



**TAXONOMY AND PHYLOGENY OF MICROFUNGI FROM
MARINE BASED HABITATS IN THAILAND**

RAHELEH ASGHARI

**DOCTOR OF PHILOSOPHY
IN
BIOLOGICAL SCIENCE**

**SCHOOL OF SCIENCE
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RAHELEH ASGHARI

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

Marine and coastal habitats are highly productive ecosystems that support diverse biological communities and provide essential ecosystem services. Coastal vegetation forms a critical interface between terrestrial and marine environments, providing habitat and shelter for organisms, contributing to coastal protection against flooding, erosion, and pollution, and supporting food resources and tourism related activities. However, these habitats are threatened by climate change and human activities. Fungi play a crucial role in coastal ecosystems through decomposition and nutrient recycling, yet fungal diversity in these ecosystems remains insufficiently explored, especially in tropical regions. This study provided a detailed reference for genera of salt marsh fungi and investigated saprobic fungi associated with decaying wood submerged in seawater and seashore plants, with particular emphasis on the salt marsh hosts *Suaeda maritima* and *Sesuvium portulacastrum*, which provide habitat for diverse organisms and contribute to coastal ecosystem stability in Thailand. Fungal identification was based on morphological characteristics and multigene phylogenetic analyses. Four new genera, *Catenomycella*, *Halomaris*, *Littoraliplantomyces* and *Neoloratospora*, and 33 new species were introduced; *Acremonium pluchaeae*, *Alloperoneutypa suaedae*, *Amphisphaeria leucaenae*, *Catenomycella sesuvii*, *Catenomycella thailandica*, *Chromolaenicola leucaenae*, *Cylindrotrichum marinum*, *Didymella lantanae*, *Emericellopsis limonii*, *Halocryptovalsa suaedae*, *Halomaris sexualis*, *Halomaris suaedae*, *Laburnicola suaedae*, *Leptospora lantanae*, *Littoraliplantomyces haylingensis*, *Myrmecridium hydei*, *Neoacremonium maritimum*, *Neocamarosporium littoraliplantae*, *Neocamarosporium pranburiense*, *Neocamarosporium salinum*, *Neocamarosporium sesuvii*, *Neocucurbitaria lantanae*,

Neoloratospora suaedae, *Paramyrothecium appendiculatum*, *Phaeosphaeria lantanae*, *Phaeosphaeria sesuvii*, *Preussia suaedae*, *Rosellinia maritima*, *Stachybotrys sesuvii*, *Tetraploa maritima*, *Torpedospora suaedae*, and *Waltergamsia maritima*. Additionally, 22 new host records, 11 geographic records, 9 first marine habitat records and 12 new collections were reported. Each identified species is provided with detailed descriptions and illustrations. A total of 117 fungal strains were analyzed, including 53 isolates from submerged decaying wood and 64 from seashore plants. Fungal composition across substrates and hosts was assessed using statistical analyses and visualized with heatmaps and charts. Submerged wood fungi were dominated by *Sordariomycetes* (72%), *Microascales* (46%) and *Halosphaeriaceae* (43%), particularly at higher salinities. Seashore plants fungi showed greater taxonomic diversity, with *Dothideomycetes* (56%) and *Pleosporales* (39%) predominating. Fungal overlap between substrates was limited, with only five genera and two species shared. Salinity influenced community composition, with higher fungal diversity at lower salinities and increased dominance of *Halosphaeriaceae* at higher salinities. Fungal morphs also differed between substrates, with hyphomycetous asexual morphs prevalent on submerged wood and coelomycetous asexual morphs dominating aerial plant tissues. This study highlights the high diversity and substrate specificity of saprobic fungi in marine based habitats and underscores the influence of environmental factors, particularly salinity, on fungal community structure.

Keywords: Ascomycota, Aquatic Fungi, Halophyte, Marine Fungi, Salt Marsh Fungi, Salt Tolerant, Taxonomy and Phylogeny

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ABBREVIATIONS AND SYMBOLS

cm	centimeter
diam.	diameter
e.g.	for example
et al.	and others
gen.	genus (singular) and genera (plural)
i.e.	that is
mm	millimeter
nov.	novum (Latin for new thing)
sp.	species
spp.	species (plural)
$\bar{x}$	average
°C	degree centigrade
μm	micrometer
μl	microliter
%	percent

CHAPTER 1

INTRODUCTION

1.1 Coastal Habitats and Fungi

Marine habitats are natural environments that can be broadly classified into oceanic and coastal systems (Kress 2019). Oceanic habitats extend from the deep sea to the water surface, and coastal habitats include seashores, intertidal zones, and the continental shelf (Kress 2019; Wijayawardene et al. 2022a). Coastal vegetation occupies the transitional zone between terrestrial and marine environments and includes submerged or partially submerged plants such as seagrasses, macroalgae, mangroves, salt marshes, and other coastal plant communities (Duarte et al. 2013; Wijayawardene et al. 2022a).

