



**TAXONOMY AND PHYLOGENY OF DISCOMYCETES WITH
EMPHASIS ON LIGNOCELLULOSE SUBSTRATES AND
ESTABLISHMENT OF DISCOMYCETES.ORG WEBSITE**

ANIS SRI LESTARI

**DOCTOR OF PHILOSOPHY
IN
BIOLOGICAL SCIENCE**

**SCHOOL OF SCIENCE
MAE FAH LUANG UNIVERSITY**

2024

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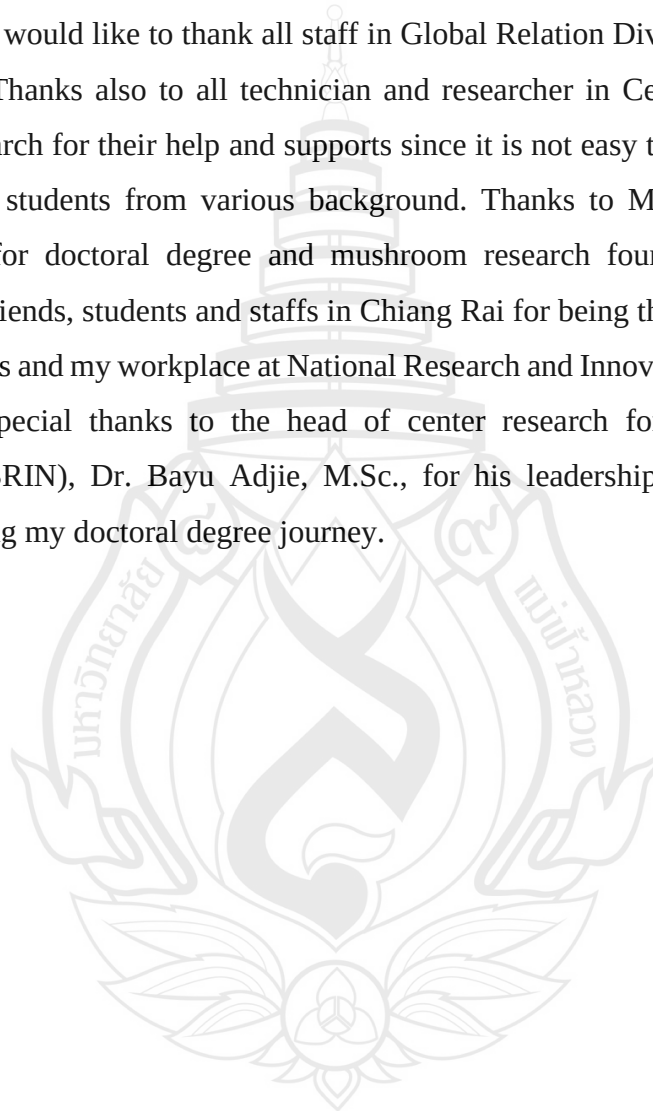
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Anis Sri Lestari



Dissertation Title	Taxonomy and Phylogeny of Discomycetes with Emphasis on Lignocellulose Substrates and Establishment of Discomycetes.org Website
Author	Anis Sri Lestari
Degree	Doctoral of Philosophy (Biological Science)
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ABSTRACT

Discomycetes, an artificial group in Ascomycota, comprises fungal species bearing saucer-, cup- or disc-like ascoma. While discomycetes are mostly found on lignocellulose substrates, they are also present in soil, on rocks, and dung. Most exploration studies collected discomycetes on lignocellulose substrates as saprobes, some as pathogens or parasites, and a few as endophytes. Among the eleven classes that accommodate discomycetes, Leotiomyces has proven to be the most challenging. This dissertation focuses on finding and redescribing discomycete specimens as saprobes in Leotiomyces families and reviews pathogenic and parasitic discomycetes on lignocellulose substrates.

Our exploration of discomycetes, particularly in northern Thailand, has yielded significant findings, particularly those found on lignocellulose substrates as saprobes. In this study, the exploration of discomycetes on lignocellulose substrates in Chiang Mai, Chiang Rai, and Tak provinces, northern Thailand, resulted in the identification of novel taxa, host and geographical records. The identification of these new species, based on a polyphasic approach consisting of morphology, phylogeny analyses and morphological observation of the herbarium material, has addressed taxonomic issues and deepened our understanding of discomycete classification. Notably, in the current

study, *C. montana* and *C. shangrila*, formerly under *Bisporella*, have been re-assigned in *Calycina* based on the morphology, chemical reactions and multi-gene phylogeny, and *C. papaeana* has been introduced as a new species, marking a significant contribution to the *Calycina* taxonomy.

Furthermore, this study not only led to the discovery of five novel species and two geographical records of *Lambertella* within Rutstroemiaceae, but also contributed to the expansion of available sequence data in public repositories. Our polyphasic approach, incorporating the morphology derived from loaned herbarium material and fresh *Lambertella* specimens, and phylogenetic analyses based on ITS, LSU, SSU and *RPB2*, has confirmed the introduction of *L. Chiangraiensis*, *L. fusioidea*, *L. sessilis*, *L. phanensis* and *L. takensis* as novel species, and *L. aurantiaca*, and *L. himalayensis* as geographical records to Thailand. Moreover, the morphology and phylogenetic analyses based on ITS and LSU also revealed a new species in Helotiaceae from Northern Thailand, as well as two novel species from Italy: *Dicephalospora irregularis* and *Cyathicula dioscorea*, with *C. rusci* being introduced in Helotiales. This polyphasic approach also determined a new geographical record, *Chlorencoelia torta*, belonging to Cenangiaceae.

This dissertation encompasses a literature review on discomycetes identified as pathogenic or parasitic on live lignocellulose substrates or designated as phytopathogenic discomycetes. It presents phytopathogenic, discomycetous fungal taxa and offers notes on representative species, their economic importance, and available management strategies. Phytopathogenic discomycetes span six classes of fungi: Dothideomycetes (distributed across three orders, two families and seven genera), Eurotiomycetes (across two orders, two families and two genera), Lecanoromycetes (across three orders, three families and four genera), Leotiomycetes (across nine orders, 23 families and 104 genera), and Pezizomycetes (across one order, seven families and 18 genera). These fungi are recognized as biotrophs, hemibiotrophs, and necrotrophs

in spermatophytes, pteridophytes, and bryophytes, showing varied disease symptoms. The study also highlights that most of the discomycetous phytopathogens reside in Leotiomyces, comprising approximately 104 fungal genera, infecting economically important plant families such as Brassicaceae, Cupressaceae, Ericaceae, Fagaceae, Pinaceae, Poaceae, Rosaceae and Solanaceae. Additionally, it briefly reports on the economic significance and current phytopathogenic status of key species, including *Botrytis cinerea*, *Diplocarpon rosae*, *Diplocarpon brunnea*, *Gremmeniella abietina*, *Neofabrae perenans*, *Oculimacula yallundae*, *Pseudopeziza medicaginis*, and *Rhizina undulata*. The impact of phytopathogenic fungi on important agricultural and forestry commodities is massive, with *B. cinerea* alone causing substantial financial losses ranging from 10–100 billion USD. Furthermore, the financial losses of other phytopathogenic discomycetes in Leotiomyces, such as *Ascocorticium anomalum*, *Ascosorus floridanus*, *Ascodichaena rugosa*, *Monilinia* sp., and *Sclerotinia sclerotiorum*, are noted to be significant, although exact numbers are not detailed as they are reported separately in certain regions. It is stated that chemical applications remain the most predominant solution for managing phytopathogenic discomycetes to reduce economic damage and yield loss in agricultural products, which are essential for food security.

The online platform <https://discomycetes.org>, established in this study, serves as a comprehensive resource for all discomycetes. It compiles disjointed published morphological and phylogeny information in one website, ensuring that all taxa in discomycetes are up to date. The author and other mycologists with expertise in discomycetes regularly update the classification of discomycetes on the online platform <https://discomycetes.org>, providing a reliable and constantly updated source of information for the academic and research community.

Lastly, a checklist of discomycetes from Thailand was provided in this dissertation. A total of 122 novel species out of 690 extant species were recorded from

Thailand, belonging to ten classes, 23 orders, and 57 families. Lecanoromycetes and Leotiomyces were the dominant groups, accounted for 81% (553 species) and 7% (50 species), respectively. Discomycetes, either novel or extant species collected from Thailand, are mostly growing on lignocellulose substrates (83%), with some found on soil, rock, dung other organisms. The number of newly discovered discomycetes peaked from 1992 to 2022, reaching 97 species.

Keywords: Cup fungi, Helotiales, Leotiomyces, Phylogenetic Analyses, Taxonomy

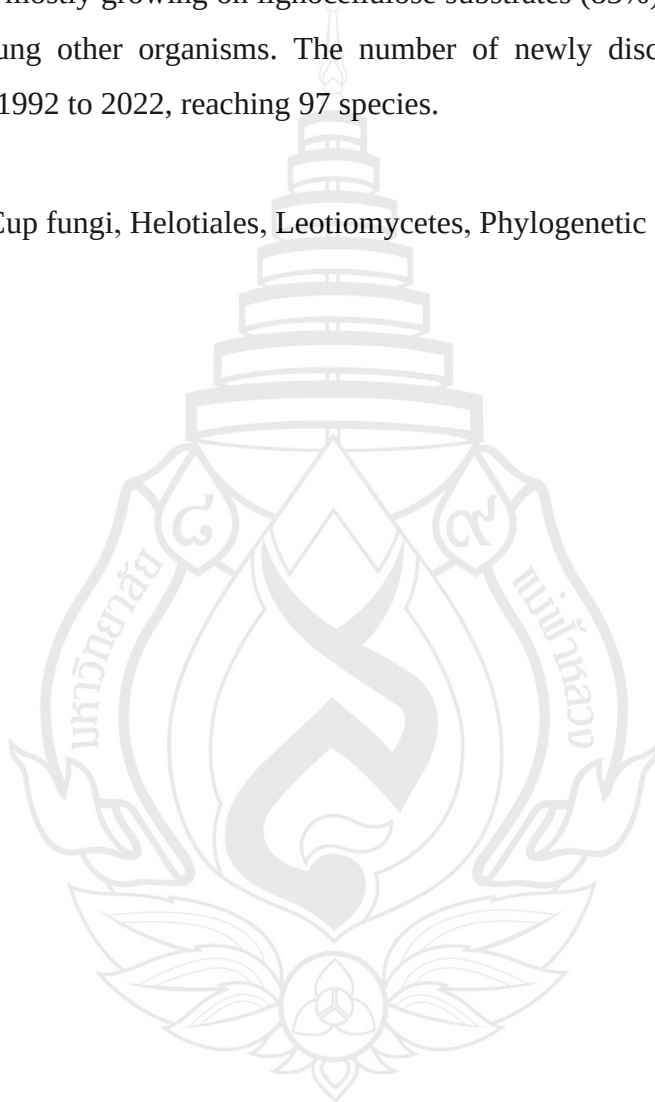


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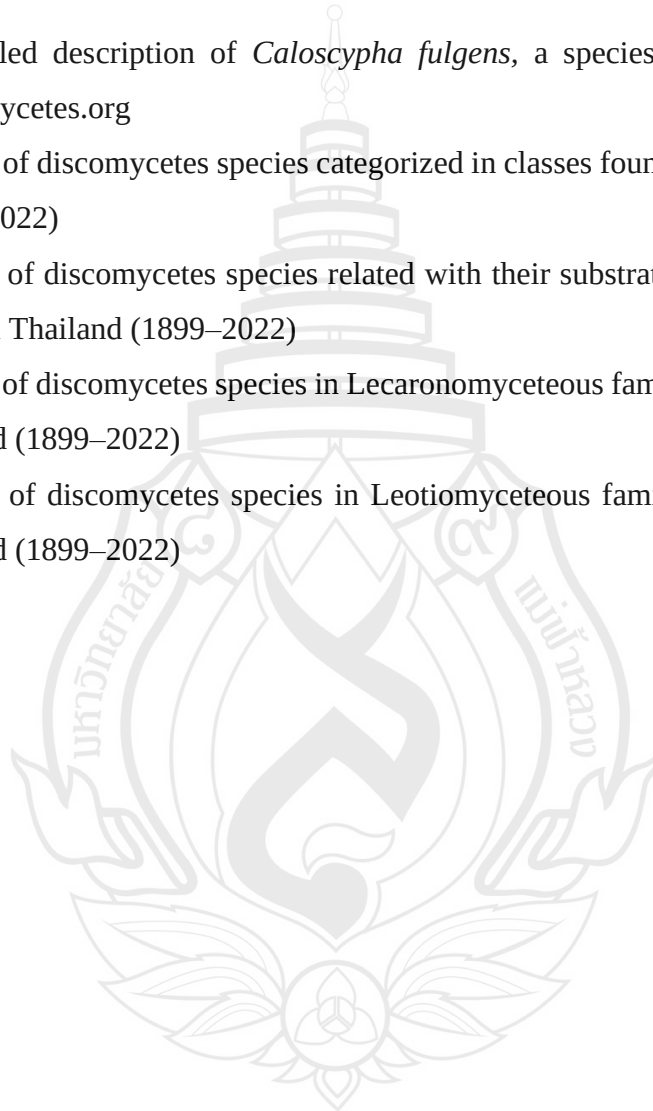
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ABBREVIATIONS AND SYMBOLS

cm	centimeter
comb.	combination
diam.	diameter
e.g	for example
et al.	and others
i.e	that is
mm	millimeter
nov.	novum (Latin for novel thing)
sp.	species
spp.	species (plural)
$\bar{x}$	average
°C	degree centigrade
%	percent
μm	micrometer
μl	microliter
=	heterotypic (taxonomic, facultative) a synonym
≡	homotypic (nomenclature, obligate) a synonym

CHAPTER 1

INTRODUCTION

1.1 Lignocellulose Substrates and Discomycetes

Lignocelluloses are the primary substances of plant materials (branches, leaves, seeds and grasses) composed of lignin, cellulose and hemicellulose (Igarashi et al., 2007). Lignocellulose materials are found in agricultural wastes and forest litter on land (Berg et al., 1984) or aquatic ecosystems (Moran et al., 1988). They are abundant and the most common living substrate for fungi, either basidiomycetes (Pointing & Hyde, 2000) or ascomycetes (Kubartová et al., 2009), including discomycetes (Sherwood, 1981; Suková, 2005).

Discomycetes are ascomycetous fungi recognized from their ascomatal structures, which are of cup-, disc-, saucer-, honey-comb-, cocktail glass-, horse saddle- or club-like shapes. Most discomycetous species bear above-ground ascomata, except for the order Tuberales (truffle fungi), which have underground, mature ascomata (Korf, 1973; Hansen, 2006). Discomycetes grow on various substrates, such as dung (Spooner & Butterfill, 1999; Doveri, 2012), other fungi (Sun et al., 2019), in or on soil (Hansen, 2006), but mostly on lignocellulose substrates (Jaklitsch, 2016).

Discomycetes have undergone significant modifications in their classification and nomenclature in recent years, and this cosmopolitan class now encompasses 11 orders and 70 families, as documented by various studies (Ekanayaka et al., 2017; Ekanayaka et al., 2019; Johnston et al., 2019; Wijayawardene et al., 2022). Traditionally, discomycetes have been defined based on their apothecial macromorphology, micromorphology, and chemical reactions (Pfister & Kimbrough, 2001). However, the generic concept of some discomycetous taxa has been misleading due to the grouping of species based on similar morphologies in the past. The incorporation of molecular data into research has revealed unexpected results that

mycologists never anticipated. For example, *Lichinodium*, which was originally placed in Lichinomycetes due to its lichenized form, was later transferred to Leotiomyces based on morphology (particularly due to lack of haustoria) and multi-gene phylogeny (Prieto et al., 2019). Advances in DNA sequencing technologies and phylogenetic studies have shown that discomycetes are phylogenetically diverse (Spatafora et al., 2006; Wang et al., 2006; Quandt & Haelewaters, 2021), with some families being paraphyletic (Peterson & Pfister, 2010) or polyphyletic (Johnston et al., 2019). Currently, discomycetes are accommodated in two subphyla: Taphrinomycotina (Neoelectomyces) and Pezizomycotina (Arthoniomyces, Coniocybomyces, Dothideomyces, Eurotiomyces, Geoglossomyces, Lecanoromyces, Leotiomyces, Lichinomycetes, Orbiliomyces, Pezizomyces) (Landvik et al., 1993; Ekanayaka et al., 2017).

1.2 Discomycetes in the Classification of Ascomycota

1.2.1 Discomycetes in Arthoniomyces

Discomycetes characterized by mostly lichenized, minute, dark-colored (with red pigments in some species), discoid to hysteroform apothecia are classified into Arthoniomyces (Grube, 2001; Kirk et al., 2008; Ertz et al., 2015; Lee & Hur, 2016). Discomycete members of Arthoniomyces are predominantly crustose lichens, as opposed to discomycetous Lecanoromyces, which grow on crustose, foliose, and fruticose-thalli structures (Schoch & Grube, 2015). Micromorphology of the apothecia in Arthoniomyces revealed a hymenial layer bordered on the outside by poorly defined excipulum cells (Ertz et al., 2009). The hymenium consists of gelatinous substances that are interspersed with paraphysoid and fissitunicate asci, bearing septate and ornamented ascospores (Schultz et al., 2001; Kirk et al., 2008). Discomycetous Arthoniomyces have pycnidial or hyphomycetous asexual morphs (Frisch et al., 2015; Vobis et al., 1992). Arthoniomycetous discomycetes are classified in a single order, Arthoniales, with the majority acting as mutualists and others as saprobes (Gargas et al., 1995; Ekanayaka et al., 2017).

1.2.2 Discomycetes in Coniocybomycetes

Discomycetes in Coniocybomycetes are characterized by mazaediate-form apothecia that are small, dark, and stalked (Prieto et al., 2013). The hymenial layer in apothecia is bordered by less to well-defined excipulum cells (Prieto et al., 2013). Asci in the hymenium are prototunicate and cylindrical, with smooth to ornamented ascospores (Prieto et al., 2013). Coniocybomycetous discomycetes belong to a single order (Coniocybales), a single family (Coniocybaceae), accommodating two genera (*Chaenotheca* and *Sclerophora*), with most species acting as mutualists (mycobionts) in lichens (Lücking et al., 2016; Wijayawardene et al., 2022). Discomycetes in this class have pycnidial or hyphomyceteous asexual morphs (Tibell, 1993; Prieto et al., 2013).

1.2.3 Discomycetes in Dothideomycetes

Discomycetes in Dothideomycetes are categorized by medium to minute, dark-colored apothecia that are discoid, cupulate to hysteriform (Greif et al., 2007; Hongsanant et al., 2020). The hymenium is bordered by well-developed excipulum cells that are largely pigmented, pseudoparenchyma cells of *textura subangularis*, *textura angularis* to *textura globulosa* (Greif et al., 2007; Boehm et al., 2009). Unitunicate to bitunicate asci in the hymenial layer are interspersed with pseudoparaphyses to paraphyses with swollen apices (Kutorga & Hawksworth, 1997; Greif et al., 2007; Thambugala et al., 2016). Discomycetous Dothideomycetes have hyaline to pigmented, septate-ascospores (Greif et al., 2007; Thambugala et al., 2016) and are found in Catinellales, Eremithallales, Hysteriales, Mytilinidiales, Patellariales and Pleosporales (Ekanayaka et al., 2017), with most species serve as mutualists (Lücking et al., 2008), saprobes (Yacharoen et al., 2015) and biotrophic pathogens (Inácio & Canon, 2008; Lestari et al., 2023). Dothideomycetous discomycetes are typically found on lignocellulose substrates in terrestrial or occasionally marine habitats (Boehm et al., 2009; Jones et al., 2015). The asexual morphs in this class are often coelomycetous or sometimes hyphomyceteous (Boehm et al., 2009; Yacharoen et al., 2015).

1.2.4 Discomycetes in Eurotiomycetes

In Eurotiomycetes, discomycetes are characterized by minute, dark-colored, sessile or stalked apothecioid sexual morph or mazaedial ascomata (Alexopoulos

et al., 1996; Döbbeler & Feuerer, 2004; Jaklitsch et al., 2016; Olariaga et al., 2019; Prieto et al., 2021). The hymenial layer comprises cylindrical asci, that contain pigmented ascospores (Wedin & Tibell, 1997). Discomycetes are divided into two orders and two families in Eurotiomycetes (Ekanayaka et al., 2017; Réblová et al., 2017), with the majority being saprobes on lignocellulose substrates (Vinuesa et al., 2001) and biotrophic pathogens (Döbbeler & Feuerer, 2004). Discomycetes in Eurotiomycetes are mostly found as hyphomyceteous asexual morphs (Geiser et al., 2006).

1.2.5 Discomycetes in Geoglossomycetes

All Geoglossomycetes members are discomycetes with dark to brightly colored, stalked apothecia that range from medium to large (Hustad et al., 2013). The apothecial cross section shows pigmented, filiform ascospores in cylindrical clavate asci (Schoch et al., 2009). Geoglossomycetes accommodates a single order, Geoglossales, a single family Geoglossaceae and seven genera (Schoch et al., 2009; Hustad et al., 2013; Wijayawardene et al., 2022). Most Geoglossomycetes are saprobes in the soil, while some are root endophytes (Hustad et al., 2013; Wang et al., 2011). Unlike other discomycetes in other classes, asexual morphs for Geoglossomycetes are not recorded (Wang et al., 2006).

1.2.6 Discomycetes in Lecanoromycetes

Discomycetes in Lecanoromycetes are characterized by medium to small, lichenized or non-lichenized apothecia (Miadlikowska et al., 2006; Schoch et al., 2009a). Lichenized apothecia with bright to dull colors can be found in crustose, foliose, and fruticose thalli structures (Honegger, 1978; Ekanayaka et al., 2019b). The hymenial layer in apothecia is made up of branched paraphyses and inoperculate asci that bear hyaline, aseptate to septate ascospores (Magain & Sérusiaux, 2012; Lumbsch et al., 1995). Lecanoromycetes is the most speciose class of discomycetes among the Ascomycota classes, containing 16 orders (Kirk et al., 2008; Ekanayaka et al., 2017). Discomyceteous Lecanoromycetes are found mostly as mutualists on lignocellulose substrates (Brodo et al., 2001; Wedin et al., 2004), some as parasites on other lichens (Lawrey & Diederich, 2003) as saprobes (Sherwood-Pike, 1987). In Lecanoromycetes,

the asexual morphs are pycnidial or hyphomycetous (Ertz et al., 2012; Miadlikowska et al., 2014).

1.2.7 Discomycetes in Leotiomyces

Leotiomyces is the second-largest class encompassing approximately 80,000 discomycetous species after Lecanoromycetes (Ekanayaka et al., 2017; Johnston et al., 2019). Leotiomyces are characterized by medium to minute, bright to dull colored, stipitate or sessile, immersed apothecia that are typically disc-, saucer-, or honeycomb-shaped (Wang et al., 2006; Johnston et al., 2019). This class of apothecia has a hymenial layer with mostly inoperculate asci carrying hyaline to brown and ovoid, ellipsoid, fusoid to filiform ascospores (Karakehian et al., 2019; Quijada et al., 2022).

Leotiomyces is the most perplexing class, with controversial taxa placements (Berbee et al., 2001; Quandt & Haelewaters, 2021). The majority of Leotiomyces are saprobes (Hansen, 2006; Laessle & Hansen, 2007), others are phytopathogens (Peterson et al., 2010), and some are mutualists as endophytes, ectomycorrhizal fungi and lichens (Chang et al., 2016; Tanney et al., 2016; Prieto et al., 2019). Currently, Leotiomyces accommodates more than 50 families in which accommodating more than 620 genera (Quandt & Haelewaters, 2021; Wijayawardene et al., 2022). The asexual morphs of this class are mostly hyphomycetous (Ingold, 1979), pycnidial (Crous et al., 2014) and coelomycetous (Lantz et al., 2011).

1.2.8 Discomycetes in Lichinomycetes

Discomycetes in Lichinomycetes are characterized by lichenized, small and immersed apothecia (Schultz et al., 2007; Ortiz-Alvarez et al., 2015). The apothecia consist of protunicate asci, enveloped by a gelatinized layer (Schultz & van den Boom, 2007). Kirk et al. (2008) describe ascospores enclosed in asci as hyaline and aseptate. Discomycetes in Lichinomycetes are found in a single order (Lichinales), accommodating a single family (Gloeohelpeaceae) and three genera (*Gloeohelpea*, *Gudelia*, and *Pseudopeltula*) (Ekanayaka et al., 2017; Wijayawardene et al., 2022). The asexual morphs of this class are mostly pycnidial (Schultz et al., 2001).

1.2.9 Discomycetes in Neoelectomycetes

The only class accommodating discomycetes in the subphylum Taphrinomycotina is Neoelectomycetes, with Neoelectales as the only order (Landvik et al., 1993; Eriksson & Winka, 1997). Members of Neoelectales have club-like apothecia, similar to *Microglossum* (Leotiales, Leotiomyces). They differ, however, in that they have a truncated ascus and lack paraphyses and croziers (Landvik et al., 2003; Ekanayaka et al., 2019b). All members of Neoelectomycetes are discomycetes having diverse ecological roles, mostly saprobes with a few parasitic biotrophs (Redhead, 1979; Landvik et al., 2003). The asexual morphs of this class produce conidia to a yeast form (Redhead, 1977).

1.2.10 Discomycetes in Orbiliomycetes

Orbiliomycetes was previously enlisted as a family, Orbiliaceae, in Helotiales (Nannfeldt, 1932; Kimbrough, 1970). Orbiliales is the only order in this class (Eriksson et al., 2003). Orbiliomycetes apothecia are disc-shaped, medium to small, stipitate to sessile, translucent, and brightly or dull colored (Baral, 1994; Baral et al., 2021). The apothecia comprised a waxy to gelatinous matrix, inoperculate asci with variously shaped ascospores, and bordered by textura globulosa cells (Baral et al., 2021). Discomycetous Orbiliomycetes play diverse ecological roles, mostly as saprobes, parasites and mutualists (Baral et al., 2020). Pfister (2015) discovered orbiliomyceteous specimens in dung, soil, and plant-associated materials. The asexual morph of this class is primarily hyphomycetous (Baral et al., 2017).

1.2.11 Discomycetes in Pezizomycetes

Pezizomycetes are discomycetes with medium to large apothecia, mostly operculate asci that discharge ascospores via rupturing or through lid-like ascal tip (Hansen & Pfister, 2006). Pezizomycetes apothecia are distinguished not only by their large sizes but also by their attractive colors, which include pink, orange, red, yellow, and white, with others being brown, grey and black (Denison, 1963; Hansen & Pfister, 2006). Apothecial shapes of Pezizomycetes varied from discoid, cupulate, and applanate to bizarre shapes, such as honeycomb-like to elfin-saddle-like (Clements & Shear, 1954). The cross-section of the apothecium shows a hymenial layer with a well-

developed ectal excipulum and a variety of asci and ascospores (Spooner, 2001; 2002; Ekanayaka et al., 2018).

Most species in Pezizomycetes live above ground and have active ascospore dispersal mechanisms, whereas Tuberales species live beneath the soil and have diminished ascospore dispersal mechanisms (Hansen, 2006; Læssøe & Hansen, 2007). Discomycetes in Pezizomycetes are found in 18 families, including Pezizales genera incertae sedis (Wijayawardene et al., 2022), and play predominantly saprobic (Perry et al., 2007), others as pathogenic (Cha et al., 2009; Lestari et al., 2023) and mutualistic ecological roles (Wei et al., 2010). The asexual morphs of Pezizomycetes are mostly hyphomycetous (Hansen & Pfister, 2006).

1.3 The Significance of Studying Discomycetes on Lignocellulose Substrates

Discomycetous fungi are prevalent in subtropic, tropic, and subarctic regions (Whetzel & Solheim, 1943; Korf, 1997; Ekanayaka et al., 2019). In environments such as forests, freshwater and marine ecosystems, discomycetous fungi play essential roles as endophytes, symbionts (mycorrhizas and lichens), saprobes and pathogens (Warcup, 1990; Suetrong & Jones, 2006; Filippova, 2012; Cantrell, 2014; Gueidan et al., 2015).

Discomycetes fungi on lignocellulose substrates (dead plant materials) serve as saprobes (Jaklitsch, 2016), even though some saprobic discomycetes are isolated from dung (Spooner & Butterfill, 1999; Doveri, 2012), other fungi (Sun et al., 2019), and soil (Hansen, 2006). Discomycetes on lignocellulose materials can also be parasitic, causing nonlethal symptoms on plant substrates, while pathogenic discomycetes cause lethal diseases (Bogacheva, 2005; Gadgil, 2009; Dean et al., 2012; Çolak & Kaygusuz, 2017). Saprobic and phytopathogenic nonlichenized discomycetes are primarily grouped in Leotiomyces, with some species listed in Dothideomyces, Eurotiomyces, Lecanoromyces, and Pezizomycetes (Denton-Giles et al., 2019; Quand & Haelewaters, 2021; Lestari et al., 2022).

1.4 Research Objectives

1.4.1 To study taxonomy and phylogeny of discomycetes found on lignocellulosic substrates with emphasize on Leotiomyces

1.4.2 To update and revise selected families in Leotiomyces (Cenangiaceae, Helotiaceae, Hyaloscyphaceae, Lachnaceae, Pezizellaceae and Rutstroemiaceae)

1.4.3 To establish and update the discomycete website: Discomycetes.org

1.5 Research Contents

This dissertation provides:

Chapter 1 contains the general introduction of discomycetes, discomycetes on lignocellulose substrates, and the significance of studying discomycetes on lignocellulose substrates.

Chapter 2 presents an account of saprobic discomycetes on lignocellulose substrates in Cenangiaceae, Helotiaceae, Hyaloscyphaceae, Lachnaceae, Pezizellaceae and Rutstroemiaceae.

Chapter 3 encompasses discomycetes on lignocellulose substrates as phytopathogens, including their economic importance and control.

Chapter 4 introduces the establishment of Discomycetes.org

Chapter 5 provides the overall conclusions, research advances and works

CHAPTER 2

SAPROBIC DISCOMYCETES ON LIGNOCELLULOSE SUBSTRATES EMPHASIZING SOME FAMILIES IN HELOTIALES

2.1 Introduction

Saprobic discomycetes on lignocellulose substrates are those fungi bearing apothecia found on dead plant materials (branches, twigs, wood barks, logs and leaf litters). Although some discomycetes are also found on other substrates such as soil (Hansen, 2006), dung (Spooner & Butterfill, 1999; Doveri, 2012) and other fungi (Sun et al., 2019), most discomycetes are saprobic (Jaklitsch, 2016), and the majority were found on lignocellulose substrates (Jaklitsch, 2016).

Leotiomyces are morphologically and ecologically diverse fungal taxa in Ascomycota. It encompasses fungi bearing various types of ascocarps, apothecia (most families), cleistothecia (mostly within Erysiphaceae) and perithecia (Loramycetaceae) (Eriksson, 2003; Baral, 2016). Leotiomycetous fungi inhabit terrestrial ecosystems, such as forests, plantations, and agricultural areas (Blein et al., 2008), but also inhabit aquatic ecosystems (freshwater and marine habitats) (Pointing & Hyde 2000; Baschien et al., 2013).

Helotiales was introduced in Ascohymeniales by Nanfeldt (1932) to accommodate six families, namely Dermateaceae, Helotiaceae, Hyaloscyphaceae, Phacidiaceae, Orbiliaceae and Geoglossaceae with their superficial apothecia, inoperculate asci, and ellipsoid to fusiform ascospores. Heterospermales replaced Helotiales based on the differences in wall formation and ornamentation among inoperculate and operculate discomycetes (Le Gal, 1947). Later, discomycetes were classified in Helotiales, Lecanorales, Pezizales, Ostropales and Phacidiales, with eight

families accommodated in Helotiales, namely Ascocorticiaceae, Caliciaceae, Dermeateaceae, Geoglossaceae, Helotiaceae, Hyaloscyphaceae, Orbiliaceae and Sclerotiniaceae (Dennis, 1968).

The first phylogenetic analysis of discomycetes was conducted by Gargas and Taylor (1995) using rSSU sequences. With the advances in DNA sequencing technology, discomycetous classification achieved breakthroughs with subsequent phylogenetic and evolutionary studies. Based on three genes combined phylogeny, Helotiales was placed within Leotiomyces along with four other orders (Wang et al., 2006a). In contrast, several families formerly placed by Nanfeld (1932) and Dennis (1968) within Helotiales were transferred to other classes. Geoglossaceae and Orbiliaceae were excluded from Helotiales (Gernandt et al., 2001; Wang et al., 2006a; b). Helotiales was revised based on new specimens and genomic data, resolving the uncertainties in their phylogeny and classification (Ekanayaka et al., 2019a; Johnston et al., 2019; Wijayawardene et al., 2020). To date, 34 families (including inoperculate discomycetes) in three lineages (*Hyteropezizella*, *Stamnaria*, *Strossmayeria*) and Helotiales genera *incertae sedis* were accepted (Quandt & Haelewaters, 2021). However, more studies are necessary on Helotiales, especially for certain families, such as Cenangiaceae, Helotiaceae, Hyaloscyphaceae, Lachnaceae and Rutstroemiaceae.

Lahmiales, an order in Ascomycota, accommodates only the family Lahmiaceae with its sole genus *Lahmia*, which comprises two species (Wijayawardene et al., 2022). Lahmiales was introduced and described by Eriksson (1986) in Dothideomycetes, which then transferred to Lecanoromycetes (Raitviir & Spooner, 1994), but Baral (2016) suggested to include this order in Leotiomyces. According to Baral (2016), Lahmiales was placed in Leotiomyces based on the similar ascomatal morphologies shared with Rhytismatales. However, it differs from the latter by having bitunicate asci and lacking clypeate stroma. Evolutionary, Eriksson (1986) suggested that Lahmiales is a monotypic family based on the distinct morphology. Micraspidales in Leotiomyces comprises only three species assigned to its only genus, *Micraspis*, which belongs to Micraspidaceae, the sole family in Micraspidales (Quijada et al., 2020). Historically, based on the absence of amyloid ascal tip and vertically oriented covering layer, *Micraspis* was reassigned to *Tympaneae* (Korf, 1973; DiCosmo et al., 1983, 1984). Baral (2016) placed *Micraspis* in Tympanidaceae (Phacidiales) based on

asexual morph characters, especially the formation of microconidia from phialides and septate macroconidia. A study documented a multi-gene phylogenetic tree of Leotiomyces by Johnston et al. (2019), including several genera of Tympanidaceae (the family which formerly accommodated *Micraspis*), but *Micraspis* sequences were not included in the analysis. Later, Quijada et al. (2020) resolved taxonomic issues on *Micraspis* by providing a multi-gene phylogenetic tree, confirming the previously identified distinct characters; hence, *Micraspis* was placed in the new family, Micraspidaceae in the new order Micraspidales.

2.1.1 Cenangiaceae, Helotiales

Cenangiaceae was established by Rehm (1889) with *Encoelia* as the type genus and included *Cenangiopsis*, *Encoeliella*, *Encoeliopsis*, and *Velutarina* as the members. Rehm (1889) characterized Cenangiaceae as having erumpent or superficial, urn-shaped to cupulate, leathery apothecia with a rough exterior. Asci are cylindric to clavate, hemispherical to conical apex with inamyloid or apical ring. Ascospores are hyaline or brown in some species, ellipsoidal, ovoid, fusoid or allantoid; aseptate, rarely 1–3-septate (Pärtel et al., 2017). Nanfeldt (1932), however, included the aforementioned genera in Encoelioideae, a subdivision of Helotiaceae, based on Höhnelt's observation (Höhnelt, 1923). Pärtel et al. (2017) then resurrected Cenangiaceae, which included genera *Cenangiopsis*, *Cenangium*, *Chlorencoelia*, *Crumenulopsis*, *Encoelia*, *Fabrella*, *Heyderia*, *Rhabdocline*, *Sarcotrochila*, *Trochila* and *Velutarina* that show morphological and phylogenetic affinities, while some genera such as *Didymascella*, *Hysterostegiella* and *Korfia* are only morphologically supported.

2.1.2 Helotiaceae, Helotiales

Helotiaceae was established by Rehm (1892) with *Helotium* as the genus type, and this family is large and the most heterogenous in Helotiales (Leotiomyces) (Dennis, 1968). Members of Helotiaceae are characterized by bright to dark colored soft, fleshy to leathery apothecia. The asci are inoperculate, 8-spored, amyloid or inamyloid ascus tips (Kimbrough, 1970; Phutthacharoen et al., 2022). The excipular cells are characterized by *textura prismatica* to *textura intricata* or woven hyphae covered by a thin layer of cuboid or globose cells (Dennis, 1968). Currently, 31 genera

are accommodated in Helotiaceae, including *Cyathicula* and *Dicephalospora* (Wijayawardene et al., 2022).

2.1.3 Hyaloscyphaceae, Helotiales

Nanfeld (1932) introduced Hyaloscyphaceae, which encompasses three tribes, namely Arachnopezizeae, Hyaloscypheae and Lachneae. Arachnopezizeae was characterized by ≤ 2 mm of apothecia surrounded with protruding hyphae forming a web-like structure (Kirk et al., 2008), thin to thick-walled apothecial hairs and *textura angularis* ectal excipulum (Kosonen et al., 2021). Hyaloscypheae comprised fungi with less than 1 mm apothecia, cylindrical paraphyses and various shaped hairs, while Lachneae was defined by characters, such as ≥ 1 mm apothecia, granulate hairs and lanceolate paraphyses (Han et al., 2014).

Hyaloscyphaceae is typified by *Hyaloscypha*, which is a sexual morph characterized by minute apothecia (< 1 mm), conical to lageniform hairs and filiform paraphyses (Han et al., 2014). The asexual morph of Hyaloscyphaceae is known in hyphomycetes genera such as *Cheiromycella*, *Clathrosphaerina*, *Monodictys* and *Pseudaegerita* (Descal & Webster, 1976; Abdullah & Webster, 1983; Huhtinen, 1989; Hosoya & Huhtinen, 2002). Currently, more than 30 genera are included, namely *Aeruginoscyphus*, *Ambrodiscus*, *Arbusculina*, *Cheiromycella*, *Clavidisculum*, *Clathrosphaerina*, *Dematioscypha*, *Dimorphotricha*, *Echinula*, *Eupezizella*, *Glutinomyces*, *Graddonidiscus*, *Grahamiella*, *Haplographium*, *Hegermilla*, *Hyaloscypha*, *Hyalopeziza*, *Hyphopeziza*, *Incrupila*, *Meliniomyces*, *Mimicoscypha*, *Mycoarthris*, *Olla*, *Polaroscyphus*, *Proprioscypha*, *Protoungicularia*, *Pseudaegerita*, *Psilocistella*, *Resinoscypha*, *Rhizoscyphus*, *Thindiomyces*, *Ungiculariella* and *Unguiculella* (Ekanayaka et al., 2019a; Kosonen et al., 2020; Wijayawardene et al., 2020; Index Fungorum, 2021).

Hyaloscyphaceae includes fungal species with various ecological roles, such as endophytes (Nakamura et al., 2019), primarily saprobes on lignocellulosic materials (Han et al., 2014; Kosonen et al., 2020), parasitic on mosses (Baral et al., 2009) and root symbionts (Fehrer et al., 2019). Following extensive studies, several genera were introduced and transferred to Hyaloscyphaceae (Hosoya & Otani, 1997; Raitviir, 1970; Raitviir, 1987; Spooner, 1987; Svrček, 1987; Korf, 1980; Haines, 1989; Cantrell &

Hanlin, 1997). Hence, more than 70 genera were included in this family (Kirk et al., 2008). Several genera were comprehensively reviewed, and some genera, such as *Lachnum*, were transferred to Lachnaceae (Raitviir, 2004).

2.1.4 Lachnaceae, Helotiales

Lachneae was a tribe in Hyaloscyphaceae established by Nanfeld (1932), characterized by minute to medium-sized apothecia, septate, granulate hairs and lanceolate paraphyses, and its members called lachnoid fungi. Lachneae was raised to Lachnaceae by Raitvir (2004), following recommendations by Cantrell and Hanlin (1997) based on morpho-phylogenetic evidence.

Lachnaceae is typified by *Lachnum*, characterized by minute, sessile to stipitate apothecia, lanceolate paraphyses, septate, and granulate hair, sometimes with crystal materials at the top (Hosoya, 2009). *Lachnum* was listed formerly in Hyaloscyphaceae, then transferred to Lachnaceae as Lachneae was elevated to the family level by Raitviir (2004). *Lachnum* is usually paraphyletic in phylogenetic analyses (Hosoya et al, 2009; Baral, 2016). Other discomycetous genera in Lachnaceae are *Albotricha*, *Brunnipila*, *Dasyscyphella*, *Incrucipulum*, *Lachnellula*, *Lasiobelonium*, *Proliferodiscus*, *Trichopeziza*, *Trichopezizella* (Johnston et al., 2019), *Asperopilum* (Spooner, 1987), *Erioscyphella* (Ekanayaka et al., 2019a), *Lachnopsis* (Guatimosim et al., 2016), *Capitotricha*, *Neodasyscypha* (Suková, 2005), *Perrotia* (Polhorský & Červenka, 2020), *Tubolachnum* (Velenovský, 1934), and *Crucellisporiopsis* (as coelomycetes) (Crous et al., 2014).

Ecological roles of Lachnaceae species are varied, with the majority living as saprobes on miscellaneous substrates (Hosoya, 2009; Tochiara et al., 2019), while others live as endophytes (Chang et al., 2016; Durán et al., 2021) and plant parasites (Yde-Andersen, 1979; Cantrell et al., 1996; Guatimosim et al., 2016).

2.1.5 Pezizellaceae, Helotiales

Pezizellaceae was introduced with *Pezizella* as the type genus (Velenovský, 1934), while *Peziza sordida* (type species of *Pezizella*) was then transferred to *Calycina* (Baral, 1989). *Pezizella* species were also re-observed and reassigned to different genera, such as *Allophylaria*, *Arachnopeziza*, *Calloria*, *Calycellina*, *Ceratophacidium*, *Cistella*, *Clavidisculum*, *Conchatium*, *Crocicreas*, *Cyathicula*, *Dasyscyphus*, *Gemmina*,

Helotium, *Hyalinia*, *Hyalopezia*, *Hyalorbilia*, *Hyaloscypha*, *Hymenoscyphus*, *Ijuhya*, *Incrupila*, *Laetinaevia*, *Leptodontidium*, *Mniaecia*, *Mollisia*, *Mollisina*, *Naeviopsis*, *Niptera*, *Neomensularia*, *Ombrophila*, *Orbilia*, *Rodwayella*, *Pachydisca*, *Pithyella*, *Psilachnum*, *Pseudohelotium*, *Pyrenopeziza*, *Thelebolus*, *Trichopeziza* and *Unguiculella* (Baral, 1989; Baral, 1993; Baral & Quijada, 2020; Index Fungorum, 2022). The delimitation of genera in Pezizellaceae remains unresolved (Suija & Motiejūnaitė, 2017).

2.1.6 Rutstroemiaceae, Helotiales

Rutstroemiaceae was established, comprising *Lambertella*, *Lanzia*, *Poculum*, and *Verpatinia* based on nuclear rDNA phylogeny and typified with *Rutstroemia* (Kohn & Grenville, 1989; Holst-Jensen et al., 1997). The family was characterized by brownish and greenish, stipitate to substipitate apothecia or sometimes cleistothecia with inoperculate, cylindric-clavate asci, and hyaline to brown, fusiform to ellipsoid ascospores. Most species of Rutstroemiaceae are saprobes, and a few are parasites (Holst-Jensen et al., 1997; Galán et al., 2015; Wiseman et al., 2015; Zhao et al., 2016; Baral, 2017; Johnston et al., 2019). With several taxonomic revisions based on morpho-phylogeny and novel species discoveries, Rutstroemiaceae has been expanded from its initial members to include eight genera, *Bicornispora*, *Bryorutstroemia*, *Clarireedia*, *Lambertella*, *Lanzia*, *Pseudolanzia*, *Rutstroemia*, and *Torrendiella* (Švrček, 1957; Johnston & Park, 2013; Johnston et al., 2014; Galán et al., 2015; Pärtel et al., 2017; Baral, 2017; Wijayawardene et al., 2022; Baral et al., 2023).

2.1.7 Lahmiaceae, Lahmiales

Lahmiaceae sexual morphs have perithecial to apothecial ascomata, stalked on various thallus-like structures once thought to be lichenized (Nannfeldt, 1932; Eriksson, 1986). Their ascomata vary from turbinate to cup-shaped structures (Funk, 1976; Rehm, 1900; Eriksson, 1986), and the ascomatal walls are composed of hyphal cells of *textura intricata*. These scleroplectenchymous walls are filled with gelatinous materials and melanized on the hyphal surface (Eriksson, 1986). Hamathecium in young ascomata consists of filiform paraphysoids stretched between and above the asci; the upper part of the hamathecium produces paraphyses-like filaments with free, slightly swollen tips (Eriksson, 1986). Asci are clavate with a long base and bitunicate, composed of thin

exotunicate and endotunicate, which become thickened after ascospore ejection (Eriksson, 1986). Ascospores are hyaline, crescent-shaped and septate (Rehm, 1900; Eriksson, 1986). The sexual morph is only reported by Funk (1976).

2.1.8 Micraspidaceae, Micraspidales

The taxa of Micraspidaceae are characterized by shining, black, orbicular to elliptic apothecia with an irregular longitudinal slit, ectal excipulum arranged in *textura epidermoidea* and inamyloid, 4–8-spored asci (Quijada et al., 2020). The taxa are distributed in Canada, Denmark, Ireland, Russia, the UK and the USA, and most occur on needle leaves of *Picea* spp., the wood of *Picea sitchensis* and cones of *Pinus sylvestris* (Darker, 1963; Dennis, 1971; Graddon, 1984; Popov, 2007; Quijada et al., 2020).

Micraspidaceae taxa form apothecia, which are scattered or in small clusters, sessile, orbicular or erumpent, irregularly elongate, developing inside the host, closed at first, and then open by tearing up stromatic covering layer into rectangular lids. The shape of the apothecia can be round, irregularly ellipsoid, or elliptical (Quijada et al., 2020). Excipulum cells are composed of dark cells of *textura epidermoidea* to *textura angularis*, often faintly separated between ectal to medullary excipulum. Asci are cylindrical clavate, and the ascus size differentiates *Micraspis tetraspora* from the other two *Micraspis* species (Quijada et al., 2020). Some of the ascospores of *Micraspis tetraspora* are aborted; hence, the asci sometimes bear four ascospores. In general, the ascospores of *Micraspis* are cylindrical fusoid to clavate-ellipsoid and 1–5-transverse septate (Quijada et al., 2020). The asexual morph is pycnidial, scattered, dark brown to black, with phialidic conidiogenous cells bearing filiform, flaccate, and fusiform to allantoid conidia.

2.2 Materials and Methods

2.2.1 Collection Sites

Discomycetous specimens found on lignocellulose substrates were collected from Doi Inthanon National Park and Mushroom Research Foundation Forest, Chiang Mai and Chiang Rai regions, Tak Province, Thailand. In contrast, herbarium specimens

were obtained from Forlì-Cesena, Perugia province, Italy and some from various herbarium institutions from Belgium (Meise Botanic Garden: BR), China (Herbarium Mycologium Institute of Microbiology Chinese Academy of Sciences: HMAS), Croatia (Croatian National Fungarium: CNF), Japan (The National Museum of Nature and Science: TNS), Estonia (Institute of Agricultural and Environmental Sciences of Estonian University of Life Sciences: TAAM), Norway (Natural History Museum Botanical Museum, University of Oslo: O), USA (The Cornell Plant Pathology Herbarium: CUP; Botany and Plant Pathology Department, Oregon State University: OSC).

2.2.2 Morphological Studies

Macromorphology of apothecia was observed, dissected using a Leica EZ4 stereomicroscope (Leica Microsystems Company, Germany), and photographed by an Olympus SC 180 digital camera (Olympus Corp., Japan) connected to the microscope. Apothecial micromorphology includes examining excipular cells, paraphyses, asci, and ascospores on a compound microscope, Nikon Eclipse Ni-U (Nikon Corp., Japan) connected to the Nikon DS-Ri2 digital camera for photographing. Tarosoft (R) Image Frame Work software version 0.9.7 was used for the measurement (Senanayake et al. 2020). Chemical reactions during micromorphology observation were observed by mounting the apothecial section in distilled water or 2–5% KOH, stained in Congo red and Melzer's reagent (MLZ) for the amyloid test. The dried herbarium specimens were deposited at the Mae Fah Luang University Herbarium (MFLU), Thailand. Faces of fungi numbers and Index Fungorum numbers were obtained as in Jayasiri et al. (2015), Index Fungorum (2022, 2023, 2024) and Mycobank (2023).

2.2.3 DNA Extraction, Amplification, and Sequencing

Genomic DNA was extracted from the apothecia using the E.Z.N.A Fungal DNA Mini Kit D3390-02 (Omega Bio-Tek, USA) following Dissanayake et al. (2020). Apothecia were collected into 1.5 ml microtubes and ground using pestles with liquid nitrogen. DNA extractions followed the manufacturer's protocol with slight modifications to the additional incubation and reduced elution volume of the extracted DNA. The extracted DNA was then stored at -20°C until further processing. The PCR reactions were conducted to amplify the necessary loci and genes. The primers listed in

Table 2.1 were used. The PCR products were stained with DL5000-DNA fluorescent loading dye (Smobio Technology Inc., Taiwan), visualized on 1.5% agarose gels, and sequenced at Solgent Co. Ltd., Korea.



Table 2.1 Partial gene regions, primers and PCR amplification conditions used in this study

Gene	Primer		PCR protocol					References
	Forward (sequence)	Reverse (sequence)	Initial denaturation	Denaturation	Annealing	Extension	Final Extension	
Internal transcribed spacer (ITS)	ITS5 (GGA AGT AAA AGT CGT AAC AAG G)	ITS4 (TCC TCC GCT TAT TGA TAT GC)	94°C, 3 minutes One cycle	94°C, 30 seconds	55°C, 30 seconds 35 cycles	72°C, 10 minutes	72°C, 10 minutes One cycle	White et al. (1990)
Large subunit (LSU)	LROR (ACC CGC TGA GGG AAA CTT ACT TAA GC)	LR5 (TCC TGA CG)	94°C, 3 minutes One cycle	94°C, 30 seconds	55°C, 30 seconds 35 cycles	72°C, 1.30 minutes	72°C, 10 minutes One cycle	Vilgalys & Hester (1990)
Small subunit (SSU)	NS1 (GTA GTC ATA TGC TTG TCT C)	NS4 (CTT CCG TCA ATT CCT TTA AG)	94°C, 3 minutes One cycle	94°C, 30 seconds	55°C, 30 seconds 35 cycles	72°C, 1.30 minutes	72°C, 10 minutes One cycle	White et al. (1990)
RNA Polymerase II largest subunit (RPB2)	RPB2-5F (GAY GAY MGW GAT CAY TTY GG)	RPB2-7CR (CCC ATR GCT TGY TTR CCC AT)	95°C, 5 minutes One cycle	95°C, 1 minute	57°C, 1 minute 35 cycles	72°C for 1 minute	72°C, 10 minutes One cycle	Liu et al. (1999)

Table 2.1 (continued)

Gene	Primer		PCR protocol					References
	Forward (sequence)	Reverse (sequence)	Initial denaturation	Denaturation	Annealing	Extension	Final Extension	
	RPB2-6F (TGG GGK GTY WTG TGY CCT GC)	RPB2-P7R (GAY TGR TTR TCR GGG AAV GG)	95°C, 5 minutes	95°C, 1 minute	58°C, 1 minute	72°C for 1 minute	72°C, 10 minutes	Liu et al. (1999)
			One cycle		35 cycles		One cycle	
Mitochondrial small subunit (mt SSU)	Mr SSU 1 (AGC AGTGAGGAAT ATTGGTC)	Mr SSU 3 (ATG TGGCACGTCTA TAGCCC)	95°C, 5 minutes	95 °C, 1 minute	56 °C, 1 minute	72 °C, 1-1.5 minutes	72°C, 10 minutes	Zoller et al. (1999)
			One cycle		35 cycles		One cycle	

2.2.4 Sequencing and Phylogenetic Analyses

The obtained sequences were quality-checked and assembled with SeqMan V.7.0.0 (DNASTAR, Madison, WI) and edited in BioEdit v 7.0.9.0 (Hall, 1999). The newly obtained sequences were browsed in the National Center for Biotechnology (NCBI BLASTn) search engine available at the NCBI Information and selected sequences were downloaded as reference sequences from related literature.

Phylogenetic analyses were performed for individual genes and the combined multi-genes. The multi-gene phylogenetic analysis was conducted based on ITS, LSU, SSU and RPB2 combined datasets containing sequences from 118 fungal sequences, including the newly introduced ones. For all datasets, sequences were aligned in MAFFT v. 7 (Kato et al., 2019) with default parameters, trimmed using trimAl v1.2 with parameter option -gappyout (Capella-Gutiérrez et al., 2009), and adjusted manually where necessary in BioEdit v 7.0.9.0 (Hall, 1999). The Maximum Likelihood (ML) analysis was performed on the IQ-tree web server (Trifinopoulos et al., 2016) with 1000 bootstrap replications, and the model of evolution that fit the data was automatically selected. For the BI analyses, the substitution models were estimated using JModeltest 2.3 in the CIPRES platform (Nylander, 2004), and the evolution model fit to the gene was chosen. The BI analyses were conducted in MrBayes v. 2.2.2 (Ronquist & Huelsenbeck, 2003) with six simultaneous Markov Chain Monte Carlo (MCMC) chains, ran for 2-5 million generations (for the combined dataset), and sampled the trees at every 1000th generation.

A single gene phylogenetic analysis was performed using each dataset, including the newly generated ones. For the single gene dataset, sequences were aligned in MAFFT v. 7 with default parameters (Kato et al., 2019), trimmed using trimAl v1.2 with option -gappyout (Capella-Gutiérrez et al., 2009), and adjusted manually where necessary in BioEdit v 7.0.9.0 (Hall, 1999). The Maximum likelihood analysis was performed on the IQ-tree web server (Trifinopoulos et al., 2016) with 1000 bootstrap replications, and a specific evolution model was automatically selected. For the BI analyses, the substitution models were estimated using JModeltest 2.3 in the CIPRES platform (Nylander, 2004), and the evolution model fit to the model data was selected. The BI analyses were conducted in MrBayes v. 2.2.2 (Ronquist & Huelsenbeck, 2003)

with six simultaneous Markov Chain Monte Carlo (MCMC) chains, ran for 1-2 million generations, and sampled the trees at every 1000th generation.

For BI multi-gene and single gene analyses, from the resulting trees, 25% were discarded as 'burn-in', and the remaining trees were used to calculate the BI posterior probabilities of the majority-rule consensus tree. Phylogenetic trees were visualized using FigTree v. 1.4.4 (Rambaut, 2012) and edited in Adobe Illustrator CS v. 6.

2.3 Results

2.3.1 Cenangiaceae, Helotiales

Dark-stipitate apothecia was found while exploring Doi Inthanon National Park, Chiang Mai, Thailand. Further morphology and phylogenetic analyses using maximum likelihood and Bayesian inference analysis based on ITS and LSU combined data set confirmed that the specimen belongs to *Chlorencoelia* species. The list of sequence data used in the phylogenetic analysis is listed in Table 2.2.

Multigene phylogenetic analyses based on the combined ITS and LSU gene regions of Cenangiaceae taxa resulted in well-supported clades in BI, as depicted in the phylogram (Figure 2.1). The combined alignment of ITS and LSU contains 41 fungal taxa, including the new geographical record taxon. The final optimization likelihood value for ML is -6924.87 and was generated from nucleotide alignments of 468 and 835 bp of ITS and LSU, respectively. The matrix comprises 1303 characters with 367 distinct alignment patterns and 25.9 % of gaps and undetermined characters. Base frequencies were estimated as follows; A = 0.235293, C = 0.242697, G = 0.290546, T = 0.231464 with substitution rates AC = 1.435792, AG = 1.774141, AT = 1.062782, CG = 0.915799, CT = 7.140609, GT = 1.00; gamma distribution shape parameter α = 0.220285. The BI analysis generated 1000 trees after 1,000,000 generations. The burn-in phase in the analysis discarded the first 250 trees and retained the remaining results to determine the posterior probabilities distribution. The final average standard of split frequencies of BI posterior probability was 0.009.

Table 2.2 Accession numbers and origin of fungal taxa used in the phylogenetic analysis of Cenangiaceae

Taxon name	Specimen code ^a	GenBank accession no.		Origin
		ITS	LSU	
<i>Cenangiopsis alpestris</i>	KL375	LT158421	KX090837	Switzerland
<i>Cenangiopsis alpestris</i>	KL378	LT158470	KX090839	Montenegro
<i>Cenangium ferruginosum</i>	KL390	LT158471	KX090840	Montenegro
<i>Cenangium ferruginosum</i>	CBS:556.70	MH859846	MH871625	Netherlands
<i>Cenangium ferruginosum</i>	CBS:111.24	MH854762	MH866266	Netherlands
<i>Chlorencoelia torta</i>	KUS-F52256	JN033400	JN086703	Korea
<i>Chlorencoelia torta</i>	ICMP:21732	MH682234	–	New Zealand
<i>Chlorencoelia torta</i>	JAC14068	MK432798	MK431490	New Zealand
<i>Chlorencoelia torta</i>	JAC14135	MK432802	MK431494	New Zealand
<i>Chlorencoelia torta</i>	KL167	LT158424	KX090810	Taiwan
<i>Chlorencoelia torta</i>	MFLU 23-0016	OP64490	OP622874	Thailand
<i>Chlorencoelia versiformis</i>	DAOMC251598	MH457140	MH455361	Canada
<i>Chlorencoelia versiformis</i>	KL21	LT158427	KX090795	Estonia
<i>Chlorencoelia versiformis</i>	TU:104550	LT158411	–	Estonia
<i>Chlorencoelia</i> sp.	ZW-Geo55-Clark	AY789352	AY789351	USA
<i>Crumenulopsis sororia</i>	KL254	LT158442	KX090826	France
<i>Crumenulopsis sororia</i>	G.M. 2015-05-02.3	KY941133	–	Luxembourg
<i>Crumenulopsis sororia</i>	H.B. 6920c	OM808934	–	Luxembourg
<i>Encoelia furfuracea</i>	KL107	LT158416	KX090798	Estonia
<i>Encoelia furfuracea</i>	KL108	–	KX090799	Estonia
<i>Encoelia furfuracea</i>	KL92	LT158482	KX090796	Estonia
<i>Encoelia furfuracea</i>	G.M. 2016-01-02.1	MT508552	–	Luxembourg
<i>Fabrella tsugae</i>	66499	U92304	–	USA
<i>Heyderia abietis</i>	KL20	LT158426	–	Estonia
<i>Heyderia abietis</i>	HMAS71954	AY789297	AY789296	China
<i>Heyderia abietis</i>	OSC60392	AY789290	AY789289	USA
<i>Heyderia pusilla</i>	KL216	LT158430	–	Estonia
<i>Heyderia pusilla</i>	K(M):126590	MZ159347	–	UK
<i>Rhabdocline parkeri</i>	ATCC 201660	AF260813	–	USA
<i>Rhabdocline parkeri</i>	RP-COE	AF462427	–	USA
<i>Rhabdocline parkeri</i>	RP-WA103	AF462426	–	USA
<i>Rhabdocline parkeri</i>	RP-OCMI	AF462429	–	USA

Table 2.2 (continued)

Taxon name	Specimen code ^a	GenBank accession no.		Origin
		ITS	LSU	
<i>Sarcotrochila longispora</i>	CBS:272.74	KJ663836	KJ663877	Canada
<i>Sarcotrochila longispora</i>	ATCC 26761	AY645899	–	Canada
<i>Sarcotrochila macrospora</i> (T)	ATCC 26762	NR154602	–	Canada
<i>Trochila urediniophila</i> (T)	PUL F18316	NR172795	NG075390	Trinidad and Tobago
<i>Trochila viburnicola</i> (T)	CBS:144206	NR159070	NG063960	UK
<i>Trochila bostonensis</i>	BHI-F974b	MT873948	MT873953	USA
<i>Trochila bostonensis</i>	BHI-F974a	MT873947	MT873952	USA
<i>Sclerotinia sclerotiorum</i>	CBS:537.77	AB926090	AB926148	Japan
<i>Rutstroemia firma</i>	KL291	LT158449	KX090831	Estonia

Note ^aATCC: American Type Culture Collection, Manassas, VA, USA; BHI: Boston Harbor Islands, Purdue University, Indiana, USA; CBS: Central Bureau voor Schimmelcultures, Utrecht, The Netherlands; DAOMC: Canadian Collection of Fungal Cultures, Agriculture and Agri-Food Canada, Ottawa, Canada; F: Fundación Medina's Fungal Culture collection, Spain; GM: herb. G. Marson, Luxembourg; HB: herb. H.O. Baral, Germany; HMAS: Herbarium Mycologicum Academiae Sinicae Beijing, China; ICMP: International Collection of Microorganisms from Plants, New Zealand; JAC: J.A. Cooper collection, New Zealand; K(M): Kew Mycology collection, Royal Botanic Garden, London, UK; KL: Landesmuseum für Kärnten, Austria; KUS: Korea University Herbarium, Seoul, Korea; MFLU: Mae Fah Luang University Herbarium, Chiang Rai, Thailand; OSC: Oregon State University, Corvallis, USA; PUL: Purdue University, Indiana, USA; RP: *Rhabdocline parkeri*, Catal M collection, Michigan State University, Michigan, USA; ZW: Zheng Wang, Clark University, Worcester, Massachusetts, USA; Type strains are labelled by (T), newly obtained sequences in this study are in bold, and “–” indicates unavailable sequences

Family: Cenangiaceae Rehm

Genus: *Chlorencoelia* J.R. Dixon

Chlorencoelia, a discomycete group in Cenangiaceae, was introduced by Dixon (1975) with *Chlorencoelia versiformis* (basonym: *Peziza versiformis*) as the type species. This genus is characterized by superficial, medium-sized apothecia, filiform, septate, 8-spored, J+, cylindrical asci, and ellipsoid to allantoid ascospores. Morphologically, our specimen (MFLU 23-0016) fits the generic term of *Chlorencoelia* and is similar to the holotype of *C. torta* (CUP 51760) designated by Dixon (1975), even though the paraphyses septation in our specimen is irregular.

***Chlorencoelia torta* (Schwein.) J.R. Dixon**

Figure 2.1; 2.2

Index Fungorum number: IF311053

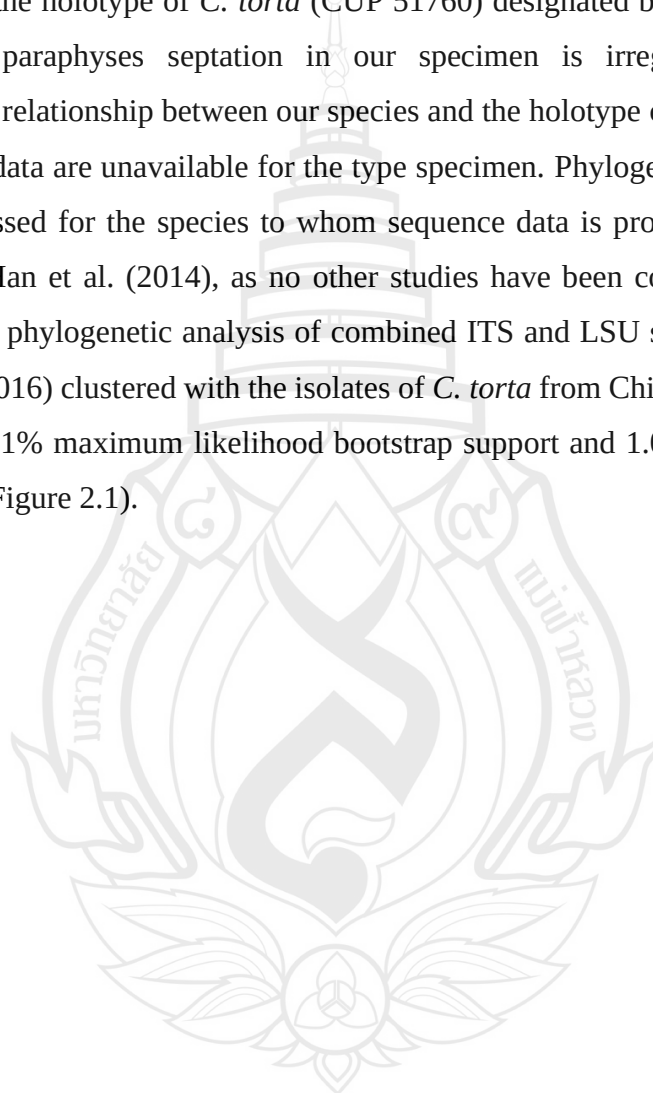
Facesoffungi number: FoF13909

Material examined: Thailand, Kew Mae Pan trail, Doi Inthanon, Chomthong District, Chiang Mai Province, bark of an unknown host, 20 October 2021, Pi Usa, KMP3-7B (MFLU 23-0016), GenBank number ITS: OP64490, LSU: OP622874.

Description: *Saprobic* on decayed wood barks. **Sexual morph:** *Apothecia* 2–4 × 2–2.1 mm ($\bar{x}$ = 2.1 × 2.5 mm, n = 5) in dry condition, arising singly or in small clusters, stipitate. Receptacle cupulate, olivaceous dark brown to black. *Stipe* 1.1–1.9 × 0.6–0.9 mm ($\bar{x}$ = 1.5 × 0.8 mm, n = 5) in dry condition, concolorous with receptacle, rugose. *Discs* dark brown, shallow cupulate to infundibuliform convex with enrolling edges upon drying. *Ectal excipulum* 54–106 µm ($\bar{x}$ = 79.5 µm, n = 15), composed of thin to thick-walled, hyaline to dark brown cells of *textura angularis*. *Medullary excipulum* 119–169 µm ($\bar{x}$ = 142.4 µm, n = 15) in lower flanks, composed of thin-walled, hyaline to yellowish cells of *textura intricata*. *Hymenium* 129–181 µm ($\bar{x}$ = 170.6 µm, n = 15). *Paraphyses* 2.4–2.7 µm in diam. ($\bar{x}$ = 2.8 µm, n = 30) at the apex, filiform, occasionally slightly swollen at the apex, septate, sometimes guttulate. *Asci* 95–115 × 4.4–6.9 µm ($\bar{x}$ = 105.3 × 6 µm, n = 15), unitunicate, 8-spored, cylindrical, rounded to subconical apex, amyloid, long substipitate base, arising from croziers. *Ascospores* 6.2–8.4 × 2.4–2.4 µm ($\bar{x}$ = 7.3 × 3 µm, n = 20), uniseriate, ellipsoid, hyaline, biguttulate, rounded at both ends. **Asexual morph:** Undetermined.

Notes: Our species fit the description of *Chlorencoelia torta* by having black to olivaceous dark apothecia, ectal excipulum of *textura angularis* cells, medullary

excipulum of *textura intricata* cells, and ellipsoidal ascospores (Figure 2.2). *Chlorencoelia torta* has been previously recorded in Japan, New Zealand, North America, Puerto Rico, the Soviet Union, and Tasmania on decayed wood of *Acer*, *Betula*, *Fagus*, *Quercus*, *Tabebuia*, coniferous and unidentified wood (Dixon, 1975; Han et al., 2014; Pärtel et al., 2016). Morphologically, our specimen (MFLU 23-0016) is similar to the holotype of *C. torta* (CUP 51760) designated by Dixon (1975), even though the paraphyses septation in our specimen is irregular. However, the phylogenetic relationship between our species and the holotype cannot be ascertained, as sequence data are unavailable for the type specimen. Phylogenetic comparison can only be assessed for the species to whom sequence data is provided by Pärtel et al. (2017) and Han et al. (2014), as no other studies have been conducted on *C. torta*. Based on the phylogenetic analysis of combined ITS and LSU sequences, our isolate (MFLU 23-0016) clustered with the isolates of *C. torta* from China, New Zealand, and Korea with 91% maximum likelihood bootstrap support and 1.00 Bayesian posterior probability (Figure 2.1).



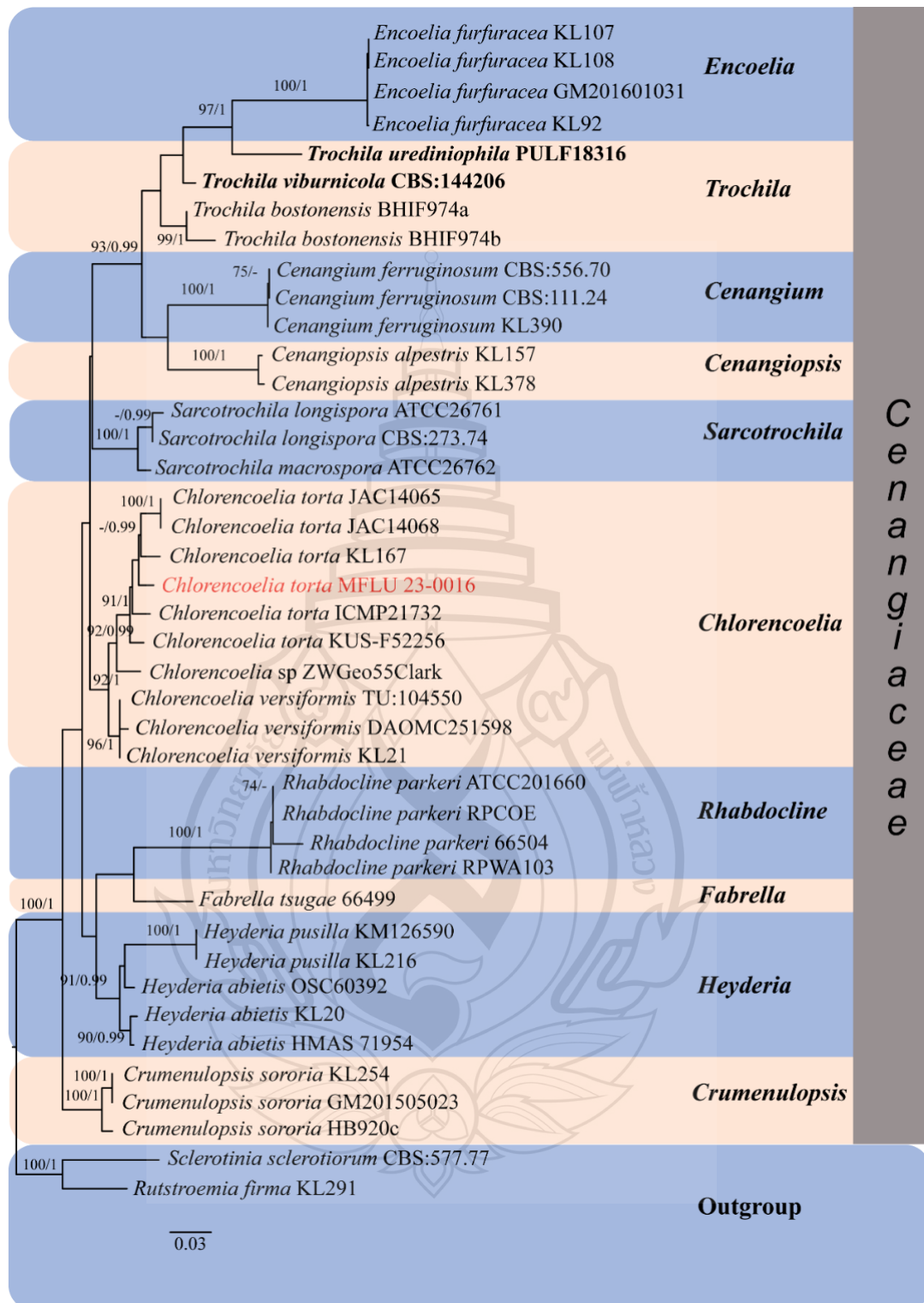


Figure 2.1 Phylogram generated from RaxML analysis based on the combined ITS and LSU sequence data of Cenangiaceae

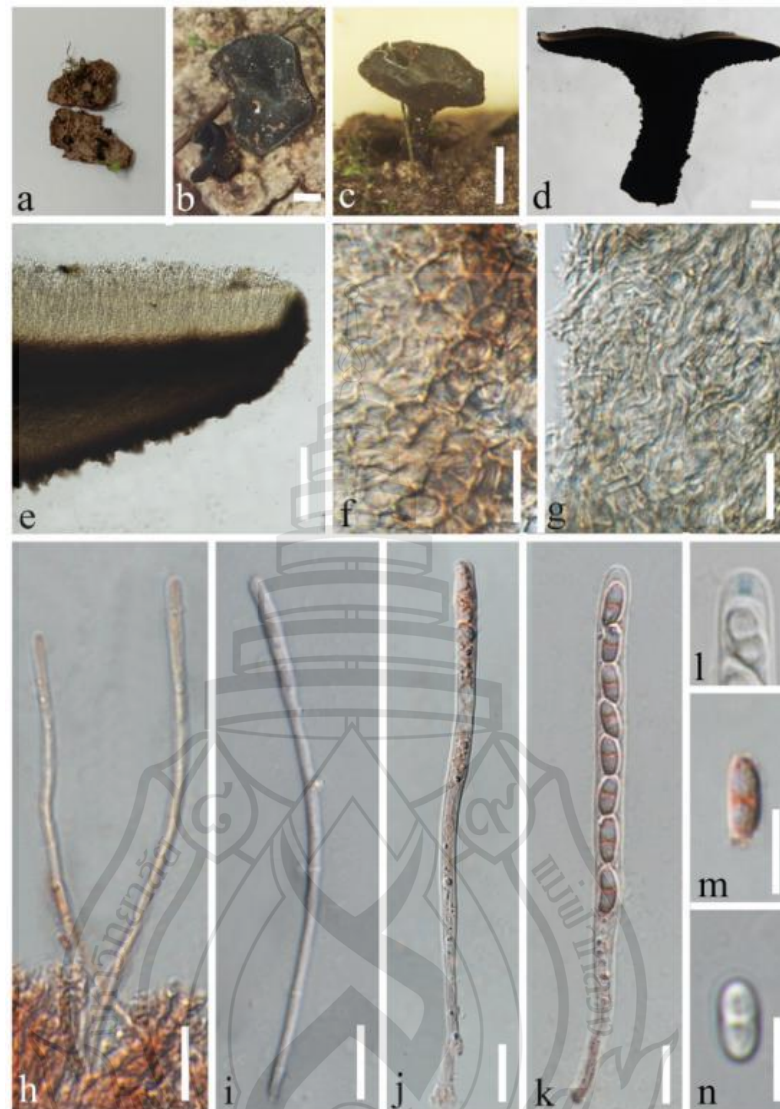


Figure 2.2 *Chlorencoelia torta* (MFLU 23-0016, new geographical record)

Figure 2.2, a Bark pieces of a decayed log. b–c Apothecia on the substrate. d Cross section of an apothecium. e Close up of the hymenium at the margin. f Close up of the ectal excipular cells. g Close up of the medullary excipular cells. h–i Slightly apically swollen paraphyses (mounted in Congo red). j–k Asci (mounted in Congo red). l J+ ascus tip (mounted in Melzer agent without KOH). m–n Ascospores (m mounted in Congo red). Scale bars: b–c = 1 mm, d = 450 μ m, e = 155 μ m, f–g = 17 μ m, h–k = 15 μ m, m–n = 8 μ m.

2.3.2 Helotiaceae, Helotiales

While exploring the Mushroom Research Foundation Forest in Chiang Mai, Thailand, and observing herbarium specimens from Italy, a new species of *Dicephalospora* and two novel species of *Cyathicula* were found. These newly found specimens belong to Helotiaceae and are classified based on molecular phylogenetic analyses and morphological characteristics. The list of sequence data used in the phylogenetic analyses is listed in Table 2.3.

Eighty-four strains were included in the data set, which comprised 1,322 characters (455 characters for ITS and 832 characters for LSU, including the gap regions). The matrix had 485 distinct alignment patterns with 29.6% undetermined characters and gaps. Estimated base frequencies were as follows: A = 0.2424, C = 0.1082, G = 0.3617, T = 0.9371; substitution rates AC = 2.2394, AG = 2.3421, AT = 2.2394, CG = 1.0, CT = 8.6577, GT = 1.0; gamma distribution shape parameter α = 0.688. The new species is indicated in blue bold. Bootstrap value (ML) is greater than 70%, and Bayesian posterior probabilities (BI) greater than 0.90 are given at the nodes. The BI analysis generated 1000 trees after 2,000,000 generations. The burn-in phase in the analysis discarded the first 250 trees and retained the remaining results to determine the posterior probabilities distribution. The final average standard of split frequencies of BI posterior probability was 0.008.

