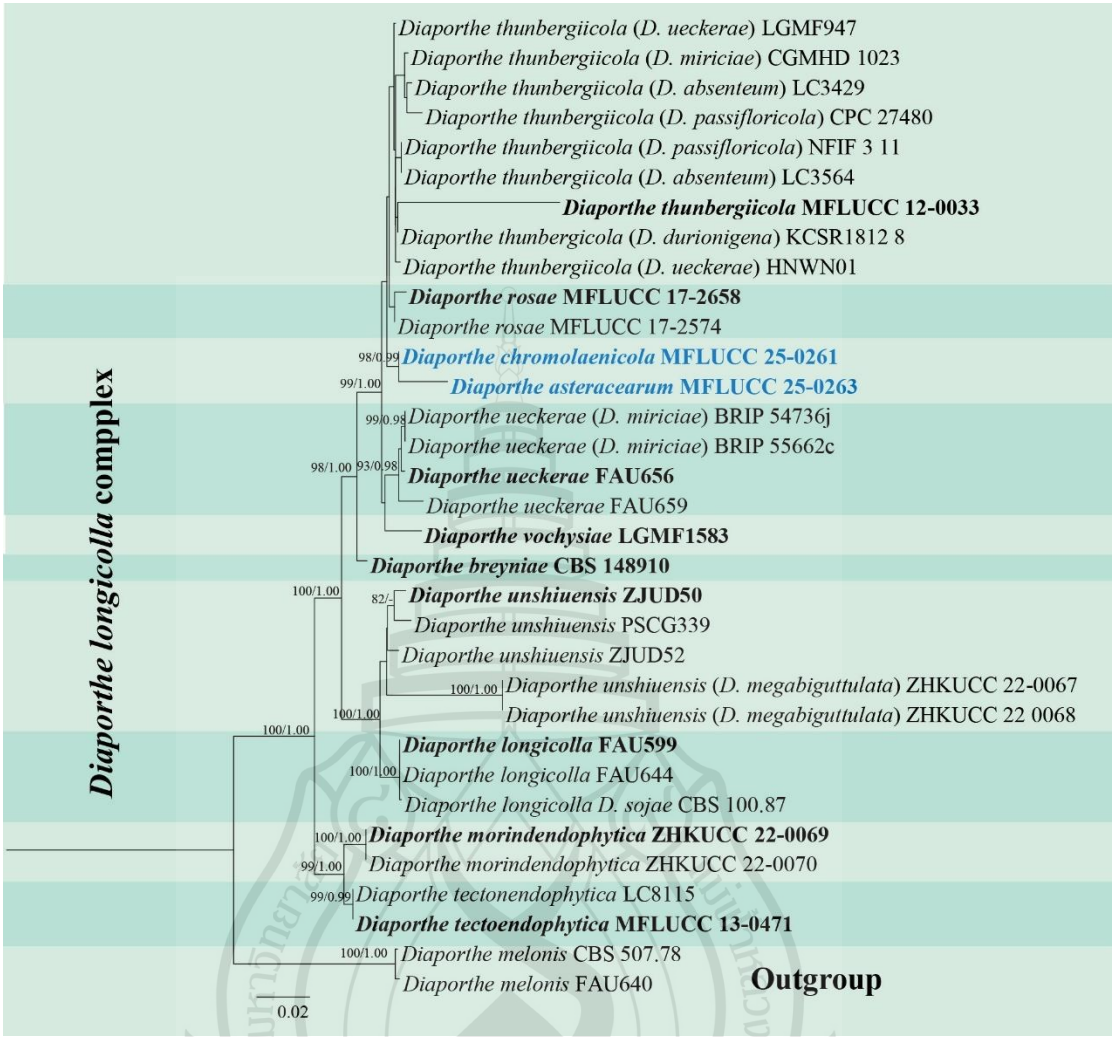



**Figure 3.59** Phylogram generated from ML analysis based on the combined dataset of ITS, *tef*1-*α*, and *tub*2 sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Diaporthe melonis* (CBS 507.78 and FAU640)

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

*Index Fungorum number*: IF904376*, Facesoffungi number*: FoF18044*,* Figure 3.60

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

*Holotype*: MFLU 25-0281

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

*Culture characteristics*: Ascospores 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, 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*: **ITS**: PV870625; ***tef*1-*α***: PX282658; ***tub*2**: 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:* Morphologically, the strain (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). Based on the phylogenetic analysis (Figure 3.59), the 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). The strain (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 (Hongsanan et al., 2023). Therefore, the morphology between them could not be compared. A comparison of base pairs difference between the strain (MFLUCC 25-0263) and *D. rosae* (MFLUCC 17-2574) reveals ITS 0.5% (3/573), *tef*1-*α* 2.7 % (10/372) and *tub*2 2.7% (13/489), while a comparison between the strain (MFLUCC 25-0263) and *D. chromolaenicola* (MFLUCC 25-0261) reveals ITS 0% (0/573), *tef*1-*α* 0% (0/372) and *tub*2 4% (20/489), respectively.Therefore, *Diaporthe asteracearum* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand.


**Note** **a, b** Appearance of ascomata on host substrate. **c** Section through 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 µm, c = 100 µm, d, e = 20 µm, f, k, l, m, n, o = 5 µm, g, h, i, j = 10 µm.

**Figure 3.60** *Diaporthe asteracearum* (MFLU 25-0281, holotype)

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

*Index Fungorum number*: IF810578, *Faces of fungi number*: FoF08406, Figure 3.61

Saprobic on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: *Conidiomata* 80–150 × 100–150 µm ($\overline{x}$ = 98 × 123 µm, 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 ($\overline{x}$ = 3 × 3 µm, n = 5), holoblastic, phialidic, globose to subglobose, or ampulliform, terminal. *Alpha conidia* 5–10 × 1.5–3 µm ($\overline{x}$ = 7.5 × 2 µm, n = 20), hyaline, aseptate, fusoid to ovoid, hyaline, aseptate, tapering at both ends, 2–4-guttules. *Beta conidia* 20–25 × 1–2 µm ($\overline{x}$ = 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.

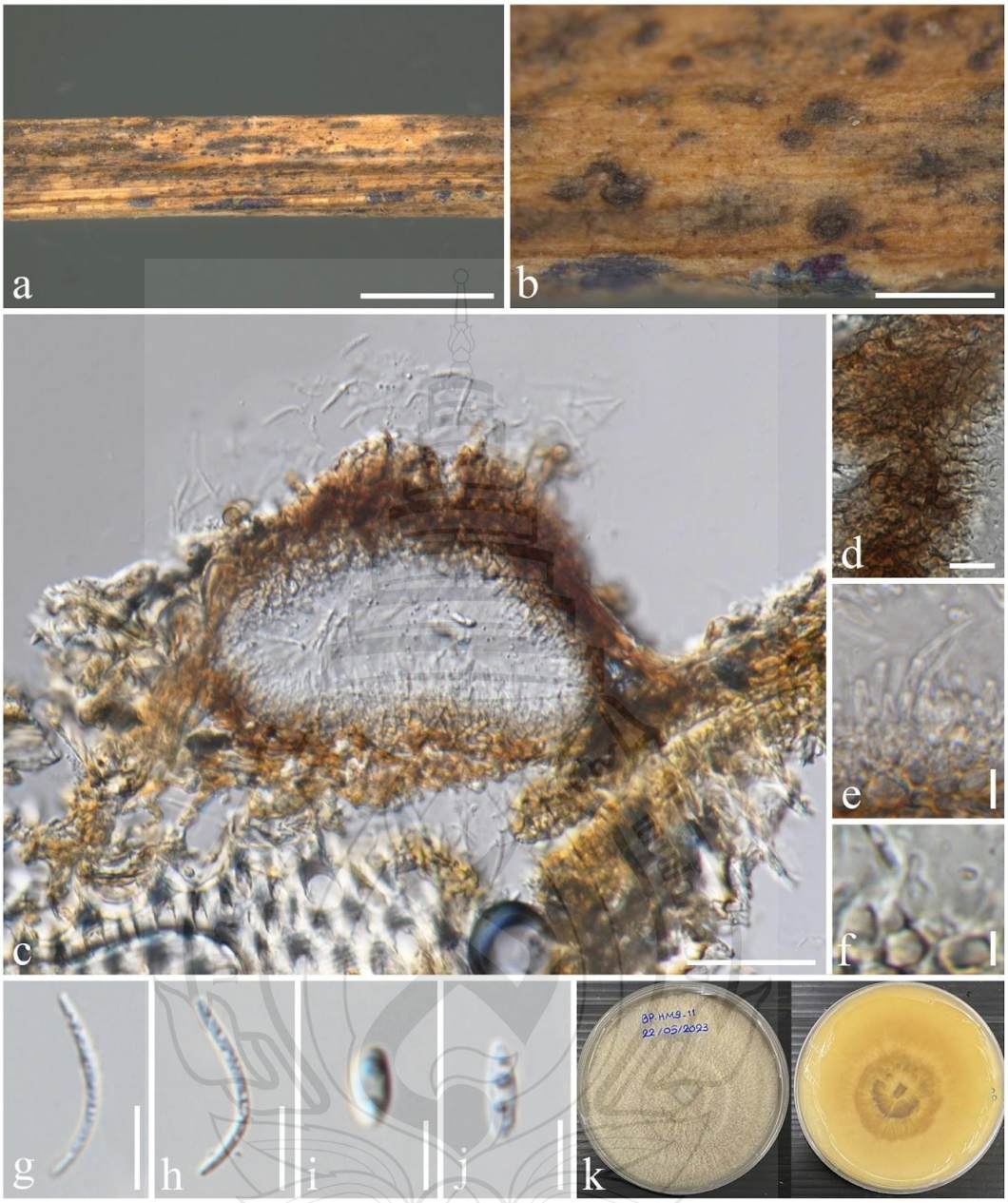
*GenBank*: **ITS**: PV870626; ***tef*1- *α***: PX282659; ***tub*2**: PX255053.

*Pre-screening for antibacterial activity*: *Diaporthe biconispora* (MFLUCC 25-0257) 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 (Rossman 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.* Later, 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 (Figure 3.58), my isolate (MFLUCC 25-0257) clustered within *D. biconispora* complex with 100% ML and 1.00 BYPP bootstrap support. There are no base pair differences between species. Therefore, this collection is reported as a new host record of *D. biconispora* on *Bidens pilosa* (Asteraceae) and a new geographical record in Thailand.




**Note** **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 µm, c = 50 µm, d, g, h = 10 µm, e, f, i, j = 5 µm.

**Figure 3.61** *Diaporthe biconispora* (MFLU 25-0282, a new host record)

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

*Index Fungorum number*: IF904377*, Facesoffungi number*: FoF18045*,* Figure 3.62

*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:** *Conidiomata* 130–150 × 90–120 µm ($\overline{x}$ = 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 papillate in central. *Peridium* 20–25 µm wide, comprising 2–3-layered brown cells of *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–10 × 2–3 µm ($\overline{x}$ = 5.5 × 2 µm, n = 5), phialidic, ampulliform, terminal. *Alpha conidia* 5–10 × 1–3 µm ($\overline{x}$ = 7 × 2.4 µm, n = 20), hyaline, aseptate, fusoid to ovoid, tapering at both ends, 2-guttules. *Beta conidia* 20–28 × 1–2 µm ($\overline{x}$ = 25×1.3 µm, n = 20), hyaline, aseptate, filiform, curved, granular appearance, wider at the middle and tapering towards both ends.

*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.

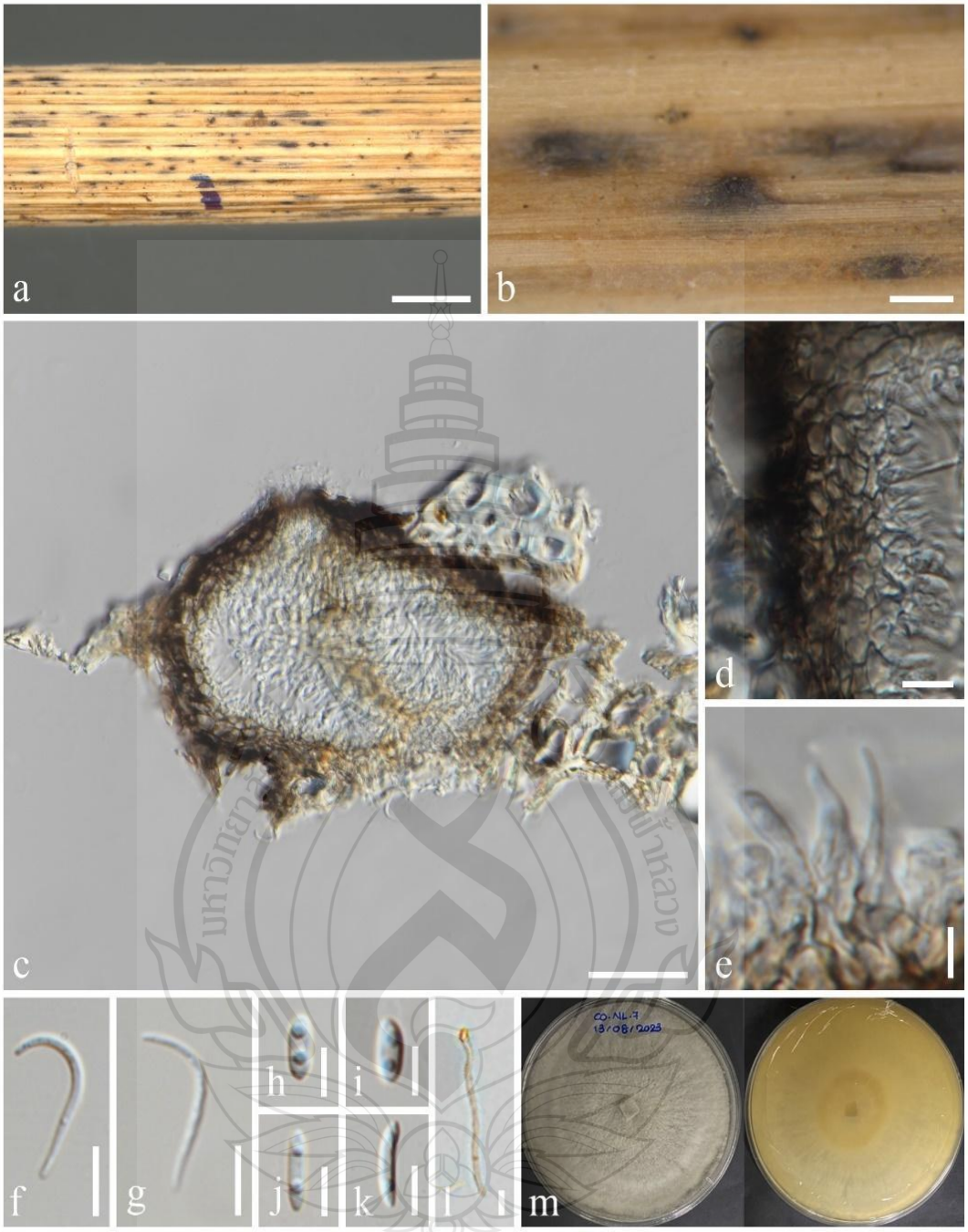
*GenBank*: **ITS**: PV870627; ***tef*1- *α***: PX282660; ***tub*2**: PX246147.

*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 (Figure 3.59), the strain (MFLUCC 25-0261) is clustered sister to *D. asteracearum* (MFLUCC 25-0263), with 98% ML and 0.99

BYPP bootstrap support. The strain (MFLUCC 25-0261) is found as an asexual morph in nature, and *D. asteracearum* (MFLUCC 25-0263) is found as a sexual morph. Therefore, the morphology between them could not be compared. Furthermore, the strain (MFLUCC 25-0261) and *D. asteracearum* clustered separately from the isolates of *D. thunbergiicola* and *D. rosae* (Figure 54). Morphologically, the 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 (8–10 × 2–3 µm vs. 13 × 1–2.5 µm), and longer alpha conidia (5–10 × 1–3 µm vs. 5.5–7.5 × 2–3 µm) and longer beta conidia (20–28 × 1–2 µm vs. 12.5–18 × 1–2 µm). When the base pair difference is compared between this strain (MFLUCC 25-0261) and *D. asteracearum* (MFLUCC 25-0263), the result reveals ITS 0% (0/573), *tef*1-*α* 0% (0/372) and *tub*2 4% (20/489), respectively. Therefore, *Diaporthe chromolaenicola* is introduced as a new species on *Chromolaena odorata* (Asteraceae) in Thailand.




**Note** **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.

**Figure 3.62** *Diaporthe chromolaenicola* (MFLU 25-0284, holotype)

**Subclass Hypocreomycetidae O.E. Erikss. & Winka**

**Glomerellales** Chadef. ex Réblová, W. Gams & Seifert

### 3.2.16 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*. (Bhunjun et al., 2021; Liu et al., 2022; Zhang et al., 2024). In my study, I introduced two new records in *Colletotrichum gigasporum* and *C. truncatum* complexes (Figures 3.63 and 3.64).

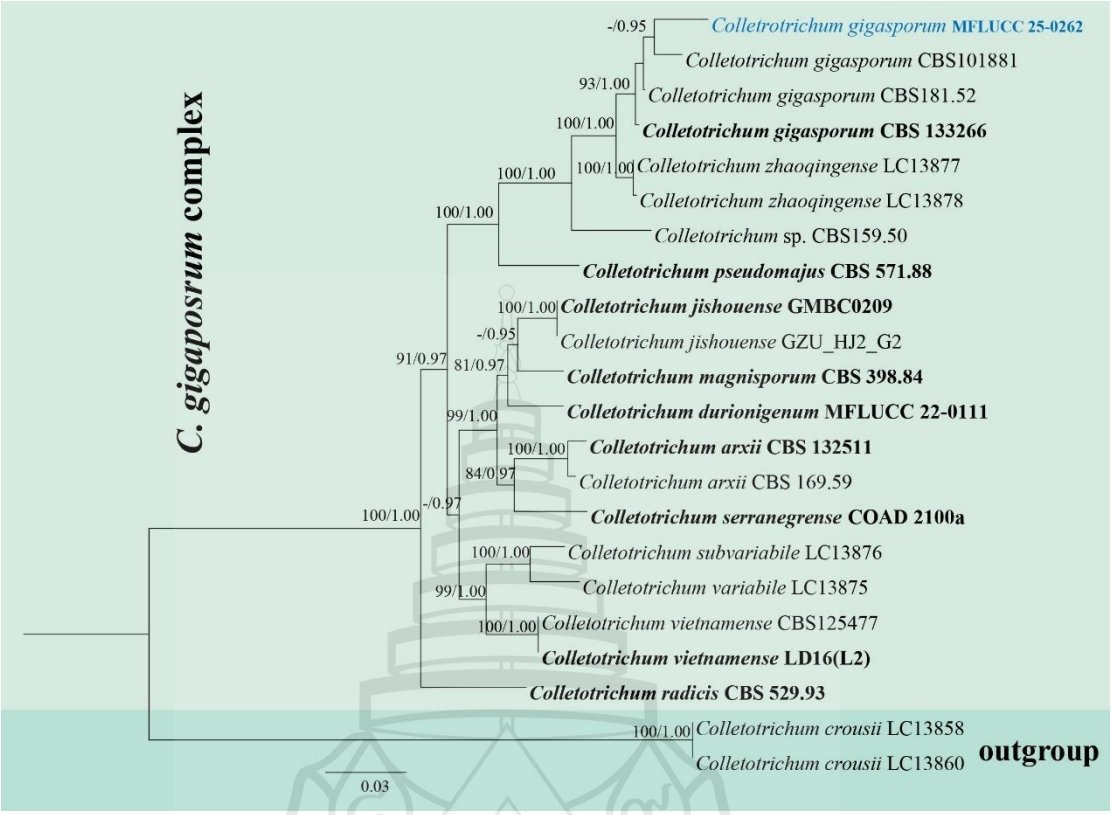



**Figure 3.63** Phylogram generated from ML analysis based on the combined dataset of ITS, *ACT*, *CHS*, *GAPDH*, and *tub*2 sequence data of *Colletotrichum gigasporum* complex. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Colletotrichum crousii* (LC13858 and LC13860)

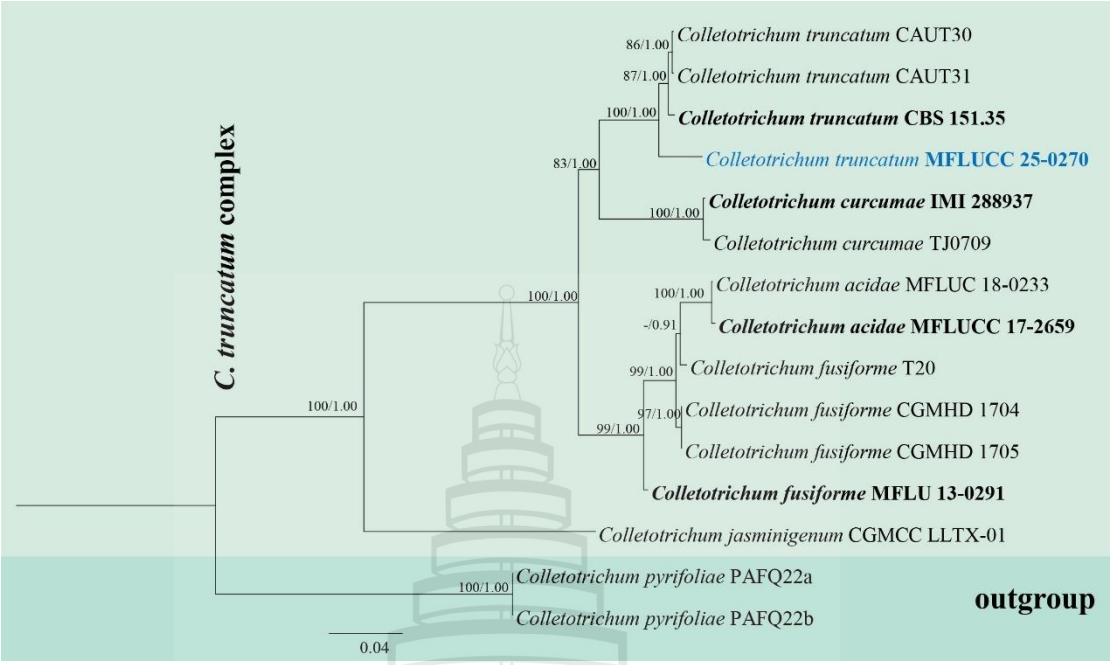



**Figure 3.64** Phylogram generated from maximum parsimony analysis of a combined dataset of ITS, *ACT*, *CHS*, *GAPDH*, and *tub*2 sequence data of *Colletotrichum truncatum* complex. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Colletotrichum pyrifoliae* (PAFQ22a and PAFQ22b)

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

*Index Fungorum number*: IF800175*, Facesoffungi number*: FoF10777*,* Figure 3.65

*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. *Coidiogenous cells* 3–5 µm long, phialidic, hyaline, ovoid to cylindrical, smooth, unbranched. *Conidia* 17–22 × 7–9 µm ($\overline{x}$ = 20 × 8 µm, n= 20), hyaline, aseptate, verruculose, cylindrical, rounded at both ends.

*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*: **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; *Stylosanthes guianensis* (Faboideae) in Mexico; *Coffea arabica* (Rubiaceae) in Colmbia; *Diospytos kaki* (Ebenaceae) in Japan; *Solanum betaceum* (Solanaceae) in New Zealand, *Homo sapiens* (Homonidae) in Brazil; *Theobromae cacao* (Malvaceae) in Panama and East Africa; *Persea americana* (Lauraceae) in Sri Lanka, *Virola surinamensis* (Myristicaceae) in Panama; *Coffea* sp. (Rubiaceae) in Vietnam; *Trichilia tuberculata* (Meliaceae) in Panama; *Acacia auriculiformis* (Fabaceae) in Thailand; *Musa* sp. (Musaceae) in Mexico; *Centella asiatica* (Apiaceae) in Madagascar, durian fruit (Malvaceae) in Thailand; dead stems of *Chromolaena odorata* (Asteraceae) in Thailand (Rakotoniriana et al., 2013; Liu et al., 2014; Hunupolagama et al., 2015; this study).

*Notes*: In *Colletotrichum*, species delimitation based only on morphology is nearly impossible due to the overlapping morphological features. Morphologically, my strain (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 (Figure 3.63), the new strain (MFLUCC 25-0262) formed a sister clade to *Colletotrichum gigasporum* (CBS 101881) with 73% ML and 0.95 BYPP bootstrap support. Therefore, herein, *C. gigasporum* is reported as a new host record on *Chromolaena odorata* (Asteraceae) in Thailand.


**Note** **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.

**Figure 3.65** *Colletotrichum gigasporum* (MFLU 25-0285, a new host record)

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

*Index Fungorum number*: IF280780*, Facesoffungi number*: FoF03827*,* Figure 3.66

*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. *Coidiogenous cells* 3–5 µm long, hyaline, cylindrical to ellipsoidal, smooth, unbranched. *Conidia* 20–28 × 2–4 µm ($\overline{x}$ = 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.