Coastal ecosystems are highly productive and provide a wide range of ecosystem services (Calabon et al. 2021). They are important carbon and nitrogen sinks and remove excess nitrogen from runoff water (Valiela and Teal 1979; Gedan et al. 2009). Coastal vegetation provides habitat and shelter for many terrestrial and marine organisms, including insects, birds, fish, and crustaceans, supporting coastal livelihoods and recreational activities such as fishing, hunting, and birdwatching. (Pennings and Bertness 2001; Gedan et al. 2009). Additionally, coastal plant communities act as natural barriers against tidal currents, waves, storms, coastal erosion, and flooding. They also protect shorelines from pollution and human-induced disturbances (Shepard et al. 2011; Duarte et al. 2013; Calabon et al. 2021).

Within coastal vegetation, salt marshes are key habitats that are regularly flooded by seawater with high salinity (Weis and Butler 2009). These ecosystems are dominated by halophytic herbaceous plants and comprise more than 500 known species, including *Salicornia*, *Juncus*, *Spartina*, *Atriplex*, *Suaeda*, and *Sesuvium* (Silliman 2014; Calabon et al. 2021). Some species, including *Suaeda maritima* (*Amaranthaceae*, *Caryophyllales*), and *Sesuvium portulacastrum* (*Aizoaceae*, *Caryophyllales*), are edible and show antibacterial activity (Chandrasekaran et al. 2011, Nayak et al. 2018; Shakthi et al. 2024). These plant species occur in both salt marsh

and mangrove habitats and are well adapted to highly saline environmental conditions (Calabon et al. 2021; Devadatha et al. 2021).

Marine fungi have traditionally been classified as obligate or facultative following the concept proposed by Kohlmeyer and Kohlmeyer (1979), later refined by Pang et al. (2016). To better reflect the ecological breadth of marine and coastal fungi, Wijayawardene et al. (2022a) proposed a habitat-based classification that divides coastal environments into coastal terrestrial ecosystems, semi-coastal marine ecosystems, coastal marine ecosystems, and deep marine ecosystems. This framework provides a useful conceptual basis for categorizing fungal habitats in transitional coastal environments where terrestrial and marine influences overlap.

Numerous studies have been conducted in coastal areas, including research on ecology (Duarte et al. 2013), ecosystem services and conservation (Deegan et al. 2012), and bacterial and fungal diversity (Calado and Barata 2012; Farrer et al. 2022). Fungi in coastal environments have been studied on a wide range of substrates, including water, sediments, driftwood, seagrasses, corals, mangroves, and salt marsh plants (Kohlmeyer and Kohlmeyer 1979; Hyde et al. 2000; Dayarathne et al. 2020a; Jones et al. 2019; Abdel-Wahab et al. 2021; Pang and Jones 2023).

Fungi are key decomposers that facilitate the transfer of organic matter in coastal ecosystems (Grossart et al. 2019; Peng et al. 2024). They contribute significantly to ecosystem functioning through their involvement in nutrient cycling (Hyde and Lee 1998). In addition, fungi represent a promising source of bioactive compounds and enzymes with potential applications in medicine, biotechnology, industry, bioremediation, and environmental management (Bonugli-Santos et al. 2015; Jones et al. 2019; Burgaud et al. 2022).

Although the oceans cover about 70% of the Earth's surface and fungi can thrive in almost all environments, only about 1.2% of cultured fungi belong to marine fungi (Zhang et al. 2024c). Of the approximately 100,000 accepted species of fungi and fungus-like taxa, only 2,252 species (about 2.25%) have been reported as marine fungi (Hyde et al. 2020c, www.marinefungi.org). This indicates that marine fungi have received considerably less attention compared to other fungal groups (Jones 2023). In recent years, studies on marine fungi have increased, with the number of recorded marine fungal species rising by about 1,000, from 1,692 species in 2020 to 2,252

species in 2025 (www.marinefungi.org, accessed 31 December). However, this still represents only about 20% of the estimated total marine fungal diversity (Jones 2011).

Lignicolous fungi are the most studied group of marine fungi and were initially reported from driftwood, trapped wood, and submerged test blocks (Jones et al. 2019). Over time, a considerable diversity of fungi has been documented from coastal plants. Devadatha et al. (2021) and Calabon et al. (2021) reported fungal associations from approximately 60 mangrove and 60 salt marsh plant species, respectively. In total, about 850 mangrove fungal taxa and 486 salt marsh fungal taxa were recorded, with *Ascomycota* being the dominant phylum (Calabon et al. 2021; Devadatha et al. 2021). Although these studies highlight coastal regions and seashore vegetation as important reservoirs of fungal diversity, many challenges remain, and numerous habitats and host plants are still underexplored. Studies on fungi associated with many seashore plants are limited. For example, only eight fungal taxa have been reported from *Suaeda maritima* and four taxa from *Sesuvium portulacastrum* (Calabon et al. 2021; Devadatha et al. 2021).