Table 2.3 Accession numbers and origin of fungal taxa used in the phylogenetic analysis of Helotiaceae

Taxon name	Specimen codes ^a	GenBank accession no.		Origin
		ITS	LSU	
<i>Amylocarpus encephaloides</i>	CBS:129.60	MH857920	MH869464	USA
<i>Amylocarpus encephaloides</i>	017cN	KM272369	KM272361	Norway
<i>Bryoscyphus dicrani</i>	M141	EU940183	EU940107	Germany
<i>Connersia rilstonii</i>	CBS:537.74	KJ755499	AF096189	Canada
<i>Crocicreas amenti</i>	F-147481	FJ005093	FJ005124	Spain
<i>Crocicreas cacaliae</i>	F-148706	FJ005107	FJ005126	Spain
<i>Crocicreas cf tomentosum</i>	MFLU 17-0082	MK584988	MK592008	Uzbekistan
<i>Cudoniella clavus</i>	AFTOL-ID 166	DQ491502	DQ470944	USA
<i>Cyathicula cyathoidea</i>	MFLU 16-0613	MK584998	MK591957	UK
<i>Cyathicula cyathoidea</i>	MFLU 18-0698	MK584943	MK591970	Russia
<i>Cyathicula dioscorea</i>	MFLU 23-00461	OR652408	OR652435	Italy
<i>Cyathicula microspora</i>	M267	EU940165	EU940088	Sweden
<i>Cyathicula rusci</i>	MFLU 23-00462	OR652405	OR652432	Italy
<i>Cyathicula rusci</i>	MFLU 23-00463	OR652406	OR6524343	Italy
<i>Cyathicula rusci</i>	MFLU 23-00464	OR652407	OR652434	Italy
<i>Dicephalospora albolutea</i>	HMAS 279693	MK425601	–	China
<i>D. aurantiaca</i>	MFLU 16-0591a	MK584962	MK591988	Thailand
<i>D. aurantiaca</i>	MFLU 16-0591b	MK584958	–	Thailand
<i>D. Chiangraiensis</i>	MFLU 21-0018	MZ241819	MZ241828	Thailand
<i>D. Chiangraiensis</i>	MFLU 21-0019	MZ241818	MZ241827	Thailand
<i>D. Chiangraiensis</i>	MFLU 21-0020	MZ241817	MZ241826	Thailand
<i>D. chrysotricha</i>	PDD:93932	MH578487	–	New Zealand
<i>D. chrysotricha</i>	PDD:91762	KF727411	–	New Zealand
<i>D. chrysotricha</i>	PDD:81537	KF727410	–	New Zealand
<i>D. chrysotricha</i>	PDD:58197	KF727409	–	New Zealand
<i>D. dentata</i>	3093	KP204263	–	China
<i>D. Huangshanica</i>	MFLU 18-1828	MK584979	MK591979	China
<i>D. Huangshanica</i>	HMAS 279694	MK425602	–	China
<i>D. Huangshanica</i>	HMAS 74836	DQ986485	–	China
<i>D. Huangshanica</i>	HMAS 81363	DQ986483	–	China

Table 2.3 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.		Origin
		ITS	LSU	
<i>D. huangshanica</i>	HMAS 81364	DQ986484	–	China
<i>D. huangshanica</i>	KUS-F52405	JN033408	JN086711	Korea
<i>D. inthanonensis</i>	MFLU 22-0050	ON604634	ON606312	Thailand
<i>D. inthanonensis</i>	MFLU 22-0053	ON604635	ON606313	Thailand
<i>D. irregularis</i>	MFLU 22-0054	ON511117	ON514038	Thailand
<i>D. rufocornea</i>	10106	KU668565	–	China
<i>D. rufocornea</i>	MFLU 19-2071	MZ241813	–	Thailand
<i>D. rufocornea</i>	MFLU 19-2089	MZ241822	MZ241831	Thailand
<i>D. rufocornea</i>	MFLU 19-2087	MZ241821	MZ241830	Thailand
<i>D. rufocornea</i>	MFLU 19-2083	MZ241816	MZ241825	Thailand
<i>D. rufocornea</i>	MFLU 19-2082	MZ241824	MZ241815	Thailand
<i>D. rufocornea</i>	MFLU 19-2073	MZ241814	–	Thailand
<i>D. rufocornea</i>	MFLU 19-2085	MZ241820	MZ241829	Thailand
<i>D. rufocornea</i>	TNS:F-40024	AB926055	AB926123	Japan
<i>D. rufocornea</i>	MHHNU 8663	MK253761	–	China
<i>D. rufocornea</i>	MFLU 18-1827	MK584978	MK591978	Thailand
<i>D. rufocornea</i>	MFLU 18-1825	MK584949	MK591976	Thailand
<i>D. rufocornea</i>	MFLU 18-0675	MK584961	MK591987	Thailand
<i>D. rufocornea</i>	MFLU 18-0674b	MK584960	MK591989	Thailand
<i>D. rufocornea</i>	MFLU 18-0674a	–	MK584959	Thailand
<i>D. rufocornea</i>	MFLU 16-1860	MK584989	MK592011	Thailand
<i>D. rufocornea</i>	MFLU 16-1858	MK592010	MK584991	Thailand
<i>D. rufocornea</i>	MFLU 16-0585	MK584955	MK591984	Thailand
<i>D. rufocornea</i>	HMAS 275559	–	MH729336	China
<i>D. rufocornea</i>	HMAS 279695	MK425603	–	China
<i>D. rufocornea</i>	KUS-F52274	JN033401	JN086704	Korea
<i>D. rufocornea</i>	JS140813-06	–	KP161277	Korea
<i>D. rufocornea</i>	HMAS 75518	DQ986480	–	China
<i>D. rufocornea</i>	HMAS 279696	MK425605	–	China
<i>D. rufocornea</i>	HMAS 279697	MK425604	–	China
<i>D. sessilis</i>	MFLU 18-1823	NR163779	MK591974	Thailand
<i>D. shennongjiana</i>	HMAS 279698	MK425606	–	China
<i>D. yunnanica</i>	HMAS 279701	MK425609	–	China

Table 2.3 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.		Origin
		ITS	LSU	
<i>D. yunnanica</i>	HMAS 279700	MK425608	–	China
<i>D. yunnanica</i>	HMAS 279699	MK425607	–	China
<i>D. yunnanica</i>	HMAS 61850	DQ986486	–	China
<i>Endoscypha perforans</i>	PDD:102231	MK039717	KF727424	New Zealand
<i>Glarea lozoyensis</i>	ATCC 20868	NR137138	–	USA
<i>Glarea</i> sp.	C2B	KX610435	–	UK
<i>Gloeotinia granigena</i>	CBS:417.50	–	MH868212	Netherlands
<i>Hymenoscyphus fructigenus</i>	CBS:186.47	MH867741	MH856211	USA
<i>Hymenoscyphus occultus</i>	KUS-F52847	KP068064	–	Korea
<i>Hymenoscyphus pseudoalbidus</i>	Hokk14	KJ511191	–	Japan
<i>Hymenotorrendiella eucalypti</i>	PDD:70105	MH578483	–	New Zealand
<i>Lanzia berggrenii</i>	ICMP:19614	KC164645	KC164640	New Zealand
<i>Ombrophila violacea</i>	WZ0024	AY789366	AY789365	China
<i>Phaeohelotium epiphyllum</i>	TNS:F-40042	AB926061	AB926130	Japan
<i>Pirottaea palmicola</i>	PDD:60282	KM677208	–	New Zealand
<i>Pirottaea palmicola</i>	PDD:65971	KM677206	–	New Zealand
<i>Pleuroascus nicholsonii</i>	CBS:345.73	KJ755519	AF096196	USA
<i>Roesleria subterranea</i>	CBS:339.96	EF060308	EF608074	Germany
<i>Roesleria subterranea</i>	CBS:407.51	MH856922	–	Italy
<i>Torrendiella eucalypti</i>	CPC 11050	DQ195788	DQ195800	Indonesia
<i>Torrendiella madsenii</i>	PRJ D672	AY755336	KJ606676	New Zealand

Note ^aAFTOL: Assembling the Fungal Tree of Life, Oregon State University, USA; ATCC: American Type Culture Collection, Manassas, VA, USA; CBS: Central Bureau voor Schimmelcultures, Utrecht, The Netherlands; cN: Tromsø University Museum, University of Tromsø, Norway; F: Fundación Medina's Fungal Culture collection, Spain; GM: herb. G. Marson, Luxembourg; HMAS: Herbarium Mycologicum Academiae Sinicae Beijing, China; Hokk: Hokkaido, Hosoya collection, Japan; ICMP: International Collection of Microorganisms from Plants, New Zealand; JS: Jin Sung Lee collection, Chonnam National University, South Korea; KL: Landesmuseum für Kärnten, Austria; KUS: Korea University Herbarium, Seoul, Korea; MFLU: Mae Fah Luang University Herbarium, Chiang Rai, Thailand; OSC: Oregon State University, Corvallis, USA; PRJ: P. R. Johnston collection, PDD: Manaaki Whenua - Landcare

Research, New Zealand Fungarium, New Zealand; TAAM: Institute of Agricultural and Environmental Sciences of the Estonian University of Life Sciences, Estonia; TNS: National Museum of Nature and Science, Tsukuba, Japan; WZ: Wang Zheng collection, Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang, China. Type strains are labeled by (T), newly obtained sequences in this study are in bold, “–” indicates unavailable sequences



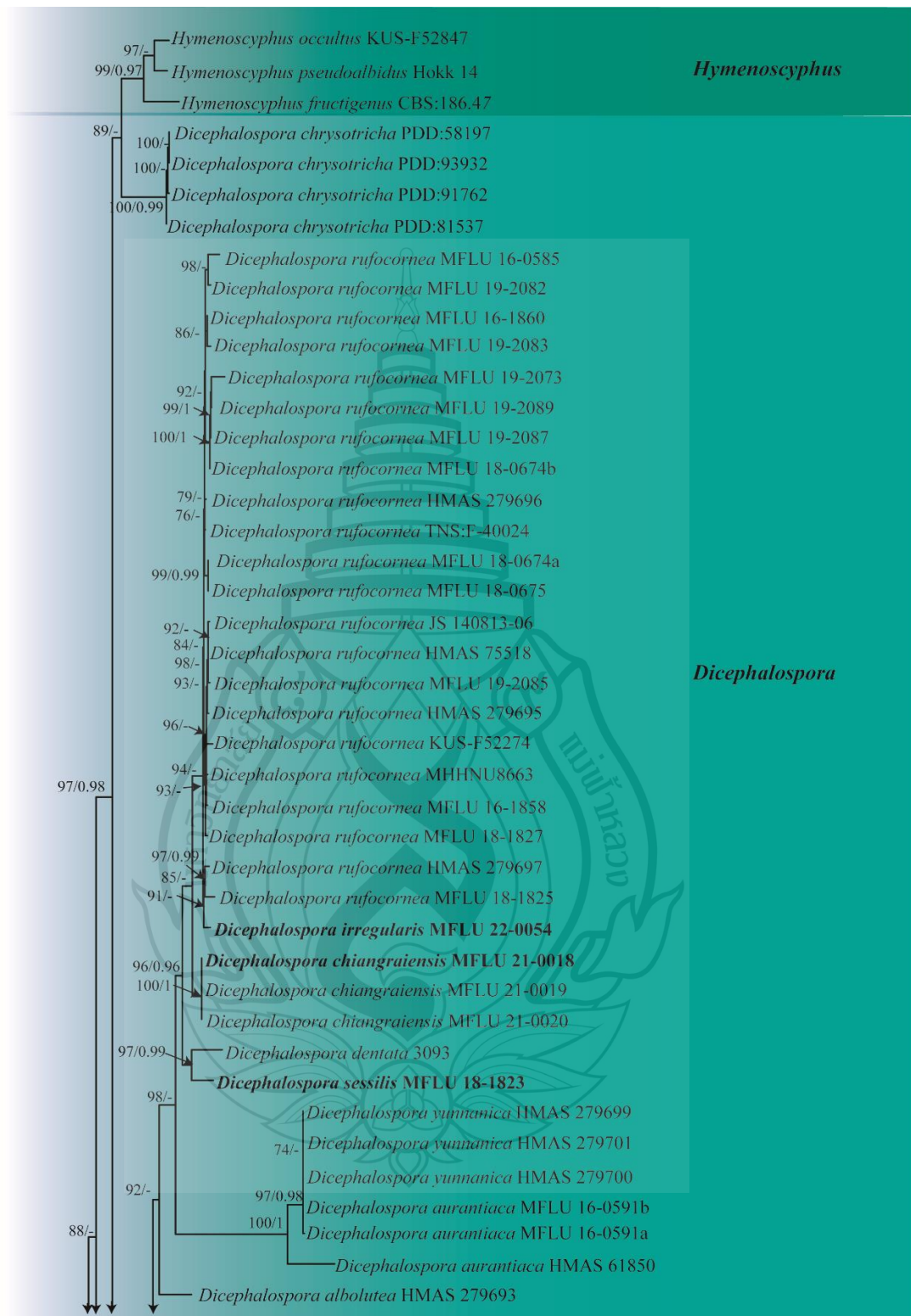


Figure 2.3 Phylogram generated from the maximum likelihood analysis based on the combined ITS and LSU sequence data of Helotiaceae members

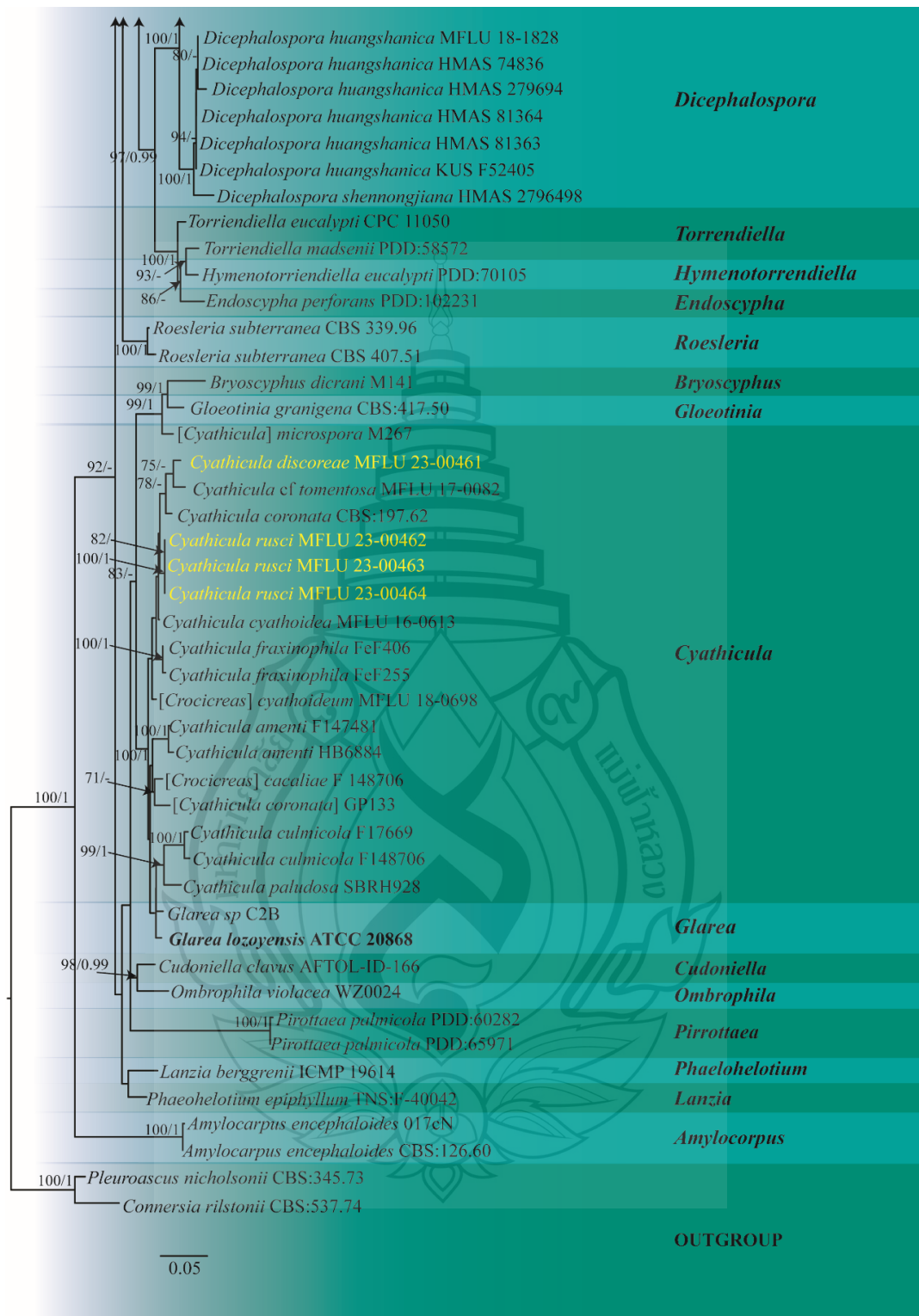


Figure 2.3 (continued)

Family: Helotiaceae Rehm

Genus: *Cyathicula* De Not

Cyathicula was introduced with the type species *C. coronata* (Clement & Shearer, 1931). Initially, some *Cyathicula* specimens were identified as *Conchatium* or *Crocicreas* (Svrček, 1985), yet phylogenetic analyses and morphological observation showed that they differ (Chlebická & Chlebicki, 2007; Baral et al., 2015). *Cyathicula* species are characterized by cylindric to clavate paraphyses, which differ from lanceolate or cylindrical paraphyses in *Crocicreas* (Carpenter, 1981). Most *Cyathicula* species have been reported in Asia, Europe and the USA (Rehm, 1893; Carpenter, 1981; Chlebická & Chlebicki, 2007). Currently, 30 species are listed in this genus (Wijayawardene et al., 2022). Herein, we provide an updated phylogeny for the *Cyathicula* taxa (Figure 2.3).

Cyathicula dioscoreae Lestari, Camporesi and Hyde, sp. nov.

Figure 2.3; 2.4

Index Fungorum number: IF901542

Facesoffungi number: FoF 15280

Etymology: Referring to the host genus name '*Dioscorea*'

Material examined: Italy, Province of Perugia, near Valfabbrica, on a dead and aerial stem of *Dioscorea communis* (Dioscoreaceae), 20 November 2020, Erio Camporesi, IT 4757 (MFLU 23- 0461). GenBank numbers – MFLU 23-0461: ITS: OR652408, LSU: OR652435.

Description: *Saprobic* on a dead aerial stem of *Dioscorea communis*. **Sexual morph:** Apothecia 262–802 μm high $\times$ 222–420 μm diam. ($\bar{x}$ = 489 $\times$ 347 μm , n = 10) in dried form, solitary or in small clusters, stipitate. *Receptacle* cupulate, greyish white. *Discs* concave. *Ectal excipulum* 40–51 μm ($\bar{x}$ = 41.6 μm , n = 10) in the lower part, composed of thick-walled, dark to pale brown, gelatinous cells of *textura porrecta*. *Medullary excipulum* 29–40 μm ($\bar{x}$ = 34 μm , n = 10) in the lower part, composed of thin-walled, hyaline cells of *textura porrecta*. *Paraphyses* 2–2.1 μm ($\bar{x}$ = 2.8 μm , n = 10) wide, filiform to cylindric, numerous, smooth, aseptate, sometimes branched at 1/3 length, rounded at the apex, similar to the length with the asci. *Asci* 45–52 $\times$ 4.9–6.3 μm ($\bar{x}$ = 48 $\times$ 5.7 μm , n = 10), unitunicate, 8-spored, cylindrical, short pedicellate, mostly conical at the apex, arising from croziers. *Ascospores* 8.7–11 $\times$ 2.3–2.8 μm ($\bar{x}$

= $10 \times 2.5 \mu\text{m}$, $n = 10$), 1–2-seriate, fusoid, hyaline, aseptate, smooth-walled, with guttules at both ends. **Asexual morph:** Undetermined.

Notes: In the combined LSU and ITS phylogenetic analysis (Fig 36), our strain (MFLU 23-0461) clustered with *C. cf tomentosa* (MFLU 17-0082) with 75% ML and 0.92 BYPP bootstrap support. The nucleotide differences between in ITS and LSU of our collection and *C. cf tomentosa* (MFLU 17-0082) are 2.2 % and 0.98 %, respectively (Table 2.4). These two collections exhibit distinct habits of apothecia, excipulum cells and asci. The apothecia of our collection (MFLU 23-0461) have greyish white with cupulate receptacle whereas *C. cf tomentosa* (MFLU 17-0082) is characterized by dark apothecia with mostly enclosed, goblet receptacles (Table 2.6). Excipulum cells of our collection is *textura porrecta* vs *textura oblita-prismatica* (*C. cf tomentosa*). Also, our collection (MFLU 23-0461) has smaller ($45\text{--}52 \times 4.9\text{--}6.3$ vs $50\text{--}65 \times 5.5\text{--}7 \mu\text{m}$) asci than *C. cf tomentosa* (Table 2.6). Hence, based on morphology and multi-gene phylogeny, we introduce *Cyathicula dioscoreae* as a new species (Figure 2.3; 2.4).

Table 2.4 Comparison of ITS and LSU sequences of closely related *Cyathicula* species with *C. dioscorea* (MFLU 23-00461)

Species	ITS (%)	LSU (%)
<i>Cyathicula cf tomentosa</i> (MFLU 17-0082)	2.2	0.98
<i>Cyathicula coronata</i> (CBS:197.62)	3.3	1.4
<i>Cyathicula rusci</i> (MFLU 23-0462)	2.9	1.1
<i>Cyathicula cyathoidea</i> (MFLU 16-0613)	3.7	0.86
<i>Cyathicula fraxinophila</i> (FeF255)	5.1	N/A
<i>Cyathicula fraxinophila</i> (FeF406)	4.6	N/A
[<i>Crocicreas</i>] <i>cyathoideum</i> (MFLU 18-0698)	4.4	1.2

Table 2.5 Comparison of ITS and LSU sequences of closely related *Cyathicula* species with *C. rusci* (MFLU 23-00462)

Species	ITS (%)	LSU (%)
<i>Cyathicula</i> cf <i>tomentosa</i> (MFLU 17-0082)	3.4	1.9
<i>Cyathicula coronata</i> (CBS:197.62)	2.9	0.6
<i>Cyathicula cyathoidea</i> (MFLU 16-0613)	1.3	0.6
<i>Cyathicula fraxinophila</i> (FeF255)	3.1	N/A
<i>Cyathicula fraxinophila</i> (FeF406)	2.6	N/A
[<i>Crocicreas</i>] <i>cyathoideum</i> (MFLU 18-0698)	3.1	0.4

Table 2.6 Morphological comparison of newly specimens *Cyathicula* with other other fungal species phylogenetically closely related

Species	Apothecia	Excipulum cells	Paraphysis Size (µm)	Asci Size (µm)	Ascospore characters Size (µm)	References
<i>Cyathicula</i> cf <i>tomentosa</i> (MFLU 17-0082)	Black, stipitate with hair	Ectal: <i>textura oblita - prismatica</i> Medulary: <i>t. oblita - porrecta</i>	2–2.5; cylindrical	50–65 × 5.5–7; cylindrical with stipitate base, J+, conical to obtuse apex, arising from croziers	9–12 × 2–3.5; ellipsoid to fusoid, hyaline with guttules	Ekanayaka et al. (2019)
<i>Cyathicula coronata</i>	Cream with crown-like structure, stipitate	Ectal: <i>textura oblita</i> Medulary: <i>t. oblita - intricata</i>	3-3.3; filiform, septate	127–133 × 10–11; cylindrical, J+ (faintly), rounded apical, arising from croziers	20.5–24.2 × 4.5–5.9; fusoid with guttules, hyaline, 1-septate	Domínguez (2020)
<i>Cyathicula</i> cf <i>cyathoidea</i> (MFLU 16-0613)	Cream, stipitate	Ectal: <i>textura porrecta</i> Medulary: <i>textura oblita-intricata</i>	1.5–2; filiform	35–45 × 4–5.5; cylindrical, conical to rounded apex, J+, arising from simple septa	8–9 × 1.6–1.8; fusoid with rather flattened at one side, hyaline, smooth	Ekanayaka et al. (2019); Baral (2010)
<i>Cyathicula dioscorea</i> (MFLU 23-0461)	Cream (dried state), stipitate	Ectal: <i>textura prismatica</i> Medulary: <i>textura intricata-oblita</i>	2–3.1; filiform (with slight apically swollen at terminal cells) to cylindrical, branched	45–52 × 4.9–6.3; cylindrical with short pedicellate, J+, conical to rounded apical, arising from croziers	8.7–11 × 2.3–2.8; fusoid with rather flattened at one side, hyaline smooth	This study
<i>Cyathicula fraxinophila</i>	White, stipitate	Ectal: <i>textura porrecta</i> Medulary: <i>textura porrecta-oblita</i>	3–3.5; cylindrical, septate	90–95 × 8–8.5; cylindrical, J+, conical to rounded apex, arising from croziers	46–48 × 2.5–3; fusoid, hyaline, 1-septate	Baral (2014)
<i>Cyathicula rusci</i>	Cream (dried state), stipitate	Ectal: <i>textura porrecta</i> Medulary: <i>textura porrecta-oblita</i>	2.2–3.8; cylindrical	45–53 × 4.3–5; cylindric with pedicellate, J+, rounded apex, arising from croziers, 8 spored	5.4–8 × 2.3–3; fusoid with guttules, hyaline	This study

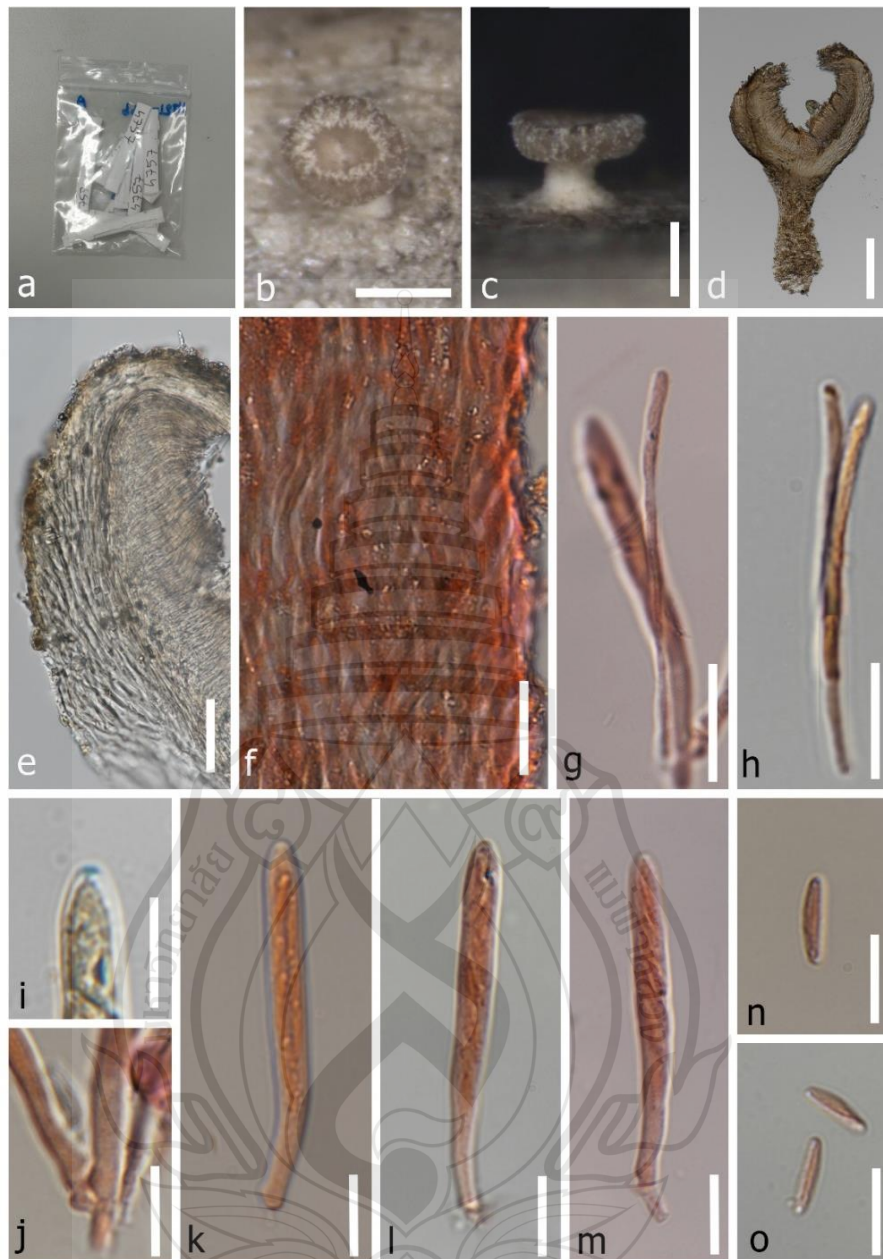


Figure 2.4 Sexual morph of *Cyathicula dioscoreae* (MFLU 23-0461, holotype)

Figure 2.4, a, b Appearance of apothecia on the host surface. c Close-up section of an apothecium. d Medullary excipulum cells. e, f Paraphyses. g Ascus tip (mounted in Melzer's agent without KOH). h A crozier at the base of asci (mounted in Congo red). i–k Asci (mounted in Congo red). l–m Ascospores (mounted in Congo red). Scale bars: a = 300 μ m, b, c = 200 μ m, d, e = 30 μ m, f–m = 10 μ m.

Cyathicula rusci Lestari, Camporesi and Hyde, sp. nov.

Figure 2.3; 2.5

Index Fungorum number: IF 901455

Facesoffungi number: FoF 15215

Etymology: The epithet represents the host genus '*Ruscus*'

Material examined: Italy, Province of Forlì-Cesena [FC], near Meldola, on a dead and aerial stem of *Ruscus aculeatus* (Asparagaceae), 18 February 2021, Erio Camporesi, IT 4684b (MFLU 23-0462, holotype); *ibid.*, 20 November 2020, Erio Camporesi, IT 4684 (MFLU 23-0463, paratype); *ibid.*, IT 4684a (MFLU 23-0464). GenBank numbers – MFLU 23-0462: ITS: OR652405, LSU: OR652432; MFLU 23-0463: ITS: OR652406, LSU: OR652433; MFLU: 23-0464: ITS: OR652407, LSU: OR652434.

Description: *Saprobic* on dead aerial of stems of *Ruscus aculeatus*. **Sexual morph:** *Apothecia* 718–917 μm high $\times$ 526–736 μm diam. ($\bar{x}$ = 805 $\times$ 597 μm , n = 10), white to creamy color, solitary or in small clusters, stipitate. *Discs* concave. *Ectal excipulum* comprising 44–65 μm ($\bar{x}$ = 55.2 μm , n = 10) at the lower flanks, composed of thick-walled, golden color cells of *textura porrecta*. *Medullary excipulum* 47–60 μm ($\bar{x}$ = 54.4 μm , n = 10) in lower flanks, composed of thin-walled, hyaline cells of *textura porrecta*. *Paraphyses* 2.2–2.8 μm ($\bar{x}$ = 2.7 μm , n = 10) wide, cylindric, numerous, sometimes guttulate, septate near the base, rounded at the apex, similar length with the asci. *Asci* 45–53 $\times$ 4.3–5 μm ($\bar{x}$ = 49 $\times$ 4.7 μm , n = 10), unitunicate, 8-spored, cylindric, with pedicels, rounded at the apex, arising from croziers. *Ascospores* 5.4–8 $\times$ 2.3–3 μm ($\bar{x}$ = 7 $\times$ 2.6 μm , n = 10), 1–2-seriate, cylindrical-fusoid, hyaline, aseptate, smooth-walled, guttulate. **Asexual morph:** Undetermined.

Notes: According to the phylogenetic analysis, our strains of *Cyathicula rusci* (MFLU 23-0462, MFLU 23-0463, MFLU 23-0464) formed a distinct clade from *C. coronata* (CBS 197.62) and *C. tomentosa* (4757, MFLU 17-0082) with 44% ML and 0.68 BYPP bootstrap support (Figure 2.3). *Cyathicula cyathoidea* (MFLU 16-0613) also forms a separate lineage to our collections (MFLU 23-0462, MFLU 23-0463, MFLU 23-0464) with 45% ML and 0.66 BYPP bootstrap value (Figure 2.3). The nucleotide differences in ITS and LSU sequences of our collection and phylogenetically close *Cyathicula* species are listed in Table 2.6. *Cyathicula rusci*

differs from *C. tomentosa* by its apothecia appearance, asci and ascospore size. The new collected *Cyathicula* is characterized by creamy color apothecia while *C. cf tomentosa* has dark or black apothecia color. In addition, *C. rusci* has smaller asci ($45\text{--}53 \times 4.3\text{--}5$ vs $50\text{--}65 \times 5.5\text{--}7$ μm) and ascospore size ($5.4\text{--}8 \times 2.3\text{--}3$ vs $9\text{--}12 \times 2\text{--}3.5$ μm) than *C. cf tomentosa*. Our collection differs from *C. cyathoidea* (MFLU 16-0613) in having wider paraphysis cells ($2.2\text{--}3.8$ vs $1.5\text{--}2$ μm), longer asci ($45\text{--}53$ vs $35\text{--}45$ μm) and smaller ascospores ($5.4\text{--}8 \times 2.3\text{--}3$ vs $8\text{--}9 \times 1.6\text{--}1.8$ μm) (Figure 2.5, Table 2.6). *Cyathicula rusci* differs from *C. coronata* by lacking prominent teeth-like or crown-like structures on the apothecial disc, smaller asci ($45\text{--}53 \times 4.3\text{--}5$ vs $127\text{--}133 \times 10\text{--}11$ μm) and ascospores ($5.4\text{--}8 \times 2.3\text{--}3$ vs $20.5\text{--}24.2 \times 4.5\text{--}5.9$ μm) (Figure 2.5, Table 2.6). Hence, the current study presents *C. rusci* as a new species on *Ruscus aculeatus*.

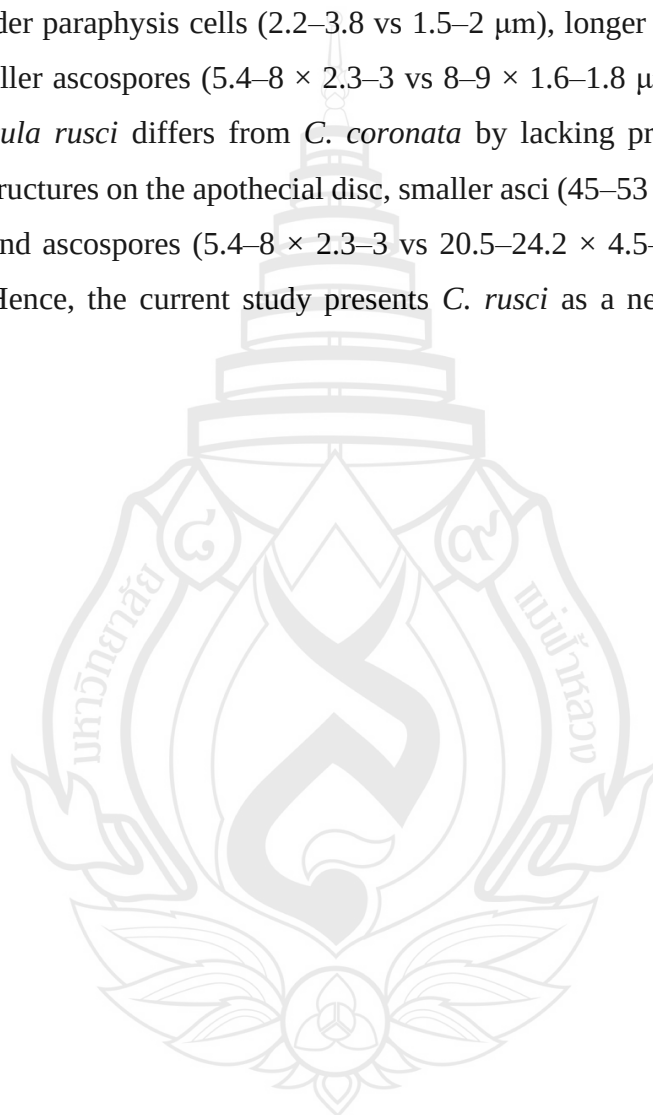




Figure 2.5 Sexual morph of *Cyathicula rusci* (MFLU 23-0462, holotype)

Figure 2.5, a A herbarium package. b Appearance of an apothecium on the host tissue. c A vertical section of an apothecium. d Close-up of excipulum cells. e–f Paraphyses. g Tip of the ascus (mounted in Meltzer reagent without KOH). h A crozier at the base of asci (mounted in Congo red). i–k Asci (mounted in Congo red). l–m Ascospores (mounted in Congo red). Scale bars: b = 500 mm, c = 350 μ m, d–k = 20 μ m, l–m = 10 μ m.

Genus: *Dicephalospora* Spooner

Dicephalospora is a distinctive genus within the Helotiaceae family, exemplified by its species such as *D. calochroa* (Spooner, 1987; Ekanayaka et al., 2019a). Initially established to accommodate cup fungi found on stromatized plant tissues, *Dicephalospora* stands out for its unique features (Spooner, 1987). Characterized by an ectal excipulum of *textura prismatica*, asci with amyloid tips, and mucilaginous-capped ascospores, it has been historically associated with various fungal families, including Rutstroemiaceae, Helotiaceae, and Sclerotiniaceae (Spooner, 1987; Ekanayaka et al., 2019a). However, recent phylogenetic studies have firmly placed it within the Helotiaceae family (Han et al., 2014; Zhao et al., 2016; Ekanayaka et al., 2019a). Typically inhabiting rotten wood, twigs, and leaf petioles, *Dicephalospora* species exhibit erumpent or superficial, stipitate apothecia in shades ranging from yellow to blackish. Their distinguishing features include an ectal excipulum of *prismatica* cells, a medullary excipulum of *intricata* cells, and hyaline, guttulate ascospores with mucilaginous caps (Ekanayaka et al., 2019a). With a considerable number of species recorded, including recent discoveries in Thailand, *Dicephalospora* continues to be an intriguing subject of study for mycologists due to its diverse morphology and bioactive secondary metabolites.

Dicephalospora irregularis Lestari, Pasouvang and K.D Hyde, sp. nov

Figure 2.3; 2.6

Index Fungorum number: IF555157

Facesoffungi number: FOF11034.

Etymology: “irregularis” refers to the irregular shape of apothecia.

Material examined: Thailand, Chiang Mai Province, Mae Taeng District, Pa Pae, on dead stem and twig of an unknown tree, 09 September 2020, Pahua Pasouvang, CM 31 (MFLU 22-0054, holotype). GenBank accession numbers: ITS-ON511117, LSU-ON514038.

Description: It is saprobic on dead twigs of an unidentified tree. **Sexual morph:** *Apothecia* 0.5–1.3 × 0.3–1.2 mm, arising singly or in small groups, sessile, erumpent, and irregular in shape. *Receptacle* cupulate and orange to yellow-brown. *Margins* smooth and brown to dark orange. *Discs* slightly convex and orange. *Ectal*

excipulum 30–45 μm ($\bar{x}$ = 40 μm , n = 15) in lower flanks and composed of thick-walled, yellowish cells of *textura globulosa* to *textura angularis*. *Medullary excipulum* 42–63 μm ($\bar{x}$ = 48.8 μm , n = 15) in lower flanks and composed of thin-walled, yellowish to hyaline cells of *textura porrecta* to *textura intricata*. *Hymenium* hyaline to yellowish. *Paraphyses* 2.5–4.0 μm wide ($\bar{x}$ = 3 μm , n = 15) at the terminal cell, filiform, and numerous, with the length exceeding the asci, unbranched to branched at the top with gelatinous matters, and are apically rounded, aseptate, and guttulate. *Asci* 125–150 $\times$ 15–20 μm ($\bar{x}$ = 135 $\times$ 17 μm , n = 15), eight-spored, unitunicate, cylindrical clavate, and non-amyloid (J- when mounted in Melzer agent with or without KOH treatment), with a rounded apex, arising from simple septa without basal protuberance. *Ascospores* 25–35 $\times$ 5.5–7.5 μm ($\bar{x}$ = 33 $\times$ 7.5 μm , n = 15), uniseriate to biseriate, and fusoid-clavate to ellipsoid, with rounded to sub-acute ends, capped with gelatinous obconical collar, and are hyaline and guttulate. **Asexual morph:** Undetermined.

Notes: Phylogenetically, our species clusters basal to the *Dicephalospora rufocornea* clade with 81% ML bootstrap support. Our specimen, *D. irregularis*, is morphologically distinct from *D. rufocornea* by having sessile apothecia, ectal excipulum of *textura globulosa* to *textura angularis*, non-amyloid asci, and fusoid-clavate to ellipsoid ascospores, while *D. rufocornea* is characterized by having stipitate apothecia, ectal excipulum of *textura porrecta* to *prismatica*, hymenoscyphus-type apical ring, and fusoid or fusoid-clavate ascospores (Spooner, 1987; Ekanayaka et al., 2019a). *Dicephalospora irregularis* differs from *D. sessilis* in apothecial shape and branched, filiform paraphyses (Ekanayaka et al., 2019a), and our species is more distantly related to *D. sessilis* than *D. rufocornea* in the phylogenetic tree (Figures 2.3).

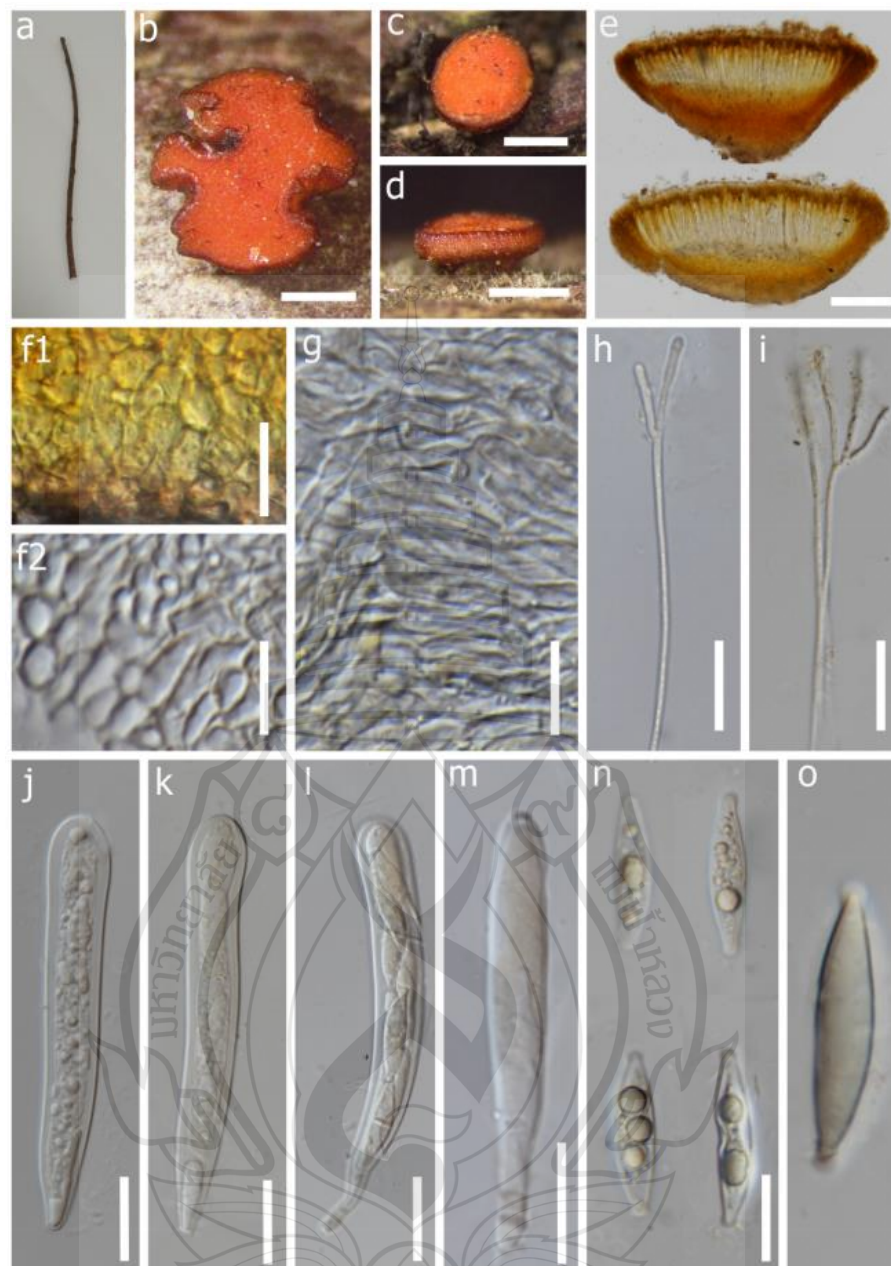


Figure 2.6 *Dicephalospora irregularis* (MFLU 22-0054, holotype)

Figure 2.6, a Dead twig substrate. b–d Top and side view of apothecia. e A cross-section of an apothecium. f1,2 Cells of ectal excipulum. g Cells of medullary excipulum. h–i A branched paraphyses. j–m Asci (mounted in Melzer agent with KOH treatment. n–o Ascospores (mounted in KOH 5%). Scale bars: b–d = 500 μm , e = 200 μm , f–g = 13 μm , h–l = 25 μm , n = 20 μm .

2.3.3 Hyaloscyphaceae, Helotiales

In Thailand, family members of Hyaloscyphaceae were not found, some herbarium specimens from various herbarium institutions were observed and redescribed in this dissertation.

Family: Hyaloscyphaceae Nannf.

Genus: *Hyalopeziza* Fuckel

Hyalopeziza characterized by glassy-walled hairs and filiform to clavate paraphysis with glassy and granulate walls (Huhtinen, 1997). *Hyalopeziza* is a notable genus within the family Hyaloscyphaceae, established by Fuckel with *Hyalopeziza patula* as the type species (Fuckel, 1870). Taxonomic reevaluation studies transferred some taxa members including the type species in to new families such as Calloriaceae, Cordieritidaceae, Lachnaceae and Niaceae (Rehm, 1893; Seaver, 1951; Korf & Kohn, 1980; Raitviir, 2004, Baral et al., 2020).

Hyalopeziza pygmaea (Mouton) Huhtinen

Synonym: *Hyphopeziza pygmaea* (Mouton) J.G. Han, Hosoya & H.D. Shin

Index Fungorum number: IF130698

Facesoffungi number: FoF 15674

Material examined: Belgium, Beaufays (Vierset), on unknown leaf substrate, unknown date, Mouton V (BR5020088313439), Type.

Description: *Saprobic* on an unidentified leaf. **Sexual morph:** Sessile discomycetes. *Apothecia* 50–66 × 45–58 µm ($\bar{x}$ = 57.7 × 50.7 µm, n = 10), arising singly. *Receptacle* cupulate. *Discs* concave. *Hairs* up to 90 µm long, 3–5 µm at the base, superficially rough or warts at the surface, spine-like with pointed tips. *Ectal excipulum* cannot be observed but it is written composed of thin-walled cells of *textura prismatica* in the note provided in the herbarium package. *Medullary excipulum* cannot be observed, and there is no cell description in the species note. *Paraphyses* 0.9–1.2 µm wide, filiform, smooth. *Asci* 21–25 × 2.8–5.4 µm ($\bar{x}$ = 22.6 × 4.8 µm, n = 10), 8-spored, unitunicate, cylindrical-clavate, rounded at the apex, J+ with and without KOH treatment, arising from croziers. *Ascospores* 3–5 × 1.2–1.5 µm (according to specimen description), partially biseriate to biseriate, fusoid, aseptate, hyaline. **Asexual morph:** Undetermined.

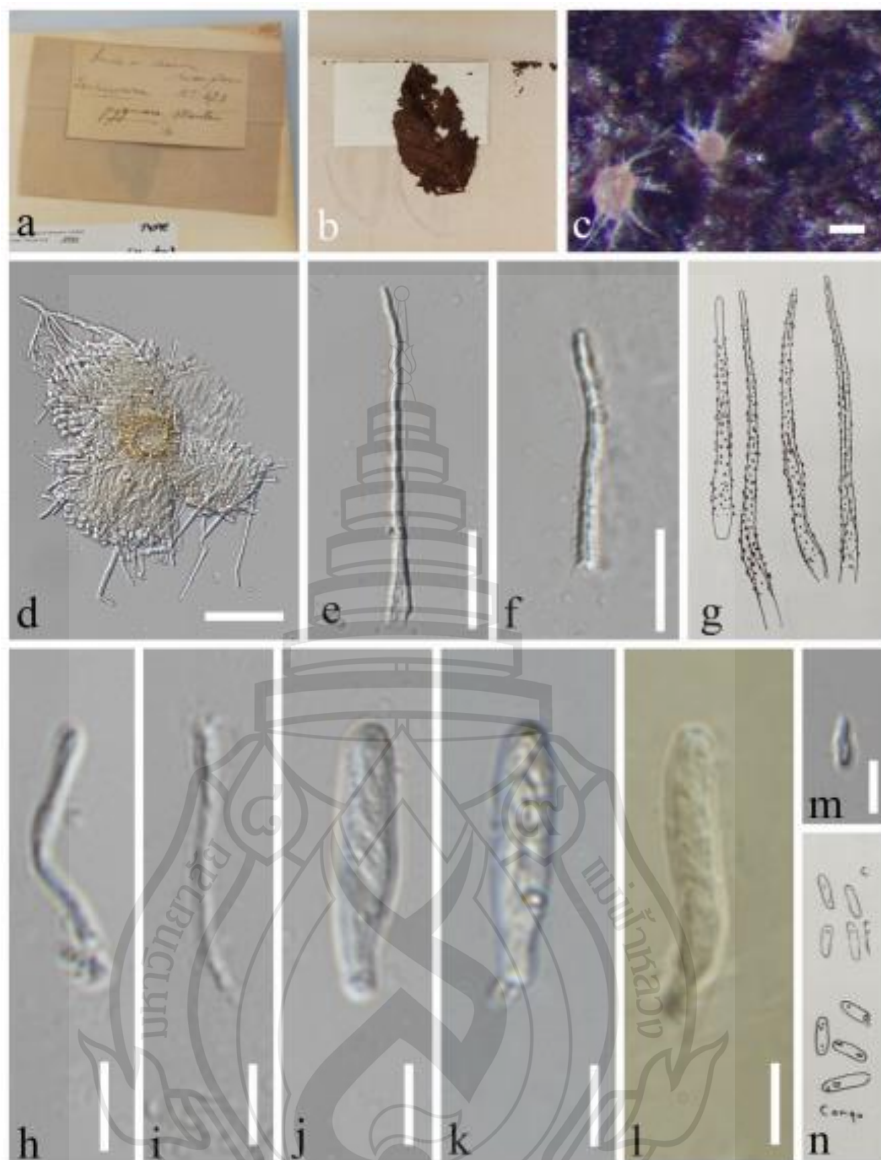


Figure 2.7 Sexual morph of *Hyalopeziza pygmaea* (BR5020088313439)

Figure 2.7, a–b Details of herbarium material. c Habit and appearance of the apothecium. d Crushed form of an apothecium. e, g Hairs. h–i Filiform paraphyses. j, k, l Asci (l mounted in Melzer agent). m, n Ascospores. Scale bars: c–d = 50 µm, e–f = 16 µm, h–l = 6 µm, m = 4 µm.

Genus: *Protounguicularia* Raitv. and R. Galán

Protounguicularia is established by Raitvir & Galán (1986) with *Protounguicularia brevicapitata* as the type species. This genus characterized by

having long, cylindrical and septate hairs (Huhtinen et al., 2008). Subsequent studies transferred *P. brevicapitata* to *Pezizellaster transiens* (Engel & Svrček, 1983) and *Olla* (Baral, 1993). However, Huhtinen et al. (2008) insisted that *Protounguicularia* is generically different from *Olla* based on the distinct hair character ornamented on the apothecia. The striking character is on septa on hair and possible lichenized habit which other genera (*Arachnopeziza*, *Corticifraga*, *Hyalopeziza*, *Olla*, *Unguiculariopsis*) are lacking (Huhtinen et al., 2008). Currently, eight species are registered (Species Fungorum, 2024).

Protounguicularia brevicapitata Raitv. and R. Galán

Index Fungorum number: IF 103735

Facesoffungi number: FoF 15684

Material examined: Spain, Andalusia, Granada, Alhama de Granada -2.98963 37.00689, on decaying wood of *Quercus rotundifolia*, 24 February 1982, Ricardo Galán and A. Ortega, (TAAM194206), Isotype.

Description: *Saprobic* on decaying wood of *Quercus rotundifolia*. **Sexual morph:** Sessile discomycetous. *Apothecia* $163 \times 86 \mu\text{m}$, arising singly, erumpent. *Receptacle* discoid to cupulate. *Discs* concave. *Hairs* $26\text{--}53 \times 2.7\text{--}4.2 \mu\text{m}$ ($\bar{x} = 36.3 \times 2.6 \mu\text{m}$, $n = 15$), at middle cells, glassy, septate, cylindrical with slightly narrower-obtuse tips. *Ectal excipulum* composed of hyaline cells of *textura prismatica* to *angularis*, cells $2.3\text{--}4.9 \mu\text{m}$ wide ($\bar{x} = 4.2 \mu\text{m}$, $n = 10$). *Hymenium* hyaline. *Paraphyses* $0.9\text{--}1.3 \mu\text{m}$ wide ($\bar{x} = 1.1 \mu\text{m}$, $n = 15$) at the middle cells, numerous, apically swollen, aseptate, branched at the base, smooth. *Asci* $31\text{--}39 \times 4.2\text{--}6.5 \mu\text{m}$ ($\bar{x} = 34.9 \times 5.3 \mu\text{m}$, $n = 15$), 8-spored, unitunicate, cylindrical clavate, conical to rounded at the apex, nonamyloid, arising from croziers. *Ascospores* $4.4\text{--}5.9 \times 1.2\text{--}1.7 \mu\text{m}$ ($\bar{x} = 5.3 \times 1.5 \mu\text{m}$, $n = 13$), fusoid, aseptate, hyaline, smooth to guttulate. **Asexual morph:** Undetermined.

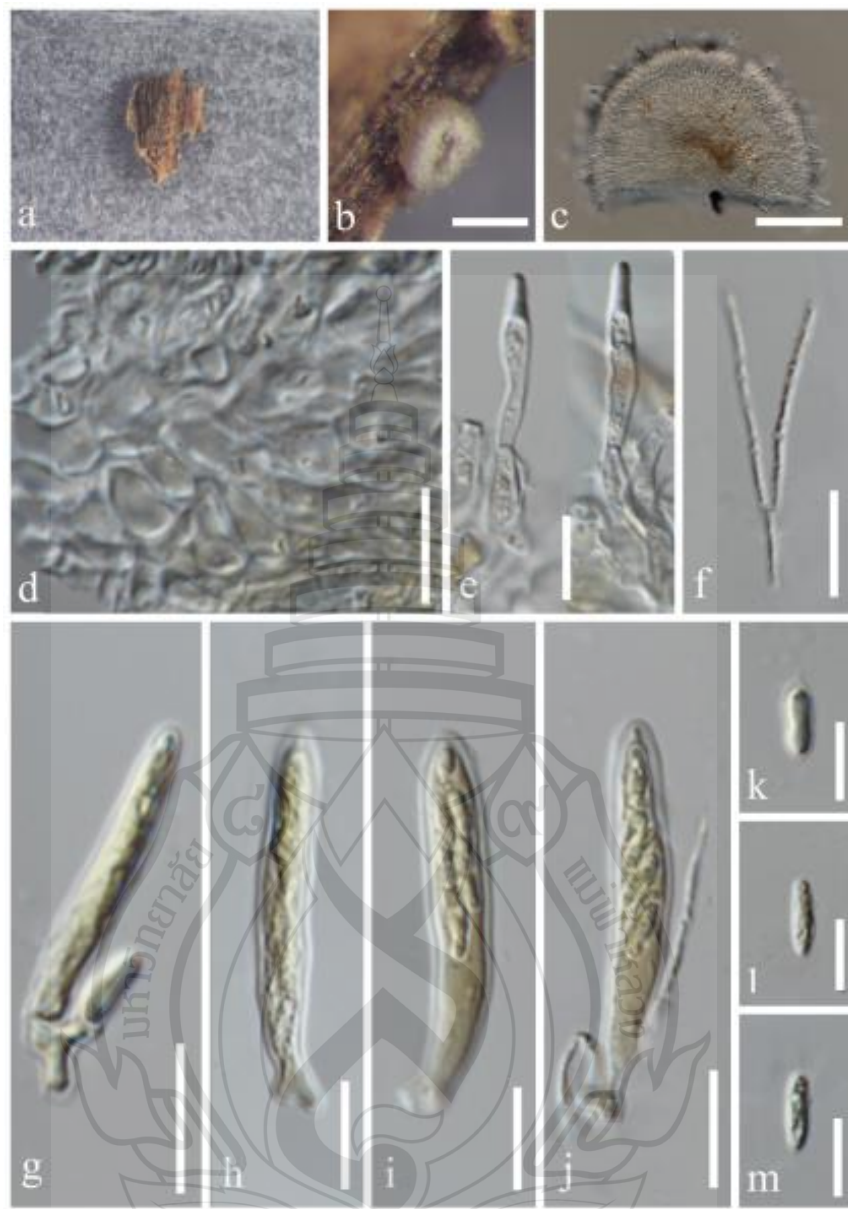


Figure 2.8 Sexual morph of *Protounguicularia brevicapitata* (TAAM194206)

Figure 2.8, a A piece of woody substrate from herbarium. b Habit and appearance of an apothecium on the host surface. c Back view of an apothecium. d Cells of ectal excipulum. e Glassy hairs. f Filiform paraphyses. g Asci with the crozier at the bottom. h–j Asci (g–j mounted in Meltzer agent). k–m Ascospores (mounted in Melzer agent). Scale bars: b = 135 μ m, c = 120 μ m, d–f = 12 μ m, g–j = 10 μ m, k–m = 5 μ m.

Genus: *Unguiculariella* K.S. Thind and R. Sharma

Unguiculariella, a genus of fungi in the family Hyaloscyphaceae, established by Thind and Sharma (1990) and characterized by having turbinate apothecia and glassy hairs. The differences compare to other genus in Hyaloscyphaceae is on its positive reaction of paraphysis by turning blue (similar to its glassy hair chemical reaction) after tested in Melzer agent (Thind & Sharma, 1990).

Unguiculariella bhutanica K.S. Thind and R. Sharma

Index Fungorum number: IF 128525

Facesoffungi number: FoF 15683

Material examined: Bhutan, Thimphu, Begana 27.473932 89.635305, on decaying leaf stalks of angiosperm. 07 August 1981, Raghunandan Sharma (CUP-IN-000623).

Description: *Saprobic* on decaying leaf stalks of angiosperm. **Sexual morph:** Sessile discomycetous. *Apothecia* 155–243 × 143–222 µm, arising singly or in a small cluster. *Receptacle* turbinate, cupulate, campanulate. *Discs* concave. *Hairs* 7.3–10.6 × 1.9–2.3 µm ($\bar{x}$ = 8.7 × 2.7 µm, n = 10), glassy at margin, cylindrical with slightly narrower-obtuse tips. *Ectal excipulum* 16–26 µm wide ($\bar{x}$ = 21.7 µm, n = 10), composed of hyaline cells of *textura porrecta*. *Medullary excipulum* 18–29 µm ($\bar{x}$ = 25.2 µm, n = 10) at lower flanks, composed of thin-walled hyaline cells of *textura intricata*. *Hymenium* hyaline. *Paraphyses* 2.1–2.3µm wide ($\bar{x}$ = 2.5µm, n = 15) at the top, numerous, apically swollen, aseptate, exceeding the asci in length, smooth. *Asci* 78–121 × 9–12 µm ($\bar{x}$ = 89.1 × 9.9 µm, n = 15), 8-spored, unitunicate, cylindrical clavate, conical to rounded at the apex, amyloid, stipitate, arising from croziers. *Ascospores* 11–14 × 2.5–5.4 µm ($\bar{x}$ = 12.1 × 4.6 µm, n = 20), partially biseriate, ellipsoid, uniseptate, hyaline, guttulate. **Asexual morph:** Undetermined.

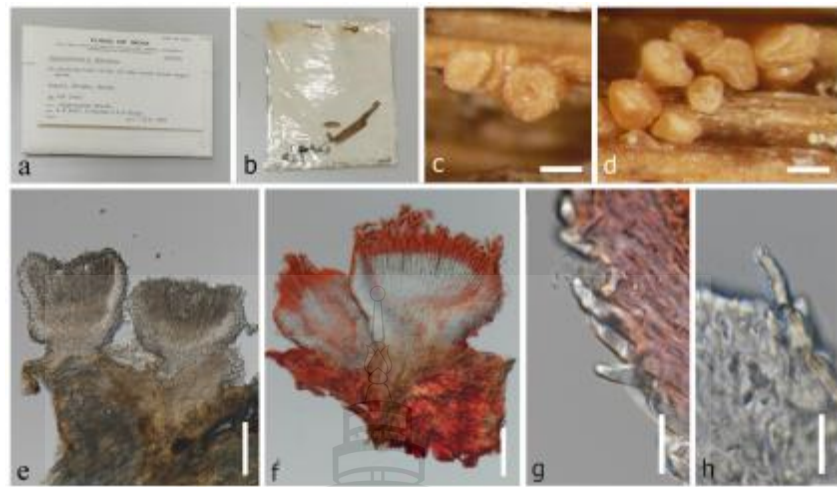


Figure 2.9 Apothecia and glassy hairs of *Unguiculariella bhutanica* (CUP-IN-000623)

Figure 2.9, a, b Details of the herbarium material. c, d Habit and appearance of apothecia on the host surface. e, f Cross section of apothecia (f mounted in Congo red). g, h Hairs (g mounted in Congo red). Scale bars: c–d = 220 μm , e–f = 45 μm , g–h = 11 μm .

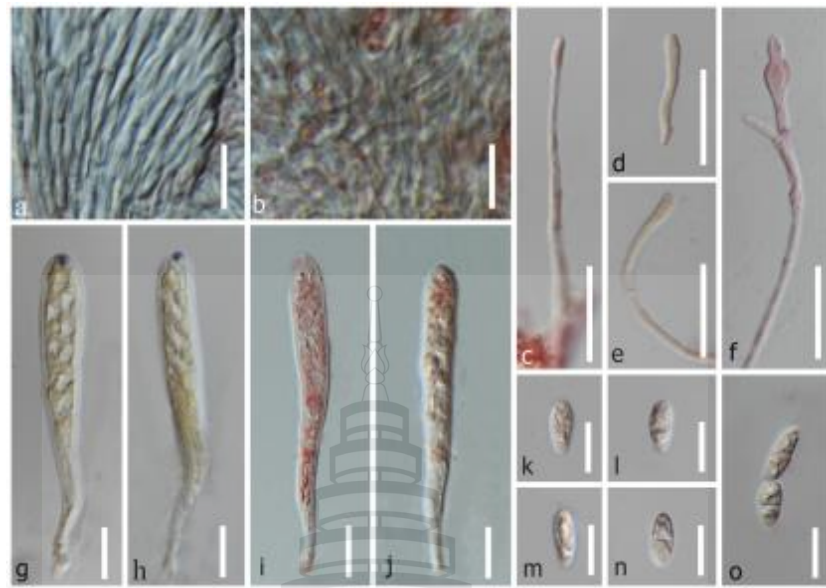


Figure 2.10 Excipulum cells, paraphysis, asci and ascospores of *Unguiculariella bhutanica* (CUP-IN-000623)

Figure 2.10, a Cells of ectal excipulum. b Cells of medullary excipulum. c–f Filiform paraphyses. g–j Asci (g, h mounted in Melzer agent, i, j mounted in Congo red). k–o Ascospores. Scale bars: a–b = 22 μm , c–f = 18 μm , g–j = 16 μm , g–h = 12 μm .

2.3.4 Lachnaceae, Helotiales

In this study, a Lachnum-like fungal specimen was found on *Tectona grandis* in Chiang Mai province, Thailand. These newly found specimens were classified based on molecular phylogenetic analyses, and morphological characteristics. Hence, the newly found specimen, *Erioscyphella abnormis* are introduced as a new host record with provided taxonomic diagnosis and photoplates. The list of sequence data used in the phylogenetic analysis is listed in Table 2.15.

The multi-gene phylogram based on the combined ITS, LSU, RPB2, and mtSSU data contains 137 Lachnaceae taxa, including the new geographical record (Figure 2.15). The final optimization likelihood value for ML is -33894.82 and was generated from nucleotide alignments of 491, 850, 739 and 892 bps of ITS, LSU, RPB2 and mt SSU, respectively. The matrix comprises 3035 characters with 1404 distinct alignment

patterns and 42.5 % of gaps and undetermined characters. Base frequencies were estimated as follows; A = 0.262040, C = 0.206953, G = 0.261128, T = 0.269879 with substitution rates AC = 1.441681, AG = 2.889861, AT = 2.390752, CG = 1.027305, CT = 7.00863, GT = 1.00; gamma distribution shape parameter $\alpha = 0.236094$. The BI analysis generated 1000 trees after 9,000,000 generations. The burn-in phase in the analysis discarded the first 250 trees and retained the remaining results to determine the posterior probabilities distribution. The final average standard of split frequencies of BI posterior probability was 0.009.



Table 2.7 Accession numbers and origin of fungal taxa used in the phylogenetic analysis of Lachnaceae

Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Albotricha acutipila</i>	FC-2262	AB481234	LC438571	AB481354	LC431751	Japan
<i>Albotricha acutipila</i>	K(M):170694	MZ159436	–	–	–	England
<i>Albotricha albotestacea</i>	FC-2094	AB481235	LC424943	AB481340	LC431747	Japan
<i>Albotricha albotestacea</i>	PRM 908618	LS997507	–	–	–	Poland
<i>Brunnipila fuscescens</i>	FC2200	AB481255	LC424945	AB48134	LC431750	Japan
<i>Brunnipila fuscescens</i>	KUS-F52031	JN033392	JN086695	JN086846	JN086769	Korea
<i>Brunnipila palearum</i>	PRM 900741	LT904856	–	–	–	Czech Republic
<i>Brunnipila palearum</i>	PRM 953071	LR963468	–	–	–	Czech Republic
<i>Capitotricha bicolor</i>	TNS:F-65670	AB481234	LC438571	AB481354	LC431751	Switzerland
<i>Capitotricha bicolor</i>	GM201504121	MK956790	–	–	–	Luxemburg
<i>Capitotricha rubi</i>	TNS:F-65752	LC438560	–	LC440395	LC533243	Switzerland
<i>Capitotricha rubi</i>	PRM 915575	LT904866	–	–	–	Czech Republic
<i>Dasyscyphella longistipitata</i>	TNS:F-16439	AB481239	LC424947	AB481331	LC533228	Japan
<i>Dasyscyphella longistipitata</i>	DL-1014	LC427964	–	–	–	Japan
<i>Dasyscyphella longistipitata</i>	DL-891	LC427954	–	–	–	Japan
<i>Dasyscyphella montana</i>	TNS:F-16527	AB481242	LC438577	AB481336	LC533241	Japan
<i>Dasyscyphus macrolanceolatus</i>	PDD:104603	ON426410	–	–	–	New Zealand

Table 2.7 (continued)

Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Dasyscyphus macrolanceolatus</i>	PDD:108742	ON426411	—	—	—	New Zealand
<i>Erioscyphella abnormis</i>	TNS:F-80478	LC424837	LC424949	LC425009	LC533283	Japan
<i>Erioscyphella abnormis</i>	KUS-F52080	JN033395	JN086698	JN086849	—	Korea
<i>Erioscyphella abnormis</i>	FC-2172	AB481250	AB481309	AB481346	—	Japan
<i>Erioscyphella abnormis</i>	MFLU 18-1826	MK584950	MK591977	MK614730	—	China
<i>Erioscyphella abnormis</i>	TNS:F-46841	LC669474	LC533170	LC533209	LC533279	Japan
<i>Erioscyphella abnormis</i>	FC-2118	AB705234	AB705274	—	—	Japan
<i>Erioscyphella abnormis</i>	E1	AB267634	—	—	—	Japan
<i>Erioscyphella abnormis</i>	MFLU 23-0489	OR652409	OR652436	OR662059	OR669152	Thailand
<i>Erioscyphella alba</i>	MFLU 16-0614	NR163782	NG066457	—	—	Thailand
<i>Erioscyphella aseptata</i>	MFLU 16-0590	NR163780	NG066456	MK388223	—	Thailand
<i>Erioscyphella curvispora</i>	KL381	MH190414	MH190415	—	—	Montenegro
<i>Erioscyphella euterpes</i>	Cantrell PR147	U58640	—	—	—	Puerto Rico
<i>Erioscyphella boninensis</i>	TNS:F-26520	LC669437	LC533151	LC533196	LC533254	Japan
<i>Erioscyphella brasiliensis</i>	TNS:F-46419	LC669456	LC533133	LC549672	LC533278	Taiwan
<i>Erioscyphella brasiliensis</i>	MFLU 16-0577a	MK584953	MK591983	MK388221	—	Thailand
<i>Erioscyphella brasiliensis</i>	MFLU 16-0577b	MK584967	MK591993	—	—	Thailand

Table 2.7 (continued)

Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Erioscyphella brasiliensis</i>	MLWU F7IIT4	U59000	—	—	—	Taiwan
<i>Erioscyphella brasiliensis</i>	3384	JF937580	—	—	—	China
<i>Erioscyphella brasiliensis</i>	2751	JF937579	—	—	—	China
<i>Erioscyphella griseibambusicola</i>	HKAS 124656	OP451796	OP451790	OP432251	OP451843	China
<i>Erioscyphella griseibambusicola</i>	HKAS 124657	OP451797	OP451791	OP432252	OP451844	China
<i>Erioscyphella hainanensis</i> (T)	TNS:F-35056	LC669453	LC533169	LC533206	LC533275	Japan
<i>Erioscyphella hainanensis</i>	TNS:F-35049	LC669452	LC533168	LC533205	LC533274	Japan
<i>Erioscyphella insulae</i> (T)	TNS:F-39720	LC669451	LC533177	LC533207	LC533261	Japan
<i>Erioscyphella insulae</i>	TNS:F-26500	LC669448	LC533149	LC533194	LC533252	Japan
<i>Erioscyphella latispora</i>	HKAS 124389	OP310823	OP113844	—	—	China
<i>Erioscyphella latispora</i>	HKAS 124391	OP113850	OP113850	—	—	China
<i>Erioscyphella lunata</i>	S.T. 13021602	KX501132	KX501133	—	—	Spain
<i>Erioscyphella lushanensis</i>	3631	JF937582	—	—	—	China
<i>Erioscyphella lushanensis</i>	205934	AF505515	—	—	—	China
<i>Erioscyphella otanii</i>	TNS:F-81472	LC669473	LC533179	—	LC533286	Japan
<i>Erioscyphella papillaris</i>	TNS:F-81272	LC669469	LC533161	LC533204	LC533285	Japan
<i>Erioscyphella paralushanensis</i>	TNS:F-61920	LC669463	LC533141	LC533220	LC533267	Japan

Table 2.7 (continued)

Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Erioscyphella sasibrevispora</i>	TNS:F-80399	LC669470	LC533173	LC533216	LC533268	Japan
<i>Erioscyphella sasibrevispora</i>	TNS:F-81401	LC669472	LC533174	LC533217	LC533269	Japan
<i>Erioscyphella sclerotii</i>	MFLU 18-0688	MK584969	MK591995	MK614726	–	Thailand
<i>Erioscyphella sclerotii</i>	MFLU 16-0569	MK584951	MK591980	MK388219	–	Thailand
<i>Erioscyphella sinensis</i>	TNS:F-32161	LC669449	LC533167	LC533219	LC533273	Japan
<i>Erioscyphella sinensis</i>	TNS:F-16837	LC669443	LC533164	AB481364	LC533235	Japan
<i>Erioscyphella subinsulae</i>	HKAS 124658	OP451798	OP451792	OP432253	OP451845	China
<i>Erioscyphella subinsulae</i>	HKAS 124659	OP451799	OP451793	OP432254	OP451846	China
<i>Incrucipulum capitatum</i>	TNS:F-81420	LC424838	LC424954	LC438592	–	Japan
<i>Incrucipulum ciliare</i>	TNS:F-81514	LC438568	LC438585	LC438598	–	Japan
<i>Incrucipulum ciliare</i>	TNS:F-81520	LC438566	LC438583	LC438596	LC533284	Japan
<i>Incrucipulum foliicola</i>	TNS:F-81526	LC438569	LC438586	LC438599	–	Japan
<i>Incrucipulum foliicola</i>	TNS:F-81508	LC438567	LC438584	LC438597	–	Japan
<i>Incrucipulum hakonechloae-macrae</i>	TNS:F-81512	LC438564	LC438581	LC438594	–	Japan
<i>Incrucipulum longispineum</i>	TNS:F-17632	AB481256	LC438579	AB481362	LC533234	Japan
<i>Incrucipulum longispineum</i>	591	AB267650	–	–	–	Japan
<i>Incrucipulum pseudosulphurellum</i>	TNS:F-81441	LC438570	LC438587	LC438600	–	Japan
<i>Incrucipulum radiatum</i>	TNS:F-16769	AB481261	AB481322	AB481359	LC431752	Japan

Table 2.7 (continued)

Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Incrucipulum radiatum</i>	TNS:F-36248	LC438559	LC438580	LC438593	–	Japan
<i>Lachnellula arida</i>	CBS:202.66	KC464635	MH870414	–	–	Switzerland
<i>Lachnellula calyciformis</i>	TNS:F-81248	LC438561	LC438574	LC438590	LC533247	Japan
<i>Lachnellula calyciformis</i>	CBS:189.66	MH858771	MH870403	–	–	Italy
<i>Lachnellula flavovirens</i>	CBS:191.66	KC464637	KC492975	–	–	Switzerland
<i>Lachnellula flavovirens</i>	CBS:190.66	MH858772	–	–	–	Switzerland
<i>Lachnellula hyalina</i>	CBS:185.66	NR165202	NG067780	XM031145866	–	Switzerland
<i>Lachnellula occidentalis</i>	FC-2034	AB481244	AB481296	AB481333	–	Japan
<i>Lachnellula occidentalis</i>	CBS:160.35	KC464639	MH867128	–	–	USA
<i>Lachnellula occidentalis</i>	CBS:159.35	MH855617	MH867127	–	–	UK
<i>Lachnellula resinaria</i>	MICH:340549	MT913605	–	–	–	USA
<i>Lachnellula subtilissima</i>	FC-2354	AB481247	AB481326	AB481363	–	Japan
<i>Lachnellula subtilissima</i>	CBS:196.66	MH858773	MH870408	–	–	Switzerland
<i>Lachnellula subtilissima</i>	CBS:197.66	MH858774	MH870409	–	–	Switzerland
<i>Lachnellula suecica</i>	TNS:F-16529	AB481248	LC424944	AB481341	LC533231	Japan
<i>Lachnellula suecica</i>	CBS:268.59	KC464642	KC492980	–	–	France
<i>Lachnellula willkommii</i>	CBS:172.35	KC464644	KC492982	–	–	Canada

Table 2.7 (continued)

Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Lachnellula willkommii</i>	CBS:200.66	KC464645	KC492983	–	–	Canada
<i>Lachniclavula thailandica</i>	BBH 50516	OR652414	OR652442	OR662059	–	Thailand
<i>Lachniclavula thailandica</i>	BBH 50526	OR652415	PQ312627	–	–	Thailand
<i>Lachnopsis catarinensis</i>	CPC 24723	NR154125	NG059651	–	–	Brazil
<i>Lachnopsis catarinensis</i>	CPC 24714	KU597795	KU597762	–	–	Brazil
<i>Lachnopsis dicksoniae</i>	CPC 24742	KU597796	KU597763	–	–	Brazil
<i>Lachnum asiaticum</i>	FC-2056	AB481251	AB481297	AB481334	–	Japan
<i>Lachnum berggrenii</i>	PDD:99185	MH921860	–	–	–	New Zealand
<i>Lachnum brevipilosum</i>	H.B. 6885	OM456227	OM456228	–	–	German
<i>Lachnum carneolum</i>	CBS:231.54	MH857305	MH868838	–	–	France
<i>Lachnum controversum</i>	K(M): 170680	MZ159434	–	–	–	UK
<i>Lachnum controversum</i>	MFLU 18-1820	MK584937	MK591964	MK368613	–	UK
<i>Lachnum diminutum</i>	CBS:232.54	MH857306	MH868839	–	–	France
<i>Lachnum fusiforme</i> (T)	MFLU 15-0230	NR154122	NG066455	MK388220	–	Thailand
<i>Lachnum fusiforme</i>	MFLU 18-1824	MK584948	MK591975	MK614728	–	Thailand
<i>Lachnum nothofagi</i>	ICMP21730	MH682233	–	–	–	New Zealand
<i>Lachnum nudipes</i>	FC-2212	AB481257	AB481314	AB481351	–	Japan
<i>Lachnum nudipes</i>	FC-2216	AB481258	–	–	–	Japan

Table 2.7 (continued)

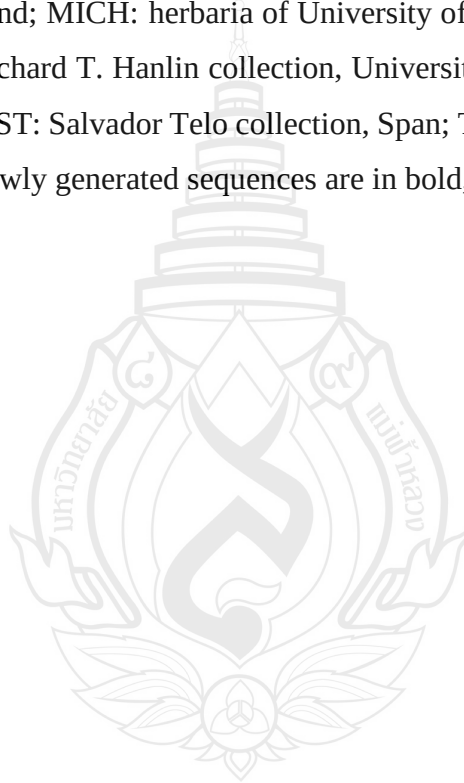
Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Lachnum palmae</i>	TNS:F-24600	LC669444	LC533145	LC533224	LC533249	Japan
<i>Lachnum palmae</i>	TNS:F-39729	LC669454	LC533178	LC533208	LC533276	Japan
<i>Lahnum palmae</i>	TNS:F-13500	LC425039	LC429382	LC431718	–	Japan
<i>Lachnum palmae</i>	PDD:60284	MH921862	–	–	–	New Zealand
<i>Lachnum papyraceum</i>	545-1	AB267648	–	–	–	Japan
<i>Lachnum pygmaeum</i>	H.B.6903	OM456203	OM456204	–	–	France
<i>Lachnum rachidicola</i>	TNS:F-81229	LC669467	LC533136	LC533189	–	Japan
<i>Lachnum rachidicola</i>	TNS:F-16649	AB745433	–	–	–	Japan
<i>Lachnum rachidicola</i>	F16801	AB745434	–	–	–	Japan
<i>Lachnum soppittii</i>	FC-2160	AB481266	AB481308	AB481344	–	Japan
<i>Lachnum spartinae</i>	RTH 1078 GAM	U58639	–	–	–	USA
<i>Lachnum spartinae</i>	SAP138	AF422970	AF422970	–	–	USA
<i>Lachnum virgineum</i>	AFTOL-ID 49	DQ491485	AY544646	DQ470877	AY544745	USA
<i>Lachnum virgineum</i>	FC-2137	AB481268	AB481306	AB481343	–	Japan
<i>Lachnum virgineum</i>	TNS-F-16583	–	AB926119	–	LC431748	Japan
<i>Lachnum virgineum</i>	420526MF0092	MG696592	MH668035	–	–	China
<i>Neodasyscypha cerina</i>	TNS:F-65625	LC424836	LC424948	LC425013	LC533242	Switzerland
<i>Pezicula chiangraiensis</i>	MFLUCC15-0170	KU310621	KU310622	KU310623	–	Thailand

Table 2.7 (continued)

Taxon name	Specimen code ^a	GenBank accession no.				Origin
		ITS	LSU	RPB2	mtssu	
<i>Pezicula neocinnamomea</i>	CBS:100248	NR155656	NG067299	KF376209	–	Denmark
<i>Proliferodiscus alboviridis</i>	TNS:F-17436	LC438558	LC424950	LC425014	–	Japan
<i>Proliferodiscus</i> cf <i>pulveraceus</i>	H.B. 6922	OM456229	–	–	–	Luxemburg
<i>Proliferodiscus Chiangraiensis</i>	MFLU 16-0588	NR164304	NG068622	–	–	Thailand
<i>Proliferodiscus dingleyae</i>	ICMP21730	MH682231	–	–	–	New Zealand
<i>Proliferodiscus earoleucus</i>	BHI-F624d	MF161304	–	–	–	USA
<i>Proliferodiscus ingens</i>	CBS:145519	NR170767	–	–	–	Germany
<i>Proliferodiscus longisporus</i>	HKAS 124388	OP113842	OP264080	–	–	China
<i>Proliferodiscus longisporus</i>	HKAS 124390	OP113840	OP310824	–	–	China
<i>Proliferodiscus tricolor</i>	CBS:122000	KC464643	KC492981	–	–	Germany
<i>Proliferodiscus</i> sp	KUS-F52600	JN033427	JN086730	JN086871	JN086796	Korea

Note ^aAFTOL: Assembling the Fungal Tree of Life, Oregon State University, USA; BHI: Boston Harbor Islands, Purdue University, Indiana, USA; Cantrell: S.A. Cantrell collection, Georgia, USA; CBS: Central Bureau voor Schimmelcultures, Utrecht, The Netherlands; CPC: Collection of Pedro Crous housed at CBS; DL: National Museum of Nature and Science, Japan; E: Takanori Miyoshi Ehime fruit tree experiment station, Ehime, Japan; F: Fundación Medina's Fungal Culture collection, Spain; FC: Tsuyoshi Hosoya National Museum of Nature and Science, Tsukuba, Japan; GM: G. Marson collection, Luxembourg; HKAS: Cryptogamic Herbarium, Kunming Institute of Botany, Chinese Academy of Sciences, China; H.B: Hans Otto Baral collection, Germany; The New Zealand Fungarium (PDD), New

Zealand, ICMP: International Collection of Microorganisms from Plants, New Zealand; K(M): Kew Mycology collection, Royal Botanic Garden, London, UK; The Kew Mycology collection, Richmond, UK; KUS: Korea University Herbarium, Seoul, Korea; MFLU: Mae Fah Luang University Herbarium, Chiang Rai, Thailand; MICH: herbaria of University of Michigan, Michigan, USA; PRM: herbaria of National Museum, Prague, Czech Republic; RTH: Richard T. Hanlin collection, University of Georgia, Georgia, USA; SAP: herbaria of Sapelo Islands University of Georgia, Georgia, USA; ST: Salvador Telo collection, Spain; TNS: National Museum of Nature and Science, Tsukuba, Japan. Ex-type strains are labeled by (T), newly generated sequences are in bold, and “–” indicates unavailable sequences



Family: Lachnaceae Raitv.

Genus: *Albotricha* Raitv.

Albotricha, a genus of fungi in the family Lachnaceae, established by Raitviir (1970) and characterized by having smooth but granulated at the base, acute hairs and long extending, lanceolate, paraphyses. Some *Albotricha* species were transferred to *Hegermila* and *Psilachnum* (Raitviir & Järv, 1995; Baral & Quijada, 2020), and currently, nineteen species registered in Species fungorum (2024)

Albotricha kamtschatica (Raitv.) Raitv.

= *Lachnaster kamtschatica* (Raitv.)

Figure 2.11

Index Fungorum number: IF103975

Facesoffungi number: FoF 15672

Material examined: Russian Federation, Kamchatka Krai, Yelizovsky District, the vicinity of Yuzhnye Koryaki 52.262461 -158.120235 on the stem of *Filipendula palmata*, 22 September 1960, Erast Parmasto (TAAM012499).

Description: *Saprobic* on the stem of *Filipendula palmata*. **Sexual morph:** Substipitate discomycetous. *Apothecia* 550–771 × 396–485 µm ($\bar{x}$ = 664.1 × 435.9 µm, n = 4), arising singly. *Receptacle* cupulate. *Discs* concave. *Hairs* 202–287 × 2.4–4.4 µm ($\bar{x}$ = 242.1 × 2.9 µm, n = 10), on margin, cylindrical with a pointed tip, sometimes topped with crystal-like structure, septate, white. *Ectal excipulum* 19–44 µm wide ($\bar{x}$ = 30.2 µm, n = 10), composed of thick-walled, hyaline cells of *textura prismatica*. *Paraphyses* 4–6.3 µm wide ($\bar{x}$ = 5.1 µm, n = 10) at the top, numerous, lanceolate, aseptate, exceeding the asci in length. *Asci* 46–77 × 4.7–5.6 µm ($\bar{x}$ = 42.2 × 5.1 µm, n = 30), 8-spored, unitunicate, cylindric, rounded at the apex, amyloid, arising from simple septa. *Ascospores* 8–11 × 2.1–2.8 µm ($\bar{x}$ = 9.3 × 2.4 µm, n = 10), uniseriate, fusoid, aseptate, hyaline, rounded at both ends. **Asexual morph:** Undetermined.

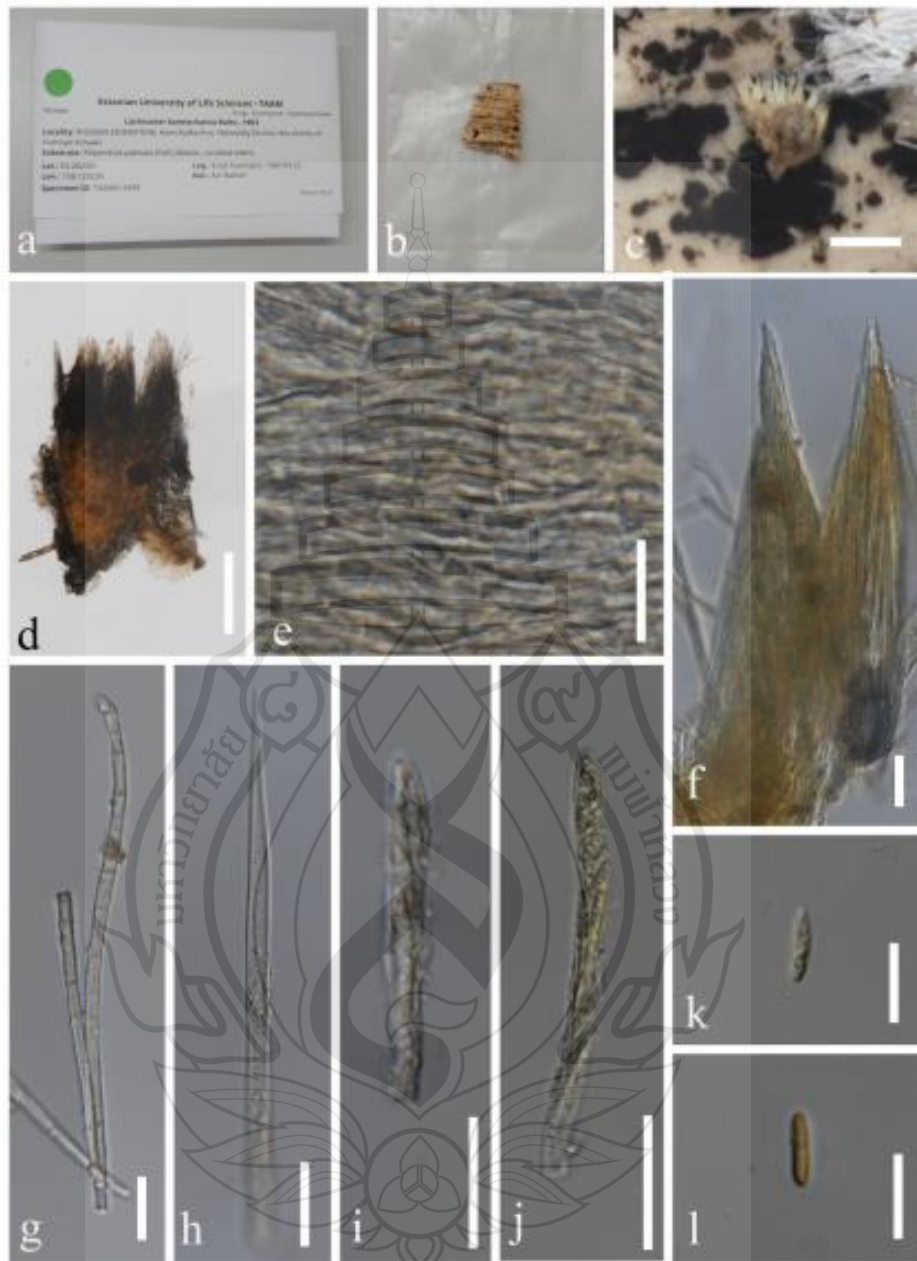


Figure 2.11 Sexual morph of *Albotricha kamtschatica* (TAAM012499)

Figure 2.11, a, b Details of herbarium material. c Habit and appearance of an apothecium on the host surface. d Cross section of an apothecium. e Cells of ectal excipulum. f–g Hairs. h Paraphyses. i–j Asci. k–l Ascospores (h, i mounted in Congo red). Scale bars: c = 619 μm , d = 180 μm , e–j = 20 μm , k–l = 9 μm .

Genus: *Brunnipila* Baral

Brunnipila, a genus of fungi in the family Lachnaceae, established by Baral (1985) and characterized by having *textura prismatica-angularis* excipulum cells, granulated hair, lanceolate paraphysis with length exceeding asci, ellipsoid to fusiform ascospores (Hosoya et al., 2019). *Brunnipila* species serves as saprophytes, growing on deciduous leaves (Hosoya et al., 2019) and currently, nineteen species registered in Species fungorum (2024).

***Brunnipila clandestina* (Bull.) Baral**

= *Peziza clandestina* Bull.

Figure 2.12

Index fungorum number: IF104069

Facesoffungi number: FoF 15673

Material examined: Lithuania, Telšiai, on the stem of *Rubus idaeus*, 17 July 1966, Ain Raitvir (TAAM-044272).

Description: *Saprobic* on the stem of *Rubus idaeus*. **Sexual morph:** Stipitate discomycetous. *Apothecia* 271–574 × 147–525 µm, arising singly or in small clusters. *Receptacle* cupulate. *Discs* concave. *Hairs* 100–159 × 4.5–5.8 µm ($\bar{x}$ = 132.1 × 5.4 µm, n = 10), on flank and margin, brown, cylindrical with hyaline, hemispherical tip and sometimes topped with crystal-like structures, septate. *Ectal excipulum* 64–71 µm wide ($\bar{x}$ = 66.6 µm, n = 10), composed of thick-walled, brown cells of *textura angularis* to *prismatica*. *Paraphyses* 3–11 µm wide ($\bar{x}$ = 6.8 µm, n = 10) at the middle cells, numerous, lanceolate, aseptate, exceeding the asci in length. *Asci* 38–50 × 2.6–4.8 µm ($\bar{x}$ = 42.2 × 4.2 µm, n = 10), 8-spored, unitunicate, cylindric, rounded to slightly conical at the apex, faintly amyloid, arising from simple septa. *Ascospores* 5.9–7 × 1.5–2.4 µm ($\bar{x}$ = 6.6 × 1.8 µm, n = 10), uniseriate to partially biseriate, fusoid, aseptate, hyaline, rounded at both ends. **Asexual morph:** Undetermined.