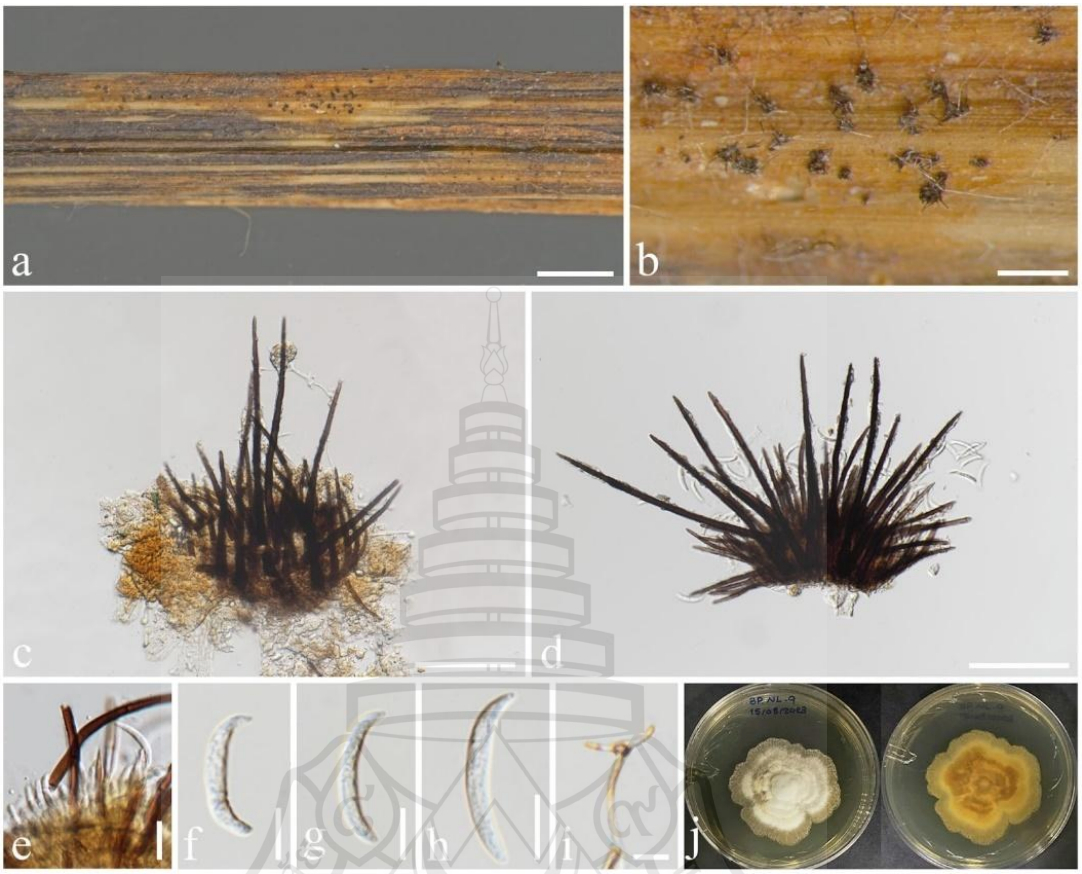
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet (BP-NL-9, MFLU25-0286, **a new host record**); living culture MFLUCC 25-0270.

*GenBank*: **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).

*Note*: 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 (Figure 3.64). 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). Therefore, *C. truncatum* is reported as a new host record on *Bidens pilosa* (Asteraceae) in northern Thailand.




**Note** **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 µm, c, d = 100 µm, e, f, g, h, i = 10 µm.

**Figure 3.66** *Colletotrichum truncatum* (MFLU 25-0286, holotype)

**Hypocreales** Lindau

### 3.2.17 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 have phialidic conidiogenesis, which produces amerosporous to phragmosporous conidia (Lombard et al., 2015). Nectriaceae species are found as saprobes, pathogens, fungicolous or insecticolous (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*, *rpb*2, *tub*2, and *CaM* (Han et al., 2023). Following the species concept of Crous et al. (2021), I conducted phylogenetic analysis and introduced two new species, *F. bidenticola*, and *F. chromolaenae* with *F. hainanense* as a new record in *Fusarium incarnatum-equiseti* complex, based on the combined dataset of ITS, *tef*1-*α*, *rpb*2, *tub*2, and *CaM* sequence data (Figure 3.67).

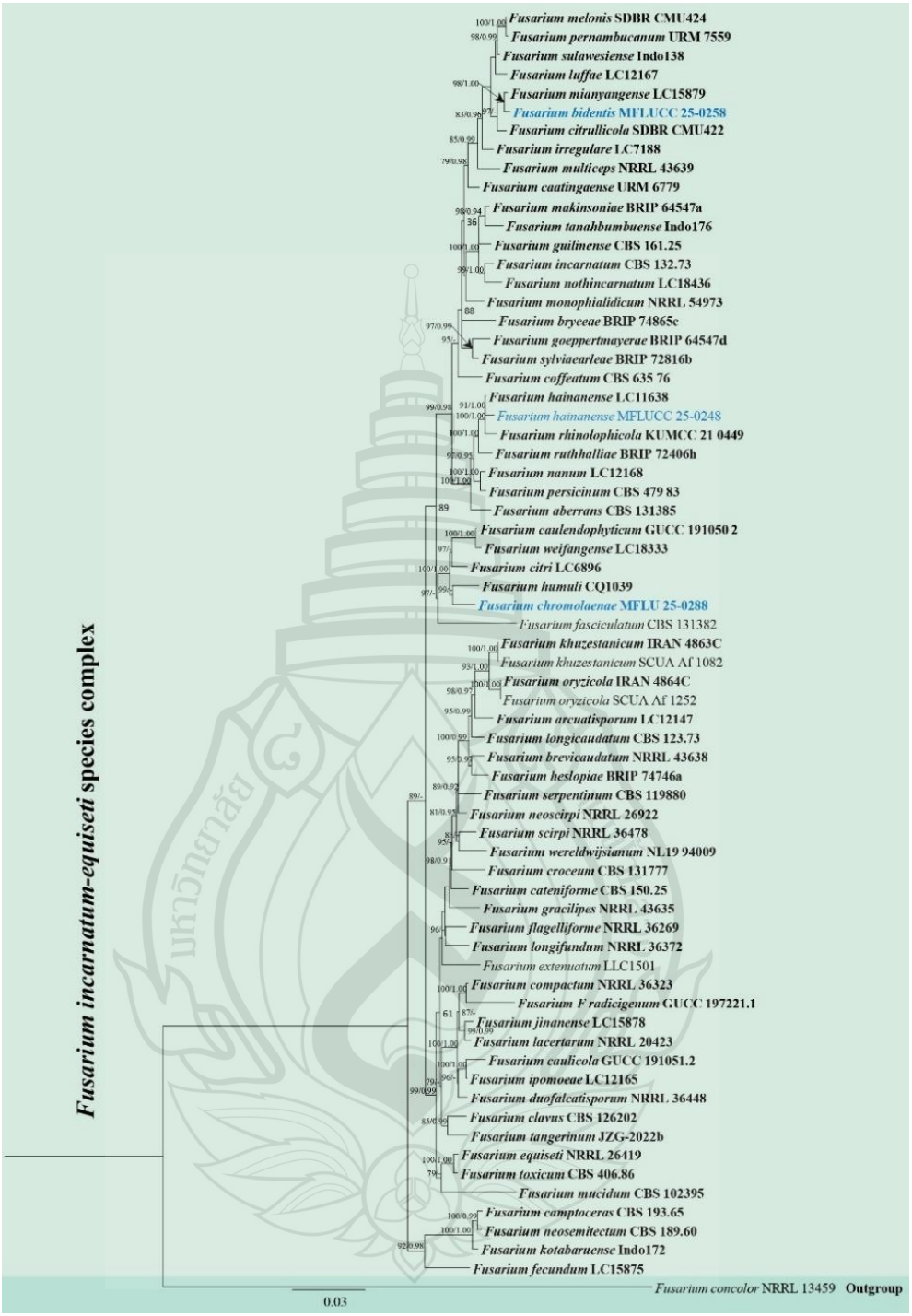



**Figure 3.67** Phylogram generated from ML analysis of a combined dataset of ITS, *tef*1-*α*, *rpb*2, *tub*2, and *CaM* sequence data of *Fusarium incatnatum-equiseti* complex. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Fusarium concolor* (NRRL 13459)

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

*Index Fungorum number*: IF904378*, Facesoffungi number*: FoF18046*,* Figure 3.68

*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**: *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 × 3–4 μm ($\overline{x}$ = 38.4 × 3.6 μm, 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.

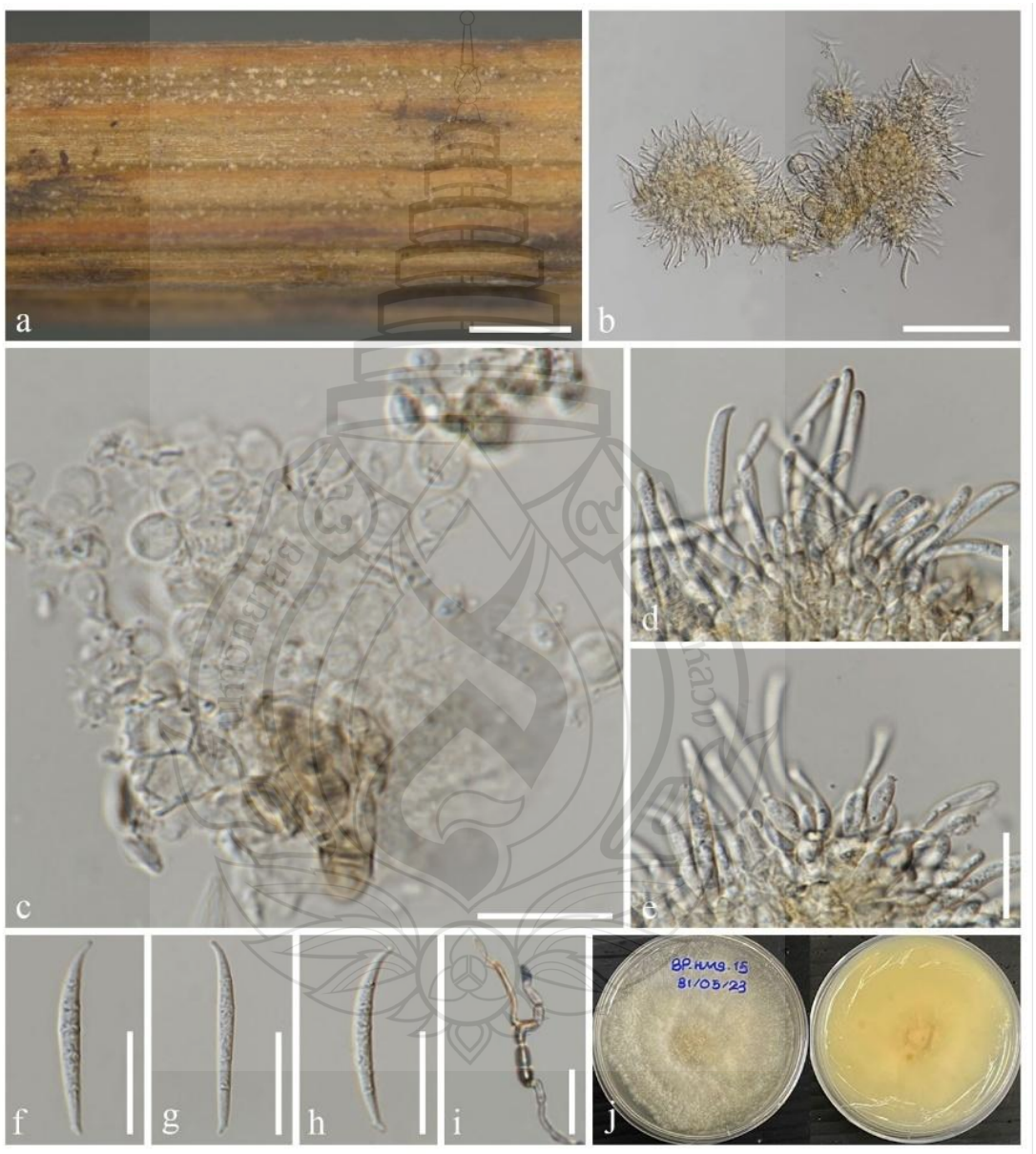
*GenBank*: **ITS**: PV870630; ***tef*1-*α***: PX282661; ***rpb*2**: PX120468

*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).

*Note*: Based on the phylogenetic analysis of *F. incarnatum-equiseti* species complex, my strain (MFLUCC 25-0258) formed a clade sister to *F. mianyangense* (LC15879) with 98% ML and 1.00 BYPP bootstrap support (Figure 3.67). *Fusarium mianyangense* (LC15879) has hyaline, falcate, smooth- and thin-walled, 3(–5)-septate conidia (Han et al., 2023), while this collection has hyaline, filiform to falcate, aseptate and

longer conidia than *F. mianyangense* (31–45 × 3–4 µm vs. 29.5–36.6 × 3.0–4.9 µm). A comparison of base pair difference reveals 0% (0/524) in *tef*1-*α* region and 1.6% (11/696) in *rpb*2 region. Therefore, this collection is introduced as a new species mainly based on multi-gene phylogenetic analyses and morphological differences with *F. mianyangense* (LC15879) (Han et al., 2023)




**Note** **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 3.68** *Fusarium bidentis* (MFLU 25-0290, holotype)

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

*Index Fungorum number*: IF904379*, Facesoffungi number*: FoF18047*,* Figure 3.69

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

*Holotype*: MFLU 25-0288

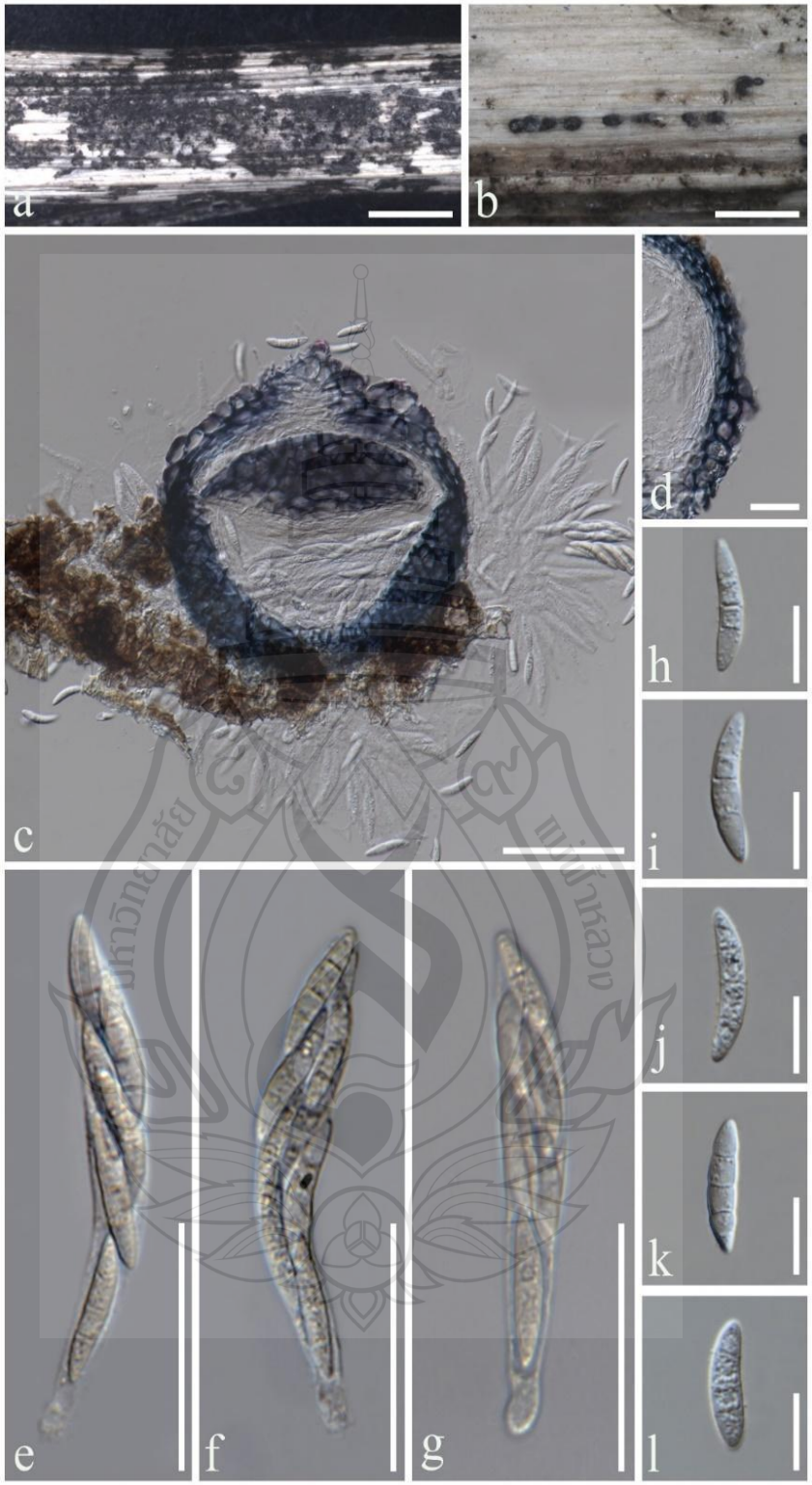
*Saprobic* on dead stems of *Chromolaena odorata.* **Sexual morph**: *Ascomata* 205–350 × 240–300 ($\overline{x}$ =290 × 288 µm, n = 5), superficial, globose to subglobose, dark blue to black on the host surface, with or without ostiole. *Peridium* 20–40 µm wide, comprising 3–4 layered of dark blue cells of *textura angularis. Asci* 95–120 × 11–15 ($\overline{x}$ = 107 × 14 µm, n = 20), 8-spored, unitunicate, hyaline, cylindric-clavate, with a short pedicel. *Ascospore* 25–35(–40) × 5–8 µm ($\overline{x}$ = 30 × 6 µm, 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.

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

*GenBank*: **ITS**: PV870631; ***tef*1-*α***: PX282662; ***rpb*2**: PX120469

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

*Notes*: Based on phylogenetic analysis (Figure 3.67), this collection is 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). My collection is found as a sexual morph in nature; therefore, the morphology could not be compared. A comparison of base pair differences of *tef*1-*α* and *rpb*2 between this 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.




**Note** **a, b** Appearance of ascomata on host substrate. **c A** Section through 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.

**Figure 3.69** *Fusarium chromolaenae* (MFLU 25-0288, a new host record)

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

*Index Fungorum number*: IF829536*, Facesoffungi number*: FoF14335*,* Figure 3.70

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph**: Undetermined. **Asexual morph**: *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 ($\overline{x}$ = 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.

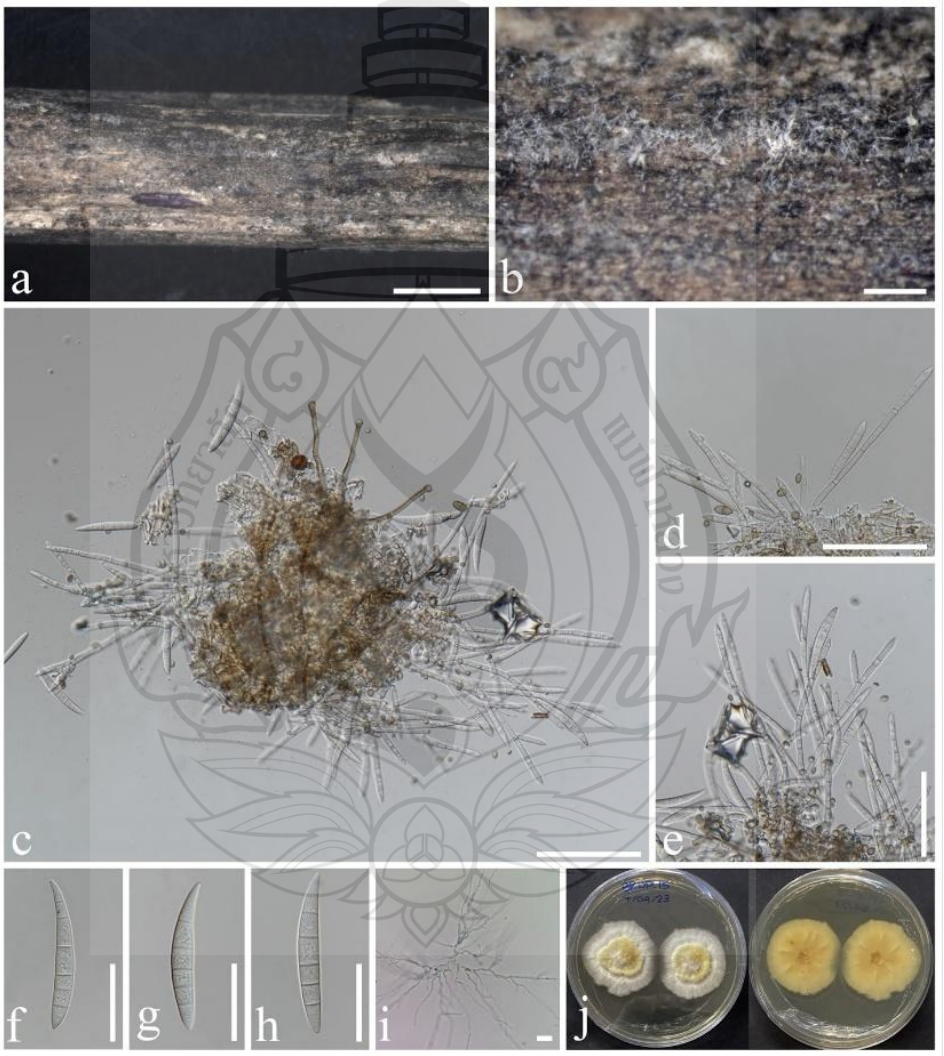
*GenBank*: **ITS**: PV870632; ***tef*1-*α***: PX282663; ***rpb*2**: PX120470

*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).

*Note*: When conducted the phylogenetic analysis of *F. incarnatum-equiseti* species complex, the strain (MFLUCC 25-0248) clustered sister to *F. hainanense* (LC11638) with 91 % ML and 1.00 BYPP bootstrap support (Figure 3.67). 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-septate (18–33 × 2–5 µm), while this collection is found as saprobes in nature and has hyaline, 5–8-septate, falcate, tapering at both ends or broader at the middle or base, rough surface conidia (40–55(69–) × 5–8 µm). When compared the base pair differences of ITS and *tef1- α*, there are no base pair differences between the strain (MFLUCC 25-0248) and *F. hainanense* (LC11638). Therefore, this collection is reported as a new host record of *F. hainanense* on *Bidens pilosa* (Asteraceae) and a new geographical record in Thailand.




**Note** **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 mm1 mm, b = 500 µm, c, d, e = 100 µm, f, g, h = 30 µm, i = 10µm.

**Figure 3.70** *Fusarium hainanense* (MFLU 25-0289, a new host record and a new geographical record)

### 3.2.18 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, 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.*

***Sarocladium*** W. Gams & D. Hawksw.

The taxonomic position of *Sarocladium* species was confirmed by Crous et al. (2018) and placed in Sarocladiaceae. The type species is *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* was introduced as a new species based on ITS, LSU, and *ACT* sequence data (Figure 3.71).

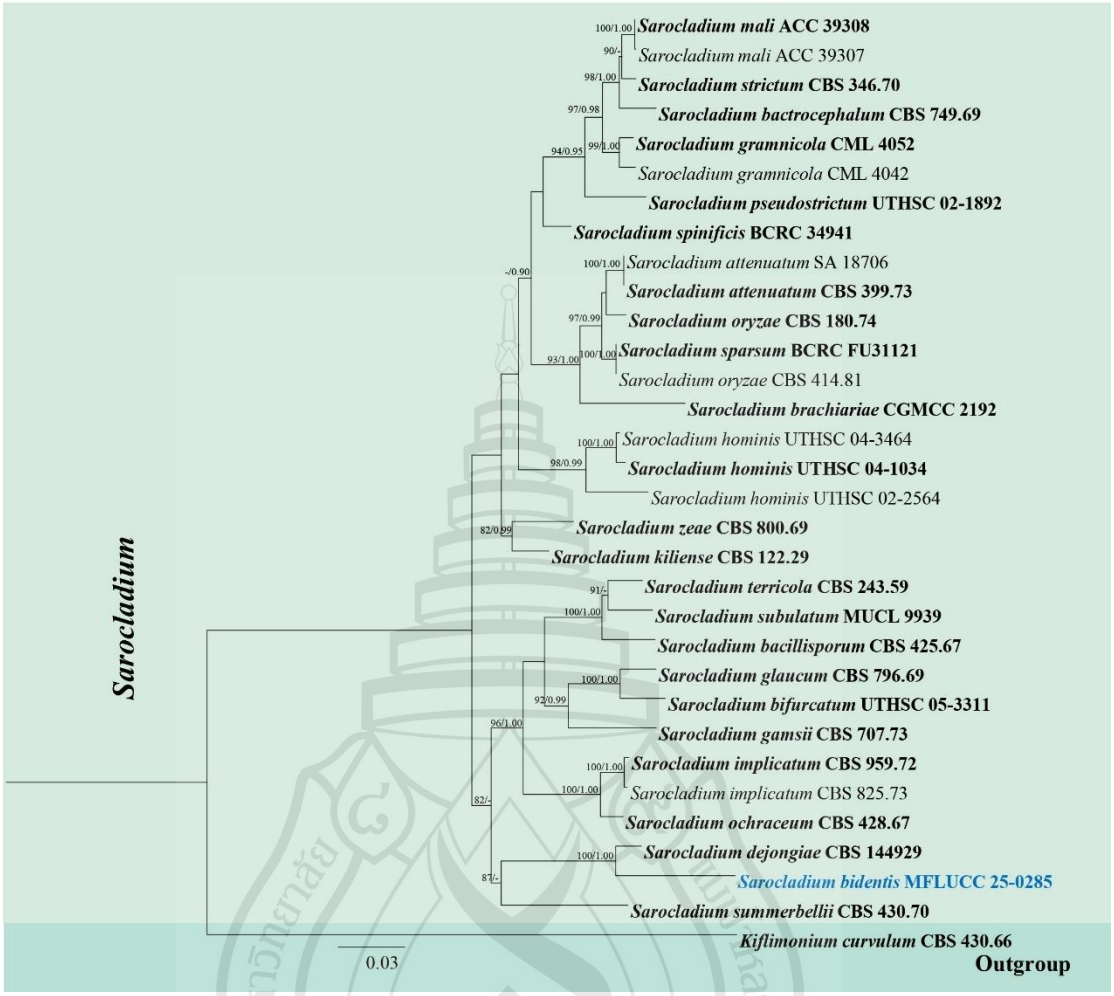



**Figure 3.71** Phylogram generated from ML analysis of a combined dataset of ITS, LSU, and *ACT* sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold. The tree is rooted to *Kifimonium curvulum* (CBS 430.66)

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

*Index Fungorum number*: IF904380*, Facesoffungi number*: FoF18048*,* Figure 3.72

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

*Holotype*: MFLU 25-0290

*Saprobic* on dried stems of *Bidens pilosa.* **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* effuse on the natural substrate, scattered, hairy, pale brown. *Mycelium* partly immersed, composed of pale brown hyphae. *Conidiophores* 250–300 × 5–7 μm ($\overline{x}$ = 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 ($\overline{x}$ = 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* 5–7 × 2–5 μm ($\overline{x}$ = 5.6 × 2.2 μm, 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.