Thailand is recognized as a hotspot of fungal diversity, with significant progress in fungal research in recent years (Hyde et al. 2018). With approximately 2,600 km of coastline, Thailand provides an ideal setting for studies of coastal ecosystems (Curoy et al. 2022). Research on fungi along the coasts of Thailand was initiated by Kohlmeyer (1984) and subsequently expanded by numerous studies, which have indicated high species richness of marine fungi in the region (Hyde 1989, 1995; Pang et al. 2013; Dayarathne et al. 2017; Suetrong et al. 2015, 2017; Apurillo 2025). Most studies in Thailand have focused on saprobic fungi associated with driftwood, mangroves, and seagrasses (Calabon et al. 2021; Devadatha et al. 2021). Recently, studies by Aumentado et al. (2025) and Mukhopadhyay et al. (2025) have addressed fungal pathogens of mangroves and saprobic fungi on mangrove associated plants, respectively. However, salt marsh ecosystems remain poorly studied, with only four fungal records listed by Calabon et al. (2021) in the recent checklist of salt marsh fungi.

This study documents fungi from marine-related habitats in Thailand, focusing on trapped submerged wood and two salt marsh halophytes (*Sesuvium portulacastrum* and *Suaeda maritima*). Specifically, we (i) assess fungal diversity across these substrates (ii) introduce novel taxa and report new records supported by morphological

comparisons and multi-locus phylogenetic analyses and (iii) re-evaluate the taxonomy of selected previously described species using newly generated collections and cultures. Voucher specimens and living cultures were deposited in recognized herbaria/culture collections and DNA sequences were generated to support phylogenetic placement and species delimitation.

Research Hypothesis of this study includes: (i) Taxonomic studies integrating molecular and morphological data will reveal undescribed and previously known fungal taxa, contributing to a more comprehensive taxonomic framework for fungi from marine based habitats, and (ii) Marine submerged substrates and seashore plants harbor both overlapping and distinct fungal communities, reflecting the influence of substrate type.

1.2 Research Objectives

1.2.1 To investigate the taxonomy of saprobic marine fungi on trapped wood inhabiting rocky shores in Thailand.

1.2.2 To identify and document of Ascomycota on selected seashore plants in Thailand, with emphasis on *Suaeda maritima* and *Sesuvium portulacastrum*.

1.2.3 To document salt marsh fungi by providing molecular data, living cultures and herbarium specimens, and to create a detailed reference of salt marsh fungal genera through the FungalPedia publication.

1.3 Research Contents

This thesis is divided into 6 chapters.

Chapter 1 provides a general introduction, covering the research background on marine based habitats, fungi from coastal vegetation, and marine related fungi in Thailand.

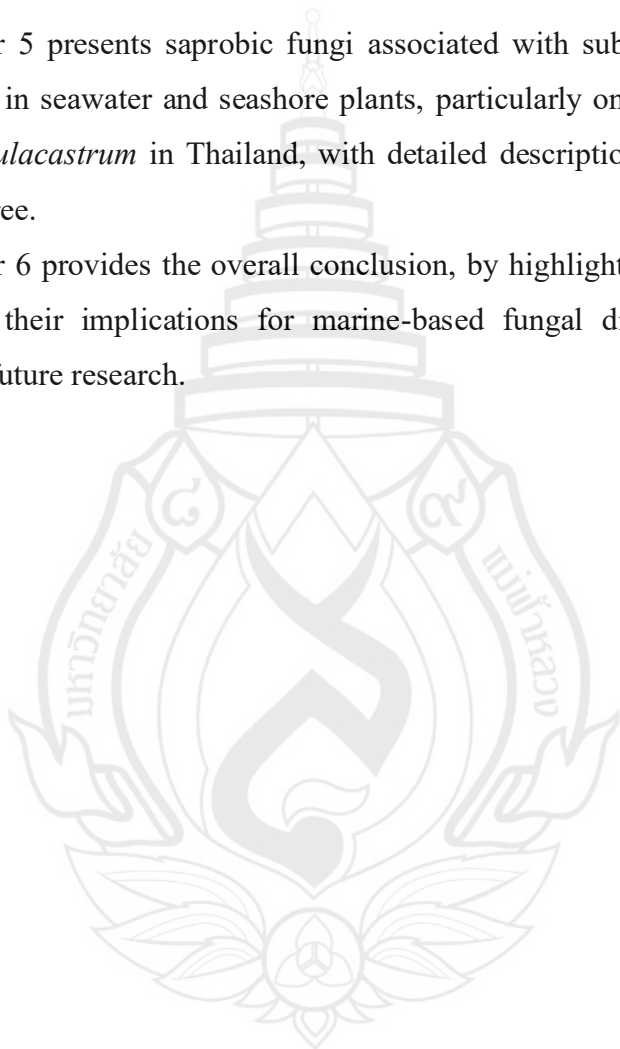
Chapter 2 provides a comprehensive literature review on the roles of fungi associated with marine ecosystems, highlighting their importance and challenges.