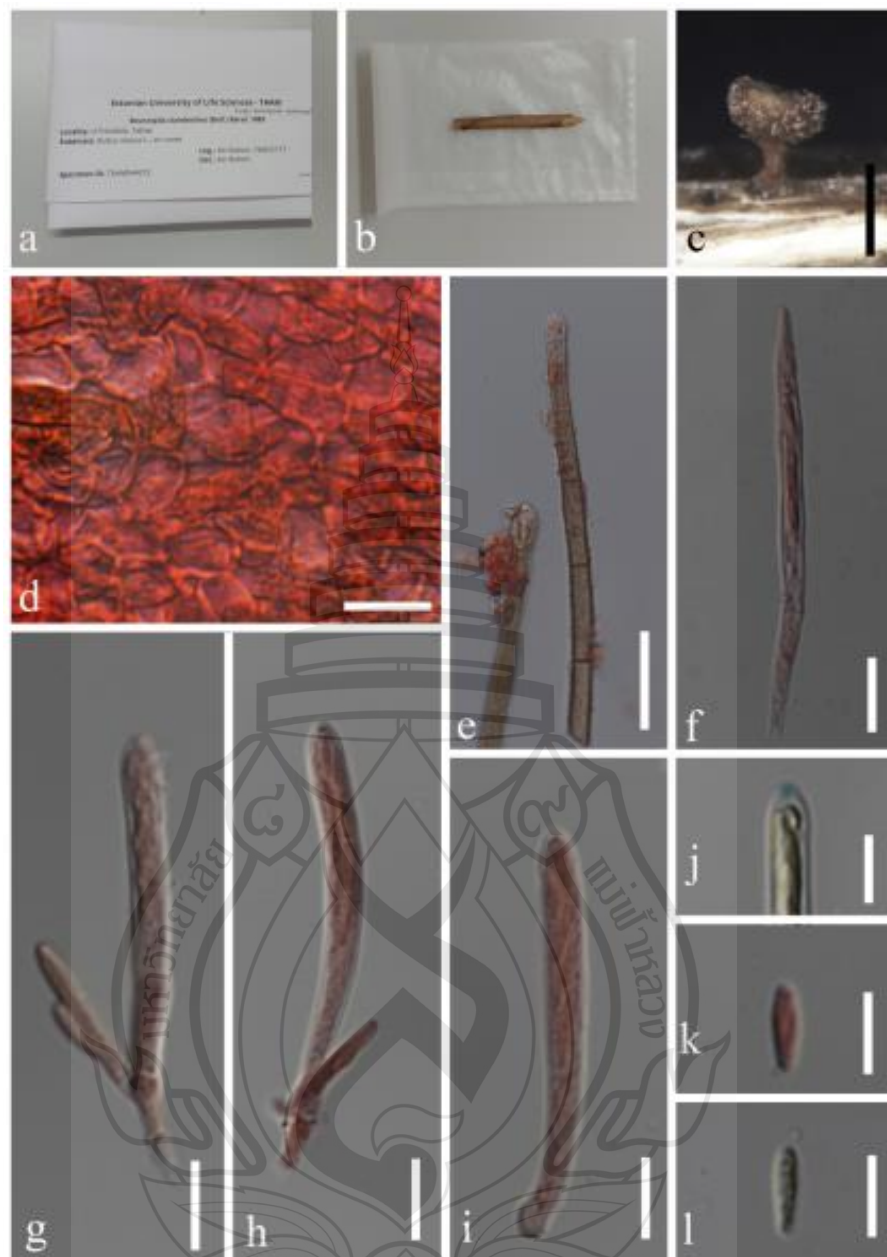


Figure 2.12 Sexual morph of *Brunnipila clandestina* (TAAM-044272)

Figure 2.12, a, b Details of the herbarium material. c Habit and appearance of an apothecium on the host surface. d Cells of ectal excipulum. e Hairs. f Paraphyses. g–i Asci. j Tip of an ascus (mounted in Melzer agent). k–l Ascospores. Scale bars: c = 475 μ m, d–i = 13 μ m, j = 10 μ m, k–l = 7 μ m.

Genus: *Dasyscyphella* Tranzschel

Dasyscyphella, a genus of fungi in the family Lachnaceae, established by Tranzschel (1899) and characterized by having hyaline hairs with smooth apex, lanceolate paraphysis, fusiform ascospores (Hosoya et al., 2019; Suková, 2005). *Dasyscyphella* species serves as saprophytes, growing on coniferous cones or deciduous woody litter (Suková, 2005) and currently, 30 species registered in Species fungorum (2024).

Dasyscyphella cassandrae Tranzschel

Figure 2.13; 2.14

Index Fungorum number: IF 199043

Facesoffungi number: FoF15676

Material examined: United States of America, New York, Tompkins, McLean, 42.552016 -76.291044 +-6359m, on dead twigs of *Chamaedaphne calyculata*, 17 June 1964, Korf (CUP-054631).

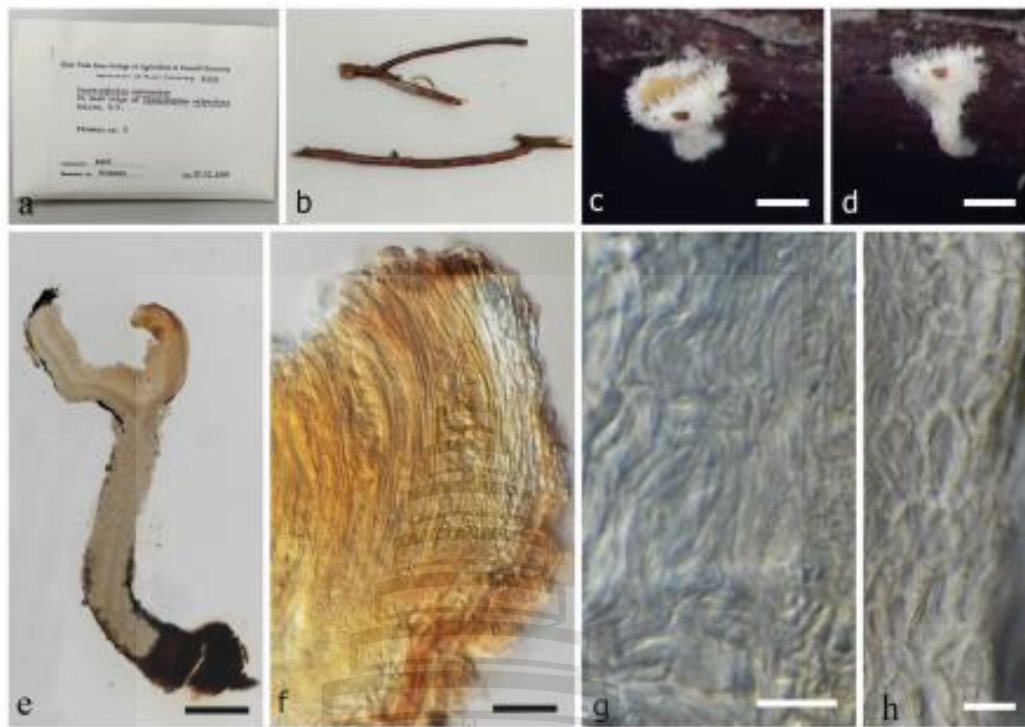


Figure 2.13 Apothecia and excipulum cells of *Dasyscyphella cassandrae* (CUP-054631)

Figure 2.13, a, b Details of the herbarium material. c, d Habit and appearance of an apothecium on the host surface. e Cross section of an apothecium. f Close-up of an apothecium at the margin. g Cells of medullary excipulum. h Cells of the ectal excipulum. Scale bars: c–d = 500 μm , e = 300 μm , f = 22 μm , g–h = 13 μm .

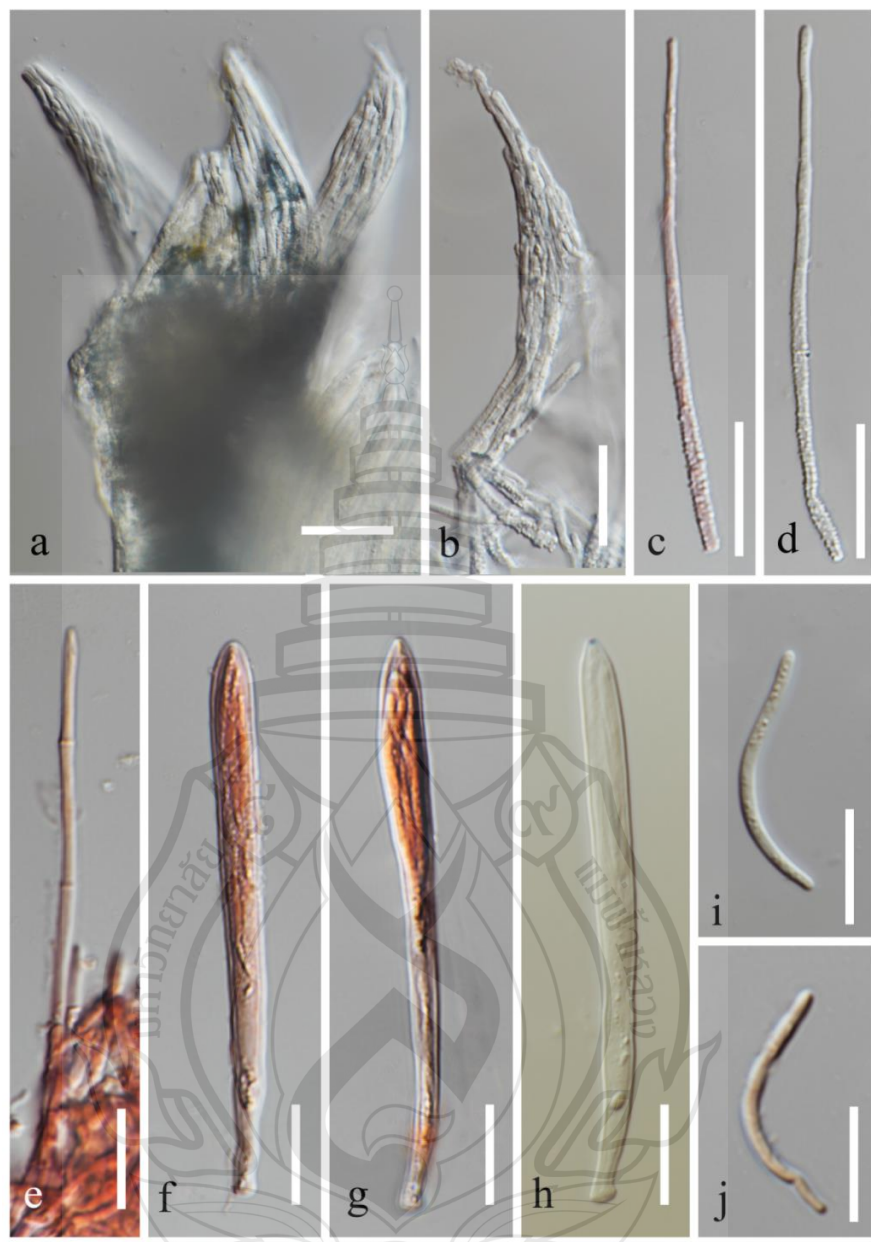


Figure 2.14 Hair, paraphysis, asci and ascospores of *Dasyscyphella cassandrae* (CUP-054631)

Figure 2.14, a–b Hairs at the apothecium margin. c–d Single hair. e Filiform paraphyses. f–g Asci (mounted in Congo red). h An ascus with J+ ring (mounted in Meltzer agent). i–j Ascospores (j. mounted in Congo red). Scale bars: a–b = 25 μm , c–d = 45 μm , f = 22 μm . e–h = 17 μm , g–h = 15 μm .

Description: *Saprobic* on dead twigs of *Chamaedaphne calyculata*. **Sexual morph:** Stipitate discomycetous. *Apothecia* 398–729 × 235–388 µm, arising singly. *Receptacle* cupulate. *Discs* concave. *Hairs* 70–90 × 3–4 µm ($\bar{x}$ = 79.4 × 2.5 µm, n = 10) on flanks, margin and stipe, cylindrical with hemispherical tip, slightly bent, septate, white, densely covered with granules at the base. *Ectal excipulum* 22–31 µm wide ($\bar{x}$ = 27.8 µm, n = 15), composed of thin-walled, pale yellowish cells of *textura prismatica*. *Medullary excipulum* 16–19 µm ($\bar{x}$ = 17.4 µm, n = 15) at flanks, composed of yellowish to hyaline cells of *textura intricata*. *Hymenium* yellow. *Paraphyses* 2.2–2.6 µm wide ($\bar{x}$ = 2.8 µm, n = 30), numerous, filiform, obtuse at the apex, septate, not exceeding the asci in length, smooth. *Asci* 75–120 × 6.1–8.8 µm ($\bar{x}$ = 94.8 × 7.7 µm, n = 20), 8-spored, unitunicate, cylindric-clavate, rounded or medium conical at the apex, amyloid, arising from croziers. *Ascospores* 32–47 × 1.9–2.5 µm ($\bar{x}$ = 36.9 × 2.2 µm, n = 30), multi-seriate, fusoid, aseptate, hyaline, small guttulate to smooth, tapered towards the base. **Asexual morph:** Undetermined.

Genus: *Erioscyphella* Kirschst.

Erioscyphella, a genus of fungi in the family Lachnaceae, established by Kirschstein (1938) and characterized by having short to long stipitate apothecia, cylindrical to lanceolate paraphysis with length mostly exceeding asci, fusiform to filiform ascospores (Tochihara & Hosoya, 2022). *Erioscyphella* species serves mainly as saprophytes, rarely pathogens (Miyoshi et al., 2007), growing on various of rotten and/or decayed lignocellulose substrates (Perić & Baral, 2014; Tochihara & Hosoya, 2022) and currently, 21 species registered in Species fungorum (2024).

Erioscyphella abnormis (Mont.) Baral, Šandová and B. Perić

= *Lachnum abnorme* (Mont.) J.H. Haines and Dumont

Figure 2.15; 2.16; 317

Index Fungorum number: IF570309

Facesoffungi number: FoF 10812

Material examined: Thailand, Chiang Rai Province, Phan District, Sai Khao, Phra That Wang Chom Thong Monastery, 31 August 2021, Anis S. Lestari, PTW 2 (MFLU 23-0489), GenBank number ITS: OR652409, LSU: OR652436, RPB2: OR662059, mtSSU: OR669152.

Description: *Saprobic* or *parasitic* on an alive tree of *Tectona grandis*. **Sexual morph:** *Apothecia* 0.6–1.5 × 0.6–1.3 mm ($\bar{x}$ = 87.7 × 2.3 mm, n = 10), sessile to substipitate, arising singly or in small clusters. *Receptacle* cupulate, yellow. *Margin* concolorous to the receptacle, covered with brown and white hair at the outer layer. *Discs* concave. *Hairs* 39–114 × 2.7–2.8 μm ($\bar{x}$ = 87.7 × 2.3 μm, n = 10), cylindric, septate, rough walls, covered with granules, pigmented, hyaline to pale brown. *Ectal excipulum* 27–47 μm ($\bar{x}$ = 37.4 μm, n = 10) in lower flanks, composed of thick-walled cells of *textura angularis* to *prismatica*. *Medullary excipulum* 79–110 μm ($\bar{x}$ = 95.3 μm, n = 10) in lower flanks, composed of thin-walled, hyaline cells of *textura intricata*. *Hymenium* yellowish. *Paraphyses* 2.7–2.1 μm wide ($\bar{x}$ = 2.8 μm, n = 10), numerous, filiform, conical apex, septate, sometimes exceeding the asci in length, smooth. *Asci* 103–116 × 8.4–11 μm ($\bar{x}$ = 111 × 9.6 μm, n = 30), 8-spored, unitunicate, cylindric-clavate, conical apex, amyloid, arising from croziers. *Ascospores* 41–66 × 2–2.7 μm ($\bar{x}$ = 56.8 × 2.7 μm, n = 30), multi-seriate, filiform, hyaline, guttulate, tapered at one end. **Asexual morph:** Undetermined.

Notes: The morphology of our new lachnoid specimen (MFLU 23-0489) fits with the species description of *Erioscyphella abnormis* by having filiform ascospores and paraphyses and yellowish hymenium (Ekanayaka et al., 2019a). However, our newly found differed on the apothecial characters. Our specimen (MFLU 23-0489) differs by having sessile to substipitate apothecia, in contrast to the description of *E. abnormis* by Haines and Dumont (1984), Hosoya et al. (2009) and Ekanayaka et al. (2019a).

Our specimen *Erioscyphella abnormis* (MFLU 23-0489) formed a sister relationship to the cluster of *E. abnormis* (FC-2172 and FC-2118) with 89% maximum likelihood bootstrap support and 0.97 BI posterior probability. Apothecial morphology can indeed vary significantly not only between different genera but also within species in Lachnaceae. These variations can be influenced by environmental factors and genetic differences (Tochihara & Hosoya, 2022).

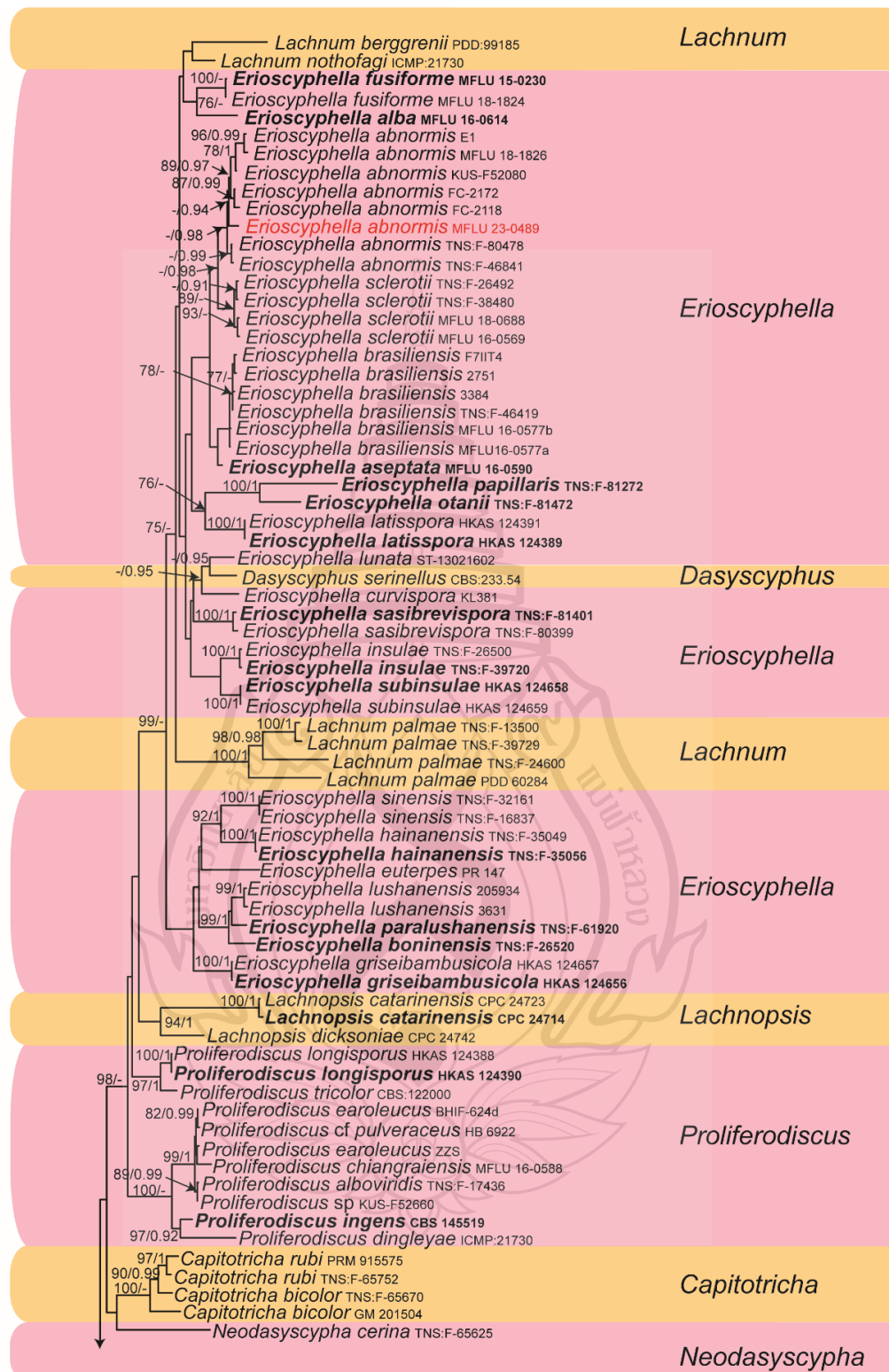


Figure 2.15 Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU, RPB2 and mt SSU sequence data of Lachnaceae

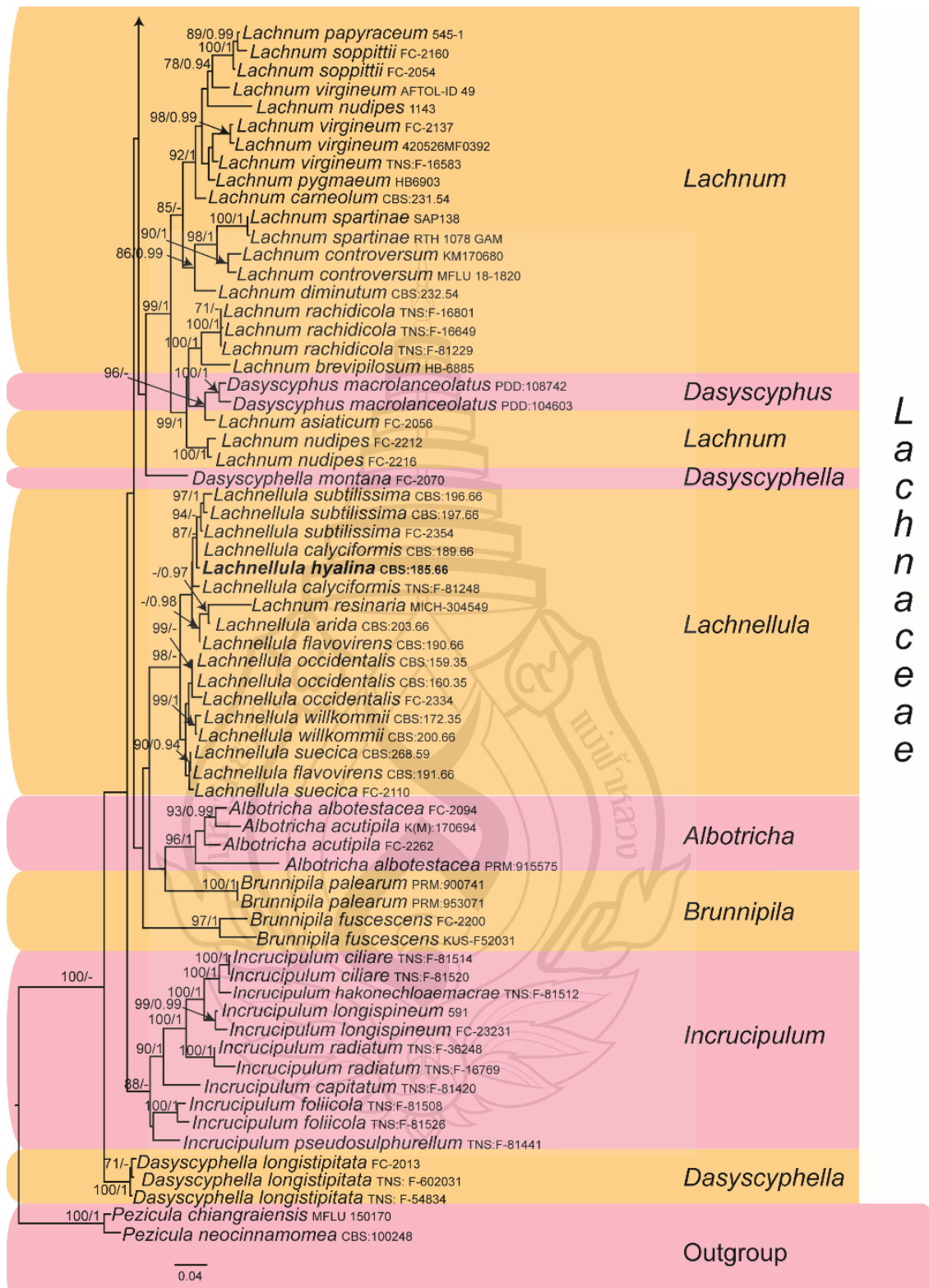


Figure 2.15 (continued)



Figure 2.16 Apothecia and hair of *Erioscyphella abnormis* (MFLU 23-0489, new host record)

Figure 2.16, a A piece of wood of an alive *Tectona grandis* tree. b–c Apothecia on the substrate. d Close-up of an apothecium in a median section. e Close-up of hymenium at the margin. f–h Hairs. Scale bars: b–c = 600 μm , d = 300 μm , e = 150 μm , g–h = 20 μm .

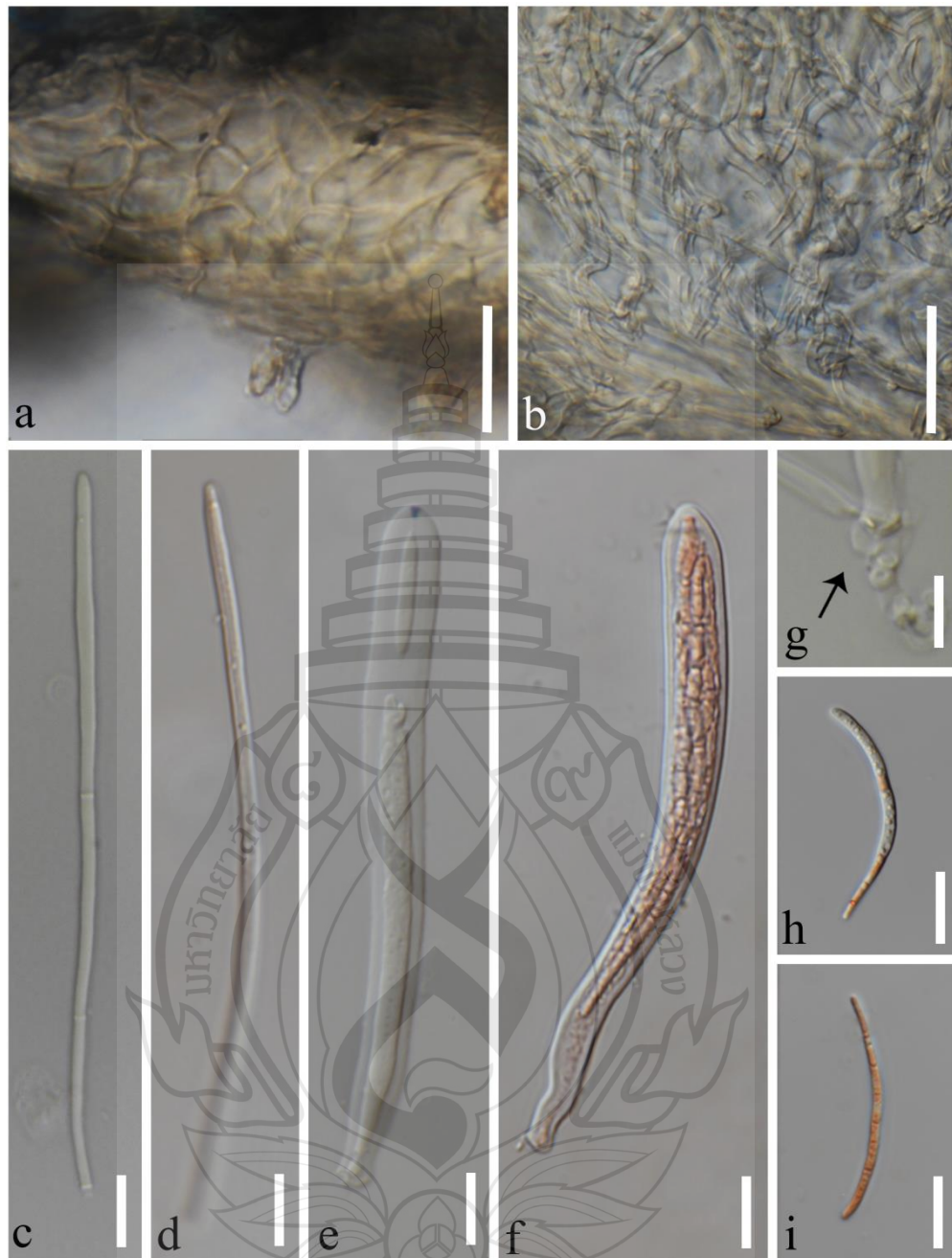


Figure 2.17 Excipulum cells, paraphysis, asci and ascospores of *Erioscyphella abnormis* (MFLU 22-0055, new host record)

Figure 2.17, a–b Excipulum cells. c–d Paraphyses. e–f Asci. g A crozier at the ascus base. h–i Ascospores. Scale bars: a–b = 45 μm , c–f = 30 μm , g–i = 15 μm .

Genus: *Incrucipulum* Baral

Incrucipulum, a genus of fungi in the family Lachnaceae, established by Baral (1985) and characterized by having *textura prismatica* excipulum cells, granulated hair, narrowly lanceolate paraphysis, fusiform ascospores (Hosoya et al., 2019). *Incrucipulum* species serves as saprophytes, growing on deciduous leaves (Hosoya et al., 2019) and currently, ten species registered in Species fungorum (2024).

Incrucipulum ciliare (Schrad. ex J.F. Gmel.) Baral

= *Peziza ciliaris* Schrad. ex J.F. Gmel.

Figure 2.18

Index Fungorum number: IF 104379

Facesoffungi number: FoF 15675

Material examined: Belgium, on unidentified leaves, Mouton, V. (BR5020089087414).

Description: *Saprobic* on unidentified leaves. **Sexual morph:** Stipitate discomycetous. *Apothecia* 132–211 × 90–197 µm, arising singly. *Receptacle* cupulate. *Discs* concave. *Hairs* 34–54 × 2.8–2.7 µm ($\bar{x}$ = 45.3 × 2.4 µm, n = 10) on flank and margin, cylindrical with hemispherical tip, septate, white, densely covered with granules at the top to base. *Excipulum* composed of thin-walled cells of *textura prismatica*. *Hymenium* hyaline. *Paraphyses* 1.5–2.5 µm wide ($\bar{x}$ = 2.3 µm, n = 10) at the top, numerous, lanceolate, septate around the base, exceeding the asci in length. *Asci* 42–47 × 4.7–7 µm ($\bar{x}$ = 40.7 × 5.4 µm, n = 10), 8-spored, unitunicate, cylindric, rounded at the apex, euamyloid, arising from simple septa. *Ascospores* 8–11 × 2.2–2.8 µm ($\bar{x}$ = 9.8 × 2.2 µm, n = 10), partially biseriate, fusoid, aseptate, hyaline, smooth, rounded at both ends. **Asexual morph:** Undetermined.

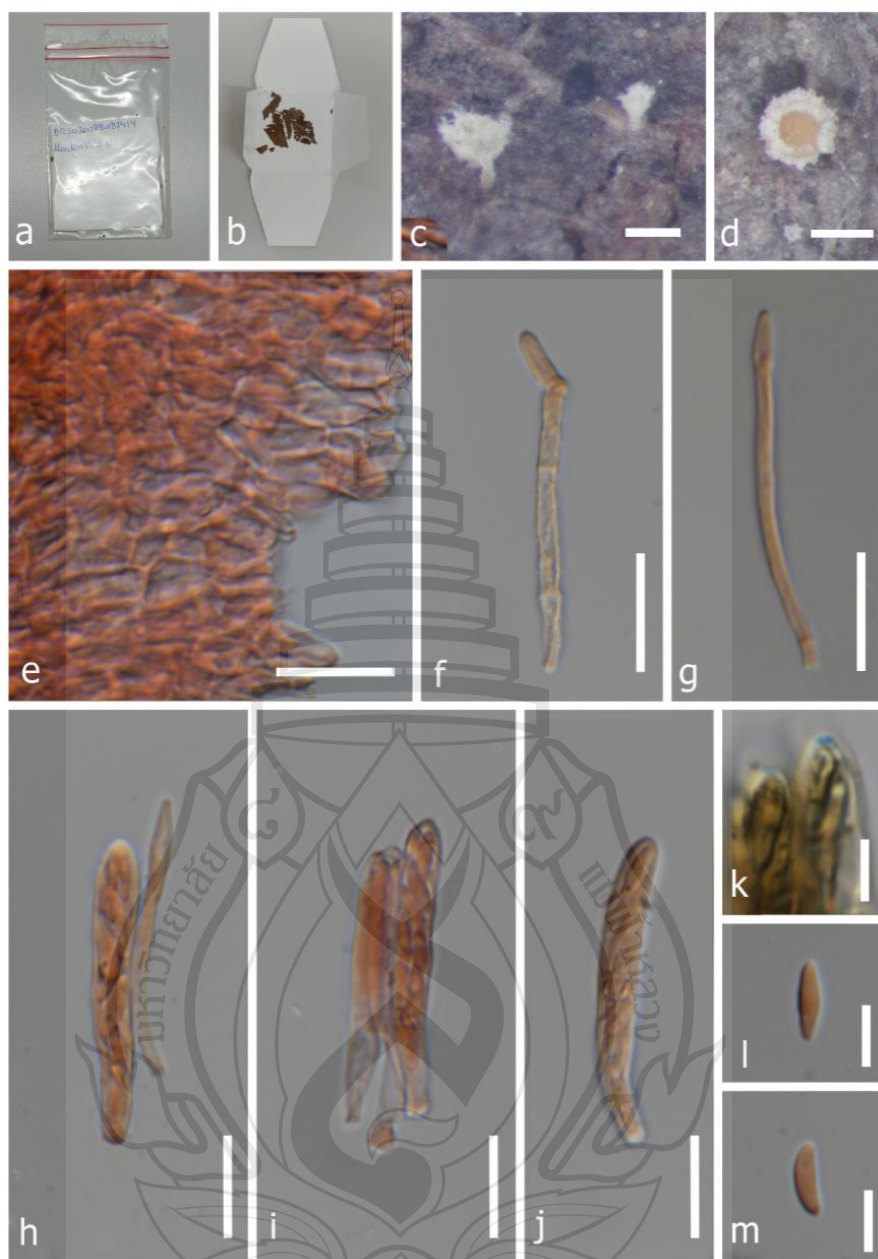


Figure 2.18 Sexual morph of *Incrucipulum ciliare* (BR5020089087414)

Figure 2.18, a–b Details of the herbarium material. c–d Apothecia on the host surface. c Cross-section of an apothecium. e Close-up of ectal excipulum cells. f Hair. g Paraphyses. h–j Asci. k Ascus tips (in Melzer agent). l–m Ascospores. Scale bars: c–d = 200 μ m, e–j = 18 μ m, k–m = 9 μ m.

Genus: *Lachnellula* P. Karst.

Lachnellula, a genus of fungi in the family Lachnaceae, established by Kars (1884) and characterized by having *textura prismatica-intricata-globulosa*, hyaline, smooth hair, cylindrical paraphysis with length sometimes exceeding asci and globose, globose, ellipsoid to tear-shaped ascospores (Hosoya et al., 2019). *Lachnellula* species serves as saprophytes or parasites, growing on coniferous wood and leaves (Hosoya et al., 2019) and currently, 46 species registered in Species Fungorum (2024).

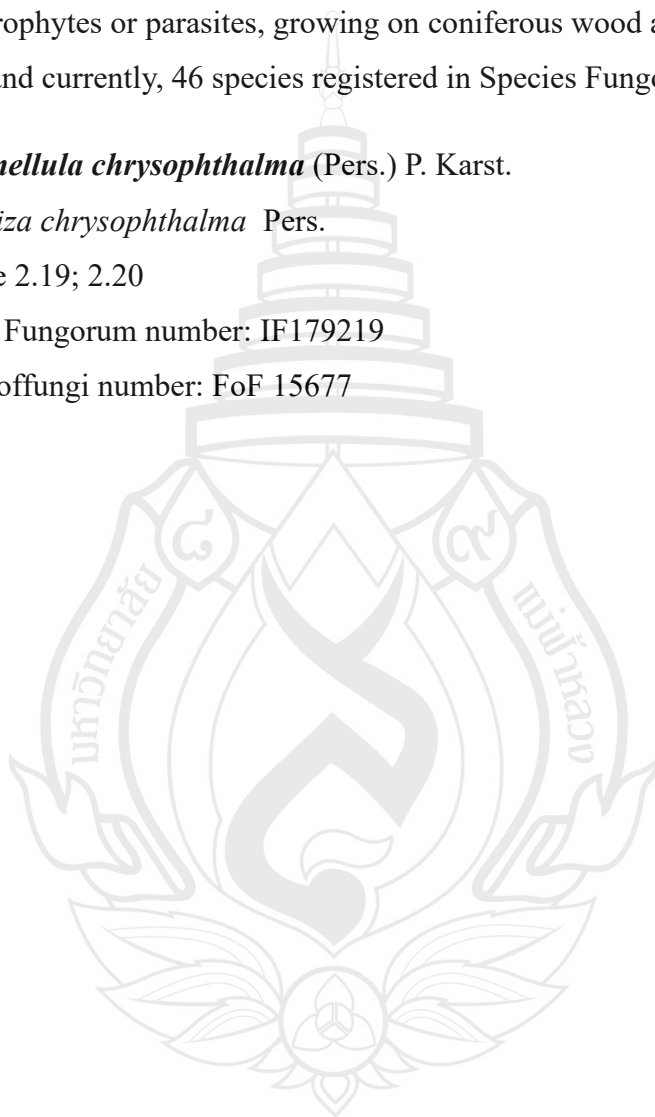
***Lachnellula chrysophthalma* (Pers.) P. Karst.**

= *Peziza chrysophthalma* Pers.

Figure 2.19; 2.20

Index Fungorum number: IF179219

Facesoffungi number: FoF 15677



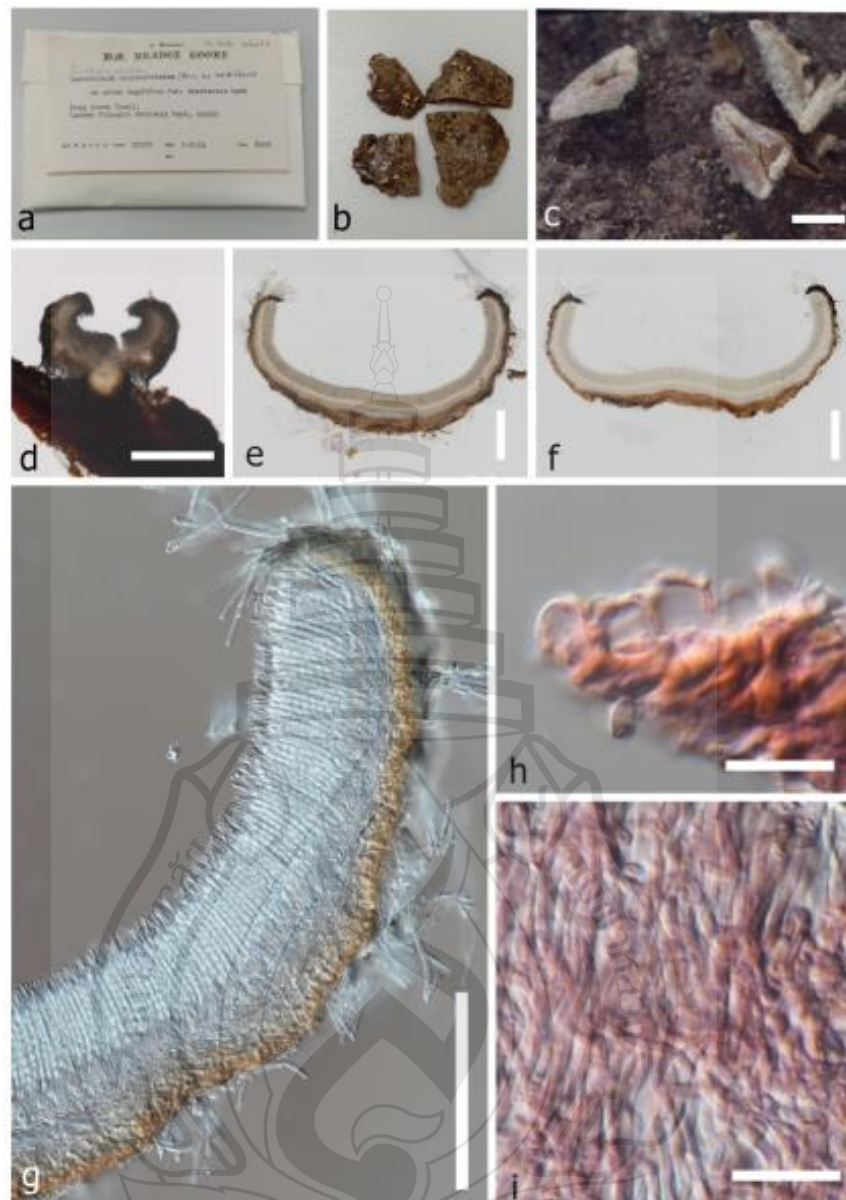


Figure 2.19 Apothecia and excipulum cells of *Lachnellula chrysophthalma* (CUP-046452)

Figure 2.19, a, b Details of the herbarium material. c Appearance of apothecia on the host surface. d–f Cross section of an apothecium. g Close-up of an apothecium at the margin. h Cells of ectal excipulum. i Cells of medullary excipulum (h, i mounted in Congo red). Scale bars: c = 1000 μ m, d = 235 μ m, e–g = 100 μ m, h–i = 15 μ m.

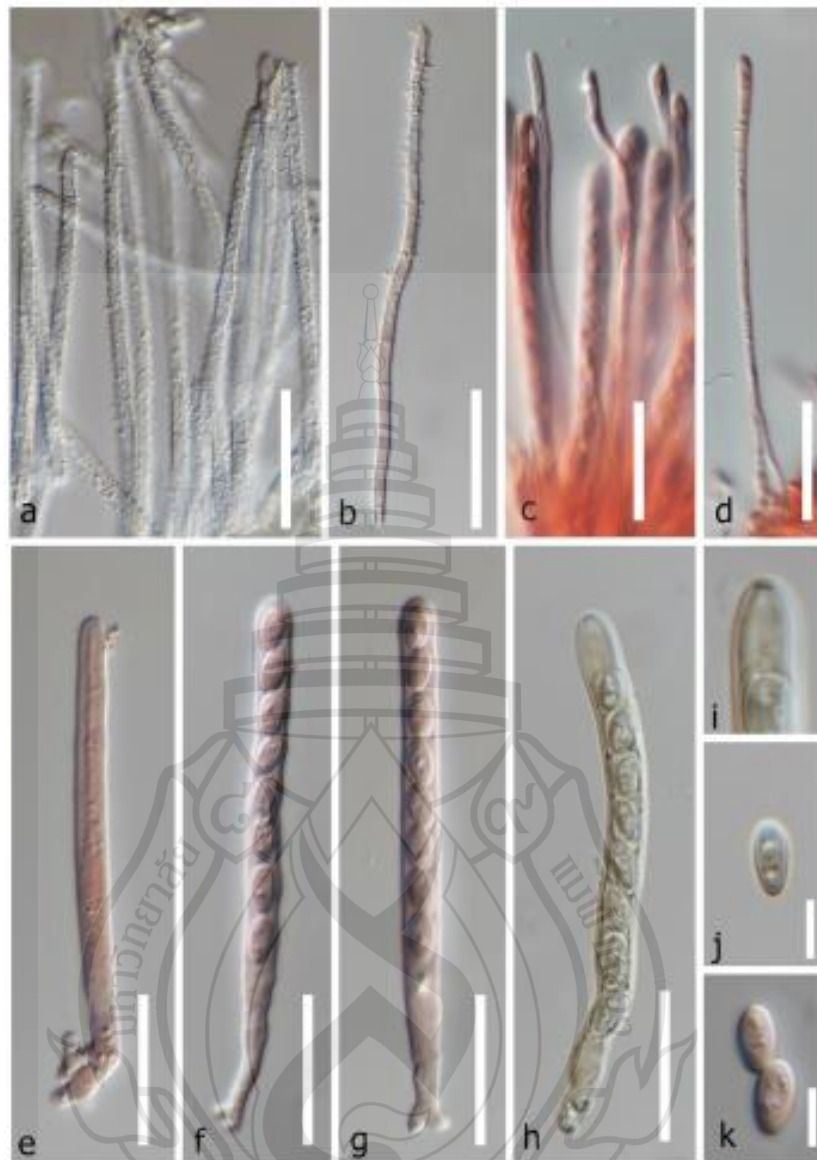


Figure 2.20 Hair, paraphysis, asci and ascospores of *Lachnellula chrysophthalma* (CUP-046452)

Figure 2.20, a Hairs at the apothecium margin. b A single hair. c Paraphyses among asci. d Filiform paraphyses. e–h Asci. i An ascus with J+ ring (mounted in Meltzer agent). j–k Ascospores (b–g, k mounted in Congo red). Scale bars: a–b = 34 μm , c–d = 22 μm , e–h = 23 μm , j–k = 6 μm .

Material examined: United states, California, King Creek Trail, Lassen Volcanic National Park 40.493683 -121.407348 +-15351m, on the barks of *Abies magnifica-shastensis*, 02 July 1954, W.B. Cooke (CUP-046452).

Description: *Saprobic* on the barks of *Abies magnifica-shastensis*. **Sexual morph:** Stipitate discomycetous. *Apothecia* 1.3–2.1 × 0.7–1.2 mm, arising singly. *Receptacle* cupulate. *Discs* concave. *Hairs* 97–132 × 2.8–2.9 µm ($\bar{x}$ = 112.1 × 2.4 µm, n = 15) on flank and margin, cylindrical with hemispherical tip, septate, white, densely covered with granules at the top to base. *Ectal excipulum* 20–26 µm wide ($\bar{x}$ = 22.7 µm, n = 30), composed of thick-walled, brown cells of *textura angularis* to *prismatica*. *Medullary excipulum* 8–12 µm ($\bar{x}$ = 9.7 µm, n = 30) at flanks, composed of hyaline cells of *textura intricata*. *Hymenium* hyaline. *Paraphyses* 2.1–2.3 µm wide ($\bar{x}$ = 2.7 µm, n = 30) at the top, numerous, filiform, slightly swollen at the apex, septate, exceeding the asci in length, smooth. *Asci* 65–81 × 4.7–5.6 µm ($\bar{x}$ = 72.3 × 5.1 µm, n = 30), 8-spored, unitunicate, cylindric, rounded at the apex, faintly amyloid, arising from croziers. *Ascospores* 5–7 × 2.9–2.6 µm ($\bar{x}$ = 6.3 × 2.3 µm, n = 30), uniseriate, ellipsoid, aseptate, hyaline, 1–2 guttules, rounded at both ends. **Asexual morph:** Undetermined.

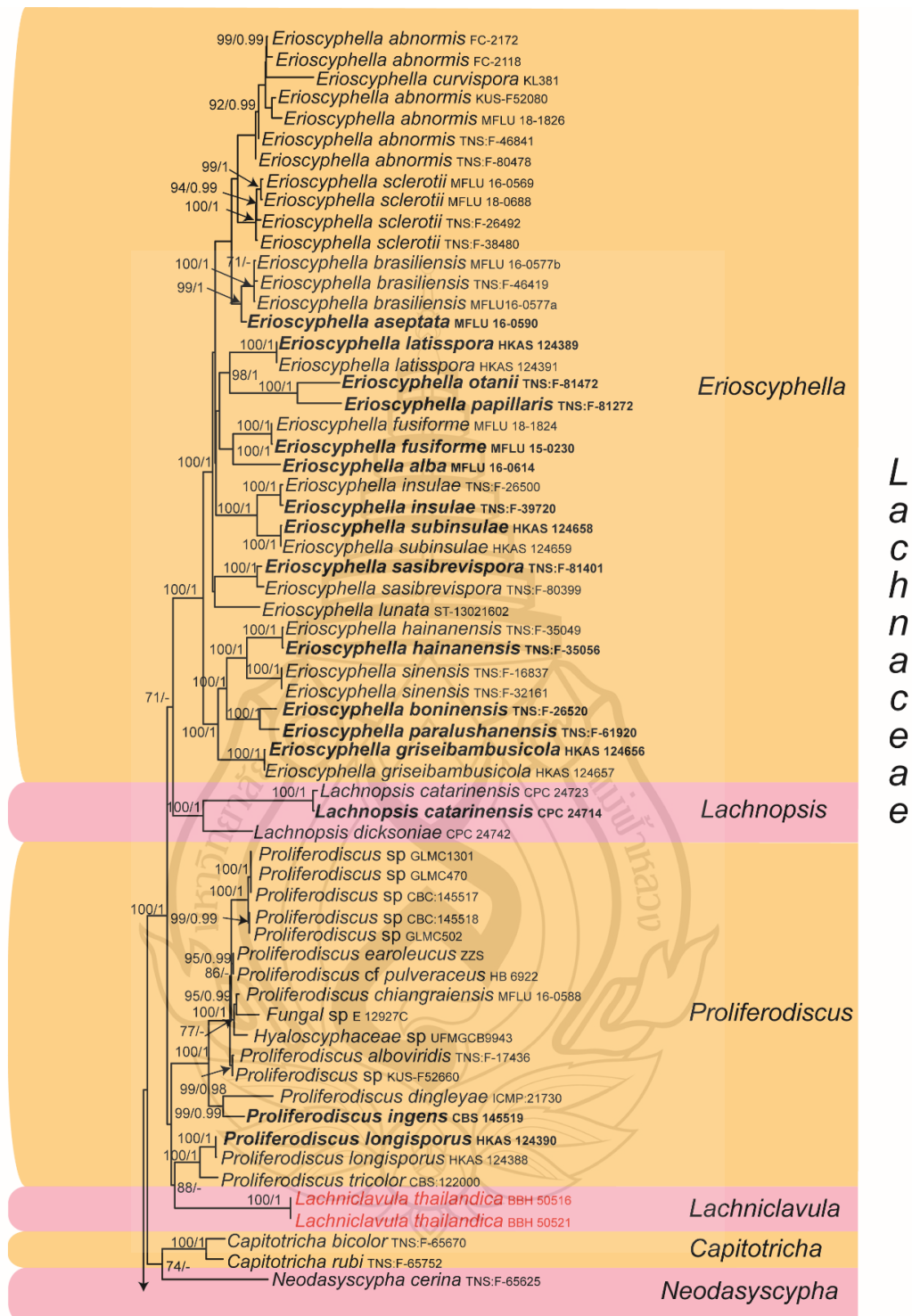


Figure 2.21 Phylogram generated from the maximum likelihood analysis based on the combined ITS, LSU and RPB2 sequence data of taxa in Lachnaceae

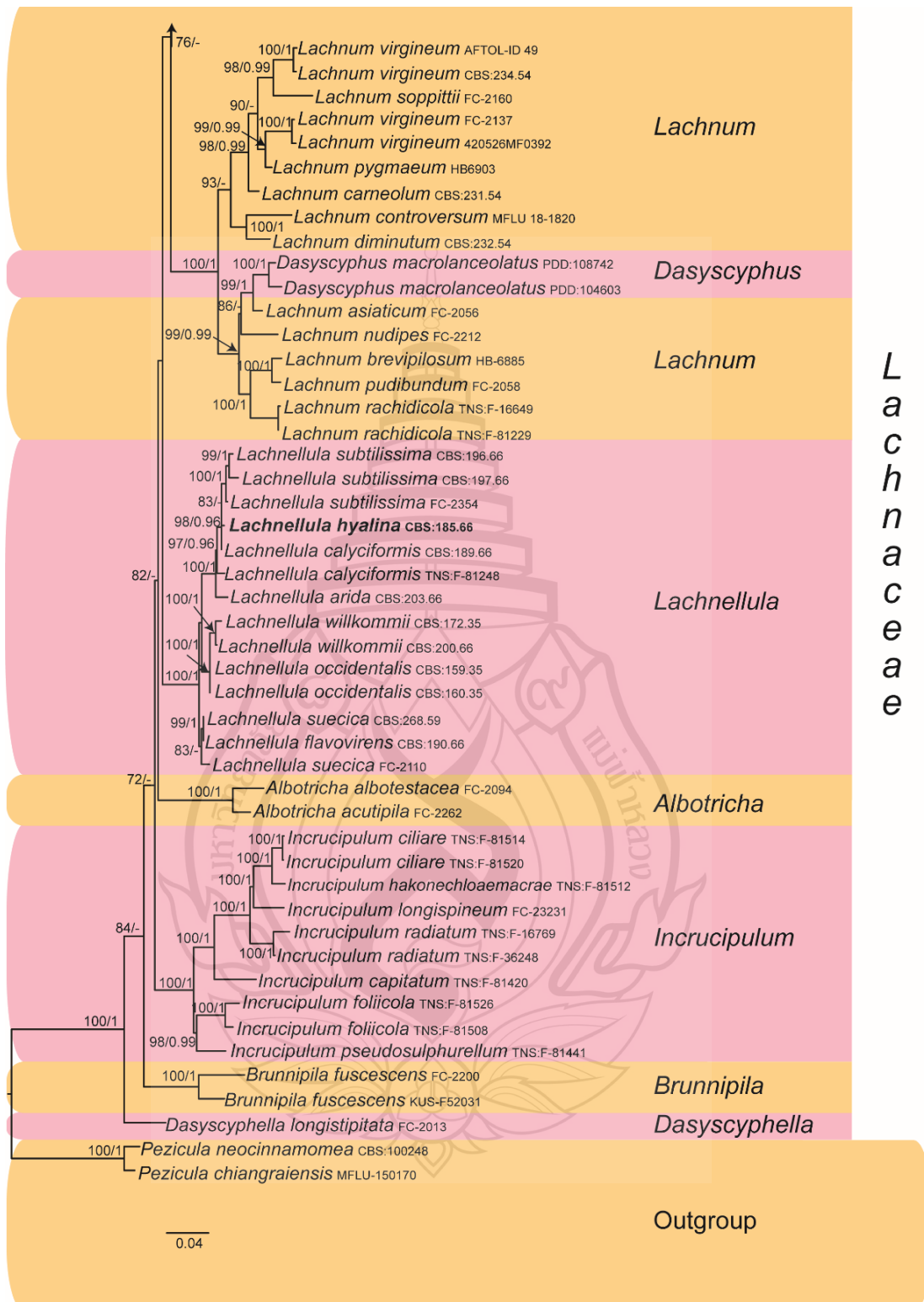


Figure 2.21 (continued)

Genus: *Lachniclavula* Lestari & Chethana

Lachniclavula thailandica Lestari & Chethana

Figure 2.21; 2.22; 2.23

Material examined: Thailand, Chiang Mai Province, Chomthong district, Doi Inthanon National Park, Kew Mae Pan Natural Trail, on rooten wood, 20 October 2021, Anis S. Lestari, KMP3 22 (BBH 50516, holotype); *ibid.*, 20 October 2021, Anis S. Lestari, INT 21 (BBH 50526, isotype).

Description: *Saprobic* on dead stems. **Sexual morph:** *Apothecia* 1.3–2.5 × 0.9–2.2 mm ($x = 1.8 \times 1.4 \mu\text{m}$, $n = 10$), club-like, arising singly or in a small cluster, stipitate. Stipe brown with minute hairy-like structure. *Receptacle* cupulate, concolorous with hymenium. *Margins* concolorous to receptacle. *Disc* convex, cream to light brown. *Ectal excipulum* 24–58 μm ($x = 27.5 \mu\text{m}$, $n = 10$) at the margin down to lower flanks, composed of thin-walled, brown to hyaline cells of *textura porrecta-angularis*. *Medullary excipulum* 32–79 μm ($x = 53.3 \mu\text{m}$, $n = 10$) in lower flanks, composed of thin-walled, hyaline to bluish cells of *textura epidomoidea*. *Hymenium* hyaline. *Paraphyses* 1.6–2.5 μm wide ($x = 1.9 \mu\text{m}$, $n = 10$), numerous, filiform, aseptate, not exceeding the asci in length. *Asci* 54–67 × 4.2–5.7 μm ($x = 61.1 \times 5 \mu\text{m}$, $n = 10$), 8-spored, unitunicate, cylindrical, apex conical to rounded, amyloid arising from simple septa. *Ascospores* 6–7.7 × 2.2–2.9 μm ($x = 6.8 \times 2.6 \mu\text{m}$, $n = 10$), 1–2-seriate, ellipsoid to fusoid, aseptate, hyaline, guttulate. **Asexual morph:** Undetermined.

Notes: *Lachniclavula thailandica* (BBH 50516 and BBH 50526) form a distinct lineage in the combined ITS, LSU and RPB2 sequence analyses with statistical support (ML/BI = 88%/less than 0.95, Figure 2.21). In the phylogram, the cluster of *Lachniclavula thailandica* (BBH 50516 and BBH 50526) is associated with *Proliferodiscus* cluster but distinctive in the morphology of apothecia habit and paraphysis. Apothecia of *Lachniclavula thailandica* are club-like and no hair ornamentation as in those in *Proliferodiscus* or even in all *Lachnaceae* species members. *Lachniclavula thailandica* (BBH 50516 and BBH 50526) characterized by filiform instead of lanceolate paraphysis as those in most of *Lachnaceae* species members.

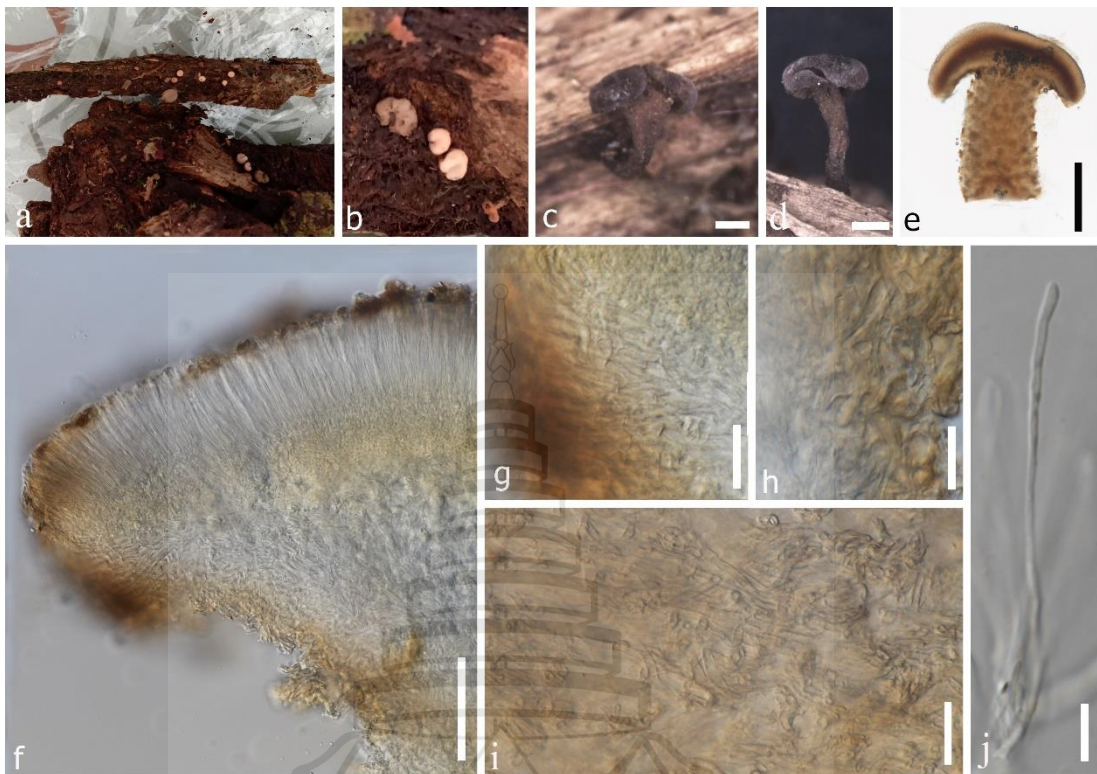


Figure 2.22 Apothecia, exipulum cells and paraphysis of *Lachniclavula thailandica* (BBH 50516)

Figure 2.22, a wood substrates b. Apothecia on the substrates. c–d Close up of apothecia on the substrates. e Close-up of an apothecium sectioning. f Close-up of hymenium at the margin. g–h Ectal excipulum. i Medulary excipulum. j Slightly apically swollen paraphysis. Scale bars: c–d = 600 μm , e= 375 μm , f = 75 μm , g–i = 20 μm , j = 10 μm .

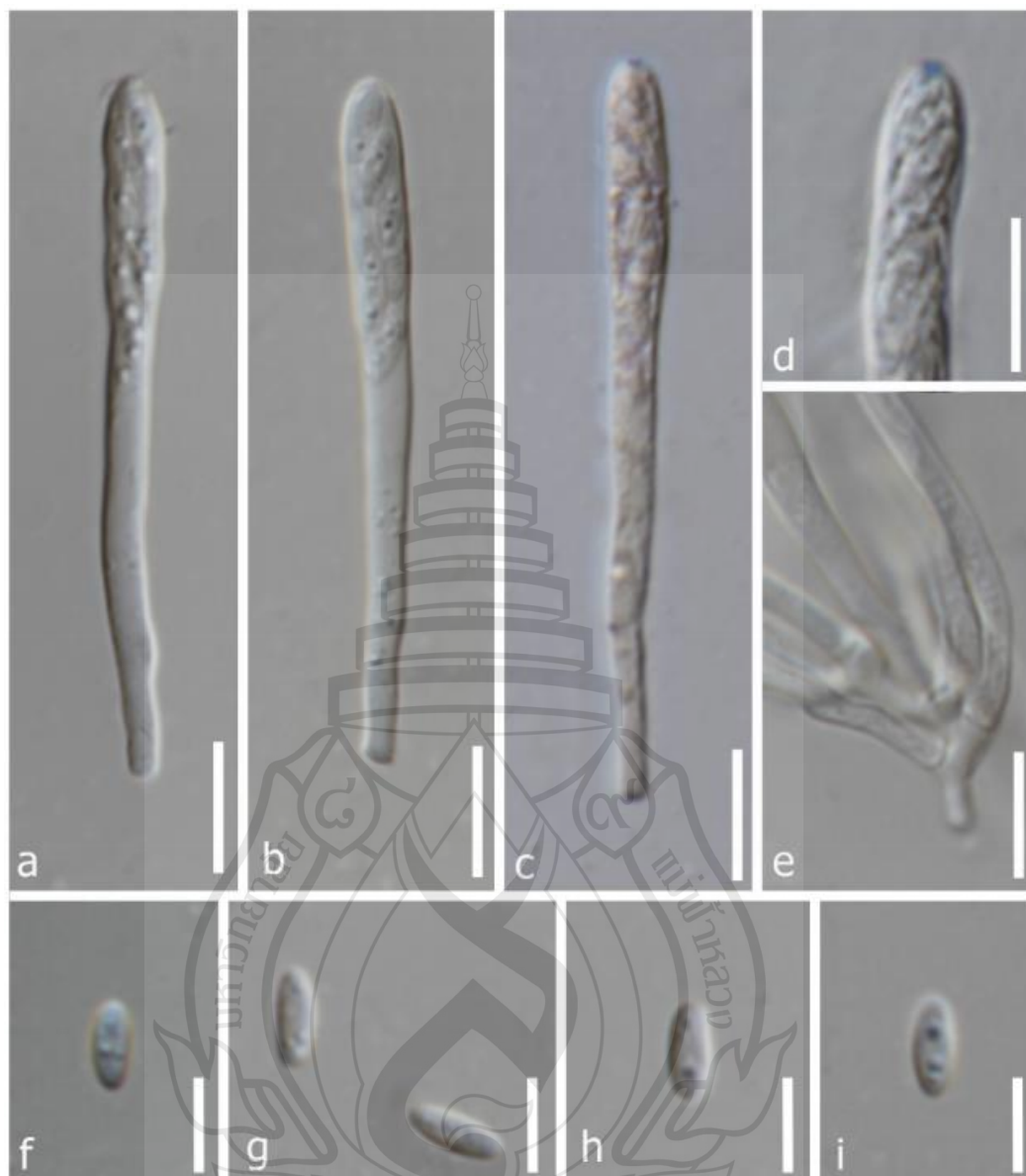


Figure 2.23 Asci and ascospores of *Lachniclavula thailandica* (BBH 50516)

Figure 2.23, a–c Asci. d Tip of the ascus (mounted in MLZ reagent without KOH pretreatment). d Filiform paraphyses. e Arising from simple septa. f–i Ascospores (c–d mounted in Melzer agent). Scale bars: a–c = 15 μm , d = 10 μm , e–i = 6 μm .

Genus: *Lachnum* Retz.

Lachnum, a genus of fungi in the family Lachnaceae, established by Retzius (1779) and characterized by sessile to stipitate apothecia with hyaline or brown colored,

granulate hairs, cylindrical to lanceolate paraphysis with the length usually exceeding the asci (Raitviir, 2004). *Lachnum* species serves mainly as saprophytes, growing on ferns and herbaceous, coniferous to deciduous lignocellulose litter (Hosoya et al., 2019) and currently, more than 100 species registered in Species fungorum (2024).

***Lachnum agaricinum* (Retz.) K.**

Figure 2.24; 2.25

Index Fungorum number: IF 217264

Facesoffungi number: FoF 15681

Material examined: United States of America, New York, Hamilton, Blue Mountain Lake 42.86138 -74.451145 +-8260 m on a bark of undetermined host. 06 August 1911, Charles E. Fairman (CUP-F-0321).

Description: *Saprobic* on the bark of an unidentified host. **Sexual morph:** Stipitate discomycetous. *Apothecia* 349–617 × 285–586 µm, arising singly or in a small cluster. *Receptacle* cupulate. *Discs* concave. *Hairs* 49–71 × 2.8–4.1 µm ($\bar{x}$ = 58.3 × 2.2 µm, n = 15) on flanks, margin and stipe, cylindrical with hemispherical to spherical tip, septate, white, densely covered with granules at the top to base. *Ectal excipulum* 23–35 µm wide ($\bar{x}$ = 27.5 µm, n = 20), composed of thick-walled, dark to light brown cells of *textura prismatica*. *Medullary excipulum* 30–43 µm ($\bar{x}$ = 38.4 µm, n = 20) at flanks, composed of light brown to hyaline cells of *textura oblita*. *Hymenium* yellowish. *Paraphyses* 2.2–3 µm wide ($\bar{x}$ = 2.6 µm, n = 30) at the top, numerous, lanceolate, septate, exceeding the asci in length, smooth. *Asci* 31–45 × 2.6–5 µm ($\bar{x}$ = 37.4 × 4.2 µm, n = 15), 8-spored, unitunicate, cylindrical, conical to rounded at the apex, amyloid, short stipitate, arising from croziers. *Ascospores* 2.7–6.1 × 1.1–1.7 µm ($\bar{x}$ = 4.9 × 1.4 µm, n = 30), partially biseriate, ellipsoid to fusoid, aseptate, hyaline, guttulate. **Asexual morph:** Undetermined.

Notes: Sukova (2005) re-described *L. agaricinum* and synonymized it into *Lachnum virgineum* or *Dasyscyphus virgineum* by Sukova (2005). However, this synonymization has not been registered in Index Fungorum (2022).

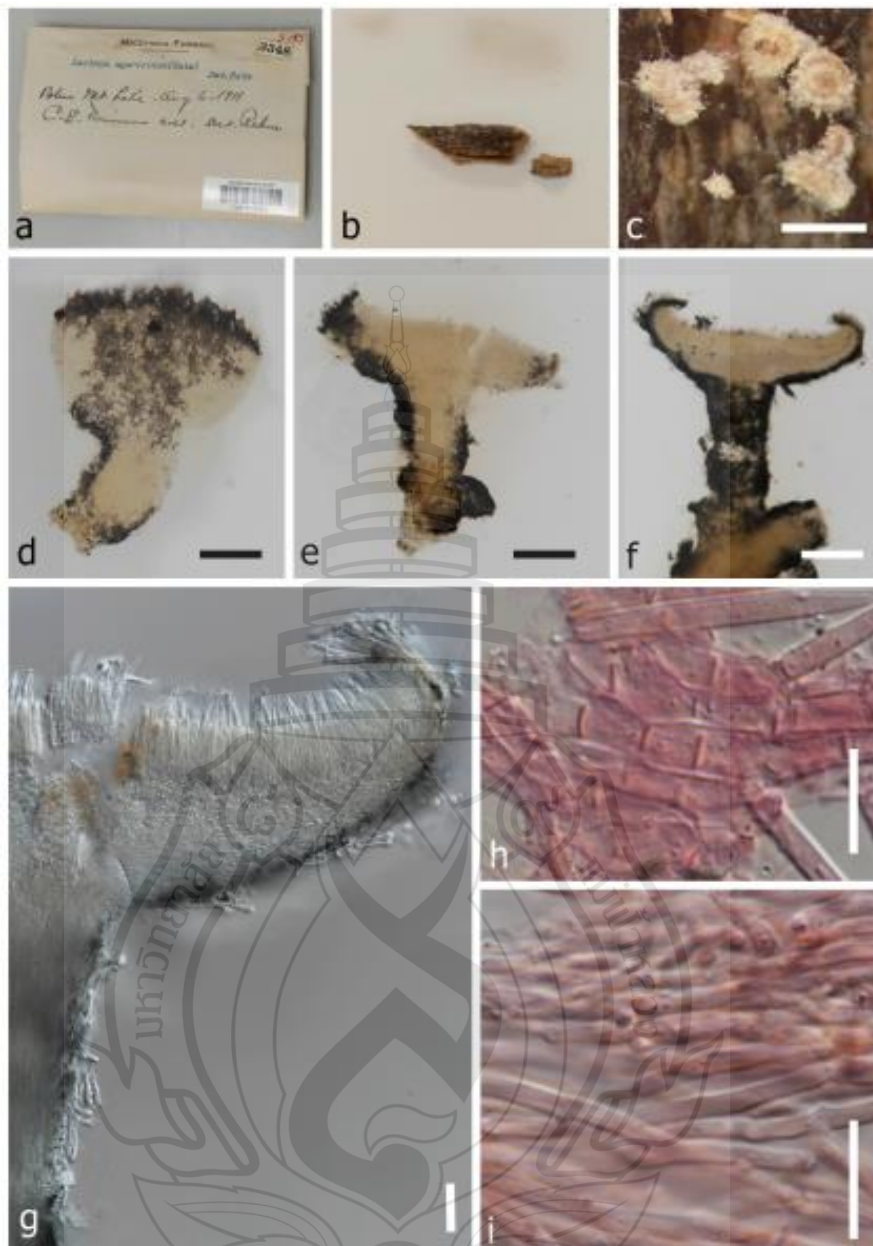


Figure 2.24 Apothecia and excipulum cells of *Lachnum agaricinum* (CUP-F-0321)

Figure 2.24, a, b Details of the herbarium material. c Habit and appearance of apothecia on the host surface. d–f Cross section of an apothecium. g. Close-up of an apothecium at the margin. h Cells of ectal excipulum. i Cells of medullary excipulum (h, i mounted in Congo red). Scale bars: c = 500 μ m, d–e = 160 μ m, g = 35 μ m, h–i = 12 μ m.

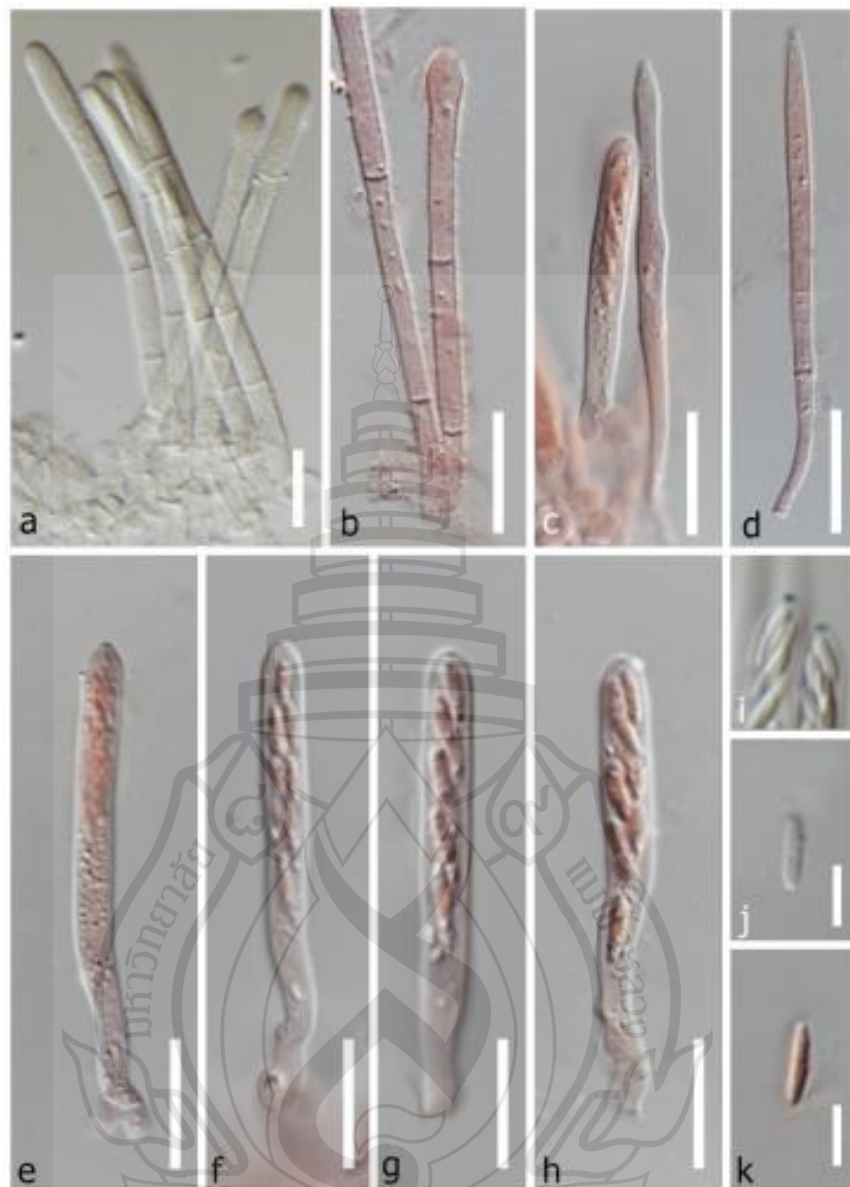


Figure 2.25 Hair, paraphysis, asci and ascospores of *Lachnum agaricinum* (CUP-F-0321)

Figure 2.25, a–b Hairs at the apothecium margin. c Paraphyses with an ascus (mounted in Congo red). d Lanceolate paraphyses (mounted in Congo red). e–h Asci (mounted in Congo red). i Asci with J+ ring (mounted in Meltzer agent). j–k Ascospores (k mounted in Congo red). Scale bars: a–h = 13 μ m, j–k = 6 μ m.

Lachnum virgineum (Batsch) P. Karst.

Figure 2.26

Index Fungorum number: IF356658

Facesoffungi number: FoF 15678

Material examined: Japan, on dead twigs, 2 July 2005, R. Sasagawa (TNS-F-16583).

Description: *Saprobic* on dead twigs. **Sexual morph:** Stipitate discomycetous. *Apothecia* 360–714 × 189–443 µm, arising singly, white in dried condition. *Receptacle* cupulate, concolorous with the margin. *Discs* concave. *Hairs* 44–67 × 4.1–5.5 µm ($\bar{x}$ = 55.6 × 4.7 µm, n = 10) on flanks, margin and stipe, cylindrical with hemispherical tip, slightly bent, septate, white, densely covered with granules at the base. *Ectal excipulum* 19–27 µm wide ($\bar{x}$ = 22.7 µm, n = 10), composed of thin-walled cells of *textura prismatica* to *porrecta*. *Medullary excipulum* 18–32 µm ($\bar{x}$ = 25.8 µm, n = 10) at flanks, composed of hyaline cells of *textura intricata*. *Hymenium* yellow. *Paraphyses* 2.4–5.7 µm wide ($\bar{x}$ = 4.6 µm, n = 20) at the widest apex, numerous, lanceolate, septate, exceeding the asci in length, smooth. *Asci* 49–52 × 4.2–4.5 µm ($\bar{x}$ = 50.5 × 7.7 µm, n = 10), 8-spored, unitunicate, cylindric, rounded or medium conical at the apex, J + with Melzer agent without KOH treatment amyloid, arising from croziers. *Ascospores* 6–10 × 1.2–1.9 µm ($\bar{x}$ = 7.6 × 1.6 µm, n = 10), partially biseriate, fusoid, aseptate, hyaline, smooth, rounded at both ends. **Asexual morph:** Undetermined.

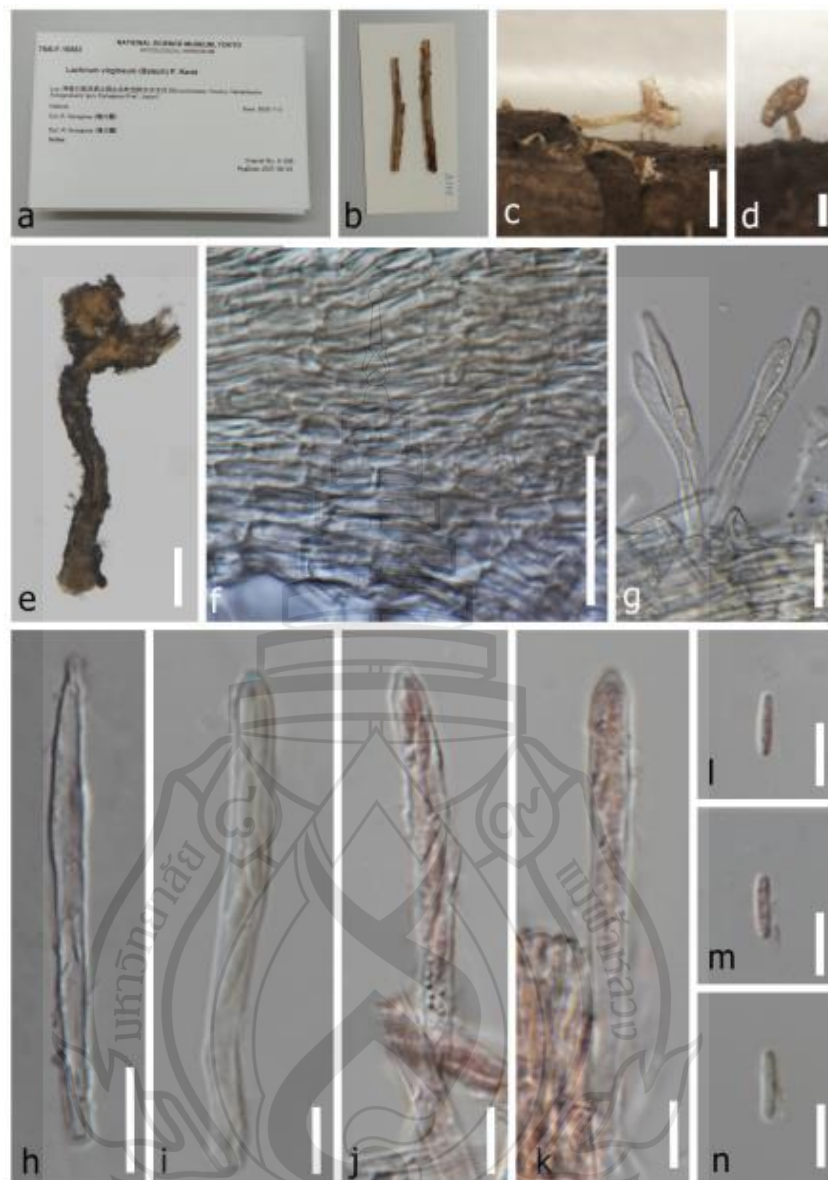


Figure 2.26 Sexual morph of *Lachnum virgineum* (TNS-F-16583)

Figure 2.26, a, b Details of the herbarium material. c, d Habit and appearance of an apothecium on the host surface. e Cross section of an apothecium. f Ectal excipulum cells. g Hairs. h Paraphyses. i–k Asci (i mounted in Melzer agent without KOH, j–k mounted in Congo red). l–m Ascospores (l–m mounted in Congo red). Scale bars: b = 430 μ m, c = 350 μ m, e = 200 μ m, f = 39 μ m, g = 16 μ m, h = 13 μ m, i–n = 7 μ m.

Genus: *Perrotia* Boud.

Perrotia, a genus of fungi in the family Lachnaceae, established by Baral (1985) and characterized by having sessile to short-stipitate apothecia, thick-walled hairs with granulate walls, asci with non-amyloid apex, ellipsoid to fusiform, aseptate to multiseptate ascospores (Polhorský & Červenka, 2020). *Perrotia* species serves as saprophytes, mostly growing on woody substrates sometimes on herbaceous plants or dicotyledon leaves (Zhuang & Yu, 2001), and currently, twenty species registered in Species fungorum (2024).

Perrotia flammea (Alb. and Schwein) Boud.

= *Peziza flammea* Alb. and Schwein.

Figure 2.27; 2.28

Index Fungorum number: IF 196568

Facesoffungi number: FoF 15682

Material examined: Norway, Trøndelag, Oppdal, Kongsvold 62.3067 9.6075 +-707m., on *Betula* twig, 31 May 1948, Axel Blytt (F-72629, Paratype).

Description: *Saprobic* on *Betula* twigs. **Sexual morph:** Sessile to short stipitate discomycetes. *Apothecia* 0.5–1.2 × 0.4–0.8 mm ($\bar{x}$ = 0.9 × 0.6 mm, n = 10) in dried state, arising singly, gregarious. *Receptacle* cupulate at first then becoming to flat. *Discs* discoid, concave. *Hairs* up to 250 µm long, 3–5 µm multi-septate, tapering, blunt; walls 0.6–1.6 µm thick, apically hyaline, basally brown, densely covered with yellowish to reddish granules and oxalate crystals. *Ectal excipulum* 42–59 µm ($\bar{x}$ = 48 µm, n = 10), wide at the lower flank, composed of dark brown cells of *textura angularis-globulosa*. In the previous description, the ectal excipulum has inner cells of *textura oblita*, but it cannot be observed clearly. *Medullary excipulum* 37–50 µm ($\bar{x}$ = 41.8 µm, n = 10), wide at the margin, composed of *textura intricata*. *Paraphyses* 2–2.5 µm ($\bar{x}$ = 41.8 µm, n = 10) wide, filiform, smooth. *Asci* 83–108 × 5.5–8.5 µm ($\bar{x}$ = 92.4 × 6.9 µm, n = 10), 8-spored, unitunicate, cylindric, rounded at the apex, J-, arising from croziers. *Ascospores* 9.2–15.7 × 2–2.8 µm ($\bar{x}$ = 11.3 × 2.4 µm, n = 10), biseriate to uniseriate, allantoid, aseptate, smooth. **Asexual morph:** Undetermined.

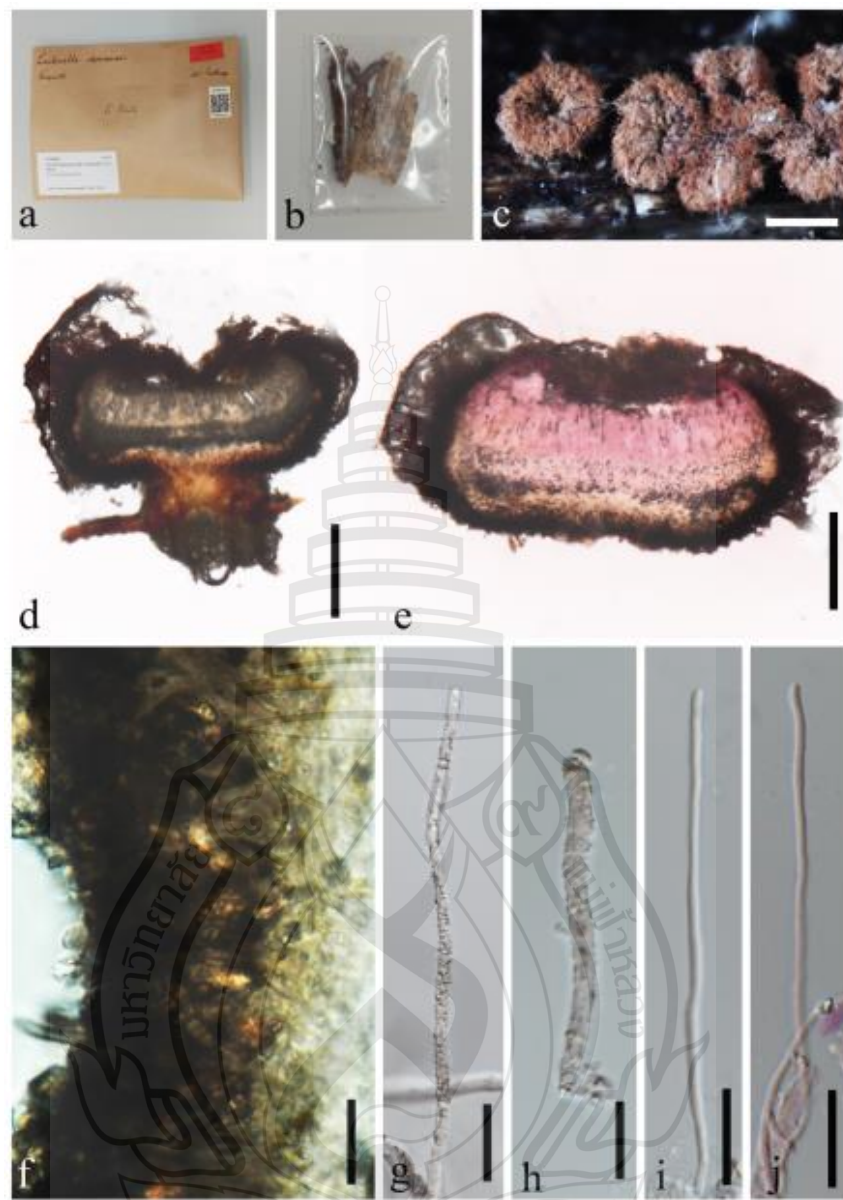


Figure 2.27 Apothecia, hair, excipulum cells and paraphysis of *Perrotia flammea* (F-72629)

Figure 2.27, a–b Details of the herbarium material. c Habit and appearance of apothecia on the substrate. e Close-up of an apothecium. f Close-up of ectal excipulum cells. g–h Hairs. h–i Filiform paraphyses. Scale bars: c = 500 μ m, d–e = 220 μ m, f–j = 19 μ m.