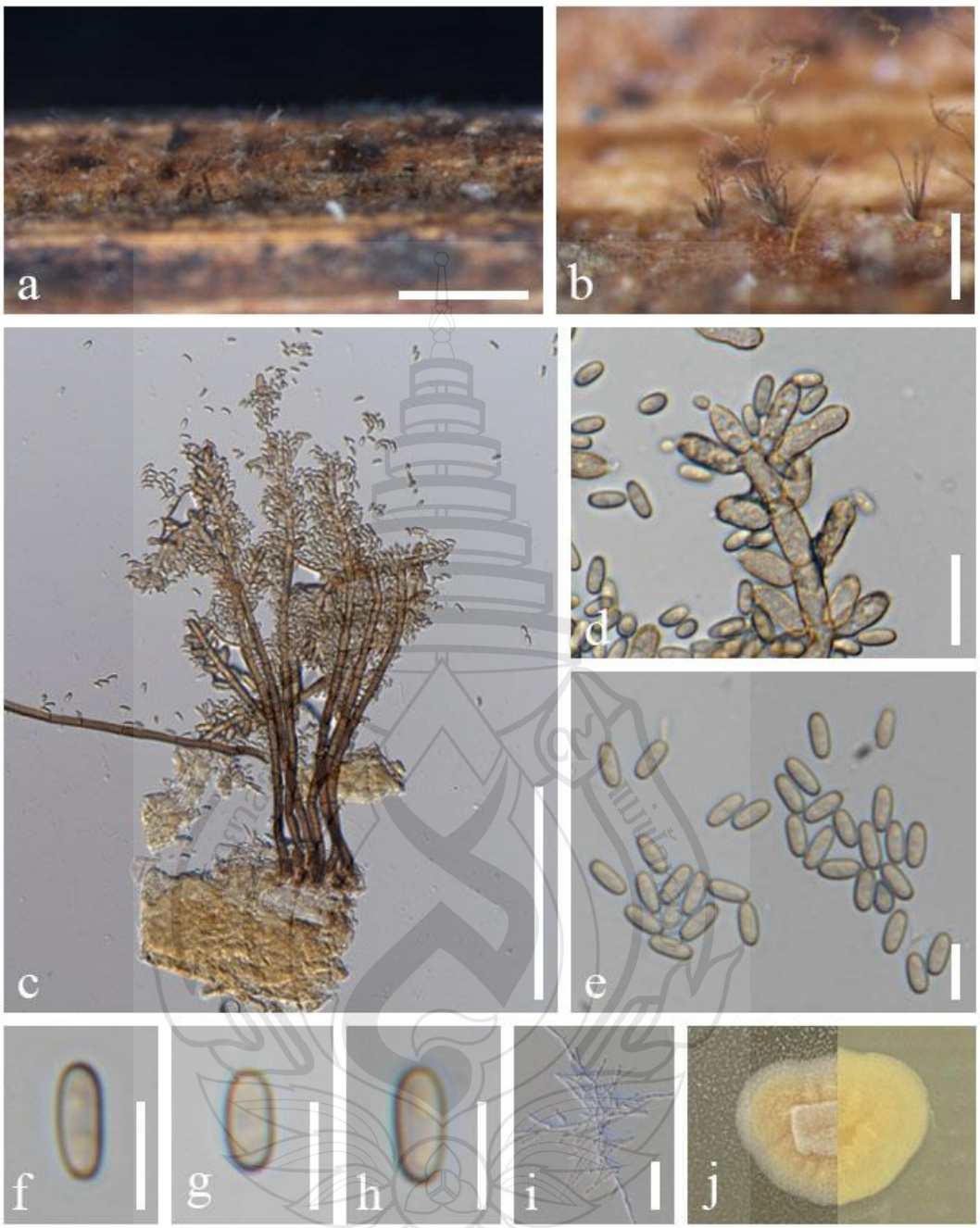
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 12 May 2023, Zin Hnin Htet (BP-HMS-1, MFLU 25-0290, **holotype**); ex-type MFLUCC 25-0285.

*GenBank*: **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).

*Note*: In phylogenetic analysis (Figure 3.71), the strain (MFLUCC 25-0285) clustered with *Sarocladium dejongiae* (CBS 144929) with 100% ML and 1.00 BYPP bootstrap support. Morphologically, this collection differs from *S. dejongiae* (CBS 144929) in having macronematous, synnematous, tree-like conidiophores (250–300 × 5–7 μm), polyphialidic, integrated or terminal, pale yellow, cylindrical, straight to slightly curved conidiogenous cells (3–5 × 3–4 μm), unicellular, aseptate, cylindrical conidia (5–7 × 2–5 μm), whereas *S. dejongiae* has 1–2.5 μm wide, septate, hyaline, vegetative hyphae, conidiophores (up to 35 μm long) arising directly from vegetative hyphae or from ropes of hyphae, simple or rarely branched, subcylindrical, phialidic conidiogenous cells (17–24 × 1–2 μm) and aseptate, cylindrical, ellipsoidal, ovoid to irregular conidia (3–5 × 1–2 μm ) formed in slimy heads. A comparison of base pair differences between this 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.




**Note** **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 µm, c = 100 µm, d = 10 µm, e, f, g, h = 5 µm, i = 10 µm.

**Figure 3.72** *Sarocladium bidentis* (MFLU 25-0290, holotype)

### 3.2.19 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 synnematous 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, *rpb*2, *tef*1- *α*, *tub*2 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, 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). This study introduced *Albifimbria bidentis* as a new species based on combined ITS, *rpb*2, and *tub*2 sequence data (Figure 3.73).

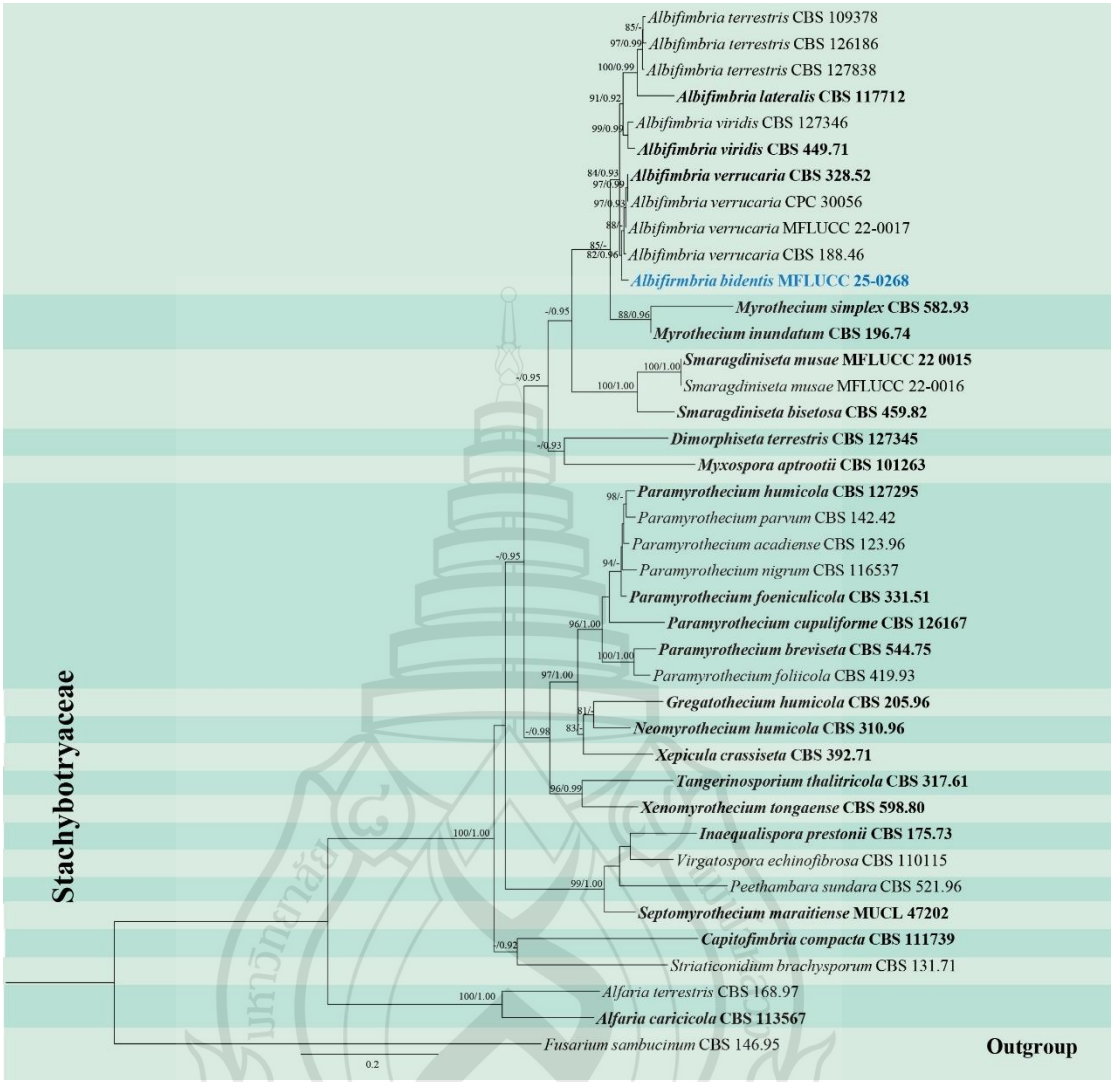



**Figure 3.73** Phylogram generated from ML analysis of a combined dataset of ITS, *rpb*2, and *tub*2 sequence data. Bootstrap support values for ML ≥ 75% and BYPP ≥ 0.90 are given at the nodes. Newly generated sequences are in blue, and type species are in bold. The tree is rooted to *Fusarium sambucinum* (CBS 146.95)

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

*Index Fungorum number*: IF904381, *Faces of fungi* number: FoF18049, Figure 3.74

*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**: *Conidiomata* sporodochial, superficial, stromatic, discoid, gregarious, irregular, a dark green conidia mass surrounded by a white setose fringe. *Conidiophores* 30–50 × 2–3 ($\bar{x}$ = 46 ×2.5 µm, n=20) arising from the basal stroma, branched, hyaline to olive green, smooth. *Conidiogenous cells* 10–15 × 1–3 µm ($\bar{x}$ = 13 × 2 µm, n=30) phialidic, cylindrical, hyaline to olive green, smooth. *Conidia* 7–8 × 2–3 µm ($\bar{x}$ = 7.7×2.8 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.

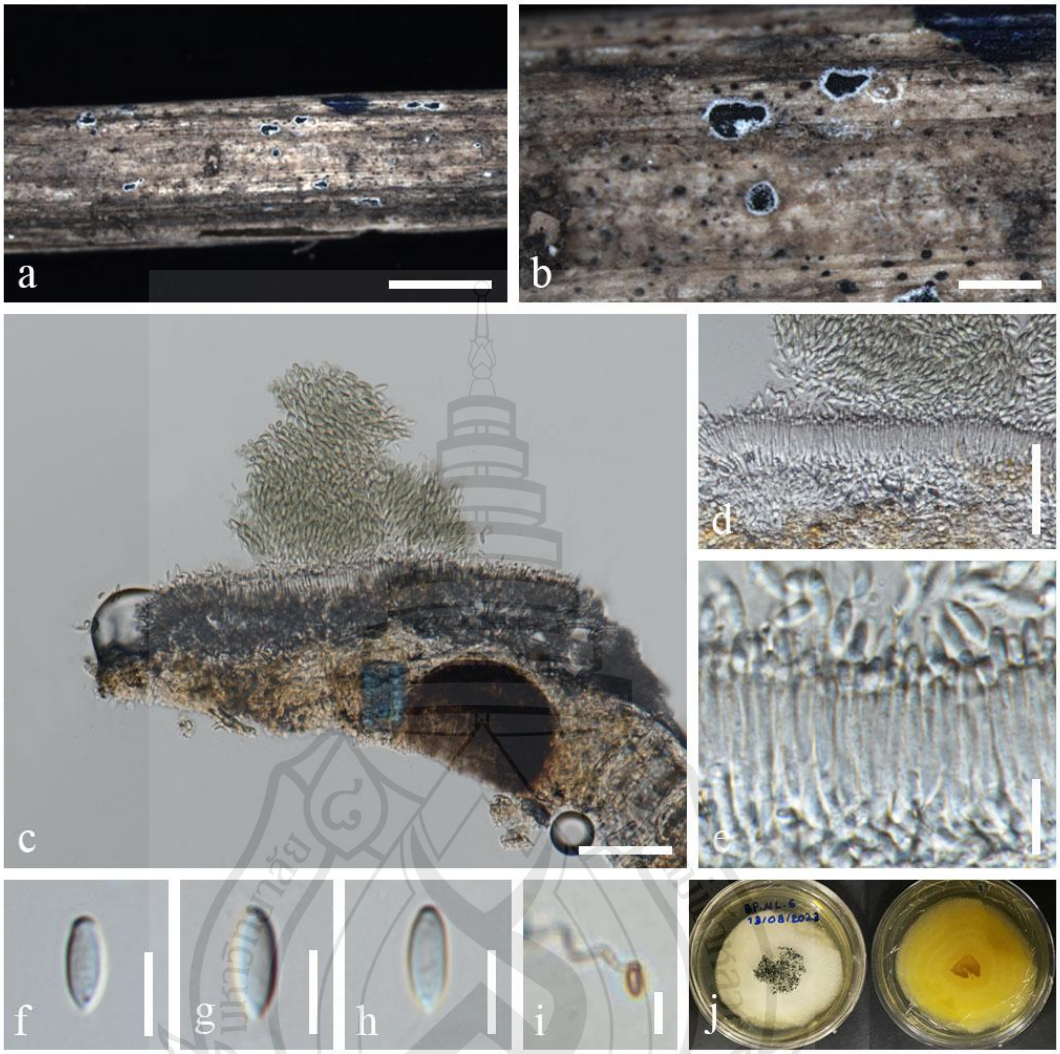
*GenBank*: **ITS**: PV870634; ***tef1-α***: PX282664; ***tub2***: PX246148; ***rpb2*:** PX120471

*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 (Figure 3.73), 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* (MFLUCC 22-0017) in having sporodochial, superficial, stromatic, discoid conidiomata, with broadly fusiform, aseptate conidia, but the current strain differs from *A. verrucaria* (MFLUCC 22-0017) in having unbranched conidiophores, hyaline to olive green, smooth, shorter conidiogenous cells (10–15 × 1–3 μm vs. 30–48 × 1–2 μm), 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.




**Note** **a, b** Appearance of colonies 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.

**Figure 3.74** *Albifimbria bidentis* (MFLU 25-0291, holotype)

***Memnoniella*** Höhn.

*Memnoniella*, a genus within the family Stachybotryaceae (Hypocreales, Hypocreomycetidae, Sordariomycetes), was first introduced by Höhnel (1923). Morphologically, *Memnoniella* shares characteristics similar to Stachybotrys. This genus was previously considered a synonym of *Stachybotrys* and the taxonomic confusion between these genera was discussed (Wang et al., 2015a). Later, a study conducted by Lombard et al. (2016) on the Stachybotryaceae family indicated that species of Memnoniella were found to cluster in a well-supported clade distinct from the *Stachybotrys* based on the combined cmdA, ITS, rpb2, *tef1- α* and *tub2* sequence data. Lombard et al. (2016) epitypified the type, *M. echinata*. Several new species and records were continuously described from *Memnoniella* (Li et al., 2003; Prasad et al., 2003; Lombard et al., 2016; Zheng et al., 2019; Mapook et al., 2020; Phukhamsakda et al., 2020; Samarakoon et al., 2021; Yeh et al., 2023). Additionally, Wang et al. (2015b) explored the chemical and bioactive secondary metabolites produced by *Memnoniella* species. This study introduced *M. asteracearum* as a new species and *M. levispora* as new host records (Figure 3.75).

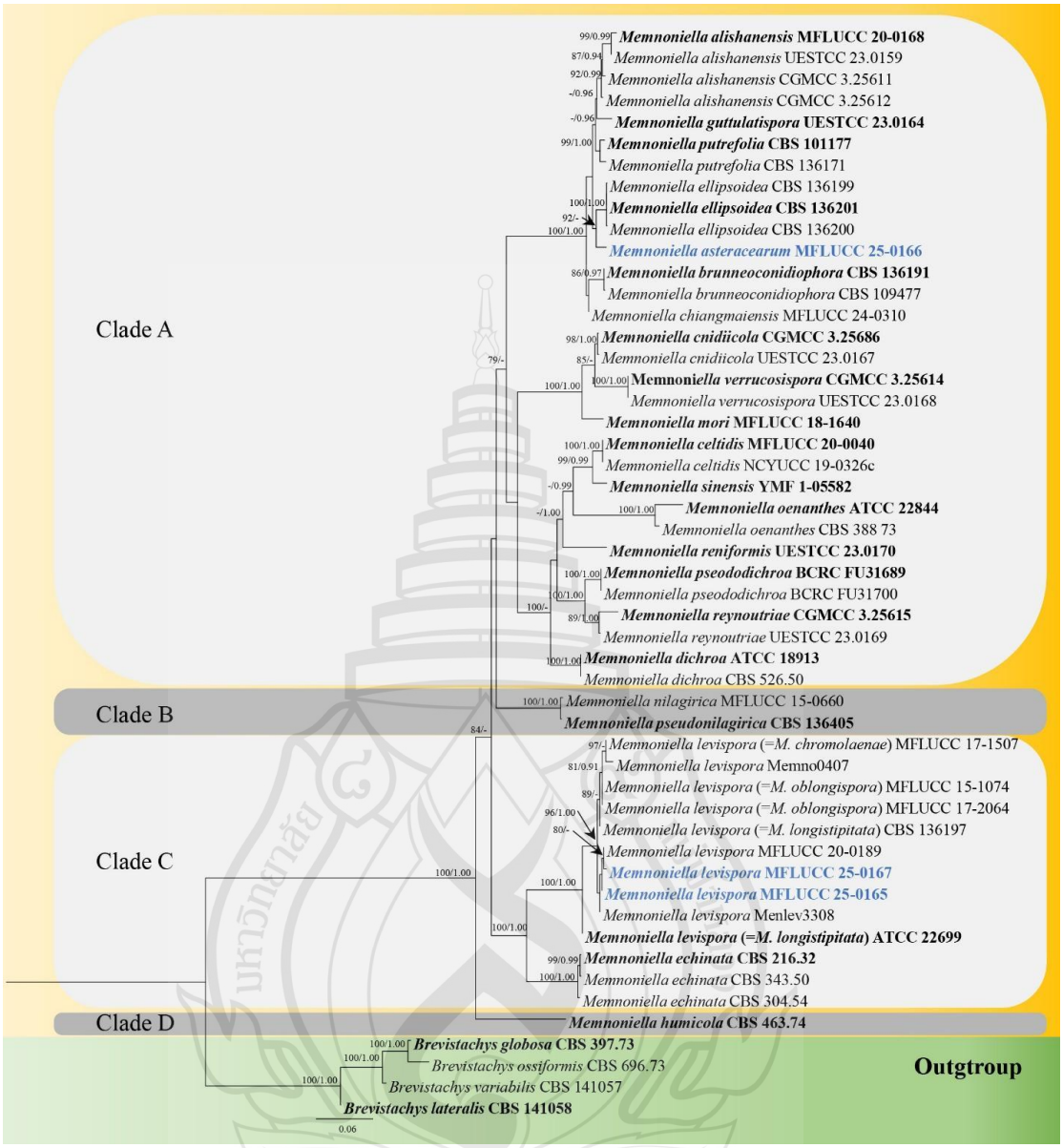



**Figure 3.75** Phylogram generated from maximum likelihood analysis based on the combined dataset of ITS, *tef1*-α, *rpb2* and *tub2* sequence data. Bootstrap support values for ML equal to or greater than 75% and BYPP equal to or greater than 0.90 are given at the nodes. Newly generated sequences are in blue and type species are in bold

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

*Index Fungorum number*: IF904382, *Facesoffungi number*: FoF17968, Figure 3.76

*Etymology*: Name reflects the host plant family "Asteraceae", from which this species was found.

*Holotype*: MFLU 25-0084

Saprobic on dead stems of *Bidens pilosa* (Asteraceae). **Sexual morph:** Undetermined. **Asexual morph:** Colonies superficial, erect, scattered on the host substrate. *Mycelium* partly superficial and partly immersed. *Conidiophores* 120–150 × 7.5–8.5 µm ($\overline{x}$ =130 × 8.1µm, n = 5), macronematous, mononematous, erect, simple, straight or flexuous, unbranched, smooth, thick-walled, septate, hyaline to pale brown, bearing conidiogenous cells at the apex. *Conidiogenous cells* 8–12 × 5–10 µm ($\overline{x}$ =11 × 6 µm, n = 5), phialidic, monophialidic, discrete, determinate, terminal, obovate, smooth, hyaline to pale brown. *Conidia* 9–13 × 5–7 µm ($\overline{x}$ = 11.1 × 5.5 µm, n = 20), acrogenous, aseptate, ellipsoidal, olivaceous brown to dark brown, verrucose, 1–2 guttules on the surface, thick-walled, rounded at both ends.

*Culture characteristics*: Conidia germinating on MEA within 24 hours, reaching 34 mm after 10 days at room temperature, irregular, filamentous, concentric, pale yellow, flat, transparent, slightly wrinkled on the surface, irregular, concentric, yellow to pale pink 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-2, MFLU 25-0084, **holotype**); ex-type MFLUCC 25-0166.

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

*Notes*: In the phylogenetic analysis, the isolate (MFLUCC 25-0166) was sistered with *M. ellipsoidea* (CBS 136199, CBS 136201 and CBS 136200) with 92% ML and 0.84 BYPP support (Figure 3.75). When comparing morphology, this new isolate shares several morphological characters with the type strain of *M. ellipsoidea* (CBS 136201), such as macronematous, mononematous, straight or flexuous, unbranched conidiophores bearing phialidic conidiogenouse cells at the apex and acrogenous, aseptate, ellipsoidal conidia. However, the isolate (MFLUCC 25-0166) differs from *M. ellipsoidea* in having longer conidiophores (120–150 × 7.5–8.5 µm vs. 55–140 × 4–8 µm), larger conidiogenous cells

(8–12 × 5–10 µm vs. 8–12 × 4–6 µm), and larger conidia (9–13 × 5–7 µm vs. 8.5–9.5 × 4.5–5.5µm). The base pair difference between this isolate and *M. ellipsoidea* (CBS 136201) revealed ITS: 1.8% (10/553), *rpb2*: 1.9% (14/720), *tef1*-α: 5.1% (22/427), *tub2*: 0.3% (1/313). Therefore, *Memnoniella asteracearum* is introduced as a new species found on *Bidens pilosa* (Asteraceae) in northern Thailand.


**Note** **a, b** Appearance of colonies on host substrate. **c, d** Conidiophores with conidiogenous cells. **e–i** Conidia. **j** A germinating conidium. **k** Culture on MEA. Scale bars: **a** = 200 µm, **b** = 100 µm, **c** = 50 µm, **d** = 30 µm, **e–i** = 5 µm, **j** = 10 µm, **k** = 1 mm.

**Figure 3.76** *Memnoniella asteracearum* (MFLU 25-0084, holotype)

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

=*Memnoniella longistipitata* Li, Yang, Haugland & Vesper, Mycotaxon 85: 254 (2003)

=*Memnoniella oblongispora* C.G. Lin, McKenzie, Yong Wang bis & K.D. Hyde, Mycosphere 7(9): 1280 (2016)

=*Memnoniella chromolaenae* Mapook & K. D. Hyde, Fungal Diversity 101: 135 (2020)

*Index Fungorum number*: IF552085, *Facesoffungi number*: FoF09573, Figure 3.77

Saprobic on dead stems of *Bidens pilosa* (Asteraceae). **Sexual morph**: undetermined. **Asexual morph**: *Colonies* black and velvety on the substrate surface. *Conidiophores* 40–65 × 3–5 µm ($\overline{x}$ =51.9 × 4 µm, n = 5), macronematous, mononematous, often simple, erect, straight or flexuous, irregularly or sympodially branched, rough, thick-walled, septate, olivaceous brown, bearing a crown of phialides at the apex. *Conidiogenous cells* 6–7 × 3–5 µm ($\overline{x}$ = 6.4 × 4.1 µm, n = 5), monophialidic, discrete, determinate, terminal, globose to subglobose, sometimes ellipsoidal, smooth, hyaline to olive-brown. *Conidia* 4–6 × 4–6 µm ($\overline{x}$ = 5.6 × 4.9 µm, n = 20), unicellular, simple, catenate, acrogenous, globose to subglobose, aseptate, olivaceous-grey to black, smooth, thick-walled, formed 5-10 conidia in long chains.