Chapter 3 provides the materials and methods employed in the study, detailing the host selection, sampling techniques, laboratory procedures, and analytical methods used to investigate the fungal communities.

Chapter 4 provides entries of saprobic fungal genera from salt marsh plants, covering their main morphological characteristics, taxonomic placements, ecological roles, and illustrations.

Chapter 5 presents saprobic fungi associated with submerged wood trapped between rocks in seawater and seashore plants, particularly on *Suaeda maritima* and *Sesuvium portulacastrum* in Thailand, with detailed descriptions, illustrations, and a phylogenetic tree.

Chapter 6 provides the overall conclusion, by highlighting the major findings of the study, their implications for marine-based fungal diversity, and potential directions for future research.



CHAPTER 2

LITERATURE REVIEW

2.1 Marine Fungi: History and Diversity

Marine fungi are a diverse group thriving in marine environments across a range of substrates, including algae, animals, corals, decaying driftwood, trapped plant materials, mangroves, sea grasses, saltmarsh plants, tunicates, muds, sands, sediments, detritus, soils, sea water, sea foam as well as oil spills (Jones and Moss 1978; Kohlmeyer and Kohlmeyer 1979; Hyde et al. 1990; Hyde and Lee 1998; Jones et al. 2006, 2015, 2019; Bovio et al. 2016; Grossart et al. 2019; Dayarathne et al. 2020; Li et al. 2023; Braconciniet et al. 2024). They occupy various ecological niches spanning from the water surface to extreme deep-sea environments, hydrothermal vents, and methane cold seep locations (Nagahama et al. 2011; Vargas-Gastélum and Riquelme 2020; Pang and Jones 2023; Nagano et al. 2024). Marine fungi have the ability to colonize any submerged piece of wood in marine or estuarine environments over an extended period (Hyde and Jones 1988; Hyde and Lee 1998; Hyde et al. 2000).

Various definitions of marine fungi have been proposed, often based on their ability to grow, or their physiological requirements for growth at specific seawater concentrations (Johnson and Sparrow 1961; Jones and Jennings 1964; Hyde 2000). The frequently cited definition is that provided by Kohlmeyer and Kohlmeyer (1979), who defined marine fungi and grouped them under two categories, obligate and facultative marine fungi. Pang et al. (2016a) expanded upon Kohlmeyer's definition and introduced a more comprehensive definition considering marine fungi and marine-derived fungi. According to their updated definition, a marine fungus is "any fungus that is recovered repeatedly from marine habitats, because: (1) it is able to grow and/or sporulate (on substrata) in marine environments; (2) it forms symbiotic relationships with other marine organisms; or (3) it is shown to adapt and evolve at the genetic level or be metabolically active in marine environments".

The initial documentation of a marine fungus was *Typhicola typharum* (Basionym = *Sphaeria scirpicola*) discovered as a facultative marine taxon by

Desmazieres 'in 1849 (Jones 2023). Since then, numerous researchers have significantly contributed to the study of marine fungi (Sutherland 1915, 1916; Sparrow 1936; Barghoorn and Linder 1944; Kohlmeyer 1974; Jones and Moss 1978; Hyde 1988; 1989). The classification of marine fungi initially relied on morphology, with only a few mycologists involved (Johnson and Sparrow 1961; Jones 1976; Kohlmeyer and Kohlmeyer 1979). However, the introduction of sequence data for *Halosphaeriopsis mediosetigera* by Spatafora and Blackwell (1994) marked a significant advancement in this field, helping to resolve the phylogenetic relationships among marine fungi (Jones et al. 2009, 2014, 2015; Suetrong et al. 2009; Sakayaroj et al. 2010; Jones 2011; Pang 2012; Singh et al. 2012; Hyde et al. 2013; Richards et al. 2015; Abdel-Wahab et al. 2020). Diverse methodologies have been used to monitor marine fungi, incorporating various approaches to collection, observation, and isolation methods (Höhnk 1961; Sarma and Hyde 2001; Abdel-Wahab et al. 2010; Pang et al. 2016b; Jones et al. 2019; Overy et al. 2019; Amend et al. 2019; Pang et al. 2023).

Marine fungi are distributed in over 12 phyla, 36 classes, 117 orders, 301 families, 882 genera and 2254 species ([www/marinefungi.org](http://www.marinefungi.org), accessed January 2026). The diversity of marine fungi can be influenced by various factors, availability and nature of substrates, competition, geographical variation, temperature, pH, and salinity (Jones 2000, 2019; Jones et al. 2022). Marine fungi have been categorized based on different habitats, including species from cold water, tropical regions, cosmopolitan and deep-water environments (Pugh and Jones 1986; Jones and Pang 2012; Raghukumar 2017; Xu et al. 2018; Jones et al. 2019; Hagestad et al. 2020). Pang et al. (2020) categorized isolated fungi near hydrothermal vent based on three factors of temperature, salinity and pH. These groupings highlight the impact of environmental factors and local conditions on fungal diversity.