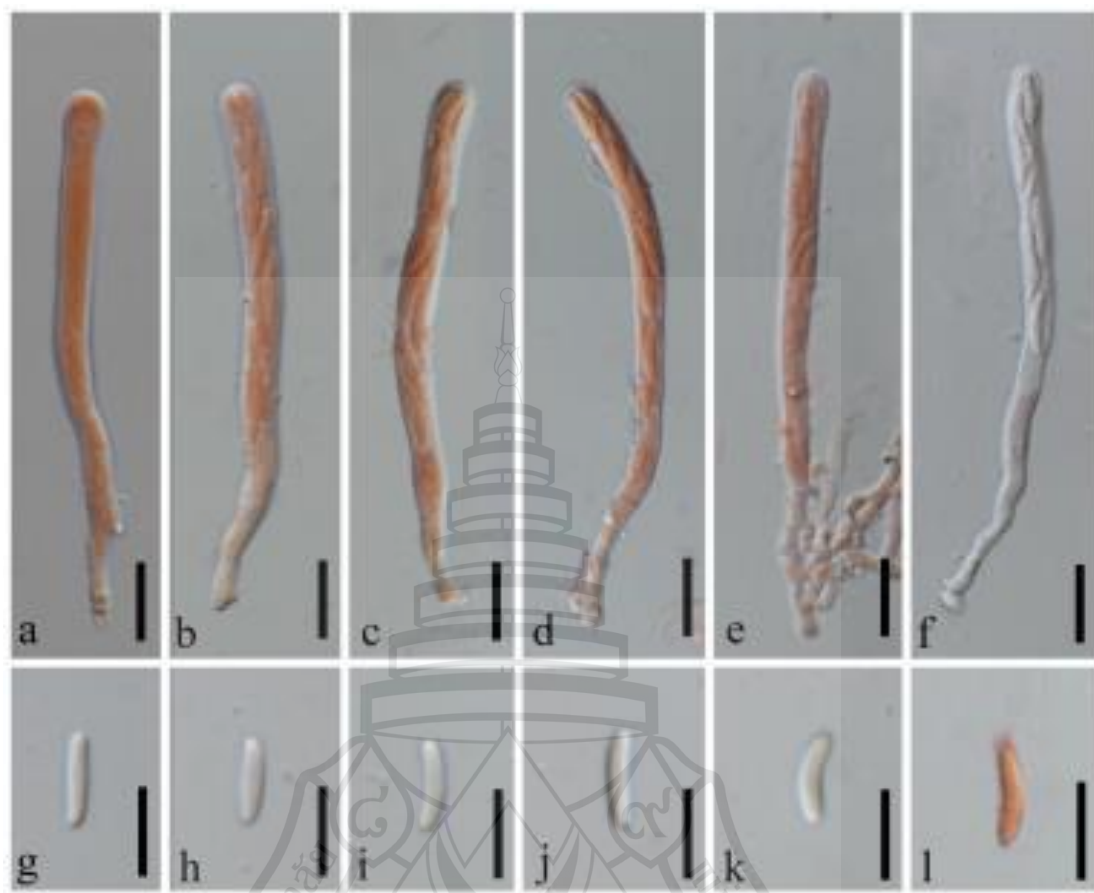


Figure 2.28 Asci and ascospore morphology of *Perrotia flammea* (F-72629)

Figure 2.28, a–f Asci (a–e mounted in Congo red). g–l Allantoid ascospores (l mounted in Congo red). Scale bars: a–f = 13 μm , g–l = 11 μm .

2.3.5 Pezizellaceae, Helotiales

In this study, calycina-like fungi were collected from Chiang Mai province, Thailand. These newly found specimens were classified based on molecular phylogenetic analyses, and morphological characteristics. The results showed that some of the fungi were new to Thailand while others are distinct from currently known species of *Calycina*. Hence, the newly found specimens are introduced as a new geographical record and species in *Calycina* with provided taxonomic diagnosis and photoplates.

The combined alignment of ITS and LSU contains 60 fungal taxa, including the new geographical record. Sixty strains were included in the dataset, which comprised

1,322 characters (466 characters for ITS and 854 characters for LSU including the gap regions). The matrix had 901 distinct alignment patterns with 68.15% undetermined characters and gaps. Estimated base frequencies were as follows: A = 0.2424, C = 0.1082, G = 0.3617, T = 0.9371; substitution rates: AC = 2.2394, AG = 2.3421, AT = 2.2394, CG = 1.0, CT = 8.6577, GT = 1.0; gamma distribution shape parameter α = 0.688. The new species is indicated in blue bold. Bootstrap value (ML) is greater than 70% and Bayesian posterior probabilities (BI) greater than 0.90 are given at the nodes. The BI analysis generated 1000 trees after 1,000,000 generations. The first 250 trees were discarded as the burn-in phase of the analysis, and the remaining results were used to determine the posterior probabilities distribution. The final average standard of split frequencies of BI posterior probability was 0.008.

Multi-gene phylogenetic analyses based on the ITS and LSU gene regions of *Pezizellaceae* taxa resulted in well-supported clades as depicted in the phylogram (Figure 2.26). The *Calycina* clade encompasses 11 species with available molecular data, including our geographical records species, *C. montana* (MFLU 22-0055 and MFLU 22-0056) and *C. papaeana* (MFLU 23-0015), a novel species. In the phylogram, *C. montana* (MFLU 22-0055 and MFLU 22-0056) form a sister relationship with *B. montana* (HMAS 275566) with statistical support of 99% ML and 0.99 BI. Additionally, both type strains of *B. montana* (HMAS 275566) and *B. shangrilana* (HMAS 275568) are positioned in the *Calycina* clade instead of the *Bisporella*, *Helotiaceae* clade (Figure 2.26).

Table 2.8 Accession numbers and origin of fungal taxa used in the phylogenetic analysis of Pezizellaceae

Taxon name	Specimen codes ^a	GenBank accession no		Origin
		ITS	LSU	
<i>Bisporella pallescens</i>	DMS-10078235T	MW203182	–	Denmark
<i>Bisporella pallescens</i>	DMS-10075832T	MW203180	–	Denmark
<i>Bisporella subpallida</i>	GM20160214	KY462818	KY462818	Luxembourg
<i>Calycellina fagina</i>	SBRH 840	OL744073	–	Netherlands
<i>Calycellina fagina</i>	SBRH925	OL752703	OM218631	Netherlands
<i>Calycellina punctata</i>	Cantrell GA18	U57494	–	USA
<i>Calycellina lachnobrachyoides</i>	KUS-F52576	JN033424	JN086727	Korea
<i>Calycellina lachnobrachyoides</i>	KUS-F52183	JN033412	JN086715	Korea
<i>Calycellina ulmarie</i>	K(M):200003	MZ159550	–	UK
<i>Calycina alstrupii</i> (T)	BILAS Motiejunaite 10761	NR154846	NG068538	Norway
<i>Calycina alstrupii</i>	Pz167	KY305096	KY305098	Norway
<i>Calycina citrina</i>	G.M. 2014-12-14-4	KY462815	KY462815	Luxembourg
<i>Calycina citrina</i>	ICMP 16997	GQ411507	–	New Zealand
<i>Calycina citrina</i>	F14046	AF335454	AF335454	Canada
<i>Calycina citrina</i>	HMAS 275570	KX781361	–	China
<i>Calycina citrina</i>	F115889	KC412004	–	Spain

Table 2.8 (continued)

Taxon name	Specimen codes ^a	GenBank accession no		Origin
		ITS	LSU	
<i>Calycina citrina</i>	FH LQH-9a	MW203183	MW115642	USA
<i>Calycina claroflava</i>	F132983	KC412006	–	Spain
<i>Calycina claroflava</i>	MFLU 18-2673	MK584952	MK591982	Thailand
<i>Calycina claroflava</i>	TNS F37025	LC169492	–	Japan
<i>Calycina cortegadensis</i>	MSS906	MN017444	MN017503	Spain
<i>Calycina herbarum</i>	KUS-F52362	JN033407	JN086710	Korea
<i>Calycina herbarum</i>	KUS-F51458	JN033390	JN086693	Korea
<i>Calycina lactea</i>	iNAT:18000156	MZ209003	–	USA
<i>Calycina lactea</i>	HB7224	KC412007	–	Germany
<i>Calycina languida</i>	F116599	KC412002	–	Spain
<i>Calycina languida</i>	F116600	KC412003	–	Spain
<i>Calycina marina</i>	TROM F26093	KT185677	KT185670	Norway
<i>Calycina marina</i>	TROM F26101	KT185674	–	Norway
<i>Calycina montana</i>	MFLU 22-0055	ON156524	ON156523	Thailand
<i>Calycina montana</i>	MFLU 22-0056	ON176689	ON325438	Thailand
<i>Calycina montana</i> (T)	HMAS 275566	NR 153627	–	China

Table 2.8 (continued)

Taxon name	Specimen codes ^a	GenBank accession no		Origin
		ITS	LSU	
<i>Calycina shangrilana</i> (T)	HMAS 275568	NR153628	–	China
<i>Calycina shangrilana</i>	HMAS 275569	KX781360	–	China
<i>Calycina shangrilana</i>	HKAS 90655a	MK584972	MK591998	China
<i>Calycina shangrilana</i>	HKAS 90655b	MK584971	MK591997	China
<i>Chalara pseudoaffinis</i> (T)	CCF 3979	NR154761	NG067520	Czech Republic
<i>Chalara pseudoaffinis</i>	CBS 261.75	FR667225	MH872651	France
<i>Chlorencoelia torta</i>	KUS-F52256	JN033400	JN086703	Korea
<i>Chlorencoelia torta</i>	ICMP 21732	MH682234	–	New Zealand
<i>Chlorencoelia torta</i>	JAC14068	MK432798	MK431490	New Zealand
<i>Gemmina gemmarum</i>	H.B. 6883	OM456209	–	Germany
<i>Gemmina gemmarum</i>	SBRH 862	KX501127	OM218628	Netherlands
<i>Gemmina</i> sp.	H.B. 6910	OM456210	OM456211	Netherlands
<i>Micropeziza umbrinella</i>	K(M):168087	MZ159422	–	UK
<i>Micropeziza umbrinella</i>	ZT-Myc-64170	MW489557	–	Switzerland
<i>Microscypha ellisii</i>	KUS-F52489	JN033418	JN086721	Korea

Table 2.8 (continued)

Taxon name	Specimen codes ^a	GenBank accession no		Origin
		ITS	LSU	
<i>Microscypha ellisii</i>	KUS-F52663	JN033428	JN086731	Korea
<i>Microscypha</i> sp.	TNS:F-18016	JN033444	JN086745	Japan
<i>Mollisia uncinata</i>	TNS:F-38901	JN033457	JN086757	Japan
<i>Mollisia uncinata</i>	KUS-F52307	JN033404	JN086707	Korea
<i>Psilachnum staphyleae</i>	KUS-F52105	JN033396	JN086699	Korea
<i>Rodwayella citrinula</i>	KUSF52443	JN033414	JN086717	Korea
<i>Rubropezicula thailandica</i> (T)	MFLU 16-0592	NR163781	–	Thailand
<i>Scleropezicula alnicola</i>	CBS 200.46	MH856161	MH867686	Canada
<i>Scleropezicula alnicola</i>	CBS 119905	MH863066	–	Lithuania
<i>Zymochalara lygodii</i> (T)	CPC 24699	NR154510	NG059653	Brazil
<i>Zymochalara cyatheae</i> (T)	CPC 24665	NR154509	NG059652	Brazil

Note ^aCantrell: S.A. Cantrell collection, Georgia, USA; CBS: Central Bureau voor Schimmelcultures, Utrecht, The Netherlands; CPC: Collection of Pedro Crous housed at CBS; F: Fundación Medina's Fungal Culture collection, Spain; FH: Farlow Herbarium of Cryptogamic Botany, Cambridge, USA; GM: G. Marson collection, Luxembourg; H.B: Hans Otto Baral collection, Germany; HKAS: Cryptogamic Herbarium, Kunming Institute of Botany, Chinese Academy of Sciences, China; HMAS: Herbarium Mycologicum Academiae Sinicae

Beijing, China; ICMP: International Collection of Microorganisms from Plants, New Zealand; iNAT: inaturalist.org collection, California, USA; K(M): Kew Mycology collection, Royal Botanic Garden, London, UK; JAC: J.A. Cooper collection, New Zealand; The Kew Mycology collection, Richmond, UK; KUS: Korea University Herbarium, Seoul, Korea; MFLU: Mae Fah Luang University Herbarium, Chiang Rai, Thailand; SBRH: S.B. Helleman collection, Netherlands; TNS: National Museum of Nature and Science, Tsukuba, Japan; TROM: Tromso University Museum, Norway; ZT: Zuercherstrasse, Zurich, Switzerland. Ex-type strains are labeled by (T), newly generated sequences are in bold, “–” indicates unavailable sequences



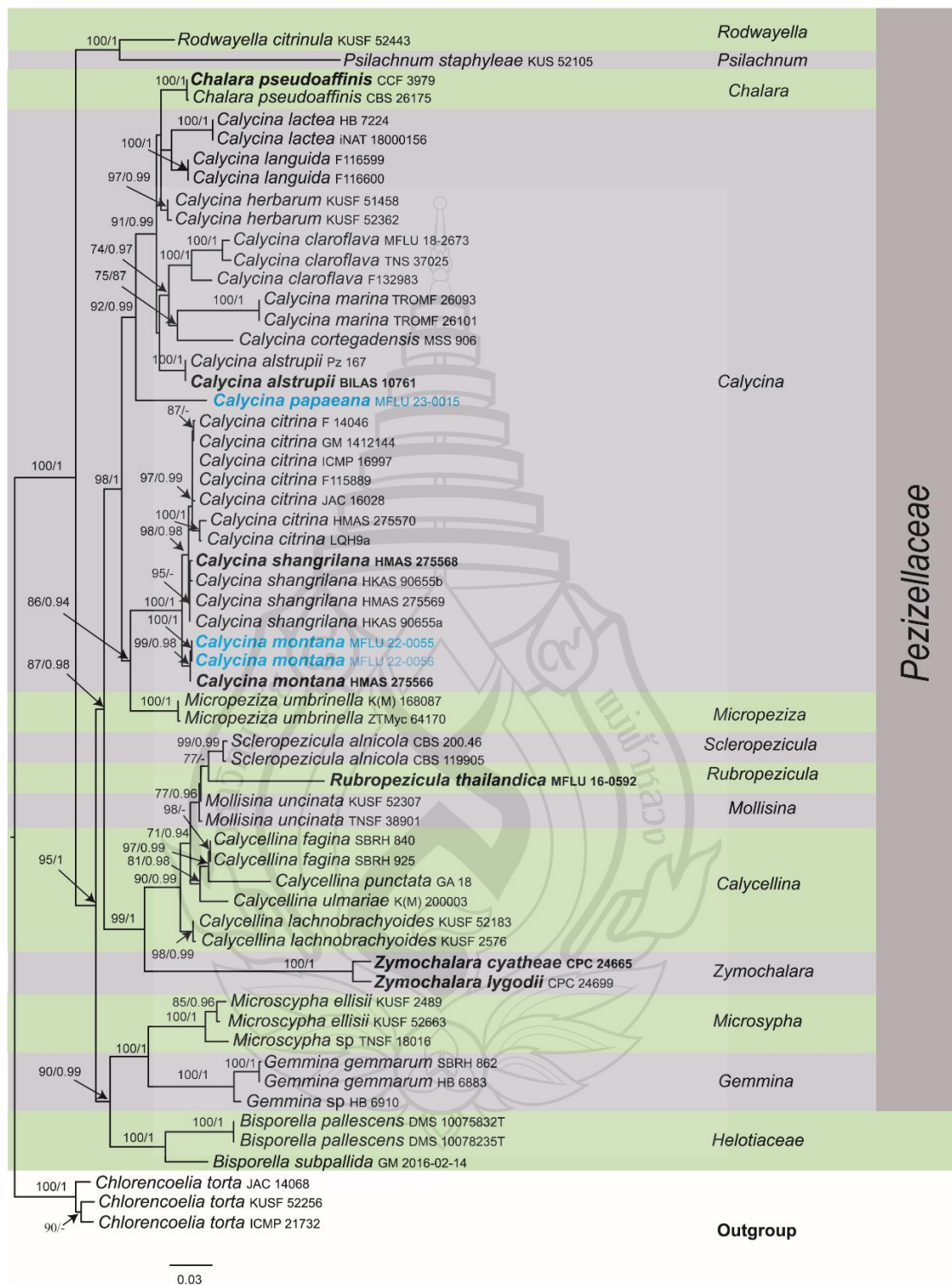


Figure 2.29 Phylogram generated from the maximum likelihood analysis based on the combined ITS and LSU sequence data of taxa in Pezizellaceae

Family: Pezizellaceae Velen.

Genus: *Calycina* Nees ex Gray

Calycina montana (W.Y. Zhuang and H.D. Zheng) Lestari and Chethana, *comb. nov.*

Basionym: *Bisporella montana* W.Y. Zhuang and H.D. Zheng

Figure 2.29; 2.30; 2.31; 2.32

Index Fungorum number: IF570309

Facesoffungi number: FoF10812

Holotype: HMAS 275566

Material examined: Thailand, Chiang Mai Province, Chomthong District, Doi Inthanon, Kew Mae Pan nature trail, 20 October 2021, Anis S. Lestari, KMP3 21 (MFLU 22-0055), KMP3 41 (MFLU 22-0056); China, Yunnan, Shangrila, Pingbian, Daweishan on rotten hardwood, 5 September 1999, X.Q. Zhang and D.Z. Ren, (HMAS 275566, holotype)

Description: *Saprobic* on decayed woods covered with mosses. **Sexual morph:** *Apothecia* 1.1–1.6 × 0.6–1.4 mm, gregarious, arising singly or in clusters, amber-colored, stipitate. *Stipe* 0.6–1.2 × 0.2–0.4 mm in dried condition. *Receptacle* discoid, bright amber color to hyaline. *Margin* hyaline with a brown outer layer at the flank. *Discs* concave. *Ectal excipulum* 55–68 µm ($\bar{x}$ = 59.8 µm, n = 10) at the flank near the stipe, composed of gelatinized thick-walled, hyaline cells of *textura porrecta*. *Medullary excipulum* 36–80 µm ($\bar{x}$ = 57.7 µm, n = 10) at the flank near the stipe, distinctively separate from the ectal excipulum, composed of thin-walled, hyaline cells of *textura oblita*, hypha with refractive guttules. *Hymenium* 141–180 µm ($\bar{x}$ = 168.9 µm, n = 15), amber-colored. *Paraphyses* 1.8–2.5 µm in diam. ($\bar{x}$ = 2.1 µm, n = 15) at the terminal, filiform, septate, branched at the 1/3 length from the base, guttulate. *Asci* 101–118 × 4.7–6.3 µm ($\bar{x}$ = 108.6 × 5.5 µm, n = 15), unitunicate, 8-spored, cylindrical and subclavate at the top, rounded (in alive state) to conical apex (dead state), J+ (eu-amyloid, in Melzer's with and without KOH treatment), long substipitate base, arising from croziers. *Ascospores* 7.1–9.2 × 4.1–5 µm ($\bar{x}$ = 8 × 4.4 µm, n = 20), ellipsoid, 0–1-septate, partially biserial to uniserial, hyaline, rounded at both ends with guttules. **Asexual morph:** Hypomycetous, on the lower flank and receptacle of the apothecia's surface. *Conidiogenous cells* 12–19 × 2.7–5.1 ($\bar{x}$ = 14.3 × 4.3 µm, n = 10) µm, phialidic,

black to dark brown. *Conidiophore* $1.5\text{--}2.7 \times 1.6\text{--}2.4$ ($\bar{x} = 3 \times 1.9$, $n = 5$) μm , black to dark brown. *Conidia* $2.2\text{--}2.8 \times 1.7\text{--}2$ ($\bar{x} = 2.5 \times 1.9$ μm , $n = 2$) μm ellipsoid, aseptate, hyaline, smooth.



Figure 2.30 Apothecia and asexual morph of *Calycina montana* (MFLU 22-0055, new geographical record)

Figure 2.30, a Rotten wood substrate covered with mosses. b–c Apothecia on the substrate. d Close-up of an apothecium sectioning. g Close-up of hymenium at the margin. f Phialide cells on the lower flank surface. g–h Conidiogenous cells bearing conidiospore. i–j A conidiogenous cell (j mounted in Congo red). Scale bars: b = 950 μm , c = 470 μm , d = 315 μm , e = 141 μm , f = 40 μm , g = 17 μm , h–j = 13 μm .

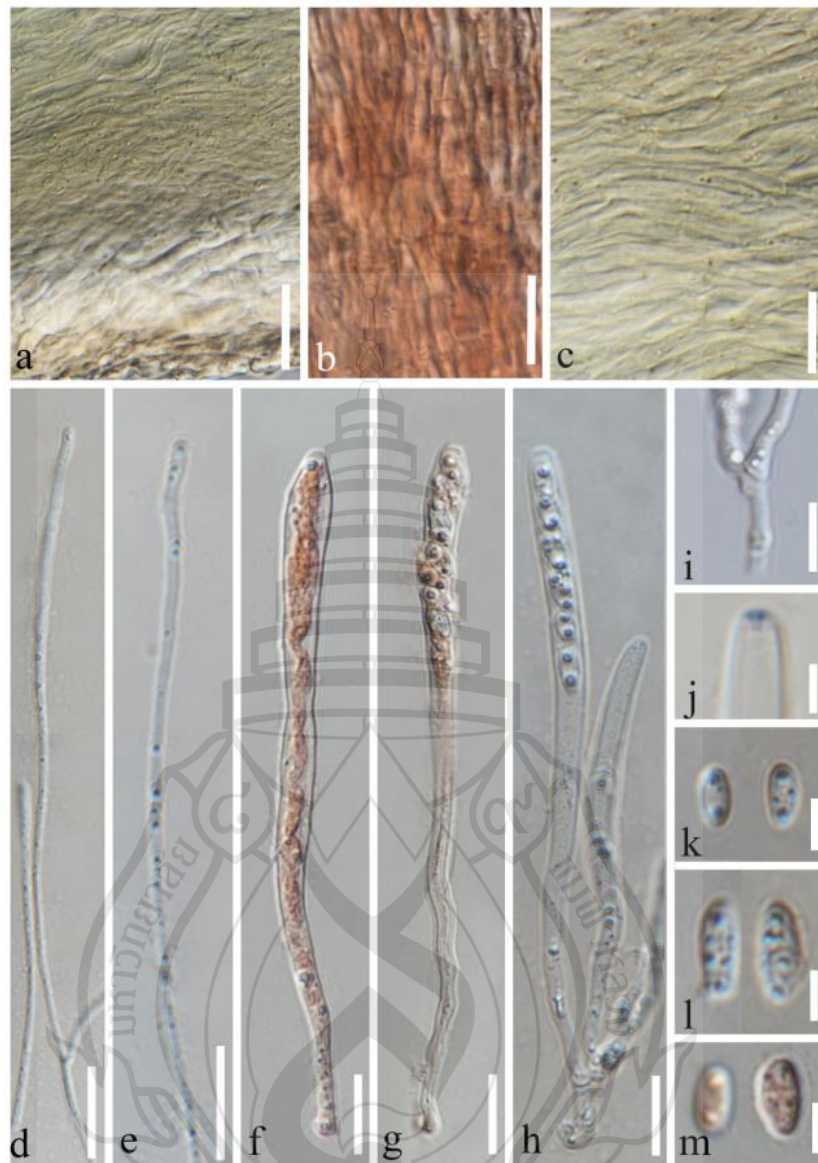
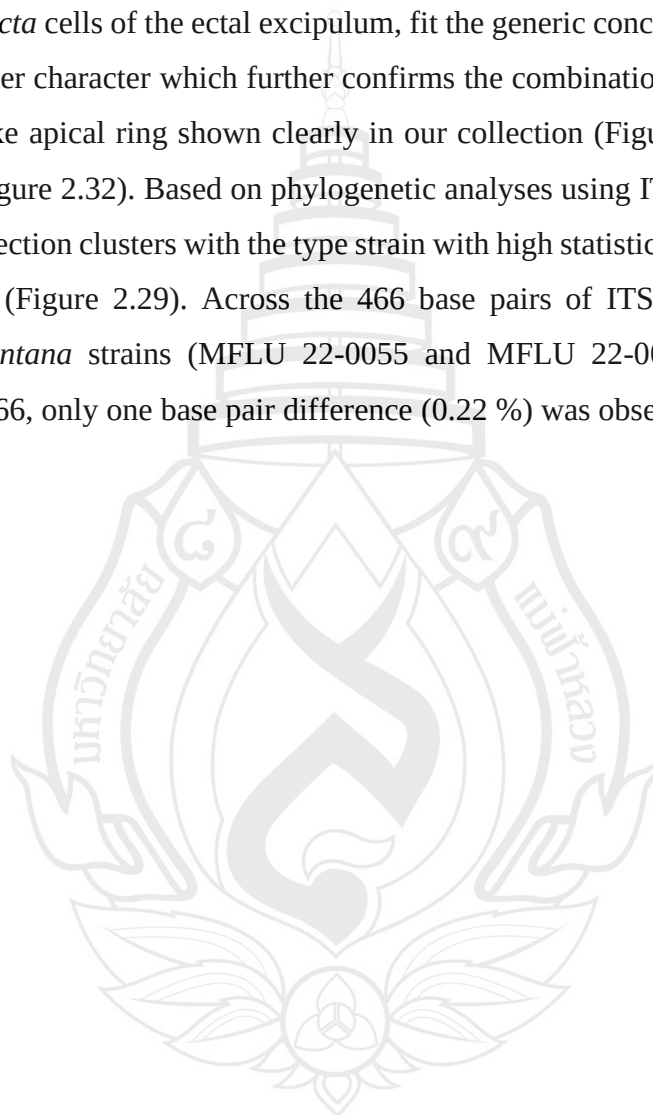


Figure 2.31 Excipulum cells, paraphysis, asci and ascospores *Calycina montana* (MFLU 22-0055, new geographical record)

Figure 2.31, a Close-up of excipulum cells. b Ectal excipulum cells (b mounted in Congo Red). d Medullary excipulum cells. d–e Filiform paraphyses with refractive guttules. f–g Asci (mounted in Congo red). h Asci (alive state). i Close-up of the crozier. j Tip of the ascus (J+, in Melzer agent with KOH treatment). k–m Ascospores (m mounted in Congo red). Scale bars: a = 40 μm , b–c = 25 μm , d–h = 14 μm , i = 10 μm , j–m = 4 μm .

Notes: In the current study, *Bisporella montana* (HMAS 275566, holotype) and our specimens clustered under *Calycina*, as *Calycina montana*. *Calycina montana* (HMAS 275566), previously known as *Bisporella montana*, was discovered in a mountainous area in China as a saprobe on woody substrates (Zhuang et al., 2017). The characters of both specimens, especially the amber-colored apothecia and gelatinized *textura porrecta* cells of the ectal excipulum, fit the generic concept of *Calycina* (Baral 1993). Another character which further confirms the combination is the appearance of a calycina-like apical ring shown clearly in our collection (Figure 2.31) and the type specimen (Figure 2.32). Based on phylogenetic analyses using ITS and LSU sequence data, our collection clusters with the type strain with high statistical support of 99% ML and 0.99 BI (Figure 2.29). Across the 466 base pairs of ITS (+5.8S) gene of our *Calycina montana* strains (MFLU 22-0055 and MFLU 22-0056) and the ex-type HMAS 275566, only one base pair difference (0.22 %) was observed.



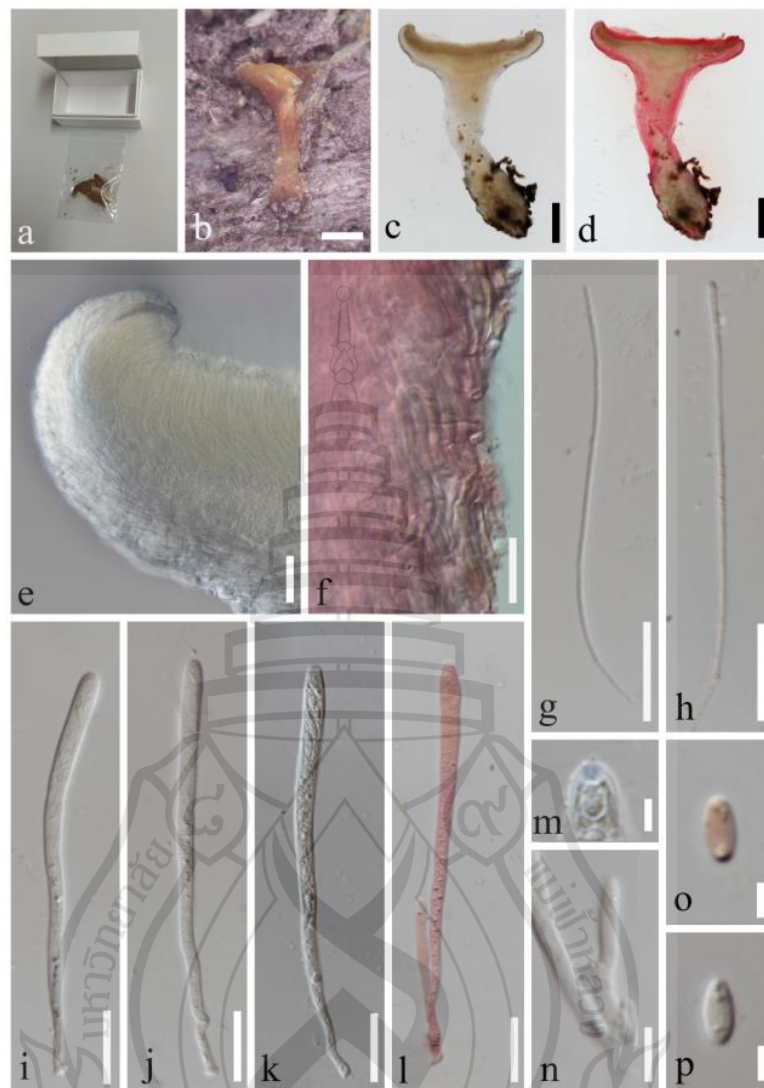


Figure 2.32 *Calycina montana* (HMAS 275566, holotype)

Figure 2.32, a A herbarium package. b An apothecium on the woody substrate. c–d Cross sections of an apothecium (d mounted in Congo red). e Close-up of hymenium at the margin. f Close up of ectal excipulum cells. g–h Filiform paraphyses (dead state). i–l Asci (k mounted in Melzer agent, l mounted in Congo red). m Tip of the ascus (J+, in Melzer agent with KOH treatment). n Close-up of crozier at the base of an immature ascus. o–p Ascospores (o mounted in Congo red). Scale bars: b = 500 μm , c–d = 380 μm , e = 43 μm , f = 25 μm , g–h = 23 μm , i–l = 19 μm , m = 4 μm , n = 8 μm , o–p = 4 μm .

Calycina shangrilana (W.Y. Zhuang and H.D. Zheng) Lestari and Chethana, *comb. nov.*

Basionym: *Bisporella shangrilana* W.Y. Zhuang and H.D. Zheng, Zhuang, Zheng and Ren, *Mycosystema* 36(4): 407 (2017)

Figure 2.29; 2.33

Index Fungorum number: IF570312

Facesoffungi number: FoF 05942

Holotype: HMAS 275566

Material examined: China, Yunnan, Shangrila, Bitahai, 12 August 2008, on rotten wood, X.Q. Zhang and D.Z. Ren, (HMAS 275568, holotype).

Description: *Saprobic* on woody substrate. **Sexual morph:** *Apothecia* 0.4–1.7 × 0.3–1.3 mm in a dried state, gregarious, arising singly or in clusters, pinkish-orange, stipitate. *Stipe* 0.3–0.7 × 0.1–0.4 mm in dried condition, white to cream color different from the disc. *Receptacle* discoid, bright orange to yellow color. *Margin* cream color to hyaline. *Discs* concave. *Ectal excipulum* 33–59 µm ($\bar{x}$ = 42.7 µm, n = 10) at flank near the stipe, composed of gelatinized-hyaline cells of *textura intricata*. *Medullary excipulum* 24–31 µm ($\bar{x}$ = 27.1 µm, n = 10) at flank near the stipe, distinctively separate from ectal excipulum, composed of thin-walled, hyaline cells of *textura oblita*. *Hymenium* 109–140 µm ($\bar{x}$ = 125.3 µm, n = 10). *Paraphyses* 1.4–1.9 µm in diam. ($\bar{x}$ = 1.8 µm, n = 10) at the terminal, filiform, septate. *Asci* 119–146 × 5.4–8 µm ($\bar{x}$ = 133 × 6.7 µm, n = 10), unitunicate, 8-spored, cylindrical, subclavate at the top, rounded apex, J+ (euamyloid), long substipitate base, arising from croziers. *Ascospores* 7.3–11 × 2.1–4.2 µm ($\bar{x}$ = 8.3 × 2.8 µm, n = 10), ellipsoid, 0–1-septate, partially biseriate to uniseriate, hyaline, guttulate, rounded at both ends. **Asexual morph:** Undetermined.

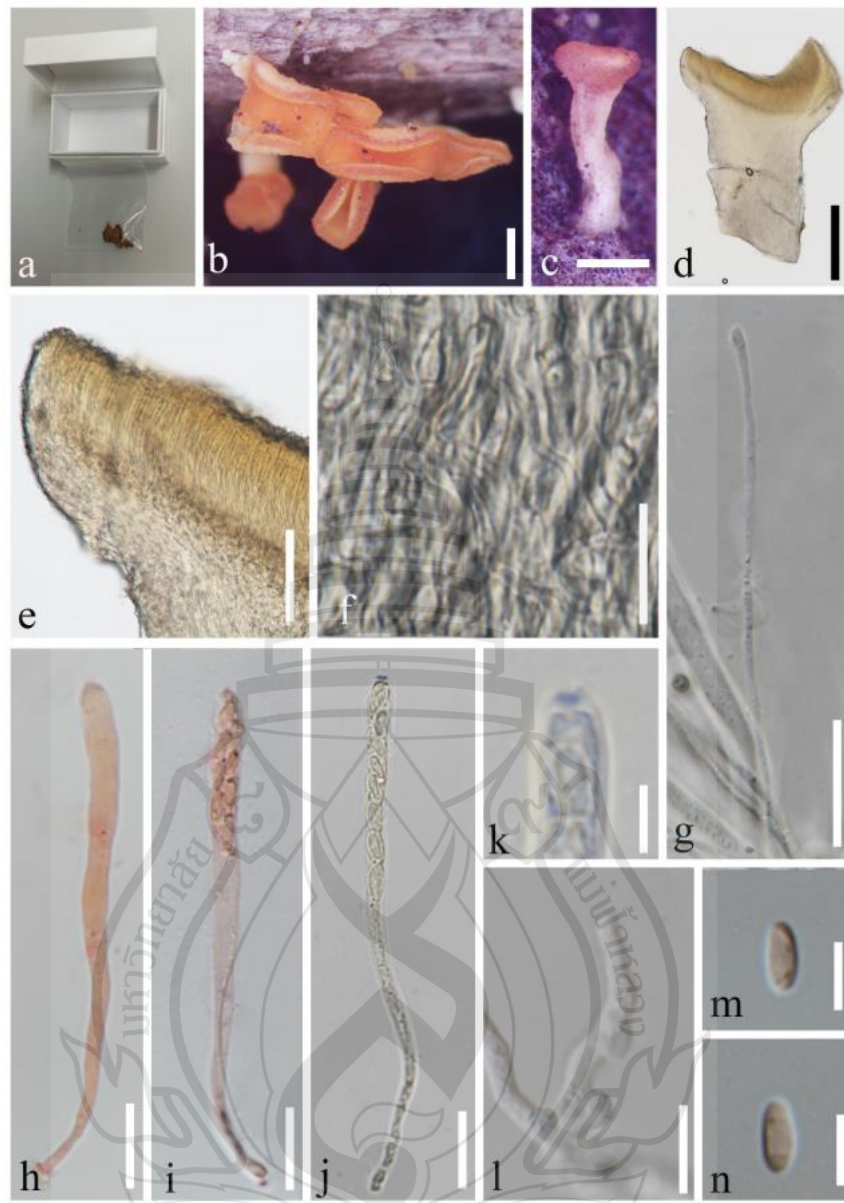


Figure 2.33 *Calycina shangrilana* (HMAS 275568, holotype)

Figure 2.33, a A herbarium package. b–c Apothecia on the woody substrate. d Cross sections of an apothecium. e Close-up of hymenium at the margin. f Close-up of ectal excipulum cells. g Filiform paraphyses (mounted in Congo red). h–j Asci (h, i mounted in Congo red, j mounted in Melzer agent). k Tip of the ascus (J+, in Melzer agent with KOH treatment). l Close-up of croziers at the base of an immature ascus. m–n Ascospores (mounted in Congo red). Scale bars: b–c = 475 μm , d = 350 μm , e = 100 μm , f = 15 μm , g = 20 μm , h–j = 17 μm , k = 5 μm , l–n = 9 μm .

Notes: This specimen is the type strain of *Bisporella shangrilana* (HMAS 275568), synonymized under *Calycina* as *C. shangrilana* in the current study. *Calycina shangrilana* is characterized by orange-pinkish apothecia, gelatinized *textura intricata* cells in the ectal excipulum, and a calycina-like apical ring, which fit with the generic concept of *Calycina* (Baral & Marson, 2005). Based on ITS and LSU phylogenetic analyses, the type strain (HMAS 275568) clusters with the other *C. shangrilana* strains within the *Calycina* clade (Figure 2.33).



Table 2.9 Synopsis of *Calycina* and calycina-like species with molecular data

Species	Apothecia	Paraphyses	Ectal excipulum	Medullary excipulum	Asci Size (µm)	Ascospore characters Size (µm)	References
<i>Calycina alstrupii</i>	0.24–0.47 mm in diam., cream yellowish to orange, sessile	Filiform, aseptate, not exceeding asci at length	<i>Textura prismatica</i> to <i>angularis</i>	<i>Textura prismatica</i> to <i>porrecta</i>	44–67 × 5–7; cylindrical to subcylindrical, J+, arising from simple septa, 8-spored	5–7 × 1.5–2.5; ellipsoid, obtuse or with apices attenuated at one or both ends, hyaline, uniseriate	Suija & Motiejūnaitė (2017)
<i>Calycina citrina</i>	0.5–2.5 mm in diam., bright yellow, very short stipe.	Filiform, somewhat swollen at the apex	<i>Textura prismatica</i> to <i>porrecta</i>	<i>Textura intricata</i>	5–135 × 8–10; cylindrical, rounded apex, J- to J+	9–14 × 3–5; ellipsoidal, hyaline, sometimes eventually becoming 1-septate, uniseriate	Dennis (1956), Carpenter & Dumont (1978), Milekhin and Prokhorov (2007)
<i>Calycina claroflava</i>	0.7–1 mm in diam., bright greenish-yellow in fresh condition, sessile	Filiform, septate	<i>Textura porrecta</i>	<i>Textura epidermoidea</i>	71–101 × 5.5–6; cylindrical-clavate, rounded apex, J-, arising from simple septa	7–12.5 × 2–3; subcylindrical to fusoid, hyaline, obtuse to narrow ends, 1-septate, uniseriate to biseriate	Quijada & Beltrán-Tejera (2017), Ekanayaka et al. (2019a)
<i>Calycina cortegadensis</i>	0.2–0.5 cm in diam., translucent brown to pale yellowish-brown in fresh condition	Filiform, septate at the base, not exceeding asci at length	<i>Textura oblita</i> to <i>intricata</i>	<i>Textura porrecta</i>	40–53 × 2.5–5; cylindrical to subcylindrical, a conical or obtuse apex, J+, arising from simple septa	4–7.5 × 2–2.8; ellipsoid, hyaline, obtuse apices, aseptate, uniseriate to biseriate	Crous et al. (2019)
<i>Calycina herbarum</i>	2–3 mm in diam., whitish to cream broad, short stipitate	Filiform with apex sometime apically swollen	<i>Textura porrecta</i>	N/A	82–86 × 4–5; cylindric to cylindrical clavate, J+	12–14 × 1.5–2.5; fusoid	Milekhin & Prokhorov (2007), Uzun et al. (2014)

Table 2.9 (continued)

Species	Apothecia	Paraphyses	Ectal excipulum	Medullary excipulum	Asci Size (µm)	Ascospore characters Size (µm)	References
<i>Calycina lactea</i>	0.3–0.7 mm in diam., milky white, with hairs at the margin	Filiform with rounded apex, not exceeding asci at length	<i>Textura prismatica</i> to <i>oblita</i>	N/A	120–135 × 8–9.5; cylindric with subclavate at the top, J+ (IKI), arising from croziers (not clear), 8 spored but only with 2–4 mature ascospores	17–19 × 22–26; fusoid with 1–3 septate and guttulate	Baral (2013)
<i>Calycina languida</i>	Up to 0.5 mm in diam., white to yellowish with robust short stipe	Filiform with rounded apex, slightly exceeding asci at length	<i>Textura oblita</i> to <i>intricata</i>	<i>Textura intricata</i>	52–68 × 4–4.3; cylindrical with long base, J+ (IKI), arising from simple septa	4.8–7.8 × 2.3–2.2; fusoid mostly with two big guttules and small guttules, partially biseriate to uniseriate, aseptate	Baral (2021)
<i>Calycina marina</i>	0.25–0.65 mm in diam., whitish to bright yellowish-orange-ochraceous, sessile	Slightly to rather strongly clavate-capitate at the apex	Gelatinized <i>textura prismatica-globulosa</i>	<i>Textura angularis-prismatica</i>	38–96 × 5.5–8; cylindrical clavate with rounded apex, arising from simple septa	5.5–15 × 2.5–5.5; subcylindrical to subfusoid or ellipsoid, obtuse at both ends, uniseriate to biseriate	Baral & Rämä (2015)
<i>Calycina montana</i>	1.1–1.6 mm in diam., amber color, long stipitate	Filiform	Gelatinized <i>textura porrecta</i>	<i>Textura oblita</i>	101–118 × 4.7–6.3, cylindrical with subclavate at the top, J+ (MLZ without and with KOH treatment), rounded to conical apex, long substipitate base, arising from croziers, 8-spored	7.1–9.2 × 2.2–4.2; ellipsoidal, uniseriate to partially biseriate	This study
<i>Calycina shangrilana</i>	1–3 mm in diam., pinkish-orange, stipitate	Filiform	Gelatinized <i>textura intricata</i>	<i>Textura oblita</i>	88–105 × 4.5–5.5; cylindric, J+ (with KOH treatment), arising from croziers, 8-spored	5–8 × 2.2–2.3; ellipsoidal, uniseriate	Zhuang <i>et al.</i> (2017)

Note “IKI” Iodine-Potassium Iodide, “MLZ” Melzer agent, “N/A” Not Available

Calycina papaeana Lestari and K. D. Hyde, sp. nov.

Figure 2.29; 2.34

Index Fungorum number: IF900437

FacesofFungi number: FoF13908

Etymology: Epithet represents Pa Pae sub-district where the specimen was collected.

Material examined: Thailand, Mushroom Research Center, Pa Pae sub-district, Chiang Mai Province, 08 September 2020, Anis S. Lestari, CM 11 (MFLU 23-0015, holotype).

Description: *Saprobic* on decaying root of an unidentified plant. **Sexual morph:** *Apothecia* 165–487 × 145–450 µm ($\bar{x}$ = 142.4 × 229 µm, n = 10), dark yellow in dry condition, arising singly or in small clusters, stipitate. *Receptacle* cupulate, olivaceous dark brown to black. *Stipe* 1–2 × 0.5–1 mm in dry condition, concolorous with receptacle, rugose. *Discs* yellow, shallow cupulate, slightly concave. *Ectal excipulum* 23–50 µm ($\bar{x}$ = 31.8 µm, n = 10), composed of thin-walled, hyaline to pale brown cells of *textura porrecta*. *Medullary excipulum* 23–57 µm ($\bar{x}$ = 39.2 µm, n = 10) in lower flanks, composed of thin-walled, hyaline cells of *textura oblita*. *Hymenium* 62–75 µm ($\bar{x}$ = 70.1 µm, n = 10), hyaline. *Paraphyses* 1.2–2.3 µm in diam. ($\bar{x}$ = 1.7 µm, n = 10), filiform with occasional subclavate at the apex, sometimes branched at around the base, guttulate. *Asci* 38–58 × 3–6 µm ($\bar{x}$ = 50.2 × 4.6 µm, n = 10), 8-spored, unitunicate, cylindrical, rounded, amyloid, long substipitate base, arising from croziers. *Ascospores* 4–9 × 2–5 µm ($\bar{x}$ = 5.7 × 2.2 µm, n = 15), ellipsoid, uniseriate or partially biseriate, hyaline, 2-guttules, rounded at both ends. **Asexual morph:** Undetermined.

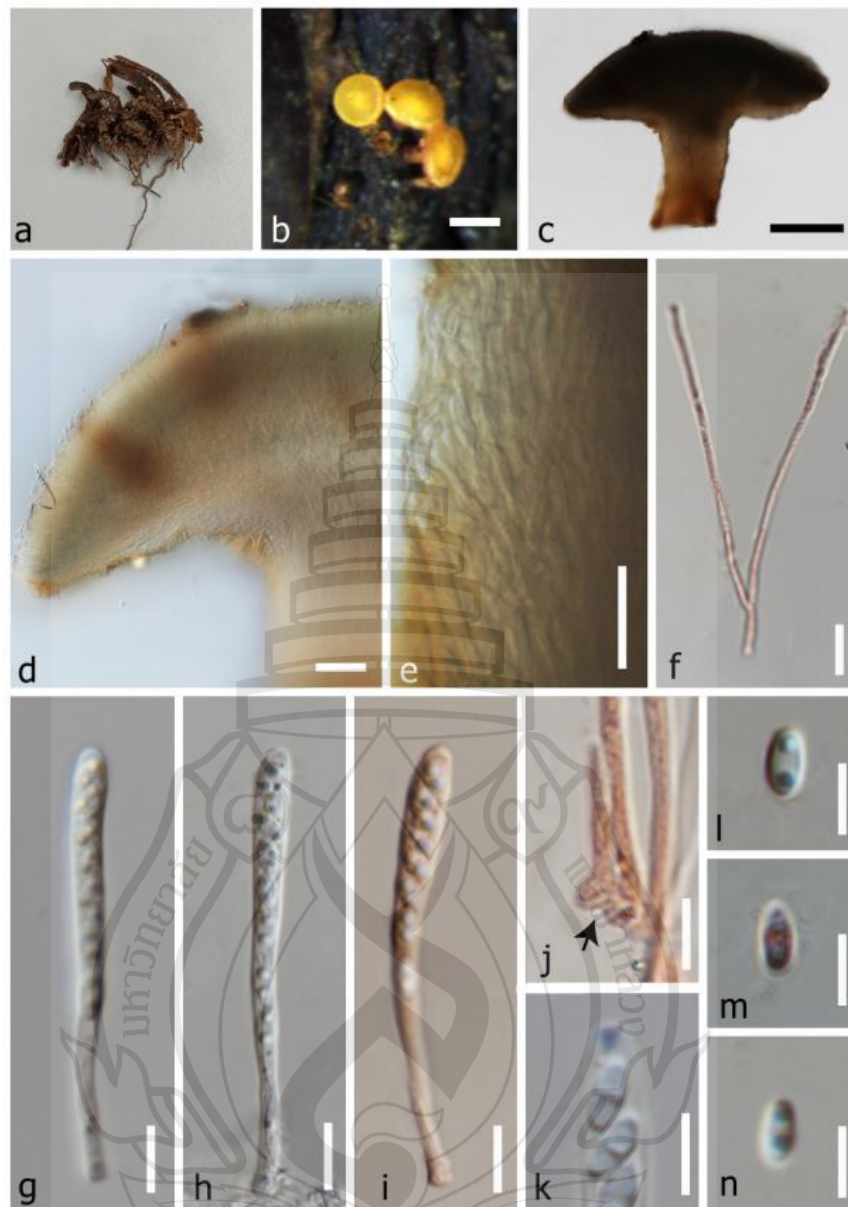


Figure 2.34 *Calycina papaeana* (MFLU 23-0015, holotype)

Figure 2.34, a Examined material. b Apothecia on the substrate. c A vertical cross-section through the apothecium. d Close-up of hymenium at the margin. e Ectal excipulum cells. f Paraphyses. g–i Asci (i mounted in Congo red). j Crozier at the base of a young ascus (arrowed). k Ascus tip (J+ without KOH treatment). l–n Ascospores. Scale bar: b = 380 μ m, c = 200 μ m, d = 60 μ m, e = 25 μ m, f–n = 10 μ m.

Notes: *Calycina papaeana* (MFLU 23-0015) forms a distinct lineage in the combined ITS and LSU sequence analyses with strong statistical support (ML/BI = 91%/0.99, Figure 2.26), and it fits with the generic term of *Calycina* by having gelatinized ectal excipulum, filiform paraphyses, cylindrical asci with calycina-like apical rings and ellipsoidal ascospores (Baral & Marson, 2005; Baral & Rämä, 2015; Suija & Motiejūnaitė, 2017; Lestari & Chethana, 2022). Despite the ITS and LSU base pair difference (Table 2.10), *Calycina papaeana* is morphologically distinguished from other phylogenetically closely related species (Table 2.11). Therefore, based on morphological and phylogenetic evidence, we introduce our collection as *Calycina papaeana* sp. nov. The nucleotide differences in ITS and LSU sequences of our collection and phylogenetically close *Calycina* species are listed in Table 2.10.

Table 2.10 Comparison of ITS and LSU sequences of closely related *Calycina* species with *C. papaeana*

Species	ITS (466 bp)	LSU (852 bp)
<i>Calycina alstrupii</i> (BILAS 10761)	61	13
<i>Chalara pseudoaffinis</i> (CCF3979)	43	16
<i>Calycina lactea</i> (HB7224)	41	-
<i>Calycina languida</i> (F116599)	41	-
<i>Calycina herbarum</i> (KUSF51458)	34	13
<i>Calycina claroflava</i> (F132983)	43	-
<i>Calycina marina</i> (TROMF26093)	51	34
<i>Calycina cortegadensis</i> (MSS 906)	57	17

Table 2.11 Morphological comparison of *C. papaena* with other fungal species phylogenetically closely related

Species	Apothecia	Asci	Ascospore characters Size (µm)	Asexual morph	References
<i>Calycina alstrupii</i>	sessile	Cylindrical to subcylindrical, J+, arising from simple septa, 8-spored	5–7 × 1.5–2.5; ellipsoid, obtuse or with apices attenuated at one or both ends, hyaline, uniseriate	-	Suija & Motiejūnaitė (2017)
<i>Calycina claroflava</i>	sessile	Cylindric-clavate, rounded apex, J-, arising from simple septa	7–12.5 × 2–3; subcylindrical to fusoid, hyaline, obtuse to narrow ends, 1-septate, uniseriate to biseriate	-	Quijada & Beltrán-Tejera (2017)
<i>Calycina cortegadensis</i>	short stipe	Cylindrical to subcylindrical, a conical or obtuse apex, J+, arising from simple septa	Ellipsoid, hyaline, obtuse apices, aseptate, uniseriate to biseriate	-	Crous et al. (2019)
<i>Calycina herbarum</i>	short stipe	Cylindric to cylindrical clavate, J+	Fusoid, guttulates (more than 2-guttules)	-	Milekhin & Prokhorov (2007), Uzun et al. (2014)
<i>Calycina lactea</i>	stipitate	Cylindric with subclavate at the top, J+ (IKI), arising from croziers (not clear), 8 spored but only with 2–4 mature ascospores	Fusoid with 1-3 septate and guttulate	-	Baral (2013)
<i>Calycina languida</i>	short stipe	Cylindrical with long base, J+ (IKI), arising from simple septa	Fusoid mostly with two big guttules and small guttules, partially biseriate to uniseriate, aseptate	-	Baral (2021)
<i>Calycina marina</i>	sessile	Cylindrical clavate with rounded apex, arising from simple septa	Subcylindrical to subfusoid or ellipsoid, obtuse at both ends, uniseriate to biseriate	-	Baral & Rämä (2015)

Table 2.11 (continued)

Species	Apothecia	Asci	Ascospore characters Size (µm)	Asexual morph	References
<i>Calycina papaeana</i>	stipitate	Cylindrical with rounded apex, J+ (MLZ without KOH treatment) arising from crozier, 8 spored	Fusoid to ellipsoid, bigutulate	-	This study
<i>Chalara pseudoaffinis</i>	-	-	-	Multiseptate conidiophore, phialide lageniform with cylindric phialoconidia	Koukol (2011)

Note “MLZ: Melzer agent, IKI: Iodine-Potassium Iodide”

2.3.6 Rutstroemiaceae, Helotiales

During our surveys for discomycetes from 2019–2021 in forests and plantations in northern Thailand, several *Lambertella*-like specimens were found. Morphological observation and BLAST search confirmed that seven newly collected specimens belong to *Lambertella*. Further phylogenetic analyses using maximum likelihood and Bayesian inference analysis based on combined the internal transcribed spacer region of rDNA (ITS), large subunit region of 28S rRNA (LSU), small subunit region of 18S rRNA (SSU) and RNA polymerase II gene (RPB2) sequence data and morphological examination coupled with chemical reactions confirmed seven *Lambertella* species.

The multi-gene phylogenetic analysis based on the ITS, LSU, SSU and RPB2 gene regions of the Rutstroemiaceae and Sclerotiniaceae taxa is depicted (Figure 2.32). The best-scored ML tree with a final optimization likelihood value of -26607.925 is shown. The matrix comprises 887 distinct alignment patterns with 41.3% of gaps and undetermined characters (ITS = 500 bp, LSU = 848 bp, SSU = 654 bp, and RPB2 = 639 bp). Base frequencies were estimated as follows: A = 0.8938, C = 1.187, G = 0.733, T = 0.2153 with substitution rates AC = 1.59611, AG = 2.4341, AT = 1.59611, CG = 1.00, CT = 6.20064, GT = 1.00; gamma distribution shape parameter $\alpha = 0.62$. The BI analysis generated 3,750 trees after 5,000,000 generations.

In the multi-gene phylogram, the cluster of newly collected specimens and extant *Lambertella*: *L. chiangraiensis* (MFLU 23-0088, MFLU 23-0488), *L. sessilis* (MFLU 23-0092, MFLU 23-0487), *L. himalayensis* (MFLU 23-0087, CBS 230.77), *L. pyrolae* (TNS:F-40132) form a sister relationship with the cluster of *L. corni-maris* with 77% maximum likelihood bootstrap support and 0.96 BI posterior probability. The cluster of *L. chiangraiensis* (MFLU 23-0088, MFLU 23-0488) and *L. sessilis* (MFLU 23-0092, MFLU 23-0487) forms a sister relationship with *L. himalayensis* (CBS 230.77, MFLU 23-0087) with 99% maximum likelihood bootstrap support. *Lambertella himalayensis* (MFLU 23-0087) forms a sister relationship with *L. himalayensis* (CBS 230.77) with 99% maximum likelihood bootstrap support and 1.00 BI posterior probability. Meanwhile, the other newly collected *Lambertella*, *L. aurantiaca*, *L. fusoides*, *L. phanensis*, and *Lambertella takensis*, form a distinct lineage

to *L. chiangraiensis-himalayensis-sessilis-pyrolae* cluster with 100% maximum likelihood bootstrap support and 1.00 BI posterior probability. *Lambertella phanensis* (MFLU 23-0091, MFLU 23-0485) form a sister relationship to *Lambertella fusioidea* (MFLU 23-0086) with 91% ML bootstrap support and 0.80 BI posterior probability. *Lambertella takensis* (MFLU 23-0089, MFLU 23-0486) develops a sister relationship with *Lambertella aurantiaca* (MFLU 23-0090) with 100% maximum likelihood bootstrap support and 1.00 BI posterior probability. In our phylogram (Figure 2.32), three newly found *Lambertella* from Northern Thailand form sister relationships to the *Lambertella* core clade (which is indicated by the green color in the multi-gene phylogram in Figure 2.35) comprising *L. corni-marais* (the type species of *Lambertella*), which confirmed their phylogenetic placement in the Rutstroemiaceae as *Lambertella sensu stricto*. The *Lambertella sensu stricto* encompasses eight species with available molecular data and is phylogenetically related to the newly collected *Lambertella* specimens: *L. himalayensis* (MFLU 23-0087), and two novel species, *L. chiangraiensis* (MFLU 23-0088, MFLU 23-0488) and *L. sessilis* (MFLU 23-0092, MFLU 23-0487). While the other newly collected: *L. aurantiaca* (MFLU 23-0090), *L. fusioidea* (MFLU 23-0086), *L. phanensis* (MFLU 23-0091, MFLU 23-0485) and *L. takensis* (MFLU 23-0089, MFLU 23-0486) are categorized in *Lambertella sensu lato* based on the new phylogram of combine data set.

The single-gene phylogenetic analysis based on the ITS gene region of the Rutstroemiaceae taxa is depicted (Figure 2.36). The best-scored ML tree with a final optimization likelihood value of -6702.934 is shown. The alignment comprises 310 distinct alignment patterns with 2.85% gaps and undetermined characters (ITS = 500 bp). Base frequencies were estimated as follows: A = 0.8964, C = 1.192, G = 0.1777, T = 0.2658 with substitution rates AC = 1.49537, AG = 2.05294, AT = 1.49537, CG = 1.00, CT = 4.20922, GT = 1.00; gamma distribution shape parameter α = 0.885. The BI analysis generated 1,500 trees after 2,000,000 generations.

In the single gene phylogram, the newly collected specimen, *L. himalayensis* (MFLU 23-0087), forms a sister relationship with 99 % maximum likelihood bootstrap support and 1.00 BI posterior probability with *L. himalayensis* (CBS 230.77). *Lambertella himalayensis* (MFLU 23-0087, CBS 230.77) form a sister relationship with a cluster of *L. chiangraiensis* (MFLU 23-0088, MFLU 23-0488) and *L. sessilis*

(MFLU 23-0092, MFLU 23-0487) with less than 70% maximum likelihood bootstrap support and less than 0.95 BI posterior probability. *Lambertella phanensis* (MFLU 23-0091, MFLU 23-0485) form a sister relationship to *L. fusoides* (MFLU 23-0086) and the cluster of *L. aurantiaca-takensis* with 89% ML bootstrap support and less than 0.95 BI posterior probability and develops a distinct lineage to the cluster of *L. himalayensis-chiangraiensis-sessilis* with 97% maximum likelihood bootstrap support and 1.00 BI posterior probability. *Lambertella takensis* (MFLU 23-0089, MFLU 23-0486) forms a sister relationship with *Lambertella aurantiaca* (MFLU 23-0090) with 100% maximum likelihood bootstrap support and 1.00 BI posterior probability.



Table 2.12 Accession numbers and origin of fungal taxa used in the phylogenetic analysis of Rutstroemiaceae

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>Amphobotrys ricini</i>	CPC 36573	NR169724	NG073869	–	–	USA
<i>Amphobotrys ricini</i>	CPC 36710	MT223776	MT223873	–	MT223676	USA
<i>Amphobotrys ricini</i>	CPC 36709	MT223775	MT223872	–	MT223675	USA
<i>Bicornispora seditiosa</i>	AH:44702	KF499362	KF499362	–	–	Spain
<i>Bicornispora seditiosa</i>	WU:32446	KF499360	–	–	MW001932	Spain
<i>Bicornispora seditiosa</i>	AH:44701	KF499361	KF499361	–	–	Spain
<i>Bicornispora exophiala</i>	AH:15779	KF499363	KF499363	–	–	Spain
<i>Botrytis aclada</i>	F15	KF263922	–	–	MG780067	South Korea
<i>Botrytis aclada</i>	DAOM 152574	–	JN938890	JN939018	–	Canada
<i>Botrytis caroliniana</i> (T)	ATCC MYA-4856	NR111839	KC171322	–	–	USA
<i>Botrytis cinerea</i>	AFTOL-ID 59	DQ491491	AY544651	AY544695	DQ247786	USA
<i>Botrytis fabae</i>	CBS:120.29	MH855020	NG067342	–	–	Spain
<i>Botrytis fabae</i>	CBS:109.57	MH857663	MH869203	–	–	Spain
<i>Bryorutstroemia fulva</i>	Z.S.7	OP035830	OP035830	–	–	Czech Republic
<i>Bryorutstroemia fulva</i>	Z.S.9	OP035829	OP035829	–	–	Czech Republic

Table 2.12 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>Bryorutstroemia fulva</i>	Z.S.19	OP035828	OP035828	–	–	Czech Republic
<i>Ciboria americana</i>	CBS:117.24	KF859925	MH866271	–	KF545419	USA
<i>Ciborinia erythronii</i> (T)	CBS:300.31	NR159764	NG063974	–	–	USA
<i>Ciboria conformata</i>	F145906	KJ941075	KJ941057	–	–	Spain
<i>Ciboria conformata</i>	CBS:518.75	AB926156	AB926156	–	AB926204	Japan
<i>Ciboria conformata</i>	C-F26964	LT158453	–	–	–	Denmark
<i>Clarireedia maritima</i>	F159519	KJ941084	KJ941064	–	–	Spain
<i>Clarireedia maritima</i>	F118839	KF588372	KJ941063	–	–	Spain
<i>Clarireedia paludosa</i>	CBS:46473	AB926158	–	–	AB926206	USA
<i>Cristulariella depraedans</i>	KUS-F25920	KT462571	KX098505	–	–	South Korea
<i>Cristulariella depraedans</i>	KUS-F26976	KT462570	KX098502	–	–	South Korea
<i>Dumontinia tuberosa</i>	CBS:304.31	MH855223	MH866674	–	–	USA
<i>Dumontinia tuberosa</i>	CBS:220.46	MH856167	MH867692	–	–	Netherlands
<i>Dumontinia tuberosa</i>	TU:109263	LT158412	KX090843	KX090897	–	Estonia
<i>Elliottinia kernerii</i>	ZTMyc_66401	OP325832	OP325826	OP325819	OP346980	Switzerland
<i>Grovesinia moricola</i>	KUS-F26901	KC460209	KX098504	–	–	South Korea
<i>Grovesinia moricola</i>	KUS-F26055	KC460210	KX098503	–	–	South Korea

Table 2.12 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>Haradamyces foliicola</i> (T)	MAFF 411026	NR137642	–	AB329718	–	Japan
<i>Haradamyces foliicola</i>	MAFF 411027	AB329721	–	AB329717	–	Japan
<i>Rutstroemia johnstonii</i>	C:F32113	LT158456	–	KX090884	KX090733	Denmark
<i>Lambertella aurantiaca</i>	MFLU 23-0090	OP967479	OP965344	OR656474	PP156569	Thailand
<i>Lambertella chiangraiensis</i> (T)	MFLU 23-0088	OP967477	OP965341	OR656471	OR940519	Thailand
<i>Lambertella chiangraiensis</i>	MFLU 23-0488	OR855989	–	–	–	Thailand
<i>Lambertella corni-marais</i>	CBS:197.47	MH856215	MH867745	–	–	Switzerland
<i>Lambertella corni-marais</i>	TNS:F-40083	AB926069	AB926139	–	–	Japan
<i>Lambertella corni-marais</i>	CLX3872	KC958559	KC964855	KC964865	–	USA
<i>Lambertella corni-marais</i>	CLX3892	KC958560	KC964856	KC964866	–	USA
<i>Lambertella fusioidea</i> (T)	MFLU 23-0086	OP967481	OP965340	OR793898	PP156567	Thailand
<i>Lambertella hicoriae</i>	CBS:294.54	MH856216	MH867746	KF545532	–	USA
<i>Lambertella hicoriae</i>	CBS:198.47	–	MH867746	KF545539	–	USA
<i>Lambertella himalayensis</i>	<u>CBS:230.77</u>	MH861053	MH872822	–	AB926201	Myanmar
<i>Lambertella himalayensis</i>	MFLU 23-0087	OP967476	OP965342	OR656473	OR940518	Thailand

Table 2.12 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>Lambertella langei</i>	285.2	Z81435	Z81411	Z81383	–	Norway
<i>Lambertella palmeri</i>	AH s.n.	KF499365	–	–	–	Spain
<i>Lambertella palmeri</i>	AH:7576	KF499364	–	–	–	Spain
<i>Lambertella phanensis</i> (T)	MFLU 23-0091	OP967478	OP965343	OR656475	–	Thailand
<i>Lambertella phanensis</i>	MFLU 23-0485	OR652416	OR652444	OR656478	–	Thailand
<i>Lambertella pruni</i>	CBS:199.47	MH856217	MH867747	–	–	USA
<i>Lambertella pruni</i>	WMA1-4	DQ335471	–	–	–	USA
<i>Lambertella pyrolae</i> (T)	TNS:F-40132	AB926081	AB926164	–	–	Japan
<i>Lambertella sessilis</i> (T)	MFLU 23-0092	OQ650294	OQ650293	OR656472	PP156570	Thailand
<i>Lambertella sessilis</i>	MFLU 23-0487	OR855987	–	–	–	Thailand
<i>Lambertella subrenispora</i> (T)	CBS:811.85	MH861915	MH873604	–	AB926220	Japan
<i>Lambertella takensis</i> (T)	MFLU 23-0089	OP967480	OP965339	OR656476	PP156568	Thailand
<i>Lambertella takensis</i>	MFLU 23-0486	OR855988	–	–	–	Thailand
<i>Lambertella tetrica</i>	F142281	KJ941068	–	–	–	Spain
" <i>Lambertella</i> " <i>tubulosa</i>	CBS:202.79	MH861201	MH872970	–	–	Netherlands
" <i>Lambertella</i> " <i>tubulosa</i>	CBS:281.51	MH856859	MH868377	–	–	Sweden

Table 2.12 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>"Lambertella" tubulosa</i>	CBS:125202	MH863518	MH875004	–	–	Austria
<i>Lanzia allantospora</i>	CBS:1242.34	AB926099	–	–	–	Japan
<i>Lanzia echinophila</i>	F132998	KF588371	KJ941053	–	–	Spain
<i>"Lanzia" ovispora</i>	PDD:70881	MH578500	MH587172	–	–	New Zealand
<i>Martininia panamaensis</i>	CBS:358.72	MH860497	MH872212	–	–	France
<i>Martininia panamaensis</i>	CBS:207.47	MH856219	MH867749	–	–	Panama
<i>Microstrobilinia castrans</i>	ZTMyc_66363	OP325830	OP325824	OP325816	OP346978	Switzerland
<i>Microstrobilinia castrans</i>	ZTMyc_66365	OP325831	OP325823	OP325820	OP346979	Switzerland
<i>Monilinia fructicola</i>	CBS:329.35	MH855692	MH867207	–	–	USA
<i>Monilinia fructicola</i>	CBS:127259	MH864497	MH875934	–	–	Australia
<i>Monilinia fructicola</i>	AFTOL-ID 279	DQ491506	AY544683	AY544724	KP143827	USA
<i>Mycopappus alni</i>	KUS-F28171	KY696716	KY696723	–	–	South Korea
<i>Mycopappus alni</i>	KUS-F27033	KC753529	KY696722	–	–	South Korea

Table 2.12 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>Myriosclerotinia caricis-ampullaceae</i>	SCL14704	KX574456	KX670973	–	–	USA
<i>Myriosclerotinia caricis-ampullaceae</i>	1898.P	Z99694	AJ226082	AJ226069	–	Norway
<i>Pseudolanzia piceetorum</i> (T)	H.B.10139	MK679683	–	–	–	Germany
<i>Pycnopeziza sejournei</i>	KL267	LT158443	KX090827	KX090878	KX090726	France
<i>Pycnopeziza sympodialis</i>	CBS:332.39	MH856037	MH867534	–	–	USA
<i>Piceomphale bulgarioides</i>	TNS:F-40005	AB926053	AB926122	–	AB926176	Japan
<i>Piceomphale bulgarioides</i>	TAAM:165289	LT158483	KX090797	–	KX090700	Estonia
<i>Piceomphale bulgarioides</i>	TAAM:198322	LT158469	KX090836	–	–	Estonia
<i>Piceomphale bulgarioides</i>	HB6899	KJ941086	KJ941062	–	–	Switzerland
<i>Rutstroemia calopus</i>	CBS:854.97	–	AB926155	KF545544	AB926213	Netherlands
<i>Rutstroemia calopus</i>	F148155	KF588373	–	–	–	Spain
<i>Rutstroemia firma</i>	CBS:115.86	MH861930	MH873619	–	–	Netherlands
<i>Rutstroemia firma</i>	CBS:341.62	MH858174	MH869768	–	–	France
<i>Rutstroemia firma</i>	TU:104481	LT158450	KX090832	–	KX090731	Estonia
<i>Rutstroemia fruticeti</i>	KL590	MK501759	–	–	–	Montenegro
<i>Rutstroemia fruticeti</i>	F163001	KF588370	–	–	–	Spain

Table 2.12 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>Rutstroemia juniperi</i>	KL234	–	KX090820	KX090871	–	Norway
<i>Rutstroemia longipes</i>	TNS:F-40097	AB926073	AB926142	–	AB926187	Japan
<i>Rutstroemia luteovirescens</i>	TU:104450	LT158431	KX090814	–	KX090716	Estonia
<i>Rutstroemia pruni-serotinae</i>	TNS:F-40119	AB926083	AB926173	–	AB926226	Japan
<i>Rutstroemia punicea</i>	KL497	MK501758	MK501758	–	–	Montenegro
<i>Rutstroemia tiliaceae</i>	KL160	LT158423	KX090808	KX090860	KX090711	Germany
<i>Scleromitrla shiraiana</i>	NBRC:30255	AB926089	AB926147	–	AB926198	Japan
<i>Scleromitrla shiraiana</i>	Hirayama062001	AY789408	AY789407	AY789406	–	–
<i>Sclerencoelia fraxinicola</i>	KL156	LT158420	KX090805	–	–	Germany
<i>Sclerencoelia fraxinicola</i>	G.M. 2017-04-07.1	MZ676713	MZ676713	–	–	Luxembourg
<i>Sclerotinia sclerotiorum</i>	CBS:499.50	MH856725	MH868246	DQ471013	DQ470916	Netherlands
<i>Seaverinia geranii</i>	CBS:168.24	MH854790	MH866294	–	–	USA
<i>Septotinia populiperda</i>	CBS:339.53	MH857235	MH868771	–	–	Germany
<i>Septotinia populiperda</i>	CBS:422.51	MH856925	MH868449	–	–	Netherlands
<i>Schroeteria decaisneana</i>	A.U. 2274	MZ048346	MZ048346	–	–	Germany
<i>Schroeteria decaisneana</i>	S1346	MW915644	MW915644	–	–	Germany
<i>Schroeteria delastrina</i>	P1652-26	MW915646	MW915646	–	–	Germany

Table 2.12 (continued)

Taxon name	Specimen codes ^a	GenBank accession no.				Origin
		ITS	LSU	SSU	RPB2	
<i>Schroeteria delastrina</i>	P1652-27	MW915645	MW915645	–	–	Germany
<i>Streptotinia caulophylli</i>	CBS:419.63	MH858318	MH869931	–	–	Canada
<i>Streptotinia caulophylli</i>	CBS:488.72	MH860540	MH872245	–	–	Brazil
<i>Stromatinia narcissi</i>	CBS:330.55	MH857496	MH869036	–	–	N/A
<i>Stromatinia narcissi</i>	CBS:328.55	MH857494	MH869034	–	–	N/A
<i>Torrendiella ciliata</i>	F132996	KC412008	KJ627220	–	–	Spain
<i>Torrendiella setulata</i>	HB9775	KF588367	KJ941052	–	–	Canada
<i>Valdensinia heterodoxa</i>	485.2	Z81447	Z81423	Z81399	–	Norway

Note ^aAFTOL: Assembling the Fungal Tree of Life, Oregon State University, USA; AH, AHsn: University of Alcalá, Spain; ATCC: American Type Culture Collection, Manassas, VA, USA; C: University of Copenhagen, Denmark; CBS: Central Bureau voor Schimmelcultures, Utrecht, The Netherlands; Canadian Collection of Fungal Cultures, Agriculture and Agri-Food Canada, Ottawa, Canada; F: Fundación Medina's Fungal Culture collection, Spain; GM: herb. G. Marson, Luxembourg; HB: herb. H.O. Baral, Germany; ICMP: International Collection of Microorganisms from Plants, New Zealand; KL: Landesmuseum für Kärnten, Austria; KUS: Korea University Herbarium, Seoul, Korea; MFLU: Mae Fah Luang University Herbarium Chiang Rai, Thailand; OSC: Oregon State University, Corvallis, USA; PDD: Manaaki Whenua - Landcare Research, New Zealand Fungarium, New Zealand; TAAM: Institute of Agricultural and Environmental Sciences of the Estonian University of Life Sciences, Estonia; TNS: National Museum of Nature and Science, Tsukuba,

Japan; TU: University of Tartu, Estonia; Z.S.: Zuzana Sochorova collection, Czech Republic; WU: University of Vienna, Ex-type strains are labeled by (T), newly generated sequences are in bold, “–” indicates unavailable sequences



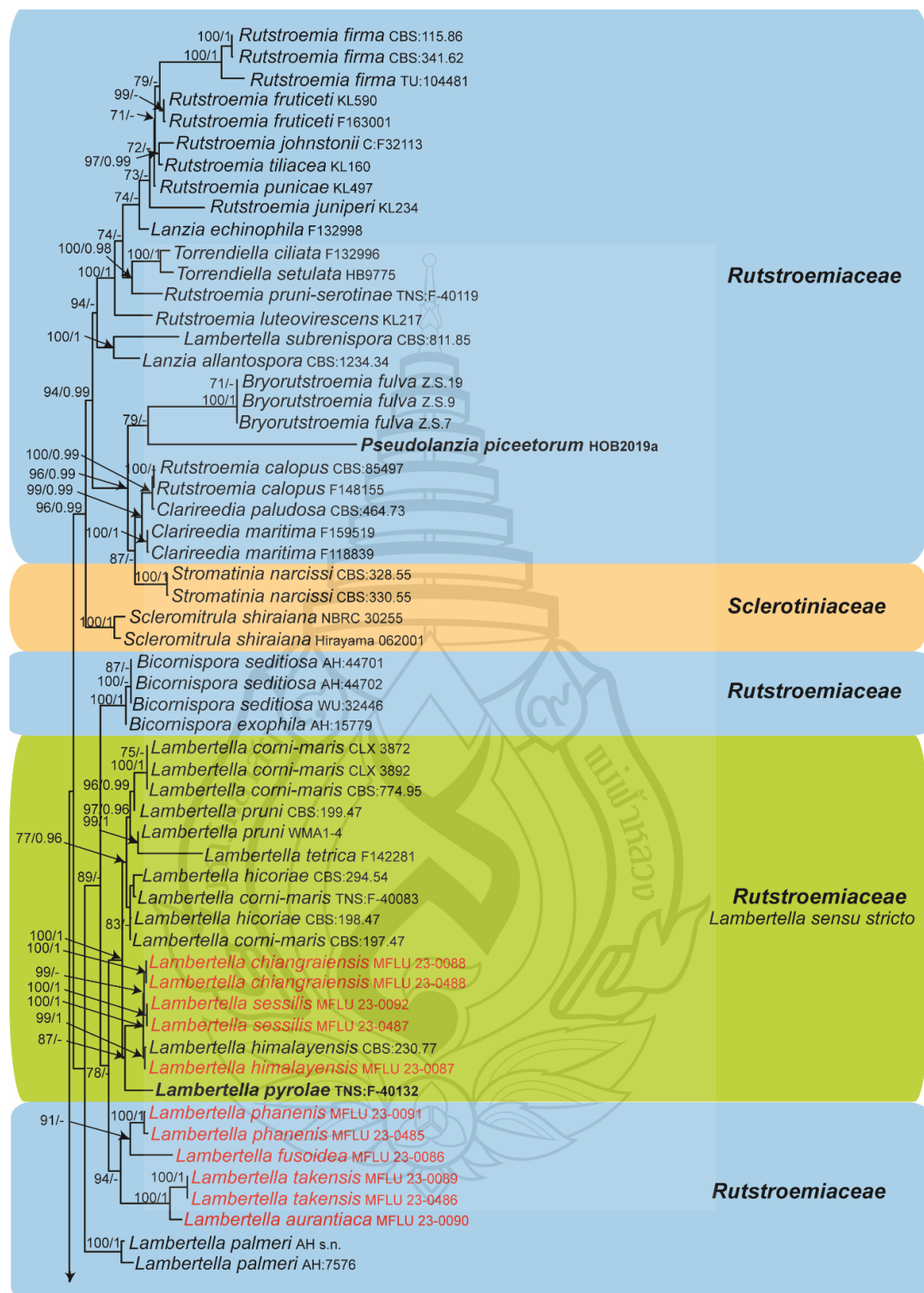


Figure 2.35 The phylogram of combined ITS, LSU, SSU and RPB2 sequence data for genera in Rutstroemiaceae and Sclerotiniaceae

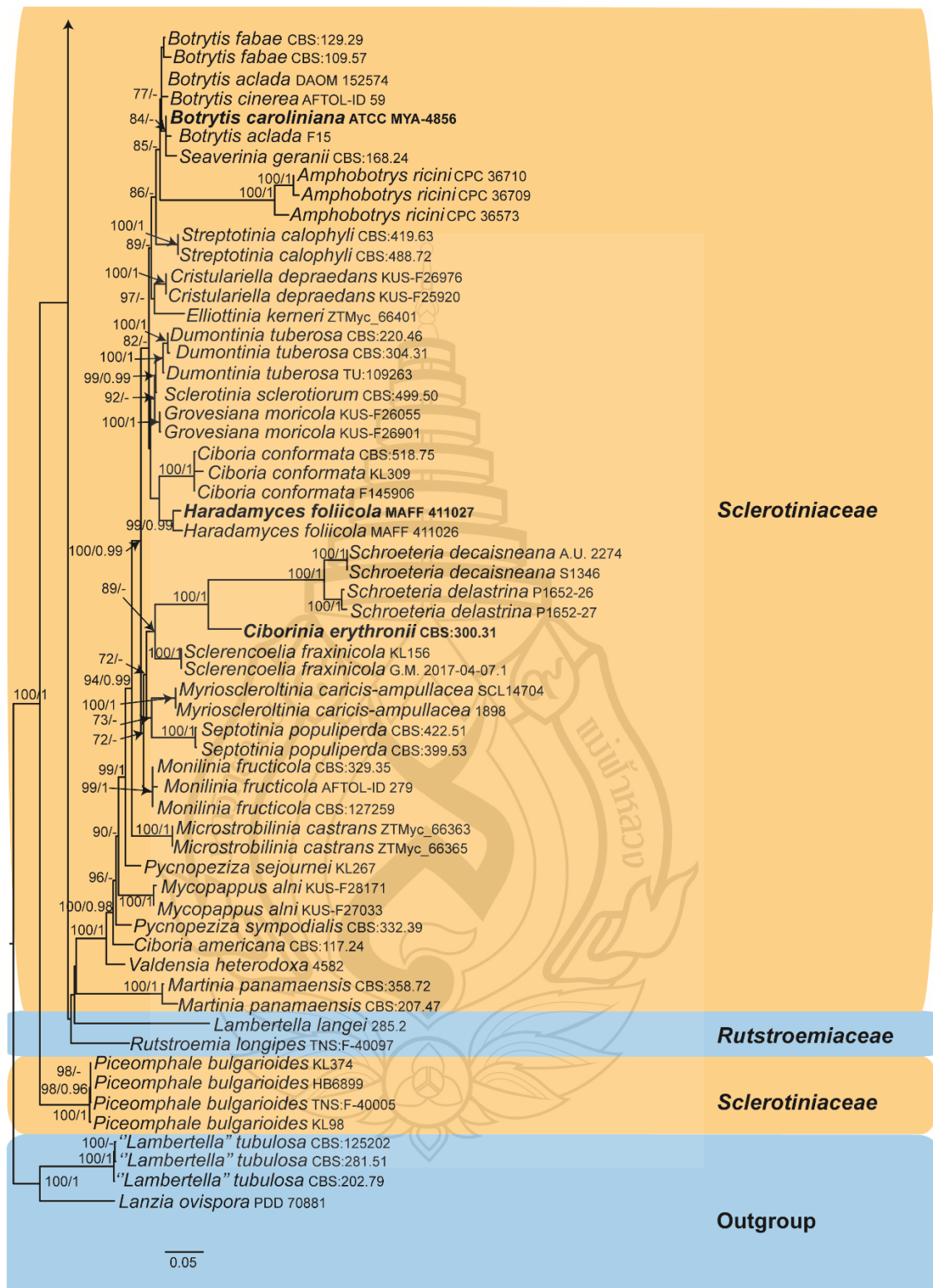


Figure 2.35 (continued)

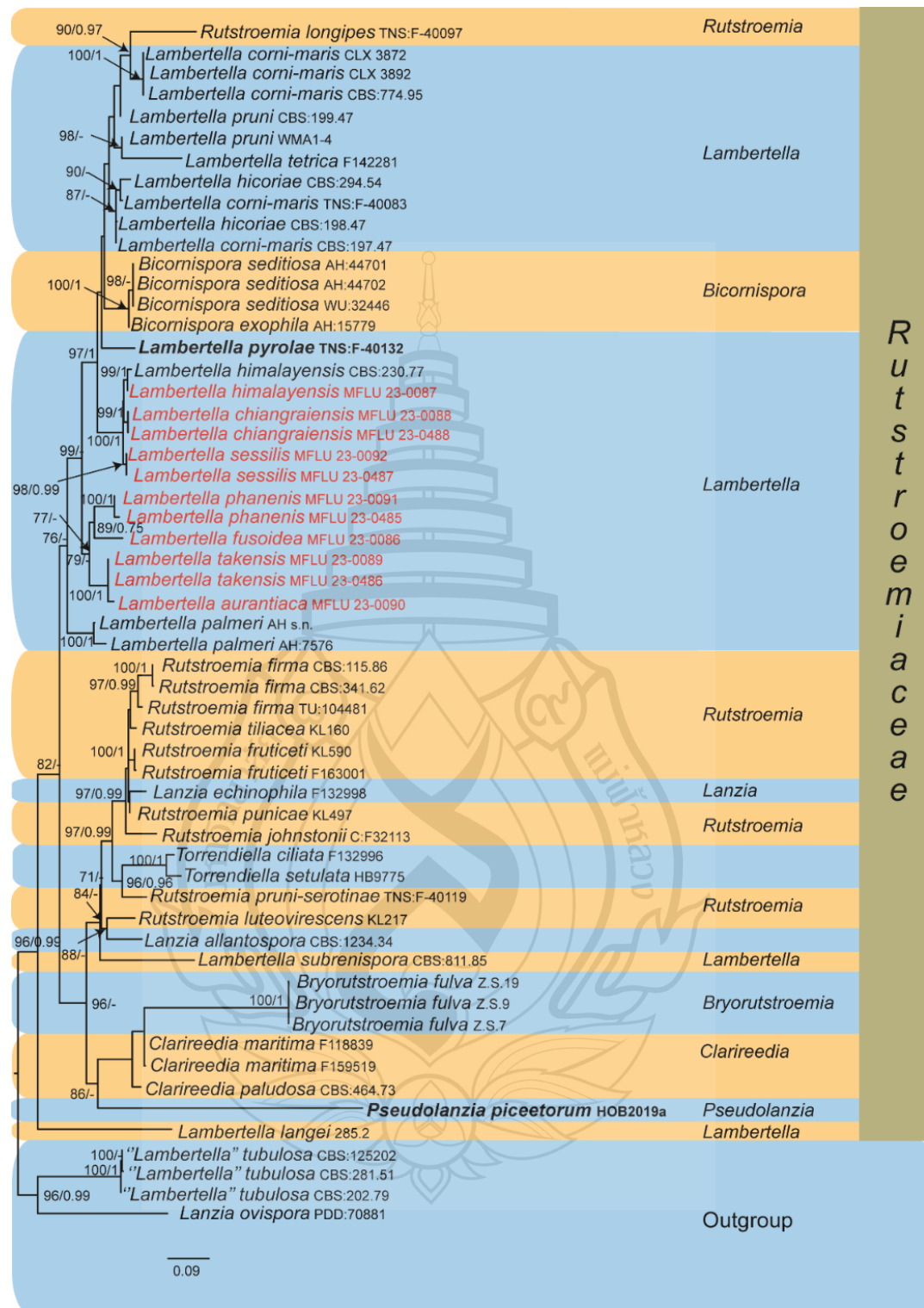


Figure 2.36 The phylogram of the ITS sequence data for genera in Rutstroemiaceae

Family: Rutstroemiaceae Holst-Jensen, L.M. Kohn and T. Schumach.