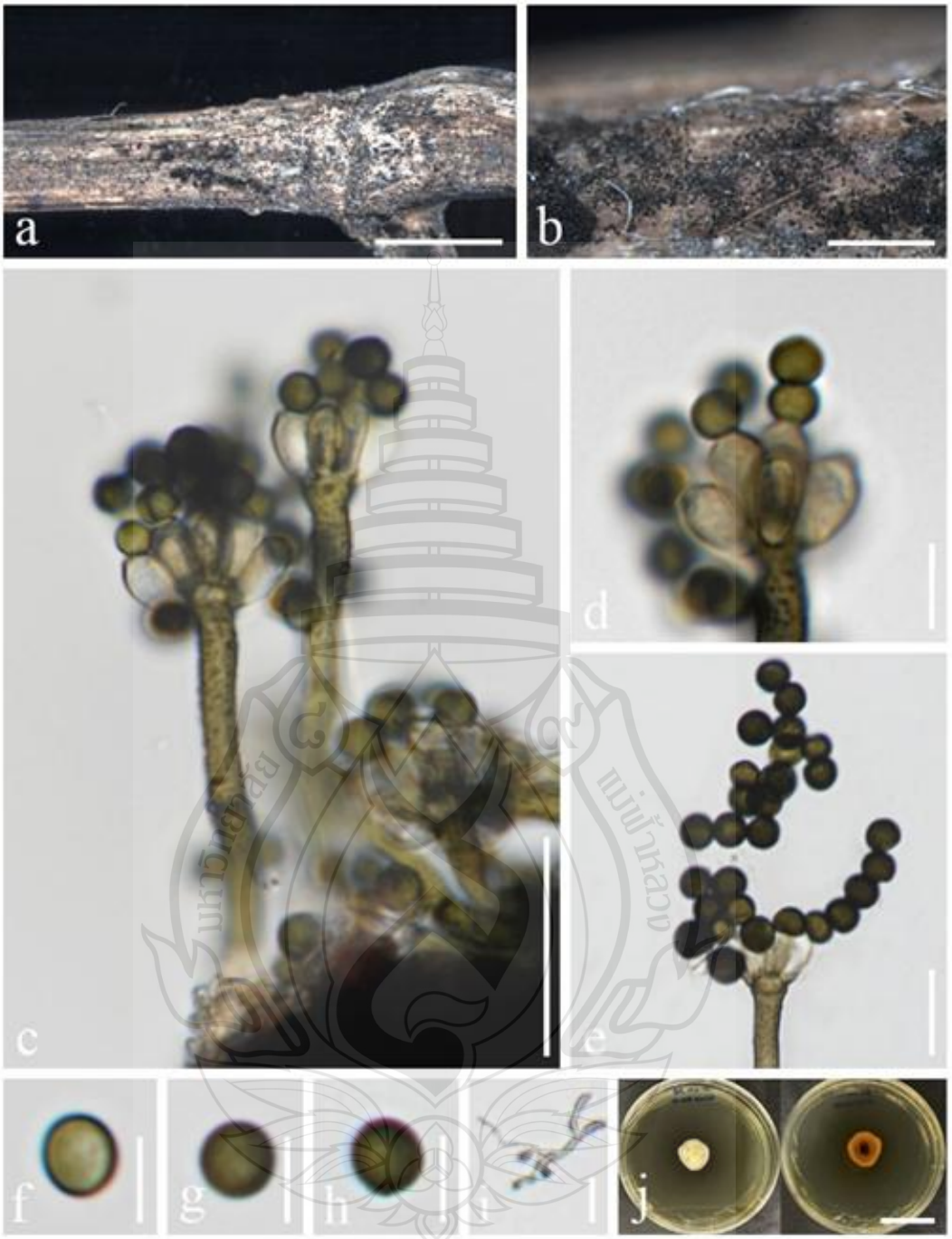
*Culture characteristics*: Conidia germinating on MEA within 24 hours, reaching 30 mm after 10 days at room temperature, irregular, entire, concentric, flat, white, changed to red on the culture media (MEA); irregular, concentric, pink to red in the reverse surface.

*Material examined*: Thailand, Chiang Rai Province, Nang Lae District, on dead stems of *Bidens pilosa* (Asteraceae), 3 August 2023, Zin Hnin Htet (BP-NL-11, MFLU 25-0086, new host); living culture MFLUCC 25-0165. *ibid*., Mueang Chiang Rai District, on dead stems of *Chromolaena odorata* (Asteraceae), 12 May 2023, Zin Hnin Htet (CO-DP-1, MFLU 25-0085, new host); living culture MFLUCC 25-0167.

*Known host and distribution*: *Morus* (Moraceae) in India (Subramanian 1954), *Musa* sp. (Musaceae) in China (Samarakoon et al. 2021), *Oryza sativa* (Poaceae) in Cuba (Barrios & Pérez 2005), *Roystonea regia* (Arecaceae) in Cuba (Arnold 1986),

*Sanchezia* sp. (Acanthaceae) in India and Pakistan (Gond et al. 2013), *Tectona grandis* (Lamiaceae) in Thailand (Doilom et al. 2017).

*Notes*: The isolates MFLUCC 25-0165 and MFLUCC 25-0167 clustered with other isolates of *Memnoniella levispora* (MFLUCC 20-0189 and Menlev3308) with 100% ML and 1.00 BYPP support (Figure 3.75). Morphologically, the isolates are similar to *M. levirspora* in having straight or flexuous, macronematous, mononematous conidiophores bearing phialidic conidiogenous cells, and spherical to subspherical conidia. Comparisons of ITS, *tef*1- *α*, *rpb*2, and *tub*2 sequences between phylogenetically related species revealed no base pairs difference between species. Thus, the two isolates are identified as new host records of *M. levispora* on *Bidens pilosa* and *Chromolaena odorata*, respectively.




**Note** **a, b** Appearance of colonies on the host substrate. **c, d, e** Conidiophores and conidiogenous cells. **f, g, h** Conidia. **i** A germinating conidium. **j** Culture on MEA. Scale bars: **a, b** = 500 µm, **c** = 20 µm, **d–i** = 5 µm, **j** = 10 mm.

**Figure 3.77** *Memnoniella levispora* (MFLU 25-0086, a new host record)

**Subclass Xylariomycetidae** O.E. Erikss & Winka

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

### 3.2.20 Sporocadaceae Corda

Sporocadaceae was described by Corda (1842), with *Sporodocadus* as the type genus. Sporocadaceae species are reported as saprobes, pathogens, and endophytes from a variety of hosts and habitats (Nag Raj, 1993; Tanaka et al., 2011; Hyde et al., 2020a; 2020b; 2020c; Peng et al., 2022; Razaghi et al., 2024). Currently, Sporocadaceae comprises 35 genera (Hyde et al., 2024; Razaghi et al., 2024).

***Bartalinia*** Tassi

*Bartalinia* was established by Tassi (1900) and is classified within the family *Sporocadaceae* (Hyde et al., 2020a; 2020b; 2020c; Wijayawardene et al., 2022; Razaghi et al., 2024). *Bartalinia* is characterized by pycnidial conidiomata and fusiform, 3–4-septate, appendage bearing conidia with an acute or blunt apex (Senanayake et al., 2015). Currently, there are 20 species accepted in *Bartalinia* (Hyde et al., 2024). This study introduced *B. bidenticola* as a new species (Figure 3.78).

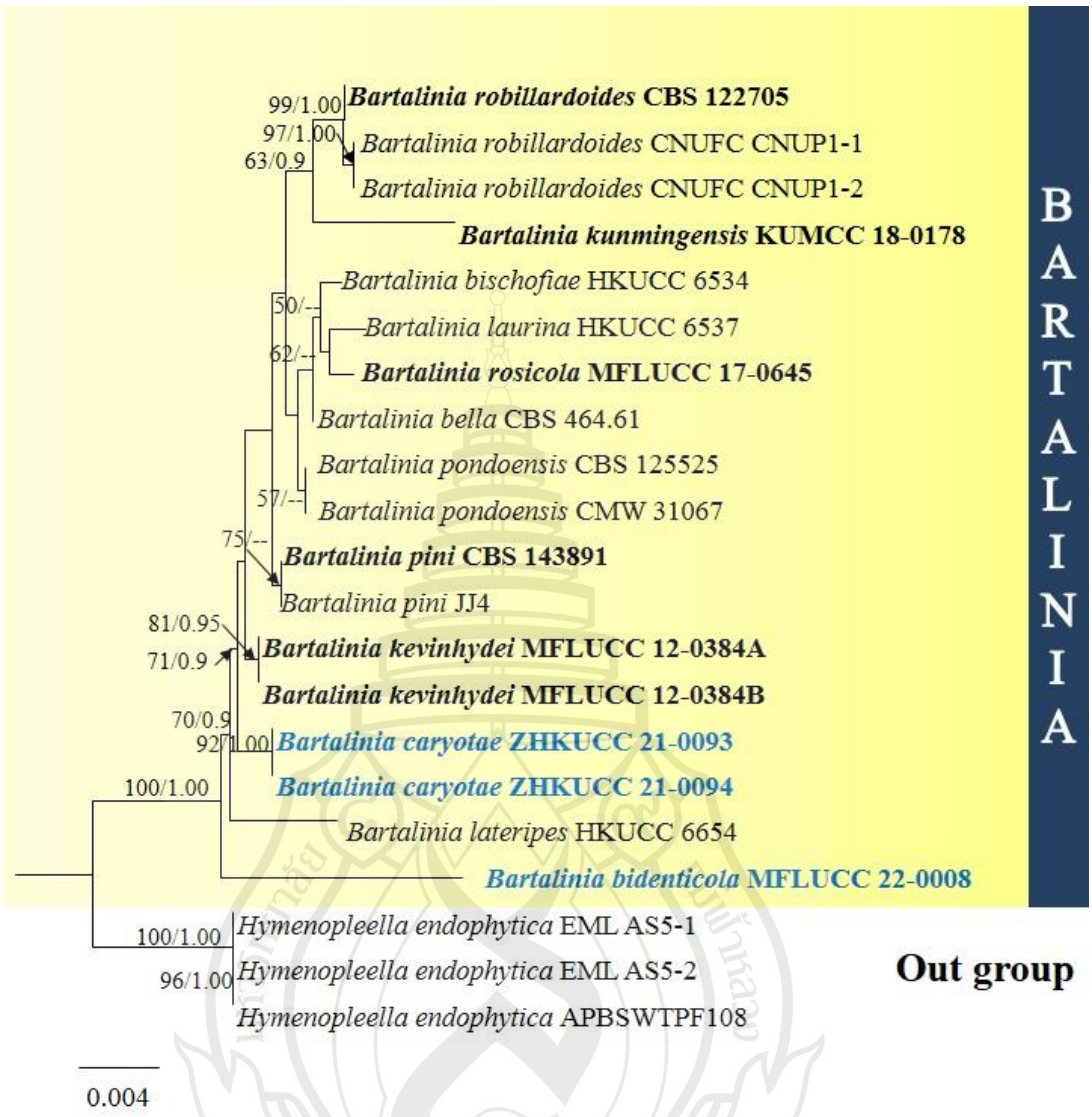



**Figure 3.78** Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data for *Bartalinia*. Ex-type strains are in bold and the new isolate is indicated in blue bold. *Hymenopleella endophytica* (APBSWTPF108, EML AS5-1, EML AS5-2) were used as the outgroup taxa

***Bartalinia bidenticola*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde, *Fungal Diversity* 117, 1–272 (2023)

*Index fungorum number*: IF559553, *Faces of fungi* number: FoF10766, Figure 3.79

*Holotype*: MFLU 22-0103

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

*Saprobic* on dead stems of *Bidens pilosa*. **Sexual morph:** Not observed. **Asexual morph:** *Conidiomata* 120–130 × 190–200 µm ($\bar{x}$= 123 × 196 µm, n = 5**)**, uniloculate, solitary, immersed to semi-immersed, globose to subglobose. *Ostiole* absent. *Peridium* 23–30 µm wide, 3–4 layered, comprised of brown cells of *textura globulosa***.** *Conidiogenous cells* 1–2 µm wide, filiform, hyaline. *Conidia* 23–27 × 4–6 µm, ($\bar{x}$ ± SD = 24.9 ± 0.8 × 4.9 ± 0.3 µm), fusoid to ellipsoid, straight to slightly curved at the apex, 4-septate, constricted ate the septa, brown in three middle cells and hyaline at the basal and apical cells; basal cells 2–4 µm long, hyaline, obconic to conic with a truncate base, thin-walled; three median cells 14–18 µm long, ($\bar{x}$ ± SD = 15.8 ± 0.8 µm), (second cell from the base pale brown, 6–7 µm long; third cell pale brown, 4–6 µm long; fourth cell pale brown, 4–7 µm long), doliiform, wall rugose, versicoloured; apical cells 3–6 µm long, hyaline, subcylindrical, smooth-walled; with 2–3 tubular appendages (mostly 2), unbranched, filliform (13–)17–24(–24) µm long, ($\bar{x}$ ± SD = 22.7 ± 2.7 µm); basal appendage single, tubular, unbranched, centric 4–8(–10) µm long.

*Culture characteristics*: Conidia germinating on MEA within 24 h, reaching 50 mm after 7 days at room temperature, irregular, undulate, concentric, flat, leathery surface, grey.

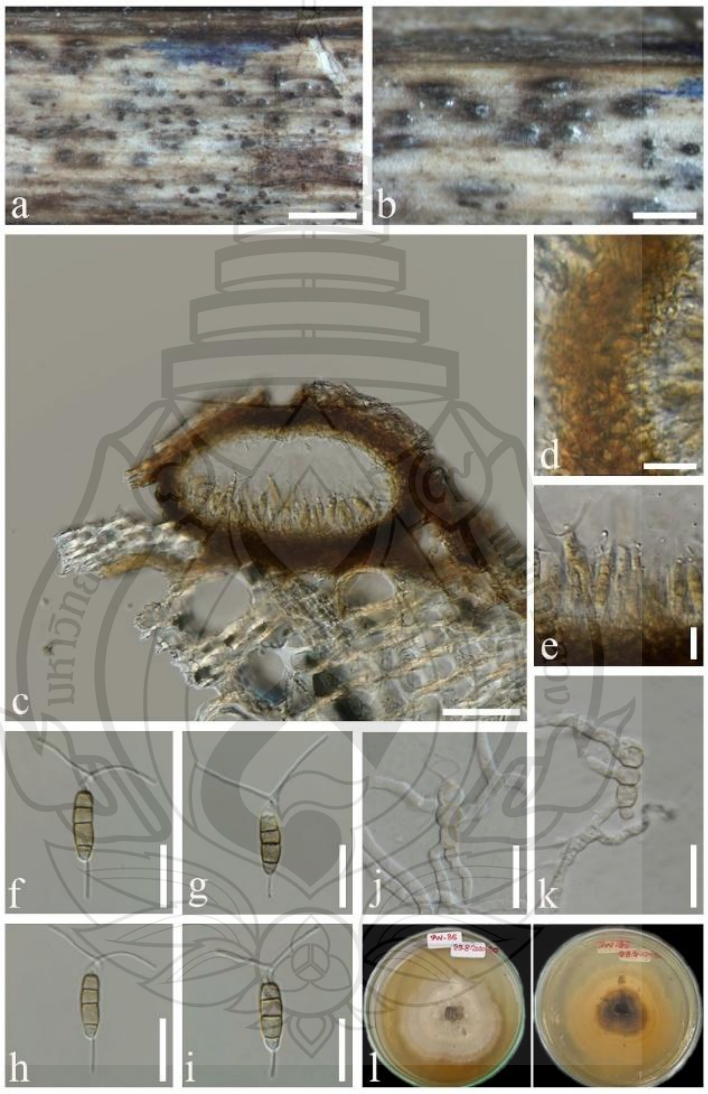
*Material examined*: Thailand, Chiang Rai Province, Mueang Chiang Rai District, on dead stems of *Bidens pilosa* (Asteraceae), 10 July 2020, Zin Hnin Htet (SW35, MFLU 22-0103, **holotype**), ex-type (MFLUCC 22-0008)

*GenBank*: **LSU**: ON715467; **ITS**: ON715520.

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

*Notes*: *Bartalinia bidenticola* (MFLUCC 22-0008) resembles *Bartalinia* in having subcylindrical to fusoid, pale yellow septate conidia, with an apical cell modified into branched appendages. According to the BLASTn results, the closest match for the LSU sequence of *Bartalinia bidenticola* (MFLUCC 22-0008) was *Bartalinia kevinhydei*

(MFLUCC 12-0384) with 97.32% similarity and the closest match for ITS sequence was *Bartalinia pondoensis* (CCTU 459) with 98.85% similarity. Phylogenetic analyses of a combined ITS and LSU sequence dataset (Figure 3.78) show that *Bartalinia bidenticola* (MFLUCC 22-0008) is phylogenetically well distinguished and branched off from all other species in *Bartalinia* with ML = 100% and BYPP = 1.00 support. Therefore, this isolate is identified as a new species which was found from *Bidens pilosa*.




**Source** Jayawardena et al. (2022)

**Note** **a, b** Appearance of conidiomata on host substrate. **c** Section through conidioma. **d** Peridium. **e** Conidia and conidiogenous cells. **f–i** Conidia. **j–k** Germinating conidia. **l** Culture on MEA. Scale bars: a = 300 µm, b = 200 µm, c = 50 µm, d = 20 µm, e = 10 µm, f–k = 20 µm

**Figure 3.79** *Bartalinia bidenticola* (MFLU 22-0103, holotype)

## 3.3 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 findings 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).

**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. ***Dictyocheirospora 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 (This study)

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

Thailand (This study)

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

Thailand (This study)

8. ***Montagnula bidentis*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (This study)

9. ***Pseudoithomyces 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

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

Thailand (This study)

**Periconiaceae** Nann

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

Thailand (This study)

**Phaeosphaeriaceae** M.E. Barr

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

Thailand (This study)

**Pleosporaceae** Nitschke

13. ***Alternaria*** **sp.**

Brazil (Mendes, 1998), Venezuela (Urtiaga, 2004)

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

Kenya (Nattrass, 1961)

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

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

Thailand (This study)

16. ***Pseudoroussoella bidenticola*** Htet, A. Mapook & K.D. Hyde, MycoKeys 111: 139 (2024)

Thailand (This study)

**Sporormiaceae** Munk

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

Thailand (This study)

**Tetraplosphaeriaceae** Kaz. Tanaka & K. Hiray

18. ***Tetraploa aristata*** Berk. & Broome, Ann. Mag. nat. Hist., Ser. 2 5: 459 (1850)

Cuba (Mercado Sierra, 1984)

**Torulaceae** Corda

19. ***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

20. ***Cercospora bidentis*** Tharp, Mycologia 9(2): 108 (1917)

Brazil (Mendes, 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 (Nattrass, 1961), Malaysia (Turner, 1971), Mauritius (Wiehe, 1948), Papua New Guinea (Shaw, 1984), Samoa (McKenzie, 1996), South Africa (Crous & Braun, 1996), Taiwan (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)

21. ***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).

22. ***Cercospora maculicola*** Thirum. & Govindu, Sydowia 8(1-6): 344 (1954)

Brazil (Guatimosim et al., 2015), India (Thirumalachar & Govindu, 1954; Vasudeva, 1963; Kamal 2010)

23. ***Cercospora bidentis-pilosae*** Sawada, Rep. Govt Res. Inst. Dep. Agric., Formosa 85: 98 (1943)

Taiwan (Chupp, 1954)

24. ***Mycosphaerella*** **sp.**

Cuba (Urtiaga, 1986), Venezuela (Urtiaga, 1986)

25. ***Pseudocercospora vitis*** (Lév.) Speg., Anal. Mus. nac. B. Aires, Ser. 3 13: 438 (1910) [1911]

Brazil (Pereira et al., 2019)

26. ***Ramularia concomitans*** Ellis & Holw., in Ellis & Everhart, J. Mycol. 4(1): 2 (1888)

China (Zhang et al., 2003; Zhang, 2006)

27. ***Septoria balansae*** Speg., Anal. Soc. cient. argent. 22(4): 196 (1886)

Colombia (Dennis, 1970)

**Myriangiales** Starbäck

**Elsinoaceae** Höhn. ex Sacc. & Trotter

28. ***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)

29. ***Sphaceloma sp.*** (=*Elsinoe* sp.)

Zimbabwe (Whiteside, 1966)

30. ***Sphaceloma bidentis*** (Bitanc. & Jenkins) X.L. Fan & Crous, Stud. Mycol. 87: 14 (2017)

Brazil (Mendes, 1998)

**Dothideomycetes** orders incertae sedis

**Botryosphaeriales** C.L. Schoch, Crous & Shoemaker

**Botryosphaeriaceae** Theiss. & Syd.

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

Cuba (Urtiaga, 2004); Egypt (Mullen et al., 1991); Thailand (this study)

**Phyllostictaceae** Fr.

32. ***Phyllosticta*** **sp.**

Brazil (Mendes, 1998), Cuba (Urtiaga, 1986)

**Dothideomycetes** families incertae sedis

**Englerulaceae** Henn

33. ***Sarcinella pulchra*** (Sacc.) Seifert, in Rossman et al., IMA Fungus 7(2): 303 (2016) (=*Schiffnerula pulchra*)

Cuba (Mercado Sierra, 1984)

**Kirschsteiniotheliales** genera incertae sedis

34. ***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

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

Thailand (This study)

36. ***Diaporthe phaseolorum*** (Cooke & Ellis) Sacc., *Syll. fung.* (Abellini) 1: 692 (1882) (=*Diaporthe phaseolorum* f. sp. *meridionalis*)

Brazil (Mendes, 1998)

**Subclass Hypocreomycetidae** O.E. Erikss. & Winka

**Glomerellales** Chadef. ex Réblová, W. Gams & Seifert

**Glomerellaceae** Locq. ex Seifert & W. Gams

37. ***Colletotrichum*** **sp.**

United States (Alfieri et al., 1984)

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

Thailand (This study)

39. ***Colletotrichum bidentis*** Damm, Guatim. & B.S. Vieira, in Damm, Cannon, Liu, Barreto, Guatimosim & Crous, Fungal Diversity 61: 34 (2013)

Brazil (Guatimosim et al., 2015)

40. ***Colletotrichum dematium*** (Pers.) Grove, J. Bot., Lond. 56: 341 (1918)

Cuba (Urtiaga, R. 1986; Jayawardena et al., 2016), Venezuela (Urtiaga, R. 1986; Jayawardena et al., 2016)

41. ***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

42. ***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.

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

Thailand (This study)

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

Thailand (This study)

**Stachybotryaceae** Lombard & Crous

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

Thailand (This study)

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

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

Thailand (Mapook et al., 2020, 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

45. ***Nigrospora oryzae*** (Berk. & Broome) Petch, J. Indian bot. Soc. 4: 24 (1924)

Brazil (Mendes, 1998)

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

46. ***Bartalinia bidenticola*** Htet, Mapook & K.D. Hyde, in Jayawardena et al., Fungal Diversity 117: 147 (2023) [2022]

Thailand (Jayawardena et al., 2023)

**Class Leotiomycetes** O.E. Erikss. & Winka

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

**Helotiales** Nannf

**Erysiphaceae** Tul. & C. Tul.

47. ***Erysiphe galeopsidis*** (DC.) U. Braun, Schlechtendalia 3: 50 (1999)

Cuba (Amano, 1986)

48. ***Golovinomyces ambrosiae*** (Schwein.) U. Braun & R.T.A. Cook, Mycol. Res. 113(5): 628 (2009)

China (Mukhtar et al., 2022)

49. ***Neoerysiphe cumminsiana*** (U. Braun) U. Braun, Schlechtendalia 3: 50 (1999)

Argentina (Braun et al., 2001), Brazil (Cook et al., 2006; Guatimosim et al., 2015)

50. ***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)

51. ***Podosphaera fuliginea*** (Schltdl.) U. Braun & S. Takam., Schlechtendalia 4: 29 (2000) (=*Sphaerotheca fuliginea*)

China (Tai, 1979), India (Pande, 2008), South Africa (Gorter, 1981)

52. ***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)

53. ***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

54. ***Botrytis cinerea*** Pers., Syn. meth. fung. (Göttingen) 2: 690 (1801)

China (Zhang, 2006)

55. ***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

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

Zimbabwe (Whiteside, 1966)

**Cantharellales** Gäum.

**Ceratobasidiaceae** G.W. Martin

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

Brazil (Mendes, 1998)

**Subphylum Ustilaginomycotina** Doweld

**Class Exobasidiomycetes** Begerow, M. Stoll & R. Bauer

**Entylomatales** R. Bauer & Oberw

**Entylomataceae** R. Bauer & Oberw

58. ***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 (Piepenbring, 1999), Uganda (Zambettakis, 1971), United States (Zundel, 1953; Piepenbring, 1999), Zambia (Vanky & Vanky, 2002), Zimbabwe (Zambettakis, 1971).

59. ***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)

60. ***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 (Anonymous, 1979), Thailand (Shivas et al., 2007), Zambia (Riley, 1956), Zimbabwe (Whiteside, 1966; Vanky & Vanky, 2002)

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

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

62. ***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

63. ***Uredo* sp.**

Cuba (Urtiaga, 1986)

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

Australia (McAlpine, 1906)

65. ***Uromyces* sp.**

Colombia (Salazar-Yepes et al., 2002)

66. ***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; Urtiaga, 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., 2002), 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 (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 Zorron de Rosengurtt, 1967), Venezuela (Chardon & Toro, 1934; Kern et al., 1934; Urtiaga, 1986), Vietnam (Kaneko, 207), Yemen (Gjaerum, 1987), Zimbabwe (Whiteside, 1966)

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

Brazil (Jackson, 1932; Hennen et al., 1982; Mendes, 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 (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. Beketov

**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)

## 3.4 Checklist of Fungi Associated with *Chromolaena odorata*

The USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr and 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).

**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, Rodríguez-Hernández & Mena Portales, 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, Farr & Lip, 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 Breeyen 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 Breeyen et al., 2006; Videira et al., 2017)

7. ***Passalora*** **sp.**

Jamaica, USA (den Breeyen et al., 2006)

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

= *Phaeoramularia capsicicola* (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 Breeyen 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 el 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 Breeyen 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 Breeyen et al., 2006; Guatimosim, Schwartsburd, Barreto & Crous, 2016), USA (den Breeyen 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, Thirumalachar & Nag Raj, 1970; Yen, 1974; Urtiaga, 1986; Barreto & Evans 1994), Andaman Islands (Hosagoudar & Mathew 2000), India (Kamal, 2010), Thailand (Meeboon, Hidayat & To-anun, 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, Wingfield & Morris, 1997; Liu & Guo 1998; Guo, 1999a, b; Zhuang et al., 2001), India (Barreto & Evans 1994), Laos (Phengsintham, Chukeatirote, Abdelsalam, Hyde & Braun, 2010), Malaysia (Barreto & Evans 1994), Myanmar (Thaung, 1984; Barreto & Evans 1994), Taiwan (Kirschner and 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 (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, Quaedvlieg, Shin & Crous, 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. ***Rhytidhysteron bruguierae*** Dayarathne, in Dayarathne et al., Mycosphere 11(1): 20 (2020)

Thailand (Dayarathne et al., 2020; Mapook et al., 2020; this study)

26. ***Rhytidhysteron 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 cassiicola*** (Berk. & M.A. Curtis) C.T. Wei, Mycol. Pap. 34: 5 (1950)

Palau (Dixon, Schlub, Pernezny & Datnoff, 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)

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. ***Trematеia asteracearum*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

48. ***Trematеia chiangraiensis*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

49. ***Trematеia chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

50. ***Trematеia thailandensis*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

**Hermatomycetaceae** Locq.

51. ***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.