The estimation of fungal numbers, including those of marine fungi, has been an ongoing topic among researchers (Jones and Mitchell 1996; Jones 2011; Hawksworth 2012; Hyde et al. 2020, 2024). The list of identified marine fungi has been consistently revised and expanded (Jones et al. 2009, 2015, 2019; Abdel-Wahab and Bahkali 2012). Jones et al. (2019) created an open-access resource at www.marinefungi.org, providing classification, number of marine fungi, as well as detailed descriptions and illustrations. Calabon et al. (2023) provided updated data, listing 1,898 species belong to

Aphelidiomycota, *Ascomycota*, *Basidiomycota*, *Blastocladiomycota*, *Chytridiomycota*, *Microsporidia*, *Mortierellomycota*, *Mucoromycota* and *Olpidiomycota*. *Ascomycota* are the most representative group including *Halosphaeriaceae*, which is the largest family of marine fungi with 77 genera and 203 species (Dayarathne et al. 2026). Hyde et al. (2023) initiated the development of Fungalpedia, an extensive online platform offering descriptions and illustrations of various fungi and fungal-like taxa, including marine, mangrove and salt marsh fungal genera.

2.2 Marine Fungi: Ecological Function and Application

Marine fungi associate with marine organisms as saprobes, endophytes, symbionts and pathogens. Primarily they involve transformation and incorporation of organic material into the food web (Grossart et al. 2019; Peng et al. 2024; Cunliffe 2023). The most studied marine fungi are saprophytes which are the major decomposers in marine ecosystems (Raghukumar 2017). Fungi employ enzymatic and non-enzymatic approaches to decompose dead woody and herbaceous plants (e.g., mangrove plants, salt marsh halophytes, and drift wood) as well as dead animals (Hyde et al. 1989; Eraslan 2023). They play a pivotal role in regulating energy flow within the marine food web (Fell 2012; Wang et al. 2014a, b; Liu et al. 2017a, b). The degradative ability of lignicolous marine fungi has been reported in various research studies (Mouzouras 1986; Bucher et al. 2004).

The marine environment, characterized by high pressure, high salinity, low temperature, and oxygen deficiency, fosters the production of compounds that are not found in terrestrial organisms (Wan et al. 2021). The unique characteristics of their habitat influence their metabolic and enzymatic functions allowing them to thrive (Rocha et al. 2012; Virués-Segovia et al. 2023). Marine fungi are an important source of natural products (Pang et al. 2016a; Pang and Jones 2017; Raghukumar 2017; Ebel 2012). Drug discovery of marine and marine-derived fungi has significantly increased in recent years, with over 3,500 natural products registered (Rateb and Ebel 2011; Jones et al. 2019; Gonçalves et al. 2022). They have significant potential in drug discovery, bioremediation, medical, pharmaceutical, nutraceutical, agricultural, food production, industry and cosmetic research (Tarman et al. 2020; Vitale et al. 2020).

Enzymes from marine sources have a wide range of applications in environmental, cosmetic, industrial, and medical fields. Fungal strains isolated from marine substrates have been reported to produce a range of enzymes such as amylase, cellulase, chitinase, keratinase, ligninase, lipase, protease, and xylanase (Velmurugan and Lee 2012; Bonugli-Santos et al. 2015). Bonugli-Santos et al. (2015), categorized five groups, based on their application in the market place, namely: technical enzymes primarily utilized in industries, enzymes used in food and beverage production, enzymes for animal feed, enzymes relevant to environmental applications, and enzymes with pharmaceutical and cosmetic applications.

2.3 Marine Fungi: Challenges

Different stresses affect fungal growth in marine environments, such as high salinity, extreme pressure, ultraviolet light, limited substrates and nutrients, and low oxygen concentrations (Brock 1979; Oren 2002). Marine fungi may show adaptations to life in the sea: chytrids are dispersed as motile zoospores; many Ascomycota have appendaged ascospores that aide in their dispersal and produce mucilage or sheaths for attachment to suitable substrates; while arenicolous fungi produce subicula for the attachment of ascomata to sand grains and other hard calcareous materials (Hyde et al. 1986, 1989, 1993; Hyde and Jones 1989; Jones 2000; Gleason et al. 2011; Gladfelter et al. 2019; Gonçalves et al. 2022).

Salinity of seawater is a major challenge for marine fungi which have adapted in various ways. Based on their salt responses, fungi are broadly classified as halophilic or halotolerant. However, halophilic fungi, such as *Wallemia ichthyophaga*, require salt for their growth (Zalar et al. 2005; Piñar et al. 2016). In contrast, halotolerant fungi, like *Hortaea werneckii*, can thrive in both normal and highly salty conditions (Gunde-Cimerman et al. 2000; Gostinčar et al. 2011; Suryanarayanan and Ravishankar 2023). Several physiological and cellular mechanisms contribute to salinity tolerance in fungi. Melanisation provides protection against environmental stresses such as UV radiation, temperature fluctuations, and toxic compounds (van Baarlen et al. 2007). In addition, fungi regulate cellular water balance and maintain turgor pressure by synthesizing compatible solutes, including polyols such as glycerol, arabitol, and mannitol

(Jeennings 1985; Noiraud et al. 2001; Gunde-Cimerman et al. 2018; de Nadal and Posas 2022). The accumulation of these osmolytes enables osmotic adjustment without disrupting cellular metabolism, thereby preventing dehydration and supporting survival under high-salinity conditions (Plemenitas et al. 2008).