Genus: *Lambertella* Höhn

Lambertella was established by Höhnelt (1918), with *Lambertella corni-marisi* as the type species in Sclerotiniaceae (Seaver, 1951). Whetzel (1943) published the first monograph for *Lambertella*, contributing eight novel species: *Lambertella cephalanthi*, *L. colombiana*, *L. hicoriae*, *L. jasmine*, *L. pruni*, *L. tropicalis*, *L. viburni*, and *L. corni-marisi*. Subsequently, the genus was re-evaluated and placed in the Rutstroemiaceae together with *Lanzia*, *Poculum*, *Rutstroemia*, and *Verpatinia* based on rDNA phylogeny and substratal stroma (Kohn & Grenville, 1989; Holst-Jensen et al., 1997). Several *Lambertella* species were reported from China (Korf & Zhuang, 1985), Europe (Dumont, 1971; Schumacher & Holøs, 1989), India (Tewari & Pant, 1967; Elliot & Sharma, 1976; Gautam et al., 1982; Sharma, 1985), Japan (Korf & Zhuang, 1985; Hosoya & Otani, 1997), Malaysia (Dumont, 1974), North America (Cash, 1958; Tewari, 1963), South America (Dumont, 1974), the Philippines (Dumont, 1971) and the UK (Abdullah & Webster, 1981). Additionally, some species in the genera *Helotium* (Dumont, 1974), *Humaria* (Dumont, 1971), *Moellerodiscus* (Hosoya & Otani, 1997), *Mollisia* (Dumont, 1971), *Phaeociboria* (Dumont, 1971), *Rutstroemia* (Dumont, 1974), *Phialea* (Korf, 1982) and *Velutaria* (Dumont, 1971) were synonymized under *Lambertella*. For example, *Moellerodiscus advenulus* has been previously synonymized under *Phialea advenula* and *Lambertella advenulum* by Hosoya and Otani (1997) due to the recognition of brown pigmentation on ascospores before germination and substratal rind formation *in vivo* and *in vitro*.

Currently, 69 *Lambertella* species are listed in the Index Fungorum (Gautam et al., 1982; Sharma, 1985; Schumacher & Holøs, 1989; Index Fungorum, 2024; Species Fungorum, 2024). *Lambertella* is characterized by sub- to stipitate apothecia, *textura prismatica* ectal excipulum, substratal stroma formation from vegetative hyphae, and brown-pigmented ascospores (Dumont, 1971; Korf & Zhuang, 1985; Holst-Jensen et al., 1997). Baral et al. (2023) observed that these brown ascospores of *Lambertella* are present in the living apothecia at maturity. Furthermore, similar brown-pigmented ascospores have been documented in other Helotiales genera, such as *Hymenoscyphus*, *Lanzia*, *Pseudolanzia*, and *Rutstroemia* (Zhao & Hosoya, 2015; Zhao et al., 2016; Baral 2017). Zhao et al. (2016) defined *Lambertella* sensu stricto to accommodate

Lambertella species characterized by stipitate apothecia, with *textura prismatica* ectal excipulum, sclerotiniaceous apical ring and brown ascospores in the asci.

Phylogenetically, Holst-Jensen et al. (1997) demonstrated polyphyletic relationships among the *Lambertella*-morphologically defined group, which was further confirmed by Zhao et al. (2016) with the arrangement of *Lambertella sensu stricto* and suggested species reevaluation in *Lambertella sensu lato*. Some *Lambertella* species still have taxonomic issues, such as *Lambertella hicoriae*, which, according to Dumont (1971), was a synonym of *L. corni-maris*. In Zhao et al. (2016), those two were in similar clades. Additionally, *L. corni-maris* and *L. hicoriae* isolates from different countries are unstable (Vu et al., 2019). Another species is *Lambertella tubulosa*, whose characters fit the generic term of *Lambertella*, yet its phylogenetic placement is not included in *Lambertella sensu stricto* (Zhao et al., 2016).

The majority of *Lambertella* species were found as saprobes on lignocellulose substrates, such as petioles, twigs, and fallen fruits in freshwater or terrestrial habitats (Dumont, 1971; Abdullah & Webster, 1981; Zhao et al., 2013), while some were found on dung (Dumont, 1976) or associated with other fungi (Dumont, 1971; Korf & Zhuang, 1985). In the genus *Lambertella*, the most important species is *Lambertella corni-maris* due to its life mode as a fungal pathogen causing mummified fruits on several horticultural commodities such as apples (*Malus prunifolia*), berries (*Sorbus aucuparia*) and cherries (*Cornus mas*) (Palmer et al., 1994). *Lambertella corni-maris* is a postharvest fungal pathogen on fruits first found in Austria in 1917, also known for causing disease on some vegetables such as turnip (*Brassica rapa*) and parsnip (*Pastinaca sativa*) (Harrison & El-Helaly, 1935). Currently, *L. corni-maris* brown rot disease is reported in Europe and the US (Wiseman et al., 2015). Even though *L. corni-maris*'s life mode is pathogenic, the vital chemical properties of *L. corni-maris*, which may potentially suppress other fungal diseases, have also been studied. For example, a recent study by Vasić et al. (2022) documented the antagonistic properties of the apple post-harvest pathogen *L. corni-maris* against the brown fruit rot pathogen *Monilia polystroma*. Further studies extracted the metabolites with antagonistic properties against bacteria and fungi from *L. corni-maris* (Sproston, 1963; Murakami et al., 2008) and patented them later as bactericides and fungicides (Dumont, 1971). *Lambertella*

species also exhibited mycoremediation properties, reducing toxicity in intermediate and old landfill leachates (Siracusa et al., 2020).

In Thailand, helotian discomycetes have been documented by Phanichapol (1986), Ekanayaka et al. (2019a) and Phutthacharoen et al. (2022); however, there are no records of Rutstroemiaceae members, especially *Lambertella*. Hence, this study aims to study and explore *Lambertella* collected in Northern Thailand and document new species and extant species as new geographical or host records.

Lambertella aurantiaca V.P. Tewari and D.C. Pant

Figure 2.35; 2.36; 2.37; 2.38

MycoBank number: MB 332943

Facesoffungi number: FoF 14252

Typus: India, Varanasi, old Botanical Garden B.H.U., on petioles and vein leaves of *Madhuca latifolia*, *Mangifera indica* and an unidentified twig, 19 August and 31 August 1965, V.P Tewari and D.C. Pant (holotype BHUPP 223; paratype BHUPP 211).

Material examined: Thailand, Chiang Rai, Phan District, Mae Ao, Ang Kep Nam Huai Tonyang Reservoir, 19.67568037694373, 99.79873968293234, on unidentified the petioles of decaying leaves, 27 September 2021, Anis S. Lestari, NHT1 (MFLU 23-0090). Sequences: OP967479 (ITS), OP965344 (LSU), OR656474 (SSU), PP156569 (RPB2).

Description: *Stroma* elliptic to irregular blackened zones on the host substrates, visible through naked eyes and stereomicroscopes, color change from cadmium yellow to purple on the receptacle when after tested with KOH 2%. **Sexual morph:** *Apothecia* 0.5–1.7 × 0.3–0.45 cm ($\bar{x}$ = 1.2 × 0.9 cm, n = 10) in dried condition, cadmium yellow or orange, arising solitary, stipitate. *Stipe* 0.3–1.2 × 0.2–0.4 cm ($\bar{x}$ = 0.8 × 0.3 cm, n = 10) in dried condition, concolorous to the receptacle. *Receptacle* cupulate to discoid, golden brown or deep cadmium yellow. *Margin* concolorous to the receptacle. *Discs* brown when dried, convex. *Hairs* absent. *Ectal excipulum* 33–44 µm ($\bar{x}$ = 39 µm, n = 10) at lower flanks, composed from thin-walled cells of *textura prismatica* to *textura porrecta*. *Medullary excipulum* 37–79 µm ($\bar{x}$ = 54 µm, n = 10) in lower flanks, composed of thin-walled, hyaline cells of *textura intricata*. *Hymenium* 75–88 µm ($\bar{x}$ =

81 μm , $n = 15$), hyaline at immaturity, becomes dark brown at maturity. *Paraphyses* 1.6–2.2 μm wide ($\bar{x} = 1.9 \mu\text{m}$, $n = 10$), numerous, filiform, septate, similar length with asci, 2–3 branched. *Asci* 66–81 $\times$ 4.1–7.3 μm ($\bar{x} = 76 \times 5.8 \mu\text{m}$, $n = 10$), 8-spored, unitunicate, cylindric, rounded apex, stained light blue in MLZ (with and without KOH-pretreatment), ascus ring is not sclerotinia-type, arising from croziers. *Ascospores* 6.6–9.5 $\times$ 2.7–4.6 μm ($\bar{x} = 8 \times 4.2 \mu\text{m}$, $n = 30$), uniseriate, hyaline when immature, becoming yellowish brown to dark brown at maturity, with 1–2 guttules. **Asexual morph:** Undetermined.

Notes: Morphologically, *L. aurantiaca* (MFLU 23-0090) fits the generic term of *Lambertella* characterized by having substratal stroma, *textura prismatica* ectal excipulum, filiform paraphyses, and the characteristic brown, ellipsoid ascospores (Figure 2.37–2.38). In addition, some characters of the newly collected specimen (MFLU 23-0090) fit *Lambertella aurantiaca* (BHUPP 223) which was previously described by Tewari and Pant (1967), based on similar morphology and chemical tests as sequence data are unavailable. Morphology of MFLU 23-0090 resembles the type species of *Lambertella aurantiaca* (BHUPP 223) by encompassing stalked apothecia with deep cadmium yellow-colored receptacle, cylindric asci, and brown, ellipsoid ascospores (Tewari & Pant, 1967; Figure 2.37). The identity was also confirmed by a chemical test using 2% KOH on the apothecial receptacle of MFLU 23-0090, which resulted in a color change from cadmium yellow to purple, concise with the description of the type species (Figure 2.38; Tewari & Pant, 1967).

Despite the fact that the characters of *Lambertella aurantiaca* (MFLU 23-0090) also fit the morphology of *Lambertella sensu stricto*, previously established by Zhao et al. (2016), however, the *Lambertella*-clade containing *L. aurantiaca* (MFLU 23-0090) do not phylogenetically relate with the *L. corni-maritima* clade which serves as the type species of *Lambertella sensu stricto* (Figure 2.35). The branch of *Lambertella* clade containing *L. aurantiaca* (MFLU 23-0090) forms a sister relationship to the clade of *L. chiangraiensis*, *L. sessilis*, *L. himalayensis*, *L. pyrolae* with 100 ML bootstrap support and 1.00 BI posterior probability (Figure 2.35). Hence, *L. aurantiaca* (MFLU 23-0090) is excluded from *Lambertella sensu stricto* but still placed in the genus *Lambertella* based on the morphology comparison and chemical reaction. *Lambertella aurantiaca*

(MFLU 23-0090) is introduced as a new geographical record in Thailand. Through this study, the sequence data of *Lambertella aurantiaca* is provided for the first time.

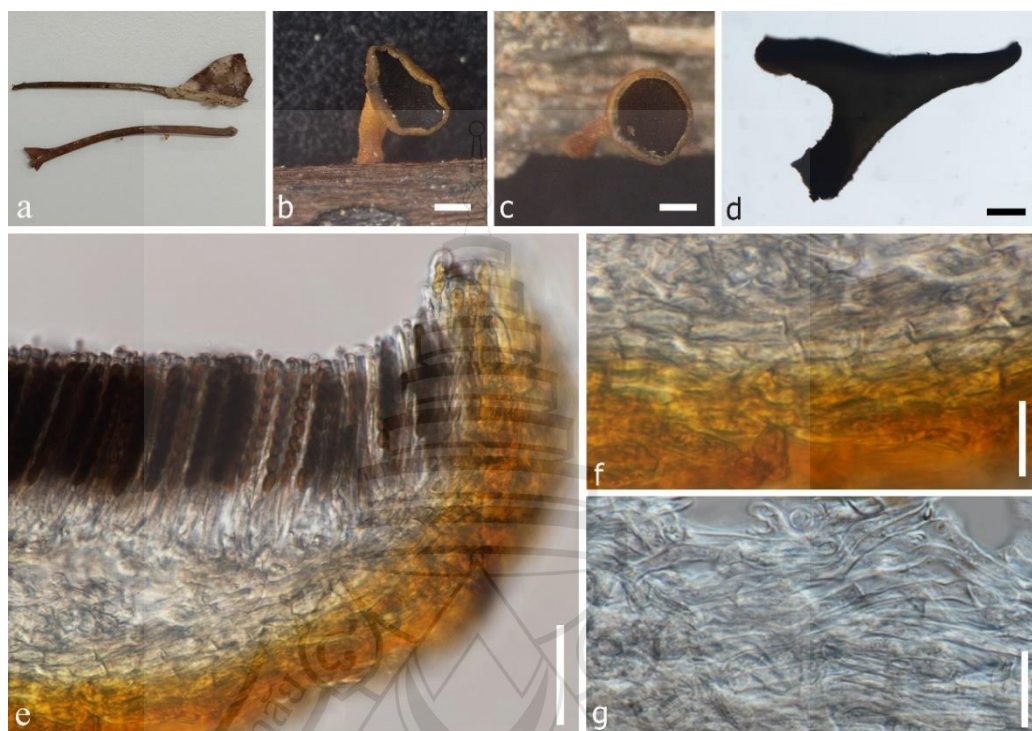


Figure 2.37 Apothecia and excipulum cells *Lambertella aurantiaca* (MFLU 23-0090, a new geographical record)

Figure 2.37, a Petiole leaves. b–c An apothecium on the leaf petiole. d Close-up of an apothecium cross-section. e Close-up of the hymenium at the margin. F Ectal excipulum cells. g Medullary excipulum cells. Scale bars: b–c = 500 μm , d = 350 μm , e = 35 μm , f–g = 15 μm .

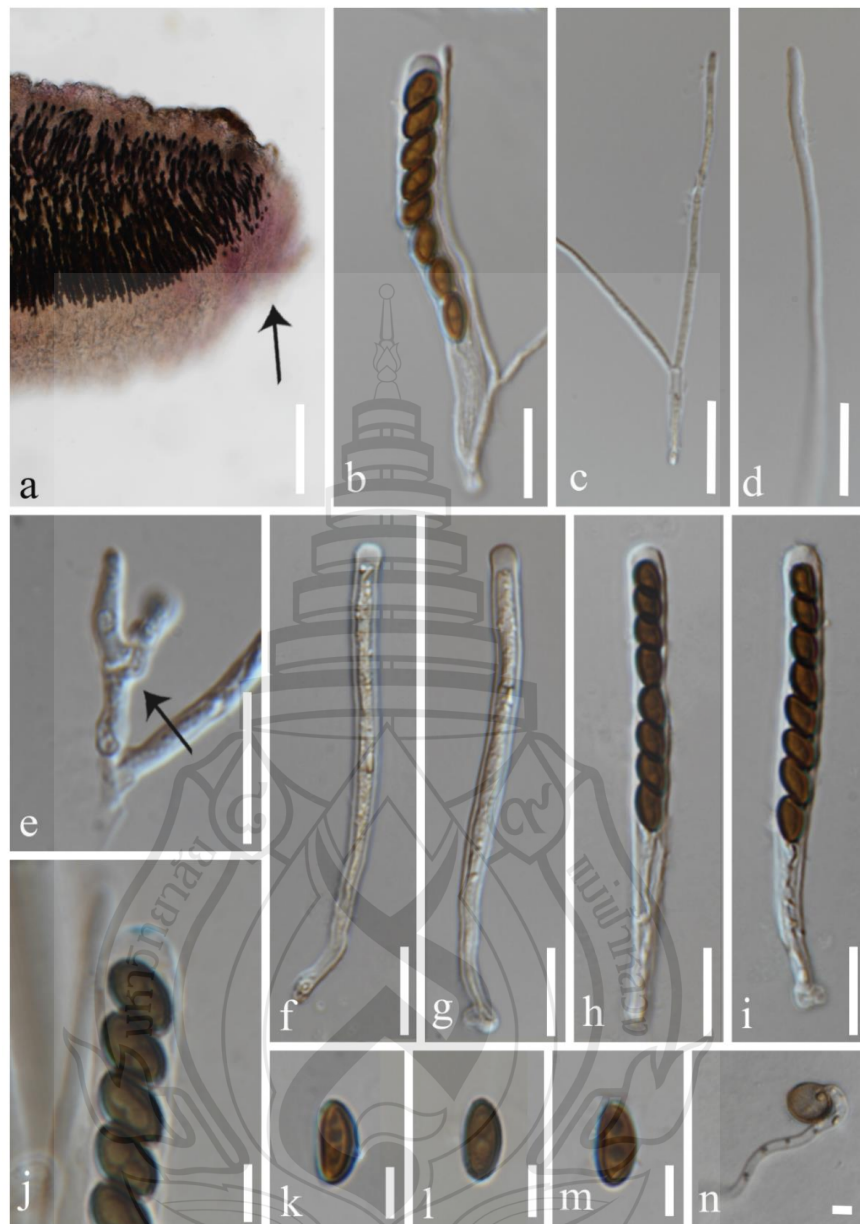


Figure 2.38 Paraphysis, asci and ascospores of *Lambertella aurantiaca* (MFLU 23-0090, a new geographical record)

Figure 2.38, a Purple color at the excipular cells (Mounted in KOH 2%). b Ascus with paraphyses. c–d Filiform paraphyses. e An immature ascus with a crozier at the base. f–i Asci. j Tip of ascus (mounted in MLZ reagent without KOH pretreatment). k–m Ascospores. n A germinated ascospore. Scale bars: a = 45 μm , b–i = 15 μm , j–n = 5 μm .

Lambertella Chiangraiensis Lestari and Chethana, sp. nov.

Figure 2.35; 2.36; 2.39, 2.40

MycoBank number: MB851087

Facesoffungi number: FoF 15214

Etymology: Epithet represents the province where the specimen was found.

Material examined: Thailand, Huai Sak, Ang Kep Nam Nong Buak Tao Reservoir, 19.792211684477675, 99.87910786250163, on leaf petioles of unidentified leaves, 27 September 2021, Anis S. Lestari, BTR5 (holotype MFLU 23-0088). Thailand, Ang Kep Nam Nong Buak Tao Reservoir, Huai Sak, Chiang Rai, 27 September 2021, Anis S. Lestari, BTR3 (MFLU 23-0488). Sequences (MFLU 23-0088): OP967477 (ITS), OP965341 (LSU), OR656471 (SSU), OR940519 (RPB2); MFLU0488: OR855989 (ITS).

Description: *Stroma* irregular blackened zones on petioles, visible through naked eyes and stereomicroscope. **Sexual morph:** *Apothecia* 0.5–2.6 × 0.4–1.7 cm ($\bar{x}$ = 1.3 × 0.9 cm, n = 10) in dried condition, solitary, stipitate, brown in dried condition. *Stipe* 348–540 × 250–349 µm ($\bar{x}$ = 442 × 360 µm, n = 10) in dried condition. *Receptacle* cupulate to discoid, brown to grey when it is dried. *Margin* concolorous to the receptacle. *Discs* whitish brown, convex, discoid. *Hairs* 41–88 × 7.4–8.5 µm ($\bar{x}$ = 71 × 7.7 µm, n = 10), arising from the outer layer of ectal excipulum, up to 3-septate, hyaline to pale brown, cylindric with rounded to conical apex. *Ectal excipulum* 99–116 µm ($\bar{x}$ = 110 µm, n = 10) at lower flanks, composed from brown to pale brown walled cells of *textura prismatica* to *textura porrecta*. *Medullary excipulum* 71–147 µm ($\bar{x}$ = 110 µm, n = 10) in lower flanks, composed of thin-walled, brown cells of *textura intricata*. *Hymenium* 133–146 µm ($\bar{x}$ = 139 µm, n = 10), hyaline to pale brown. *Paraphyses* 1.7–2.2 µm wide ($\bar{x}$ = 2.5 µm, n = 12), numerous, filiform, aseptate, similar length with asci, branched at 1/3 length and at the base. *Asci* 81–95 × 5.6–8.8 µm ($\bar{x}$ = 70 × 6.9 µm, n = 11), 8-spored, unitunicate, cylindric, rounded apex, stained light blue in MLZ (with and without KOH-pretreatment), ascal ring is sclerotinia-type, arising from croziers. *Ascospores* 7–11 × 2.8–4.9 µm ($\bar{x}$ = 9.5 × 4.3 µm, n = 30), uniseriate to partially biseriate, hyaline, ellipsoid, smooth. **Asexual morph:** Undetermined.

Notes: Our specimens (MFLU 23-0088 and MFLU 23-0488) fit the generic description of *Lambertella* by having substratal stroma, stipitate apothecia, *textura*

prismatica ectal excipulum except brown ascospores. In addition, our specimens (MFLU 23-0088 and MFLU 23-0488) are included in the *Lambertella sensu stricto*, which supports its taxonomic placement in *Lambertella*. Hence, based on phylogeny and some similarity in morphology to *Lambertella*, we include *L. chiangraiensis* (MFLU 23-0088 and MFLU 23-0488) in the *Lambertella sensu stricto* and emend its defined *Lambertella* character.

Morphologically, our *Lambertella* specimens (MFLU 23-0088, MFLU 23-0488), at a glance, resemble our newly collected *Lambertella himalayensis* (MFLU 23-0087) due to their cylindric asci, branched paraphysis and ellipsoid ascospores. However, *Lambertella* specimens (MFLU 23-0088 and MFLU 23-0488) differed based on the apparent hairs on the apothecial receptacle and hyaline ascospores while *L. himalayensis* (MFLU 23-0087) has no hairs on its receptacle and pale brown ascospores (Figure 2.39–2.40, 2.43–2.44). In addition, in the phylogram, our specimens (MFLU 23-0088 and MFLU 23-0488) form a distinct lineage to the cluster of *L. himalayensis* (CBS 230.77, MFLU 23-0087) with 99% ML bootstrap support and 0.76 BI posterior probability (Figure 2.35). Furthermore, there are base pair differences of ITS, SSU and RPB2 between our species and *L. himalayensis* (Table 2.13); hence, our *Lambertella* specimens (MFLU 23-0088, MFLU 23-0488) introduced as a new species, *Lambertella chiangraiensis*.

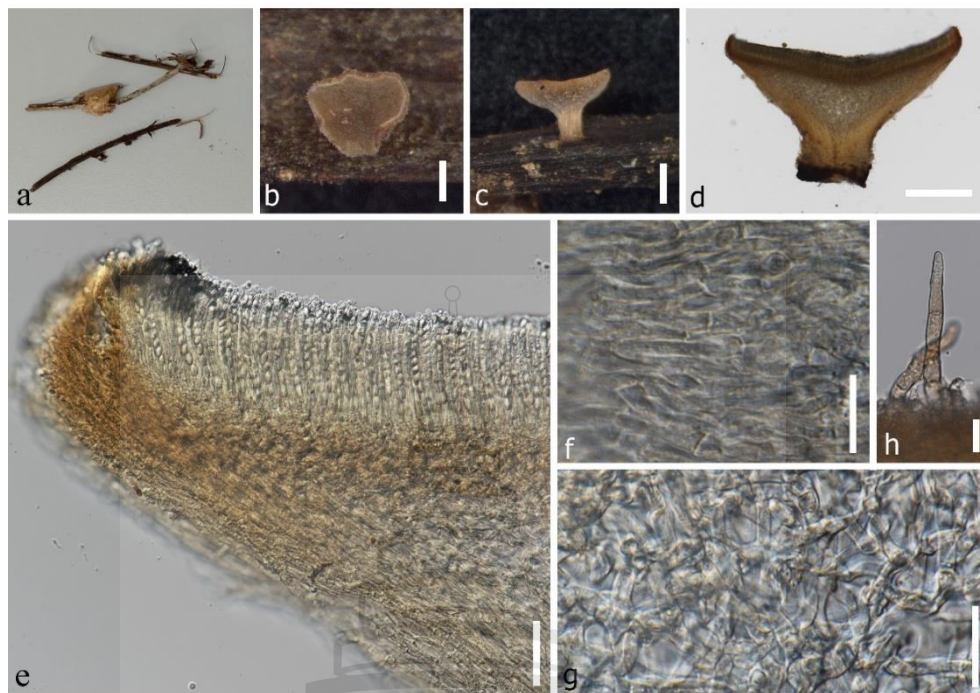


Figure 2.39 Apothecia, excipulum cells and hair of *Lambertella chiangraiensis* (MFLU 23-0088, holotype)

Figure 2.39, a Dead leaves. b–c Apothecia on the petiole leaves. d Close-up of an apothecium sectioning. e Close-up of hymenium at the margin. f Ectal excipulum cells. g Medullary excipulum cells. h A hair. Scale bars: b–c = 550 μm , d = 450 μm , e = 50 μm , f–g = 25 μm , h = 15 μm .

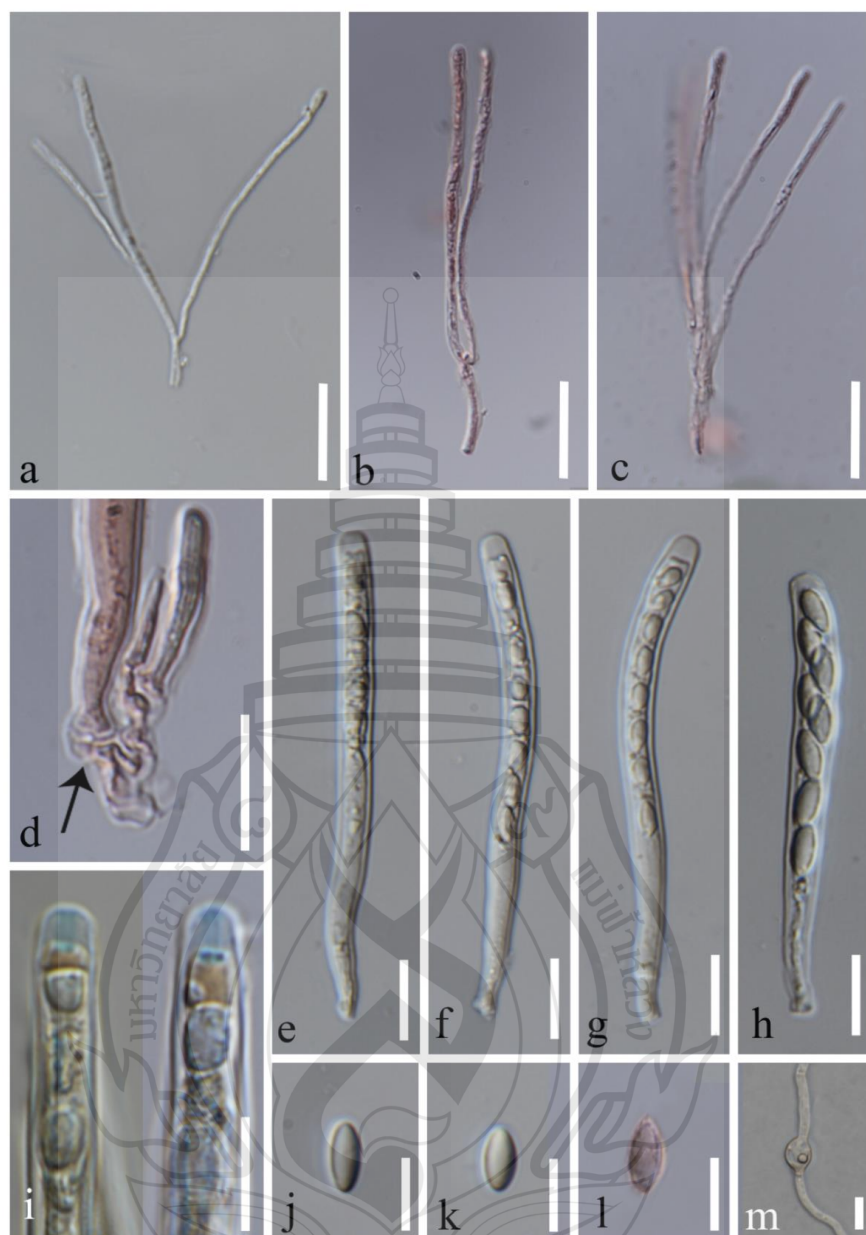


Figure 2.40 Paraphysis, asci and ascospores of *Lambertella chiangraiensis* (MFLU 23-0088, holotype)

Figure 2.40, a–c Filiform paraphyses. d A crozier at the base of the ascus. e–h Asci. i Tips of asci (mounted in MLZ reagent without KOH treatment). j–k Ascospores. m A germinated ascospore. Scale bars: a–h = 15 μm , i–m = 10 μm .

Lambertella fusoides Lestari and Chethana, sp. nov.

Figure 2.35; 2.36; 2.41; 2.42

MycoBank number: MB 849025

Facesoffungi number: FoF 14253

Etymology: The epithet reflects the shape of the ascospores of the new species.

Typus: Thailand, Chiang Rai Province, Forest nearby Huay Mae Sai Waterfall, 20.005648312575723, 99.71441705353928, on unidentified rotten leaf surface, 24 June 2020, Anis S. Lestari (holotype MFLU 23-0086, original code: HMS1). Sequences: OP967481 (ITS), OP965340 (LSU), OR793898 (SSU), PP156567 (RPB2).

Description: *Stroma* on the rotten leaf surface, blackened zones, visible through naked eyes and the stereomicroscopes. **Sexual morph:** *Apothecia* 442–894 × 413–724 µm ($\bar{x}$ = 686 × 564 µm, n = 10) in dried condition, arising solitary, stipitate, without hairs, brown in dried condition. *Stipe* 350–478 × 160–185 µm ($\bar{x}$ = 429 × 174 µm, n = 10) in dried condition, concolorous to the receptacle. *Receptacle* discoid to applanate, brown. *Margins* concolorous to the receptacle. *Discs* brown, slightly concave, discoid. *Ectal excipulum* 25–34 µm ($\bar{x}$ = 30 µm, n = 12) in lower flanks, composed from thick-walled cells of *textura angularis* to *textura prismatic*. *Medullary excipulum* 31–49 µm ($\bar{x}$ = 39 µm, n = 15) in lower flanks, composed of hyaline to light brown, thick-walled cells of *textura porrecta* to *textura angularis*. *Hymenium* 73–81 µm ($\bar{x}$ = 76 µm, n = 10), hyaline to pale brown. *Paraphyses* 1.6–3 µm ($\bar{x}$ = 2.1 µm, n = 10) wide at the terminal cells, numerous, filiform, septate, similar with asci in length, guttulate. *Asci* 76–86 × 7.3–8.7 µm ($\bar{x}$ = 82 × 7.6 µm, n = 10), unitunicate, 8-spored, cylindric to cylindric-clavate, with rounded apex, stained light blue in MLZ (with and without KOH-pretreatment), ascal ring is not sclerotinia-type, arising from croziers. *Ascospores* 10–15 × 2.2–2.6 µm ($\bar{x}$ = 12.5 × 2.1 µm, n = 30), uniseriate to biseriate, fusoid, hyaline, smooth, 1–3 guttules, with rounded ends. **Asexual morph:** Undetermined.

Notes: In the phylogram, our specimen (MFLU 23-0086) forms a sister relationship with *L. phanensis* (MFLU 23-0091, MFLU 23-0485), *L. aurantiaca* (MFLU 23-0090), *L. takensis* (MFLU 23-0089) to the cluster of *L. chiangraiensis-sessilis-himalayensis-pyrolae* with 100 % ML bootstrap support and 1.00 BI posterior probability but do not develop phylogenetic affinities to the *L. corni-maris* clade defined as *Lambertella sensu stricto* (Figure 2.35). Morphologically, our specimen

(MFLU 23-0086) only fits some characters of *Lambertella* generic description such as having substratal stroma and filiform paraphysis, however, the ascospores are hyaline, fusoid which are distinctive from brown, ellipsoid ascospores. The *Lambertella* identity of our specimen (MFLU 23-0086) as *L. fusoides* is based on some character similarity and the phylogenetic affinity with the cluster of *L. chiangraiensis*-*sessilis-himalayensis-pyrolae* clade with 100 % ML bootstrap support and 1.00 BI posterior probability.

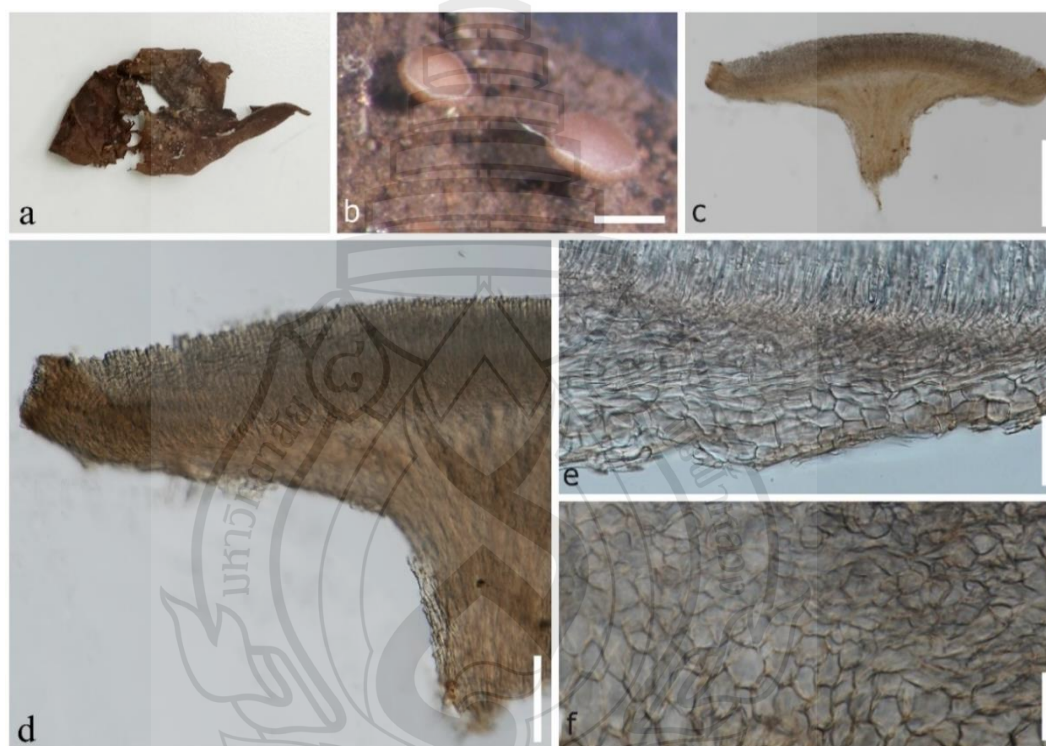


Figure 2.41 Apothecia and excipulum cells of *Lambertella fusoides* (MFLU 23-0086, holotype)

Figure 2.41, a Dead leaves. b Apothecia on the leaf midribs. c Close-up of an apothecium section. d Close-up of hymenium at the margin. e Ectal excipulum cells. f Medullary excipulum cells. Scale bars: b = 550 μm , c = 350 μm , d = 135 μm , e = 40 μm , f = 30 μm .

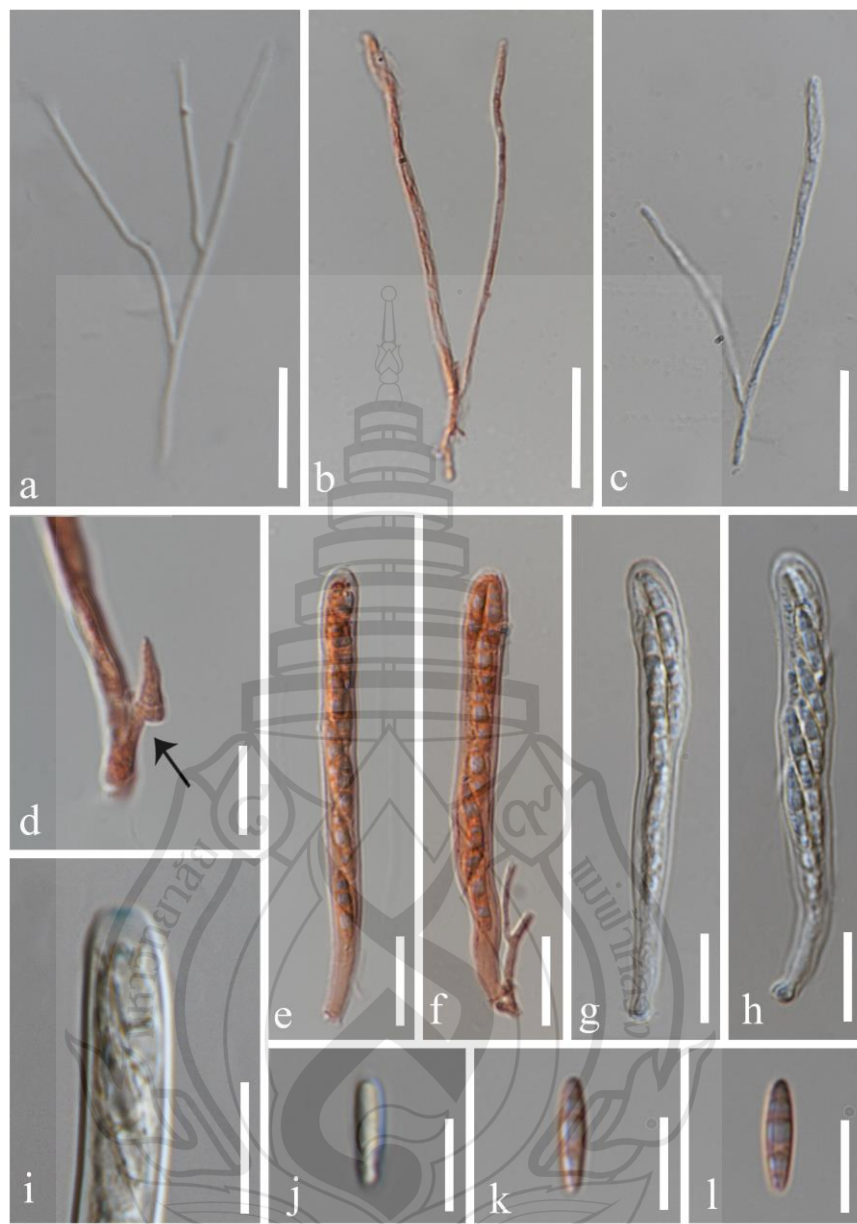


Figure 2.42 Paraphysis, asci and ascospores of *Lambertella fusoidea* (MFLU 23-0086, holotype)

Figure 2.42, a–c Filiform paraphyses. d A crozier at the base of the ascus. e–h Asci. i Tip of the ascus (mounted in MLZ reagent without KOH pretreatment). j–l Ascospores. Scale bars: a–c = 20 μm , d–h = 15 μm , i–l = 10 μm .

Lambertella fusoides (MFLU 23-0086) forms a sister relationship to the *L. phanensis* with a 91 % maximum likelihood bootstrap support. Our specimen (MFLU23-0086) is morphologically distinct from the *L. phanensis* holotype (MFLU 23-0091) with its excipulum cells, asci, and ascospores. The medullary excipulum of the specimen (MFLU 23-0086) is composed of *textura angularis-prismatica* compared to *textura prismatica-porrecta* in *L. phanensis* (MFLU 23-0091, MFLU 23-0485) (Figure 2.41, 2.46). Our specimen (MFLU 23-0086) has wider asci (7.3–8.7 μm vs. 2.7–6.1 μm) and longer ascospores (10–15 μm vs. 6.2–8.8 μm) than those of *L. phanensis* (MFLU 23-0091). Hence, based on morphology and phylogeny, *L. fusoides* (MFLU 23-0086) is introduced as a new species.

Lambertella himalayensis V.P. Tewari and D.C. Pant

Figure 2.35; 2.36; 2.43; 2.44

MycoBank number: MB 332945

FacesofFungi number: FoF 14257

Material examined: Thailand, Chiang Rai, Phan District, Sai Khao, Phra That Wang Chom Thong Monastery, 19.67835471370441, 99.74994242011047, on leaf petioles of *Tectona grandis*, 31 August 2021, Anis S. Lestari (MFLU 23-0087, original code: PTW1). Sequences: OP967476 (ITS), OP965342 (LSU), OR656473 (SSU), OR940518 (RPB2).

Typus: India, Ayarpata, near Bisht Bhawan, Nainital, on dead twigs of *Quercus leucotrichophora* and two unidentified herbaceous stems, 29 August 1965, D.C. Pant (holotype BHUPP 297; isotype BHUPP 221).

Description: *Stroma* on the surface of leaf petioles, inconspicuous on the mid rib of leaves, blackened zones, visible through the stereomicroscope and naked eyes.

Sexual morph: *Apothecia* 0.9–2.6 $\times$ 0.9–2.6 mm ($\bar{x}$ = 1.9 $\times$ 1.8 mm, n = 10) in dried condition, arising solitary, short stipitate, white to pale brown when fresh, brown in dried condition. *Stipe* 400–778 $\times$ 267–640 μm ($\bar{x}$ = 566 $\times$ 424 μm , n = 10) in dried condition. *Receptacle* cupulate to discoid, brown to grey when it is dried. *Margin* concolorous to the receptacle. *Discs* white when fresh, convex. *Hairs* absent. *Ectal excipulum* 74–138 μm ($\bar{x}$ = 101 μm , n = 10) at lower flanks, composed of pale brown to hyaline, thin-walled cells of *textura prismatica* to *textura porrecta*. *Medullary*

excipulum 95–366 μm ($\bar{x}$ = 223 μm , n = 10) in lower flanks, composed of thin-walled, hyaline cells of *textura intricata*. *Hymenium* 94–99 μm ($\bar{x}$ = 95 μm , n = 11), hyaline to pale brown. *Paraphyses* 1.9–2.8 μm wide ($\bar{x}$ = 2.3 μm , n = 12) at the terminal cell, numerous, filiform, septate, similar length with asci, branched at 1/2 and 1/3 length. *Asci* 74–82 $\times$ 6.4–8.1 μm ($\bar{x}$ = 78 $\times$ 7.4 μm , n = 11), 8-spored, unitunicate, cylindric, rounded apex, stained deep blue in MLZ (with and without KOH pretreatment), ascal ring is sclerotinia-type, arising from croziers. *Ascospores* 7.4–12 $\times$ 2.1–5.2 μm ($\bar{x}$ = 10 $\times$ 4.1 μm , n = 30), uniseriate to partially biseriate, hyaline to pale brown, fusoid to ellipsoid, smooth. **Asexual morph:** Undetermined.

Notes: Our specimen (MFLU 23-0087) fits the generic description of *Lambertella* by having substratal stroma, stipitate apothecia, *textura prismatica* ectal excipulum except pale brown ascospores. In addition, our specimen (MFLU 23-0087) is included in the *Lambertella sensu stricto* which supports its taxonomic placement in *Lambertella* (Figure 2.35).

Our *Lambertella* specimen (MFLU 23-0087) forms a sister relationship to *L. himalayensis* (CBS 230.77); the only available sequence data for *L. himalayensis* originated from the culture CBS 230.77 isolated from *Cassia siamea* in Myanmar with 99% maximum likelihood bootstrap support and 1.00 BI posterior probability (Figure 2.35). However, the culture of *L. himalayensis* (CBS 230.77) is neither the holotype nor the isotype of *L. himalayensis* (CUP-050013) described in Tewari and Pant (1967) and lacks complete morphological descriptions (Salgado-Salazar et al., 2018; Vu et al., 2019). In this study, we observed the isotype of *L. himalayensis* (CUP-050013) to confirm the presence of any characters similar to our newly introduced species, especially the sexual forms of our *Lambertella* specimens. We found that the morphology of apothecia and ascospores of *L. himalayensis* (CUP-050013) were distinct from *L. himalayensis* (MFLU 23-0087). *Lambertella himalayensis* (CUP-050013) has long stipitate apothecia (up to 2 mm) with 4–5-spored asci and brown ascospores (Tewari & Pant, 1967), while *L. himalayensis* (MFLU 23-0087) have shorter stipe apothecia (up to 0.8 mm), 8-spored asci and pale brown ascospores (mostly hyaline ascospores) (Figure 2.43–2.44; Table 2.14). However, the morphology of *L. himalayensis* (CBS 230.77) is lacking, thus, we cannot compare it to our specimen (MFLU 23-0087) despite the fact that the nucleotide base comparison of ITS, LSU,

SSU and RPB2 between our specimen and *L. himalayensis* (CBS 230.77) showed only one base pair difference on ITS (Table 2.13). Hence, we conclude that our specimen is to be conspecific to *L. himalayensis* (CBS 230.77) based on the sequence data.



Figure 2.43 Apothecia and excipulum cells of *Lambertella himalayensis* (MFLU 23-0087, new host and geographical records)

Figure 2.43, a Dead leaves. b–c Apothecium on a leaf petiole. d Close-up of an apothecium in a cross-section. e Close-up of hymenium at the margin. f Ectal excipulum cells. g Medullary excipulum cells. Scale bars: b = 850 μm , c = 640 μm , d = 480 μm , e = 50 μm , f–g = 25 μm .

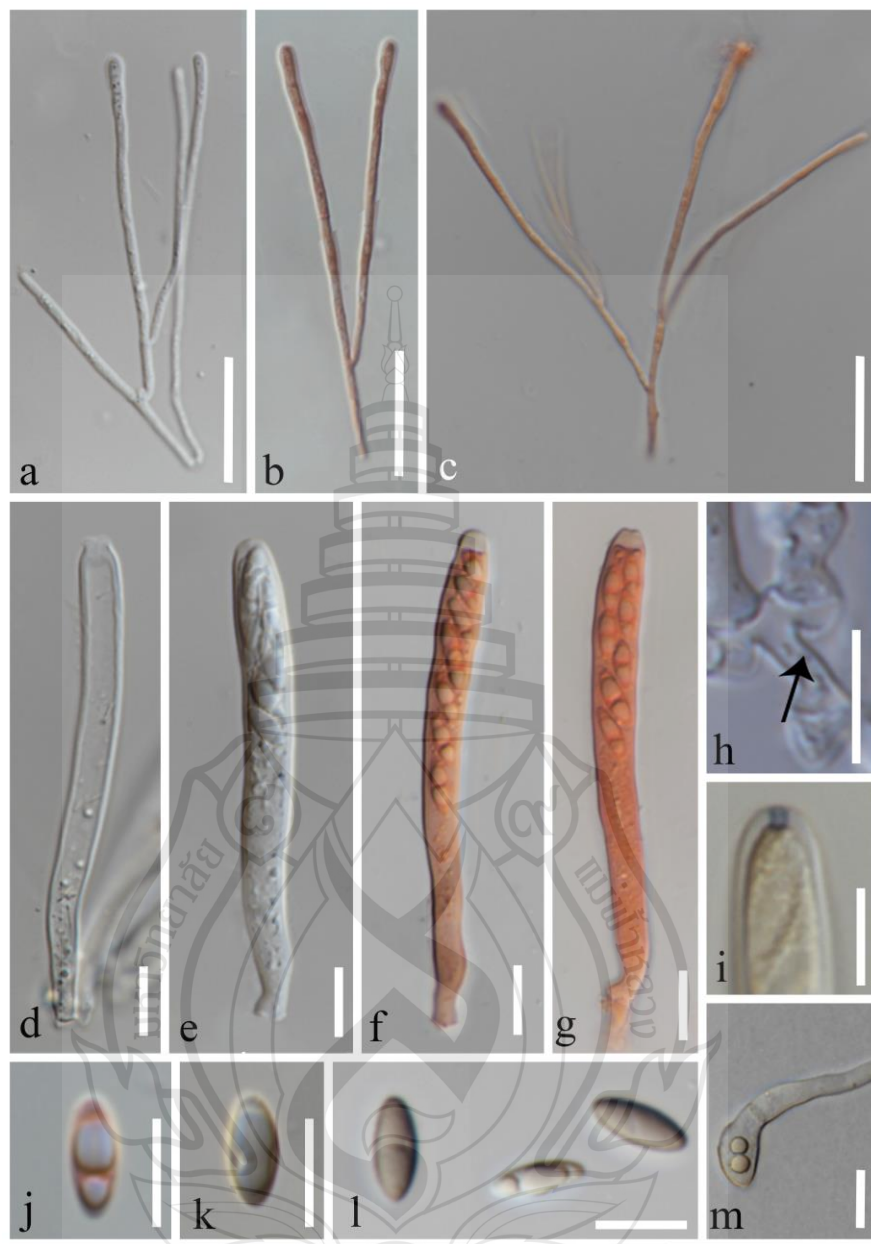


Figure 2.44 Paraphysis, asci and ascospores of *Lambertella himalayensis* (MFLU 23-0087, new host and geographical records)

Figure 2.44, a–c Filiform paraphyses. d–g Asci (f–g mounted in Congo red). h A crozier at the base of an ascus. i Tip of an ascus (mounted in MLZ reagent without KOH pretreatment). j–k Ascospores. l An immature, hyaline ascospore and pale brown ascospores. m A germinated ascospore. Scale bars: a–c = 25 μm , d–m = 10 μm .

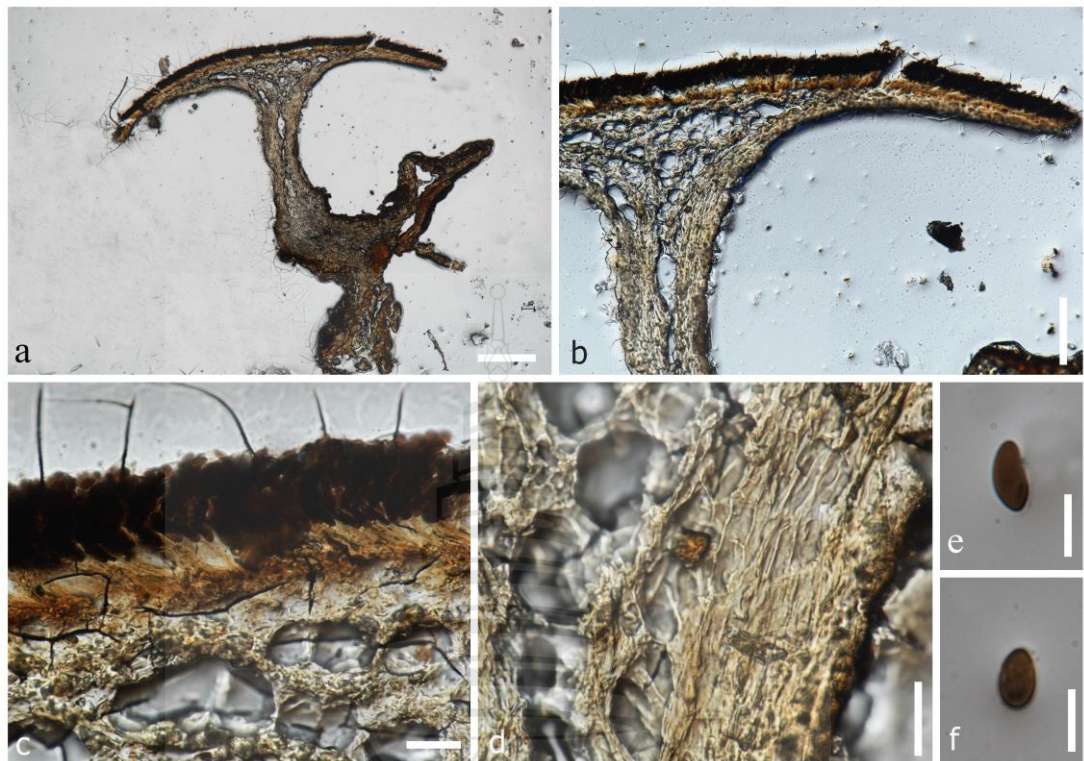


Figure 2.45 *Lambertella himalayensis* (CUP-050013, isotype)

Figure 2.45, a–b An apothecium section. c A Close-up of the hymenium. d Ectal excipular cells. e–f Ascospores. Scale bars: a = 330 μm , b = 170 μm , c–d = 35 μm , e–f = 15 μm

Lambertella phanensis Lestari and Chethana, sp. nov.

Figure 2.35; 2.36; 2.46; 2.47

MycoBank number: MB 849026

Facesoffungi number: FoF 14254

Etymology: Epithet represents the district where the specimen was found

Typus: Thailand, Chiang Rai, Phan District, Mae Ao, Ang Kep Nam Huai Tonyang Reservoir, 19.67734726710035, 99.79890061546585, on leaf petioles of an unidentified plant, 27 September 2021, Anis S. Lestari (holotype MFLU 23-0091, original code NHT2). Sequences: MFLU 23-0091 - OP967478 (ITS), OP965343 (LSU), OR656475 (SSU).

Additional material examined: Thailand, Chiang Rai province, Huai Kang Pla Forest, on flower petioles of unidentified leaves, 11 November 2020, Anis S. Lestari, HKP3 (MFLU 23-0485). Sequences: MFLU 23-0485- OR652416 (ITS), OR652444 (LSU), OR656478 (SSU).

Description: *Stroma* elliptical to irregular blackened zones, visible on the surface of leaf petioles through naked eyes and the stereomicroscope. **Sexual morph:** *Apothecia* 0.6–1.3 × 0.5–0.9 mm ($\bar{x}$ = 0.9 × 0.7 mm, n = 10) in dried condition, arising solitary, stipitate, brown in dried condition. *Stipe* 181–578 × 162–302 μ m ($\bar{x}$ = 287 × 204 μ m, n = 10) in dried condition, concolorous to the receptacle. *Receptacle* cupulate to discoid, brown. *Margin* concolorous to the receptacle. *Discs* convex to applanate. *Hairs* absent. *Ectal excipulum* 30–45 μ m ($\bar{x}$ = 38 μ m, n = 11) at lower flanks, composed of brown to hyaline cells of *textura prismatica* to *textura porrecta*. *Medullary excipulum* 19–31 μ m ($\bar{x}$ = 25 μ m, n = 12) in lower flanks, composed of thin-walled, brown cells of *textura prismatica* to *textura angularis*. *Hymenium* 75–85 μ m ($\bar{x}$ = 80 μ m, n = 15), hyaline. *Paraphyses* 1.1–1.7 μ m wide ($\bar{x}$ = 1.3 μ m, n = 10), numerous, filiform, aseptate, similar length with asci, branched at 1/3 of the length and at the base. *Asci* 59–82 × 2.7–6.1 μ m ($\bar{x}$ = 70 × 5.2 μ m, n = 10), 8-spored, unitunicate, cylindric, rounded apex, stained deep blue in MLZ (with and without KOH pretreatment), ascal ring is not sclerotinia-type, arising from croziers. *Ascospores* 6.2–8.8 × 2.5–2.1 μ m ($\bar{x}$ = 7.3 × 2.7 μ m, n = 30), uniseriate to partially biseriate, ellipsoid, 1–2 guttules, smooth or seems with 1-septate, hyaline. **Asexual morph:** Undetermined.

Notes: In the phylogram, our specimens (MFLU 23-0091, MFLU 23-0485) form a sister relationship to the cluster of *L. chiangraiensis-sessilis-himalayensis-pyrolae* with 100 % ML bootstrap support and 1.00 BI posterior probability but not develop phylogenetic affinities to the *L. corni-maris* clade defined as *Lambertella* sensu stricto (Figure 2.35). Morphologically, our specimen (MFLU 23-0086) only fits some characters of the *Lambertella* generic description such as having substratal stroma and filiform paraphysis, however, the ascospores are hyaline instead of brown, ellipsoid ascospores (Figure 2.47). The *Lambertella* identity of our specimens (MFLU 23-0091, MFLU 23-0485) as *L. phanensis* is based on some character similarity and the phylogenetic affinity with the cluster of *L. chiangraiensis-sessilis-himalayensis-pyrolae* clade with 100 % ML bootstrap support and 1.00 BI posterior probability.

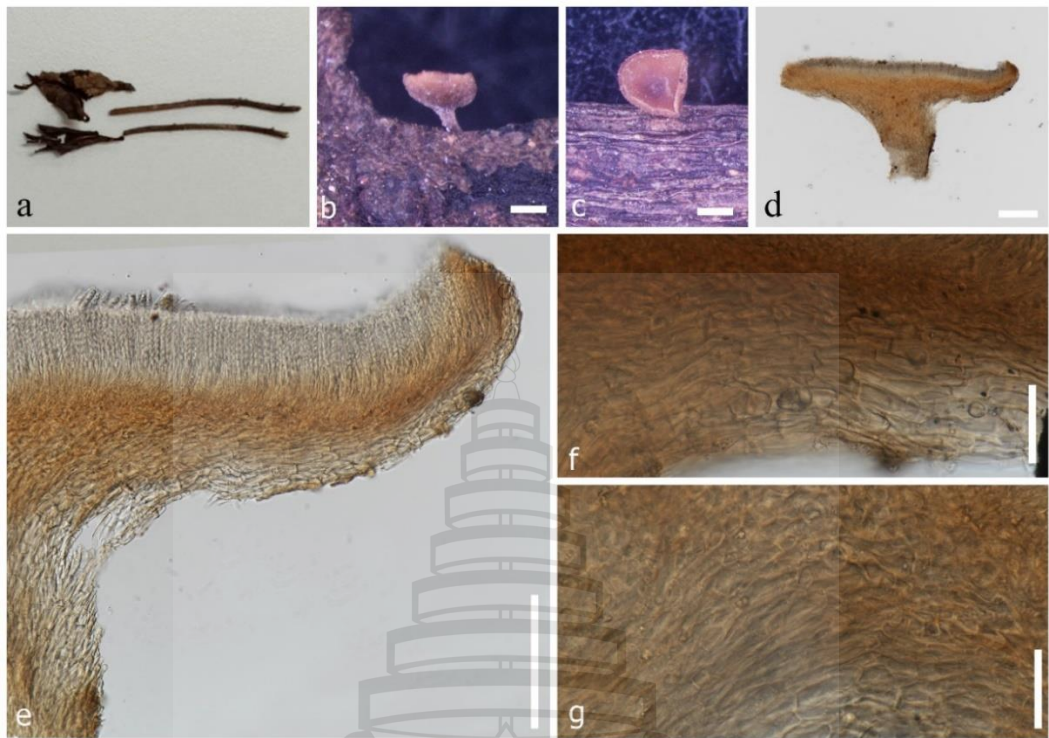


Figure 2.46 Apothecia and excipulum cells of *Lambertella phanensis* (MFLU 23-0091, holotype)

Figure 2.46, a Dead leaves. b–c Apothecia on the leaf petioles. d Close-up of an apothecium section. e Close-up of hymenium at the margin. f Ectal excipulum cells. g Medullary excipulum cells. Scale bars: b–c = 325 μm , d = 210 μm , e = 120 μm , f–g = 35 μm .

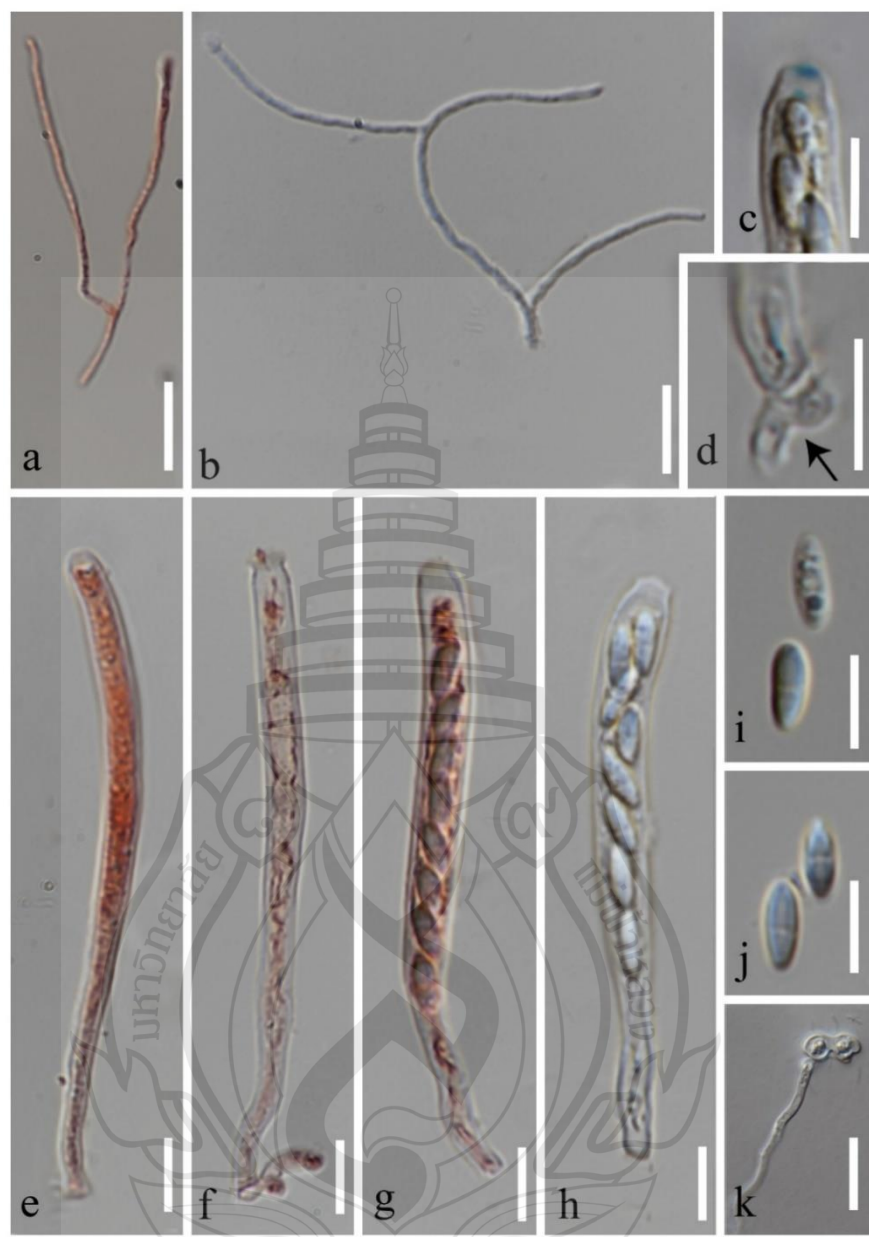


Figure 2.47 Paraphysis, asci and ascospores of *Lambertella phanensis* (MFLU 23-0091, holotype)

Figure 2.47, a–b Filiform paraphyses. c Tip of the ascus (mounted in MLZ reagent without KOH pretreatment). d A crozier at the base of the ascus. e–h Asci (e–g Mounted in Congo red). i–j Ascospores. k A germinated ascospore. Scale bars: a–k = 10 µm.

Lambertella sessilis Lestari and Chethana, sp. nov.

Figure 2.35; 2.36; 2.48; 2.49

MycoBank number: MB 849027

Facesoffungi number: FoF 14255

Etymology: The epithet represents the sessile apothecia of this species.

Material examined: Thailand, Chiang Rai province, Omkoi district, Sop Khong, 17.639554620869404, 98.24246141202575, on the barks of an unidentified dead plant, 16 October 2019, Anis S. Lestari (holotype MFLU 23-0092, original code OMK2). Sequences: OQ650294 (ITS), OQ650293 (LSU), OR656472 (SSU), PP156570 (RPB2); Thailand, Tak province, Omkoi district, Sop Khong, 17.639554620869404, 98.24246141202575, on the barks of an unidentified dead plant, 16 October 2019, Anis S. Lestari, OMK2b (MFLU 23-0487). Sequences: OR855987 (ITS).

Description: *Stroma* irregular blackened zones, visible on the surface of the bark of an unidentified dead plant, through naked eyes and the stereomicroscope. **Sexual morph:** *Apothecia* 311–848 × 303–708 µm ($\bar{x}$ = 590 × 530 µm, n = 5) in dried condition, arising solitary, sessile to subsessile, greyish brown when fresh, brown in dried condition. *Receptacle* cupulate to discoid, exterior brown when dried. *Margin* concolorous to the receptacle. *Discs* brown, convex. *Hairs* absent. *Ectal excipulum* 55–62 µm ($\bar{x}$ = 60 µm, n = 10), thick at lower flanks, composed of brown to hyaline cells of *textura angularis* to *textura prismatica*. *Medullary excipulum* 62–171 µm ($\bar{x}$ = 116 µm, n = 10) thick at lower flanks, composed of thin-walled, brown cells of *textura epidermoidea*. *Hymenium* 89–97 µm ($\bar{x}$ = 92 µm, n = 10), grey, pale brown to brown. *Paraphyses* 1.7–2.5 µm wide ($\bar{x}$ = 2.6 µm, n = 12) at the terminal cells, numerous, filiform, septate, similar length with asci, branched at 1/2 length and at the base. *Asci* 74–88 × 6.9–10.2 µm ($\bar{x}$ = 82 × 8.4 µm, n = 10), 8-spored, unitunicate, cylindric to cylindric-clavate, with rounded apex, stained light blue in MLZ (with and without KOH pretreatment), ascus ring is not sclerotinia-type, arising from croziers. *Ascospores* 7.6–10 × 2.8–4.9 µm ($\bar{x}$ = 8.7 × 4.1 µm, n = 30), uniseriate to partially biseriate, hyaline when immature, becoming yellowish brown to dark brown at maturity ellipsoid, 1–2-guttulate. **Asexual morph:** Undetermined.

Notes: Our specimens (MFLU 23-0092, MFLU 23-0487) fit the generic description of *Lambertella* by having substratal stroma, *textura prismatica* ectal excipulum, cylindric asci, brown ellipsoid ascospores except sessile to substipitate apothecia. In addition, our specimens (MFLU 23-0092, MFLU 23-0487) are included in the *Lambertella sensu stricto* which supports its taxonomic placement in *Lambertella* (Figure 2.35).

Lambertella sessilis (MFLU 23-0092, MFLU 23-0487) forms a sister relationship with *L. chiangraiensis* isolates (MFLU 23-0088, MFLU 23-0488) and *L. himalayensis* (CBS 230.77, MFLU 23-0087) with 99% maximum likelihood bootstrap support (Figure 2.35). Morphologically, the new species, *Lambertella sessilis* (MFLU 23-0092, MFLU 23-0487), differs from *L. chiangraiensis* by sessile to subsessile apothecia, medullary excipulum comprising *textura epidermoidea*, and shorter 74–88 µm cylindric-clavate asci, while *L. chiangraiensis* has apothecia with stipes, medullary excipulum comprising *textura intricata*, and longer 81–95 µm cylindric asci. *Lambertella sessilis* forms ellipsoid, dark ascospores from hyaline, immature ascospores in contrast to *L. chiangraiensis* (MFLU 23-0088) and *L. himalayensis* (MFLU 23-0088). However, the formation of ellipsoid, dark ascospores from hyaline, immature ascospores is also observed in the isotype of *L. himalayensis* (CUP-050013), which is incomparable to *L. himalayensis* (CBS 230.77) due to data inaccessibility. Additionally, base pair comparison of *L. sessilis* (MFLU 23-009) to *L. chiangraiensis* (MFLU 23-0088), *L. himalayensis* (MFLU 23-0088) and *L. himalayensis* (CBS 230.77) show differences in the ITS, LSU, SSU and RPB2 sequences (Table 2.13). Hence, based on morphology and phylogeny, *L. sessilis* (MFLU 23-0092) is introduced as a new species.

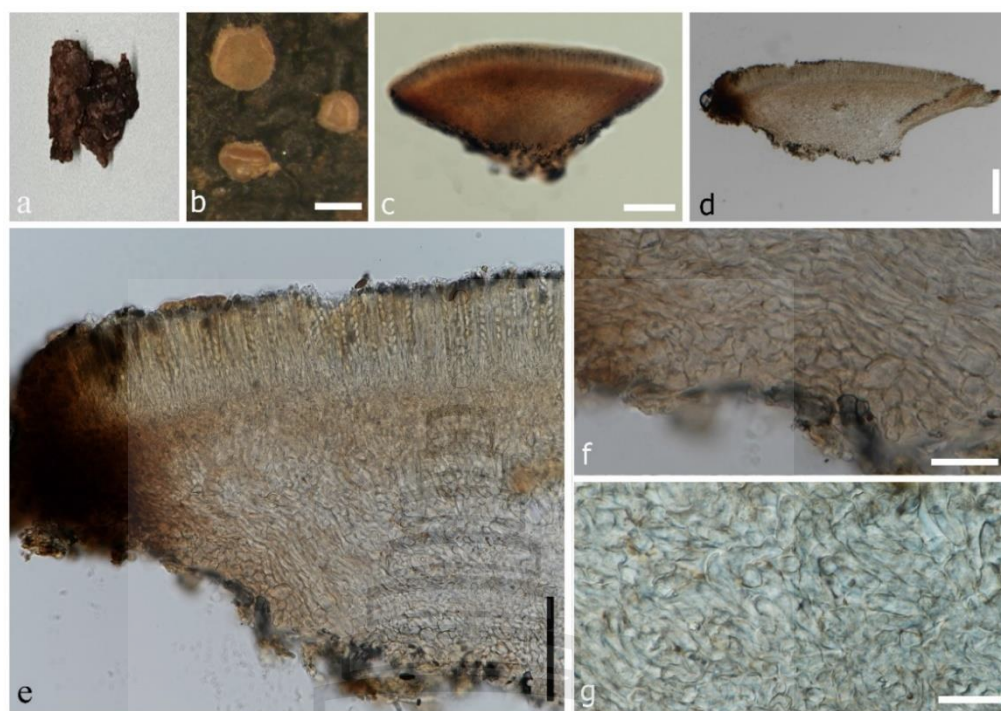


Figure 2.48 Apothecia and excipulum cells of *L. sessilis* (MFLU 23-0092, holotype)

Figure 2.48, a A bark piece of an unidentified dead plant. b Apothecia on the natural substrate. c–d Close-up of an apothecium in a median section. e Close-up of hymenium at the margin. f Ectal excipulum cells. g Medullary excipulum cells. Scale bars: b = 500 μm , c = 180 μm , d = 130 μm , e = 90 μm , f = 40 μm , g = 25 μm .



Figure 2.49 Paraphysis, asci and ascospores of *Lambertella sessilis* (MFLU 23-0092, holotype)

Figure 2.49, a–d Filiform paraphyses. e–h Asci. i Tip of the ascus (mounted in MLZ reagent without KOH pretreatment). j A crozier at the ascus base. k–m Ascospores. Scale bars: a–d = 20 μ m, e–m = 10 μ m.

Lambertella takensis Lestari and K.D. Hyde, sp. nov.

Figure 2.35; 2.36; 2.50; 2.51

MycoBank number: MB 849028

Facesoffungi number: FoF 14256

Etymology: Epithet represents the province where the holotype was found.

Typus: Thailand, Tak province, Tha Song Yang district, Mae Wa Luang, 17.712253372145504, 97.99567621471674, on leaf petioles of *Tectona grandis*, 17 October 2019, Anis S. Lestari (holotype MFLU 23-0089, TAK1). Sequence: OP967480 (ITS), OP965339 (LSU), OR656476 (SSU), PP156568 (RPB2).

Additional material examined: Thailand, Chiang Rai province, Huai Kang Pla Forest, on flower petioles of unidentified leaves, 11 November 2020, HKP2 (MFLU 23-0486). Sequences: OR855988 (ITS).

Description: *Stroma* irregular blackened zones, visible on the surface of leaf petioles through naked eyes and the stereomicroscope. **Sexual morph:** *Apothecia* 0.7–2.6 × 0.5–2.5 mm ($\bar{x}$ = 1.7 × 0.3 mm, n = 10) in dried condition, solitary, brown, stipitate, without hairs. *Stipe* 0.3–1.4 × 0.2–0.5 mm ($\bar{x}$ = 0.6 × 0.3 mm, n = 10) in dried condition, brown. *Receptacle* cupulate to discoid. *Margin* concolorous to the receptacle. *Discs* creamy to light brown, convex. *Ectal excipulum* 31–46 µm ($\bar{x}$ = 40 µm, n = 15) at lower flanks, composed from thin-walled, hyaline to light brown cells of *textura prismatica*. *Medullary excipulum* 44–58 µm ($\bar{x}$ = 49 µm, n = 10) in lower flanks, composed of thin-walled, hyaline cells of *textura intricata*. *Hymenium* 61–79 µm ($\bar{x}$ = 65 µm, n = 15), hyaline to brown. *Paraphyses* 2.6–2.3 µm wide ($\bar{x}$ = 2.9 µm, n = 10), numerous, filiform, septate, similar length with asci, some branched at 1/3 of the length from the base. *Asci* 56–71 × 5–6 µm ($\bar{x}$ = 65 × 5.6 µm, n = 10), 8-spored, unitunicate, cylindric, rounded apex, stained light blue in MLZ (with and without KOH pretreatment), ascus ring is not sclerotinia-type, arising from croziers. *Ascospores* 6.2–8.4 × 2.4–4 µm ($\bar{x}$ = 7 × 2.7 µm, n = 30), uniseriate, hyaline when immature, becoming yellowish brown to dark brown at maturity, ellipsoid, with 2–3 guttules. **Asexual morph:** Undetermined.

Notes: The characters of the newly found specimens (MFLU 23-0089, MFLU 23-00486) fit the descriptions of those *Lambertella sensu stricto* previously established by Zhao et al. (2016), however, phylogenetically, the *Lambertella*-clade containing *L.*

takensis (MFLU 23-0089) do not directly related with the *L. corni-maris* clade which serve as the type species of *Lambertella* sensu stricto clade (Figure 2.35). The branch of *Lambertella*-clade containing *L. takensis* (MFLU 23-0089) forms a sister relationship to the clade of *L. chiangraiensis*, *L. sessilis*, *L. himalayensis*, *L. pyrolae* with 100 ML bootstrap support and 1.00 BI posterior probability (Figure 2.35). Hence, *L. takensis* (MFLU 23-0089) is excluded from *Lambertella* sensu stricto but still placed in the genus *Lambertella* based on the morphology comparison.

In the phylogram of the combined dataset, our new specimens of *Lambertella* (MFLU 23-0089, MFLU 23-0486) form a cluster separated from *L. aurantiaca* (MFLU 23-0089) with 100% ML bootstrap support and 1.00 BI posterior probability (Figure 2.35). *Lambertella takensis* (MFLU 23-0089, MFLU 23-0486) has a creamy to light brown receptacle that differs from the deep cadmium yellow colour of *L. aurantiaca* (MFLU 23-0090). The length of the *L. takensis* apothecial stipe (1.4 mm) is also smaller than that of *L. takensis* (up to 5 mm) (Table 2.14). Another distinct character was revealed via a chemical test using 2% KOH on the receptacle, as described by Tewari and Pant (1967), to differentiate *L. aurantiaca* from other *Lambertella* species. The receptacle of *L. takensis* (MFLU 23-0089) tested negative (no color change), whereas *L. aurantiaca* (MFLU 23-0090) showed a color change to purple (Figure 2.28a). Additionally, the nucleotide base differences in Table 2.13 (No.1) shows that *L. aurantiaca* (MFLU 23-0090) and *L. takensis* (MFLU 23-0089) are likely different species since there are nucleotide base differences on ITS, LSU, SSU and RPB2 with 5, 4, 2 and 69 bp different, respectively.

In the case of morphology, *L. takensis* is similar at a glance to the isotype of *L. himalayensis* (CUP-050013); however, it is distinct in the number of ascospores inside the asci, the size of asci and ascospores (Tewari & Pant, 1967). *Lambertella takensis* (MFLU 23-0089) is characterized by 8-spored asci whereas *L. himalayensis* (CUP-050013) has 4–5-spored asci (Table 2.14). In addition, *Lambertella takensis* (MFLU 23-0089) are characterized by smaller asci ($56\text{--}71 \times 5\text{--}6 \mu\text{m}$ vs. $87\text{--}102 \times 6.5\text{--}18 \mu\text{m}$ on *L. himalayensis*) and smaller ascospores ($6.2\text{--}8.4 \times 2.4\text{--}4 \mu\text{m}$ vs. $9.6\text{--}14.5 \times 4.5\text{--}6.5 \mu\text{m}$ on *L. himalayensis*). Hence, we introduce *Lambertella takensis* (MFLU 23-0089), even though there are no doubts that *L. takensis* (MFLU 23-0089) has been

presumably described in previous studies (Dumont, 1971; Whetzel, 1943) under different species.

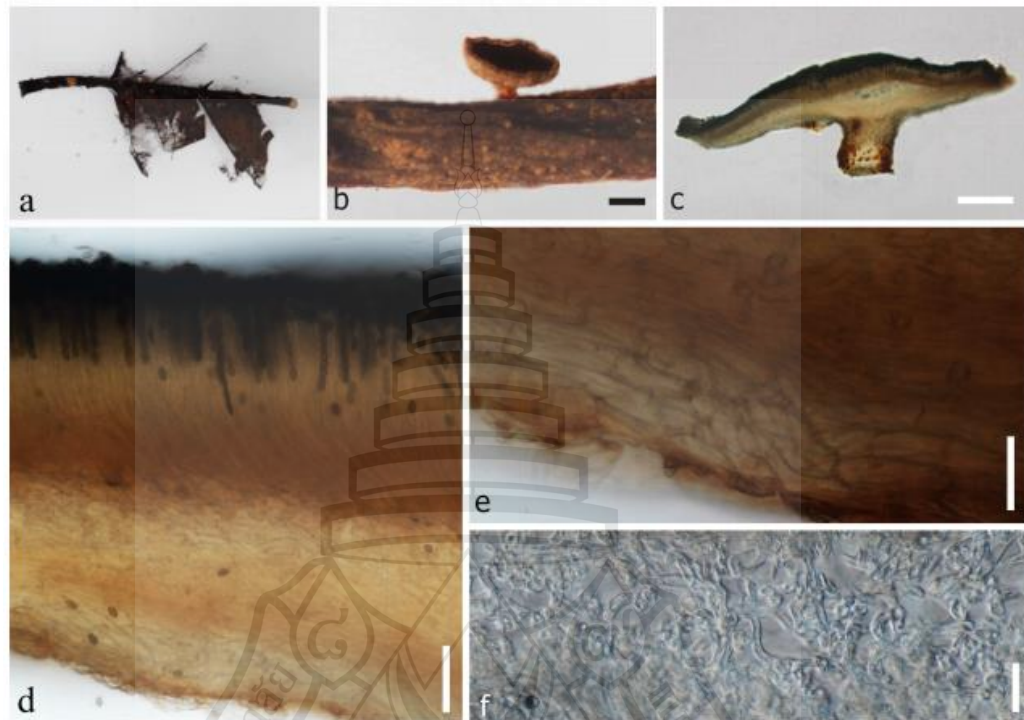


Figure 2.50 Apothecia and excipulum cells of *Lambertella takensis* (MFLU 23-0089, holotype)

Figure 2.50, a A dead leaf. b Apothecium on the leaf petiole. c Close-up of an apothecium cross-section. d Close-up of the hymenium at the margin. e Ectal excipulum cells. f Medullary excipulum cells. Scale bars: b = 450 μm , c = 250 μm , d = 45 μm , e–f = 25 μm .

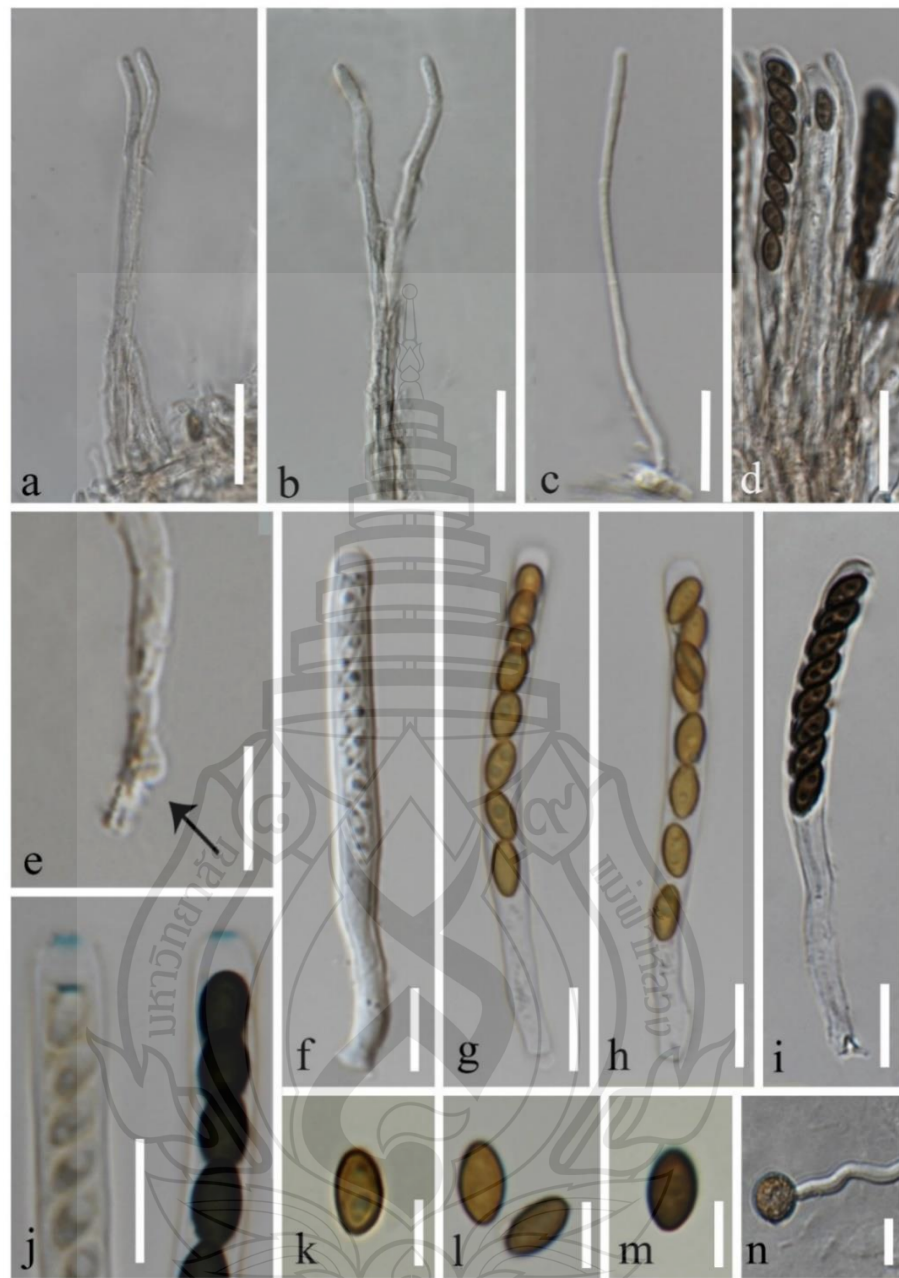


Figure 2.51 Paraphysis, asci and ascospores of *Lambertella takensis* (MFLU 23-0089, holotype)

Figure 2.51, a–c Filiform paraphyses. d Asci with paraphyses. e Crozier at the ascus base (arrow pointed). f–i Asci. j Tip of an ascus (mounted in MLZ reagent without KOH pretreatment). k–m Ascospores. n A germinated ascospore. Scale bars: a–d = 20 μm , e–j = 10 μm , k–n = 5 μm .