52. ***Lophiostoma longiappendiculata*** (Mapook & K.D. Hyde) Andreasen, Jaklitsch & Voglmayr, 2021 in Andreasen M et al., Persoonia 46 (2021)

= *Pseudocapulatispora longiappendiculata* Mapook and K.D. Hyde

(Mapook et al., 2020; this study)

53. ***Flabellascoma minimum*** A. Hashim., K. Hiray. & Kaz. Tanaka, in Hashimoto et al., Studies in Mycology 90: 169 (2018)

Thailand (Mapook et al., 2020)

54. ***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

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

Thailand (this study)

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

56. ***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)

**Nigrograna**ceae Jaklitsch & Voglmayr

57. ***Nigrograna chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

**Neomassarinaceae** Mapook & K.D. Hyde

58. ***Neomassarina chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

59. ***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.,

60. ***Neopyrenochaeta chiangraiensis*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

61. ***Neopyrenochaeta chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

62. ***Neopyrenochaeta thailandica*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

63. ***Neopyrenochaeta triseptatispora*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

**Phaeosphaeriaceae** M.E. Barr

64. ***Leptospora chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

65. ***Leptospora phraeana*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

66. ***Leptospora thailandica*** Phukhams. & K.D. Hyde, in Hyde et al., Fungal Diversity. 80: 100 (2016)

Thailand (Mapook et al., 2020)

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

Thailand (Mapook et al., 2020)

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

Thailand (Mapook et al., 2020)

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

Thailand (Htet et al., 2023)

70. ***Neoophiobolus chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

71. ***Ophiobolus ipohensis*** J.M. Yen, Cahiers Pacif. 13: 277 (1969)

Malaysia (Yen, 1969; Barreto & Evans 1994)

72. ***Ophiosphaerella eupatorii*** J.M. Yen, Cahiers Pacif. 13: 278 (1969)

Malaysia (Yen, 1969; Barreto & Evans 1994)

73. ***Paraleptospora chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

74. ***Paraleptospora chromolaenicola*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

75. ***Phaeosphaeria eupatoriicola*** J.M. Yen, Cahiers Pacif. 13: 279 (1969)

Malaysia (Yen, 1969; Barreto & Evans 1994)

76. ***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)

77. ***Pseudostaurosphaeria chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

78. ***Pseudostaurosphaeria chromolaenicola*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

79. ***Setophoma chromolaenae*** Quaedvl., Verkley, R.W. Barreto & Crous, Studies in Mycology 75: 373 (2013)

Brazil (Quaedvlieg et al., 2013)

80. ***Yunnanensis chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

**Pleosporaceae** Nitschke

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

Brazil (Barreto & Evans 1994)

**Pyrenochaetopsidaceae** Valenzuela-Lopez et al.,

82. ***Pyrenochaetopsis chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

**Roussoellaceae** J.K. Liu et al.,

83. ***Neoroussoella chromolaenae*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

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

Thailand (this study)

85. ***Pseudoneoconiothyrium thailandicum*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

86. ***Pseudoneoconiothyrium thailandicum*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

87. ***Pseudoroussoella chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

88. ***Pseudoroussoella elaeicola*** (Konta & K.D. Hyde) Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

89. ***Setoarthopyrenia chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

90. ***Xenoroussoella triseptata*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

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

91. ***Chromolaenomyces appendiculatus*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

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

Thailand (this study)

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

Thailand (Mapook et al., 2020)

94. ***Pseudothyridariella thailandica*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

**Torulaceae** Corda

95. ***Dendryphion hydei*** J.F. Li, Phookamsak & Jeewon, PLoS ONE 15(2): e0228067, 6 (2020)

Thailand (this study)

96. ***Torula canangae*** N.I. de Silva, Lumyong & K.D. Hyde, Mycosphere 13(1): 1012 (2022)

Thailand (this study)

97. ***Torula chromolaenae*** JF. 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)

98. ***Torula fici*** Crous, in Crous et al., IMA Fungus 6(1): 192 (2015)

Thailand (Li et al., 2017; Mapook et al., 2020; this study)

99. ***Torula hydei*** J.F. Li, Phookamsak & Jeewon, in Li, Jeewon, Mortimer, Doilom, Phookamsak & Promput, PLoS ONE 15(2): e0228067, 8 (2020)

Thailand (Li et al. 2020)

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

Thailand (Li et al., 2017; this study)

101. ***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**

102. ***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.,

103. ***Aplosporella chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

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

Thailand (Mapook et al., 2020; this study)

105. ***Aplosporella artocarpi*** Trakun., L. Lombard & Crous, in Trakunyingcharoen, Lombard, Groenewald, Toanun & Crous, Persoonia 34: 91 (2014)

Thailand (Jayawardena et al., 2023)

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

106. ***Dothiorella asteracearum*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

107. ***Dothiorella chromolaenae*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

108. ***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)

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)

**Dyfrolomycetales** K.L. Pang et al.,

**Pleurotremataceae** Walt. Watson (=Dyfrolomycetaceae K.D. Hyde et al.,)*

112. ***Dyfrolomyces chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

**Muyocopronales** Mapook et al.,

**Muyocopronaceae** K.D. Hyde

113. ***Muyocopron chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

114. ***Muyocopron chromolaenicola*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

115. ***Muyocopron 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**

**Dysrhynchisceae** 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 and 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

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

Thailand (this study)

126. ***Diaporthe chromolaenae*** Mapook & K.D. Hyde

Thailand (Mapook et al., 2020)

127. ***Diaporthe chromolaenicola*** Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde

Thailand (this study)

128. ***Diaporthe eupatoriicola*** Petr., Annls mycol. 20(3/4): 147 (1922)

Sri Lanka (Barreto & Evans 1994)

**Diaporthomycetidae families incertae sedis**

**Sporidesmiaceae** Fr.

129. ***Sporidesmium* sp.**

West Indies (Minter et al., 2001)

**Subclass Hypocreomycetidae** O.E. Erikss. & Winka

**Glomerellales** Chadef. ex Réblová et al.,

**Glomerellaceae** Locq. ex Seifert & W. Gams

130. ***Colletotrichum* sp.**

Cambodia - (Barreto & Evans 1994), Venezuela - (Urtiaga, 2004)

131. ***Colletotrichum gigasporum*** Rakotonir. & Munaut, in Rakotoniriana, Scauflaire, Rabemanantsoa, Urveg-Ratsimamanga, Corbisier, Quetin-Leclercq, Declerck & Munaut, Mycol. Progr. 12(2): 407 (2012) [2013]

Thailand (this study)

132. ***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**

133. ***Clonostachys byssicola*** Schroers, Stud. Mycol. 46: 80 (2001)

Thailand (Chethana et al., 2021)

134. ***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.,

135. ***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.

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

South America (Viegas, 1961)

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

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

138. ***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.

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

Thailand (this study)

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

141. ***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)

125. ***Fusarium pallidoroseum*** (Cooke) Sacc., Syll. fung. (Abellini) 4: 720 (1886)

Nigeria (Richardson, 1990)

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

Nigeria (Richardson, 1990)

**Stachybotryaceae** Lombard & Crous

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

Thailand (This study)

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

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

Thailand (Mapook et al., 2020, this study)

**Subclass Sordariomycetidae** O.E. Erikss & Winka

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

**Meliolaceae** G.W. Martin ex Hansf.

129. ***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)

130. ***Meliola*** **sp.**

India (Barreto & Evans 1994)

131. ***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.,

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

Thailand (Mapook et al., 2020)

**Xylariales** Nannf.

**Cainiaceae** J.C. Krug

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

Thailand (Mapook et al., 2020)

**Sordariomycetes genera incertae sedis**

134. ***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 unclassified**

**Ascomycota genera incertae sedis**

135. ***Alysidiopsis yunnanensis*** Y.L. Guo & X.J. Liu, Acta Mycol. Sin. 11(3): 213 (1992)

China (Zhuang et al., 2001)

136. ***Hansfordia pulvinata*** (Berk. & M.A. Curtis) S. Hughes 1958

= *Dicyma pulvinata* (Berk. & M.A. Curtis) Arx 1981

West Indies (Minter et al., 2001)

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

Brazil (Barreto & Evans 1994)

138. ***Redbia* sp.**

West Indies (Minter et al., 2001)

**Phylum Basidiomycota** R.T. Moore

**Class Agaricomycetes** Doweld

**Cantharellales** Gäum.

**Ceratobasidiaceae** G.W. Martin

139. ***Rhizoctonia solani*** J.G. Kühn, Ann. Sper. agr., N.S.: 224 (1858)

= *Thanatephorus cucumeris* (A.B. Frank) Donk, Reinwardtia 3: 376 (1956)

Taiwan (Sawada, 1931)

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

**Sebacinaceae** K. Wells & Oberw.

140. ***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

141. ***Coleosporium eupatorii*** Arthur, Bull. Torrey bot. Club 33: 31 (1906)

China (Tai, 1979; Barreto & Evans 1994; Zhuang et al., 2005)

142. ***Coleosporium steviae*** Arthur, Bot. Gaz. 40: 197 (1905)

China (Barreto & Evans 1994), Mexico (Gallegos & Cummins 1981)

**Cronartiaceae** Dietel

143. ***Cronartium praelongum*** G. Winter, Hedwigia 26: 24 (1887)

Colombia (Chardon & Toro 1930; Kern, Thurston-Jr & Whetzel 1933b), Venezuela (Chardon & Toro 1934; Kern, Thurston-Jr & Whetzel, 1934)

**Pucciniales genera incertae sedis**

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

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

**Pucciniosiraceae** Cummins & Y. Hirats.

145. ***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 Cardona, 1996; Pardo Cardona, 1998), Costa Rica (Arthur, 1918; Berndt, 2004) Guatemala (Arthur, 1918), Mexico (Gallegos & Cummins 1981), Panama (Piepenbring, 2006), West Indies (Minter et al., 2001)

## 3.5 Discussion

### 3.5.1 Antibacterial Activity of Fungi on *Bidens Pilosa* and *Chromolaena odorata*

The bacteria *Bacillus subtilis* (gram-positive), *Escherichia coli* (gram-negative), and *Staphylococcus aureus* (gram-positive) were all susceptible to the antibacterial action of fungi isolated from *Bidens pilosa*. Among 22 fungal species identified on *Bidens pilosa*, 15 species inhibited the growth of *B. subtilis*, 14 species were effective against *S. aureus*, and 11 species inhibited *E. coli*. Among them, two fungal species, *Neoroussoella entadae* and *Remotididymella fici-microcarpae* showed no inhibition zone against all three test organisms (Figure 3.43). Certain fungal species, including *Chromolaecinola siamensis*, *C. thailandensis*, *Periconia byssoides*, and *Forliomyces bidentis*, were shown to have activity against only Gram-positive bacteria, *B. subtilis* and *S. aureus*. However, certain fungal species had broad-spectrum antibacterial activity, which can inhibit the growth of both gram-positive and gram-negative bacteria (Table 3.1).

Similarly, fungal isolates from *Chromolaena odorata* showed antibacterial potential against the same bacterial strains. Among the 34 fungal species identified on *Chromolaena odorata*, eight species were not subjected to antibacterial screening due to the lack of viable cultures. The findings show that eleven fungal species inhibited the growth of *B. subtilis*, six species were effective against *S. aureus*, and ten 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 (Figure 4.38). Certain fungal species, including *Diaporthe biconispora*, *Lasiodiplodia henanica*, and *Torula canangae* showed antibacterial activity against both gram-positive and gram-negative bacteria. However, there were no specific fungal isolates that could inhibit either gram-positive bacteria or gram-negative bacteria (Table 3.2).

**Table 3.1** Preliminary screening of fungi on *Bidens pilosa* for antibacterial properties

| Number | Species name | *B. subtilis* | *E. coli* | *S. aureus* |
|---|---|---|---|---|
| 1. | *Albifimbria bidentis* | 13mm | 11mm | no inhibition |
| 2. | *Bahusandhika bidentis* | 15mm | 14mm | 15mm |
| 3. | *Bartalinia bidenticola* | Not studied | | |
| 4. | *Chromolaenicola chaingraiensis* | 10mm | no inhibition | no inhibition |
| 5. | *Chromolaenicola siamensis* | 18mm | no inhibition | 9mm |
| 6. | *Chromolaenicola thailandensis* | 17mm | no inhibition | 10mm |
| 7. | *Colletotrichum truncatum* | 19mm | 12mm | 18mm |
| 8. | *Dendryphion hydei* | no inhibition | 14mm | 20mm |
| 9. | *Diaporthe biconispora* | 15mm | 12mm | 18mm |
| 10. | *Dictyocheirospora nabanheensis* | 9 mm | no inhibition | no inhibition |
| 11. | *Forliomyces bidentis* | 19mm | no inhibition | 10mm |
| 12. | *Fusarium bidentis* | 13mm | 15mm | 17mm |
| 13. | *Lasiodiplodia theobromae* | no inhibition | 13mm | 19mm |
| 14. | *Leptospora thailandica* | 15 mm | no inhibition | no inhibition |
| 15. | *Montagnula bidentis* | no inhibition | 9mm | no inhibition |
| 16. | *Neoroussoella entadae* | no inhibition | no inhibition | no inhibition |
| 17. | *Periconia byssoides* | 15mm | no inhibition | 13mm |
| 18. | *Pseudoithomyces chartarum* | no inhibition | no inhibition | 11mm |
| 19. | *Pseudoroussoella bidenticola* | 18mm | 12mm | 13mm |
| 20. | *Remotididymella anthropophila* | 12mm | 14mm | 15mm |
| 21. | *Remotididymella fici-microcarpae* | no inhibition | no inhibition | no inhibition |
| 22. | *Sarocladium bidentis* | 19mm | 16mm | 22mm |

**Table 3.2** Preliminary screening of fungi on *Chromolaena odorata* for antibacterial properties

| Number | Species name | *B. subtilis* | *E. coli* | *S. aureus* |
|---|---|---|---|---|
| 1. | *Acrocalymma pterocarpi* | Not studied | | |
| 2. | *Aplosporella artocarpi* | Not studied | | |
| 3. | *Aplosporella hesperidica* | Not studied | | |
| 4. | *Austropleospora chromolaenae* | no inhibition | no inhibition | no inhibition |
| 5. | *Bahusandhika indica* | no inhibition | no inhibition | no inhibition |
| 6. | *Chromolaenicola nanensis* | no inhibition | no inhibition | no inhibition |
| 7. | *Colletotrichum gigasporum* | 14mm | no inhibition | no inhibition |
| 8. | *Dendryphion hydei* | 14mm | 11mm | no inhibition |
| 9. | *Diaporthe asteracearum* | 10mm | 9mm | no inhibition |
| 10. | *Diaporthe biconispora* | 17mm | 18mm | 21mm |

**Table 3.2** (continued)

| Number | Species name | *B. subtilis* | *E. coli* | *S. aureus* |
|---|---|---|---|---|
| 11. | *Acrocalymma pterocarpi* | Not studied | | |
| 12. | *Aplosporella artocarpi* | Not studied | | |
| 13. | *Aplosporella hesperidica* | Not studied | | |
| 14. | *Austropleospora chromolaenae* | no inhibition | no inhibition | no inhibition |
| 15. | *Bahusandhika indica* | no inhibition | no inhibition | no inhibition |
| 16. | *Chromolaenicola nanensis* | no inhibition | no inhibition | no inhibition |
| 17. | *Colletotrichum gigasporum* | 14mm | no inhibition | no inhibition |
| 18. | *Dendryphion hydei* | 14mm | 11mm | no inhibition |
| 19. | *Diaporthe asteracearum* | 10mm | 9mm | no inhibition |
| 20. | *Diaporthe biconispora* | 17mm | 18mm | 21mm |
| 21. | *Diaporthe chromolaenicola* | 14mm | 12mm | no inhibition |
| 22. | *Dothiorella asteracearum* | no inhibition | no inhibition | no inhibition |
| 23. | *Dothiorella chromolaenae* | no inhibition | no inhibition | no inhibition |
| 24. | *Fusarium chromolaenae* | Not studied | | |
| 25. | *Kalmusia thailandica* | Not studied | | |
| 26. | *Lasiodiplodia henanica* | 16mm | 17mm | 25mm |
| 27. | *Lasiodiplodia theobromae* | 11mm | no inhibition | no inhibition |
| 28. | *Lophiostoma longiappendiculatum* | Not studied | | |
| 29. | *Memnoniella asteracearum* | 17mm | 16mm | 20mm |
| 30. | *Memnoniella levispora* | 10mm | no inhibition | 13mm |
| 31. | *Murichromolaenicola thailandensis* | no inhibition | no inhibition | no inhibition |
| 32. | *Neodendryphiella mali* | Not studied | | |
| 33. | *Neoroussoella entadae* | 13mm | 17mm | 14mm |
| 34. | *Pseudoithomyces chartarum* | no inhibition | 10mm | no inhibition |
| 35. | *Pseudolophiostoma chromolaenicola* | Not studied | | |
| 36. | *Pseudoneoconiothyrium chromolaenae* | no inhibition | no inhibition | no inhibition |
| 37. | *Pseudoneoconiothyrium thailandicum* | no inhibition | no inhibition | no inhibition |
| 38. | *Pseudothyridariella asteracearum* | No inhibition | No inhibition | No inhibition |
| 39. | *Pseudothyridariella thailandica* | No inhibition | No inhibition | No inhibition |
| 40. | *Rhytidhysteron bruguierae* | Not studied | | |
| 41. | *Torula canangae* | 18mm | 10mm | 21mm |
| 42. | *Torula fici* | Not studied | | |
| 43. | *Torula mackenziei* | Not studied | | |
| 44. | *Trematheia asteracearum* | Not studied | | |

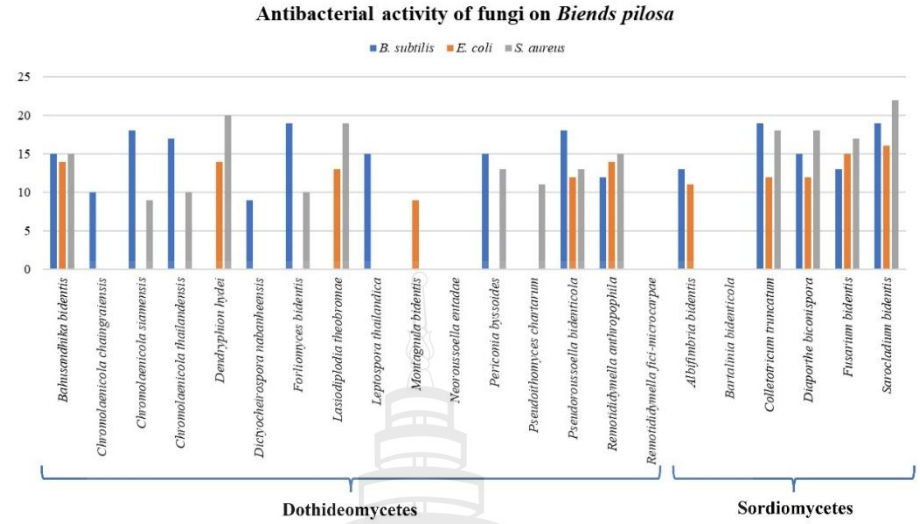



**Figure 3.80** Antibacterial activity of fungi on *Bidens pilosa* in this study

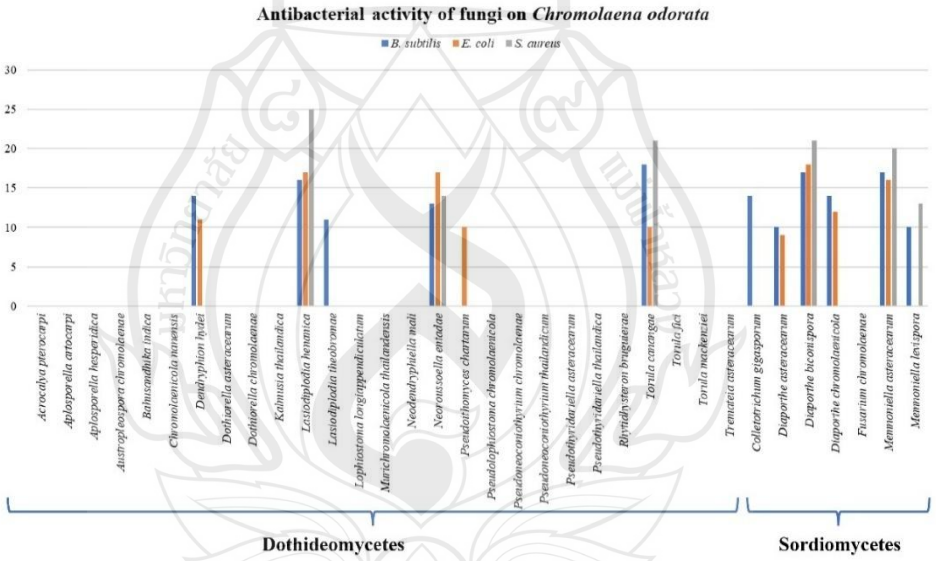



**Figure 3.81** Antibacterial activity of fungi on *Chromolaena odorata* in this study

### 3.5.2 Checklist of Fungi on *Bidens Pilosa* and *Chromolaena odorata*

A total of 76 fungal taxa has been documented on *Bidens pilosa*, which includes 10 unclassified species and new isolates identified in my research. From this total, I have observed and reported 22 distinct fungal species. According to the USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2025) and pertinent literature, 54 fungal species have been previously recorded. These species are distributed 18 orders, 33 families, and 44 genera, representing the phyla Ascomycota, Basidiomycota, Glomeromycota, and Oomycota. The Ascomycota phylum is the most dominant, comprising 32 genera across 23 families. My research contributes to the understanding of the diversity of saprobic fungi included in this checklist (Figure 3.81).

In comparison, A total of 145 fungal taxa has been documented on *Chromolaena odorata*, which includes 14 unclassified species and new isolates identified in my research. From this total, I have observed and reported 35 fungal species from my research. According to the USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2025) and pertinent literature, 109 fungal species have been previously recorded. These species are distributed 21 orders, 48 families, and 95 genera, representing two phyla Ascomycota, Basidiomycota. The Ascomycota phylum is the most dominant on *Chromolaena odorata* with 89 genera across 43 families. My research contributes to the understanding of the diversity of saprobic fungi included in this checklist (Figure 3.82).

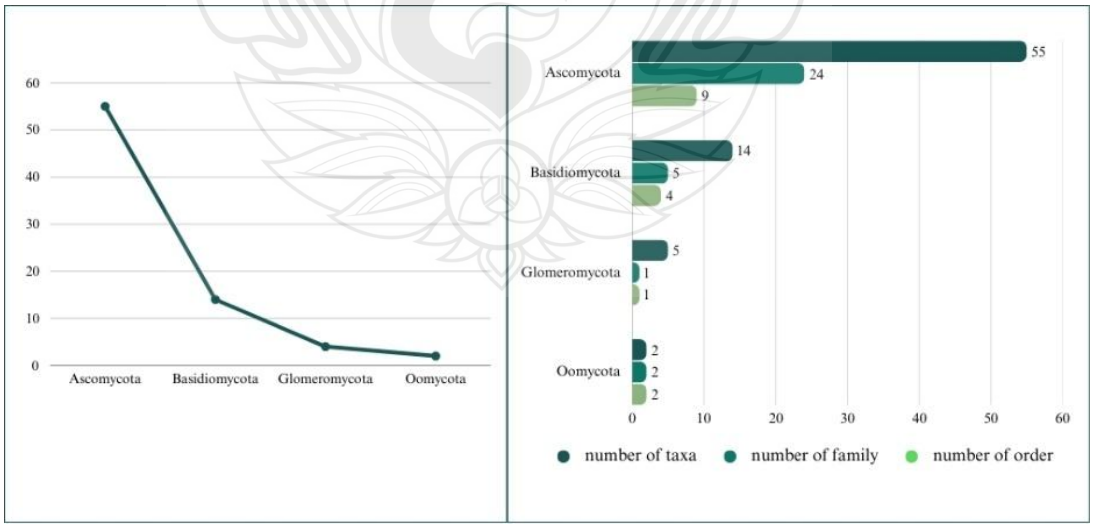



**Figure 3.82** Worldwide checklist of fungi on *Bidens Pilosa*

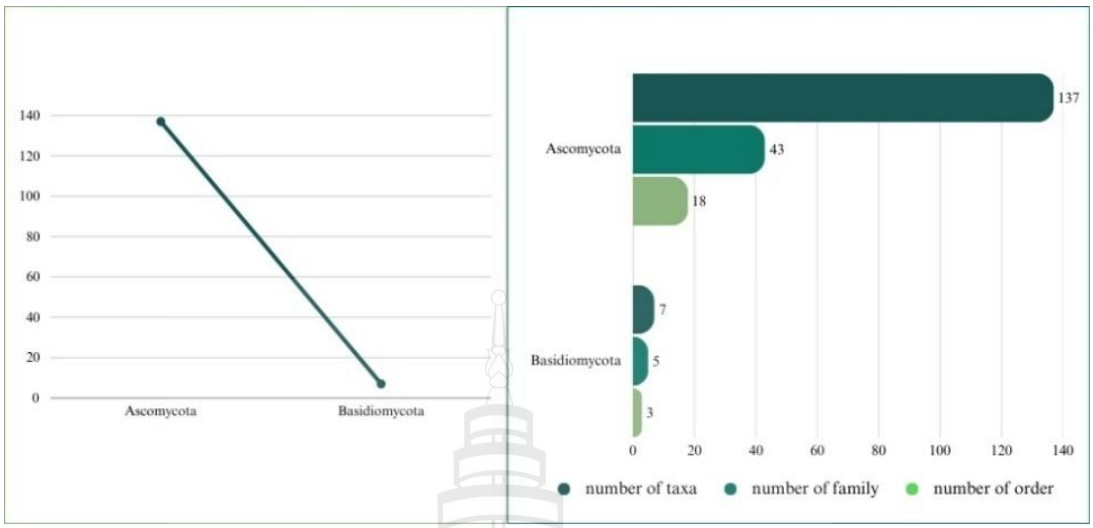



**Figure 3.83** Checklist of fungi on *Chromolaena odorata*

# CHAPTER 4

# TAXONOMY AND CHEMICAL PROFILING OF *MEMNONIELLA ASTERACEARUM* (STACHYBOTRYACEAE) USING HPLC AND LC-QTOF ANALYSIS

## 4.1 Introduction

Asteraceae is one of the largest flowering plants families (Carlquist, 1976; Bremer, 1987; Bremer et al., 1992). Many species are well-known for economic value due to their medicinal and horticultural importance (Elomaa et al., 2018; Saini et al., 2020; Agbede et al., 2023). However, several Asteraceae species are also classified as weeds, posing potential threats to natural ecosystems (Kaur et al., 2023; MG et al., 2023). Asteraceae species are well known for production of a wide range of secondary metabolites. A phytochemical investigation conducted on Brazilian Vernonieae revealed the presence of *trans*-cinnamic acid derivatives, flavonoids, polyacetylenes and sesquiterpene lactones using UHPLC-UV-MS (Lusa et al., 2016). Gallon et al. (2018) also found that sesquiterpene lactones and flavonoids are the main secondary metabolites in biosynthesis of Vernonieae species. Subsequently, a study on plant-insect interaction between *Tithonia diversifolia* and *Chlosyne lacinia* revealed flavonoid aglycones were aboundant in *T. diversifolia* (Gallon et al., 2019). Mukatay et al. (2023) identified 43 compounds from *Artemisia heptapotamica* (Asteraceae), which include alkyl p-coumarates, sesquiterpene lactones, flavonoids and phenolic acid derivatives. Lazanaki et al. (2024) also reported eleven sesquiterpene lactones, one lignan, six flavonoids, three phenolic derivatives from *Staehelina uniflosculosa* (Asteraceae).