In addition to environmental stresses, climate change and human activities such as urbanization and agriculture are disrupting natural coastal ecosystems (Zhai et al. 2020; Calabon et al. 2021). They disturb the health of salt marshes, mangroves, and seashore plants and affect nutrient availability for fungi. About 25% to 50% of coastal vegetation areas have been lost in recent decades, occurring at a rate ten times faster than the loss of tropical forests (Duarte et al. 2013). In addition to substrate limitation, plastic and hydrocarbon pollution and toxic ions increase and cause additional stress for marine organisms (Zhai et al. 2020). This may affect fungal composition and interactions with other organisms (Álvarez-Barragán et al. 2023).

Fungi that are unable to adapt to environmental changes may be replaced by other more adaptive species or become extinct (Kumar et al. 2021). Therefore, it is crucial to conserve these organisms, which play a significant role in ecosystems and are a promising source of enzymes and natural compounds.

CHAPTER 3

MATERIALS AND METHODS

3.1 Sample Collection, Morphological Study, and Isolation

Host plants and substrates were selected to represent different coastal ecosystem categories following the habitat-based classification of Wijayawardene et al. (2022a), including coastal terrestrial ecosystems, semi-coastal marine ecosystems, and coastal marine ecosystems. Coastal terrestrial hosts included plant species commonly occurring in near-shore environments that are primarily exposed to sunlight and dry conditions but may also be influenced by seawater splash and sandy soils (Wijayawardene et al. 2022a). Samples were collected from *Opuntia* sp., *Pluchea indica*, *Leucaena leucocephala*, *Lantana camara*, *Ficus macrocarpa*, and *Chromolaena odorata*. Semi-coastal marine hosts included salt marsh plants that are exposed to air and sunlight during low tide and subjected to tidal inundation during high tide (Wijayawardene et al. 2022a). Samples were collected from *Suaeda maritima*, and *Sesuvium portulacastrum*. Coastal marine substrates consisted of materials that remain permanently submerged in seawater and are exposed to sunlight through the water column (Wijayawardene et al. 2022a). Samples from this category included submerged decaying wood collected from coastal marine environments.

The collection focused on coastal areas of Thailand, including seashores and salt marsh habitats, along the Gulf of Thailand coasts, particularly in Pranburi, Prachuap Khiri Khan Province; with the permission for surveys, studies, research or academic experiments (No. 0907.4/23579) in the National Parks (book no. 02/020) and the Forest Parks, Botanic Gardens and Arboreta (book no. 02/001). Decaying woody specimens submerged in seawater and trapped between rocks were collected along rocky shores during 2022–2025. The collected specimens had a soft texture and were colonized by barnacles and other marine organisms. Dead twigs of seashore plants were also collected, with an emphasis on two abundant salt-marsh halophytes, *Suaeda maritima* and *Sesuvium portulacastrum*. The host plants were identified by experts and through bibliographic databases, including Google Scholar, POWO (Plants of the World

Online, Royal Botanic Gardens, Kew), WFO (World Flora Online), and iNaturalist. Collections were carried out during high-tide periods (October, November, December, February) and low-tide seasons (April, May, August) between 2022 and 2025. Submerged specimens were washed with seawater, placed in moist plastic bags, and transported to the laboratory, whereas dry specimens were placed in plastic bags and transferred directly to the laboratory. Salinity and pH of the water were measured using a portable refractometer and pH strips, respectively. Detailed information including substrates, collection sites and collection dates was documented.

Specimens were examined for fungal presence immediately after sorting in the laboratory or kept in moist plastic boxes for further observation of fungal structures. Plastic boxes were sprayed with sterile water for aerial specimens and with pure or 50% diluted sterile seawater for submerged specimens until fungal examination. Fungal structures were initially observed using a stereomicroscope (Leica EZ4, Leica Microsystems, Germany), and macroscopic features on the substrates were documented using an Olympus SZX16 stereomicroscope (Olympus, Japan) fitted with a digital camera (Olympus SC180, Olympus, Japan). Microscopic features were examined using freehand sections cut through ascomata and conidiomata, whereas hyphomycetous structures were directly collected with a fine needle. Microscopic preparations were mounted in water, lactoglycerol, or seawater and examined under a Nikon ECLIPSE Ni compound microscope (Nikon, Japan), with images captured using a Nikon DS-Ri2 digital camera (Nikon, Japan). Melzer's reagent was used to stain the apical structures of asci, and black ink (Guizhou Boss chemical industry, China) was used to visualize the mucilaginous sheath. Measurements of fungal structures were taken using Tarosoft® Image Framework software (Tarosoft, Thailand). Composite photoplates of fungal morphology were assembled, and scale bars were added using Adobe Photoshop CS6 Extended (version 13.1.2; Adobe Systems Inc., USA). Axenic cultures were obtained using the single-spore isolation technique described by Senanayake et al. (2020) on potato dextrose agar (PDA), corn meal agar (CMA), and CMA seawater, including CMA prepared with either 100% natural seawater or 50% seawater. Following examination and isolation, cultures were grown at room temperature for further study. Living cultures were preserved in the Mae Fah Luang University Culture Collection (MFLUCC). Natural specimens were deposited in the Mae Fah Luang