Table 2.13 Nucleotide differences of ITS, LSU, SSU and RPB2 sequences of some newly collected *Lambertella* species

No	Species	ITS (bp)	LSU (bp)	SSU (bp)	RPB2 (bp)
1.	<i>L. aurantiaca</i> (MFLU 23-0090) vs. <i>L. takensis</i> (MFLU 23-0089)	5/480	4/848	2/654	69/639
2.	<i>L. chiangraiensis</i> (MFLU 23-0088) vs. <i>L. himalayensis</i> (CBS 230.77)	8/483	0/848	0/538	5/609
3.	<i>L. chiangraiensis</i> (MFLU 23-0088) vs. <i>L. himalayensis</i> (MFLU 23-0087)	7/483	0/848	1/652	8/639
4.	<i>L. chiangraiensis</i> (MFLU 23-0088) vs. <i>L. sessilis</i> (MFLU 23-0092)	4/483	2/848	1/652	4/639
5.	<i>L. himalayensis</i> (CBS 230.77) vs. <i>L. himalayensis</i> (MFLU 23-0087)	1/483	0/848	0/538	0/609
6.	<i>L. sessilis</i> (MFLU 23-0092) vs. <i>L. himalayensis</i> (MFLU 23-0087)	4/483	2/848	0/653	6/639
7.	<i>L. sessilis</i> (MFLU 23-0092) vs. <i>L. himalayensis</i> (CBS 230.77)	5/483	2/848	2/537	6/609

Table 2.14 Synopsis of *Lambertella* species (Rutstroemiaceae) with sequence data

Species	Origin	Apothecia	Paraphyses	Ectal excipulum	Medullary excipulum	Size (µm) and ascal characters	Size (µm) and ascospore characters	References
<i>Lambertella aurantiaca</i>	Thailand	Up to 0.45 cm diam., 1.7 cm high in dried condition, orange (cadmium yellow), stipitate	Filiform with 2-3 branches, septate	<i>Textura prismatica</i> to <i>porrecta</i>	<i>Textura intricata</i>	66–81 × 4.1–7.3 µm, cylindric, rounded apex, J+ (*), ascal ring is not Sclerotinia-type, arising from croziers, 8 spored	6.6–9.5 × 2.7–4.6 µm, ellipsoid, hyaline to brown at maturity, guttulate, uniseriate	Tewari and Pant (1967); this study
<i>Lambertella Chiangraiensis</i> sp. nov.	Thailand	0.4–2.6 mm in diam., 0.3–0.5 high, brown, stipitate	Filiform aseptate, branched near the base	<i>Textura prismatica</i> to <i>porrecta</i>	<i>Textura intricata</i>	41–88 × 5.6–8.8 µm, cylindric, rounded apex, J+ (*), ascal ring is Sclerotinia-type, arising from croziers, 8-spored.	7–11 × 2.8–4.9 µm, ellipsoid, hyaline, uniseriate to partially biseriate	This study
<i>Lambertella corni-marisi</i>	Australia, Austria, Europe, Japan	1.5–7.5 mm diam., up 0.5–20 mm high, pale pink to flesh colored, stipitate	Filiform, septate, branched	<i>Textura prismatica</i>	Interwoven thin-walled, septate hyphae	70–108 × 5.5–8 µm, cylindric, rounded apex, J+, ascal ring is Sclerotinia-type, arising from croziers, 8 spored	6–10 × 2.5–5 µm, fusoid to ellipsoid, hyaline to brown at maturity, biguttulate, uniseriate	Harrison and El-Helaly (1935); Spooner (1987); Palmer et al. (1994); Zhao et al. (2016)

Table 2.14 (continued)

Species	Origin	Apothecia	Paraphyses	Ectal excipulum	Medullary excipulum	Size (µm) and ascal characters	Size (µm) and ascospore characters	References
<i>Lambertella fusoides</i> sp. nov.	Thailand	413–894 µm, 160–478 µm high, brown, stipitate	Filiform, septate, branched near the base	<i>Textura angularis</i> to <i>prismatica</i>	<i>Textura porrecta</i> to <i>angularis</i>	76–86 × 7.3–8.7 µm cylindric to cylindric-clavate, rounded apex, J+ (*), ascal ring is not Sclerotinia-type, arising from croziers, 8-spored.	10–15 × 2.2–2.6 µm, fusoid, hyaline with rounded ends, guttulate, uniseriate to biseriate.	This study
<i>Lambertella hircorae</i>	USA	N/A	N/A	<i>Textura porrecta</i> to <i>intricata</i>	N/A	cylindric-clavate	Fusoid, hyaline to brown at maturity, guttulate,	Zhao et al. (2016); Mycoportal (2023)
<i>Lambertella himalayensis</i>	India, Myanmar	2–3 mm diam., up to 2 mm high, stipitate.	Filiform, septate	<i>Textura porrecta</i>	<i>Textura intricata</i>	86.5–102 × 6.5–18 µm, cylindric, rounded apex, J+, 4-5 spored	9.6–14.5 × 4.5–6.5 µm, ellipsoid, hyaline to brown at maturity, guttulate, uniseriate	Tewari and Pant (1967); Salgado-Salazar et al. (2018)
<i>Lambertella langei</i>	Norway	0.5–2.5 mm diam., 1–2.2 mm high, stipitate	Filiform, branched, septate	<i>Textura prismatica</i>	<i>Textura intricata</i>	130–180 × 11.5–15.5 µm, cylindric, rounded apex, J+ (with KOH 5% treatment), 8 spored	14.5–21 × 5.6–8 µm, fusoid to ellipsoid, pigmented at maturity, guttulate uniseriate to partly biseriate	Schumacher and Holøs (1989)

Table 2.14 (continued)

Species	Origin	Apothecia	Paraphyses	Ectal excipulum	Medullary excipulum	Size (µm) and ascal characters	Size (µm) and ascospore characters	References
<i>Lambertella palmeri</i>	Mexico	Up to 1 mm diam, 1.5 mm high, stipitate	Cylindric	<i>Textura prismatica</i> to <i>porrecta</i>	<i>Textura intricata</i>	115–140 × 12–18 µm, cylindric to cylindric-clavate, truncate apex, J-, arising from simple septa, 8 spored	28–38 × 10–12 µm, fusoid-ellipsoid in dorsal view, ventricose in lateral view, hyaline to brown at maturity, guttulate, biseriate	Galán et al. (1994)
<i>Lambertella phaniensis</i> sp. nov.	Thailand	0.6–0.9 mm diam., 0.1–0.5 mm high, stipitate	Filiform, aseptate, branched near the base	<i>Textura prismatica</i> to <i>porrecta</i>	<i>Textura prismatica</i> to <i>angularis</i>	59–82 × 2.7–6.1 µm, cylindric, rounded apex, J+ (*), ascal ring is not Sclerotinia-type, arising from croziers, 8-spored.	6.2–8.8 × 2.5–2.1 µm, fusoid, hyaline, guttulate, uniseriate to partially biseriate.	This study
<i>Lambertella pruni</i>	USA	N/A	N/A	N/A	N/A	cylindric, J+, arising from croziers, 8-spored	13–19 × 7–10 µm, almond-shaped, hyaline to brown at maturity	Dumont (1976)
<i>Lambertella pyrolae</i>	Japan	0.5–1.6 mm diam., 1.5–2 mm high, stipitate	Filiform, branched near the base	<i>Textura prismatica</i> adorned with hairs	<i>Textura intricata</i>	81–145 × 6–9.5 µm, clavate, rounded apex, J-, arising from simple septa, 8 spored	14–22 × 3–4.5 µm, fusoid to ellipsoid, hyaline to brown at maturity, guttulate, uniseriate to biseriate	Zhao et al. (2013)

Table 2.14 (continued)

Species	Origin	Apothecia	Paraphyses	Ectal excipulum	Medullary excipulum	Size (µm) and ascal characters	Size (µm) and ascospore characters	References
<i>Lambertella sessilis</i> sp. nov.	Thailand	0.3–0.8 mm diam., 0.2–0.5 mm high, sessile	Filiform, branched at the 1/2 length, sometimes at the base	<i>Textura angularis</i> to <i>prismatica</i>	<i>Textura epidermoidea</i>	74–88 × 6.9–10.2 µm, cylindric-clavate, rounded apex, J+ (*), ascal ring is Sclerotinia-type, arising from croziers, 8- spored	7.6–10 × 2.8–4.9 µm, ellipsoid, hyaline to brown at maturity, guttulate, uniseriate to partially biseriate	This study
<i>Lambertella subrenispora</i>	Japan, India	Up to 2 mm diam., 1–1.5 mm high, substipitate or short stipe, adorned with hairs	Filiform	<i>Textura prismatica</i>	<i>Textura intricata</i>	80–95 × 8–9.5 µm, cylindric to cylindric-clavate, J+ (with KOH 10% pretreatment)	11–13 × 4.8–6.4 µm, sub-reniform, hyaline to brown at maturity, guttulate, uniseriate to biseriate	Korf and Zhuang (1985)
<i>Lambertella takensis</i> sp. nov.	Thailand	0.7–2.6 mm diam., 0.2–1.4 mm high, light brown to brown, stipitate	Filiform, septate, branched near the base	<i>Textura prismatica</i>	<i>Textura intricata</i>	56–71 × 5–6 µm, cylindric, rounded apex, J+ (*), ascal ring is not Sclerotinia-type, arising from croziers, 8- spored	6.2–8.4 × 2.4–4 µm, ellipsoid, hyaline to dark brown at maturity, guttulate, uniseriate.	This study

Note (*) euamyloid indicated by deep blue with and without KOH pretreatment

2.3.7 Lahmiaceae, Lahmiales

Family: Lahmiaceae O.E. Erikss

Genus: *Lahmia* Körb.

Lahmia, introduced by Koerber (1865), accommodated six species (Rehm 1900), among which four were transferred to other genera (Fries, 1861; Ciferri & Tomaselli, 1953; Timdal, 1991), leaving only *Lahmia kunzei* and *L. waghornii* (Species Fungorum, 2023). *Lahmia* is mainly distributed on the bark of *Populus* trees in northern Europe and North America and is often associated with *Rhytidiella baranyanyi* (Rehm, 1900; Funk, 1976; Eriksson, 1986; Quandt & Haelewater, 2021).

Koerber (1865) initially observed and documented *Lahmia kunzei* and *L. fueistingii*, but the latter was reassigned to *Arthrorhaphis grisea* (Fries, 1961; Species Fungorum, 2023). Later, Nannfeldt (1932) treated *Lahmia* as a lichenized species in Lecanorales, for which Rehm (1890) opposed as the species gave negative results in the iodine test. Koerber (1986) once included *Lahmia* in discolichenes, but the excipular cells of Caliciales published by Tibell (1984) do not fit with *Lahmia*'s asci and ascospores. Saccardo listed *Lahmia piceae*, which was then synonymized with *Lahmiomyces piceae* (Ciferri & Tomaselli, 1953). *Lahmia plumbina* was listed in Keissler (1930) but then transferred to *Toninia plumbina* (Timdall, 1991). Rehm (1900) introduced *Lahmia waghornii*, which is still accepted to this date, along with *Lahmia kunzei* (Species Fungorum, 2023).

Lahmia was known as *Parkerella* when Funk (1976) found it as a secondary colonizer along with *Rhytidiella baranyanyi*, the fungus causing the cork bark disease on *Populus tremuloides*. Funk (1976) included *Parkerella populi* in Conophorales (Sordariomycetes) due to its similarity to *Thaxteria* by having turbinate ascomata, long-stalked asci and 3-septate ascospores. However, Eriksson (1986) pointed out the difference in ascomatal tissues. *Parkerella* was characterized by scleroplectenchymous cells, while *Thaxteria* has pseudoparenchymatous cells; hence, *Parkerella* was believed to be conspecific with *Lahmia kunzei*. Subsequently, Eriksson (1986) established Lahmiales and Lahmiaceae to accommodate *Lahmia* with *Lahmia kunzei* as the type species.

***Lahmia kunzei* Körb.**

Figure 2.52

MycoBank number: MB 387185

Description: Sexual morph: *Ascomata* up to $300 \times 250 \mu\text{m}$, uniloculate, scattered or sometimes in a group consisting of 2–3 ascoma, erumpent, turbinate, black, swell in the water, with stipe up to $300 \mu\text{m}$ high. *Excipulum* composed of *textura intricata* to *epidermoidea*. *Hamathecium* comprises filiform paraphysoids between and above the asci, with the uppermost part consisting of paraphyses-like structures with slightly swollen apices. *Paraphysoids* swollen at the tips. *Asci* $85\text{--}110 \times 10\text{--}14 \mu\text{m}$, 8-spored, bitunicate, clavate, amyloid. *Ascospores* $18\text{--}37 \times 4\text{--}5 \mu\text{m}$, crescent-shaped, 1–4 septate, contorted, hyaline (Figure 2.49). **Asexual morph:** Short phialides bearing falcate conidia.

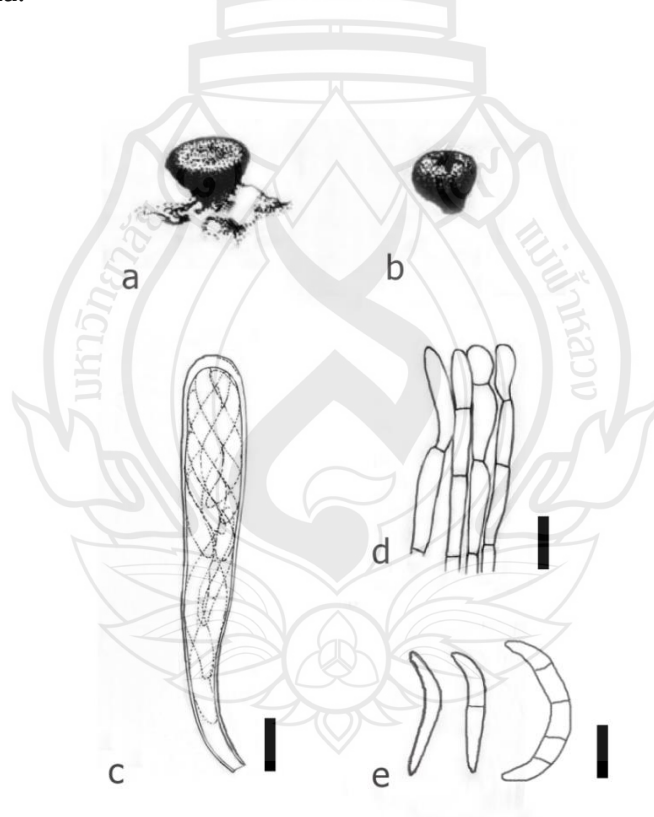


Figure 2.52 Morphology of *Lahmia kunzei*

Figure 2.52, a, b Ascomata. c An ascus. d Tips of paraphysis-like. e Ascospores. Scale bars: a, b = $35 \mu\text{m}$, c–e = $10 \mu\text{m}$ (Redrawn from Eriksson, 1986).

Lahmia is previously described as a lichenized species due to the presence of ascomata on tissue-like structures similar to those of Lecanorales (Nannfeldt, 1932) and apical structures similar to Odontotremataceae (Raitviir & Spooner, 1994). Some mycologists suggested that *Lahmia* should belong to Dothideomycetes based on its rubbery ascomata and bitunicate asci (Raitviir & Spooner, 1994). Later, Baral (2016) treated this taxon in Leotiomycetes, citing the similarities of its ascomatal morphology with Rhytismatales, even though *Lahmia* is distinct by having bitunicate asci and lacking clypeate stroma.

Lahmia kunzei have been reported in association with *Populus* barks (Eriksson, 1986), along with *Rhytidiella baranyanyi*, the fungal pathogen causing cork-bark disease on *Populus* (Funk & Zalasky, 1975; Funk, 1976). However, the role and the impact of *Lahmia kunzia*, aka *Parkerella populi*, was not known ecologically and economically until this date. The secondary metabolite diversity of *Lahmia* species has been overlooked; hence, there is no data regarding what chemical substances these taxa synthesize.

Since all reference studies and specimens of *Lahmia* were outdated, they have been overlooked regarding their morphology, phylogeny and chemical diversity. The lack of molecular data for *Lahmia* species leads to uncertain delineation and phylogeny (Quandt & Haelewaters, 2021). New collections and investigations on *Lahmia* species are required for better taxonomic and phylogenetic resolution as well as future conservation.

2.3.8 Micraspidaceae, Micraspidales

Family: Micraspidaceae Quijada & Tanney

Genus: Micraspis Darker

Studies on *Micraspis* began when Darker (1963) found a foliar disease caused by a fungus in Ontario, Canada. The disease symptoms were similar to those caused by *Phacidium* (*Lophophacidium hyperboreum*) except for the color of affected needles, which differs from the usual. Darker then described the specimen as a novel species, *Micraspis acicola*, based on both asexual and sexual morphs found on the needle leaves (Darker, 1963). *Micraspis acicola* was placed in Phacidiaceae, citing its similarities with *Phacidium*'s apothecia, except for the absence of irregular teeth and amyloid asci.

Darker (1963), then assigned *Micraspis* in the family ‘‘Cryptomyceten’’ sensu von Höhnelt, Phacidiales (Höhnelt, 1917).

Micraspis acicola Darker

Figure 2.53

Mycobank number: MB 334138

Micraspis tetraspora Graddon

Figure 2.54

Mycobank number: MB 106265

Description: Sexual morph: *Apothecia* arising singly or in small cluster, orbicular to irregularly elongate, elliptical, subcuticular or erumpent, developing inside the superficial layers of the host tissues, opening by longitudinal slits when mature forming rectangular lids. *Ectal excipulum* 20–120 µm thick, thicker at the upper flank and thinner near the margin or in the lower flanks, comprises cells of *textura epidermoidea* to *textura globosa–angularis* at the margin and flanks. *Medullary excipulum* mostly restricted beneath the hymenium, 20–100 µm thick, composed of a loose network of narrow hyphae (plectenchymatous tissue), brownish to hyaline *textura globosa* to *textura angularis*. *Paraphyses* cylindrical with uninflated to slightly medium clavate, straight or slightly sinuous, no more than 5-septate, simple or branched at the below of the apical cell. *Asci* cylindric-clavate, 4–8-spored, inamyloid, arising from croziers. *Ascospores* bi- or triseriate, cylindrical fusoid to clavate-ellipsoid, hyaline, rounded to obtuse at both ends, sometimes with one end extremely wider than the other, straight or slightly curved, with 1–3(–5) transverse septa at maturity, smooth or with tiny sparse guttules, germinating at both ends (Figures 2.53 and 2.54). **Asexual morph:** *Pycnidia* immersed, subcuticular to partly subepidermal, unilocular to multilocular or convoluted, scattered, dark brown to black, shining, outline elliptical to circular or irregular, raised to pulvinate, opening by a single longitudinal or several radial splits. *Conidiophores* lining all inner surfaces of conidioma, simple or branched, sometimes septate, subcylindrical, tapering toward apex, hyaline, smooth, frequently reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, integrated or discrete, determinate or indeterminate, simple or unbranched, hyaline, smooth, aperture minute,

collarette inconspicuous. *Conidia* filiform to falcate or fusiform to allantoid, 0–2(–3)-septate, hyaline, smooth or guttulate (Figure 2.55).

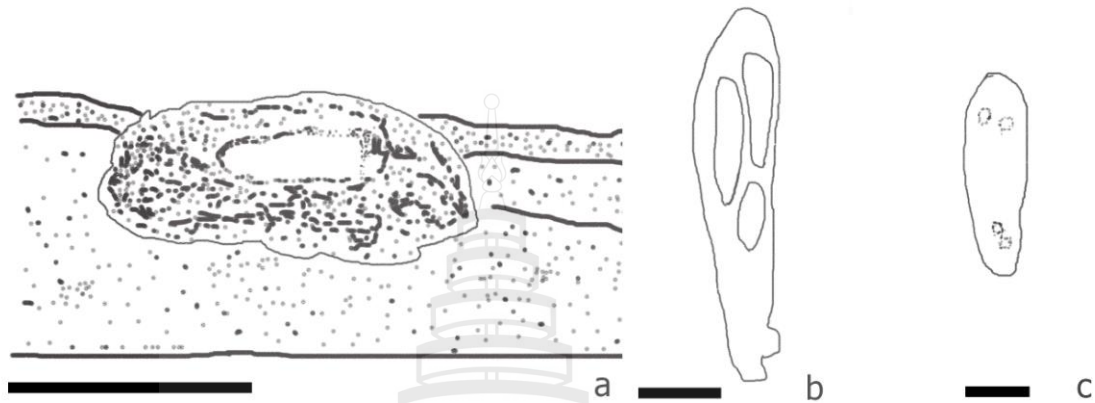


Figure 2.53 Sexual morph of *Micraspis acicola*

Figure 2.53, a An ascoma. b An ascus. c An ascospores. Scale Bars: a = 500 μm , b = 10 μm , c = 5 μm (Redrawn from Quijada et al. 2020).

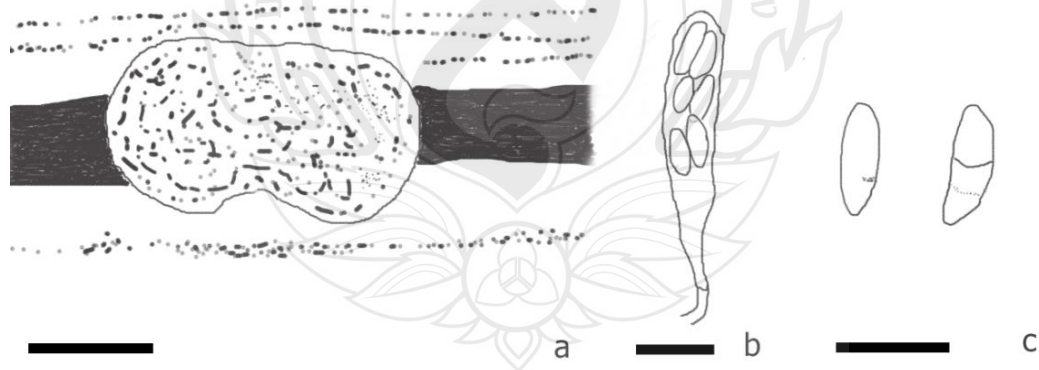


Figure 2.54 Sexual morph of *Micraspis tetraspora*

Figure 2.54, a An ascoma at the upper view. b An ascus. c An ascospores. Scale Bars: a = 500 μm , b, c = 10 μm (Redrawn from Quijada et al. 2020).

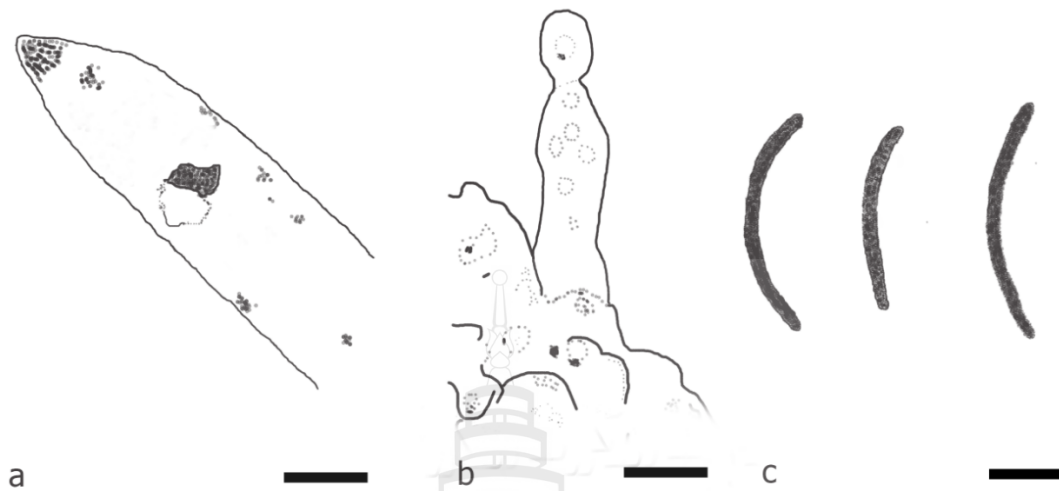


Figure 2.55 Asexual morph of *Micraspis acicola*

Figure 2.55, a Conidioma on a dead needle leave of *Picea rubens*. b. Conidiogenous cells and conidiophore of *Micraspis acicola*. c. Conidia of *Micraspis acicola*. Scale Bars: a = 500 μm , b = 5 μm , c = 10 μm (Redrawn from Quijada et al. 2020).

Micraspis is recently placed in Micraspidaceae, Micraspidales based on the multi-gene phylogeny and morphology by Quijada et al. (2020), and also relates to the *Trizodia* clade in Leotiomycetes. However, further evolution studies are required to confirm the placement of this genus in Leotiomycetes.

The placement of *Micraspis* has been uncertain since 1963, and some mycologists, based only on the morphologies, tried to assign this genus to several existing families such as Phacidiaceae (Darker, 1963), Tympaneae (DiCosmo et al., 1983; 1984) and Tympanidaceae (Baral, 2016). *Micraspis* is similar to Phacidiaceae members based on subcuticular, blackish, circular to elongate with longitudinal slit apothecia (Darker, 1963). However, they differ from Phacidiaceae by having inamyloid asci and the lack of an irregular teeth-covering layer on apothecia; Hence, Di Cosmo et al. (1984) reassigned it to Tympaneae. Baral (2016) placed *Micraspis* in Tympanidaceae (Phacidiales) based on the formation of blastic-phialidic microconidia from ascospore germination.

A multi-gene phylogeny of Leotiomycetes by Johnston et al. (2019) included several members of Tympanidaceae (Phacidiales) but none from *Micraspis* species. Later, Quijada et al. (2020) employed multi-gene phylogeny, including the sequences from *Micraspis acicola* and *M. strobilina*, along with morphological affirmation and transferred *Micraspis* species into the newly established Micraspidaceae (Micraspidales), resolving previous taxonomic issues related to the genus.

Micraspis acicola has been reported in association with needle leaves of *Picea* spp. as endophytes and pathogens in Canada (Quijada et al., 2020). However, *Micraspis strobilina* and *M. tetraspora* lack information on their ecological and economic significance due to limited studies and collections. *Micraspis strobilina* was found on fallen cones of *Pinus sylvestris* and was common in the UK, while *M. tetraspora* is native to North America and found on decorticated wood of *Picea sitchensis* which became an essential timber commodity after being introduced in the UK (Graddon, 1984; Quijada et al., 2020). Further studies on the economic and ecological values are still expected.

Prior to Quijada et al. (2020), molecular data were only available for *Micraspis acicola* in unpublished studies. Subsequently, many endophytic isolations of *M. acicola* from *Picea* spp. were conducted, which can be used in resolving taxonomic issues of *Micraspis* (Quijada et al., 2020). However, further comprehensive studies on evolution, ecology or other applications are required. *Micraspis strobilina* is the other *Micraspis* species for which molecular data are available besides *M. acicola*. *Micraspis strobilina* is ubiquitous in the UK; hence, further studies on evolution and ecology are required. Apart from the aforementioned species, *Micraspis tetraspora* lacks sequence data. The current taxonomic placement of these species in Micraspidales was mainly based on morphological affinities from three specimens (Quijada et al., 2020). Hence, more explorations are vital to discover additional specimens for further studies on this genus.

2.4 Discussion

Doi Inthanon National Park in Chiang Mai Province spanned three districts (Chom Thong, Mae Wang, and Mae Chaem) with altitudes ranging from 400 to 2562

m and temperatures ranging from 1°C to 23°C (Anonimus, 2001). Located in a mountainous area and covered with rich plant diversities (Khamyong et al., 2004), many new species of bryophytes (Akiyama et al., 2010), ferns (Iwatsuki et al., 1998), reptiles (Kunya et al., 2015) and insects (Takaoka & Choochote, 2005) were uncovered. Fungal diversity in Doi Inthanon National Park has been studied, specifically aquatic fungi (Chuaseeharonnachai et al., 2013) and Xylariaceae (Læssøe et al., 2013), however, none reported on discomycetes. In Thailand, previous research revealed novel species and geographical records of discomycetous fungi in many areas of northern Thailand (Ekanayaka et al., 2018; Ekanayaka et al., 2019a; Zeng et al., 2019), but no studies were conducted at the Doi Inthanon National Park; hence, more discoveries are expected, especially in Doi Inthanon National Park.

The topology of the maximum likelihood analysis is similar to the Bayesian analysis for the Cenangiaceae phylogram (Figure 2.1). However, the phylogenetic relationship between our species and the holotype cannot be ascertained, as sequence data are unavailable for the type specimen. Phylogenetic comparison can only be assessed for the species to whom sequence data is provided by Pärtel et al. (2017) and Han et al. (2014), as no other studies have been conducted on *C. torta*. *Chlorencoelia torta* has been previously recorded in Japan, Korea New Zealand, North America, Puerto Rico, the Soviet Union, and Tasmania on decayed wood of *Acer*, *Betula*, *Fagus*, *Quercus*, *Tabebuia*, coniferous and deciduous unidentified wood (Dixon, 1975; Han et al., 2014; Pärtel et al., 2016). Hence, this study documented *Chlorencoelia torta* as a geographical record from Thailand as it has not been found before.

Dicephalospora is mostly found on lignocellulose substrates such as rotten branches, dead stems, and leaf petioles and has been found in many regions in Europe and Asia (Spooner, 1987; Zhuang et al., 2016; Ekanayaka et al., 2019a). Previous research revealed *Dicephalospora aurantiaca* and *D. rufocornea* in Chiang Mai, Thailand (Ekanayaka et al., 2019a). However, a new species has not been recorded. This study revealed a new species of *Dicephalospora irregularis* (MFLU 22-0054) from Chiang Mai, Thailand based on morphology and phylogenetic analysis.

The topology of the phylogenetic tree with LSU and ITS sequence data is congruent to Ekanayaka et al. (2019a), and our collection MFLU 22-0054 form a sister relationship to *Dicephalospora rufocornea* MFLU 18-1825 and HMAS 279697 with

81% ML bootstrap value (Figure 2.3). The ITS sequence of our specimen shows 96.7% and 98% similarity to the *D. rufocornea* (MFLU 18-1825) and *D. rufocornea* (HMAS 279697), respectively, while the LSU data of our specimen show 99% similarity to *D. rufocornea* (MFLU 18-1825) across 829 bp. Morphologically, *D. rufocornea* is characterized by having stipitate apothecia, ectal excipulum of *textura porrecta* to *prismatica*, hymenoscaphus-type apical ring and fusoid or fusoid-clavate ascospores while our specimen, *D. irregularis* (MFLU 22-0054) characterized by sessile apothecia, *textura angularis-globosa* ectal excipulum, non-amyloid apical ring and ellipsoid ascospores (Figure 2.6).

Our epithet specimen, named after its irregular apothecia and sessile, which is different compared to other *Dicephalospora* species except for *D. sessilis* (MFLU 18-1823) (Spooner, 1987; Zhuang et al., 2016; Ekanayaka et al., 2019a). However, phylogenetically, our specimen does not form a close affinity with *D. sessilis* (MFLU 18-1823) and is characterized by having irregular discoid apothecia, *textura angularis-globulosa* and 2-3 branched filiform paraphysis vs round cupulate apothecia, *textura prismatica-intricata* and unbranched filiform paraphyses.

Another saprobic discomycete specimen among Italy herbarium packages sent was classified as *Cyathicula*. *Cyathicula* species are characterized by cylindric to clavate paraphyses, which differ from lanceolate or cylindrical paraphyses of *Crocicreas* (Carpenter, 1981). *Cyathicula* was established by De Notaris (1864) with *C. coronata* as the type species (Rehm, 1893) in Helotiaceae. Most *Cyathicula* species are recorded in Asia, Europe and the USA (Rehm, 1893; Carpenter, 1981; Chlebická & Chlebicki, 2007). Currently, 30 species are accepted in this genus (Wijayawardene et al., 2022).

Our specimens, *C. discoreae* (MFLU 23-00461) and *C. rusci* (MFLU 23-00462, MFLU 23-00463, MFLU 23-00464) fit the morphological description of *Cyathicula* by having filiform to cylindric paraphyses and phylogenetically the two *Cyathicula* species are placed within *Cyathicula* clade and form sister relationship to *C. coronata* as the type species. *Cyathicula dioscoreae* (MFLU 23-00461) is grouped with *C. coronata* (CBS 197.62) and *Cyathicula* cf. *tomentosa* (MFLU 17-0082) with 75% maximum likelihood bootstrap support, while *C. rusci* (MFLU 23-00462, MFLU 23-00463, MFLU 23-00464) form a sister relationship to *C. coronata* (CBS 197.62)

with 66% maximum likelihood bootstrap support. Morphologically, *C. coronata* is characterized by having prominent teeth-like or crown-like structures on the apothecial disc rim and faintly blue apical ring when tested in Melzer agent, while *C. dioscoreae* (MFLU 23-00461) and *C. rusci* (MFLU 23-00462, MFLU 23-00463, MFLU 23-00464) are characterized by smooth apothecia without prominent teeth-like at the edge and strongly blue apical ring at the ascus tip after tested in Melzer agent.

Cyathicula dioscoreae (MFLU 23-00461) is also morphologically distinct from *C. cf. tomentosa* on the apothecia and excipular cells. The apothecia of our isolate (MFLU 23-00461) are greyish white with cupulate receptacles, whereas the *C. cf. tomentosa* strain (MFLU 17-0082) is characterized by dark apothecia with mostly enclosed, goblet receptacles (Ekanayaka et al., 2019a). The excipulum cells of our isolate are *textura porrecta* vs *textura oblita-prismatica* (*C. cf. tomentosa*).

Cyathicula rusci (MFLU 23-00462, MFLU 23-00463, MFLU 23-00464) also relate to *C. cyathoidea* (MFLU 16-0613) with less than 70% maximum likelihood bootstrap support and less than 0.90 posterior probability. Morphologically, our collections are distinct from *C. cyathoidea* in having asci arising from crozier (Figure 2.5), while the latter has asci arising from simple septa (Quijada et al., 2017; Ekanayaka et al., 2019a). Hence, our new herbarium specimens from Italy were identified as novel species of *Cyathicula* based on morphology and phylogeny with LSU and ITS sequence data.

Previous studies have documented *Erioscyphella* from Asia such as China, Japan (Tochihara & Hosoya, 2022; Li et al., 2023; Su et al., 2023) and Thailand, and mostly found on lignocellulose substrates such as rotten wood, trunk, dead stems, dead bamboo and fallen leaves (Ekanayaka et al., 2019a; Li et al., 2022; Su et al., 2022; Tochihara & Hosoya, 2022). *Erioscyphella* characterized fusiform to filiform ascospores, filiform to lanceolate paraphysis and yellow hymenium (Korf, 1978; Haines & Dumont, 1983; Perić & Baral, 2014). However, a recent study by Tochihara and Hosoya (2022), incorporating extant *Erioscyphella* species, revealed that morphological character only cannot delineate *Erioscyphella* from *Lachnum* without phylogenetic analysis.

Erioscyphella abnormis was documented by Haines and Dumont (1983) as *Lachnum abnorme* and characterized by apothecia stipitate with brown hair on the stipe,

Erioscyphella abnormis was synonymized with *Lachnum abnorme*, *Lachnum longisporum* (Perić & Baral, 2014). Morphologically, our specimen also fits the species description of *E. abnormis*, especially with septate, fusiform to filiform ascospores (Ekanayaka et al., 2019a; Tochihara & Hosoya, 2022).

Erioscyphella abnormis have been recorded in Japan (Hosoya et al., 2009), China (Ekanayaka et al., 2019a), and Korea (Han et al., 2021) but not in Thailand. This current study revealed a geographical record and host of *E. abnormis* on *Tectona grandis* from Thailand. *Erioscyphella abnormis* have been found on citrus and caused stem canker in Japan (Miyoshi et al., 2007). Our *E. abnorme* was found growing on a live branch of the *Tectona grandis*. However, its parasitic nature on the tree should be further investigated.

This study documents a geographical record of calycina-like species found in Doi Inthanon National Park, Thailand, based on morphology and multi-gene phylogeny. Our newly collected samples were identified as *C. montana*, which was previously found in China and identified under the name *Bisporella montana* (Zhuang et al., 2017). The morphological differences between *Calycina* and *Bisporella* seem to be insignificant in terms of apothecial color, asci, paraphyses, and ascospores, except for the blueing of the apical ring visible in calycina-like fungi. In contrast to that, a hymenoscyphus-type apical ring is visible in the *Bisporella* species (Verkley, 1993; Baral & Marson, 2005).

Following observation of the holotype of *C. montana* (HMAS 275566), we confirmed the morphological similarities between the type and our specimens. The original description of *C. montana* (HMAS 275566) is incomplete and lacks several key characteristics, including details on asexual morphs and the calycina-like apical ring at the ascus tips, which confirmed its relation to *Calycina* and its taxonomic placement in Pezizellaceae (Figure 2.26). In the original description, the blue ring at the ascus tip of *C. montana* (HMAS 275566) was not confirmed by Zhuang et al. (2017). However, we managed to re-observe and verify the appearance of a calycina-like apical ring on the type strain (Figure 2.29) and its morphological similarity with our newly collected *C. montana* (Figure 2.28, 2.29). This new taxonomic placement was further supported by the ITS and LSU phylogeny, which shows different placements for

Calycina (Pezizellaceae) and *Bisporella* (Helotiaceae) fungi in different clades (Figure 2.26).

The chalara-like fungus was mentioned in Baral (2016) as the asexual morph of *Calycina* and also reported by Ekanayaka et al. (2019a) for *C. claroclava* (synonym: *B. descendens*). The asexual morph of the newly collected *C. montana* (MFLU 22-0055) is revealed to be chalara-like and grows on the surface of apothecia (Figure 2.29). However, the asexual morph was not described for the holotype (Zhuang et al., 2017); therefore, our findings update information for the asexual and sexual morphs of *C. montana*.

The Pezizellaceae phylogram's topologies (Figure 2.26) in our study are roughly similar to Baral and Rämä (2015), especially in the *Calycina* clade. However, *Calycellina populina* (CBS 247.62) was not included. *Calycellina populina* (CBS 247.62) was placed in the *Calycina* clade (Baral & Rämä, 2015; Ekanayaka et al., 2019a), hence its name was suggested to be transferred into *Calycina populina* (Baral & Rämä, 2015). Since its morphology has not been re-observed and its name transferred has not been published, this species was not included in our analysis. Our phylogenetic tree's topography is different from Ekanayaka et al. (2019a) based on the gene region and taxa selection. Our phylogenetic analysis based on ITS and LSU contrasts with ITS phylogeny in Ekanayaka et al. (2019a). The taxa selection in this study is based on genera accepted under Pezizellaceae by Wijayawardene et al. (2022). However, *B. citrina* (ILLIS 61033) and *C. herbarum* (NBRC 9520) were not included in our analyses due to their morphology and phylogeny affinities to Helotiaceae members, *Phaeohelotium monticola* (Baral et al., 2013) and *Hymenoscyphus herbarum* (Zhao et al., 2012), respectively.

Our study also synonymized *Bisporella shangrilana* into *Calycina shangrilana* comb. nov., supported by the combined phylogeny of ITS and LSU (Figure 2.26) and morphology (Figure 2.30). Also, the morphological description of the type specimen coincides with the *Calycina* generic concept (Baral, 1993; Baral & Marson, 2005). *Calycina shangrilana* (HMAS 275568) found in China was reported to have insignificant morphological differences from *C. montana* (HMAS 275566) except in highly gelatinous and larger excipular cells (Zhuang et al., 2017). While in our study, we only noticed that *C. shangrilana* differs from *C. montana* by having pinkish-orange

apothecia and a shorter stipe, which is not concolorous to the receptacle of *C. shangrilana* (Figure 2.30). However, fresh specimens of *C. shangrilana* may reveal more differences between the two species, especially in micromorphologies.

The current study resolves the taxonomic confusion related to *Bisporella* species placed in Pezizellaceae (Ekanayaka et al., 2019a). However, the delineation of other genera in Pezizellaceae remains unclear. Therefore, more global explorations combined with comprehensive studies using morphology and phylogeny are vital for resolving taxonomic confusions of other genera in Pezizellaceae or other families in Leotiomycetes.

Calycina species have been found in various regions, mainly as saprobes in plant materials (Baral & Rämä, 2015; Quijada & Beltrán-Tejera, 2017), living plants (Crous et al., 2019), and as lichenicolous (Suija & Motiejūnaitė, 2017). More than 60 records of *Calycina* species are documented in the Index Fungorum (2023), and only a few have molecular data. This study also provides a synopsis of the morphological characteristics of the *Calycina* species available with molecular data, including geographical data (Table 2.6).

Our other Pezizellaceae collection morphologically fits with *Calycina* by having gelatinized ectal excipulum, filiform paraphyses, cylindrical asci with calycina-like apical rings and ellipsoidal ascospores (Baral & Marson, 2005; Baral & Rämä, 2015; Suija & Motiejūnaitė, 2017; Lestari & Chethana, 2022). Despite the ITS and LSU base pair difference (Table 2.7), morphologically, *Calycina papaeana* distinguished from *Chalara pseudoaffinis*, *Calycina lactea*, *Calycina languida*, *C. herbarum*, *C. claroflava*, *Calycina cortegadensis* and *C. alstrupii* (Table 2.8). *Chalara pseudoaffinis* differs from *C. papaeana* by its lacking of sexual morph or apothecia and only characterized by chalara-like asexual morph (Koukol, 2011). *Calycina papaeana* characterized by its stipitate apothecia which is differed from sessile apothecia of *C. alstrupii*, *C. claroflava* and *C. marina* (Suija & Motiejūnaitė, 2017; Quijada & Beltrán-Tejera, 2017; Baral & Rämä, 2015). Another character on *C. papaeana* is the asci arising from crozier which distinct from *C. languida* and *C. cortegadensis* which its asci arising from simple septa (Baral, 2021). Ascospores of *C. papaeana* is ellipsoid biguttules which is different from *C. herbarum* and *C. lactea* which characterized with their fusoid ascospores with more than 2-guttules (Baral, 2013). Therefore, based on

morphological and phylogenetic evidences, we introduce our collection as *Calycina papaeana* sp. nov.

Previous studies have documented the presence of *Lambertella* on diverse substrates, including rotten or mummified fruits (Wiseman et al., 2015) and dead twigs and leaves (Tewari & Pant, 1967). *Lambertella* has been reported in diverse geographic regions across the tropics, northern and southern hemispheres (Whetzel, 1943; Cash, 1958; Tewari, 1963; Dumont, 1971; Dumont, 1974; Korf & Zhuang, 1985; Hosoya & Otani, 1997; Zhao et al., 2013), but no occurrences have been documented in Thailand (Phanichapol, 1986; Ekanayaka et al., 2019a; Phutthacharoen et al., 2022). This study reported seven *Lambertella* species from Northern Thailand (Chiang Mai, Chiang Rai and Tak provinces), among which five are novel species, and two are new host records that were previously undocumented in Thailand. The new species are *L. chiangraiensis* (MFLU 23-0088 and MFLU 23-0488), *L. fusoides* (MFLU 23-0086), *L. phanensis* (MFLU 23-0091 and MFLU 23-0485), *L. sessilis* (MFLU 23-0092 and MFLU 23-0487) and *L. takensis* (MFLU 23-0089 and MFLU 23-0486), while *L. aurantiaca* (MFLU 23-0090) and *L. himalayensis* (MFLU 23-0087) are the new records.

Zhao et al. (2016) showed that *Lambertella* is a polyphyletic genus based on LSU and RPB2 sequences. The phylogenetic relationships of the three newly identified *Lambertella* species are depicted in Figure 2.32, illustrating their clustering within *Lambertella* sensu stricto (highlighted in green zone). Our *Lambertella* sensu stricto clade exhibits an identical topology to that observed by Zhao et al. (2016). However, our single-gene and multi-gene trees introduce slight differences in the phylogenetic positions of certain species, such as *L. himalayensis* (CBS 230.77) and *L. pyrolae* (TNS:F-40132) (Figure 2.32 and 2.33). This perhaps, because our updated phylogram incorporates a broader set of *Lambertella* species such as *L. langei* (285.2), *L. palmeri* (AH s.n, AH:7576), *L. tetrica* (F142281), which was not previously included in the Zhao et al. (2016)'s phylogram. Our phylogram also includes more representatives from other genera such as *Bicornispora*, *Bryorutstroemia* and *Clarireedia* in Rutstroemiaceae (Figure 2.32).

Regarding the phylogenetic relationship with the *Lambertella* sensu stricto (indicated by the green highlight), the phylogenetic affinity of our three newly collected *Lambertella* (*L. chiangraiensis*, *L. himalayensis*, *L. sessilis*) and some extant

Lambertella species (*L. pyrolae*) are noticeable in the multigene phylogram compare to the ITS single gene tree (Figure 2.32 and 2.33). Morphologically, the current *Lambertella* sensu stricto encompasses features such as substratal stroma, stipitate apothecia, *textura prismatica* ectal excipulum, filiform paraphyses, sclerotinia-type ascal ring or negative, and brown, ellipsoid ascospores. Our specimens, namely *L. chiangraiensis* (MFLU 23-0088 and MFLU 23-0488), fit the generic concept of *Lambertella* description except for its hyaline ascospores (Figure 2.37), whereas our other specimen: *L. sessilis* (MFLU 23-0092 and MFLU 23-0487) is distinct on the sessile to substipitate instead of stipitate apothecia and having *t. angularis-prismatica* rather than *t. prismatica* ectal excipulum. Based on our findings, we propose an expansion of the generic concept of *Lambertella* sensu stricto to include substratal stroma, sessile to stipitate apothecia, filiform paraphyses, *t. angularis* - *t. prismatica* ectal excipulum cells, and hyaline, pale to brown, fusoid to ellipsoid ascospores.

Based on the multigene phylogram in Figure 2.32, the cluster of other newly collected specimens: *L. aurantiaca* (MFLU 23-0090), *L. fusoides* (MFLU 23-0086), *L. phanensis* (MFLU 23-0091, MFLU 23-0485) and *L. takensis* (MFLU 23-0089, MFLU 23-00486) do not form a sister relationship to *L. corni-maritima* clade but to the clade of *L. chiangraiensis-himalayensis-sessilis-pyrolae* with high bootstrap value (100 % ML bootstrap support and 1.00 BI posterior probability). Hence, they cannot be included in *Lambertella* sensu stricto, but we propose to still include them in *Lambertella* sensu lato because despite its phylogenetic affinities to our three newly found *Lambertella*, some characters (which already described in each species taxonomy description) are fit the *Lambertella* generic term. Despite the varied characters of *L. aurantiaca* (MFLU 23-0090), *L. fusoides* (MFLU 23-0086), *L. phanensis* (MFLU 23-0091, MFLU 23-0485), *L. takensis* (MFLU 23-0089, MFLU 23-00486), the similarity of these newly specimens found on the pattern of ascal ring with MLZ after with or without KOH. Regarding the ascal ring types which appear or not after tested with MLZ with or without KOH pretreatment, Zhao's et al. 2016 described that in *Lambertella* sensu stricto, the ascal ring of its members are Sclerotinia-types or negatively reacted. The ascal rings of *L. aurantiaca* (MFLU 23-0090), *L. fusoides* (MFLU 23-0086), *L. phanensis* (MFLU 23-0091, MFLU 23-0485), *L. takensis* (MFLU 23-0089, MFLU 23-00486) form light blue horizontal lines at the ascal tips without vertical lines which do

not fit *Sclerotinia*-ascal types (2.35, 2.39, 2.44, 2.48), these indicate that members of Rutstroemiaceae needs to be further explore by combining morphology and phylogeny either for new findings or taxonomic re-evaluation.

In the single gene phylogram, our newly collected and extant *Lambertella* species: *L. himalayensis* and *L. pyrolae* (which was included in *Lambertella* sensu stricto by Zhao et al. 2016) do not form sister relationships with *L. corni-marais* clade but to the *Bicornispora* clade which was not previously included in Zhao et al. 2016's phylogram. Morphologically, compare to *Lambertella*, *Bicornispora* characterized by having distinctive cleistothecia instead of apothecia and reniform with appendages instead of fusoid-ellipsoid ascospores (Galán et al., 2015). In addition, similar to in Figure 2.32, our three newly collected specimens: *L. chiangraiensis* (MFLU 23-0088 and MFLU 23-0488), *L. himalayensis* (MFLU 23-0087) and *L. sessilis* (MFLU 23-0092 and MFLU 23-0487) shows sister relationships to *L. himalayensis* (CBS 230.77) and *L. pyrolae* (TNS:F-40132). Whereas the other newly collected *Lambertella* species: *L. aurantiaca*, *L. fusioidea*, *L. phanensis* and *L. takensis* develops phylogenetic affinities to the clade of *L. chiangraiensis*-*himalayensis*-*sessilis* but not related to *L. pyrolae* as in the multigene phylogram (Figure 2.32 and 2.33). This means that the taxonomic delineation for *Lambertella* based on our phylogram analysis is better performed in the multigene phylogram.

In the multigene phylogram, despite *L. aurantiaca*, *L. fusioidea*, *L. phanensis* and *L. takensis*, another *Lambertella* species such as *L. langei* (285.2), *L. palmeri* (AH s.n., AH:7576), *L. subrenispora* (CBS:811.85) are excluded from *Lambertella* sensu stricto (Figure 2.32). Morphologically, *L. langei*, *L. palmeri*, *L. subrenispora* fit the generic description of *Lambertella* characterized by having substratal stroma, t. prismatica-ectal excipulum, filiform paraphysis except ascospores shape are distinct on *L. palmeri* (Galán et al., 2015), *L. subrenispora* (Korf & Zhuang, 1985), however the character variation differs is not clear on *L. langei* (Table 2.41). Hence, further deep taxonomic studies on *Lambertella* still necessary to address the morpho-phylogenetic issue.

The specimens of many extant *Lambertella* species are collected in long time ago, lack sequence data, and their morphological descriptions are often incomplete for comprehensive character comparison and identification. Among the currently accepted

66 *Lambertella* species (Zhao et al., 2013; Zhao et al., 2016; Vu et al., 2019; Species Fungorum, 2023), only 14 have sequence data (Table 2.41). Therefore, the current study, combining morphological descriptions, phylogenetic analyses with chemical testing, confirmed the identity of *L. aurantiaca*, which was previously reported in India without sequence data. Our research successfully contributed molecular data for the extant species, *L. aurantiaca*. Therefore, ongoing field explorations are crucial for discovering new and existing *Lambertella* specimens, facilitating updates to morphology and sequence data in public databases.

Through single spore isolation, some of the newly found *Lambertella* are able to germinate on water agar, and grew for one week once it transferred on Potato Dextrose Agar with antibiotic. However, the cultures are then parasitized by *Aspergillus* species, hence, it is suggested to carefully isolate and culture using equipments which parasitic fungal species-free.

Species of *Lambertella* have been found mostly on plant substrates, such as *Acer*, *Andromeda*, *Archontophoenix*, *Artemisia*, *Artocarpus*, *Aster*, *Astronia*, *Berberis*, *Calophyllum*, *Carya*, *Cassia*, *Cephalanthus*, *Citharexylum*, *Coccolobis*, *Coptis*, *Cornus*, *Cryptomeria*, *Dalbergia*, *Damnacanthus*, *Elaeocarpus*, *Eriobotrya*, *Eugenia*, *Euphorbia*, *Euterpe*, *Fraxinus*, *Gayrya*, *Gunnera*, *Guttifera*, *Hedera*, *Ilex*, *Ixora*, *Jasminum*, *Madhuca*, *Maesa*, *Malus*, *Mangifera*, *Melasomataceae*, *Myrica*, *Myrtaceae*, *Pachysandra*, *Palmae*, *Pinus*, *Prunus*, *Pyrola*, *Pyrus*, *Quercus*, *Rhamnus*, *Rosaceae*, *Rhubus*, *Shorea* and *Viburnum* (Korf & Zhuang, 1985; Schumacher & Holøs, 1989; Salgado-Salazar et al., 2018; Zhao et al., 2013). In this study, *Tectona grandis*, for *L. himalayensis* (MFLU 23-0087) and *L. takensis* (MFLU 23-0089) were reported as new hosts of *Lambertella*. It is remarkable that five new species in only one genus were found in a small area of northern Thailand, indicating that the tropics is an unexplored cache of novel taxa (Hyde et al., 2007, 2019).

CHAPTER 3

PHYTOPATHOGENIC DISCOMYCETES ON LIGNOCELLULOSE SUBSTRATES, THEIR ECONOMIC IMPACTS AND CONTROL

3.1 Introduction

The increasing human population and reduction of agricultural landscapes have a direct impact on global food security. For agricultural crops, fungal diseases pose one of the most significant challenges, with climate change aggravating the infection on various crops (Harvell et al., 2002). It is estimated that 16% of crop losses are due to microbial pathogens, among which approximately 75% are caused by fungal diseases (Oerke, 2006).

Fungal diseases on food crops negatively impact food availability and economic losses. One of the most devastating fungal pathogens, *Pyricularia oryzae* (basionym: *Magnaporthe oryzae*), causes the blast disease not only on rice but also on barley, millet and wheat (Couch et al., 2005; Dean et al., 2012). Blast disease caused by *Pyricularia oryzae* lowers the yield by 10–13% or around 50 million tonnes (Talbot et al., 2003; Boddy, 2016). *Fusarium oxysporum* is another phytopathogen targeting ornamental and horticultural crops, causing an economic loss of over 130 million USD to the banana industry in Australia (Cook et al., 2015). Phytopathogenic fungi not only affect food crops but also lead to substantial losses in forestry. *Ceratocystis fagacearum* is a fungal pathogen of oak that causes significant economic losses by infecting more than 260,000 oak trees in Anoka County, Minnesota, resulting in a mitigation cost of over 18 million USD (Haight et al., 2011). Annually, in the USA, fungal diseases caused more than 200 billion Euro of financial loss on pre- and post-harvest agricultural commodities, including the cost of fungicides, which exceeds 600 million USD (Arora et al., 2004).

Discomycetes is an artificial group of ascomycetes characterized by their teleomorphic discs, cups or saucer-like apothecia or ascomatal structures, composing a hymenium, with or without paraphyses and outlined by excipular cells (Pfister & Kimbrough, 2001; Ekanayaka et al., 2017). In their life cycle, discomycetes fungi have shown hyphomycetous, coelomycetous, pycnidial and yeast asexual forms (Redhead, 1977a; Hansen & Pfister, 2006; Lantz et al., 2011; Crous et al., 2014). Those asexual forms are recognized for some taxa, but some are not available due to the isolation difficulties which hinder further studies on the understanding of discomycetes' life cycle (Spooner, 1987).

Discomycetes inhabit terrestrial and aquatic environments as saprobes, symbionts (bryosymbionts, ectomycorrhizae and lichens), endophytes, fungicolous taxa, nematode trappers and phytopathogens (Hosoya & Otani, 1995; Künkele et al., 2005; Wang et al., 2011; Doveri, 2012; Gueidan et al., 2014; Hyde et al., 2014; Lücking et al., 2016). Phytopathogen discomycetes are ascomycetous fungi bearing apothecia that may cause disease or show parasitic symptoms on live plant hosts.

3.2 Materials and Methods

Literature browsing was conducted to study phytopathogenic discomycetes, their economic impacts and control. All the currently known and published discomycetes fungi cause impediments to average growth or disease symptoms of nonvascular to vascular plants. The literature browsing on the possible fungal taxa of phytopathogenic discomycetes based on the Ekanayaka et al. (2017), then the taxa targets were browsed on the Google search engine with the keyword: “fungal family or genus or species”, the related disease: for example, “dollar spot” and “control strategies”, “genomic studies on phytopathogenic discomycetes”. Not only publications but fungal databases such as CABI (Centre for Agriculture and Bioscience International) and USDA (United States Department of Agriculture) were also scrutinized regarding the disease information and their related host caused by discomycetes fungi economic impacts, and relevant information was listed.

The list of fungal taxa causing fungal diseases through mycology journals or other websites was validated for the updated classification through Index fungorum, Mycobank and Species fungorum, and each species was confirmed. The classification of phytopathogenic discomycetes based on class Leotiomycetes was based on Quandt and Haelewaters (2021). Classification of other classes was based on Wijayawardene et al. (2022) and updated if recent changes in the taxonomy were made. The analysis related to phytopathogenic discomycetes includes the taxon name, type of disease or growth impediment on plants or nutritional modes, the host (family or species or common plant names) and the geographical distribution. The literature review includes the life cycles of the selected prominent species that have impacted vital commodities or caused a wide array of damage and the genomic studies of the class of related phytopathogenic discomycetes. Regarding Leotiomycetes discomycetes, the phytopathogenic species were also searched for any studies related to the apothecial formation since many fungal pathogens in Leotiomycete families do not bear apothecia as the sexual morph. The literature review of phytopathogenic discomycetes was done after the data were listed, screened, analysed and tabulated. Important validated information was then compiled into a comprehensive overview of phytopathogenic discomycetes along with an updated classification, control strategies and ongoing molecular-based research.

3.3 Results and Discussion

3.3.1 Phytopathogenic Discomycetes

Previous records classified phytopathogenic discomycetes in various fungal taxa within Ascomycota from many host plants and regions (Dowson, 1913; Funk, 1962; 1967; Childs, 1968; Funk, 1982; Fitt et al., 1988; Batra, 1991; Annesi et al., 1997; Cho et al., 2016; Egertová et al., 2016; Elad et al., 2016; Çolak & Kaygusuz, 2017; Crous et al., 2019). Many phytopathogenic discomycetes parasitize host plants in their apothecial forms, such as Pezizomycetes. At the same time, some Leotiomycetes infect in their asexual forms (i.e., *Botrytis cinerea*, *Monilinia fructigena*, *Sclerotinia sclerotiorum*, etc.) (Groves & Drayton, 1939; Schwartz & Steadman, 1978; Batra &

Harada, 1986). Induction of apothecial formation in phytopathogenic discomycetes depends on specific conditions, such as mimicking natural habitats that vary within regions and species even within a similar genus (Bergquist & Lorbeer, 1973; Spiers & Hopcroft, 1986; Moore-Landecker, 1992; Norvell & Redhead, 1994; Terhem, 2015). For example, apothecia of *Drepanopeziza brunnea* (anamorph: *Marssonina brunnea*) were reported in Europe but not in New Zealand, Japan and Korea (Spiers & Hopcroft, 1986).

Phytopathogenic discomycetes are noteworthy for further exploration because of their economic importance and need for management strategies (Elad & Freeman, 2002; Bogacheva, 2005; Baral, 2016). However, the number of studies on these phytopathogens is not proportionately similar to those centralized on certain taxa due to their massive economic impacts on a wide range of crops (Batra, 1991; Boland & Hall, 1994; Elad et al., 2004). *Botrytis cinerea*, for example, gained tremendous research interest throughout the world, resulting in new records (on hosts, regions), host-pathogen interactions, disease incidences and management strategies (Elad & Shtienberg, 1995; Legard et al., 2000; Dean et al., 2012; Williamson et al., 2007; Sowley et al., 2010; Duan et al., 2014; Elad et al., 2016; Yang et al., 2018; Ebrahimzadeh & Abrinbana, 2019; Petrasch et al., 2019). Furthermore, *Monilinia fructigena*, several other *Monilinia* species and *Sclerotinia sclerotiorum* also received immense research interest due to their negative economic impact on food crops (Boland & Hall, 1994; Kim et al., 2008; Ivanović & Ivanović, 2001; Hily et al., 2010; Hu et al., 2014; De Miccolis Angelini et al., 2018). In addition, *Diplocarpon rosae*, *Oculimacula yallundae* and other phytopathogenic discomycetes are also gaining research interest and are still in need of more investigations (Blein et al., 2009; Marin-Felix et al., 2019).

Phytopathogenic discomycetes are diverse and unique but reported separately in individual studies. Current information on discomycete taxa, their impacts and updates on available approaches for disease mitigation are disjointed and, thus, required to be revisited as a whole. The main purpose of this review is to extract and compile information from miscellaneous resources about fungal taxa, their diseases, their economic significance, and the available mitigation strategies to provide an overview of phytopathogenic discomycetes.

Discomycete species are distributed across 11 classes: Arthoniomycetes, Coniocybomycetes, Dothideomycetes, Eurotiomycetes, Geoglossomycetes, Lecanoromycetes, Leotiomycetes, Lichinomycetes, Neoelectromycetes, Orbiliomycetes and Pezizomycetes (Ekanayaka et al., 2017), inhabiting terrestrial and aquatic environments with various ecological roles. Among these, some are phytopathogens that cause various plant fungal diseases (Hosoya & Otani, 1995; Künkele et al., 2005; Wang et al., 2011).

3.3.2 Phytopathogenic Discomycetes in Dothideomycetes

Phytopathogenic discomycetes in Dothideomycetes are characterized by semi-immersed to erumpent, black, hysteriform apothecia, bitunicate or fissitunicate asci and ellipsoid, fusiform, long clavate and septate ascospores (Samuels & Müller, 1979; Inácio et al., 2012; Guatimosim et al., 2015; Jayasiri et al., 2016; Tian et al., 2016). The sexual forms of phytopathogenic discomycetes in Dothideomycetes are grouped in Catinellales, Eremithallales, Hysteriales, Mytilinidiales, Patellariales and Pleosporales (Ekanayaka et al., 2017). Many phytopathogenic Dothideomycetes were noted (Hongsanan et al., 2020), but very few belong to discomycetes (Table 3.1).

Rhytidhysterium rufulum is a phytopathogenic species in Dothideomycetes recognized as a weak parasite on unidentified dicotyledon plants despite most studies finding this species as saprobes (Samuels & Müller, 1979; Thambugala et al., 2016). No further studies have been conducted to explore the weak pathogenicity of *Rhytidhysterium rufulum* on its hosts. Tian et al. (2016) reported *Aldona stella-nigra*, *Aldonata pterocarpi* and *Viegasella pulchella* to cause leaf necrosis by penetrating host cells and obtaining nutrients via structures under ascomata (Inácio & Canon, 2008). *Antoniomyces loranthicola* and *Dothidasteromella parvispora* also cause leaf spot diseases on *Gaiadendron punctatum* and *Olex wightiana*, respectively (Luttrell & Muthapa, 1974; Inácio et al., 2012). Guatimosim et al. (2015) reported the biotrophic pathogen *Inocyclus angularis* that causes the black tar spot disease on fern species (*Pleopeltis atrolepis*). Further studies on life cycles, infection modes, and pathogenicity factors of *Antoniomyces loranthicola*, *Dothidasteromella parvispora* and *Inocyclus angularis* are limited and need to be studied in detail (Luttrell & Muthapa, 1974; Inácio

et al., 2012). The number of phytopathogenic discomycetes is shown in Table 3.1, but the number can be more since it only represents one species for each reported genus.

3.3.3 Phytopathogenic Discomycetes in Eurotiomycetes

Eurotiomycetes is a prominent class of saprobes that switches to pathogens in humans, animals, plants and symbionts (lichens, ectomycorrhizae and myrmecophytes) (Henkel et al., 2006; Blatrix et al., 2013; Gueidan et al., 2014). Eurotiomycetes include cleistothecial and perithecial bearing phytopathogens (Döbbeler, 1997; Thambugala et al., 2014), among which most are filamentous, such as *Aspergillus* sp. (Cotty et al., 1994), while few are discomycetes (Table 3.2) (Döbbeler & Hertel, 2013). Phytopathogenic discomycetes in Eurotiomycetes are characterized by short to long stalked-apothecia, unitunicate, clavate asci, and fusiform to ellipsoid, hyaline to dark brown, septate ascospores (Marsh et al., 2010; Döbbeler & Hertel, 2013).

Stenocybe nitida is a biotroph on *Plagiochilla punctata*, causing systemic infections in its host by developing hyphae on cell walls and producing stipitate apothecia from the leafless stem of the host (Döbbeler & Feuerer, 2004). *Stenocybe nitida* was parasitic, mostly on *Plagiocilla punctata*, but sometimes found in other *Plagiochilla* species (Döbbeler & Hertel, 2013). In contrast to *S. nitida*, *Dactylospora heimerlii* not only infect axil leaves and perianth of Plagiochillaceae (Marsh et al., 2010) but also other genera of hepatic bryophytes (Döbbeler & Triebel, 1985). For both species, detailed studies on life cycles and pathogenic factors are still lacking (Davey & Currah, 2006). Phytopathogenic discomycetes in Eurotiomycetes were reported mostly on bryophytes from different regions (Döbbeler & Hertel, 2013).

3.3.4 Phytopathogenic Discomycetes in Lecanoromycetes

Lecanoromycetes consists of mostly lichenized symbionts (lichens) in addition to saprobes and phytopathogens (Sherwood et al., 1980; Huneck & Yoshimura, 1996; Lawrey & Diederich, 2003; Wedin & Wiklund, 2004). Based on ascomatal morphologies, Lecanoromycetes is divided into plectomycetes, pyrenomycetes and discomycetes (Luttrell, 1955). Phytopathogenic discomycetes in Lecanoromycetes are defined by interlamellar, sessile apothecia, unitunicate, claviform to cylindrical asci, and hyaline, ellipsoid, elongated ovate to fusiform, aseptate to septate ascospores (Vězda, 1965; Ceynowa-Gieldon, 2003; Søchting et al., 2008; Stenroos et al., 2009;

Döbbeler & Hertel, 2013). In this study, we found records of phytopathogenic discomycetes distributed across two orders and four genera in Lecanoromycetes (Table 3.3). Table 3.3 represents phytopathogenic genera with one or two species and some with more species, such as *Potriphila* (Döbbeler, 2002).

Absconditella sphagnorum, *Caloplaca nivalis*, *Potriphila navicularis* and *Puttea margaritella* are pathogenic discomycetes infecting various bryophytic families (Andreaeaceae, Grimmiaceae, Polytrichaceae, Ptilidiaceae and Sphagnaceae) (Søchting et al., 2008; Döbbeler & Hertel, 2013). *Absconditella sphagnorum* infects *Sphagnum* sp, an important bryophyte that provides the raw material for horticulture (Stenroos et al., 2010; Ludwig, 2019). In Guizhou province, China, the net revenue of *Sphagnum* farming reached € 15000 per ha annually and is considered an exported commodity to overseas countries, such as Europe, Indonesia, Japan, North America, Malaysia, Taiwan, Thailand and Vietnam (Zhu, 2019). *Potriphila navicularis* infects bryophyte species, such as *Dendrologotrichum squamosum*, but it is found mainly in *Polytrichastrum alpinum* (Döbbeler, 1996). Infection of *P. navicularis* is systemic and develops haustoria in each host cell of trichomes, following the emergence of pycnidia on upper leaves and apothecia on lower leaves (Döbbeler, 1996; Döbbeler & Hertel, 2013). These biotrophic associations with hosts prevail in the environment (Döbbeler, 1997). *Puttea margaritella* is most likely a necrophyte found mostly on diseased and decaying *Ptilidium pulcherrimum*, a bryophyte that exhibits antimicrobial and moderate cytotoxicity properties against subcutaneous tumor cells in laboratory trials (Guo et al., 2009; Stenroos et al., 2009; Veljić et al., 2010), and also found on *Lophocolea heterophylla* as a facultative host (Stenroos et al., 2009; Czarnota & Hernik, 2013). *Caloplaca nivalis* was also reported as a pathogen on *Andreaea* sp. and *Grimmia* sp. (Søchting et al., 2008).

Studies on phytopathogenic discomycetes in Lecanoromycetes are lacking (Davey & Currah, 2006). Döbbeler (2002) reported micro-niches favored by bryophytes ascomycetes and briefly discussed the niche of *P. navicularis* but did not provide details on their life cycle and virulence factors. There are no studies on infection modes, life cycles and pathogenic factors of *A. sphagnorum*, *C. nivalis* and *P. margaritella*. Most studies reported their incidence in different regions and on various bryophytes (Döbbeler, 2002; Søchting et al., 2008; Czarnota & Hernik, 2013).

However, no economic losses or control strategies against these pathogens in their related bryophytic species have been reported.

3.3.5 Phytopathogenic Discomycetes in Leotiomyces

Leotiomyces include teleomorphic fungi bearing various shapes of minute to medium-sized apothecia, cleistothecia and perithecia with anamorphic forms of hyphomycetes and coelomycetes (Quandt & Haelewaters, 2021). Leotiomyces are found in terrestrial and aquatic habitats mostly as saprobes, sometimes as endophytes, symbionts (lichen, ectomycorrhiza), and animal and plant pathogens (Tedersoo et al., 2009; Queloz et al., 2011; Blehert, 2012; Zhang & Wang, 2015). Phytopathogenic discomycetes in Leotiomyces are characterized by sessile to stipitate, immersed to superficial apothecia, inoperculate, clavate to cylindrical asci interspersed with paraphyses, and hyaline to brown, filiform, pyriform, fusoid to ellipsoid ascospores (Jones, 1919; Redhead & Spicer, 1981; Jülich & de Vries, 1982; Nannfeldt, 1984a; Petersen & Pfister, 2010; Stenroos et al., 2010; Döbbeler & Hertel, 2013; Johnston et al., 2013; Guatimosim et al., 2016). Phytopathogenic discomycetes in Leotiomyces cause various diseases and significant financial impacts on economically important plant commodities (Knight & Wheeler, 1977; Boland & Hall, 1994; Nutter et al., 2002; Parnell et al., 2008; Dean et al., 2012; Elad et al., 2016). More than 100 genera of phytopathogenic discomycetes within nine Leotiomyces orders were listed in Table 3.4. The table displays that this class has the most members of phytopathogenic discomycetes among others. Perhaps this is due to their thriving mode in man-made environments, such as agricultural lands, while other discomycetes, for example, Pezizomycetes, are mostly found in forest habitats.

In Leotiomyces, phytopathogenic species are exclusively found in Cyttariaceae, Drepanopezizaceae, Erysiphaceae, Medeloriaceae and Sclerotiniaceae (Baral, 2016). However, among these, discomycetes cannot be found in Erysiphaceae as their sexual morph characters are restricted to perithecia and cleistothecia (Salmon, 1900). Hence, this family is excluded from the current study. Phytopathogenic discomycetes in Cyttariaceae and Medeloriaceae generally affect host plants in forests, and their existence is restricted to particular regions (Petersen & Pfister, 2010; Pfister et al., 2013). Drepanopezizaceae and Sclerotiniaceae infect valuable plant commodities

mostly grown in man-made habitats (Horst, 1990; Schuster, 2004; Denton-Giles et al., 2019). Phytopathogenic species, representing Cyttariaceae, Drepanopezizaceae, Godroniaceae, Medeloriaceae, Ploettnerulaceae and Sclerotiniaceae that cause an economic impact on agricultural and forestry commodities (i.e., ornamental plants, seed crops, orchards, staple and cover crops and forestry) are selected and described here. Host plants affected by phytopathogenic Leotiomycetes are exceptionally broader compared to other discomycetous classes. These hosts range from non-vascular plants (bryophytes and pteridophytes) to agricultural and forestry commodities, including nursery material (Table 3.4) (Townsend, 1951; Redhead, 1977b; Jülich & de Vries 1982; Williamson et al., 2007; Bezerra et al., 2008; Melzer et al., 1997; Guatimosim et al., 2016; Marin-Felix et al., 2019; Baral et al., 2022). The species number of phytopathogenic discomycetes in Table 3.4 is underestimated since it only represents one or few species for each reported genus.

Cyttariceae accommodates 13 species of biotrophic discomycetes (Index Fungorum, 2022). *Cyttaria* species are endemic to South America (Argentina and Chile) (Minter et al., 1987) and Oceania (southern Australia, Tasmania and New Zealand) (Petersen & Pfister, 2010). They were documented for their associations with specific host trees (*Nothofagus* spp.) and their phylogenetic affinities (Petersen & Pfister, 2010). The disease development of three *Cyttaria* species (*Cyttaria gunnii*, *Cyttaria nigra* and *Cyttaria pallida*) was described by Gadgil (2009). Their infection started with the germination of ascospores in the young shoot of *Nothofagus* spp. The penetrated fungi secrete specific substances responsible for the functioning of cell proliferation and gall formation. The spines comprise a combination of fungal hypha and host tissues, from which the apothecia arise. The extent of mycelial colonization determines the longevity of gall existence and varies among *Cyttaria* species. Gadgil (2009) described that due to short hyphal colonization distances of *C. gunnii* and *C. nigra* localized galls are formed, whereas, for *C. pallida*, fungal hyphae grow down to the branch, resulting over the years-gall.

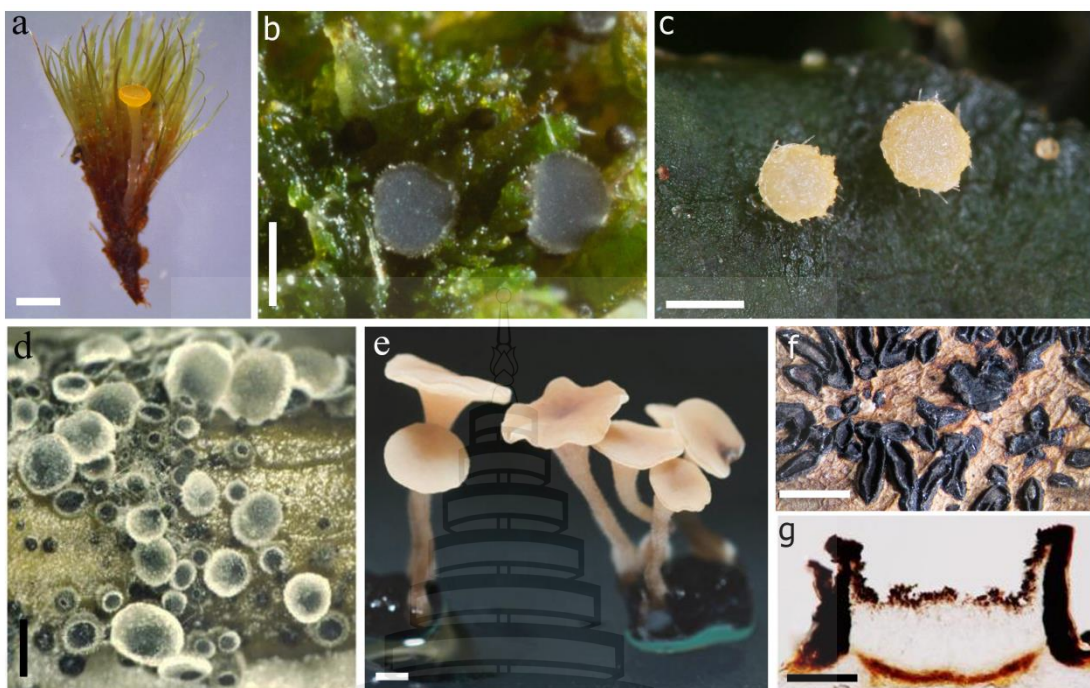


Figure 3.1 Apothecial characters of phytopathogenic discomycetes

Figure 3.1, a *Bryoclavicus campylopi* (Johnston et al., 2013). b *Hyaloscypha hepaticola* (Baral et al., 2009). c *Octosporopsis erinacea* (Egertová et al., 2018). d *Oculimacula yallundae* (Marin-Felix et al., 2019). e *Botrytis cinerea* (Rodenburg et al., 2018). f *Aldona stella-nigra* (Tian et al., 2016). g Close section of *Aldona stella-nigra*'s apothecium (Tian et al., 2016). Scale bars: a, d, e, f = 1 mm, b = 200 µm, c = 500 µm, g = 100 µm

Drepanopezizaceae accommodates eight phytopathogenic discomycete genera, namely *Blumeriella*, *Diplocarpon*, *Drepanopeziza*, *Felisbertia*, *Leptotrochila*, *Pseudopeziza*, *Spilopodia* and *Spilopodiella* (Spegazzini, 1889; Müller, 1989; Graddon, 1984; Johnston et al., 2019; Quandt & Haelewaters, 2021). There are records of *Felisbertia*, *Spilopodia* and *Spilopodiella* pathogenic species, but their disease symptoms, life cycles and virulence factors are not yet reported (Spegazzini, 1889; Müller, 1989; Graddon, 1984). Most species in Drepanopezizaceae infect dicotyledon leaves and scarcely herbaceous plants (Johnston et al., 2019). One species in Drepanopezizaceae that is important for floriculture (especially for cut roses) is *Diplocarpon rosae*.

Diplocarpon rosae (anamorph: *Marssonina rosea*) is a hemibiotrophic pathogen causing defoliation, plant weakening and even the death of susceptible rose varieties planted outdoors (Black et al., 1994; Drewes-Alvarez, 2003; Gachomo et al., 2006). A significant factor affecting the disease severity of *D. rosae* is the low humidity maintenance in greenhouses, which results in minimal infections (Horst, 1983). A large amount of free water in outdoor landscapes stimulates massive germination of *D. rosae* conidia, leading to substantial infections in host plants (Horst & Cloyd, 2007). Following the conidial germination, up to 3 germ tubes are grown from distal ends and differentiate to appressoria for cell penetration (Gachomo & Kotchoni, 2007). However, some germ tubes invade host plants regardless of appressoria formation (Gachomo & Kotchoni, 2007). Germ tubes and/or appressoria penetrate the host cuticle and develop infection vesicles that contain subcuticular and intercellular hyphae (Gachomo, 2005). Subcuticular and intercellular hyphae penetrate epidermal cells, develop an initial haustorium, and then more haustoria are formed towards the leaf periphery (Aronescu, 1934; Gachomo, 2005). Acervuli are formed along the length of the subcuticular hyphae and are visible on leaves, petioles, stems and twigs with the disease (Gachomo & Kotchoni, 2007). The formation of apothecia is suggested to be dependent on weather conditions. If the weather is suitable, apothecia can be formed at the end of winter or spring on old leaves; however, if not, asexual morphs will be developed (Aronescu, 1934; Knight & Wheeler, 1977). The assumption is that cold temperatures in the snowy winter trigger the apothecial formation of *D. rosae* (Dodge, 1931). However, the optimized weather conditions for apothecial formation are not clearly understood, as the germination trial on conidia and ascospores from overwintered infected leaves in different seasons had failed (Knight & Wheeler, 1977). Another hypothesis is that it might be related to a specific *D. rosae* strain, as all strains do not produce apothecia (Dodge, 1931), but this hypothesis requires further studies. Studies on virulence factors of *D. rosae* were conducted by Neu and Debener (2019), in which they revealed that some pectin-degrading enzymes and effector candidate genes are related to haustoria formation and penetration, but further studies are necessary.

Medeolariaceae is a Leotiomycetes family comprising only *Medeolaria farlowii*, an obligate pathogen of *Medeola virginiana* with limited occurrence in the

northeastern US (Thaxter, 1922; Pfister, 1984). Morphologically, *M. farlowii* lacks ascomata, excipular cells and ascospore characterization (LoBuglio & Pfister, 2010). Disease symptoms of this fungus include shortened internodes and swollen tissues, with brown and woolly characters (Thaxter, 1922; LoBuglio & Pfister, 2010). Infected plants were visible with lesions on stems, rhizomes and tubers, and infections spread throughout plants. However, symptoms at the onset of the disease remain unclear (Pfister et al., 2013). It was suggested that its ascospore dispersal is related to the foraging insects on infected plants (Pfister, 1984). Therefore, more studies are required, especially on its life cycle and virulence factors.