Fungi are recognized as a valuable source of bioactive compounds (Conrado et al., 2022). In response to various biotic and abiotic stresses, they produce a diverse array of secondary metabolites (Macheleidt et al., 2016). Among microbial producers, Actinomycetes and fungi generate a significantly higher number of bioactive

compounds compared to unicellular bacteria and cyanobacteria (Bérdy, 2012; Bills & Gloer, 2016; Nett et al., 2009).

Stachybotryaceae was introduced by Crous et al. (2014) and is considered an important group for the discovery of bioactive compounds (Jagels et al., 2019; Koike et al., 2022; Granados-Echegoyen et al., 2024). A diverse range of secondary metabolites has been reported from Stachybotryaceae species such as *Stachybotrys chlorohalonata* and *S. chartarum* (Jagels et al., 2019). Additionally, *Myrothecium* species have demonstrated significant toxic activity against *Aedes aegypti* mosquito larvae (Granados-Echegoyen et al., 2024). Moreover, interesting secondary metabolites found from *Stachybotrys* and *Memnoniella* were discussed by Wang et al. (2015) and documented 200 secondary metabolites such as cochlioquinone, cyclic peptide, diterpenoid, isochroman, polyketide, trichothecene, triprenyl phenol.

During a survey of weed associated fungi on *Chromolaena odorata* in northern Thailand, *Memnoniella asteracearum* (Stachybotryaceae, Hypocreales, Sordariomycetes) was identified. This fungus was only reported as a saprobic fungus on *Bidens pilosa* (Asteraceae) (Htet et al., 2025) and my study is second occurrence of *M. asteracearum* on Asteraceae plants. Since the members of Stachybotryaceae are known to produce diverse metabolites, *M. asteracearum* might be an interesting source for compound discovery.

## 4.2 Result

### 4.2.1 Phylogenetic Analyses

Fifty-two taxa were included from Stachybotryaceae and four *Brevistachys* species (CBS 141058, CBS 141057, CBS 397.73, and CBS 696.73) were selected as the outgroup. Maximum likelihood (ML) analyses and Bayesian Inference (BI) of the combined dataset were performed and tree topology of ML and BI (not shown) were similar. The best-scoring RA×ML tree with a final likelihood value of -14610.205938 is shown in Figure 5.1. RA×ML analysis yielded 1100 distinct alignment patterns, with 35.25% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.230457, C = 0.285467, G = 0.261731, T = 0.222346; substitution rates:

AC = 1.056549, AG = 3.910296, AT = 1.219557, CG = 1.008846, CT = 6.520553, GT = 1.000000; gamma distribution shape parameter α = 0.235994. My collection was sistered to *Memnoniella asteracearum* (MFLUCC 25-0166) with 85% ML and 1.00 BYPP support.

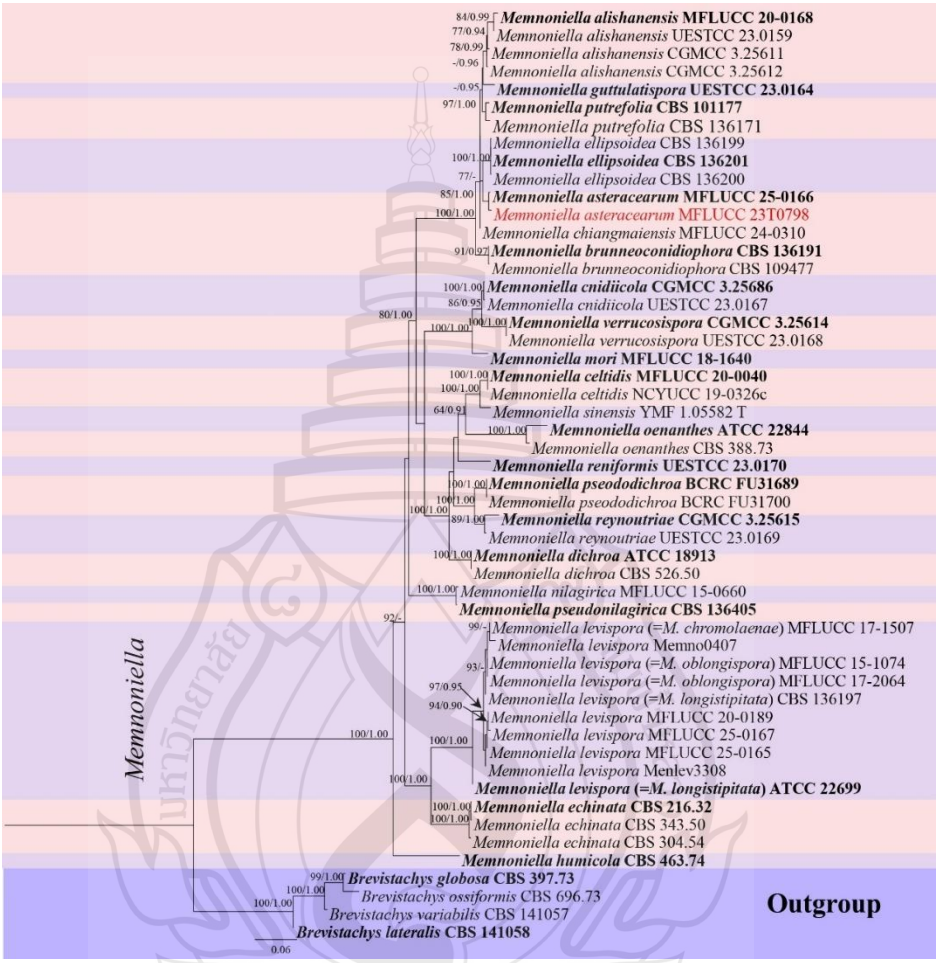



**Figure 4.1** Phylogram generated from maximum likelihood analysis of a combined dataset of ITS, *tef1-α, rpb2*, and *tub2* sequence data. Bootstrap support values for ML equal to or greater than 75% and BYPP equal to or greater than 0.90 are given at the nodes. Newly generated sequences are in red and type species are in bold

### 4.2.2 Taxonomy

***Memnoniella asteracearum*** Htet, A. Mapook &, K. W. T. Chethana (in prep)

*Index fungorum number*: IF904382, *Faces of fungi* number: FoF17968, Figure 4.2

*Saprobic* on dead stems of *Chromolaena odorata*. **Sexual morph**: Undetermined. **Asexual morph**: *Colonies* superficial, erect, scattered on the host substrate. *Mycelium* partly superficial and partly immersed. *Conidiophores* 100–130 × 6–8 µm ($\overline{x}$ =125.5 × 7.1 µm, n = 5), macronematous, mononematous, erect, simple, straight or flexuous, unbranched, smooth, thick-walled, septate, hyaline to pale brown, bearing conidiogenous cells at the apex. *Conidiogenous cells* 7–12 × 6–9 µm ($\overline{x}$ =10.5 × 6.9 µm, n = 5), phialidic, monophialidic, discrete, determinate, terminal, obovate, smooth, hyaline to pale brown. *Conidia* 8–12 × 5–9 µm ($\overline{x}$ = 10.6 × 6.8 µm, n = 20), acrogenous, aseptate, ellipsoidal, olivaceous brown to dark brown, verrucose, 1–2 guttules on the surface, thick-walled, rounded at both ends.

*Culture characteristics*: Conidia germinating on MEA within 24 hours, reaching 68 mm after 22 days at room temperature. Colonies on MEA irregular, filamentous, concentric, pale yellow, flat, transparent, slightly wrinkled on the surface, irregular, concentric, yellow to pale pink in reverse surface.

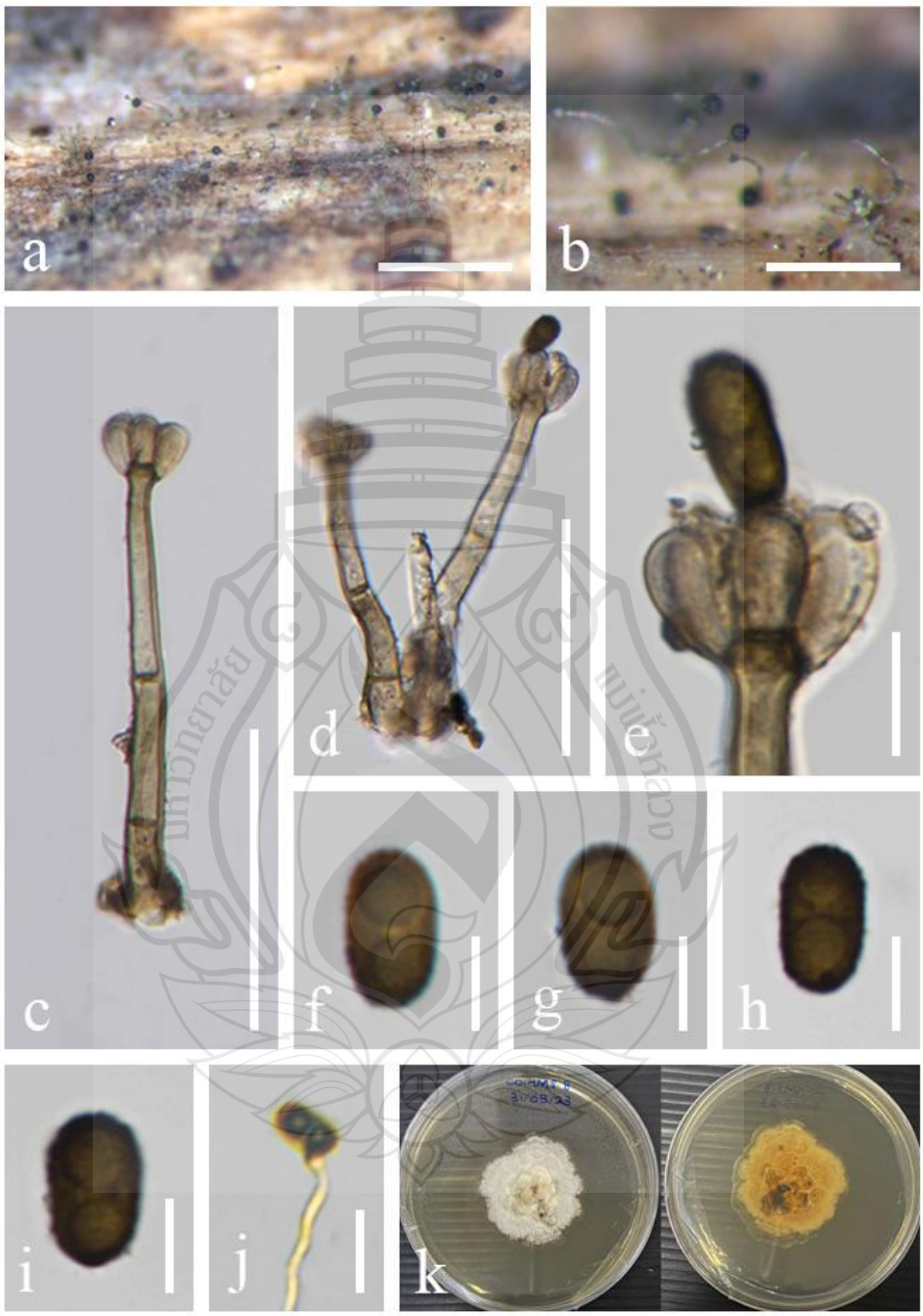
*Material examined*: THAILAND, Chiang Rai Province, Mueang Chiang Rai District, 20°0'16"N, 99°43'0.3"E, on dead stems of *Chromolaena odorata* (Asteraceae), 12 May 2023, Zin Hnin Htet (CO-HMS-8, MFLU 25-0292, new host); living culture MFLUCC 25-0254.

*Known host and distribution*: on dead stems of *Bidens pilosa* (Asteraceae) (Htet et al., 2025); on dead stems of *Chromolaena odorata* (Asteraceae) (this study).

*GenBank*: **ITS**: PV345721, ***tef1-α***: PV366414

*Notes*: Based on phylogenetic analysis (Figure 4.1), this collection (MFLUCC 25-0254) formed a sister clade to *Memnoniella asteracearum* (MFLUCC 25-0166) with 85% ML and 1.00 BYPP support. When comparing morphology, this new collection is resembling *M. asteracearum* in having similar morphological characters, such as macronematous, mononematous, straight or flexuous, unbranched conidiophores (100–130 × 6–8 µm vs. 120–150 × 7.5–8.5 µm), bearing phialidic conidiogenouse cells at the apex and acrogenous, aseptate, ellipsoidal conidia (8–12 × 5–9 µm vs. 8–12 × 5–10 µm).. Moreover, there is no base pairs difference between species. *Memnoniella*

*asteracearum* was previously reported on the dead stems of *Bidens pilosa* (Asteraceae) in northern Thailand. Therefore, the current collection is reported as a new host record of *M. asteracearum* on *Chromolaena odorata* (Asteraceae).




**Note** **a, b** Appearance of colonies on host substrate. **c, d, e** Conidiophores with conidiogenous cells. **f–i** Conidia. **j** Germinating conidia. **k** Culture on MEA. Scale bars: a, b = 500 µm, b, c = 50 µm, e = 10 µm, f, g, h, i, j = 5 µm.

**Figure 4.2** *Memnoniella asteracearum* (MFLU 25-0292, a new host record)

### 4.2.3 Preliminary Screening of Antibacterial Activity

Three bacterial test organisms, *Bacillus subtilis*, *Escherichia coli*, and *Staphylococcus aureus,* were used for preliminary screening of antibacterial activity. My isolate, *Memnoniella asteracearum* showed antibacterial activity against *B. subtilis* with a 17 mm inhibition zone, 16 mm inhibition zone against *E. coli*, and 20 mm inhibition zone against *S. aureus*. However, the inhibition zones observed for the control (ampicillin) were larger than those produced by *M. asteracearum*.

### 4.2.4 Tentative Chemical Profiling using LC-QTOF Analysis

A diverse range of compounds were detected from the extract of *Memnoniella asteracearum* using time-of-flight mass spectrometry. A total of 142 compounds, including some previously reported as bioactive, were detected and characterized based on precise mass measurements and fragment ion analysis, with comparisons to databases. (Table 4.1). The identified compounds consisted of six classes: alkaloids, carbohydrates and derivatives, heterocyclic compounds, organic acids and carboxylic acids, lipids and fatty acids, terpenoids and steroids, with lipids and fatty acids being the majority.

#### 4.2.4.1 Alkaloids (1–11)

Alkaloids are secondary metabolites composed of one or more nitrogen atoms (El Sayed, 2000; Gutiérrez-Grijalva et al., 2020). Alkaloids are one of the most important fungal metabolites in pharmaceutical and industrial aspects (Dey et al., 2020; Wieczorek et al., 2015).

In this study, six alkaloids (compounds 1–11) were identified as 2-Methoxycanthin-6-one, chalciporone, isococculidine, tabernamine, irinotecan, Clavepictine B. Some of these compounds are recognized for their biological properties in traditional medicine and modern drug development.

Compound 1–3 was detected at retention time (RT) 17.012, 17.624, 17.387 minutes with m/z 249.0672 in [M-H]- negative ion mode and characterized as 2-Methoxycanthin-6-one ($C_{15}H_{10}N_2O_2$). This compound is a plant alkaloid, previously reported as having cytotoxic and antifertility activity (Njar et al., 1995; Fausto Rivero-Cruz et al., 2005), which was also the potential antiulcer agent (Raji & Oloyede, 2012). At RT 19.172, compound 4 is characterized as chalciporone with m/z 242.1553 in [M-H]- negative ion mode, and a molecular formula of $C_{16}H_{21}NO$. Chalciporone was

previously isolated from mushroom *Chalciporus piperatus* (Basidiomycetes); however, no recent data available on its biological activity. This represents the second reported isolation of chalciporone from fungi. Irinotecan (compound 9) is a pentacyclic alkaloid, observed with m/z 631.2815 [M+HCOO]- in the negative ion mode, which is reported as an anticancer agent, especially in treating of colon cancer (Cunningham et al., 2004; Jia et al., 2020; Kciuk et al., 2020).

4.2.4.2 Carbohydrates and derivatives (12–16)

Carbohydrates are compounds composed of carbon, nitrogen, and oxygen. In this study, three carbohydrate derivatives were detected (compounds 12–16) at negative ion mode. 2,6-Dimethyl-7-octene-1,6-diol 8-O-glucoside (compound 12–14) is an O-acyl carbohydrate, detected at m/z 333.1927 in [M-H]- negative ion mode. Compound 15 and compound 16 were characterized as disaccharides with molecular formulas $C_{18}$ $H_{30}$ $O_{16}$ and $C_{12}$ $H_{22}$ $O_{11}$. However, these compounds have not yet been reported to be bioactive.

4.2.4.3 Heterocyclic compounds (17–54)

Heterocyclic compounds are important compounds in medicinal chemistry and biologically active compounds including anti-cancer, anti-inflammatory, anti-HIV, etc. (Ebenezer et al., 2022). In agriculture, these compounds are useful agents as having pesticidal, fungicidal, insecticidal properties (Gupta, 2015). In this study, heterocyclic compounds (Compound 17–54) are the most dominant compounds detected in *Memnoniella alishanensis*. Compound 25 (RT 18.727) was detected m/z 245.0817 in [M-H]- negative ion mode and characterized as Columbianetin. Columbianetin ($C_{14}H_{14}O_4$) is a furanocoumarin derivative with a 1-ring heterocyclic system with oxygen. This compound has been reported for potential biological and pharmaceutical properties such as anti-inflammatory and antiphotoaging activities (Jeong et al., 2009; J. H. Oh et al., 2020; Patel & Patel, 2023). Compound 26 and 27 (RT 18.947 and 19.125 mins) was detected with m/z 242.1554 in [M+H] + positive ion mode and m/z 240.1399 in [M-H]- negative ion mode, and was characterized as Dehydroisochalciporone. This compound was previously reported as a fungal metabolite from the ethyl acetate extract of the mushroom *Chalciporus piperaturs.* Dehydroisochalciporone has demonstrated potential antihypertensive activity, making it an interesting source for future drug development (Yang et al., 2023). Compound 50 (RT 23.955 min) was observed with

m/z 671.4905 in [M+Na] + positive ion mode and identified as uvaricin, which has antitumor activity (Jolad et al., 1982)

4.2.4.4 Organic acids and carboxylic acids (55–76)

Organic acids are the organic compounds with acidic properties (Chahardoli et al., 2020). In this study, organic acids and carboxylic acids are represented by compounds 55–76, with dicarboxylic acids being the majority. Compound 34 was observed at RT 17.873 with m/z 201.1134 in [M-H]- negative ion mode and identified as sebacic acid. Sebacic acid is a dicarboxylic acid that can serve as a valuable agent in pharmaceutical and cosmetic industries as well as pesticidal development (Allan et al., 2019; Fiume et al., 2012; Liao et al., 2024). Compound 57 was characterized as 2-Hydroxy-3-carboxy-6-oxo-7-methylocta-2,4-dienoate with m/z 229.0709 in [M+H] + positive ion mode and a formula $C_{10}H_{12}O_6$. This compound is a meta-cleavage intermediate in the p-cumate catabolic pathway of *Pseudomonas putida* F1 (Eaton, 1996). Compound 64 and 65 were identified as 3-Methyl-3Z-heptenoic acid with m/z 143.1091 in [M+H] + positive ion mode and m/z 142.0995 in [M-H]- negative ion mode. 3-Methyl-3Z-heptenoic acid is a carboxylated fatty acid derivative, which was previously obtained from sunflower and has shown to have potential allelopathic properties (Macías et al., 1998). Compounds 70–72 were detected with m/z 421.2271 in [M-H]- negative ion mode and identified as docusate ($C_{20}H_{38}O_7S$), a bioactive compound commonly used as an anti-constipation agent (Donowitz & Binder, 1975; Hurdon et al., 2000). Compounds 73–76 were detected and identified as 4-Dodecylbenzenesulfonic acid in m/z 325.185 in [M-H]- negative ion mode. 4-dodecylbenzenesulfonic acid is an acid catalyst that aids in biodiesel production, and is widely used in industrial applications (Alegría et al., 2014; Alegría & Cuellar, 2015; Wallis et al., 2017; Pellegrini et al., 2023)

4.2.4.5 Lipids and fatty acids (77–118)

Lipids and fatty acids derivatives are detected by compound 77 to 118 in this study. Compound 104 was detected with m/z 215.1295 in [M-H]- negative ion mode and characterized as butyl butyryllactate with a molecular formula of $C_{11}H_{20}O_4$. Butyl butyryllactate is a flavoring agent and is also a bioactive compound with the potential of anti-cancer activity (Holbeck & Simon, 2007). Compound 107–109 were observed in m/z 187.1343 in [M-H]- negative ion mode and identified as

3-hydroxycapric acid. 3-Hydroxycapric acid, also known as 3-Hydroxydecanoic acid, is a medium-chain fatty acid. This compound has potential agonist activity and is gaining interest for future drug development (Köse et al., 2020). Compound 110 was detected with m/z 270.1869 in [M-H]- negative ion mode and characterized as anacyclin, with a molecular formula $C_{18}H_{25}NO$. Anacyclin is a fatty amide that has been reported in plants (Althaus et al., 2014) with antiprotozoal activity. Compounds 115–116 were detected with m/z 445.3451 in [M+Na] + positive ion mode and identified as Theonellasterol B with a molecular formula ($C_{30}H_{46}O$). Theonellasterols are compounds with potential pharmacological applications in the treatment of liver disorders (De Marino et al., 2011).

4.2.4.6 Terpenoids and steroids (119-142)

Terpenoids and steroids are secondary metabolites known for their bioactive properties. In this study, terpenoids and steroids derived from *Memnoniella asteracearum* as listed in compound 119–142. Compound 119 was detected with m/z 249.1139 in [M-H]- negative ion mode and identified as helinorbisabone, a bioactive norsesquiterpene isolated from *Helianthus annuus* (sunflower), which has demonstrated potential allelopathic activity (Macías et al., 1998). Compounds 122–123 were detected with m/z 645.3521 in [M+H] + positive ion mode and m/z 689.3373 in [M+HCOO]- in negative ion mode and characterized as Goshonoside F3 ($C_{32}H_{52}O_{13}$). Goshonoside F3 is a diterpene glycoside which was isolated from the leaves of *Rubus chingii* (Chou et al., 1987). Kiwiionoside (RT 20.616 min), a terpene gycoside, was observed with m/z 451.2182 in [M+HCOO]- negative ion mode. Compounds 125 and 126 were detected with m/z 235.1716 in [M+H] + positive ion mode and m/z 233.1546 in [M-H]- negative mode and identified as Dehydrocurdione with a molecular formula $C_{15}H_{22}O_2$. Dehydrocurdione is a bioactive sesquiterpene with potential anti-inflammatory, antibacterial, and antioxidant properties (Yoshioka et al., 1998; Diastuti et al., 2014; Hamdi et al., 2015).

## 4.3 Discussion

This study identified *Memnoniella asteracearum* (MFLUCC 25-0254) based on a combined dataset of ITS, *tef1-α,* r*pb2*, and *tub2* sequence data. Morphologically, this collection (MFLUCC 25-0254) is similar to *M. asteracearum* (MFLUCC 25-0166) in having straight to flexuous conidiophores bearing phialidic conidiogenous cells at the apex and aseptate, ellipsoidal, olivaceous brown to dark brown, guttulate conidia (Htet et al., 2025). Moreover, preliminary screening of antibacterial activity of this collection, *M. asteracearum* (MFLUCC 25-0254) revealed the ability to inhibit the growth of all test bacteria organisms, *B. subtilis*, *E. coli*, and *S. aureus*. This result is also consistent with the findings of Htet et al. (2025), in which *M. asteracearum* (MFLUCC 25-0166) exhibited antimicrobial activity against all tested organisms, regardless of whether they were Gram-positive or Gram-negative.