University Herbarium, Chiang Rai, Thailand (MFLU). Newly proposed taxa were registered in Index Fungorum (2025) and the Faces of Fungi database (Jayasiri et al. 2015).

3.2 DNA Extraction, PCR Amplification, and Sequencing

Genomic DNA was extracted from fresh axenic cultures following the manufacturer's instructions for the Mega Genomic DNA Extraction Kit (Omega Bio-tek Inc., USA). Polymerase chain reaction (PCR) amplifications were carried out using primer sets and optimized cycling conditions as described in previous studies. The internal transcribed spacer (ITS) region was amplified with primers ITS5/ITS4 (White et al. 1990), the nuclear ribosomal large subunit (LSU) with LR0R/LR5 or LR0R/LR7, and the nuclear small subunit ribosomal DNA (SSU rDNA) with NS1/NS4 (Vilgalys and Hester 1990). The translation elongation factor 1-alpha (*tef1*) was amplified using EF728F/EF986R or EF983F/EF2218R (Carbone and Kohn 1999), the partial RNA polymerase II second-largest subunit gene (*rpb2*) with primers 5F/7CR, and the partial beta-tubulin gene (*tub2*) with primers T1/T22 or bt2a/bt2b (Glass and Donaldson 1995). Each PCR reaction was prepared in a total volume of 25 μ L, consisting of 8.5–9.5 μ L of double-distilled water (ddH₂O), 12.5 μ L of 2 $\times$ GoTaq® Green PCR Master Mix (Promega, Madison, WI, USA), 1 μ L of each forward and reverse primer (20 μ M), and 1–2 μ L of genomic DNA template. Amplification products were verified on 1.7% agarose gels stained with 4S Green Stain, using a D2100 DNA Ladder (ExcelBand™ 100 bp; SMOBIO Technology Inc., Hsinchu, Taiwan) as a size marker. Purified PCR products were sequenced by SolGent Co. (South Korea). Obtained sequences were annotated and submitted to GenBank and the corresponding accession numbers are provided.

3.3 Sequence Alignment and Phylogenetic Analyses

After assessing the quality of sequences in Chromas 2.6.6 (Technelysium Pty Ltd., South Brisbane, Australia), forward and reverse sequences were assembled in SeqMan software version 7.1.0 (DNASTAR Inc., WI, USA). The resulting contigs

were searched on the NCBI nucleotide BLAST platform (<https://blast.ncbi.nlm.nih.gov>) to identify the closest matching sequences. Sequence data for related taxa were retrieved from GenBank based on previous publications. Sequence alignments were generated using MAFFT v.7 (Katoh et al. 2019), subsequently trimmed with the trimAl tool via the NGPhylogeny.fr platform (Lemoine et al. 2019), and manually inspected and adjusted in BioEdit v.7.0.9 (Hall 1999). Individual locus datasets were concatenated in Mesquite v.3.10 (Maddison and Maddison 2016) following previously published studies. Maximum Likelihood (ML) phylogenetic analyses were conducted using IQ-TREE v.2.2.0 under the GTR + GAMMA model of nucleotide substitution, with branch support assessed by 1,000 bootstrap replicates (Minh et al. 2020). Bayesian inference (BI) phylogenetic analyses were conducted via the CIPRES Science Gateway portal (Miller et al. 2010) using MrBayes v.3.2.2 (Ronquist et al. 2012). Posterior probabilities were estimated based on Markov chain Monte Carlo (MCMC) sampling with simultaneous chains. A majority-rule consensus tree and posterior probability values were calculated after discarding the initial 25% of sampled trees as burn-in (Larget and Simon 1999). Phylogenetic trees were visualized using FigTree v.1.4.0 (Rambaut 2015) and further edited and refined in Inkscape v.1.3.3.