Table 3.1 Phytopathogenic discomycetes in Dothideomycetes

Fungal taxa	Diseases	Nutritional mode	Host	Region	References
<i>Rhytidhysterium rufulum</i> (Hysteriales, Hysteriaceae)	Black spot on the wood	Weak pathogen	Woods of dicotyledon	South and North America, Indonesia, Jamaica, Costa Rica, Dominican Republic	Samuels and Müller (1979)
<i>Aldona stella-nigra</i> (Parmulariales, Parmulariaceae)	Leaf spot		<i>Pterocarpus</i> spp.	Indonesia, The Philippines	Tian et al. (2016)
<i>Aldonata pterocarpii</i> (Parmulariales, Parmulariaceae)	Leaf spot		<i>Pterocarpus draco</i>	India	Tian et al. (2016)
<i>Antoniomyces loranthicola</i> (Parmulariales, Parmulariaceae)	Black spot		<i>Gaiadendron punctatum</i>	Panama	Inácio et al. (2012)
<i>Dothidasteromella parvispora</i> (Parmulariales, Parmulariaceae)	Yellowish spot		<i>Olax wightiana</i>	India	Luttrell and Muthapa (1974)
<i>Viegasella pulchella</i> (Parmulariales, Parmulariaceae)	Leaf spot		<i>Sapotaceae</i>	Paraguay	Tian et al. (2016)
<i>Inocyclus angularis</i> (Dothideomycetes order incertae sedis, Asterinales genera incertae sedis)	Tar spot		<i>Pleopeltis astrolepis</i>	Florida, Southern Brazil	Guatimosim et al. (2015)

Table 3.2 Phytopathogenic discomycetes in Eurotiomycetes

Fungal taxa	Nutrition mode	Host	Region	References
<i>Dactylospora heimerlii</i> (Sclerococomycetidae, Sclerococcales, Dactylosporaceae)	Bryophytes parasitic	<i>Plagiochila</i> <i>asplenioides</i>	Alaska, Europe, Japan, Tasmania	Marsh et al. (2010)
<i>Stenocybe nitida</i> (Mycocaliciomycetidae, Mycocaliciales, Mycocaliciaceae)	Cell wall infection	<i>Plagiochila</i> <i>punctata</i>	Europe	Döbbeler and Hertel (2013)

Table 3.3 Phytopathogenic discomycetes in Lecanoromycetes

Fungal taxa	Nutrition mode	Host	Region	References
<i>Absconditella sphagnum</i> (Ostroporales, Stictidaceae)	Bryophytic necrotrophs	<i>Sphagnum compactum</i> , <i>Sphagnum fuscum</i> , <i>Sphagnum magellanicum</i>	Europe	Vězda (1965), Ceynowa-Giełdon (2003)
<i>Caloplaca nivalis</i> (Teloschistales, Teloschistaceae)	Bryophytic necrotrophs	<i>Andreaea</i> sp., <i>Grimmia</i> sp.	Europe, USA, Scotland	Søchting et al. (2008)
<i>Potriphila navicularis</i> (Ostroporales, Odontotremataceae)	Bryophytic parasitic	<i>Polytrichastrum alpina</i>	Antarctica, Asia, Australia, Europe, USA, South America	Döbbeler and Hertel (2013)
<i>Puttea margaritella</i> (Lecanorales genera incertae sedis)	Liverwort parasitic	<i>Ptilidium pulcherrimum</i>	Europe	Stenroos et al. (2009)

Table 3.4 Phytopathogenic discomycetes in Leotiomycetes

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Allantophomopsis cytisporae</i> (Phacidiales, Phacidiaceae)	Black rot	<i>Pinus</i> sp., <i>Vaccinium</i> sp.	Latvia, USA	Crous et al. (2014, 2015)
<i>Ascocalyx pinicola</i> (Helotiales, Godroniaceae)	Canker	<i>Pinus taeda</i>	Japan	Kondo and Kobayashi (1984)
<i>Ascocorticium anomalum</i> (Helotiales, Ascocorticiaceae)	Whitish, corticoid patches	<i>Pinus</i> sp., <i>Picea</i> sp., <i>Juniperus</i> sp., <i>Larix</i> sp., <i>Acacia</i> sp., <i>Betula</i> sp., <i>Calluna</i> sp.	Europe, North Africa, USA	Jülich and de Vries (1982)
<i>Ascodichaena rugosa</i> (Helotiales, Ascodichaenaceae)	Cork wall inhabitation	<i>Fagus sylvatica</i>	Germany	Butin and Pamarewaran (1980)
<i>Ascosorus floridanus</i> (Helotiales, Ascocorticiaceae)	Corticoid patches	<i>Quercus laurifolia</i>	USA	Jülich and de Vries (1982)
<i>Atropellis piniphila</i> (Helotiales, Godroniaceae)	Canker	<i>Pinus</i> sp.	USA	Lohman and Cash (1940)
<i>Belonioscyphella hypnorum</i> (Helotiales genera incertae sedis)	Yellowish decoloration	<i>Bryum moravicum</i> , <i>Anomodon</i> sp., <i>Hypnum</i> sp.	Czech Republic, Finland, Canada, Germany	Egertová et al. (2016)
<i>Bifusella linearis</i> (Rhytismatales, Rhytismataceae)	Brown spot needle blight	<i>Pinus radiata</i>	USA	Broders et al. (2015)
<i>Bloxamia cyatheicola</i> (Helotiales, Bloxamiaceae)	Frond spot	<i>Cyathea delgadii</i> , <i>Cyathea atrovirens</i>	Brazil	Guatimosim et al. (2016)
<i>Blumeriella jaapii</i> (Helotiales, Drepanopezizaceae)	Leaf spot	<i>Prunus</i> spp.	Europe, UK, USA	Annesi et al. (1997), Schuster (2004)
<i>Botrytis cinerea</i> (Helotiales, Sclerotiniaceae)	Gray mold	Over 200 crop plant species	Worldwide	Williamson et al. (2007)
Teleomorph: <i>Botryotinia fuckeliana</i>				

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Botrytis pseudocinerea</i> (Helotiales, Sclerotiniaceae)	Gray mold	<i>Brassica napus</i> , <i>Lycopersicon esculenta</i> , berries, <i>Vitis vinifera</i>	China, France, Germany, Hungary, New Zealand, USA	Walker et al. (2011), Li et al. (2015)
<i>Bryoclavicular campylopi</i> (Helotiales, Bryoglossaceae)	A small lesion on the base of leaf axil cells	<i>Campylopus acuminatus</i>	New Zealand	Johnston et al. (2013)
<i>Bryoglossum gracile</i> (Helotiales, Bryoglossaceae)	Death patches	Tundra moss	Canada, Europe, Greenland, Iceland, USA	Kankainen (1969), Redhead (1977a)
<i>Bryoscyphus atromarginatus</i> (Helotiales, Helotiaceae)	Thallus parasitic	<i>Marchantia polymorpha</i>	The Netherlands	Verkley et al. (1997)
<i>Calycellina leucella</i> (Helotiales, Pezizellaceae)	Defoliation, leaf withering	<i>Betula</i> spp.	Japan	Bennell and Millar (1984)
<i>Cenangium ferruginosum</i> (Helotiales, Cenangiaceae)	Pine dieback	<i>Pinus sylvestris</i>	USA, South Korea, Spain	Santamaría et al. (2007)
<i>Ciboria carunculoides</i> (Helotiales, Sclerotiniaceae)	Popcorn disease	Mulberry	Korea, Japan	Hong et al. (2007)
<i>Ciborinia camelliae</i> (Helotiales, Sclerotiniaceae)	Petal blight	<i>Camellia</i> spp.	World wide	Sarachi et al. (2019)
<i>Cistella japonica</i> (Helotiales genera incertae sedis)	Stem canker	Hinoki cypress	Japan	Yamada et al. (2003)
<i>Clarireedia paspali</i> (Helotiales, Sclerotiniaceae)	Dollar spot	<i>Axonopus compressus</i> , <i>Paspalum vaginatum</i>	China, USA	Hu et al. (2019)
<i>Coccomyces strobi</i> (Rhytismatales, Rhytismataceae)	Bark death, canker	<i>Pinus strobus</i>	USA	Reid and Cain (1961), McMullin et al. (2019)
<i>Collophorina hispanica</i> (Leotiales, Tympanidaceae)	Branch canker	Almond	USA, Iran, Spain	Holland et al. (2018)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Cristulariella depraedans</i> (Helotiales, Sclerotiniaceae)	Leaf spot	<i>Acer</i> spp.	Europe, Japan, Korea, USA, Polland	Redhead (1975), Cho et al. (2016)
<i>Crumenulopsis sororia</i> (Helotiales, Cenangiaceae)	Canker	<i>Pinus</i> spp.	Europe	Vuorinen (2000)
<i>Cudoniopsis pussila</i> (Helotiales, Sclerotiniaceae)	Parasitic on branch	<i>Eugenia proba</i>	Argentina	Spegazzini (1925)
<i>Cyclaneusma minus</i> (Marthamycetales, Marthamycetaceae)	Needle cast	<i>Pinus radiata</i> , <i>Pinus nigra</i>	USA	Frederick et al. (1980)
Basionym: <i>Naemacyclus minor</i> <i>Cyttaria darwinii</i> , <i>C. espinosae</i> , <i>C. exigua</i> , <i>C. gunni</i> , <i>C. nigra</i> , <i>C. pallida</i> (Cyttariales, Cyttariaceae)	Tree cankers and galls	<i>Nothofagus</i> spp.	Australia, New Zealand, South America	Petersen and Pfister (2010)
<i>Darkera abietis</i> (Phacidiales, Phacidiaceae)	Needle blight	<i>Abies balsamiae</i>	USA	Whitney (1975)
<i>Davisomycella ampla</i> (Rhytismatales, Rhytismataceae)	Jackpine needle blight	<i>Pinus</i> spp.	Brazil, New Zealand, USA	Minter and Gibson (1978a)
<i>Dermea abietinum</i> , <i>D. prunastri</i> , <i>D. pruni</i> , <i>D. pseudotsugae</i> (Helotiales, Dermateaceae)	Dieback	Helmlock, plum	China, UK, USA	Dowson (1913), Dodge (1932), Funk (1967), Jiang and Tian (2019)
<i>Didymascella tetraspora</i> (Helotiales genera incertae sedis)	Needle blight	<i>Juniperus communis</i>	Scotland	Phillips and Burdek (1992)
<i>Diplonaevia luzulina</i> (Helotiales, Calloriaceae)	Leaf parasitic	<i>Luzulae</i> spp.	Finland, Norway, Sweden	Nannfeldt (1984a)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Diplocarpon rosae</i> (Helotiales, Drepanopezizaceae) Anamorph: <i>Marssonina rosae</i>	Leaf spot, leaf scorch	<i>Rosa</i> spp.	Canada, Pakistan, UK	Knight and Wheeler (1977)
<i>Discinella schimperi</i> (Helotiales, Discinellaceae)	Circumpolar parasitic	<i>Sphagnum squarrosum</i>	Canada, Slovakia	Redhead and Spicer (1981)
<i>Drepanopeziza brunnea</i> (Helotiales, Drepanopezizaceae) Synonym: <i>Marssonina brunnea</i>	Leaf blight	<i>Populus</i> sp.	USA	Spiers and Hopcroft (1998)
<i>Drepanopeziza ribis</i> (Helotiales, Drepanopezizaceae)	Leaf spot	<i>Ribes</i> spp.	Europe, USA, Japan, Australia and New Zealand	Booth and Waller (1979)
<i>Dumontinia tuberosa</i> (Helotiales, Sclerotiniaceae)	Root rot	<i>Hepatica nobilis</i>	Japan	Uzuhashi et al. (2010)
<i>Durandiella pseudotsugae</i> (Leotiales, Tympanidaceae)	Dime canker	Douglas fir	Canada	Funk (1962)
<i>Elliotiana kernerii</i> (Helotiales, Sclerotiniaceae)	Parasitic on branch	<i>Abies alba</i>	France	Van Vooren et al. (2009)
<i>Elytroderma deformans</i> (Rhytismatales, Rhytismataceae)	Needle cast	<i>Pinus ponderosa</i>	USA	Childs (1968)
<i>Fabrella tsugae</i> (Helotiales, Cenangiaceae)	Needle blight	<i>Tsuga</i> sp.	Canada	Korf (1962)
<i>Felisbertia melastomacearum</i> (Helotiales, Drepanopezizaceae)	Parasitic on leaves	<i>Melastomaceae</i>	Spain	Spegazzini (1889)
<i>Gloeotinia temulenta</i> (Helotiales, Helotiaceae)	Blind seed	<i>Lolium perenne</i> , <i>Secale cereale</i>	Ireland, Scotland, New Zealand, USA	Hardison (1962)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Gremmeniella abietina</i> (Helotiales, Godroniaceae) Anamorph: <i>Brunchorstia pinea</i>	Stem cancer, death of crown and seedlings	<i>Abies</i> spp., <i>Pinus</i> spp.	Turkey, Europe, USA	Özkazanç and Maden (2013)
<i>Grovesiana pyramidalis</i> (Helotiales, Sclerotiniaceae)	Zonate leaf spot	Soursop, avocado	Brazil, Japan, USA	Cline et al. (1983), Bezerra et al. (2008)
<i>Grovesiella abieticola</i> (Helotiales, Godroniaceae)	Stem canker	<i>Abies</i> sp.	USA	Chastagner et al. (2017)
<i>Godronia cassandrae</i> (Helotiales, Godroniaceae)	Canker	Blueberries	Canada	Sabaratnam (2018)
<i>Hyaloscypha hepaticola</i> , <i>Hyaloscypha albocarpa</i> (Helotiales, Hyaloscyphaceae)	Rhizoid infection	<i>Cephaloziella</i> spp.	Belgium, Finland, Germany	Baral et al. (2009)
<i>Hymenoscyphus fraxineus</i> (Helotiales, Helotiaceae)	Ash dieback	Ash trees	Europe	Baral et al. (2014)
<i>Hypodermella laricis</i> (Rhytismatales, Rhytismataceae)	Needle cast	<i>Larix</i> spp.	Asia, Europe, USA	Minter (1988)
<i>Hysteronaevia luzulicola</i> (Helotiales genera incertae sedis)	Leaf infection	<i>Luzula arcuata</i>	Canada, Sweden	Nannfeldt (1984b)
<i>Isthmiella quadrispora</i> (Rhytismatales, Rhytismataceae)	Needle blight	<i>Abies lasiocarpa</i>	USA	Ziller (1968)
<i>Kohninia linnaeicola</i> (Helotiales, Sclerotiniaceae)	Parasitic on petioles	<i>Linnaea borealis</i>	Norway	Holst-Jensen et al. (2004)
<i>Lachnellula willkommii</i> , <i>L. decidua</i> (Helotiales, Lachnaceae)	Canker	<i>Larix</i> spp.	Asia, Europe, USA	Yde-Andersen (1979)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Lachnopsis catarinensis</i> (Helotiales, Lachnaceae)	Frond blight	<i>Dicksonia sellowiana</i>	Brazil	Guatimosim et al. (2016)
<i>Lachnum spartina</i> (Helotiales, Lachnaceae)	Dead shoot	<i>Spartinae alterniflora</i>	USA	Cantrell et al. (1996)
<i>Lambertella corni-maris</i> (Helotiales, Rutstroemiaceae)	Mummified fruits	<i>Malus prunicola</i> , <i>Prunus domestica</i> , <i>Sorbus aucuparia</i>	Czech Republic, Europe	Palmer et al. (1994)
<i>Lahmia kunzei</i> (Lahmiales, Lahmiaceae)	Branch dieback	<i>Populus</i> sp.	USA	Enebak et al. (1996)
<i>Leptotrochila medicaginis</i> (Helotiales, Drepanopezizaceae)	Yellow leaf blotch	Alfalfa	USA, Canada	Malvick (1988)
<i>Lirula macrospora</i> (Rhytismatales, Rhytismataceae)	Needle blight	<i>Picea</i> sp.	USA	Walla (2016)
<i>Lophodermella concolor</i> (Rhytismatales, Rhytismataceae)	Needle cast	<i>Pinus</i> sp.	USA	Minter and Millar (1993)
<i>Lophodermium seditiosum</i> (Rhytismatales, Rhytismataceae)	Pine blight	<i>Pinus sylvestris</i>	USA, Europe	Minter and Millar (1980), Sinclair (1987)
<i>Lophophacidium dooksii</i> (Rhytismatales, Rhytismataceae)	Needle cast	<i>Pinus radiata</i>	USA	Broders et al. (2015)
<i>Marthamyces emerginatus</i> (Marthamycetales, Marthamycetaceae)	Leaf spot	Eucalyptus	Australia	Crous et al. (2019)
<i>Medeolaria farlowii</i> (Medeolariales, Medeolariaceae)	Leaf whorl, leaf brown	<i>Medeola virginiana</i>	USA	LoBuglio and Pfister (2010)
<i>Meloderma desmazieri</i> (Rhytismatales, Rhytismataceae)	Needle cast	<i>Pinus strobus</i>	Europe	Bednářová et al. (2013)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Micraspis acicola</i> (Micraspidales, Micraspidaceae)	Snow blight	<i>Picea mariana</i>	Canada	Darker (1963), Quijada et al. (2020)
<i>Mniaecia jungermanniae</i> (Leotiales, Mniaeciaceae)	Swollen rhizoid, malformed spores	<i>Cephalozia</i> , <i>Diplophyllum</i> , <i>Scapania</i>	Belgium	Raspé and Sloover (1998), Pressel and Duckett (2011)
<i>Monilinia fructigena</i> (Helotiales, Sclerotiniaceae) Anamorph: <i>Monilia fructigena</i>	Brown rot, mummy fruit	Actinidiaceae, Berberidaceae, Ebenaceae, Ericaceae, Moraceae, Rosaceae, Solanaceae, Vitaceae	Egypt, Morocco, east and south Asia, Europe, USA, Brazil, Chile, Uruguay	CABI/EPPO (2000), Leeuwen et al. (2002)
<i>Myriosclerotinia curreyana</i> (Helotiales, Sclerotiniaceae)	Black spot on stems	<i>Juncus</i> spp.	Denmark, Kroatia, Norway, UK, USA	Schumacher and Kohn (1985)
<i>Naemacyclus fimbriatus</i> (Marthamycetales, Marthamycetaceae)	Needle cast	<i>Pinus</i> spp.	Europe, USA	Vujanovic et al. (2007)
<i>Neofabraea perenans</i> (Helotiales, Dermateaceae)	Bull's eye rot	<i>Malus domestica</i>	USA	Aguillar et al. (2018)
<i>Oculimacula yallundae</i> (Helotiales, Ploettnerulaceae)	Eye spot	Poaceae, winter wheat	Africa, Australia, Europe, South America, New Zealand, USA	Marin-Felix et al. (2019)
<i>Ovulinia azaleae</i> (Helotiales, Sclerotiniaceae)	Petal blight	Azalea, rhododendron	USA, Japan, Europe, New Zealand, Australia	Backhaus (1994)
<i>Pezicula cinnamomea</i> (Helotiales, Dermateaceae)	Canker	Red oak	Europe	Kehr (1991), Ooki et al. (2003)
<i>Pezicula corticola</i> (Helotiales, Dermateaceae)	Bull's eye rot	Japanese pear	Japan	Nitta et al. (2002)
<i>Phacidium lacerum</i> (Phacidales, Phacidiaceae) Anamorph: <i>Ceuthospora pinastri</i>	Fruit rot, leaf spot	Apple, pear	USA	Wiseman et al. (2016), Crous et al. (2019)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Phaeosclerotinia nipponica</i> (Helotiales, Sclerotiniaceae) Basionym: <i>Sclerotinia phaeospora</i>	Fruit rot	<i>Malus</i> sp.	Japan	Hori (1916)
<i>Ploioderma lethale</i> (Rhytismatales, Rhytismataceae)	Pine needle blight	<i>Pinus</i> sp.	USA	Minter and Gibson (1978b)
<i>Potebniamyces piri</i> (Phacidiales, Phacidiaceae)	Fruit rot (Phacidiopycnis rot)	Pear	USA	Xiao and Boal (2007)
<i>Potridiscus polymorphus</i> (Helotiales genera incertae sedis)	Bryophytes parasitic	<i>Dendroligotrichum</i> sp.	Australia, New Zealand	Döbbeler and Hertel (2013)
<i>Pragmopora pithya</i> (Leotiales, Tympanidaceae)	Canker	Douglas fir	USA	Funk (1975)
<i>Pseudopeziza medicaginis</i> (Helotiales, Ploettnerulaceae)	Common leaf spot	Alfalfa	Europe, USA, Oceania	Jones (1919), Townsend (1951)
<i>Pseudophacidium diselmae</i> (Phacidiales, Phacidiaceae)	Stem canker	<i>Diselma archeri</i>	Australia	Yuan et al. (2000)
<i>Pyrenopeziza brassicae</i> (Helotiales, Mollisiaceae)	Light leaf spot	<i>Brassicae napus</i>	Europe, UK	Boys et al. (2007)
<i>Redheadia quercus</i> (Helotiales, Sclerotiniaceae)	Brown leaf spots	<i>Quercus acutissima</i>	Japan	Suto and Suyama (2005)
<i>Rhabdocline pseudotsugae</i> , <i>Rhabdocline parkeri</i> (Helotiales, Cenangiaceae)	Needle cast	<i>Larix</i> sp., <i>Pseudotsugae menziesii</i>	USA	Gernandt et al. (1997)
<i>Rhytisma acerinum</i> , <i>R. punctatum</i> (Rhytismatales, Rhytismataceae)	Tar spot	<i>Acer platanoides</i> , <i>A. pseudoplatanus</i>	Europe, USA	Horst (2008), Held et al. (2018)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Sarcotrichila alpina</i> (Helotiales, Cenangiaceae)	Needle cast	<i>Larix</i> spp.	Europe, USA	Jalkanen (2016)
<i>Schroeteria decaisneana</i> (Helotiales, Sclerotiniaceae)	Seed infection	<i>Veronica hederifolia</i> , <i>Veronica aarvensis</i>	Germany	Baral et al. (2022)
<i>Schizothyrioma ptarmicae</i> (Helotiales, Dermateaceae)	Leaf lesion	<i>Achillea ptarmica</i>	France, Germany, Holland, Poland	Holm (1971), Adamska (2004)
<i>Sclerencoelia pruinoso</i> (Helotiales, Sclerotiniaceae)	Sooty bark canker	<i>Populus tremuloides</i> , <i>P. grandidentata</i> , <i>Populus tremula</i>	Northern America and Northern Europe	Pärtel et al. (2017)
<i>Scleromitula shiraiana</i> (Helotiales, Sclerotiniaceae)	Popcorn disease	Mulberries	China, Japan, Korea	Schumacher and Holst-Jensen (1997)
<i>Sclerotinia minor</i> (Helotiales, Sclerotiniaceae)	Rot root	More than 90 plant species	Europe, Asia, USA, South America, Oceania	Melzer et al. (1997), CABI/EPPO (2003)
<i>Sclerotinia sclerotiorum</i> (Helotiales, Sclerotiniaceae)	Watery soft rot, cottony soft rot	More than 400 plant species and pteridophytes	USA, South America, Oceania, Asia, Canada	Boland and Hall (1994), CABI/EPPO (2005)
<i>Scolecoclachnum pteridii</i> (Helotiales, Lachnaceae)	Frond spot	<i>Pteridium arachnoideum</i>	Brazil	Guatimosim et al. (2016)
<i>Seaverinia geranii</i> (Helotiales, Sclerotiniaceae)	Rhizome parasitic	Geranium	USA	Whetzel (1945)
<i>Septotinia podophyllina</i> (Helotiales, Sclerotiniaceae)	Leaf lesion, leaf blotch	<i>Podophyllum peltatum</i>	Asia, Europe, USA	Whetzel (1937), Kam (1973)
<i>Spilopodia ranunculi</i> (Helotiales, Drepanopezizaceae)	Parasitic on epigeal stolon	<i>Ranunculi repens</i>	UK	Graddon (1984)
<i>Spilopodiella arxii</i> (Helotiales, Drepanopezizaceae)	Parasitic on leaves	<i>Caricis sempervirens</i>	Switzerland	Müller (1989)

Table 3.4 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	References
<i>Stamnaria americana</i> (Helotiales genera incertae sedis)	Fern parasitic	<i>Equisetum hyemale</i>	USA	Seaver (1932), Künkele et al. (2005)
<i>Streptotinia caulophylli</i> (Helotiales, Sclerotiniaceae)	Target spot	<i>Caulophyllum thalictroides</i> , <i>Menispermum dauricum</i>	Canada, China	Elliott (1962), Bai et al. (2014)
<i>Stromatinia narcissi</i> (Helotiales, Sclerotiniaceae)	Bulb rot	<i>Narcissus</i> , <i>Zephyranthes</i>	Canada	Drayton and Groves (1952)
<i>Symphyosirinia clematidis</i> (Helotiales, Helotiaceae)	Seed pathogen	<i>Clematis</i> spp.	Germany, Spain	Baral (1994), Gams et al. (2009)
<i>Therrya piceae</i> (Rhytismatales, Rhytismataceae)	Canker	<i>Picea glauca</i>	USA	Funk (1982)
<i>Trochila laurocerasi</i> (Helotiales, Cenangiaceae)	Leaf spot	<i>Prunus laurocerasus</i>	UK, Europe, Australia, Poland	Stoykov and Assyov (2009)
<i>Valdensinia heterodoxa</i> (Helotiales, Sclerotiniaceae)	Leaf spot	<i>Vaccinium corymbosum</i>	Japan, Canada, USA, Europe	Norvell and Redhead (1994)
Teleomorph: <i>Valdensia heterodoxa</i>				

Table 3.5 Phytopathogenic discomycetes in Neolectomycetes

Fungal taxa	Nutritional modes	Host	Region	References
<i>Neolecta vittelina</i> (Neolectales, Neolectaceae)	Rootlet parasitic	Conifers	USA, Norway	Redhead (1977b, 1979), Landvik et al. (2003)

Table 3.6 Phytopathogenic discomycetes in Pezizomycetes

Fungal taxa	Diseases or nutritional modes	Host	Region	Notes	References
<i>Anthracobia maurilabra</i> , <i>Anthracobia tristis</i> (Pezizales, Pyrenomataceae)	Radicle elongation reduction	Pine seedlings	Canada	Under certain temperatures in monoxenic culture caused disease symptom	Egger and Paden (1986a, b)
<i>Ascobolus carbonarius</i> , <i>Ascobolus epimyces</i> (Pezizales, Ascobolaceae)	Radicle elongation reduction	Pine seedlings	Canada	Under certain temperatures in monoxenic culture caused disease symptom	Egger and Paden (1986a, b)
<i>Caloscypha fulgens</i> (Pezizales, Caloscyphaceae)	Seed germination decline	Lodge pole pine	Canada		Egger and Paden (1986a)
<i>Filicupula suboperculata</i> (Pezizales genera incertae sedis)	Parasitic on phyllodia	<i>Frullania tamarisci</i>	Scotland		Yao and Spooner (1996)
<i>Geopyxis carbonaria</i> (Pezizales, Tarzettaceae)	Chlorotic seedlings	<i>Pinus contorta</i>	Canada, Norway		Egger and Paden (1986b), Vrålstad et al. (1998)
<i>Gyromitra infula</i> (Pezizales, Discinaceae)	Chlorotic seedlings	Pine seedlings	Canada	Under certain temperatures in monoxenic culture caused disease symptom	Egger and Paden (1986b)
<i>Lamprospora dictydiola</i> (Pezizales, Pyrenomataceae)	Haustoria infection	<i>Tortula muralis</i>	Germany, Gorgia, Spain, Ukraine		Vega et al. (2019)

Table 3.6 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	Notes	References
<i>Neottiella ricciae</i> (Pezizales, Pyrenomataceae)	Thallus and rhizoid infection	<i>Riccia</i> spp.	Canary island, Europe, India, USA		Németh et al. (2017)
<i>Octospora microtricha</i> , <i>O. nematospora</i> (Pezizales genera incertae sedis)	Biotrophic parasites	<i>Frullania</i> spp.	New Zealand, Spain		Döbbeler et al (2018)
<i>Octospora leucoloma</i> (Pezizales, Pyrenomataceae)	Parasitic on bryophytes	<i>Bryum</i> sp., <i>Funaria</i> sp., <i>Leptobryum</i> sp.	Bulgaria, Turkey, USA		Çolak and Kaygusuz (2017)
<i>Octosporopsis erinacea</i> (Pezizales, Pyrenomataceae)	Parasitic on bryophytic thalli	<i>Dumortiera hirsuta</i> , <i>Riccardia</i> sp.	Malaysia		Egertová et al. (2018)
<i>Peziza pratervisa</i> (Pezizales, Pezizaceae)	Seed germination decline	Lodge pole pine	Canada		Egger and Paden (1986a)
<i>Pithya cupressi</i> (Pezizales, Sarcoscyphaceae)	Twig wilting disease	<i>Juniperus</i> , <i>Cupressus</i> , <i>Thuja</i> , <i>Sequoia</i>	China, Europe, Japan, USA, Taiwan		Sawada (1931), Wu (2001)
<i>Plicaria endocarpoides</i> (Pezizales, Pezizaceae)	Seed germination decline	Lodge pole pine	Canada		Egger and Paden (1986a)
<i>Pyropyxis rubra</i> (Pezizales, Pyrenomataceae)	Seed germination decline	Oak	Canada		Egger and Paden (1986a)
<i>Rhizina undulata</i> (Pezizales, Rhizinaceae)	Root rot	Coniferous trees	Asia, Europe, USA, South Africa		Wingfield and Swart (1994)

Table 3.6 (continued)

Fungal taxa	Diseases or nutritional modes	Host	Region	Notes	References
<i>Tricharina praecox</i> (Pezizales, Pyrenomataceae)	Phloem degeneration	Pine seedlings	Canada	Under certain temperatures in monoxenic culture caused disease symptom	Egger and Paden (1986a, b)
<i>Trichophaea hemisphaerioides</i> (Pezizales, Pyrenomataceae)	Moderate chlorotic symptom	Pine seedlings	Canada	Under certain temperatures in monoxenic culture caused disease symptom	Egger and Paden (1986b)
<i>Urnula craterium</i> (Pezizales, Sarcosomataceae)	Canker	Oak, hardwood trees	Europe, USA		Davidson (1950), Wolf (1958), Ayer et al. (2000)

Sclerotiniaceae comprises 31 genera of parasitic fungi (Johnston et al., 2019; Quandt & Haelewaters, 2021; Wijayawardene et al., 2022). Their teleomorphs are recognized, except for some genera, such as *Amphobotrys* (Hennebert, 1973), *Haradamyces* (Masuya et al., 2009) and *Myrioconium* (Davidson & Cash, 1933), which are known only from their asexual morphs. Due to their massive fungal infections on agricultural and horticultural commodities (Smith, 1900; Boland & Hall, 1994; Leeuwen et al., 2002; Elad et al., 2016; De Miccolis Angelini et al., 2018), Sclerotiniaceae became the most studied group among all the families in Leotiomycetes, especially *Botrytis cinerea* (Whetzel, 1945; Holst-Jensen et al., 1997; Dean et al., 2012; Navaud et al., 2018). *Botrytis cinerea* infects more than 500 host genera ranging from agricultural to horticultural, ornamental, cover crops and non-vascular plants (Elad et al., 2016). Fungal diseases caused by *Botrytis cinerea*, such as gray mold and blight canker that damage valuable economic commodities immensely gained attention from phytopathologists (Dean et al., 2012). The life cycle of *Botrytis cinerea* was described by Williamson et al. (2007). Infection of *Botrytis cinerea* begins under wet conditions with over 93% humidity, allowing conidia to germinate (Williamson et al., 1995). Conidia are mainly spread by wind but also via water droplets, insects, and unsanitised agricultural tools and clothes (Jarvis, 1977). Conidial germination may also be affected by ethylene gas production from host plants (Elad & Volpin, 1988). Two to five germ tubes produced during conidial germination and appressoria are helpful for host cell penetration and infection (Williamson et al., 2007). On the plant surface, conidial penetration of *Botrytis cinerea* is facilitated by the cutinolytic enzyme activities (Salinas & Verhoeff, 1995), while the infections on injured tissues started by direct penetration through the injured tissues (Van Kan, 2005). The fungus produces several substances in the host tissue, such as botrydial, cellulases, polygalacturonases (ecto and endo) and oxalic acid, which are detrimental and act as virulence factors (Nakajima & Akutsu, 2014). As a host defense, plants trigger programmed cell death and hypersensitive responses upon pathogen recognition and kill the infected host tissues to prevent infection (Govrin & Levin, 2000). Vegetative mycelia, conidia and sclerotia are asexual forms of *Botrytis cinerea* used for dispersal and survival. In temperate regions, sclerotia grow in early spring and produce

conidiophores and multinucleate conidia. Spermatization of sclerotia leads to the production of apothecia and later ascospore formation (Williamson et al., 2007).

Oculimacula yallundae belongs to Ploettnerulaceae and parasitizes barley, oats, rye, some grasses and wheat (Murray et al., 1994; Chapman et al., 2008). *Oculimacula yallundae* is a soil-borne fungus causing eye spot disease or elliptical-shaped lesions on leaf sheath at the stem base (Lucas et al., 2000). Conidial germination of *Oculimacula yallundae* on coleoptile facilitated by rain splashes (Bateman & Taylor, 1976). Conidial germ tubes develop into appressoria, which directly penetrate coleoptile tissues inter- and intracellularly via colonizing leaf sheath cells and ultimately invading the stem via successive leaf sheath (Soulié et al., 1985; Daniels et al., 1991). Blein et al. (2009) report *O. yallundae* as a necrotrophic fungus (Groenewald et al., 2003) and showed that the fungus exhibits both asymptomatic and symptomatic stages in its infection cycle, which is a characteristic of a hemibiotroph (Lucas et al., 2000). The asymptomatic stage is shown during conidial colonization on coleoptile (Lucas et al., 2000; Blein et al., 2009), while the symptomatic phase is shown after the pathogen penetrates leaf sheath epidermal cells and develops in a confined space, leading to death cells (Blein et al., 2009). Apothecia of *O. yallundae* were spotted on post-harvest wheat stubble during spring and autumn (Dyer et al., 1994; Vera & Murray, 2016). However, further studies are needed to determine initial apothecia development and the environmental factors that influence it (Vera & Murray, 2016).

Gremmeniella abietina (synonym: *Scleroderris lagerbergii*) is one of the most devastating phytopathogenic discomycetes in Leotiomycetes, infecting forest and nursery commodities (Özkazanç & Maden, 2013). Initially, the pathogen is indigenous to Europe, widespread to North America, and is the causative agent of dieback and cankers on various ages of coniferous trees in Europe and North America (Setliff et al., 1975; Kaitera et al., 2000; Porta et al., 2008). Infected plants are characterized by necrotic lesions formed on needles and branches with distorted terminal twigs (Santamaría et al., 2003). A study conducted in Southern Sweden showed that the life cycle of *G. abietina* is completed within two years (Hellgren & Barklund, 1992). The infection mode of *G. abietina* in red pine seedlings was reported by Ylimartimo et al. (1996). Infection begins with the germination of conidia attached to the outermost

bracts, subtending the short shoots and the inner bracts at the needle base (Ylimartimo et al., 1996). The emerging hyphae from conidia are enveloped by a fibrillar extracellular sheath containing chitin, galactose, lipids, polygalacturonic acids and proteins (Benhamou & Ouellette, 1987a; b). The hypha then penetrates stomata and colonizes the underlying bract tissues (Ylimartimo et al., 1996). Colonization by *G. abietina* occurs from the outward growth of hypha through the epidermis into intercellular spaces of cell junctions and middle lamellae, wholly or partly embedded in host cell walls. Hypha then reached the lumen and periderm cell walls, isolating the bract from the shoot. Hyphal tips that are attached to host cell walls secrete extracellular enzymes, such as exoglucanases, laccases, peroxidases and polygalacturonases, to degrade the host cell wall (Ylimartimo et al., 1996; Simard et al., 2005; 2012). In the field, conidia (produced by pycnidia) and ascospores (released by apothecia) are the infection sources of *G. abietina* on coniferous trees (Kaitera et al., 1997). In Sweden, conidia commonly disperse from April to July and sporulate until the end of August, and ascospores are released a while later after the summer (Laflamme & Archambault, 1990; Hellgren & Barklund, 1992). Conidia and ascospores initiate the infection in the summer but penetrate further until the periderm and living tissues of pine shoots in the following winter (Lang & Schutt, 1974; Patton et al., 1984). Apothecia and pycnidia grow on dead shoots of living infected trees for at least two years (Hellgren & Barklund, 1992; Kaitera et al., 1997). Environmental factors, such as high humidity and water source availability, aid the infection of *G. abietina* (Skilling, 1972), while mild temperature increases its symptom development (Marosy et al., 1989).

Besides infecting vascular plants, discomycetes in Leotiomyces also infect non-vascular plants, such as bryophytes and pteridophytes (Redhead & Spicer, 1981; Künkele et al., 2005; Baral et al., 2009; Döbbeler & Hertel, 2013). Some discomycete Leotiomyces form biotrophic associations with bryophytes, such as *Discinella schimperi* on *Sphagnum squarrosum* (Redhead & Spicer, 1981) and *Mniaecia jungermanniae* on *Cephalozia bicuspidata* (Raspé & Sloover, 1998). Redhead and Spicer (1981) described the action mode of *Discinella schimperi* on mucilaginous cells of the hosts. Once a single hypha contacts the apical papilla of the host cell, it develops an appressorium, which then grows in branches, forming a dorm, covering most of the

cells (Redhead & Spicer, 1981). Penetration into apical papilla cells is followed by the formation of a branched haustorium-like structure inside the host cell wall. The haustorium-like structure grows excessively and spreads out until it reaches mucilaginous cells. Infected mucilaginous cells are often used to diagnose the presence of *D. schimperii* on *Sphagnum squarrosum* (Redhead & Spicer, 1981). However, further studies are needed on the virulence factors of *D. schimperii*. In contrast to *D. schimperii*, the action mode of *Mniaecia jungermanniae* as a biotroph was not described in detail, and the formation of either appressoria or haustoria on *Cephalozia bicuspidate* was never asserted (Raspé & Sloover, 1998). The biotrophic association between *M. jungermanniae* and its host is unclear as it was described merely on the swollen tip of bryophyte rhizoid responsible for rhizoid penetration (Killian, 1926). Among bryophyte species, *Marchantia polymorpha* is reported to be the most valuable due to its thallus paste for the treatment of insect bites and external inflammation (Chandra et al., 2017). However, no economic losses have been reported due to fungal damage caused by *Bryoscyphus atromarginatus* on this host.

Four discomycetes in Leotiomycetes, such as *Bloxamia cyatheicola*, *Lachnopsis catarinensis*, *Scolecoclachnum pteridii* and *Stamnaria americana*, are reported to infect pteridophytes (Guatimosim et al., 2016; Haelewaters et al., 2018). *Bloxamia cyatheicola* causes frond spots, characterized by irregular chlorotic to pale brown necrotic lesions on *Cyathea delgadii* pinnulae. *Lachnopsis catarinensis* causes frond blight, characterized by a necrotic area at the apex of *Dicksonia sellowiana* pinnulae, and *Scolecoclachnum pteridii* causes frond spots, characterized by pale brown necrotic area on individual pinnulae of *Pteridium arachnoideum* (Guatimosim et al., 2016). *Stamnaria americana* was documented by Haelewaters et al. (2018) as a pathogen on *Equisetum hyemale*, but further studies on disease symptoms were not reported. This study found that reports on the action modes of aforementioned discomycetes are lacking, and even the species records of discomycetous fungi associated with fern species are still limited (Guatimosim et al., 2016). Similar to their biotrophic associations with bryophytes, their associations with pteridophytes depend primarily on the prevalence of their hosts (Döbbeler, 1997; Davey & Curah, 2006). Due to the lack of hosts and the rarity of some plants resulting from deforestation, these pathogenic

leotiomycetous taxa can be categorized as endangered, regardless of their phytopathogenic status (Windisch, 2002).

3.3.6 Phytopathogenic Discomycetes in Neoelectomycetes

Being the only order in Neoelectomycetes (Landvik et al., 1993), Neoelectales accommodates *Neoelecta*, the only discomycetous genus in Taphrinomycotina (Eriksson & Winka, 1997). Most *Neoelecta* species are saprobes; the only pathogen reported is *Neoelecta vitellina* (Table 3.5). Phytopathogenic discomycetes in Neoelectomycetes are characterized by their yellow, club-like apothecia, unitunicate, cylindrical asci with no paraphyses, and hyaline, fusoid to globose ascospores (Landvik et al., 2003; Friebe, 2015). *Neoelecta vitellina* was reported as a pathogen on rootlets of conifers (Redhead, 1979) despite the lack of evidence on its nutrition mode (Landvik et al., 2003). To date, detailed research on the life cycle and pathogenicity factors of *N. vitellina* has not yet been studied (Healy et al., 2013).

3.3.7 Phytopathogenic Discomycetes in Pezizomycetes

Phytopathogenic discomycetes in Pezizomycetes are characterized by bright or dull colored, superficial, sessile, apothecia, sometimes with setae, unitunicate, operculate or inoperculate, long to short, cylindrical, claviform asci with paraphyses, and hyaline to brown, fusoid to ellipsoid ascospores (Fitzpatrick, 1917; Wolf, 1958; Çolak & Kaygusuz, 2017; Döbbeler et al., 2018; Egertová et al., 2018). Phytopathogenic *Pezizomycetes* cause diseases in various host plants, such as pine seedlings (Egger & Paden, 1986a; b), hardwood trees (Davidson, 1950; Hughes, 1960; Gibson, 1979; Wingfield & Swart, 1994; Cha et al., 2009) and bryophytes (Döbbeler et al., 2018; Egertová et al., 2018; Vega et al., 2019). In this study, we compiled 19 genera within eight families recognized as phytopathogenic discomycetes (Table 3.6). Table 3.6 is an underestimation since each genus is listed with at least one representative species in contrast to the actual pathogenic species numbers. The listed discomycetes infect plants with various disease symptoms, such as chlorosis, phloem degeneration (Egger & Paden, 1986a; b), canker (Davidson, 1950; Hughes, 1960), and root rot (Gibson, 1979). They are recorded in various regions (Table 3.6) (Wingfield & Swart, 1994; Wu, 2001; Cha et al., 2009).

The most prominent pathogenic discomycete in Pezizomycetes is *Rhizina undulata*, which causes root rot on coniferous plantations in Asia, Europe, South Africa and North America (Gibson, 1979; Wingfield & Swart, 1994). As a pyrophilous fungus, ascospore germination of *R. undulata* was stimulated by heat shock at 35–45 °C (Jalaluddin, 1967a). *Rhizina undulata* favors acidic soil for growth, and its mycelia spread through soil, infecting conifer roots that come in contact (Jalaluddin, 1967a; Murray & Young, 1961). The colonization of *R. undulata* negatively impacts coniferous seedlings and mature trees (Murray & Young, 1961; Weir, 1915). *Rhizina undulata* infects and kills vascular tissues of pine seedlings (Egger & Paden, 1986a; b). Annually, *R. undulata* infected conifer fields vary in their devastation lengths in different regions. In Japan and Korea, *R. undulata* infects 3–6 m irregular rings of coniferous fields (Sato et al., 1974; Lee & Kim, 1990), while in the USA and Europe, 0.6–1 m of radial fields was affected (Phillips & Burdekin, 1982; Tainter & Baker, 1996). Besides abiotic factors such as alkaline soil (pH 7–8) (Jalaluddin, 1967b), biotic factors such as the presence of broad leaves and conifer absence can be limiting factors for *R. undulata* (Semashko, 2014). Detailed studies on the life cycle, infection mode and virulence factors of *R. undulata* are still lacking. Perhaps it is due to the difficulties of inducing the disease on the hardwood (Lee et al., 2005) and culturing ascospores and conidia from *R. undulata* mycelia in the laboratory (Semashko, 2014).

In addition to *Rhizina undulata*, several pathogens from various families in Pezizomycetes are causing diseases in pine seedlings. *Caloscypha fulgens* and *Pyropyxis rubra* cause seedling death, while *Geopyxis carbonaria*, *Tricharina praecox*, and *Trichophaea hemisphaerioide* trigger moderate disease symptoms. Other pezizomycetous pathogens, such as *Anthracobia maurilabra* and *Gyromitra infula*, cause weak infections in root seedlings (Egger & Paden, 1986a). Further detailed descriptions of biotrophic associations between the aforementioned Pezizomycetes and pine seedlings were discussed by Egger and Paden (1986a, b). However, more studies are needed to confirm their pathogenicity status, especially the life cycle and virulence factors responsible for fungal diseases.

Discomycete Pezizomycetes are found mostly in humid forests, which provide suitable habitats for various host plants, including bryophytes. Six genera of

phytopathogenic Pezizomycetes, namely *Lamprospora*, *Neottiella*, *Octospora*, *Octosporopsis*, *Filicupula* and *Octosporella*, infect bryophytes (Table 3.6) and develop biotrophic associations with their related hosts. Most recent records on *Lamprospora* species were documented, including a brief description regarding its biotrophic infection on bryophytes. Vega et al. (2019) documented *Lamprospora dictydiola* as one of the three byophylous described. *Lamprospora dictydiola* develops appressoria enveloped by a hyphal layer to infect and grow on rhizoids of *Tortula muralis*. Appressoria are connected with thin-walled, irregular-shaped, aseptate haustoria. From the middle part of appressoria, infection pegs emerge and invade the rhizoid wall. Appressoria and haustoria are important structures in bryophyte infection (Döbbeler, 1980) and also reported in *Octosporella* species (Döbbeler et al., 2018).

3.3.8 Economic Importance of Selected Phytopathogenic Discomycetes

Phytopathogenic discomycetes in different classes show various degrees of economic impact. Phytopathogenic species in Dothideomycetes (e.g., *Mycosphaerella graminicola*) and Eurotiomycetes (e.g., *Aspergillus flavus* and *A. parasiticus*) were reported to reduce the yield and product quality by causing diseases on agricultural and horticultural commodities (Cotty et al., 1994; Hofmann, 2010; Orton et al., 2011; Ohm et al., 2012). However, the damage caused by discomycetes in Dothideomycetes and Eurotiomycetes (Tables 3.1, 3.2) are not significant on their related hosts, hence no records were found for their economic losses (Inácio & Canon, 2008; Guatimosim et al., 2015). Discomycetes in Lecanoromycetes mostly parasitize lichens (Lawrey & Diederich, 2003), and some infect bryophytes (Döbbeler & Hertel, 2013). Still, none have been reported as pathogens on valuable agricultural dicots and monocots (Hibbett et al., 2007; Sørø et al., 2008; Gueidan et al., 2015). Economic losses are also not documented for phytopathogenic Neolectomycetes (Healy et al., 2013), while the loss for one discomycete in Pezizomycetes was noted (Thies et al., 1979). Still, the financial damage is apparent for pathogenic discomycetes in Leotiomyces (Dean et al., 2012). Host plants affected by pathogenic Leotiomyces are exceptionally wider compared to other discomycete classes. Plants affected range from non-vascular plants (bryophytes and pteridophytes) to agricultural and forestry commodities (i.e. orchard, spice, staple,

ornamental, cover and oil seed crops), including nursery material (Table 3.4) (Boland & Hall, 1994; Künkele et al., 2005; Williamson et al., 2007; Pressel & Duckett, 2011).

3.3.9 Control Strategies for Selected Phytopathogenic Discomycetes

Diplocarpon rosae causes black spot disease on *Rosa* spp. planted in outdoor landscapes (Knight & Wheeler, 1977). *Rosa* spp. are high-valued ornamental plants with cultivation areas of more than 800 ha, and around 18 million stems are harvested annually worldwide (Blom & Tsujita, 2003). In the USA, roses are considered one of the floricultural crops worth approximately \$ 24–28 million in 2018–2019 (USDA, 2020a). Infection of *D. rosae* does not cause mortality in the plant host, but the host weakening, such as weight loss, is apparent (Gachomo et al., 2007). Lyle (1960) found that infection of *D. rosae* may cause weight loss for *Rosa* spp., up to 73–98%. Control strategies available for *D. rosae* include several cultural practices, such as proper sanitation (pruning stems bearing infected leaves and removing them from the planted area), avoiding excessive water and providing sufficient distance between each plant (Horst, 1983). However, if those sanitation efforts are insufficient or too late, fungicide applications can be used (Behe et al., 1993). Recent research found that synthetic fungicides, such as penconazole or boscalid plus pyraclostrobin combined with inducers (a stimulant beneficial in inducing host defense responses) provide control against *Diplocarpon rosae* (Percival & Graham, 2021). Another control effort to suppress *D. rosae* infection was studying potential resistant genes in new rose cultivars. The *Rdr1*, *Rdr2*, *Rdr3* and *Rdr4* genes were identified as the potential loci against *D. rosae* black spot in the latest research, and further studies on these genes are vital in building up genetic resistance in rose cultivars (Menz et al., 2017; Zurn et al., 2018).

Pseudopeziza medicaginis is a discomycete species causing common leaf spots on economically important legume crops, especially alfalfa (*Medicago sativa*) (Townsend, 1951). Alfalfa is a plant commodity cultivated in temperate regions for pasture, silage, seed, and cover crops (Bouton, 2021). Infection of *P. medicaginis* on alfalfa triggers leaf spot disease that reduces dry matter by up to 40% (Morgan & Parberry, 1977). A recent study estimated a yield reduction of 62% at the highest disease severity on alfalfa (Nutter et al., 2002). Growers must cut infected alfalfa in

severe disease cases (Frate & Davis, 2007). A recommended control strategy against *P. medicaginis* is the use of resistant cultivars (Kehr et al., 1984; Summers, 1998). Alfalfa cultivars exhibited various degrees of resistance against leaf spot disease, but a study showed the incidence of *P. medicaginis* infection in a highly resistant cultivar (Inch et al., 1993). The available method to increase alfalfa resistance was by increasing plant resistance via crossing the transgenics expressing a hydrogen peroxide/reactive oxygen species producing enzyme or an oxalate degrading enzyme in pathogen tolerant lines or inbreds obtained through conventional genetic manipulations or by the transformation of tolerant plants or plant tissues with a hydrogen peroxide/reactive oxygen species producing gene or by altering the expression of an endogenous hydrogen peroxide/reactive oxygen species producing gene (Bidney et al., 2000). The latest research on alfalfa resistance revealed that *MsPGIP2* is a gene responsible for limiting common leaf disease caused by *P. medicaginis* and further research are necessary to enhance and transform this gene on alfalfa cultivars (Gui et al., 2016).

Neofabraea perenans (anamorph: *Cryptosporiopsis perennans*) is a pathogenic species on valuable orchard crops, such as apples and pears (Dugan et al., 1993). In the USA, the production of apples and pears worth more than 2.9 billion USD and 300 million USD in 2020, respectively (USDA, 2020b, c). *Neofabraea perenans* causes bull's eye rot, a post-harvest disease and cankers on the bark of apples and pears, despite other *Neofabraea* species infecting similar fruit crops (Garipey et al., 2005; Aguillar et al., 2018). In British Columbia, depending on the apple cultivar, *Neofabraea* bull eye rot resulted in 5 % to 40% yield loss (Sholberg & Haag, 1996), while the yield loss of pear production in the USA due to bull eye rot was estimated to be around 5–50% (Lennox et al., 2004). The available control strategies to alleviate *Neofabraea* cankers include conducting thorough inspections and removal of infected plant parts to minimize the spread of disease inoculum and reduce infection rates of cankers on barks (Garipey et al., 2005). As for bull's rot disease, the latest study showed fungicide applications during pre- and post-harvest periods on fruit crops were available for domestic use but might not be for international transportation (Aguillar et al., 2018). However, each *Neofabraea* species has specific sensitivity and may develop resistance

to certain fungicides (Weber & Palm, 2010). Hence, new experiments for novel modes of action of fungicides were suggested (Garton et al., 2019).

Oculimacula yallundae is the causal agent of eyespot disease on staple crops, such as wheat and other cereals (Crous et al., 2003). Winter wheat, the third most popular crop cultivated in the USA (Vocke & Ali, 2013), represents up to 80% of overall wheat in the USA, with an economic value of more than 5 billion USD in 2020 (Vocke & Ali, 2013; USDA, 2020d). However, *Oculimacula* eyespot disease reduces grain yield, especially in the Pacific Northwest (Clarkson, 1981). *Oculimacula* pathogens damaged wheat production up to 40–50% in the UK and, in 1998, an approximate estimation of loss due to *Oculimacula yallundae* and *Oculimacula acutiformis* reached £24 million (Fitt et al., 1988; Al-Azri et al., 2015; Palicová et al., 2018). In Europe and the Pacific Northwest, infection severity depends on the weather, especially during heavy rainfall and mild winter conditions, as they increase fungal infections (Serfling et al., 2016). Effective management strategies for controlling *Oculimacula* eyespot on wheat are currently being investigated despite the recommended approaches for disease mitigation. Cultural practices, such as crop rotation and tillage, are available besides pesticide applications (Wei et al., 2011). The use of fungicides, such as prochloraz, was deemed ineffective due to the developing resistance reported in Germany, France and the UK (Parnell et al., 2008). However, prochloraz has still been proven to be effective during field tests conducted in Japan against *Oculimacula* eyespot (Takeuchi et al., 2018). The latest study on pesticide applications against more than 100 *Oculimacula* isolates showed that 58% had low to medium resistance, and one isolate had strong resistance. In contrast, 42% of isolates were still sensitive to prochloraz (Palicová & Matušinsky, 2019). Fungicide applications are effective at the beginning of the stem elongation period (Dumalasová et al., 2015). Planting resistant cultivars is the other option to mitigate *Oculimacula* infection and is currently being studied. In the Pacific Northwest, resistant cultivars are developed against *Oculimacula* infection (Jones et al., 1995). Even though the resistant cultivars do not provide 100% protection against eye spot disease, field tests on wheat cultivars bearing the resistance gene *Pch1* showed lower damage against *Oculimacula* infection in the Czech Republic (Palicová et al., 2018).

Drepanopeziza brunnea (anamorph: *Marssonina brunnea*) is a phytopathogenic discomycete in Drepanopezizaceae reported as the causative agent of leaf blight on *Populus* spp., affecting 15–45% of wood losses on harvested poplar in Europe (Spiers & Hopcroft, 1986; Castellani, 1970). Poplar trees (*Populus* spp.) are valuable as energy crops used as lignocellulosic feedstock for biofuel production, with a target production of 61 billion litres in the USA (Sissine, 2007). Hence, any diseases on *Populus* spp. may have devastating impacts on the harvested poplar products (Netzer et al., 2002). The available control strategies do not entirely protect *Populus* sp from *Drepanopeziza* leaf blight since they are mainly preventive measures, such as fungicide applications on poplar seeds, to reduce leaf blight infection at the seedling stage (Spiers & Wenilam, 1983). Research efforts focusing on the co-evolution of pathogenicity between *D. brunnea* and poplar to develop resistant varieties as an alternative control strategy had been initiated (Zhu et al., 2012), while the latest research highlighted the gene expression profiles and the roles of effectors in host specificity (Ren et al., 2020).

Gremmeniella abietina infection is widespread in Europe, North America and Asia, killing young trees and causing growth reduction in old trees (EFSA et al., 2017). In Quebec, the percentage of *G. abietina* infection in red pines reaches 86–100% and causes > 40% mortality without any treatments or control strategies (Laflamme, 1999). In 2001, the *G. abietina* epidemic covered over 400 K ha of *Pinus sylvestris* with estimated financial damage of approximately 250 million Euro in Sweden (Hansson et al., 2004; Wulff et al., 2006). Control strategies against *G. abietina* infection are being assessed, including pruning, fungicide application and endophytic inoculations. It was noted that cutting up to two-thirds of tree crown reduces *G. abietina* infection rates by 22–47% (Laflamme, 1999). Preventive measures to contain the disease on coniferous trees were studied by Hudler and Neal (1990). They documented that the sanitation method of immersing diseased seedlings of *Pinus sylvestris* and *Pinus resinosa* in water at 50 °C was able to eradicate *G. abietina* propagules. This control strategy was based on the high possibility that overwintered *G. abietina* spores in cut Christmas trees might spread the disease to new areas where they were discarded (Magasi & Manley, 1974). Certain preventive measures to avoid *G. abietina* infection, such as pine site selections, spacing between plants, chemical applications and biological control, were listed in

EFSA et al. (2017). In the worst case of *G. abietina* infection, pesticide utilization has been allowed in the nursery (Hopkin & McKenney, 1995) but not recommended in the forest, especially in Europe (Villaverde, 2009). Biological control is the other recommended control strategy against *G. abietina*. The latest research on biological control against *G. abietina* in the greenhouse revealed reduced infection in endophyte-inoculated pine seedlings (Romeralo et al., 2015).

As a biotrophic species, *Cyttaria* caused gall formation, leading to twisted branches and often breaking due to high wind. However, no studies were conducted on the impact of *Cyttaria* infection on timber production of *Nothofagus menziesii* nor their control strategies (Gadgil, 2009). Besides *Cyttaria*, *Medeolaria farlowii* infection on its host, *Medeola virginiana*, has never been reported to cause the host death or financial damages. Biotrophic discomycetes in Leotiomycetes cause fungal diseases in bryophytes, and pteridophytes also lack studies on economic losses (Guatimosim et al., 2016).

Among other phytopathogenic discomycetes, *Botrytis cinerea* is the most destructive pathogen on valuable agricultural, ornamental and forestry commodities, including non-vascular plants (Dean et al., 2012; Elad et al., 2016). The global annual financial damage caused by *B. cinerea* is more than \$10–100 billion (Jin & Wu, 2015). Economic and yield losses on various agricultural commodities vary in different regions. Yield loss caused by *B. cinerea* infection is about 20% and reached 50% as environmental conditions favour the widespread of the disease (Hu et al., 2017). Fruit rot on strawberries caused by *B. cinerea* was estimated to be 13–18% in the USA (Mertely et al., 2000), while gray mold reduces zucchini yield by 20% in Korea (Cheon & Jeon, 2013). In New Zealand, the annual loss caused by *B. cinerea* infection on wine grapes was estimated at NZ\$ 2578/hectare (Hill et al., 2019). In Croatia, the estimated loss of apple price during storage was approximately € 5–53/ton for *B. cinerea*, *Monilia fructigena* and *Colletotrichum* spp. (non-discomycete phytopathogens) infections (Ivić et al., 2013).

Control strategies to manage gray mold caused by *B. cinerea* vary, and many studies have been conducted (Elad & Shtienberg, 1995; Bika et al., 2021). *Botrytis cinerea* can infect pre- and post-harvest agricultural, horticultural and ornamental

commodities; thus, various and specific methods to reduce disease infection were tried and documented. Bika et al. (2021) reported several potential methods to manage *B. cinerea* infection on ornamental crops. Those strategies include using resistant cultivars (Takatsu et al., 1999), practicing sanitation (by removing diseased plant parts, disinfecting cutting tools and containers in the greenhouse), dipping cut roses in hot water (50 °C) (Elad & Vopin, 1991), irradiation treatment using UV and gamma rays on cut flowers (Chu et al., 2015), monitoring temperature and humidity (Holz et al., 2007), nutrient adjustment (Alvarez, 2012), and biological control or employing antagonistic organisms against *B. cinerea*, such as *Trichoderma* sp. (Elad & Shtienberg, 1995), *Clonostachys rosea* (Sutton et al., 1997), *Exophiala jeanselmei* (Zapata et al., 2016) and *Pseudomonas* sp. (Gao et al., 2018). Other control methods against *B. cinerea* include the utilization of plant growth regulators, for e.g., benzothiodiazole and gibberellins (Shaul et al., 1995; Friedrich et al., 1996), natural chemical coating (e.g., plant extract and essential oils for post-harvest treatment) (Wilson et al., 1997), nanotechnology (He et al., 2011), chemical control (Fernández-Ortuño et al., 2015) and strategies using a combination of biological control, cultural, growth regulators, chemical via ‘a system-based approach’ (Parke & Grünwald, 2012).

For Pezizomycetes, economic losses were reported for *Rhizina undulata*, a pyrophilous fungus whose apothecia emerge after forest fires (Lee et al., 2005). South Korea reported substantial economic losses from *R. undulata* infections in pine seedlings after the forest fires in 1996–2000 (Lee et al., 2005). In the Pacific Northwest USA, Thies et al. (1979) reported that 64 out of 277 burned Douglas fir cuts were infected with *R. undulata* after burning practices in Washington and Oregon, and its effect on pine seedling growth afterwards. In Africa, 1.2 million ha of forest plantations were also threatened by *R. undulata* infection since its first report in 1944 (Wingfield & Swart, 1994), and along with *Sphaeropsis sapinea*, *R. undulata* infection caused significant losses to forest plantations in South Africa (Germishuizen, 1984).

Control strategies have been applied to mitigate *R. undulata* infections, such as avoiding slash-burning practices for cleaning up agricultural wastes (Germishuizen, 1984). However, this strategy led to the emergence of other forest pathogens, such as pine bark beetles, as they survive easily without fire and develop their offspring. Hence,

the application of chemical sprays is necessary (Wingfield & Swart, 1994). Finding new and effective strategies to control rot root disease has been challenging since multiple efforts to induce disease infection on various trees failed (Lee et al., 2005). Therefore, mitigating fungal diseases while suppressing beetle infestation requires integrated pest management strategies. Slash burning avoidance is mandatory and should be coupled with the immediate removal of dead trees and debris from forest fields to avoid creating nesting grounds for bark beetles (Wingfield & Swart, 1994). Fungicide application can be substituted for on-site burning to avoid *Rhizina* infections. In case of accidental fires, several plant baiting techniques can be used, and careful monitoring of *R. undulata* infection patterns in the field is required (Wingfield & Swart, 1994).

3.3.10 Genome and -Omic Studies of Phytopathogenic Discomycetes

The use of various analytical tools and modern technologies, such as the utilization of nuclear magnetic resonance (NMR), mass spectrometry (MS) and high-throughput-next generation sequencing (HT-NGS), improve technical analyses on genomic, metabolomic, proteomic and transcriptomic research (Shiratake and Suzuki 2016). Numerous studies using genomic, metabolomic, proteomic and transcriptomic approaches are available on *Botrytis cinerea* (AbuQamar et al., 2016). *Botrytis cinerea* genomes were sequenced by Amselem et al. (2011) and Van Kan et al. (2016), who drafted the genomes of *B. cinerea* strain T4 and B05.10 to be 37.9 Mbp (14,270 genes) and 38.8 Mbp (13,664 genes), respectively. Knowledge of the whole genome sequence of *B. cinerea* allows researchers to identify critical information on pathogenesis, such as virulence factors (Nakajima & Akutsu, 2014), secondary metabolites (Collado & Viaud, 2016) and susceptibility genes in host plants (Sun et al., 2017). Virulence factors that are responsible for host surface penetration (lipase and cutinase), host cell killing (botcinolid, botcinins derivatives, botrydial metabolites, Cu–Zn-superoxide dismutase, Nep1-like proteins, sesquiterpenoid metabolites and xylanase), host tissue conversion into fungal masses (aspartic protease, *BcPGL*, *BcPG2* and pectin methylesterase), and suppressing host defense (ATP-binding cassette transporters and *BcBirl*) of *B. cinerea* were identified (Salinas & Verhoeff, 1995; Cutler et al., 1993; Have et al., 1998; Duran-

Patron et al., 2000; Valette-Collet et al., 2003; Rolke et al., 2004). Another important finding was the silencing of *DND1*, a susceptibility gene toward *B. cinerea*, reduced lesion sizes on tomato and potato leaves (Sun et al., 2017). The importance of these molecular studies is related to the control methods, which rely heavily on chemical fungicides, leading to *B. cinerea* resistance, negatively impacting non-target organisms (Leroux et al., 2002; Weber, 2011). Thus, a combination of genomic, proteomic, transcriptomic and metabolomic studies will provide valuable information, such as gene cascading of plant defense mechanism for resistant cultivars, an effective and eco-friendly control approach against *B. cinerea*.

In addition to *B. cinerea*, whole genomes have been sequenced for other phytopathogenic discomycetes in Sclerotiniaceae, such as *Sclerotinia sclerotiorum* (Amselem et al., 2011), *Sclerotinia borealis* (Mardanov et al., 2014), *Monilinia fructigena* (Landi et al., 2018), *Monilinia fructicola* (De Miccolis Angelini et al., 2018), *Monilinia laxa* (Naranjo-Ortiz et al., 2018) and *Scleromitrlula shiraiana* (Lv et al., 2021). Draft genomes have also been provided for *Drepanopeziza brunnea* (Zhu et al., 2012), *Diplocarpon rosae* (Neu et al., 2017), *Oculimacula yallundae* (Sheng & Murray, 2017), *Gremmeniella abietina* (Hamelin et al., 1993), and *Coccomyces strobili* (Stajich, 2018a). Comparative fungal genome analysis for identifying virulence factors in *Scleromitrlula borealis*, *Drepanopeziza brunnea*, *Diplocarpon rosae*, *Monilinia fructicola*, *Monilinia fructigena* and *Monilinia laxa* have been started (Neu & Debener, 2019; Ren et al., 2020; Lv et al., 2021), but not yet for *Gremmeniella abietina*, *Coccomyces strobili* and *Oculimacula yallundae* (Hamelin et al., 1993). In Pezizomycetes, phytopathogenic discomycetes with whole genome sequences are *Caloscypha fulgens*, *Geopyxis carbonaria*, *Gyromitra infula* and *Rhizina undulata* (Stajich, 2018b). However, further analysis of these genomes is still lacking.

Genome sequences are available for 101 fungal phytopathogens in Dothideomycetes, and phylogenetic analysis based on newly sequenced genomes indicated that plant pathogenicity in Dothideomycetes evolved multiple times (Haridas et al., 2020). However, whole genome sequences have not been reported for phytopathogenic discomycetes in Dothideomycetes. It will be interesting to incorporate

this group in comparative analysis with other pathogenic taxa that are not discomycetes in a genomic study.

Genomes of 41 fungal species in Lecanoromycetes have been sequenced (Pizarro et al., 2019; Resl et al., 2022). Further studies on the loss of mating gene *MAT 1* (responsible for self-fertilization or homothallism) (Pizarro et al., 2019), heterothallic ancestor revelation and carbohydrate-active enzymes gene prediction based on fungal genome analysis were reported (Resl et al., 2022). However, no genome has yet been published on phytopathogenic discomycetes in Lecanoromycetes. The phylogenetic affinities based on genome sequences between phytopathogenic discomycetes in Lecanoromycetes in plants, saprobes and lichens will be intriguing.

In Neolectomycetes, the genome sequence for *Neolecta irregularis* was documented, but not *Neolecta vittelina* (Nguyen et al., 2017). Compared to other members of Taphrinomycotina, the genome of *Neolecta irregularis* was less in size and the number of protein-coding genes, even though it has an actual teleomorph structure, is similar to fungal species in Pezizomycotina (Landvik et al., 2003; Healy et al., 2013). It will be intriguing to compare the current available fungal genome of *Neolecta irregularis* as a saprobe (Redhead, 1977a; Nguyen et al., 2017) and *Neolecta vittelina* as a biotroph (Redhead, 1979).

Genomes of *Aspergillus*, a medically and industrially important Eurotiomycete, had been sequenced (Arnaud et al., 2012), and further studies on genes responsible for spore production structures were revealed (de Vries et al., 2017; Mead et al., 2020). The loss of the *abaA* gene in *Aspergillus nidulans* (Eurotiomycetes) and other species triggered failures in the formation of phialides and conidiospores (Mead et al., 2020). Additionally, this gene was independently lost in four lineages of Eurotiomycetes based on whole genome phylogeny (Mead et al., 2020). Even though fungal genomes of some Eurotiomycetes are available, genomes for phytopathogenic discomycetes have not been sequenced. Hence, their affinities compared to those of other Eurotiomycetes based on whole genome phylogeny are still unknown.

CHAPTER 4

INTRODUCTION TO DISCOMYCETES.ORG: ONLINE PLATFORM DEDICATED TO APOTHECIAL FUNGI

4.1 Introduction

Discomycetes, with their diverse morphology and ecological roles, play a significant part in various fields of study. They are found in a range of environments, from plants to dead substrates, dung, and soil, both on land and in water (Beaton & Weste, 1976; Abdullah & Webster, 1981; Van Vooren & Moreau 2009; Elad et al., 2016; Lücking et al., 2016; Lestari et al., 2023). Some species, like *Botrytis cinerea*, have drawn attention due to their pathogenic effects on agricultural plants (Dean et al., 2012). Others are known for their ability to produce secondary metabolites with antibiotic properties (Quack et al., 1980), their culinary value (Hall et al., 1998; Tietel & Masaphy, 2018), and their role as nematode predators (Pfister, 1994). The group also includes endophytes like *Phialocephala* species (Tanney et al., 2016), coprophiles such as *Ascobolus* species (De Sloover, 2002), and pyrophiles (Dzhagan et al., 2020).

4.2 History of Discomycetes

The history of discomycetes can be traced back to Pliny in 23-79 AD, who discovered a mushroom without a root or stalk and named it '*Pezica*'. Dillenius (1719) described *Peziza* as cup-shaped fungi or discomycetes (Kimbrough, 1970). Fries established the Friesian classification of discomycetes based on apothecial macro characters, which were used for 60 years (Fries, 1821). De Notaris (1864) provided detailed observations on discomycetes, focusing on characters such as asci, paraphyses, ascospore color, and excipulum cells.

Nylander (1869) was the first to employ the iodine reaction for the classification of discomycetes. Boudier (1907) made significant contributions to discomycete classification, including the distinction between inoperculate and operculate discomycetes, the amyloid test, and oil drops in ascospores. Saccardo (1889) published his volume of *Sylloge Fungorum*, abandoning the Friesian method in favour of his prior discomycete classification system, raising many subgenera to the generic rank and describing over 200 genera with approximately 3,500 species. Nannfeldt (1932) critically re-evaluated several discomycete genera and proposed higher ascomycetes, namely Plectoascales, Ascoloculares and Ascohymeniales. Le Gal (1947) contributed to the understanding of ornaments and spore wall formations in operculate discomycetes. Dennis (1968) published *British Ascomycetes*, a widely accepted work that included five orders of discomycetes: Helotiales, Lecanorales, Pezizales, Phacidiales, and Ostropales. Kimbrough (1970) further divided inoperculate divisions into Helotiales, Ostropales, and Phacidiales.

In the 19th century, advances in molecular studies with the DNA barcoding approach revolutionized studies on taxonomy and phylogeny of discomycetes. Landvik and Erikson (1994) documented the parsimonious tree of discomycetes, which was followed by Gargas and Taylor (1995), Landvik (1996) and O'Donnell (1997). This research revealed a paraphyletic assemblage for apothecial specimens, with Helotiales and Pezizales classified into distinct clades. Phylogenetic studies focused on discomycetes and pyrenomycetes were conducted by Lutzoni et al. (2004), James et al. (2006), Spatafora et al. (2006), Wang et al. (2006a, b) and Schoch (2009a, b). Jaklitsch et al. (2016) incorporated discomycetes taxa in their Ascomycota classification. Following that, Ekanayaka et al. (2018) summarized all classes comprising apothecial bearing species. Furthermore, subsequent studies have introduced and revised discomycetous taxa based on multi-gene phylogeny and morphology (Ekanayaka et al., 2019a; Johnston et al., 2019; Pfister & Healy, 2021; Quandt & Haelewaters, 2021). These advancements have led to the current classification of Ascomycota (Wijayawardene et al., 2022).

4.3 The Significance of Discomycetes.org

Mycological research groups worldwide are conducting studies on discomycetes. For example, the Center of Excellence in Fungal Research, one such research group, contributed to the discomycete taxonomy with new geographical records, new taxa (species, genus, and family), re-descriptions and re-evaluation of certain taxonomic ranks, phylogenetic construction of new taxa and reconstruction of previously studied taxa based on molecular data (Ekanayaka et al., 2017, 2018, 2019a, b; Lestari et al., 2023). There is a trend to develop databases on various groups of fungi, e.g., Coelomycetes (Huanraluek et al., 2021); microfungi in the Greater Mekong Subregion (Chaiwan et al., 2021); Italian ascomycetes (Wijesinghe et al., 2021). Discomycete.org provides information on earlier but legitimate studies and regular updates on current studies on discomycetes worldwide. The purpose of this web-based platform is to compile all knowledge on discomycetes into a comprehensive, easily accessible system for mycologists worldwide. This website regularly updates the most recent taxonomic placements and descriptions of genera and species.

In this internet era, young mycologists prefer to access mycological information online rather than in a book. However, online platforms highlighting discomycetes specimens are rarely available, especially those that provide complete morphological descriptions with photographs and up-to-date phylogenies. Due to the lack of online resources for discomycetes, information on the macro- and micromorphologies are difficult to access, particularly for taxa with old specimen records and descriptions. According to various multi-gene phylogenetic analyses, discomycetes, which were formerly placed in taxa based on the shape and morphology of sexual morph, are widespread in various classes of Ascomycota (Spatafora et al., 2006; Lumbsch & Huhndorf, 2010; Pfister, 2015; Ekanayaka et al., 2018). Therefore, it is essential to construct a website and provide comprehensive information on taxonomy with phylogeny and their ecological roles.

4.4 Materials and Methods

The online platform includes taxonomy and phylogeny and comprises taxa from Ekanayaka et al. (2018), followed by the most recent research on discomycetes

(Ekanayaka et al., 2019a; 2019b; Tochihara & Hosoya, 2022). Descriptions, illustrations and phylogenies of discomycetes taxa were provided and updated regularly with their references. Each taxa entry on the website is linked to the Index Fungorum, Mycobank, Faces of Fungi (Jayasiri et al., 2015), Freshwaterfungi.org (Calabon et al., 2020), Fungal Genera (Monkai et al., 2019) and Outline of Fungi (Wijayawardene et al., 2022) websites. This online platform encourages mycologists to share their knowledge, suggestions and contributions, especially on discomycetes research updates. The website (Discomycetes.org) is dedicated to providing comprehensive information on pathology issues, ecology and economic importance, and industrial significance.

4.5 Database Interface and Visualization

The online platform, <https://www.discomycetes.org>, compiles classification and taxonomic information on discomycetes and provides user-friendly access to the database. The website interface consists of ten headings, of which seven are described as follows:

1. Home: provides an overview of the discomycetes.org website, a reference when using the website and enables rapid access to the most recently submitted taxa entries
2. Outline: describes the current state of classification, taxonomy and phylogeny of discomycetes
3. Archives: provides a direct path to access specific taxa at the order level
4. Curators: provides list and contact information of discomycetes.org curators (Table 4.1).
5. History: offers a synopsis of the classification and taxonomy of discomycetes.
6. References: provides a list of publications referenced in the entries on discomycetes.org
7. Notes: contains up-to-date mycological news.
8. Contact: provides contact details of the online platform, and the users can post suggestions and website-related questions.

Entries on discomycetes specimens uploaded to discomycetes.org were reviewed by the curators listed in Table 4.1, yet we are also open to suggestions from mycologists who will contribute further.



Table 4.1 List of curators of Discomycetes website

Position	Name	Affiliations	Correspondence
Head curator	Anusha H. Ekanayaka	Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand	hasinie88@gmail.com
Managing curator	Anis S. Lestari	Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand	anislestari1@gmail.com
Curators	Dhanushka Wanasinghe	Key Laboratory of Biodiversity and Biogeography, Kunming Institute of Botany Chinese Academy of Sciences Kunming, China	dnadeeshan@gmail.com
	B. Gareth Jones	Department of Botany and Microbiology, King Saud University, Riyadh, Kingdom of Saudi Arabia.	torperadgj@gmail.com
	Kevin D. Hyde	Centre of Excellence in Fungal Research, Mae Fah Luang University	kdhyde3@gmail.com
	Robert Luecking	Botanischer Garten and Botanisches Museum, Berlin-Dahlem	r.luecking@bgbm.org

Table 4.1 (continued)

Position	Name	Affiliations	Correspondence
	K.W. Thilini Chethana	Centre of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand	kandawatte.thi@mfu.ac.th
	Sajeewa Maharachchikumbura	University of Electronic Science and Technology, Sichuan, Chengdu, Chenghua, China	sajeewa83@yahoo.com
	Sinang Hongsanan	College of Life Science and Oceanography, Shenzhen University, Xili campus, Nanshan, Guangdong, China	sinang333@gmail.com
	Tian Qing	Centre of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand	tianqing124@gmail.com
	Vincent P. Hustad	Department of Natural Sciences, Northwest Missouri State University, Maryville, Missouri, USA	vhustad@nwmissouri.edu
	Zeng Ming	Centre of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand	z-ming@outlook.com

DISCOMYCETES

ISSN ****-****

[Home](#)[Outline](#)[Archives](#)[Curators](#)[History](#)[References](#)[High Level Classification](#)[Evolution](#)[Notes](#)[Contact](#)

Discomycetes.org is a website dedicated to the taxonomy and classification of discomycetes. The website focuses on providing an up-to-date outline of discomycetes with notes on orders, families, genera and species.

When using this website please cite: [References](#).

Recent Genus

[Haematomyxa](#)[Tryblidaria](#)[Stratisporella](#)

Recent Species

[Patellaria microspora](#)[Patellaria chromolaenae](#)[Patellaria atrata](#)

Figure 4.1 The homepage of Discomycetes.org

Discomycetes.org is a website dedicated to the taxonomy and classification of discomycetes. The website focuses on providing an up-to-date outline of discomycetes with notes on orders, families, genera and species.

When using this website please cite: [References](#).



Go

Orders

Helotiales

Family

Helotiaceae

Helotiales genera insertae sedis

Recent Species[Lecanora hagenii](#)[Allophylaria subciformis](#)[Tapesia fusca](#)

Figure 4.2 The search bar available for users to find specific discomycetes taxa

Outline

Phylum: **ASCOMYCOTA**Subphylum: **Taphrinomycotina**Class: **Neoelectomycetes** O.E. Erikss. & WinkaOrder: **Neoelectales** Landvik, O.E. Erikss., Gargas & P. Gust.Family: **Neoelectaceae** Redhead*Neoelecta* Speg.

- *Neoelecta irregularis* (Pk.) Korf et Rogers
- *Neoelecta vitelina* (Bres.) Korf et Rogers

Subphylum: **Pezizomycotina**Class: **Pezizomycetes** O.E. Erikss. & WinkaSubclass: **Pezizomycetidae** Locq. 1974Order: **Pezizales** J. Schröt.Family: **Ascobolaceae** Boud. ex Sacc.*Ascobolus* Pers.

- *Ascobolus albidus* P. Crouan and H. Crouan
- *Ascobolus cervinus* Berk. & Broome

Cleistodophanus J.L. Bezerra & Kimbr.*Cubonia* Sacc.*Saccobolus* Boud.

Search

Go

Recent Genus

[Micraspis](#)[Lamprospora](#)[Octosporopsis](#)

Recent Species

[Micraspis tetraspora](#)[Micraspis strobilina](#)[Micraspis acicola](#)

Figure 4.3 The snapshot of the outline page of the Discomycetes.org

Discomycetes Heirarchy

Abrothallales
Read more about Abrothallales orders »
Lichenosconiaceae
Caliciales
Catinellales
Chaetomellales
Cyttariales
Dothideomycetes, families incertae sedis
Eremithallales
Graphidales
Helotiales
Holmiellales
Lahmiales
Lecanorales
Leotiales
Lichinodiales

Go

Recent Genus

[Micraspis](#)
[Lamprospora](#)
[Octosporopsis](#)

Recent Species

[Micraspis tetraspora](#)
[Micraspis strobilina](#)
[Micraspis acicola](#)

Figure 4.4 The snapshot of the archive page in Discomycetes.org

Pezizales » Caloscyphaceae » Caloscypha

Caloscypha fulgens

Caloscypha fulgens (Pers.) Boud., Bull. Soc. mycol. Fr. 1:103 (1885)

=*Geniculodendron pyriforme* G.A. Salt, Trans. Br. mycol. Soc. 63(2): 340 (1974)

Facesoffungi number: FoF 04203

Saprobic on soil or pathogenic on endosperm and embryo of Sitka spruce seed. **Sexual morph:** Apothecia up to 5 cm diam., gregarious, sessile to short stipitate, exterior surface dull yellow to yellowish-orange, with maturity become bluish-green to olive, especially near the margin. Receptacle cupulate, sometimes discoid at maturity. Margins lobed, concolorous to receptacle. Disc yelloworange to orange, glabrous. Paraphyses filiform, granulated. Asci 8-spored, operculate, inamyloid. Ascospores 5.5–7.5 µm, globose, smooth, hyaline. **Asexual morph:** Colonies on PDA coarse, white to pale brown. Aerial mycelium densely verrucose, white to pale brown. Submerged mycelium smooth, white, orange or brown. Conidiophores straight, erect, cylindrical, septate, highly branched, forming hyaline, dendroid structures, with a main axis, ultimate branches bearing conidiogenous cells. Conidiogenous cells polyblastio, borne singly, in pairs or verticillately and proliferating sympodially. Conidia form in successive apices of conidiogenous cells from sympodial succession, dry, acropetal, holoblastic, arising in clusters, aseptate, hyaline, pyriform, smooth-walled, guttulate, truncate at the attached end (Description modified from Salt 1974; Beug et al. 2014).

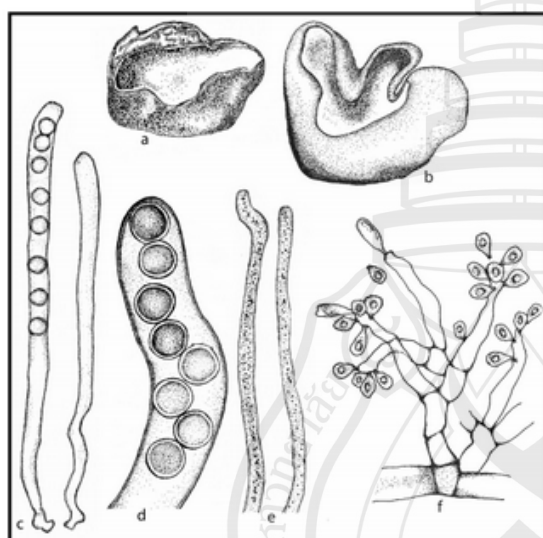
Notes: The sexual morph of *Caloscypha fulgens* is saprobic on soil and characterized by yellow apothecia which become bluish-green to olive at maturity, cylindrical operculate asci and globose hyaline ascospores (Beug et al. 2014). The asexual morph of *Caloscypha fulgens* is pathogenic on endosperm and embryo of Sitka spruce seed and characterized by its sympodially proliferating conidiogenous cells from which unicellular holoblastic conidia are formed (Salt 1974).

Recent Genus

[Lecanora](#)
[Allophylaria](#)
[Tapesia](#)

Recent Species

[Lecanora hagenii](#)
[Allophylaria subciformis](#)
[Tapesia fusca](#)



Morphology of *Caloscypha fulgens* a, b Habit of apothecia, c cylindrical asci, d ascus apex with globose ascospores, e filiform paraphyses, f conidiophore and conidia (Redrawn from Salt 1974; Jones 2017; Goodwin 2017; Stevens 2017)

Reference:

Ekanayaka AH, Hyde KD, Jones EBG, Zhao Q. 2018. Taxonomy and phylogeny of operculate discomycetes: Pezizomycetes. Fungal Diversity 90, 161–243

Figure 4.5 A detailed description of *Caloscypha fulgens*, a species uploaded in Discomycetes.org

4.6 A Short Report on the Website Update

To this date, 324 discomycetes taxa comprising order, families, genera and species description have been uploaded and linked to the index fungorum and Mycobank. The updates on incoming discomycetes studies will be periodically uploaded to the website.

CHAPTER 5

A CHECKLIST OF DISCOMYCETES FROM THAILAND

5.1 Introduction

Thailand consists of seasonal, tropical lowland forests in the south and subtropical montane forests in the north, which provide various habitats for animals and plants, including fungi (Whitmore, 1984; Napompeth & Rodcharoen, 1998). Fungal explorations of lichenized discomycetes had been conducted since the mid-1800s, with some species recorded as novel (Rostrup, 1902; Vainio, 1907). In addition, discomycetes in Pezizomycetes and other classes in Thailand were documented in the 1960s, with some specimens recorded as novel taxa (Dissing, 1963; Brummelen, 1967; 1969). Since then, studies on discomycetes relied heavily on the lichenized species (Vainio, 1921; Paulson, 1930; Alava, 1988; Boonpragob et al., 1998; Wolseley & Aguirre-Hudson, 1995; Aptroot et al., 2007) and checklists of discolichens species were provided (Buaruang et al., 2017). On the contrary, a list of nonlichenized discomycetes in Thailand was still limited in the 1960s and 1980s (Dissing, 1963; Phanichapol, 1984). Explorations and documentation of non-lichenized discomycetes in Thailand have been resuming since the early 2000s (Weinstein et al., 2002; Hongsanan et al., 2015; Ekanayaka et al., 2016; 2019a; 2019b; Zeng et al., 2020; 2023; Lestari & Chethana, 2024). However, despite the availability of various checklists of collected ascomycetes based on the ecological roles (Thanakitpipattana et al., 2020), habitats (Zhang et al., 2011), hosts (Goonasekara et al., 2018), certain morphologies (Choeyklin et al., 2011), and taxonomical groups (Chandrasrikul et al., 2011), an updated checklist of discomycetes recorded in Thailand has not been provided.

Comprehensive checklists of fungi, in general, are necessary for providing taxon data on biodiversity and distribution associated with their ecological habitats (Guarino & Napolitano, 2006; Wang et al., 2020). Specifically, a checklist of discomycete taxa from Thailand is vital for composing a road map for nature conservation, sustainable natural resource management, resource utilization and protection, including governmental decision-making (Hawksworth, 1991; Piepenbring et al., 2020). A checklist of discomycetes found in Thailand is also important for filling the knowledge gap regarding their distribution in Southeast Asia (Hyde et al., 2019). Additionally, it serves to determine the ecological relationships between discomycetous species and vegetation communities (Cantrell, 2004; Fillippova, 2012) and bioindicator species categorization (Hawksworth, 1991; Yang et al., 2023; Manici et al., 2024).

5.2 Materials and Methods

Literature browsing was conducted to find any publications or documentation of discomycetes collected in Thailand. The list of discomycetes retrieved from mycology journals or other publications was validated for extant or novel status through Index Fungorum, MycoBank and Species Fungorum databases. The classifications of some discomycetes were updated based on Quandt & Haelewaters (2021) and Wijayawardene et al. (2022).

5.3 Results

During 1899–2022, discomycete exploration in Thailand showed a significant increase in the number of newly discovered and extant species, especially in the last three decades. A total of 690 species have been documented, including 122 new species (Table 5.1). Extant and new species of discomycetes in Thailand are categorized across ten classes (Arthoniomycetes, Candelariomycetes, Coniocybomycetes, Dothideomycetes, Geoglossomycetes, Lecanoromycetes, Leotiomyces, Lichinomycetes, Orbiliomycetes and Pezizomycetes), 23 orders, 57 families. Lecanoromycetes was the predominant class, accounting for 81% (553 species),

followed by Leotiomyces with 7% (50 species) (Figure 5.1, Table 5.2). The majority of discomycete species were growing on lignocellulose substrates (83%), compared to rocks, soil, dung and other organisms (Figure 5.2).

Table 5.1 Number of discomycetes species found in Thailand in three decades period

Notes	1899–1929	1930–1960	1961–1991	1992–2022
New species	19	2	4	97
Extant species	51	17	83	416
Total species	70	119	87	514

A comprehensive checklist in Table 5.2 provides discomycetes diversity found in Thailand from 1899 to 2022. The listed discomycetes species are identified across ten classes and found on numerous substrates, displaying various ecological niches in Thailand. The largest number of discomycetes belong to Lecanoromycetes, categorized into 26 families, with Graphidaceae having the highest number of discomycetous species number (102 species) (Figure 5.3). In addition, Leotiomyces is the second largest group of discomycetes found in Thailand, with the most taxa belonging to Helotiaceae, comprising 11 species (Figure 5.4).