Bioactive compounds from fungi have gained interest in the pharmaceutical industry for treating cancer as well as the development of antibiotics (Manganyi & Ateba, 2020). Several compounds found in *M. asteracearum*, such as 2-Methoxycanthin-6-one, anacyclin, columbianetin, dehydroisochalciporone, irinotecan, and sebacic acid, have been previously documented as bioactive (Njar et al., 1995; Cunningham et al., 2004; Fausto Rivero-Cruz et al., 2005; Jeong et al., 2009; Fiume et al., 2012; Althaus et al., 2014; Allan et al., 2019; J. H. Oh et al., 2020; Jia et al., 2020; Kciuk et al., 2020; Patel & Patel, 2023; Yang et al., 2023; Liao et al., 2024). These results are consistent with the initial antibacterial investigation. Chemical characterization of ethyl acetate extract of *Memnoniella asteracearum* using LC-QTOF resulted in 142 compounds of which heterocyclic compounds, lipids and fatty acids derivatives are the most dominant compounds. Many of these compounds have been previously isolated from plants (Njar et al., 1995; Fausto Rivero-Cruz et al., 2005; Althaus et al., 2014), suggesting that fungi could serve as alternative bioresources for bioactive metabolites. Interestingly, chalciporone and dehydroisochalciporone, fungal metabolites originally identified from the ethyl acetate extract of the basidiomycete *Chalciporus piperaturs* were also detected in this study (Table 4.1). This finding suggests that fungi may have a conserved biosynthesis route, which is consistent with

the previous finding of fungal glucans in both Ascomycota and Basidiomycota (Liu et al., 2024). Additionally, two carboxylic acids derivatives, azelaic acid and sebacic acid which have promising applications in the cosmetic industry (Liao et al., 2024) are also detected. The occurrence of these bioactive compounds highlights the potential of *M. asteracearum* not only as a source of medicinal compounds but also as a valuable resource for industrial applications.

The current study presents the tentative chemical profile of *M. asteracearum* (Stachybotryaceae) and discusses its potential biological properties. Many compounds with known bioactivies were identified, which showed that *M. asteracearum* as a source of bioactive metabolites. However, further research is required to isolate the pure compounds, elucidate their structures, explore the mechanisms of action, and confirm their biological potential.

**Table 4.1** Identification and characterization of compounds in *Memnoniella asteracearum* extract using LC-QTOF in positive and negative ionization modes

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| **Alkaloids** | | | | | | | | | |
| 1 | 17.012 | 2-Methoxycanthin-6-one | $C_{15}H_{10}N_2O_2$ | 250.0745 | - | - | 249.0672 (249.0667) [M-H]- | 130.9662, 174.9561 | Raji and Oloyede (2012) |
| 2 | 17.624 | | | | | | | | |
| 3 | 17.387 | | | | | | | | |
| 4 | 19.172 | Chalciporone | $C_{16}H_{21}NO$ | 243.1626 | - | - | 242.1553 (242.155) [M-H]- | - | Sterner et al. (1987) |
| 5 | 17.976 | Isococculidine | $C_{18}H_{23}NO_2$ | 285.1762 | 286.1833 (286.1802) [M+H] + | 179.063, 207.058, 208.0613, 216.1412, 225.0881 | - | - | Chaudhary et al. (2023) |
| 6 | 19.964 | | | | | | | | |
| 7 | 21.263 | | | | | | | | |
| 8 | 21.843 | Tabernamine | $C_{40}H_{48}N_4O_2$ | 661.3819 | - | - | 661.3802 (661.3759) [M+HCOO]- | 311.1685, 319.231, 324.233, 649.3805, 650.3838 | Perera et al. (1985) |
| 9 | 23.912 | Irinotecan | $C_{33}H_{38}N_4O_6$ | 586.2833 | - | - | 631.2815 (631.2773) [M+HCOO]- | 132.9237, 531.3568, 532.3597 | Kciuk et al. (2020) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 10 | 19.814 | Clavepictine B | $C_{20}H_{35}NO$ | 305.2751 | 306.2822 (306.2791) [M+H] + | 164.9215, 258.1883, 260.1681, 261.1714 | - | - | Davis and Xu (2012) |
| 11 | 23.073 | | | | | | | | |
| **Carbohydrates and derivatives** | | | | | | | | | |
| 12 | 18.442 | 2,6-Dimethyl-7-octene-1,6-diol 8-O-glucoside | $C_{16}H_{30}O_7$ | 334.2 | - | - | 333.1927 (333.1919) [M-H]- | 275.0568, 305.2163, 325.1849, | Kong et al. (2001) |
| 13 | 21.344 | | | | | | | | |
| 14 | 22.546 | | | | | | | | |
| 15 | 17.057 | alpha-L-Rhamnopyranosyl-(1->2)-beta-D-galactopyranosyl-(1->2)-beta-D-glucuronopyranoside | $C_{18}H_{30}O_{16}$ | 50.21566 | - | - | 547.1548 (547.1516) [M+HCOO]- | 249.0672, 250.0705, 341.1147, 342.1181, 469.1387 | Lan et al. (2017) |
| 16 | 17.308 | Trehalose | $C_{12}H_{22}O_{11}$ | 342.1213 | - | - | 341.1141 (341.1089) [M-H]- | 249.0668, 265.004, 3.4.9142 | Elbein et al. (2003) |
| **Heterocyclic compounds** | | | | | | | | | |
| 17 | 17.026 | 2,3-Dihydro-6-methyl-5-(5-methyl-2-furanyl)-1H-pyrrolizine | $C_{13}H_{15}NO$ | 201.1155 | - | - | 200.1081 (200.1081) [M-H-]- | 174.9563 | Cao et al. (2022) |
| 18 | 17.595 | Thysanone | $C_{14}H_{12}O_6$ | 276.0642 | - | - | 275.0567 (275.0561) [M-H]- | 174.9563, 249.0673 | Donner and Gill (2002) |
| 19 | 18.42 | | | | - | - | | | |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 20 | 16.98 | Dictyoquinazol C | $C_{18}H_{18}N_2O_5$ | 342.1222 | - | - | 341.115 (341.1143) | 174.9561, | Oh and Song (2007) |
| | | | | | - | - | [M-H]- | 249.0673, | |
| 21 | 17.617 | | | | | | | 304.9143 | |
| 22 | 18.08 | Celereoin | $C_{14}H_{14}O_5$ | 262.0844 | - | - | 261.0772 (261.0768) | 174.956 | Jain et al. (1986) |
| | | | | | | | [M-H]- | | |
| 23 | 18.18 | Fluoromidine | $C_7H_3ClF_3N_3$ | 220.9984 | - | - | 219.9907 (219.9895) | 174.9567 | National Center for |
| 24 | 18.801 | | | | - | - | [M-H]- | | Biotechnology Information (2025) |
| 25 | 18.727 | Columbianetin | $C_{14}H_{14}O_4$ | 246.0889 | - | - | 245.0817 (245.0819) | 186.1037 | Jeong et al. (2009) |
| | | | | | | | [M-H]- | | |
| 26 | 18.947 | Dehydroisochalciporone | $C_{16}H_{19}NO$ | 241.1473 | 242.1554 | 151.1253, | 240.1399 (240.1394) | 187.1346 | Sterner et al. (1987) |
| | | | | | (242.1539) | 190.0347, | [M-H]- | | |
| 27 | 19.125 | | | | [M+H] + | 208.0455 | | | |
| 28 | 19.299 | Zapotidine | $C_7H_9N_3S$ | 167.0485 | 190.0376 | 172.0479 | - | - | Mechoulam et al. (1961) |
| | | | | | (190.0409) | | | | |
| | | | | | [M+Na] + | | | | |
| 29 | 19.359 | 1,4-Benzodioxin-2(3H)-one | $C_8H_6O_3$ | 150.0323 | - | - | 149.0248 (149.0244) | - | Bozzo et al. (2003) |
| | | | | | | | [M-H] - | | |
| 30 | 19.419 | Demethylsuberosin | $C_{14}H_{14}O_3$ | 230.0946 | - | - | 229.0873 (229.087) | - | Kim et al. (2014) |
| | | | | | | | [M-H] - | | |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 31 | 19.472 | Phenylamil | $C_{12}H_{12}ClN_7O$ | 305.0786 | 328.0675 (328.0684) [M+Na] + | 158.1564, 225.1986, 229.0711, 309.2937 | - | - | National Center for Biotechnology Information (2025) |
| 32 | 19.614 | Grevilline A | $C_{18}H_{12}O_6$ | 324.0636 | 325.0716 (325.0707) [M+H] + | 147.0938, 258.1521, 258.1885, 297.2937, 311.3093, 312.3129 | - | - | Shaker et al. (2022) |
| 33 | 19.66 | Iso-Olomoucine | $C_{15}H_{18}N_6O$ | 298.1608 | - | - | 297.1535 (297.1496) [M-H]- | 391.2004 | Price et al. (2009) |
| 34 | 19.995 | | | | | | | | |
| 35 | 19.701 | Dodemorph | $C_{18}H_{35}NO$ | 281.2754 | 282.2827 (282.2791) [M+H] + | 256.1729, 258.1883, 270.1886 | - | - | Put et al. (2016) |
| 36 | 16.931 | Coumaperine | $C_{16}H_{19}NO_2$ | 257.1443 | 258.1517 (258.1489) [M+H] + | 116.9731, 119.0301, 143.0034 | 256.1345 (256.1343) [M-H]- | - | Kitano et al. (2000) |
| 37 | 17.415 | | | | | | | | |
| 38 | 18.409 | | | | | | | | |
| 39 | 18.911 | | | | | | | | |
| 40 | 20.085 | | | | | | | | |
| 41 | 20.12 | | | | | | | | |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 42 | 20.529 | N-Hexadecanoylpyrrolidine | $C_{20}H_{39}NO$ | 309.307 | 310.3143 (310.3104) [M+H] + | - | - | - | Dutta et al. (2023) |
| 43 | 20.75 | Pridinol | $C_{20}H_{25}NO$ | 295.1974 | 296.2046 (296.2009) [M+H] + | - | 294.1864 (294.1863) [M-H]- | 265.0479 | Rodríguez-Basso et al. (2024) |
| 44 | 20.758 | | | | | | | | |
| 45 | 21.287 | Amataine | $C_{43}H_{48}N_4O_6$ | 716.3585 | - | - | 715.3511 (715.3501) [M-H]- | 284.1658, 311.1689, 319.2312, 339.1998,647.3643, 648.3678 | Macías et al. (1998) |
| 46 | 19.547 | 1,3-Dimethylpyrrolo[1,2-a]pyrazine | $C_9H_{10}N_2$ | 146.0864 | 147.0937 (147.0917) [M+H] + | 101.0196, 116.9781, 119.0301, 143.0036 | - | - | National Center for Biotechnology Information (2025) |
| 47 | 23.612 | | | | | | | | |
| 48 | 23.983 | | | | | | | | |
| 49 | 24.594 | | | | | | | | |
| 50 | 23.955 | Uvaricin | $C_{39}H_{68}O_7$ | 648.5016 | 671.4905 (671.4857) [M+Na] + | 147.0938, 499.402, 550.4008, 555.3565, 556.3595 | - | - | Jolad et al. (1982) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 51 | 24.141 | 2-Ethyl-5-methylpyridine | $C_8 H_{11} N$ | 121.091 | 122.0982 (122.0964) [M+H] + | - | - | - | Burkhardt and Coleridge (2008) |
| 52 | 29.178 | 2,3-Dihydroxy-6,7- | $C_8 H_4 Cl_2 N_2 O_2$ | 229.9674 | - | - | 228.9603 (228.9577) | 174.9561, | National Center for |
| 53 | 30.595 | Dichloroquinoxaline | | | | | [M-H]- | 178.9779, 206.9728 | Biotechnology Information (2025) |
| 54 | 24.297 | 1-(4-Fluorobenzyl) piperazine | $C_{11} H_{15} F N_2$ | 194.1183 | 217.1075 (217.1111) [M+Na] + | 136.1141, 147.0938 | - | - | Ferro et al. (2018) |
| **Organic acid & Carboxylic acid** | | | | | | | | | |
| 55 | 17.187 | Azelaic acid | $C_9 H_{16} O_4$ | 188.1046 | - | - | 187.0974 (187.0976) [M-H]- | 112.9856, 130.9661, 174.9561 | Spaggiari et al. (2023) |
| 56 | 17.873 | Sebacic acid | $C_{10} H_{18} O_4$ | 202.1207 | - | - | 201.1134 (201.1132) [M-H]- | 112.9856, 130.9664, 174.9565 | Yu et al. (2020) |
| 57 | 19.392 | 2-Hydroxy-3-carboxy-6-oxo-7-methylocta-2,4-dienoate | $C_{10} H_{12} O_6$ | 228.0633 | 229.0709 (229.0707) [M+H] + | 147.0938, 200.2397, 206.0299 | - | - | Eaton (1996) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 58 | 19.415 | S-methylcaptopril | $C_{11}H_{18}O_3S$ | 230.0975 | 231.1046 (231.1049) [M+H] + | 147.0938, 151.1248, 200.2397, 206.0299, 229.1046 | - | - | Drummer et al. (1983) |
| 59 | 19.487 | Isobutyl salicylate | $C_{11}H_{14}O_3$ | 194.0946 | - | - | 193.0873 (193.087) [M-H] - | - | He et al. (2016) |
| 60 | 19.848 | Norpropoxyphene carbinol | $C_{18}H_{23}NO$ | 269.1785 | 270.1886 (270.1852) [M+H] + | 258.1883, 260.1679 | 268.1712 (268.1707) [M-H] - | 265.1484 | Ruan and Mueck, (2024) |
| 61 | 20.095 | | | | | | | | |
| 62 | 20.178 | | | | | | | | |
| 63 | 20.226 | Didodecyl thiobispropanoate | $C_{30}H_{58}O_4S$ | 514.4038 | 515.411 (515.4129) [M+H] + | 260.1678, 270.1909, 271.1921, 272.1976, 284.2042, 359.3198, 395.3676 | - | - | National Center for Biotechnology Information (2025) |
| 64 | 21.421 | 3-Methyl-3Z-heptenoic acid | $C_8H_{14}O_2$ | 142.1018 | 143.1091 (143.1067) [M+H] + | - | 142.0995 (141.0921) [M-H] - | - | Busund et al. (2024) |
| 65 | 21.415 | | | | | | | | |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 66 | 22.091 | Dibutyl phthalate | $C_{16}H_{22}O_4$ | 278.1554 | 279.1627 (279.1591) [M+H] + | 121.0316, 149.026, 150.0293 | - | - | Roy et al. (2006) |
| 67 | 22.131 | 2-Oxo-8-methylthiooctanoic acid | $C_9H_{16}O_3S$ | 148.0187 | 149.0258 (149.0267) [M+H] + | - | - | - | National Center for Biotechnology Information (2025) |
| 68 | 22.56 | Acetyl tributyl citrate | $C_{20}H_{34}O_8$ | 402.2301 | 403.2375 (403.2326) [M+H] + | 391.2889 | - | - | Kim et al. (2018) |
| 69 | 17.527 | 2-Chloro-3-oxoadipate | $C_6H_7ClO_5$ | 193.9986 | - | - | 192.9909 (192.9909) [M-H] - | 130.9659, 174.9557, 176.9791, 178.9773, 181.0712 | National Center for Biotechnology Information (2025) |
| 70<br>71<br>72 | 18.964<br>19.116<br>24.82 | Docusate | $C_{20}H_{38}O_7S$ | 422.2344 | - | - | 421.2271 (421.2265) [M-H] - | 305.2159, 325.1847, 353.2009 | Hurdon et al. (2000) |
| 73<br>74<br>75<br>76 | 19.265<br>19.96<br>20.372<br>22.113 | 4-Dodecylbenzenesulfonic acid | $C_{18}H_{30}O_3S$ | 326.1923 | - | - | 325.185 (325.1843) [M-H] - | 242.1555, 243.1593, 291.2006, 305.2158, 323.0535 | Alegría and Cuellar (2015) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| **Lipids and fatty acids** | | | | | | | | | |
| 77 | 12.676 | 3-O-(alpha-L- | $C_{22}H_{40}O_{11}$ | 480.2581 | 481.2663 | 116.9782, | 479.2508 (479.2498) | 130.9664, | Fahy et al. (2009) |
| 78 | 17.948 | rhamnopyranosyl-(1-2)- | | | (481.2643) | 119.9782, | [M-H]- | 174.9563, | |
| 79 | 12.676 | alpha-L-rhamnopyranosyl)- | | | [M+H] + | 119.0301, | | 219.0233, | |
| 80 | 21.805 | 3-hydroxydecanoic acid | | | | 143.0035, | | 291.2005, | |
| | | | | | | 459.2843, | | 325.1843 | |
| | | | | | | 476.3114, | | | |
| | | | | | | 477.3143 | | | |
| 81 | 18.54 | Norethindrone acetate | $C_{22}H_{28}O_3$ | 340.2066 | - | - | 339.2006 (339.1966) | 275.0566, | Morotti et al. (2017) |
| 82 | 20.428 | | | | | | [M-H]- | 305.216, | |
| 83 | 20.781 | | | | | | | 325.1847 | |
| 84 | 21.05 | | | | | | | | |
| 85 | 21.226 | | | | | | | | |
| 86 | 22.101 | | | | | | | | |
| 87 | 21.322 | 24R-methylcholest-22E-en-3beta,4beta,5alpha,6alpha,8beta,14alpha,15alpha,25R,26-nonol | $C_{28}H_{48}O_9$ | 528.3316 | - | - | 573.33 (573.328) [M+HCOO]- | 311.1683, 319.2308, 339.1992 | Riccio et al. (1989) |
| 88 | 21.35 | 2-deoxy-20-hydroxyecdysone 22-phosphate | $C_{27}H_{45}O_9P$ | 544.2855 | - | - | 543.2784 (543.2728) [M-H]- | 311.169, 475.2913, 476.295 | Tsoupras et al. (1982) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 89<br>90<br>91 | 21.673<br>21.924<br>21.805 | 3-O-(alpha-L-rhamnopyranosyl-(1-2)-alpha-L-rhamnopyranosyl)-3-hydroxydecanoyl-3-hydroxydecanoic acid | $C_{32}H_{58}O_{13}$ | 650.3943 | 673.3835 (673.377) [M+Na] + | 326.2518, 359.2835, 668.4279, 669.4314 | - | - | Fahy et al. (2009) |
| 92 | 22.708 | 14-methyl-all-trans-retinoic acid | $C_{21}H_{30}O_2$ | 314.2244 | - | - | 313.217 (313.2173) [M-H]- | 116.9282, 132.9232, 297.1524, 311.1686 | Tanaka et al. (1992) |
| 93<br>94<br>95 | 21.741<br>22.489<br>22.941 | 9,12-dimethoxy-13-hydroxy-10-octadecenoic acid | $C_{20}H_{38}O_5$ | 358.2721 | 359.2833 (359.2792) [M+H] + | 171.1403, 341.2728 | 357.2647 (357.2646) [M-H]- | 132.9237, 187.1345, 265.1484, 311.1696, 319.2317, 339.2009 | Fahy et al. (2009) |
| 96 | 23.223 | (25S)-5alpha-cholestan-3beta,4beta,6alpha,8beta,15alpha,16beta,26-heptol | $C_{27}H_{48}O_7$ | 484.3396 | - | - | 529.3378 (529.3382) [M+HCOO]- | 132.9231, 265.1477 | Kerr and Baker, (1991) |
| 97 | 25.998 | 13-methoxy-heneicosanoic acid | $C_{22}H_{44}O_3$ | 356.3294 | - | - | 355.3221 (355.3218) [M-H]- | 115.9207, 132.9236, 311.1681, 325.1848, 337.206 | Barnathan et al. (1998) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 98 | 17.422 | 14-fluoro-myristic acid | $C_{14}H_{27}FO_2$ | 246.2006 | - | - | 291.2006 (291.1977) | 130.9661, | Gribble (2006) |
| 99 | 17.748 | | | | | | [M+HCOO]- | 174.956, | |
| 100 | 18.096 | | | | | | | 178.9782 | |
| 101 | 19.279 | | | | | | | | |
| 102 | 19.69 | | | | | | | | |
| 103 | 18.095 | 3-Chloro-2-methylmaleylacetate | $C_7H_7ClO_5$ | 205.9986 | - | - | 204.9913 (204.9909) [M-H]- | 130.9964, 174.9563 | Magrane and UniProt Consortium (2011) |
| 104 | 18.438 | Butyl butyryllactate | $C_{11}H_{20}O_4$ | 216.1368 | - | - | 215.1295 (215.1289) [M-H]- | 112.9856, 130.9964, 174.9564 | Api et al. (2024) |
| 105 | 18.479 | 11,12,13-TriHOME | $C_{18}H_{34}O_5$ | 330.2402 | - | - | 329.233 (329.233) [M-H]- | 130.966, 275.0562, 305.2156, 325.1841 | Fahy et al. (2009) |
| 106 | 19.056 | 3-Chloro-2-hydroxymuconic semialdehyde | $C_6H_5ClO_4$ | 175.9878 | - | - | 220.986 (220.9858) [M+HCOO]- | 112.9856 | Riegert et al. (1998) |
| 107 | 19.086 | 3-Hydroxycapric acid | $C_{10}H_{20}O_3$ | 188.1415 | | | 187.1343 (187.134) | 112.9856, | National Center for |
| 108 | 19.353 | | | | - | - | [M-H]- | 173.1184, | Biotechnology |
| 109 | 22.883 | | | | | | | 182.9898 | Information (2025) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 110 | 20.303 | Anacyclin | $C_{18}H_{25}NO$ | 271.1942 | - | - | 270.1869 (270.1863) [M-H]- | 268.171, 269.1746 | Crombie (1955) |
| 111 | 20.907 | Ethyl (R)-3-hydroxyhexanoate | $C_8H_{16}O_3$ | 160.1102 | - | - | 159.1029 (159.1027) [M-H]- | - | Schomburg et al. (1993) |
| 112 | 24.228 | (5E)-isovitamin D2 / (5E)-isoergocalciferol | $C_{28}H_{44}O$ | 396.3397 | 397.3471 (397.3465) [M+H] + | 136.1142, 147.0938, 217.1075 | - | - | National Center for Biotechnology Information (2025) |
| 113 | 24.231 | (5Z)-isovitamin D2 / 5,6-cis-isovitamin D2 / (5Z)-isoergocalciferol / 5,6-cis-isoergocalciferol | $C_{28}H_{44}O$ | 396.3399 | 419.3292 (419.3284) [M+Na] + | 136.1141, 147.0938, 217.1075, 397.347 | - | - | National Center for Biotechnology Information (2025) |
| 114 | 24.292 | Palmitic amide | $C_{16}H_{33}NO$ | 255.2591 | 256.2664 (256.2635) [M+H] + | 230.2509, 242.1571 | - | - | Pan et al. (2023) |
| 115 | 24.394 | Theonellasterol B | $C_{30}H_{46}O$ | 422.3558 | 445.3451 (445.3441) [M+Na] + | 122.0984, 136.1142, 147.0939, 217.1076, 423.3623 | - | - | De Marino et al. (2011) |
| 116 | 24.405 | | | | | | | | |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 117 | 20.42 | 5-Dehydro-avenasterol | $C_{29}H_{46}O$ | 410.3582 | 433.3475 (433.3441) [M+Na] + | 272.2042, 274.1841, 325.3252, 339.3412, 340.3446, 341.3103, 359.3198 | - | - | Islam et al. (2023) |
| 118 | 24.835 | 1-Monopalmitin | $C_{19}H_{38}O_4$ | 330.2806 | 331.2879 (331.2843) [M+H] + | 147.0938, 313.2773 | - | - | Nicholson et al. (2022) |
| **Terpenoids and Steroids** | | | | | | | | | |
| 119 | 19.562 | Helinorbisabone | $C_{14}H_{18}O_4$ | 250.1211 | - | - | 249.1139 (249.1132) [M-H]- | - | Macías et al. (1998) |
| 120 | 20.329 | 3beta-Acetoxy-11alpha-methoxy-12-ursen-28-oic acid | $C_{34}H_{54}O_5$ | 542.3929 | 543.4001 (543.4044) [M+H] + | 288.1994 | 541.3809 (541.3898) [M-H]- | 268.1712, 270.1872, 271.1904, 286.1816, 325.185, 447.2609 | Liang et al. (2022) |
| 121 | 20.326 | | | | | | | | |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 122 | 20.543 | Goshonoside F3 | $C_{32}H_{52}O_{13}$ | 644.3391 | 645.3521 (645.3481) [M+H] + | 327.3443, 328.3449, 341.3093, 351.3411, 359.3198, 640.3967 | 689.3373 (689.339) [M+HCOO] - | 311.1693, 325.1849,339.2005,621.3511, 622.3539, 623.357 | Chou et al. (1987) |
| 123 | 20.565 | | | | | | | | |
| 124 | 21.11 | Acetylvalerenolic acid | $C_{17}H_{24}O_4$ | 292.168 | - | - | 291.161 (291.1602) [M-H]- | 265.1489 | Bianconi et al. (2020) |
| 125 | 21.589 | Dehydrocurdione | $C_{15}H_{22}O_2$ | 234.1619 | 235.1716 (235.1693) [M+H] + | 147.0935, 211.1713 | 233.1546 (233.1547) [M-H]- | - | Qu et al. (2009) |
| 126 | 21.6 | | | | | | | | |
| 127 | 20.12 | Valdiate | $C_{17}H_{26}O_5$ | 310.1748 | - | - | 309.1713 (309.1707) [M-H]- | 256.1345, 268.171, 293.1796, 305.2159 | Gaur and Annapure (2022) |
| 128 | 21.523 | | | | | | | | |
| 129 | 27.676 | | | | | | | | |
| 130 | 20.616 | Kiwiionoside | $C_{19}H_{34}O_9$ | 406.2199 | - | - | 451.2182 (451.2185) [M+HCOO] - | 311.1689, 325.1842, 339.2001 | Murai et al. (1992) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 131 | 20.933 | Peposterol | $C_{29}H_{48}O$ | 412.3742 | 435.3635 (435.3597) [M+Na] + | 197.1564, 286.2202, 298.2202, 299.2236, 341.3091, 341.3565, 359.3201 | - | - | Rahman et al. (2019) |
| 132 | 21.242 | Lyciumoside III | $C_{32}H_{56}O_{13}$ | 648.3723 | - | - | 647.3651 (647.3648) [M-H]- | 305.2158, 311.1695, 319.2315, 339.2003, 635.365 | Terauchi et al. (1995) |
| 133 | 22.182 | Ganoderic acid Mc | $C_{36}H_{54}O_9$ | 630.3839 | - | - | 675.3823 (675.375) [M+HCOO]- | 297.1491, 311.1645, 311.1951, 319.2266, 339.1952 | Liu et al. (2015) |
| 134<br>135 | 22.282<br>22.291 | 3-O-trans-Feruloyleuscaphic acid | $C_{40}H_{56}O_8$ | 664.4037 | - | - | 663.3966 (663.3902) [M-H]- | 297.1533, 311.1692, 319.2313, 339.2003 | National Center for Biotechnology Information (2025) |