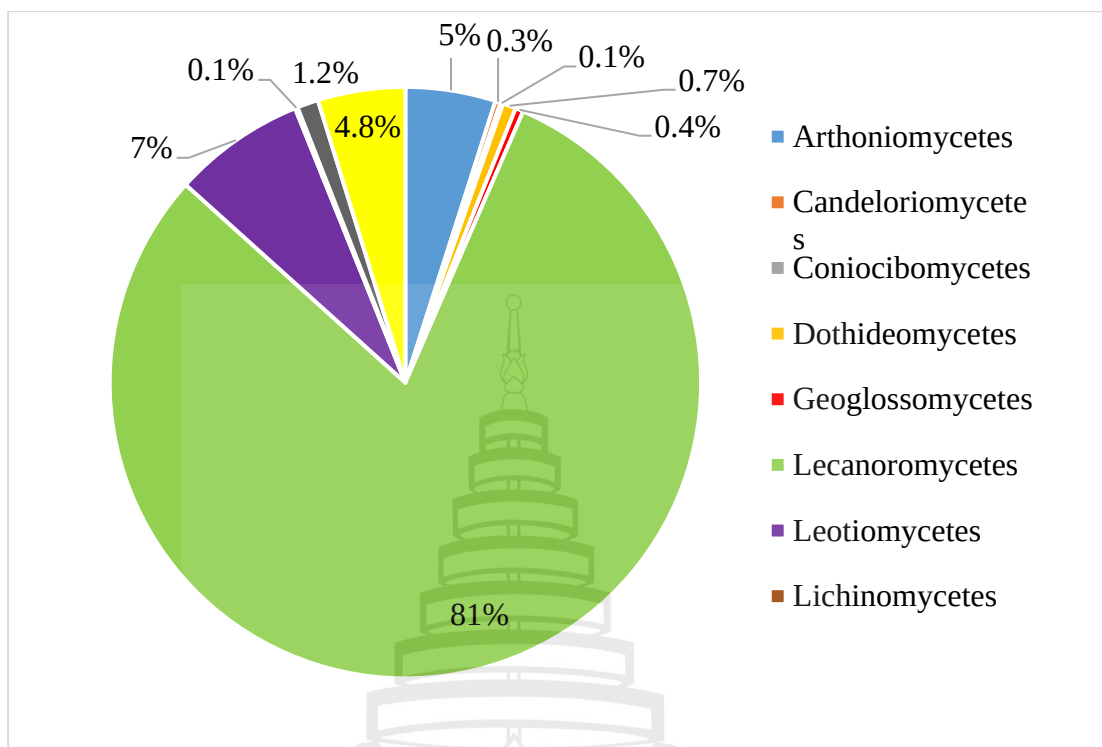


Figure 5.1 Number of discomycetes species categorized in classes found in Thailand (1899–2022)

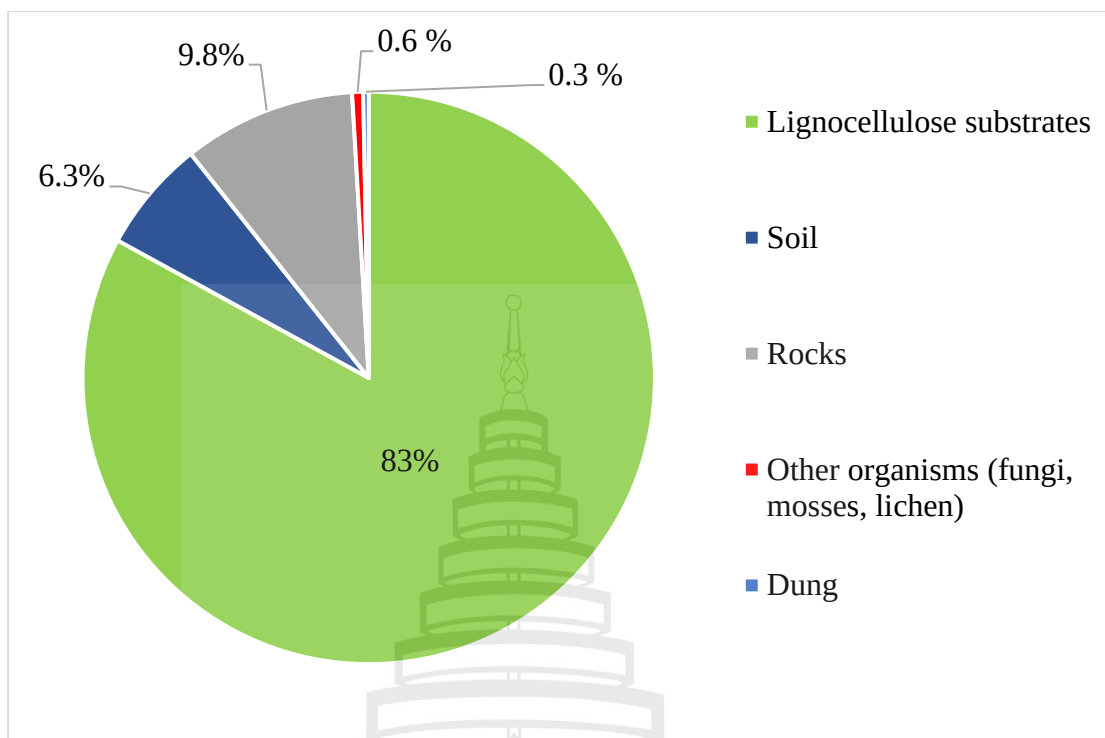


Figure 5.2 Number of discomycetes species related with their substrates associated found in Thailand (1899–2022)

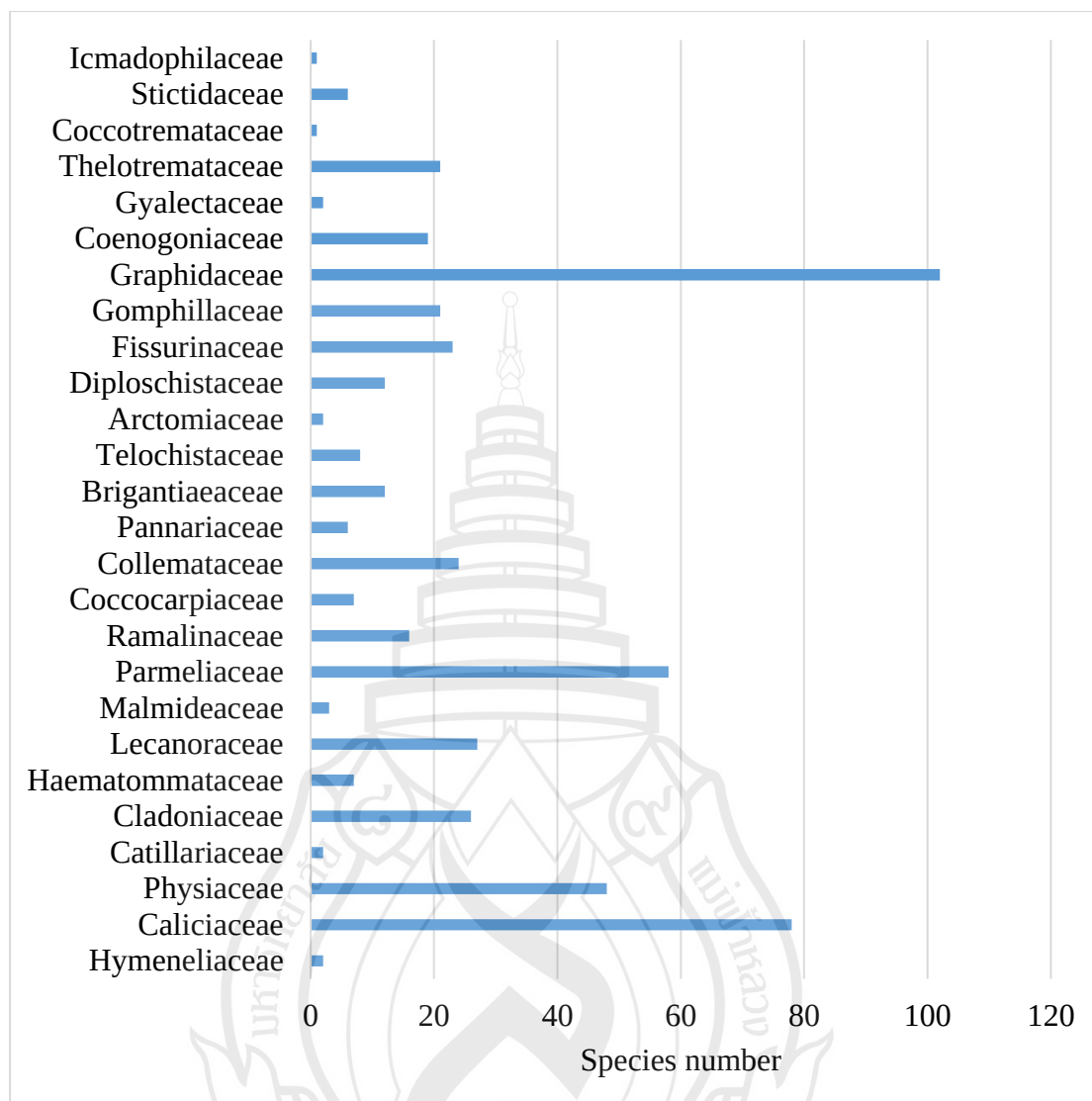


Figure 5.3 Number of discomycetes species in Lecanoromycetous families found in Thailand (1899–2022)

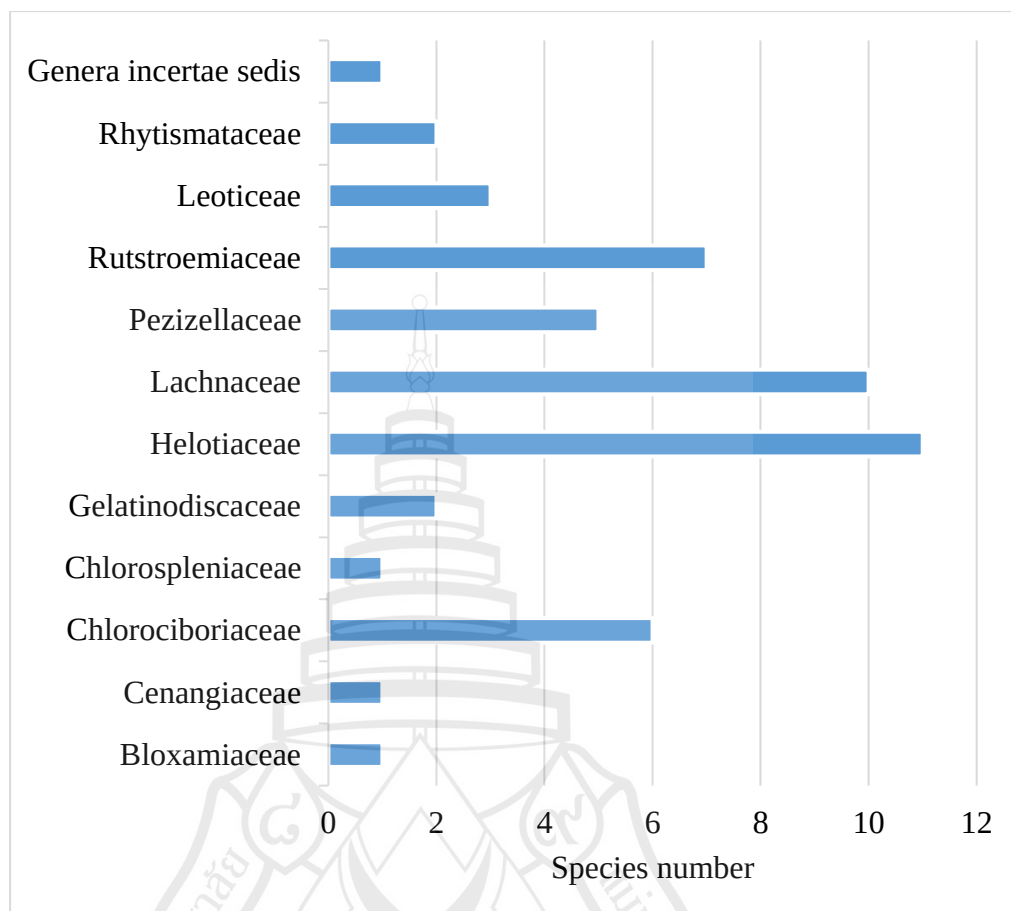


Figure 5.4 Number of discomycetes species in Leotiomycetous families found in Thailand (1899–2022)

Table 5.2 A checklist of the discomycetes species found in Thailand

Class	Order	Family	Species	Host	Novel status
Arthoniomycetes	Arthoniales	Arthoniaceae	<i>Arthonia cyanea</i> var. <i>cyanea</i>	On bark	
			<i>Arthonia lividula</i>	On bark	
			<i>Arthonia mira</i>	On palms	
			<i>Arthonia obscuratula</i>	On bark	
			<i>Arthonia perpallens</i>	On bark	
			<i>Arthonia ramosii</i>	On leaves	
			<i>Arthonia rhizophorae</i>	On bark	
			<i>Arthonia trilocularis</i>	On leaves	
			<i>Arthonia varia</i> var. <i>stenographella</i>	On bark	
			<i>Eremothecella calamicola</i>	On leaves	
			<i>Eremothecella macrocephala</i>	On leaves	
			<i>Synarthonia ochrodes</i>	On bark	
		Lecanographaceae	<i>Heterocyphelium leucampyx</i>	On bark	
			<i>Lecanographa atropunctata</i>	On bark	New species
		Roccellaceae	<i>Chiodecton congestulum</i>	On bark	
			<i>Chiodecton leptosporum</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Chiodecton subsphaerale</i>	On bark	
			<i>Cresponea chloroconia</i>	On bark	
			<i>Cresponea leprieurii</i>	On bark	
			<i>Cresponea proximata</i>	On bark	
			<i>Dichosporidium boschianum</i>	On bark	
			<i>Enterographa anguinella</i>	On bark	
			<i>Enterographa angustissima</i>	On leaves	
			<i>Enterographa inthanonensis</i>	On bark	
			<i>Enterographa mesomela</i>	On bark	New species
			<i>Enterographa pallidella</i>	On leaves, bark	
			<i>Lecanactis flavisedella</i>	On bark	
			<i>Lecanactis platygraphoides</i>	On bark	
			<i>Lecanactis platygraphoides</i>	On bark	
		Roccellographaceae	<i>Fulvophyton subseriale</i>	On bark	
			<i>Graphidastra byssiseda</i>	On dead stem	
			<i>Graphidastra laii</i>	On smooth bark	New species

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
Candelariomycetes	Candelariales	Candelariaceae	<i>Phyllopsora gossypina</i>	On bark	
			<i>Phyllopsora pyxinoides</i>	On bark	
			<i>Candelaria concolor</i>	On bark	
			<i>Candelariella reflexa</i>	On bark	
Coniocibomycetes	Coniocybales	Coniocybaceae	<i>Chaenotheca trichialis</i>	On bark	
Dothideomycetes	Bezerromycetales	Bezerromycetaceae	<i>Neorhamphoria garethjonesii</i>	On dead wood	New species
	Botryosphaeriales	Aplosporellaceae	<i>Aplosporella thailandica</i>	On dead stems	New species
			<i>Rhytidhysterion neorufulum</i>	On bark	New species
			<i>Rhytidhysterion thailandicum</i>	On bark	New species
Geoglossomycetes	Patellariales	Patellariaceae	<i>Patellaria chromolaenae</i>	On dead stems	New species
	Geoglossales	Geoglossaceae	<i>Geoglossum nigratum</i>	On soil	
			<i>Trichoglossum hirsutum</i>	On soil	
			<i>Trichoglossum septatum</i>	On soil	New species
Lecanoromycetes	Baeomycetales	Arctomiaceae	<i>Arctomia fascicularis</i>	On bark	
			<i>Arctonia complanata</i>	On bark	
		Hymeneliaceae	<i>Hymenelia lacustris</i>	On rock	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Ionaspis tropica</i>	On rocks	
	Caliciales	Caliciaceae	<i>Allocalicium adaequatum</i>	On bark	
			<i>Amandinea diorista</i>	On bark	
			<i>Amandinea diorista</i> var. <i>hypopelidna</i>	On bark	
			<i>Amandinea efflorescens</i>	On bark	
			<i>Amandinea extenuata</i>	On bark	
			<i>Amandinea melaxanthella</i>	On palms	
			<i>Amandinea montana</i>	On bark	
			<i>Amandinea pelidna</i>	On rock	
			<i>Amandinea placodiomorpha</i>	On palms	
			<i>Amandinea punctata</i>	On bark	
			<i>Baculifera remensa</i>	On bark	
			<i>Buellia aethalea</i>	On sandstone	
			<i>Buellia alboatrior</i>	On bark	
			<i>Buellia almeriensis</i>	On rocks	
			<i>Buellia amblyogona</i>	On rock	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Buellia bahiana</i>	On bark	
			<i>Buellia blastenioides</i>	On bark	New species
			<i>Buellia curatellae</i>	On bark	
			<i>Buellia demutans</i>	On bark	
			<i>Buellia desertica</i>	On bark	
			<i>Buellia disciformis</i>	On bark	
			<i>Buellia dispersa</i>	On rock	
			<i>Buellia erubescens</i>	On bark	
			<i>Buellia homophylia</i>	On rock	
			<i>Buellia leptocline</i>	On rock	
			<i>Buellia leptoclinoides</i>	On rock	
			<i>Buellia ocellata</i>	On sandstone	
			<i>Buellia pallidomarginata</i>	On bark	
			<i>Buellia parastata</i>	On bark	
			<i>Buellia pinicola</i>	On bark	
			<i>Buellia pleiophoroides</i> var. <i>meiospermoides</i>	On bark	New species

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Buellia pleiotera</i>	On bark	
			<i>Buellia proximata</i>	On wood	
			<i>Buellia pruinosa</i>	On rock	
			<i>Buellia polyspora</i>	On dead stem	
			<i>Buellia rechingeri</i>	On bark	
			<i>Buellia sequax</i>	On rock	
			<i>Buellia saxorum</i>	On rock	
			<i>Buellia schaereri</i>	On bark	
			<i>Buellia stellulata</i>	On rock	
			<i>Buellia stillingiana</i>	On bark	
			<i>Buellia subdisciformis</i>	On sandstone	
			<i>Buellia sublauri-cassiae</i>	On dead stem	New species
			<i>Buellia subnexa</i>	On bark	
			<i>Buellia subsororioides</i>	On rock	
			<i>Buellia substigmaea</i>	On rock	
			<i>Buellia triseptata</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Buellia viridula</i>	On dead stems	New species
			<i>Calicium hyperelloides</i>	On bark	
			<i>Cratiria amphorea</i>	On bark	
			<i>Cratiria dissimilis</i>	On bark	
			<i>Cratiria lauricassiae</i>	On bark	
			<i>Cratiria melanochlora</i>	On bark	
			<i>Cratiria obscurior</i>	On bark	
			<i>Cratiria rutilans</i>	On bark	
			<i>Cratiria rutilantoides</i>	On bark	
			<i>Dimelaena tenuis</i>	On sandstone	
			<i>Dimelaena thysanota</i>	On rock	
			<i>Dimelaena weberi</i>	On rock	
			<i>Diplotomma alboatrum</i>	On bark, rock	
			<i>Diplotomma venustum</i>	On rocks	
			<i>Dirinaria aegialita</i>	On bark, rock	
			<i>Dirinaria applanata</i>	On bark, rock	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Dirinaria confluens</i>	On bark	
			<i>Dirinaria confusa</i>	On bark	
			<i>Dirinaria consimilis</i>	On bark	
			<i>Dirinaria papillulifera</i>	On bark	
			<i>Dirinaria picta</i>	On bark	
			<i>Dirinaria purpurascens</i>	On bark	
			<i>Endohyalina circumpallida</i>	On bark	
			<i>Gassicurtia chermesina</i>	Pine bark	
			<i>Gassicurtia clathrisidiata</i>	On bark	New species
			<i>Gassicurtia coccifera</i>	On bark	
			<i>Hypoflavia crustosa</i>	On bark	New species
			<i>Pyxine nubila</i>	On bark or rock	
			<i>Stigmatochroma glaucothecum</i>	On bark	
			<i>Tetramelas chloroleucus</i>	On bark	
			<i>Tetramelas insignis</i>	On soil	
		Physiaceae	<i>Heterodermia albicans</i>	On bark	New record

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Heterodermia angustiloba</i>	On bark	
			<i>Heterodermia antillarum</i>	On bark	New record
			<i>Heterodermia archeri</i>	On bark	New record
			<i>Heterodermia comosa</i>	On bark	
			<i>Heterodermia coralloidea</i>	On rock	New record
			<i>Heterodermia dactyliza</i>	On rock	
			<i>Heterodermia diademata</i>	On bark	
			<i>Heterodermia dissecta</i>	On rock	New record
			<i>Heterodermia formula</i>	On bark, rock	
			<i>Heterodermia flabellata</i>	On bark	
			<i>Heterodermia galactophylla</i>	On bark	
			<i>Heterodermia hypochraea</i>	On bark	
			<i>Heterodermia. incana</i>	On bark	
			<i>Heterodermia isidiophora</i>	On bark	
			<i>Heterodermia koyana</i>	On rock	New record
			<i>Heterodermia koyanoides</i>	On bark	New record

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Heterodermia lepidota</i>	On trees	
			<i>Heterodermia obscurata</i>	On bark	
			<i>Heterodermia pacifica</i>	On bark	
			<i>Heterodermia palpebrata</i>	On bark	
			<i>Heterodermia pandurata</i>	On bark	
			<i>Heterodermia paradoxa</i>	On tree	
			<i>Heterodermia podocarpa</i>	On bark	
			<i>Heterodermia pseudospeciosa</i>	On bark	
			<i>Heterodermia rubescens</i>	On bark	New record
			<i>Heterodermia speciosa</i>	On bark	
			<i>Heterodermia stellata</i>	On bark	
			<i>Heterodermia verdonii</i>	On bark	
			<i>Hyperphyscia adglutinata</i>	On bark	
			<i>Hyperphyscia cochlearis</i>	On tree trunk	
			<i>Hyperphyscia granulata</i>	On bark	
			<i>Hyperphyscia pandani</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Leucoderma borphyllidiata</i>	On tree	
			<i>Leucoderma. boryi</i>	On bark	
			<i>Leucoderma leucomelos</i>	On bark	
			<i>Polyblastidium appendiculatum</i>	On bark	
			<i>Polyblastidium flavosquamosum</i>	On bark	
			<i>Polyblastidium fragilissimum</i>	On bark	
			<i>Polyblastidium fragilissimum</i>	On trees	
			<i>Polyblastidium hypocaustium</i>	On bark	
			<i>Polyblastidium hypoleucum</i>	On bark	
			<i>Polyblastidium japonicum</i>	On bark	
			<i>Polyblastidium microphyllum</i>	On wood, rock	
			<i>Polyblastidium propaguliferum</i>	On bark	
			<i>Polyblastidium queenslandicum</i>	On bark	
			<i>Polyblastidium togashii</i>	On bark	
			<i>Polyblastidium violostriatum</i>	On bark	
	Graphidales	Diploschistaceae	<i>Ampliotrema palaeoamplius</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Ampliotrema rimosum</i>	On bark	
			<i>Asteristion alboannuliforme</i>	On bark	
			<i>Compositrema thailandicum</i>	On bark	New species
			<i>Fibrillithecis argentea</i>	On wood	
			<i>Glaucotrema costaricense</i>	On bark	
			<i>Glaucotrema glaucophaenum</i>	On bark	
			<i>Glaucotrema thailandica</i>	On bark	New species
			<i>Heiomasia sipmanii</i>	On bark	New species
			<i>Phaeographopsis indica</i>	On bark	
			<i>Phaeographopsis palaeotropica</i>	On bark	
			<i>Wirthiotrema glaucopallens</i>	On bark	
		Fissurinaceae	<i>Clandestinotrema clandestinum</i>	On bark	
			<i>Cruentotrema cruentatum</i>	On bark	
			<i>Cruentotrema kurandense</i>	On bark	
			<i>Cruentotrema lirelliforme</i>	On bark	New species
			<i>Cruentotrema thailandicum</i>	On bark	New species

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Dyplolabia afzelii</i>	On bark	
			<i>Dyplolabia chumphonensis</i>	On tree	New species
			<i>Dyplolabia ochrocheila</i>	On bark	
			<i>Fissurina albonitens</i>	On bark	
			<i>Fissurina cingalina</i>	On bark	
			<i>Fissurina dumastii</i>	On bark	
			<i>Fissurina elaiocarpa</i>	On bark	
			<i>Fissurina incrustans</i>	On bark	
			<i>Fissurina inabensis</i>	On bark	
			<i>Fissurina inquinata</i>	On bark	
			<i>Fissurina insculpta</i>	On bark	
			<i>Fissurina niveoalba</i>	On bark	New species
			<i>Fissurina phuluangii</i>	On bark	New species
			<i>Fissurina pseudostromatica</i>	On bark	
			<i>Fissurina quadrispora</i>	On bark	
			<i>Fissurina radiata</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Fissurina rubiginosa</i>	On bark	
			<i>Fissurina rufula</i>	On bark	
		Gomphillaceae	<i>Aderkomyces armatus</i>	On leaves	
			<i>Aderkomyces thailandicus</i>	On leaves	New species
			<i>Asterothyrium microsporum</i>	On leaves	
			<i>Asterothyrium pittieri</i>	On leaves	
			<i>Aulaxina microphana</i>	On leaves	
			<i>Aulaxina quadrangula</i>	On leaves	
			<i>Calenia aspidota</i>	On leaves	
			<i>Calenia depressa</i>	On leaves	
			<i>Calenia graphidea</i>	On leaves	
			<i>Calenia leptocarpa</i>	On leaves	
			<i>Calenia phyllogena</i>	On leaves	
			<i>Calenia thelotremella</i>	On leaves	
			<i>Echinoplaca epiphylla</i>	On leaves	
			<i>Echinoplaca leucotrichoides</i>	On leaves	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Echinoplaca pellicula</i>	On leaves	
			<i>Echinoplaca tetrapla</i>	On leaves	
			<i>Gyalidea luzonensis</i>	On rock, soil	
			<i>Gyalideopsis altamirensis</i>	On bark	
			<i>Gyalideopsis lambinonii</i>	On bark	
			<i>Gyalideopsis rubescens</i>	On leaves	
			<i>Gyalideopsis vainioi</i>	On bark	
		Graphidaceae	<i>Allographa stictilabiata</i>	On bark	
			<i>Allographa leptospora</i>	On bark	New species
			<i>Allographa norvestitoides</i>	On bark	New species
			<i>Allographa pavoniana</i>	On bark	
			<i>Allographa rimulosa</i>	On bark	
			<i>Allographa rhizicola</i>	On bark	
			<i>Allographa rustica</i>	On bark	
			<i>Allographa sauroidea</i>	On bark	
			<i>Allographa seminuda</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Allographa semirigida</i>	On bark	
			<i>Allographa striatula</i>	On bark	
			<i>Allographa subdisserpens</i>	On bark	
			<i>Allographa subdussii</i>	On tree	New species
			<i>Allographa trichospora</i>	On bark	New species
			<i>Allographa verminosa</i>	On bark	
			<i>Austrotrema terebrans</i>	On bark	
			<i>Creographa subbrasiliensis</i>	On bark	New species
			<i>Diorygma angusticarpum</i>	On the trunk	New species
			<i>Diorygma chumphonense</i>	On tree	New species
			<i>Diorygma citri</i>	On <i>Citrus maxima</i>	New species
			<i>Diorygma conprotocetraricum</i>	On tree	New species
			<i>Diorygma erythrellum</i>	On bark	
			<i>Diorygma fuscopruinosum</i>	On the trunk	New species
			<i>Diorygma hieroglyphicum</i>	On <i>Durio zibethinus</i>	New species
			<i>Diorygma inexpectatum</i>	On tree	New species

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Diorygma junghuhnii</i>	On bark	
			<i>Diorygma pruinosum</i>	On bark	
			<i>Diorygma reniforme</i>	On bark	
			<i>Diorygma salazinicum</i>	On tree	New species
			<i>Diorygma soozanum</i>	On wood	
			<i>Diorygma subpruinosum</i>	On <i>Citrus maxima</i>	New species
			<i>Diorygma thailandicum</i>	on <i>Areca catechu</i>	New species
			<i>Diploschistes actinostomus</i>	On sandstone	
			<i>Diploschistes cinereocaesius</i>	On soil	
			<i>Glyphis cicatricosa</i>	On dead steam	
			<i>Glyphis scyphulifera</i>	On bark	
			<i>Graphis acharii</i>	On bark	
			<i>Graphis analoga</i>	On bark	
			<i>Graphis arbusculiformis</i>	On wood	
			<i>Graphis aphaneomicrospora</i>	On bark	
			<i>Graphis aphanes</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Graphis assimilis</i>	On bark	
			<i>Graphis australosiamensis</i>	On <i>Areca catechu</i>	New species
			<i>Graphis balaghatensis</i>	On bark	
			<i>Graphis caesiella</i>	On bark	
			<i>Graphis cincta</i>	On wood	
			<i>Graphis concolor</i>	On bark	
			<i>Graphis consimilis</i>	On bark	
			<i>Graphis dendrogramma</i>	On bark	
			<i>Graphis dussii</i>	On bark	
			<i>Graphis emersa</i>	On bark	
			<i>Graphis fissurinoidea</i>	On bark	
			<i>Graphis furcata</i>	On bark	
			<i>Graphis glaucescens</i>	On bark	
			<i>Graphis glaucocinerea</i>	On bark	New species
			<i>Graphis glaucorufa</i>	On bark	
			<i>Graphis handelii</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Graphis hossei</i>	On bark	New species
			<i>Graphis implicata</i>	On bark	
			<i>Graphis indica</i>	On bark	
			<i>Graphis intermedians</i>	On bark	New species
			<i>Graphis irosina</i>	On bark	
			<i>Graphis jejuensis</i>	On bark	
			<i>Graphis koratensis</i>	On bark	New species
			<i>Graphis librata</i>	On bark	
			<i>Graphis lineola</i>	On bark	
			<i>Graphis longiramea</i>	On bark	
			<i>Graphis longispora</i>	On bark	
			<i>Graphis lumbricina</i>	On bark	
			<i>Graphis marginata</i>	On bark	
			<i>Graphis nanodes</i>	On bark	
			<i>Graphis nigrocarpa</i>	On bark	
			<i>Graphis novopalmicola</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Graphis nuda</i>	On bark	
			<i>Graphis persimilis</i>	On rock	New species
			<i>Graphis perstriatula</i>	On bark	
			<i>Graphis phaeospora</i>	On bark	
			<i>Graphis proserpens</i>	On bark	
			<i>Graphis pyrrhocheiloides</i>	On bark	
			<i>Graphis renschiana</i>	On bark	
			<i>Graphis rongklaensis</i>	On bark	New species
			<i>Graphis schmidtii</i>	On rock	New species
			<i>Graphis stenotera</i>	On bark	
			<i>Graphis streblocarpa</i>	On bark	
			<i>Graphis subinsulana</i>	On tree	New species
			<i>Graphis subobtecta</i> var. <i>feracior</i>	On bark	New species
			<i>Graphis subrigida</i>	On wood	New species
			<i>Graphis subserpentina</i>	On bark	
			<i>Graphis subregularis</i>	On wood	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Graphis subvittata</i>	On wood	
			<i>Graphis supracola</i>	On decayed wood	
			<i>Graphis tenella</i>	On bark	
			<i>Graphis tenella</i> var. <i>epiphaea</i>	On bark	New species
			<i>Graphis vittata</i>	On bark	
			<i>Leiorreuma hypomelaenoides</i>	On bark	New species
			<i>Leiorreuma sericeum</i>	On bark	
			<i>Platygramme australiensis</i>	On bark	
			<i>Platygramme commutabilis</i>	On bark	
			<i>Platygramme discurrens</i>	On trunk	
			<i>Platygramme subcolubrosa</i>	On bark	New species
			<i>Pseudotopeliopsis longispora</i>	On bark	
			<i>Sarcographina heterospora</i>	On bark	
	Gyalectales	Coenogoniaceae	<i>Coenogonium barbatum</i>	On leaves	
			<i>Coenogonium convexum</i>	On leaves	New species
			<i>Coenogonium coronatum</i>	On leaves	New species

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Coenogonium dilucidum</i>	On leaves	
			<i>Coenogonium disciforme</i>	On leaves	New species
			<i>Coenogonium epiphyllum</i>	On leaves	
			<i>Coenogonium flavicans</i>	On leaves	
			<i>Coenogonium frederici</i>	On bark	
			<i>Coenogonium geralense</i>	On bark	
			<i>Coenogonium interplexum</i>	On trunk	
			<i>Coenogonium isidiiferum</i>	On leaves	
			<i>Coenogonium leprieurii</i>	On bark	
			<i>Coenogonium luteum</i>	On tree	
			<i>Coenogonium nepalense</i>	On bark	
			<i>Coenogonium pineti</i>	On wood	
			<i>Coenogonium queenslandicum</i>	On leaves	
			<i>Coenogonium subborinquense</i>	On bark	New species
			<i>Coenogonium subluteum</i>	On leaves	
			<i>Coenogonium verrucimarginatum</i>	On bark	New species

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
		Gyalectaceae	<i>Cryptolechia subincolorella</i>	On bark	
			<i>Ramonia minima</i>	On bark	New species
		Thelotre mataceae	<i>Astrochapsa astroidea</i>	On bark	
			<i>Astrochapsa calathiformis</i>	On trunk	New species
			<i>Astrochapsa kalbii</i>	On bark	New species
			<i>Astrochapsa zahlbruckneri</i>	On bark	
			<i>Astrochapsa pseudophlyctis</i>	On bark	
			<i>Chapsa alborosella</i>	On bark	
			<i>Chapsa discoides</i>	On bark	
			<i>Chapsa imperfecta</i>	On trees	
			<i>Chapsa indica</i>	On bark	
			<i>Chapsa laemensis</i>	On bark	New species
			<i>Chapsa leprocarpa</i>	On bark	
			<i>Chapsa patens</i>	On bark	
			<i>Chroodiscus australiensis</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Chroodiscus defectus</i>	On leaves	New species
			<i>Chroodiscus homchantarae</i>	On leaves	New species
			<i>Chroodiscus khaolungensis</i>	On leaves	New species
			<i>Chroodiscus khaosokensis</i>	On leaves	New species
			<i>Chroodiscus parvisporus</i>	On leaves	
			<i>Chroodiscus verrucosus</i>	On leaves	
			<i>Leucodecton occultum</i>	On bark	
			<i>Thelotrema leprocarpoides</i>	On trees	
	Lecanorales	Catillariaceae	<i>Catillaria testaceolivens</i>	On bark	New species
			<i>Catillaria unicolor</i>	On bark	New species
		Cladoniaceae	<i>Cladia aggregata</i>	On wood	
			<i>Cladonia calyciformis</i>	On soil	New species
			<i>Cladonia ciliata</i> var. <i>tenuis</i>	On soil	
			<i>Cladonia corymbescens</i>	On soil	
			<i>Cladonia didyma</i> var. <i>vulcanica</i>	On wood	
			<i>Cladonia fruticulosa</i>	On soil	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Cladonia furcata</i>	On soil	
			<i>Cladonia gymnopoda</i>	On Soil	
			<i>Cladonia homchantarae</i>	On soil	New species
			<i>Cladonia macilenta</i>	On soil, wood	
			<i>Cladonia mongkolsukii</i>	On rock	New species
			<i>Cladonia mauritiana</i>	On damp soil	
			<i>Cladonia ochrochlora</i>	On trees	
			<i>Cladonia ochrochlora</i>	On wood	
			<i>Cladonia ramulosa</i>	On soil	
			<i>Cladonia rangiferina</i>	On soil	
			<i>Cladonia rappii</i>	On rock	
			<i>Cladonia recticaulis</i>	On rock	New species
			<i>Cladonia rudis</i>	On soil	New species
			<i>Cladonia scabriuscula</i>	On soil	
			<i>Cladonia siamea</i>	On soil	New species
			<i>Cladonia singhii</i>	On soil	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Cladonia squamosa</i>	On mosses	
			<i>Cladonia subcervicornis</i>	On soil	
			<i>Cladonia subpityrea</i>	On rock	
			<i>Cladonia transindica</i>	On soil	
		Haematommataceae	<i>Haematomma africanum</i>	On bark	
			<i>Haematomma collatum</i>	On bark	
			<i>Haematomma flexuosum</i>	On bark	
			<i>Haematomma parda</i>	On bark	New species
			<i>Haematomma puniceum</i>	On bark	
			<i>Haematomma rufidulum</i>	On bark	
			<i>Haematomma wattii</i>	On bark	
		Lecanoraceae	<i>Traponora macrospora</i>	On bark	
			<i>Lecanora achroa</i>	On bark	
			<i>Lecanora argentata</i>	On bark	
			<i>Lecanora arthothelinella</i>	On bark	
			<i>Lecanora austrotropica</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Lecanora caesiorubella</i>	On bark	
			<i>Lecanora coronulans</i>	On bark	
			<i>Lecanora ecoronata</i>	On bark	
			<i>Lecanora farinacea</i>	On rocks	
			<i>Lecanora flavoviridis</i>	On rock	
			<i>Lecanora fumigata</i>	On rocks	New species
			<i>Lecanora helva</i>	On sandstone	
			<i>Lecanora interjecta</i>	On bark	
			<i>Lecanora kansriae</i>	On bark	New species
			<i>Lecanora leproplaca</i>	On bark	
			<i>Lecanora leprosa</i>	On bark	
			<i>Lecanora melaleuca</i>	On bark	
			<i>Lecanora phaeocardia</i>	On bark	New species
			<i>Lecanora plumosa</i>	On rock	
			<i>Lecanora pseudargentata</i>	On bark	
			<i>Lecanora pseudistera</i>	On granite	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Lecanora subimergens</i>	On rock	
			<i>Lecanora subimmersa</i>	On granite	
			<i>Lecanora toroyensis</i>	On bark	
			<i>Lecanora tropica</i>	On bark	
			<i>Lecanora ulrikii</i>	On bark	New species
			<i>Lecanora vainioi</i>	On granite	
		Malmideaceae	<i>Malmidea subaurigera</i>	On dead stem	
			<i>Crustospathula khaoyaiana</i>	On bark	New species
			<i>Kalbionora palaeotropica</i>	On bark	New species
		Parmeliaceae	<i>Bulbothrix bulbochaeta</i>	On tree trunk	
			<i>Bulbothrix goebelii</i>	On bark	
			<i>Bulbothrix hypocraea</i>	On bark	
			<i>Bulbothrix isidiza</i>	On bark	
			<i>Bulbothrix laevigatula</i>	On bark	
			<i>Bulbothrix meizospora</i>	On bark	
			<i>Bulbothrix papyrina</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Bulbothrix pigmentacea</i>	On bark	
			<i>Bulbothrix queenslandica</i>	On bark	
			<i>Bulbothrix sensibilis</i>	On bark	
			<i>Bulbothrix setschwanensis</i>	On bark	
			<i>Bulbothrix tabacina</i>	On bark	
			<i>Bulbothrix ventricosa</i>	On bark	
			<i>Canoparmelia ecaperata</i>	On bark	
			<i>Canoparmelia owariensis</i>	On rock	
			<i>Canoparmelia texana</i>	On bark	
			<i>Flavoparmelia caperata</i>	On bark	
			<i>Hypogymnia pseudobitteriana</i>	On bark	
			<i>Hypogymnia subphysodes</i>	On wood	
			<i>Hypogymnia vittata</i>	On rock	
			<i>Hypotrachyna addita</i>	On wood	
			<i>Hypotrachyna adjuncta</i>	On wood	
			<i>Hypotrachyna bahiana</i>	On trees, rocks	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Hypotrachyna brevirhiza</i>	On trees, rocks	
			<i>Hypotrachyna chlorobarbatica</i>	On bark	New species
			<i>Hypotrachyna cirrhata</i>	On wood	
			<i>Hypotrachyna coorgiana</i>	On bark	
			<i>Hypotrachyna corneola</i>	On fallen branch	
			<i>Hypotrachyna crenata</i>	On bark	
			<i>Hypotrachyna dactylifera</i>	On trees	
			<i>Hypotrachyna ducalis</i>	On wood	
			<i>Hypotrachyna expallida</i>	On wood	
			<i>Hypotrachyna exsecta</i>	On wood	
			<i>Hypotrachyna formosana</i>	On trees	
			<i>Hypotrachyna granulans</i>	On bark	New species
			<i>Hypotrachyna heterochroa</i>	On bark	
			<i>Hypotrachyna horrescens</i>	On rock	
			<i>Hypotrachyna imbricatula</i>	On trees	
			<i>Hypotrachyna immaculata</i>	On trees	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Hypotrachyna infirma</i>	On trees	
			<i>Hypotrachyna mason-halei</i>	On bark	
			<i>Hypotrachyna massartii</i>	On trees	
			<i>Hypotrachyna microlobulata</i>	On trees, rocks	
			<i>Hypotrachyna minarum</i>	On bark	
			<i>Hypotrachyna nepalensis</i>	On twigs and branches	
			<i>Hypotrachyna orientalis</i>	On bark	
			<i>Hypotrachyna osseoalba</i>	On bark	New species
			<i>Hypotrachyna physcioides</i>	On trees, rocks	
			<i>Hypotrachyna ramkhamhaengiana</i>	On bark	New species
			<i>Hypotrachyna scabrida</i>	On coniferous trees	New species
			<i>Hypotrachyna scytodes</i>	On trees	
			<i>Hypotrachyna sorocheila</i>	On wood	
			<i>Hypotrachyna vexans</i>	On twigs, branches	
			<i>Imshaugia placorodia</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Parmelia coilocarpa</i>	On bark	New species
			<i>Xanthoparmelia australiensis</i>	On rocks	
			<i>Xanthoparmelia congensis</i>	On rocks	
			<i>Xanthoparmelia mougeotina</i>	On rocks	
		Pilocarpaceae	<i>Byssolecania fumosonigrans</i>	On leaves	
			<i>Byssolecania hymenocarpa</i>	On leaves	
			<i>Byssoloma annuum</i>	On leaves	
			<i>Byssoloma chlorinum</i>	On leaves	
			<i>Byssoloma fadenii</i>	On leaves	
			<i>Byssoloma gahavisukanum</i>	On leaves	
			<i>Byssoloma guttiferæ</i>	On leaves	
			<i>Byssoloma leucoblepharum</i>	On bark	
			<i>Byssoloma subdiscordans</i>	On rock	
			<i>Byssoloma tricholomum</i>	On leaves	
			<i>Calopadia fusca</i>	On leaves	
			<i>Calopadia puiggarii</i>	On leaves	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Calopadia subcoerulescens</i>	On leaves	
			<i>Eugeniella micrommata</i>	On leaves, trees	
			<i>Fellhanera bouteillei</i>	On leaves	
			<i>Fellhanera fuscata</i>	On leaves	
			<i>Fellhanera mastothallina</i>	On leaves	
			<i>Fellhanera raphidophylli</i>	On leaves	
			<i>Lasioloma phycophilum</i>	On leaves	
		Ramalinaceae	<i>Bacidia heterochroa</i>	On bark	
			<i>Bacidia hostheleoides</i>	On bark	
			<i>Bacidia manilensis</i> var. <i>siamensis</i>	On bark	
			<i>Bacidia medialis</i>	On bark	
			<i>Bacidia squamellosa</i>	On bark	
			<i>Bacidia subareolata</i>	On dead stem	New species
			<i>Bacidina pallidocarnea</i>	On leaves	
			<i>Bacidina penicillata</i>	On tree	New species
			<i>Bacidiopsora orizabana</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Bacidiopsora squamulosula</i>	On bark	
			<i>Bactrospora metabola</i>	On bark	
			<i>Bactrospora dispersa</i>	On bark	New species
			<i>Bactrospora myriadea</i>	On bark	
			<i>Bactrospora perspiralis</i>	On bark	New species
			<i>Bactrospora subdryina</i>	On bark	New species
			<i>Badimia multiseptata</i>	On leaves	New species
	Ostropales	Stictidaceae	<i>Absconditella delutula</i>	On rock	
			<i>Fitzroyomyces cyperacearum</i>	On woody stem	
			<i>Fitzroyomyces hyaloseptisporus</i>	On dead stem	New species
			<i>Ostropomyces thailandicus</i>	On dead stem	New species
			<i>Stictis anomianthi</i>	On dead twigs	New species
			<i>Trinathotrema stictideum</i>	On bark	
		Coccotremataceae	<i>Coccotrema porinopsis</i>	On bark	
	Peltigerales	Coccocarpiaceae	<i>Coccocarpia adnata</i>	On trunk	
			<i>Coccocarpia dissecta</i>	On tree	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Coccocarpia erythroxyli</i>	On bark	
			<i>Coccocarpia glaucina</i>	On bark	
			<i>Coccocarpia palmicola</i>	On trunks	
			<i>Coccocarpia pellita</i>	On trunks	
			<i>Coccocarpia smaragdina</i>	On barks	
		Collemataceae	<i>Collema coilocarpum</i>	On bark	
			<i>Collema furfuraceum</i>	On trees	
			<i>Collema leptaleum</i>	On bark	
			<i>Collema leptaleum</i> var. <i>bilosum</i>	On bark	
			<i>Collema pulchellum</i> var. <i>subnigrescens</i>	On bark	
			<i>Collema rugosum</i>	On bark	
			<i>Leptogium austroamericanum</i>	On bark	
			<i>Leptogium azureum</i>	On bark	
			<i>Leptogium burgessii</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Leptogium caesium</i>	On trunk	
			<i>Leptogium chloromelum</i>	On bark	
			<i>Leptogium cochleatum</i>	On trunk	
			<i>Leptogium coralloideum</i>	On bark	
			<i>Leptogium corticola</i>	On bark	
			<i>Leptogium cyanescens</i>	On leaves	
			<i>Leptogium denticulatum</i>	On rocks	
			<i>Leptogium javanicum</i>	On branches	
			<i>Leptogium marginellum</i>	On wood	
			<i>Leptogium moluccanum</i>	On bark	
			<i>Leptogium pedicellatum</i>	On bark	
			<i>Leptogium phyllocarpum</i>	On bark	
			<i>Leptogium resupinans</i>	On bark	
			<i>Leptogium trichophorum</i>	On bark	
			<i>Toniniopsis subincompta</i>	On bark	
		Pannariaceae	<i>Fuscopannaria siamensis</i>	On soil among bryophytes	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Gibbosporina boninensis</i>	On bark	
			<i>Lepidocollema brisbanense</i>	On bark	
			<i>Lepidocollema marianum</i>	On bark	
			<i>Lepidocollema papillatum</i>	On bark	
			<i>Lepidocollema wainioi</i>	On bark	
	Pertusariales	Icmadophilaceae	<i>Dibaeis arcuata</i>	On roadside mosses	
	Telochistales	Brigantiaeaceae	<i>Brigantiaea leucoxantha</i>	On bark	
			<i>Brigantiaea lobulatisidiata</i>	On bark	New species
			<i>Brigantiaea pulchra</i>	On wood	
			<i>Brigantiaea tricolor</i>	On lichen	
			<i>Letrouitia corallina</i>	On bark	
			<i>Letrouitia domingensis</i>	On bark	
			<i>Letrouitia flavocrocea</i>	On bark	
			<i>Letrouitia leprolyta</i>	On bark	
			<i>Letrouitia magenta</i>	On dead stem	New species
			<i>Letrouitia subvulpina</i>	On bark	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
Leotiomyces	Helotiales	Telochistaceae	<i>Letrouitia transgressa</i>	On dead stem	
			<i>Letrouitia vulpina</i>	On bark	
			<i>Athallia holocarpa</i>	On rock	
			<i>Athallia inconnexa</i>	On rock	
			<i>Blastenia testaceorufa</i>	On bark	
			<i>Caloplaca cinnabarina</i>	On rock	
			<i>Caloplaca flavorubescens</i>	On bark	
			<i>Caloplaca pulicarioides</i>	On bark	
			<i>Flavoplaca oasis</i>	On rock	
			<i>Gyalolechia flavovirescens</i>	On rock	
		Bloxamiaceae	<i>Bloxamia discedens</i>	On dead log	
		Cenangiaceae	<i>Chlorencoelia torta</i>	On rotten wood	
		Chlorociboriaceae	<i>Chlorociboria aeruginascens</i>	On wood	
			<i>Chlorociboria aeruginosa</i>	On wood	
			<i>Chlorociboria macrospora</i>	On wood	
			<i>Chlorociboria poutoensis</i>	On dead stems	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Chlorciboria</i> sp1	On wood	
			<i>Chlorociboria</i> sp2	On wood	
		Chlorospleniaceae	<i>Chlorocplenium sinicum</i>	On rotten wood	
		Gelatinodiscaceae	<i>Ascocoryne cylichnium</i>	On wood	
			<i>Ascocoryne sarcoides</i>	On wood	
		Helotiaceae	<i>Dicephalospora aurantiaca</i>	On dead stems	
			<i>Dicephalospora. chiangraiensis</i>	On dead stems	New species
			<i>Dicephalospora inthanonensis</i>	On dead stems	New species
			<i>Dicephalospora irregularis</i>	On dead stems	New species
			<i>Dicephalospora rufocornea</i>	On dead stems	
			<i>Dicephalospora</i> sp1	On dead stems	
			<i>Dicephalospora</i> sp2	On dead stems	
			<i>Dimorphospora foliicola</i>	On submerged wood	
			<i>Helotiales</i> sp1	On dead branch	
			<i>Hymenoscyphus cf calyculus</i>	On dead stems	
			<i>Phaeohelotium</i> sp	On wood litter	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
		Lachnaceae	<i>Erioscyphella abnormis</i>	On dead stems	
			<i>Erioscyphella alba</i>	On dead stems	New species
			<i>Erioscyphella. aseptata</i>	On dead stems	New species
			<i>Erioscyphella brasiliensis</i>	On dead stems	
			<i>Erioscyphella. sclerotii</i>	On dead stems	
			<i>Erioscyphella papillaris</i>	On dead wood	
			<i>Erioscyphella sp</i>	On dead stems	
			<i>Lachniclavula thalandica</i>	On dead wood	New species
			<i>Proliferodiscus chiangraiensis</i>	On dead stems	New species
			<i>Proliferodiscus sp</i>	On dead wood	
		Pezizellaceae	<i>Calycina citrina</i>	On dead wood	
			<i>Calycina claroflava</i>	On dead stems	
			<i>Calycina montana</i>	On dead stems	
			<i>Calycina papaeana</i>	On dead stems	New species
			<i>Rubropezicula thailandica</i>	On dead stems	New species
		Rutstroemiaceae	<i>Lambertella aurantiaca</i>	On dead stems	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
Lichinomycetes	Lichinales	Lichinaceae	<i>Lambertella chiangraiensis</i>	On dead stems	New species
			<i>Lambertella fusoides</i>	On dead leaves	New species
			<i>Lambertella himalayensis</i>	On dead stems	
			<i>Lambertella phanensis</i>	On dead stems	New species
			<i>Lambertella sessilis</i>	On rotten wood	New species
			<i>Lambertella takensis</i>	On dead stems	New species
			<i>Microglossum macrosporum</i>	On soil	New species
			<i>Leotia atrovirens</i>	On soil	
			<i>Leotia lubrica</i>	On soil	
			<i>Coccomyces macronatus</i>	On dead leaves	
			<i>Terriera elliptica</i>	On dead stems	
			<i>Strossmayeria bakeriana</i>	On dead stem	
			<i>Lecidopyrenopsis corticola</i>	On trunk	New species
			<i>Arthrobotrys superba</i>	On deads wood	
			<i>Hyalorbilia erythrostigma</i>	On <i>Annulohypoxylon</i> sp.	
Orbiliomycetes	Orbiliales	Orbiliaceae	<i>Hyalorbilia fagi</i>	On dead wood	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
Pezizomycetes	Pezizales	Ascobolaceae	<i>Hyalorbilia inflatula</i>	On wood	
			<i>Orbilia caudata</i>	On wood	
			<i>Orbilia cf. paracaudata</i>	On dead branches	
			<i>Orbilia leucostigma</i>	On wood	
			<i>Orbilia stipitata</i>	On wood	New species
			<i>Saccobolus succineus</i>	On elephant dung	New species
			<i>Saccobolus diaphanus</i>	On horse dung	New species
		Helvellaceae	<i>Helvella guttata</i>	On soil	
			<i>Helvella orentitomentosa</i>	On soil	
		Pezizaceae	<i>Peziza tomentosa</i>	On soil	
		Pulvinulaceae	<i>Pulvinula anthracobia</i>	On soil	New species
			<i>Pulvinula carbonaria</i>	On charred wood	
			<i>Pulvinula cinnabarina</i>	On soil	
			<i>Peziza convexella</i>	On soil	
			<i>Pulvinula etiolata</i>	On soil	
			<i>Pulvinula tetraspora</i>	On soil	

Table 5.2 (continued)

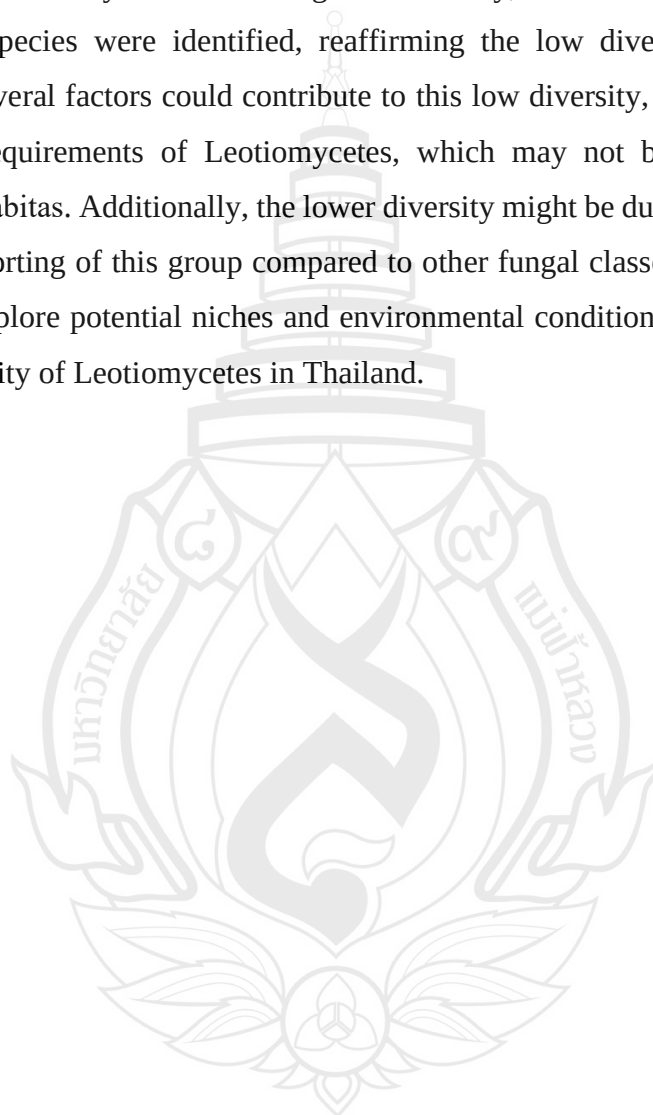
Class	Order	Family	Species	Host	Novel status
		Pyrenomataceae	<i>Acervus globulosus</i>	On soil	
			<i>Lamprospora lobata</i>	On soil	
			<i>Lasiobolidium boudieri</i>	On dead wood	
			<i>Otidea</i> sp	On soil	
			<i>Scutellinia badio-berbis</i>	On decay trunk	
			<i>Scutellinia colensoi</i>	On decay wood	
			<i>Scutellinia jungneri</i>	On soil	
			<i>Scutellinia superba</i>	On soil	
			<i>Sowerbyella phlyctispora</i>	On soil	
			<i>Sphaerosporella brunnea</i>	On soil	
		Rhizinaceae	<i>Phillipsia carnicolor</i>	On dead wood	
			<i>Phillipsia domingensis</i>	On rotten wood	
			<i>Phillipsia gelatinosa</i>	On rotten wood	New species
			<i>Phillipsia hydei</i>	On dead wood	New species
		Sarcoscyphaceae	<i>Cookeina indica</i>	On dead wood	
			<i>Cookeina sinensis</i>	On dead branch	

Table 5.2 (continued)

Class	Order	Family	Species	Host	Novel status
			<i>Cookeina speciosa</i>	On dead branch	
			<i>Cookeina sulcipes</i>	On dead branch	
			<i>Cookeina tricholoma</i>	On dead branch	
			<i>Nanoscypha aequispora</i>	On dead wood	New species
		Sarcosomataceae	<i>Plectania rhytidia</i>	On herbaceous stem	
			<i>Pseudoplectania nigrella</i>	On soil among mosses	

5.4 Discussion

According to the checklist, the number of Leotiomyces species found in Thailand is relatively low, with only 50 species documented. This indicates a limited diversity of Leotiomyces in the region. Similarly, in the current study, a modest number of species were identified, reaffirming the low diversity of this class in Thailand. Several factors could contribute to this low diversity, including the specific ecological requirements of Leotiomyces, which may not be abundantly met in Thailand's habitats. Additionally, the lower diversity might be due to under-exploration or under-reporting of this group compared to other fungal classes. Further studies are needed to explore potential niches and environmental conditions that could support a higher diversity of Leotiomyces in Thailand.



CHAPTER 6

CONCLUSIONS

6.1 Overall Conclusion

The exploration and diversity of discomycetes within the Leotiomyces globally have garnered increasing attention in mycological studies over the years (Tewari & Pant, 1967; Baral & Rämä, 2015; Galán et al., 2015; Quijada & Beltrán-Tejera, 2017; Tochiara et al., 2019). Despite this, the taxonomic exploration of discomycetes within Leotiomyces, particularly in tropical regions like Southeast Asia, remains largely uncharted territory despite the significant genetic diversity present (Hyde et al., 2018; Wong et al., 2021). Thailand, known for its remarkable fungal diversity and increasing documentation of novel taxa (Hyde et al., 2018), has seen limited exploration studies focusing on discomycetes within Leotiomyces (Phanichapol, 1986; Ekanayaka et al., 2019; Lestari et al., 2022; Phutthacharoen et al., 2022). This dissertation addresses these gaps through a research study focusing on saprobic discomycetes on lignocellulose substrates, with redescription of selected species in Hyaloscyphaceae and the introduction of taxonomic novelties within *Calycina*, *Dicephalospora*, *Lambertella*, and *Cyathicula*, along with new host and geographical records, along with a review study focusing on phytopathogenic discomycetes on lignocellulose substrates.

The taxonomic investigations identified 17 Helotiales species, primarily collected in northern Thailand, with additional specimens from Italy. Through morphological and phylogenetic analyses of ITS and LSU sequence data, *Chlorencoelia torta* and *Calycina montana* were introduced as new geographical records, while *Calycina papaeana* and *Dicephalospora irregularis* were introduced as novel species from Thailand. From Italy, *Cyathicula dioscorea* and *Cyathicula rusci* were introduced. Notably, seven species of *Lambertella* were also documented from Thailand; *L. aurantiaca* and *L. himalayensis* were presented as geographical records while *L. chiangraiensis*, *L. fusoidea*, *L. phanensis*, *L. sessilis* and *L. takensis* were introduced as novel species based on morphology and phylogeny of ITS, LSU, SSU and RPB2 sequence data.

Additionally, this study expands our understanding of host associations, with *Erioscyphella abnormis* documented as a new host record on *Tectona grandis* based on morphology and phylogeny of ITS, LSU, RPB2 and mtSSU. Synonymizing efforts were also undertaken, consolidating our taxonomic knowledge. For e.g., *Bisporella montana* and *B. shangrilana* were synonymized into *Calycina montana* and *C. shangrilana*.

This dissertation documented seven new species of genera *Calycina*, *Dicephalospora*, and *Lambertella*, two host records of genera *Erioscyphella*, *Lambertella* and two geographical records of genera *Calycina* and *Chlorencoelia*. Despite the limited novel findings of this study, it underscores the importance of continued exploration and documentation of fungal diversity, particularly in regions like Thailand. The diversity of fungi, in general, including discomycetes, depends on the combination of weather and richness of the substrates (Talley et al., 2002; Niu et al., 2021). This study was done in Northern Thailand with various habitats such as National Park Forest Doi Inthanon and nearby forests in Mushroom Research Center, which are both located in Chiang Mai and *Tectona grandis* plantations in Chiang Rai and Tak provinces. The most abundant discomycetes specimens are collected from Doi Inthanon National Park, in which various sources of lignocellulose substrates are abundant, of which discomycetous specimens of more than three helotian families are collected. Even a few specimens were collected if the collection trip was conducted in the dry season (unpublished data, 2022).

This study also presents a checklist of discomycetes from Thailand. The checklist encompasses extant and newly discovered discomycetes from Thailand from 1889 to 2022, providing an unprecedented record of their presence. While this list is not encyclopedic, it serves as initial data on the distribution of discomycetes from Thailand. By compiling this checklist, a total of 690 extant species were discovered in Thailand, distributed across ten classes, 23 orders, and 57 families. The checklist showed that Lecanoromycetes and Leotiomyces were the major groups, accounting for 81% (553 species) and 7% (50 species) respectively (Figure 5.1).

Novel species of discomycetes were discovered from 1889 to 1929 (19 species) but then decreased during 1930 to 1991 (6 species). Subsequently, the number of new species discovered rose significantly and reached a peak during 1992 to 2022, reaching 97 species (Table 5.1). Based on the table list, it is apparent that discomycetes in Thailand have been immensely overlooked, hence, this signifies the need for further research and exploration to fully comprehend the extent and ecological significance of discomycetes in Thailand. The checklist serves as a valuable resource for future studies, facilitating a better understanding of the diversity and distribution patterns of discomycetes in Thailand. It highlights the importance of bolstering research efforts in discomycetes explorations and encourages further scrutiny into the ecological function and potential applications of these fungi in Thailand's ecosystems.

Additionally, this dissertation provides a comprehensive literary review of phytopathogenic discomycetes on lignocellulose substrates, offering insights into their taxonomy, life cycle, economic impacts, and control strategies. While the list of phytopathogenic genera may not be exhaustive, it offers a snapshot of the current understanding and highlights the need for further research in this area. This study also establishes an online database of discomycetes, consolidating research from various regions and spanning across different years into the accessible website discomycetes.org. Overall, this study contributes to ongoing efforts to unravel the diversity and ecological significance of discomycetes, emphasizing the importance of continued exploration and research in this field.

6.2 Research Advances

This thesis builds upon previous studies by further exploring the diversity of discomycetes, primarily in northern Thailand and Italy. In addition to introducing new species, it documents new host and geographical records of discomycetes, particularly within certain families of Helotiales. Furthermore, this study addresses taxonomic issues concerning species in *Bisporella* within the Helotiaceae family, which were previously highlighted by other mycologists. Through the observation of new specimens and comparison with herbarium material, our study synonymizes our newly found *Bisporella* species into *Calycina*, based on morphological and taxonomic criteria. Additionally, *Lambertella sensu stricto* is emended in this study by expanding its description based on newly found specimens, including previously undescribed characteristics. Moreover, *L. aurantiaca* is redescribed based on newly discovered specimens, and the associated gene regions have been deposited in NCBI for future reference.

This thesis holds significant importance in the field of mycology as it contributes new sequence data for discomycete taxa, a crucial element that was lacking in the literature. By providing the molecular data, the thesis not only enhances our understanding of discomycete diversity but also facilitates more accurate taxonomic classifications and phylogenetic analyses. This newfound data opens avenues for further research, allowing for more comprehensive investigations into the evolutionary relationships, ecological roles, and potential applications of discomycetes. Overall, the inclusion of new sequence data in this thesis marks a substantial advancement in our knowledge of these fungi and underscores the ongoing efforts to unravel their complexities.

Studies focusing on discomycetes species causing diseases or growth impediments on lignocellulose substrates have predominantly centered on those affecting economically significant host plant commodities. However, there is an imbalance in research attention towards other phytopathogenic species causing disease symptoms on non-economical host plants, along with their updated classification and recent studies related to economic impacts and control strategies. Therefore, this study

addresses this gap by presenting the most recent documentation of lists and classifications from the class to the general level of phytopathogenic discomycetes, including their economic impacts and control strategies. The comprehensive overview of phytopathogenic discomycetes provided in this thesis, covering various countries, updated classifications, and recent study status, offering valuable insights for mycologists. This knowledge not only enhances our understanding of saprobic discomycetes but also sheds light on the unexplored scope of phytopathogenic discomycetes.

The construction of the discomycetes.org website stands as a pivotal step forward in the study and appreciation of discomycetes fungi. By providing a centralized platform for comprehensive information, data, and resources pertaining to discomycetes, this website serves as a beacon for researchers, educators, and enthusiasts alike. Its establishment marks a concerted effort to bridge the gap in understanding and exploring the diversity, taxonomy, ecology, and distribution of discomycetes globally. As a dynamic repository, discomycetes.org not only facilitates knowledge dissemination but also fosters collaboration, innovation, and conservation efforts within the mycological community. Through ongoing updates, contributions, and engagement, this website promises to be a cornerstone in advancing our understanding of discomycetes and their integral role in ecosystems worldwide.

6.3 Future Works

Research in discomycete exploration, particularly in Southeast Asia, remains essential due to the challenges in finding specimens of these fungi. Discomycetes, especially those belonging to the Leotiomycetes, are predominantly found in humid environments with rich vegetation, such as national parks. Therefore, exploration efforts in these areas are highly encouraged. Additionally, fungal exploration in homogenous plantation areas can also be conducted, particularly during the high rainy season when conditions are conducive to fungal growth. Culturing newly found specimens is vital for studying the asexual morph of discomycetes, providing comprehensive insights into their life cycle. However, culturing discomycete

specimens requires additional focus and support with sufficient sterile facilities, as these cultures are often targeted by other parasitic fungi. The other significance of culture availability for discomycetes will also broaden advance researches such as detection for secondary metabolites which potential for medicine, biological control and varied other industries. For example, secondary metabolite of *Dicephalospora* called dicephalosterol which inhibit testosterone pathway and useful in prostatic hypertrophy. Another helotian fungi, *Lachnum papyraceum* detected for Lachnumon which are known for its nematicidal ability.

In this thesis, attempts have been made to re-observe herbarium specimens for all genera within Hyaloscyphaceae, Lachnaceae, and Rutstreomiaceae, as some genera required redescrptions and updates. However, gathering herbarium materials from overseas herbaria poses challenges, as some are inaccessible, and the availability of type materials is limited, making loans impossible. Depending on the family in question, future work would benefit from focusing on redescrbing one family in morphology and, if feasible, extracting DNA from the type or reference materials. This approach may help resolve taxonomic issues by analyzing phylogenetic affinities with the type materials.

Finally, the discomycetes.org website requires continuous updates with the latest research findings on all classes of discomycetes, ensuring that the platform remains current and comprehensive.

6.4 Publications

A total of five first-author and eight co-author papers have been published and or submitted in international journals. The following is the list of the publications.

Lestari, A. S, Wanasinghe, D. N., Gafforov, Y., Tennakoon, D. S., Chethana, K. W. T., Aburazakov, A., . . . Hyde, K. D. (2021). Taxonomy and phylogenetic appraisal of *Leptosphaeria chatkalica* sp. nov. (Leptosphaeriaceae, Pleosporales) from Uzbekistan. *Phytotaxa*, 520 (2), 155–168.
<https://doi.org/10.11646/phytotaxa.520.2.3>

- Lestari, A.S., & Chethana, K.W.T. (2022). Morpho-phylogenetic insights reveal *Bisporella montana* as *Calycina montana* comb. nov. (Pezizellaceae, Helotiales). *Phytotaxa*, 558, 185–202.
<https://phytotaxa.mapress.com/pt/article/view/phytotaxa.558.2.3>
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APPENDICES



APPENDIX A

MEDIA AND CHEMICAL REAGENTS

1. Potato Dextrose Agar used for fungal cultivation

Potato Starch (from infusion) 4 g

Dextrose 20 g

Agar 15 g

Dissolve 39 g of Potato dextrose agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the powder and bring volume to 1000 ml. Autoclave at 121°C for 15 minutes.

2. Potassium hydroxide (KOH) used in the rehydration of dried specimens in 5% aqueous solution
3. Melzer's Reagent is a good general mounting medium that clears the material somewhat and allows particularly brilliant resolution with a microscope, and used for identification of ascomycete fungi. Amyloid reaction of asci changed to blue or heavily purple colours.

Chloral hydrate 100 g

Potassium iodide 5 g

Iodine 1.5 g

Distilled water 100 ml

APPENDIX B

DISCOMYCETES SPECIMENS FROM HERBARIUM INSTITUTIONS

Table B1 List of discomycetes specimens from abroad herbarium institutions

No	Name of Species	Reference / Accession number
1.	<i>Albotricha kamtschatica</i> (Raitv.) Raitv., 1985 Basionym: <i>Lachnaster kamtschatica</i> (Raitv.)	<i>Folia cryptog. Estonica</i> 17: 3 (1985) Herbarium Number: TAAM012499, Non-type Location: USA, Oregon, Lane County, Andrews Experimental Forest LTER Site #1 Host: <i>Pseudotsuga menziesii</i> Collector: Steven E. Carpenter Collection Date: 1986-09-10
2.	<i>Ambrodiscus pseudotsugae</i> S.E. Carp., 1988	<i>Mycologia</i> 80(3): 320 (1988) Herbarium Number: 46720, Holotype Location: Russian Federation, Kamchatka Krai, Yelizovsky District, the vicinity of Yuzhnye Koryaki 52.262461 -158.120235 Host: on the stem of <i>Filipendula palmata</i> . Collector: Erast Parmasto Collection Date: 1960-09-22

Table B1 (continued)

No	Name of Species	Reference / Accession number
3.	<i>Belonidium macounii</i> Dearn., 1916	<i>Mycologia</i> 8(2): 98 (1916) Herbarium Number: CUP-061849, Holotype Location: Canada, British Columbia, Vancouver Island 49.666667 -125.833333 +-301m. Host: on dead stems of <i>Spiraea menziensis</i> Collector: John Macoun Collection Date: 1915-00-00
4.	<i>Bisporella montana</i> W.Y. Zhuang and H.D. Zheng, 2017	<i>Mycosystema</i> 36: 401–420 (2017) Herbarium Number: HMAS 275566, Holotype Location: China, Yunnan, Shangrila, Pingbian, Daweishan Host: on rotten hardwood Collector: X.Q. Zhang and D.Z. Ren Collection Date: 1999-09-05
5.	<i>Bisporella shangrilana</i> W.Y. Zhuang and H.D. Zheng, 2017	<i>Mycosystema</i> 36: 401–420 (2017) Herbarium Number: HMAS 275566, Holotype Location: China, Yunnan, Shangrila, Bitahai Host: on rotten wood Collector: X.Q. Zhang and D.Z. Ren Collection Date: 2008-08-12

Table B1 (continued)

No	Name of Species	Reference / Accession number
6.	<i>Brunnipila clandestina</i> (Bull.) Baral, 1985 Basionym: <i>Peziza clandestina</i> Bull. 1791	Baral & Krieglsteiner, <i>Beih. Z. Mykol.</i> 6: 49 (1985) Herbarium Number: TAAM044272, Non-type Location: Lithuania, Telšiai Host: Unspecified Collector: Ain Raitviir Collection Date: 1966-7-17
7.	<i>Dasyscyphella cassandrae</i> Tranzschel, 1899	<i>Hedwigia</i> 38(Beibl.): (11) (1899) Herbarium Number: CUP-054631, Non- type Location: United States, New York, Tompkins, McLean 42.552016 -76.291044 +-6359m. Host: <i>Chamaedaphne calyculata</i> Collector: Korf Collection Date: 1964-06-17
8.	<i>Hyalopeziza pygmaea</i> (Mouton), 1987 Basionym: <i>Trichopeziza pygmaea</i> Mouton 1897 Bull. Soc. R. Bot. Belg. 36 (no. 2): 19 (1897)	Huhtinen, <i>Mycotaxon</i> 29: 279 (1987) Herbarium Number: BR5020088313439, Type Location: Belgium, Beaufays (Vierset) Host: Unspecified Collector: Mouton V Collection Date: s.d.

Table B1 (continued)

No	Name of Species	Reference / Accession number
9.	<i>Incrucipulum ciliare</i> (Schrad. ex J.F. Gmel.) Baral, 1985 Basionym: <i>Peziza ciliaris</i> Schrad. ex J.F. Gmel. 1792	<i>Beih. Z. Mykol.</i> 6: 72 (1985) Herbarium Number: BR5020089087414, Type Location: Belgium Host: Unspecified Collector: Mouton V. Collection Date: Unspecified
10.	<i>Lachnellula chrysophthalma</i> (Pers.) P. Karst., 1884 Basionym: <i>Peziza chrysophthalma</i> Pers., 1822	<i>Meddn Soc. Fauna Flora fenn.</i> 11: 138 (1884) Herbarium Number: CUP-046452, Non-type Location: United States, California, King Creek Trail, Lassen Volcanic National Park 40.493683 -121.407348 +-15351m. Host: <i>Abies magnifica shastensis</i> Collector: W.B. Cooke Collection Date: 1954-07-02
11.	<i>Lachnum agaricinum</i> Retz., 1769	<i>K.svenska Vetensk-Akad. Handl.</i> , ser. 1 30: 255 (1769) Herbarium Number: CUP-F-0321, Non-type Location: United States, New York, Hamilton, Blue Mountain Lake 43.86138 -74.451145 +-8260m. Host: Undetermined Collector: Charles E. Fairman Collection Date: 1911-08-06

Table B1 (continued)

No	Name of Species	Reference / Accession number
12.	<i>Lachnum virgineum</i> (Batsch) P. Karst., 1871 Basionym: <i>Peziza virginea</i> Batsch 1783	<i>Bidr. Känn. Finl. Nat. Folk</i> 19: 169 (1871) Herbarium Number: 16583, Nontype Location: Japan, Kanagawa, Ashigarakami- gun 35.42503 138.97411 Host: Wood Collector: Unspecified. Collection Date: 2005-07-02
13.	<i>Lahmia kunzei</i> Flot. ex Körb., 1861) [1865]	<i>Parerga lichenol.</i> (Breslau) 3: 282 (1861) [1865] Herbarium Number: BR5030045331321, Non-type Location: Germany Host: Unspecified Collector: Kalchbrenner C. Collection Date: Unspecified
14.	<i>Lambertella himalayensis</i> V.P. Tewari & D.C. Pant, 1967	<i>Mycologia</i> 59(1): 117 (1967) Herbarium Number: CUP-050013, Isotype Location: Unspecified Host: Unspecified Collector: Unspecified Collection Date: Unspecified

Table B1 (continued)

No	Name of Species	Reference / Accession number
15.	<i>Micraspis acicola</i> Darker, 1963	<i>Can. J. Bot.</i> 41(10): 1390 (1963) Herbarium Number: CUP-054914, Holotype Location: Canada, Ontario, Nipissing District, north of long portage into Gull Lake, Lake Timagami 46.25 -79 Host: <i>Picea marina</i> Collector: G.D. Darker Collection Date: 1927-07-27
16.	<i>Mitrula gracilis</i> P. Karst, 1833 Current name: <i>Bryoglossum gracile</i> (P. Karst.) Redhead 1977	<i>Hedwigia</i> 22: 17 (1883) Herbarium Number: CUP-D-00649(3- 199), Iso-type Location: Finland Host: Mosses Collector: Karsten, Petter (Peter) Adolf Collection Date: 1861-08-05
17.	<i>Neocudoniella jezoensis</i> (S. Imai) S. Imai, 1941 Basionym: <i>Cudoniella jezoensis</i> S. Imai [as 'jezoënsis'] 1934	<i>J. Fac. agric.</i> , Hokkaido Imp. Univ. 45: 234 (1941) Herbarium Number: CUP-JA-000465, Holo-type Location: Japan, Ishikari, Sapporo, Hokkaido, Mt. Moiwa 43.02308 141.322368 +-15605m. Host: Undetermined Collector: K. Sasaki Collection Date: Unspecified

Table B1 (continued)

No	Name of Species	Reference / Accession number
18.	<i>Perrotia flammea</i> (Alb. & Schwein.) Boud., 1901 Basionym: <i>Peziza flammea</i> Alb. & Schwein., 1805	<i>Bull. Soc. mycol. Fr.</i> 17: 24 (1901) Herbarium Number: 72629, Paratype Location: Norway, Trøndelag, Oppdal, Kongsvold 62.3067 9.6075 +-707m. Host: på birk Collector: Axel Blytt Collection Date: 1887-0-0
19.	<i>Pezizella hamulata</i> Feltgen, 1903 Current name: <i>Unguiculella hamulata</i> (Feltgen) Höhn., Sber. Akad. Wiss. Wien, Math.-naturw. Kl., Abt. 1 115: 1281 (1906)	<i>Vorstud Pilzfl. Luxemb.</i> , Nachtr. III: 51 (1903) Herbarium Number: CUP-058171, Iso- type Location: Luxembourg, Schonfelser Klaus 49.6 6.133333 +-301m. Host: <i>Trifolium medium</i> Collector: J. Feltgen Collection Date: 1901-06-00
20.	<i>Protounguicularia brevicapitata</i> Rait v. & R. Galán, 1986	<i>Int. J. Mycol. Lichenol.</i> 2(2-3): 222 (1986) Herbarium Number: TAAM194206, Isotype Location: Granada, Alhama de Granada -3.98963 37.00689 Andalusia/Andalucía, ES, Spain Host: Unspecified Collector: Ricardo Galán; A. Ortega Collection Date: 1982-02-24

Table B1 (continued)

No	Name of Species	Reference / Accession number
21.	<i>Unguiculariella bhutanica</i> K.S. Thind & R. Sharma, 1990	<i>Proc. Indian Acad. Sci., Pl. Sci.</i> 100(5): 280 (1990) Herbarium Number: CUP-IN-000623, Iso-type Location: Bhutan, Thimphu, Begana 27.473932 89.635305 Host: Decaying leaf stalks of angiosperm Collector: Sharma, Raghunandan Collection Date: 1981-08-07

APPENDIX C

PUBLICATIONS

<https://www.biotaxa.org/Phytotaxa/article/view/phytotaxa.520.2.3>

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Taxonomy and phylogenetic appraisal of *Leptosphaeria chatkalica* sp. nov. (Leptosphaeriaceae, Pleosporales) from Uzbekistan

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Morpho-phylogenetic insights reveal *Bisporella montana* as *Calycina montana* comb. nov. (Pezizellaceae, Helotiales)

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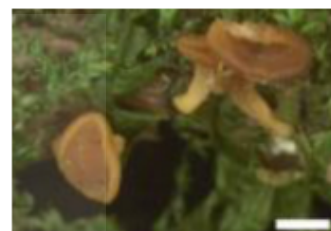
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Keywords: Fungi, 2 new combination species, Ascomycota, discomycetes, Leotiomycetes, saprobic

Abstract

Calycina-like specimens were collected in Doi Inthanon National Park, Thailand. The combined phylogeny of ITS and LSU based on maximum likelihood and bayesian inference analyses confirmed the taxonomic placement of our specimen in *Pezizellaceae*. Based on morphology and multi-gene phylogeny, the new discomycete specimen was identified as *Calycina montana* comb. nov., and was documented for the first time in Thailand. *Calycina montana* is characterized by the amber color, stipitate apothecia, gelatinized ectal excipulum, cylindrical asci and ellipsoidal ascospores. The morphology was observed together with the type strain, *Bisporella montana*. Our phylogenetic analyses and observation of the morphology of the type strain also confirmed the new combination of *Bisporella shangrilana* as *Calycina shangrilana* comb. nov., which resolves the confusion of *Bisporella* placement in *Pezizellaceae*.



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Article
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Phytopathogenic discomycetes, their economic impacts and control applications

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Abstract

Discomycetes is an artificial group in Ascomycota, comprising fungal species bearing saucer-, cup- or disc-like ascoma. There are many records of phytopathogenic discomycetes causing diseases in a wide range of vascular and non-vascular plants worldwide. In this review, we present phytopathogenic, discomycetous fungal taxa and provide notes on representative species, their economic importance and available management strategies. Phytopathogenic discomycetes are found in six classes of fungi, *Dothideomycetes* (distributed across three orders, two families and seven genera), *Eurotiomycetes* (across two orders, two families and two genera), *Lecanoromycetes* (across three orders, three families and four genera), *Leotiomycetes* (across nine orders, 23 families and 104 genera) and *Pezizomycetes* (across one order, seven families and 18 genera). The survival and completion of the life cycle of these discomycetes depend on their mode of parasitism on plant hosts in terrestrial habitats, including man-made landscapes (i.e., agricultural areas) and natural environments (i.e., forests). Agricultural and forest plant commodities are impacted by biotrophic, hemibiotrophic and necrotrophic discomycetes. Due to the complexity of their life cycles, many species have not yet been discovered and documented. Thus, this study can provide the foundation for comprehensive future studies into their taxonomy, physiology and host interactions.

Keywords – epidemiology – food security – fungal diseases – parasitic fungi – virulence

Introduction

The increasing human population and reduction of agricultural landscapes have a direct impact the global food security. For agricultural crops, fungal diseases pose one of the most significant challenges, with climate change aggravating the infection on various crops (Harvell et al. 2002). It is estimated that 16% of crop losses are due to microbial pathogens, among which approximately 75% are caused by fungal diseases (Oerke 2006).

Fungal diseases on food crops negatively impact food availability and economic losses. One of the most devastating fungal pathogens, *Pyricularia oryzae* (basionym: *Magnaporthe oryzae*) causes the blast disease not only on rice but also on barley, millet and wheat (Couch et al. 2005, Dean et al. 2012). Blast disease caused by *Pyricularia oryzae* lowers the yield by 10–13% or around 50 million tonnes (Talbot et al. 2003, Boddy 2016). *Fusarium oxysporum* is another



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Introducing Discomycetes.org: An online platform dedicated to apothecial fungi

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Abstract

There is an increase in the number of discomycetes and fungal taxonomic and phylogenetic investigations being conducted around the world. Previous research on discomycete fungi has been disjointedly documented. As a result, there is a need for an online platform to update the taxonomy and phylogeny of discomycetes. Discomycetes.org was created to provide a centralized location for updating the taxonomy, phylogeny, and ecological and economic significance of apothecial fungi.

Keywords – Ascomycota – Ascocarp – Database – Discomycetes taxa – Fungal webpage – Phylogeny – Species description – Taxonomy

Introduction

Discomycetes have undergone significant modifications in their classification and nomenclature in recent years, and this cosmopolitan class now encompasses 11 orders and 70 families, as documented by various studies (Ekanayaka et al. 2017, Ekanayaka et al. 2019a, Johnston et al. 2019, Wijayawardene et al. 2022). Traditionally, discomycetes have been defined based on their apothecial macromorphology, micromorphology, and chemical reactions (Pfister & Kimbrough 2001). However, the generic concept of some discomycetous taxa has been misleading due to the grouping of species based on similar morphologies in the past. The incorporation of molecular data into research has revealed unexpected results that mycologists never anticipated. For example, *Lichinodum*, which was originally placed in *Lichinomycetes* due to its lichenized form, was later transferred to *Leotiomyces* based on morphology (particularly due to lack of haustoria) and multigene phylogeny (Prieto et al. 2019). Advances in DNA sequencing technologies and phylogenetic studies have shown that discomycetes are phylogenetically diverse (Spatafora et al. 2006, Wang et al. 2006, Quandt & Haelewaters 2021), with some families being paraphyletic (Peterson & Pfister 2010) or polyphyletic (Johnston et al. 2019). Currently, discomycetes are accommodated in two subphyla: *Taphrinomycotina* (*Neoelectromycetes*) and *Pezizomycotina* (*Arthoniomycetes*, *Coniocybomycetes*, *Dothideomycetes*, *Eurotiomycetes*, *Geoglossomycetes*, *Lecanoromycetes*, *Leotiomyces*, *Lichinomycetes*, *Orbiliomycetes*, *Pezizomycetes*) (Landvik et al. 1993, Ekanayaka et al. 2017).

RESEARCH ARTICLE



Lambertella (Rutstroemiaceae, Helotiales) from Northern Thailand

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ABSTRACT

During our surveys for discomycetes from 2019 to 2021 in forests and plantations in northern Thailand, several *Lambertella*-like specimens were found. Morphological observation and BLAST search confirmed that seven newly collected specimens belong to *Lambertella*. Further phylogenetic analyses using maximum likelihood and Bayesian inference analysis based on combined the internal transcribed spacer region of rDNA (ITS), large subunit region of 28S rRNA (LSU), small subunit region of 18S rRNA (SSU) and RNA polymerase II gene (RPB2) sequence data and morphological examination coupled with chemical reactions confirmed seven *Lambertella* species. *Lambertella aurantiaca* and *L. himalayensis* were established as new geographical and host records, and the other five specimens, *L. chiangraiensis*, *L. fusoides*, *L. phanensis*, *L. sessilis* and *L. takensis*, were introduced as novel species. The highlight of the current study is the contribution of the morphological description for *Lambertella aurantiaca* since its introduction in 1964, emending the morphological criteria for *Lambertella* sensu stricto, and providing sequence data for all *Lambertella* species described in the current study.

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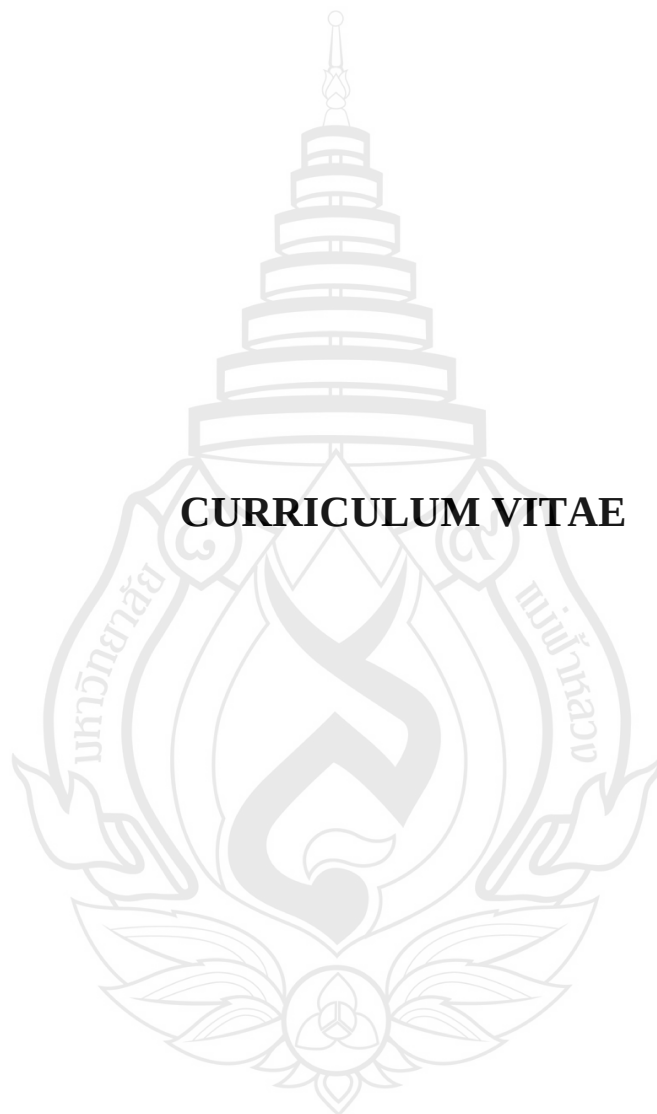
Ascomycota; discomycetes;
 Leotiomycetes; phylogenetic
 analysis; saprobes

Introduction

Rutstroemiaceae was established comprising *Lambertella*, *Lanzia*, *Poculum*, and *Verpatinia* based on nuclear rDNA phylogeny and typified with *Rutstroemia* (Kohn and Grenville 1989; Holst-Jensen et al. 1997). The family was characterised by brownish and greenish, stipitate to substipitate apothecia or sometimes cleistothecia with inoperculate, cylindric-clavate asci, and hyaline to brown, fusiform to ellipsoid ascospores. Most species of Rutstroemiaceae are saprobes and a few are parasites (Holst-Jensen et al. 1997; Galán et al. 2015; Wiseman et al. 2015; Zhao et al. 2016; Baral 2017; Johnston et al. 2019). With several taxonomic revisions based on morpho-phylogeny and novel species discoveries, Rutstroemiaceae has been expanded from its initial members to include eight genera, *Bicornispora*, *Bryorutstroemia*, *Clarireedia*, *Lambertella*, *Lanzia*, *Pseudolanzia*, *Rutstroemia*, and *Torreidiella* (Švrček 1957; Johnston and Park 2013;

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