**Table 4.1** (continued)

| No. | RT | Compound Name | Molecular Formula | Mass | Adduct (+ve mode) | Fragment Ion (+) | Adduct (-ve mode) | Fragment Ion (-) | Ref |
|---|---|---|---|---|---|---|---|---|---|
| 136 | 22.513 | 6-Hydroxysandoricin | $C_{31}H_{40}O_{12}$ | 604.2544 | - | - | 603.2477 (603.2447) [M-H]- | 503.3223, 504.3259 | Powell et al. (1991) |
| 137 | 22.662 | (22E, 24x)-Ergosta-4,6,8,22-tetraen-3-one | $C_{28}H_{40}O$ | 392.3122 | 393.3195 (393.3152) [M+H] + | 147.0939, 149.0257, 391.2919, 392.2948 | - | - | National Center for Biotechnology Information (2025) |
| 138 | 22.513 | 6-Hydroxysandoricin | $C_{31}H_{40}O_{12}$ | 604.2544 | - | - | 603.2477 (603.2447) [M-H]- | 503.3223, 504.3259 | Powell et al. (1991) |
| 139 | 23.452 | Armillarivin | $C_{23}H_{28}O_5$ | 384.1966 | - | - | 383.1898 (383.1864) [M-H]- | 132.9231, 265.1477, 311.1687 | National Center for Biotechnology Information (2025) |
| 140 | 23.653 | 4,4'-Diaponeurosporene | $C_{30}H_{42}$ | 402.3265 | 403.3338 (403.3359) [M+H] + | 147.0939, 217.1074, 381.3514, 391.334 | - | - | Siziya et al. (2022) |
| 141 | 24.22 | Fucoxanthin | $C_{42}H_{58}O_6$ | 658.4287 | - | - | 703.4268 (703.4215) [M+HCOO]- | 132.9236, 305.2158 | Din et al. (2022) |
| 142 | 24.838 | Ptilosteroid | $C_{21}H_{34}O_7S$ | 430.2026 | - | - | 429.1955 (429.1952) [M-H]- | 115.9206, 132.9234 | Gabant et al. (2009) |

# CHAPTER 5

# OVERALL CONCLUSIONS

## 5.1 Summary of Study

This study aimed to explore the fungal diversity associated with two weeds in Asteraceae, by providing worldwide checklist of fungi on host plants and potential antibacterial activities. To achieve the objectives of this study, saprobic fungi were isolated from *Bidens pilosa* and *Chromolaena odorata*. Fungal identification is carried out based on both morphology and multigene phylogeny. Preliminary antibacterial screening was conducted using the agar plug diffusion method against selected bacterial strains. Based on the prescreening result, one fungal species, *Memnoniella asteracearum*, was selected for further chemical profiling. The result of LC-QTOF analysis led to the identification of 142 compounds categorized into alkaloids, carbohydrates and derivatives, heterocyclic compounds, organic acids and carboxylic acids, lipids and fatty acids, terpenoids and steroids. Some of these compounds have been previously reported as fungal metabolites with bioactive properties. This study contributes valuable knowledge of fungal metabolites and highlights the importance of discovering fungi as a source of antimicrobial and industrially important agents.

## 5.2 Comparative Fungal Diversity and Host Association of Invasive Asteraceae Weeds

In this study, saprobic fungi were described from the dead stems of *Bidens pilosa* and *Chromolaena odorata.* 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*.

*Chromolaenicola chiangraiensis*, *C. thailandensis*, *Dendryphion hydei*, *Diaporthe biconispora*, *Lasiodiplodia theobromae*, *Leptospora thailandica*, *Neoroussoella entadae*, *Pseudoithomyces 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*, *Pseudoroussoella*, and *Pseudothyridariella* are among the taxa that Mapook et al. (2020) established. These genera were initially reported from *Chromolaena odorata*, demonstrating the fungal originality connected with *Chromolaena odorata*. Combined with the results of this study, it is obvious that the number of fungal species from these genera are 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 *B. pilosa* and *C. 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's interesting to note that two fungal species (*Remotididymella anthropophila* and *Colletotrichum gigasporum*) were discovered in Asteraceae weeds 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 fungi have features that allow for occasional human connection.

## 5.3 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*. Sixteen species occurred exclusively on *Chromolaena odorata*, viz., *Austropleospora chromolaenae*, *Dothiorella asteracearum*, *Dothiorella chromolaenae*, *Diaporthe asteracearum*, *Diaporthe chromolaenicola*, *Fusarium chromolaenae*, *Kalmusia thailandica*, *Lophiostoma longiappendiculatum*, *Murichromolaenicola thailandensis*, *Pseudothyridariella asteracearum*, *Pseudothyridariella thailandica*, *Pseudolophiostoma chromolaenae*, *Pseudoneoconiothyrium chromolaenae*, *Pseudoneoconiothyrium thailandicum*, and *Trematei a asteracearum*. 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. 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.

## 5.4 Proportion of Novel Taxa and the Unexplored Mycobiota of Invasive Weeds

This study introduces a total of 23 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. Overall, the newly recorded species are distributed across 33 genera, 21 families, and seven orders within the classes Dothideomycetes and Sordariomycetes. Notably, Dothideomycetes emerged as the dominant class (Figure 6.1), with Pleosporales being the most frequently encountered order (Figure 6.2). Within this order, the family Didymosphaeriaceae was particularly well represented (Figure 6.3), highlighting its ecological prominence on Asteraceous weed hosts.

The finding of novel taxa 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, can serve as important reservoirs of taxonomic and functional novelty. This study highlights the importance of additional sampling on Asteraceae weed in the future to know the ecological role of weed associated fungi.

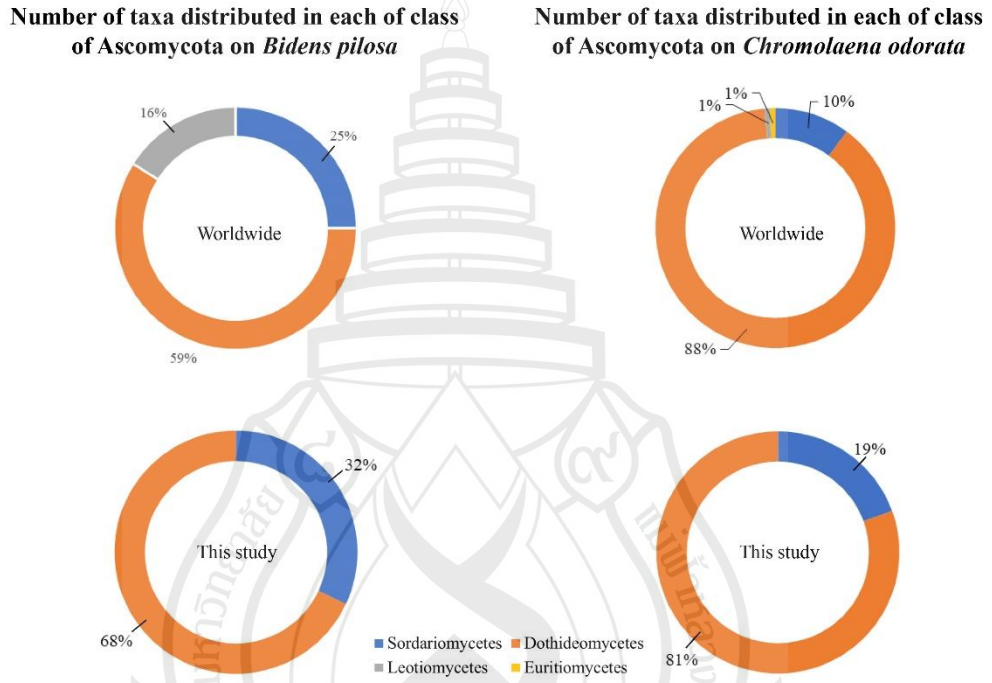



**Figure 5.1** Number of taxa distributed in classes of Ascomycota

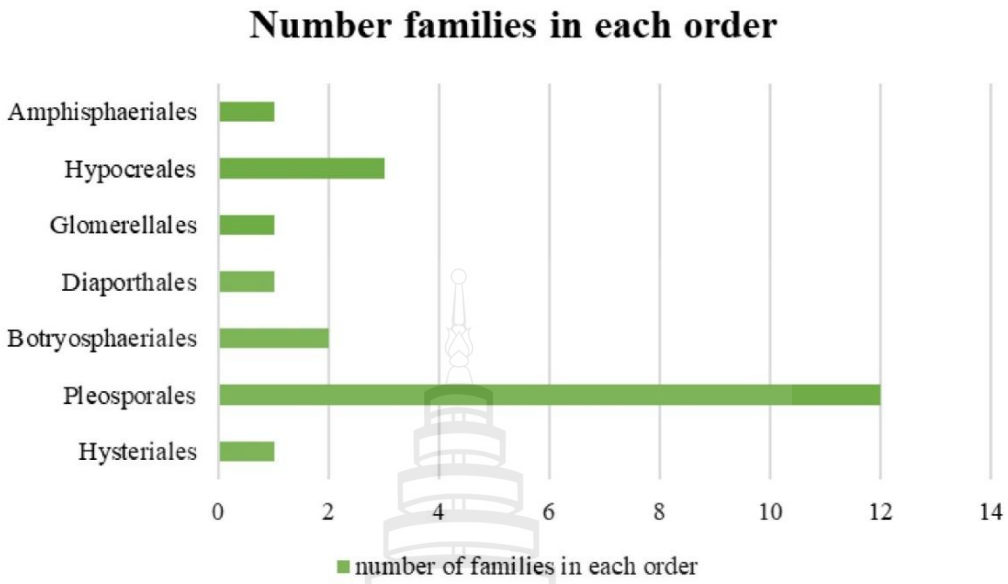



**Figure 5.2** Number of families in orders of Dothidiomycetes and Sordariomycetes found in this study

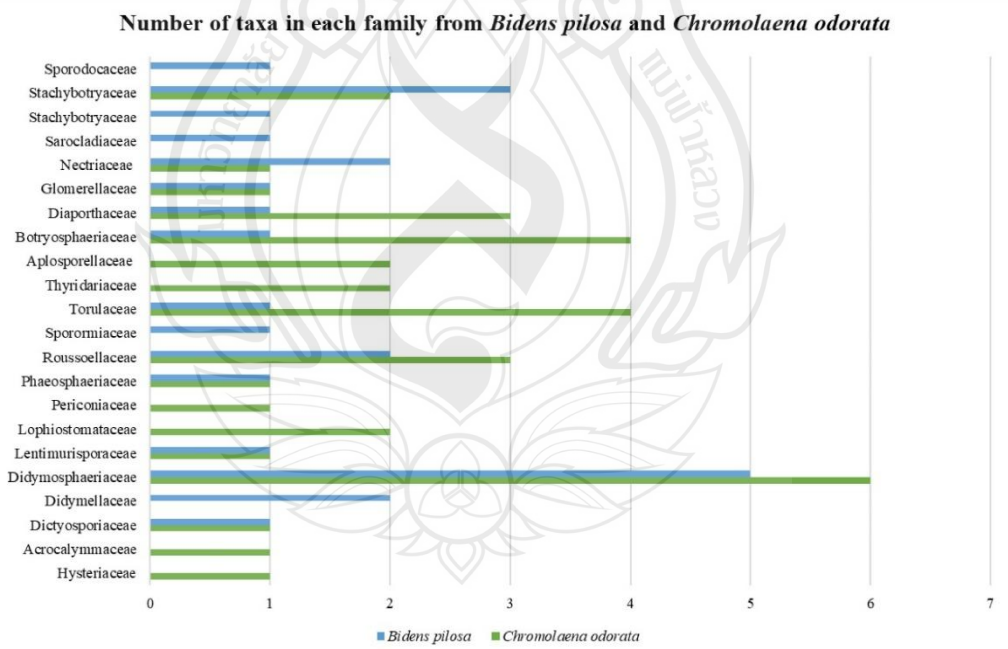



**Figure 5.3** Number of taxa in families from *Bidens Pilosa* and *Chromolaena odorata* found in this study

## 5.5 Antibacterial Potential of Fungi on *Bidens pilosa* and *Chromolaena odorata*

While 13 isolates were excluded from the screening because they lacked fungal cultures, 43 isolates from my fungal specimens that obtained fungal cultures were examined for antibacterial activity. Among the isolates tested, 26 isolates had activity against *Bacillus subtilis*, 21 isolates against *Escherichia coli*, and 20 isolates against *Staphylococcus aureus*. In addition, 12 isolates showed no action against any of the bacteria test organisms (Figure 6.4). The results show that these fungal isolates have the potential to be used as antibacterial agents, with various levels of specificity against different bacteria.

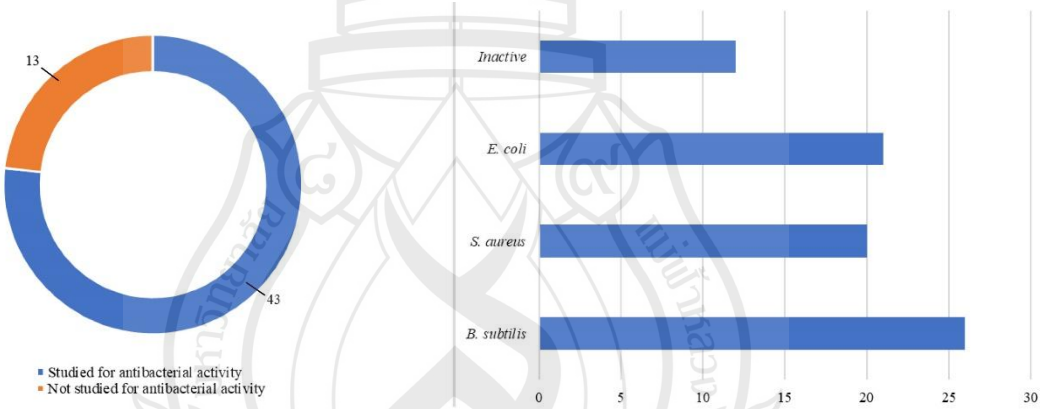



**Figure 5.4** Numbers of fungal isolates on *Bidens pilosa* and *Chromolaena odorata* with potential for antibacterial activity

## 5.6 Research Advantages

Except for Guatimosim et al. (2015) and Mapook et al. (2020), the research on weed associated fungi is limited, especially regarding the saprobic fungal community. Consistent with earlier findings, my study yielded comparable results which can increase the understanding of weed-associated fungi. This study provides an updated account of fungal diversity associated with two Asteraceae weeds, *Bidens pilosa* and

*Chromolaena odorata*, in northern Thailand, supported by detailed morphological descriptions, molecular data, phylogenetic analyses, and herbarium specimens.

In addition to these findings of the current study, this study listed the distribution of fungi on both *Bidens pilosa* and *chromolaena odorata* by providing worldwide checklists. A total of 76 fungal taxa has been documented on *Bidens pilosa* based on USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2025), relevant literature and my result. These species are distributed across 18 orders, 33 families, and 44 genera, representing the phyla Ascomycota, Basidiomycota, Glomeromycota, and Oomycota. The Ascomycota phylum is the most dominant, comprising 32 genera across 23 families (Figure 6.1). A total of 145 fungal taxa has been documented on *Chromolaena odorata* based on USDA Systematic Mycology and Microbiology Laboratory (SMML) database (Farr & Rossman, 2025), relevant literature and my result. These species are distributed across 21 orders, 48 families, and 95 genera, representing two phyla, Ascomycota and Basidiomycota. The Ascomycota is the most dominant phylum on *Chromolaena odorata* with 89 genera across 43 families (Figure 6.1).

The fundamental knowledge for future applications of fungi in advanced technology is expected to be discovered based on accessing potential antibacterial activity. Overall, this study adds the knowledge of weed associated fungal diversity and reviews the possible biological properties for future research in various fields.

## 5.7 Future Perspectives

This study compares the occurrence of saprobic fungi on two different host. Some fungal metabolites characterized in this study are reported to be useful in pharmaceutical, cosmetics and agricultural industries. Exploring ecological interactions such as observing different nutritional modes, and environmental factors affecting the distribution patterns of weeds associated with fungi would be interesting for future research. Genomics and molecular investigations will enhance the better understanding of fungal genetic composition. Studying biosynthetic gene clusters can be revealed the

genetic mechanisms of the bioactive compounds production. Potential climate-related adaptations to fungal metabolic pathways across various regions and seasons could be the subject of future research.

## 5.8 List of Publications

### 5.8.1 First Author

Htet, Z. H., Chethana, K. W. T., & Mapook, A. (2022). The role of fungi in weed biocontrol: A review. *Asian Journal of Mycology*, *5*, 38–58. https://doi.org/10.5943/ajom/5/2/4

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### 5.8.2 Co-author

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# APPENDIX

## ANTIBACTERIAL ACTIVITY RESULTS

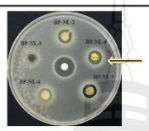
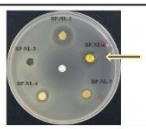
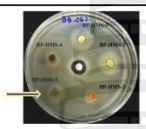
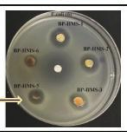
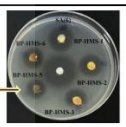
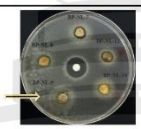
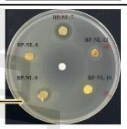
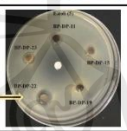
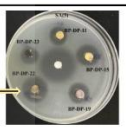
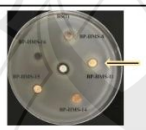
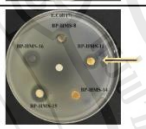
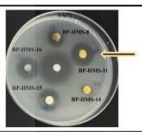
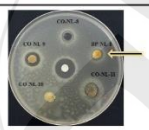
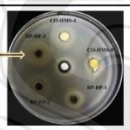
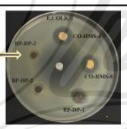
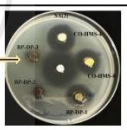
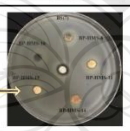
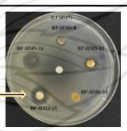
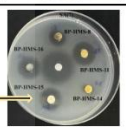
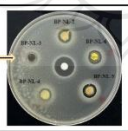
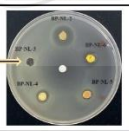
| Species name | *B. subtilis* (+) | *E. coli* (-) | *S. aureus* (+) |
|---|---|---|---|
| *Albifimbria bidentis* (MFLUCC 23T1047) |  |  | No inhibition |
| *Bahusandhika bidentis* (MFLUCC 23T0800) |  |  |  |
| *Colletotricum bidenticola* (MFLUCC 23T0790) |  |  | No inhibition |
| *Dendryphion hydei* (MFLUCC 25T0003) | No inhibition |  |  |
| *Diaporthe biconispora* (MFLUCC 23T0803) |  |  |  |
| *Dictyocheirospora nabanheensis* (MFLUCC 23T1043) |  | No inhibition | No inhibition |
| *Fusarium bidentis* (MFLUCC 23T0784) |  |  |  |
| *Forliomyces bidentis* (MFLUCC 23T0804) |  |  |  |
| *Lasiodiplodia theobromae* (MFLUCC 23T1044) |  |  | No inhibition |

**Figure A1** Antibacterial activity results of selected fungal isolates against *Bacillus subtilis*, *Escherichia coli*, and *Staphylococcus aureus*, showing inhibition zones measured in millimeters

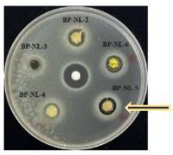
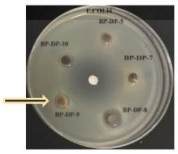
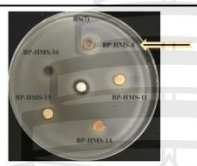
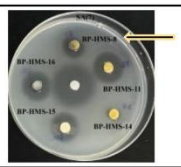
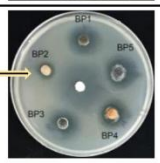
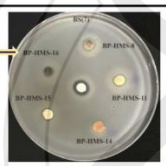
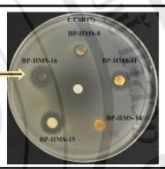
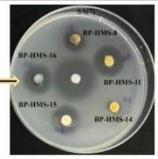
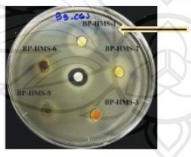
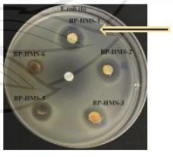
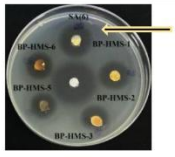
| Species name | *B. subtilis* (+) | *E. coli* (-) | *S. aureus* (+) |
|---|---|---|---|
| *Leptospora thailandica* (MFLUCC 23T1046) |  | No inhibition | No inhibition |
| *Montagnula chromolaenae* (MFLUCC 23T0787) | No inhibition |  | No inhibition |
| *Neoroussoella entadae* (MFLUCC 23T1049) | No inhibition | No inhibition | No inhibition |
| *Periconia byssoides* (MFLUCC 23T0802) |  | No inhibition |  |
| *Pseudoithomyces chartarum* (MFLUCC 23T0781) | No inhibition | No inhibition |  |
| *Remotididymella anthropophila* (MFLUCC 23T0805) |  |  |  |
| *Remotididymella fici-microcarpae* (MFLUCC 24T279) | No inhibition | No inhibition | No inhibition |
| *Sarocladium bidentis* (MFLUCC 24T564) |  |  |  |

**Figure A1** (continued)

# CURRICULUM VITAE

| | |
|---|---|
| **NAME** | Zin Hnin Htet |
| **EDUCATIONAL BACKGROUND** | |
| 2019 | Post Graduate Diploma<br>Environmental Studies<br>University of Yangon |
| 2018 | Bachelor of Science<br>Botany<br>University of Yangon |
| **WORK EXPERIENCE** | |
| 2020-Present | Doctoral Researcher (Ph.D. Candidate sponsored by Basic Research Fund through the National Science, Research and Innovation Fund (Grant Nos. 652A01001, 662A01001, and 672A16001) under the project titled *"Studies of fungi associated with Asteraceae and the discovery of biological properties"*,<br>Center of Excellence in Fungal Research,<br>Mae Fah Luang University |
| **SCHOLARSHIP** | |
| 2020-2022 | Boon Rawd Scholarship |
| 2022-2025 | Grad MFU Scholarship |
| **ADWARDS** | |
| 2018 | Academic Excellence Award (1st)<br>Department of Botany, University of Yangon |
| 2017 | Academic Excellence Award (1st)<br>Department of Botany, University of Yangon |

**PUBLICATION**

**First Author**

Htet, Z. H., Chethana, K. W. T., & Mapook, A. (2022). The role of fungi in weed biocontrol: A review. *Asian Journal of Mycology*, *5*, 38–58. https://doi.org/10.5943/ajom/5/2/4

Htet, Z. H., Hyde, K. D., Alotibi, F. O., Chethana, T. K., & Mapook, A. (2024). Multigene phylogeny, taxonomy, and potential biological properties of *Pseudoroussoella* and *Neoroussoella* species (Roussoellaceae, Dothideomycetes) from Asteraceae weeds in northern Thailand. *MycoKeys*, *111*, 129–146. http://doi.org/10.3897/mycokeys.111.136922

Htet, Z. H., Mapook, A., & Chethana, K. T. (2024). Molecular taxonomy reveals new records of *Chromolaenicola* (Didymosphaeriaceae, Pleosporales) and potential antibacterial properties. *Studies in Fungi*, *9*. http://doi.org/10.48130/sif-0024-0006

Htet, Z. H., Mapook, A., Gafforov, Y., Chethana, K. T., Lumyoung, S., & Hyde, K. D. (2021). Molecular phylogeny and diversity of *Laburnicola* (Didymosphaeriaceae): A new species from Uzbekistan. *Phytotaxa*, *527*, 177–190. http://doi.org/10.11646/phytotaxa.527.3.2

Htet, Z. H., Prematunga, C., Mapook, A., Chethana, T. K. W., & Gareth Jones, E. B. (2023). Taxonomy and phylogeny of *Paradictyoarthrinium salsipaludicola* sp. nov. (Paradictyoarthriniaceae, Pleosporales) from mangroves. *Phytotaxa*, *620*, 283–292. http://doi.org/10.11646/phytotaxa.620.4.4

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**Co-author**

Hyde, K. D., Abdel-Wahab, M. A., Abdollahzadeh, J., Abeywickrama, P. D., Absalan, S., Afshari, N., . . . Zucconi, L. (2023). Global consortium for the classification of fungi and fungus-like taxa. *Mycosphere, 14*(1), 1960–2012, https://doi.org/10.5943/mycosphere/14/1/23

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