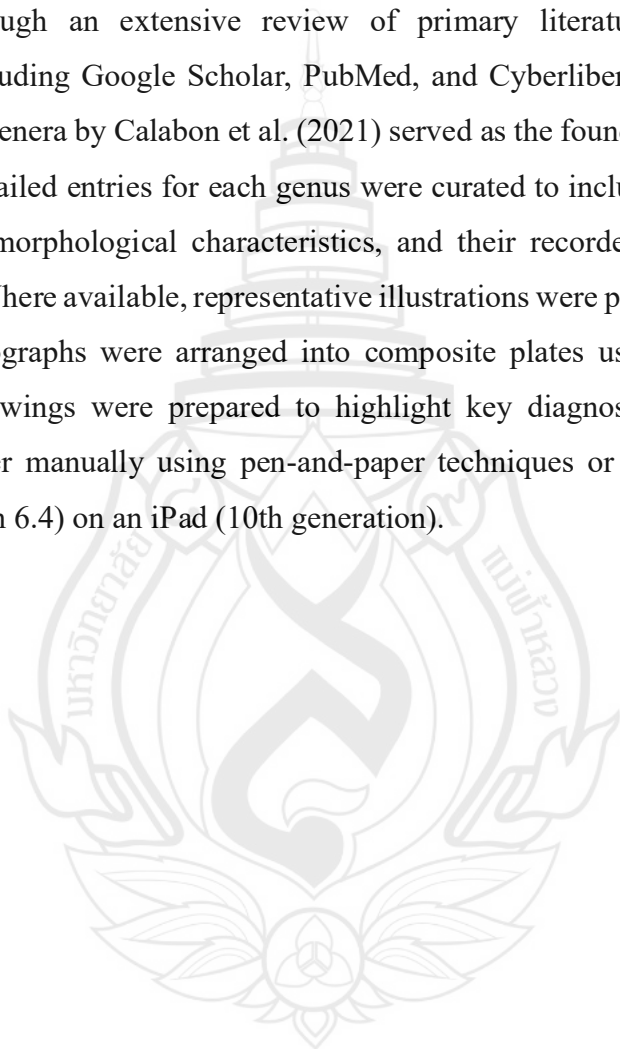
3.4 Data Analyses

After Data of isolated fungi were organized in Excel (Excel Office 365) and visualized using various data visualization tools. Bar charts, stacked bar charts, and pie charts were generated in Excel, while Venn diagrams were created using the online platform EVenn (Yang et al. 2024). Heat maps showing the distribution of fungal isolates across seashore host plants were produced in R version 4.4.2 (R Core Team 2024) using the pheatmap package, with color gradients representing isolate frequency and hierarchical clustering applied to summarize similarity patterns. Graphs were further adjusted in Adobe Photoshop where necessary. Fungal taxonomic composition for saltmarsh hosts was visualized using an interactive sunburst chart generated in R with the dplyr, plotly, and htmlwidgets packages. Taxa were hierarchically structured

from class to genus, with frequencies aggregated at each level to represent relative abundance.

3.5 Fungalpedia Compilation

Information regarding fungal genera associated with salt marsh plants was compiled through an extensive review of primary literature and bibliographic databases, including Google Scholar, PubMed, and Cyberliber. The checklist of salt marsh fungal genera by Calabon et al. (2021) served as the foundational framework for this study. Detailed entries for each genus were curated to include taxonomic history, type species, morphological characteristics, and their recorded occurrences on salt marsh hosts. Where available, representative illustrations were provided for each genus. Original photographs were arranged into composite plates using Adobe Photoshop CS6. Line drawings were prepared to highlight key diagnostic features and were produced either manually using pen-and-paper techniques or digitally using Adobe Fresco (version 6.4) on an iPad (10th generation).



CHAPTER 4

GENERA OF SALT MARSH FUNGI

4.1 Introduction

Salt marshes are ecologically significant coastal ecosystems characterized by herbaceous halophytes. These productive habitats, found in 43 countries, play a crucial role in shoreline protection against erosion, tidal currents, coastal flooding and storms. Salt marsh fungi are important as key decomposers, contributing to nutrient cycling and ecosystem stability. Fungi associated with salt marshes have been documented for over 150 years. The most recent checklist of salt marsh fungi has documented 486 fungal taxa from these environments, predominantly belonging to Ascomycota and Dothideomycetes (Calabon et al. 2021). This chapter creating a reference database for selected genera of salt marsh fungi, which will be published through the Fungalpedia publication. We provide taxonomic and morphological details of the genera based on the previous checklist, including photographic plates and/or drawings where possible.

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The taxa are listed according to their present classification as outlined in Hyde et al. (2024) and Thiyagaraja et al. (2025)

Phylum *ASCOMYCOTA* Caval. Sm

Subphylum *Pezizomycotina* O. E. Erikss. & K. Winka

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

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

Cladosporiales Abdollahz. & Crous

Cladosporiaceae Chalm. & R.G. Archibald

1- *Cladosporium* Link (= *Davidiella* Crous & U. Braun)

Mycosphaerellales (Nannf.) P.F. Cannon

Mycosphaerellaceae Lindau

2- *Fulvia* Cif.

- 3- *Micronectriella* Höhn
- 4- *Ramularia* (= *Mycosphaerella*) Unger
- 5- *Septoria* Sacc.
- 6- *Sphaerulina* Sacc.

Phaeothecoidiaceae K.D. Hyde & Hongsanan (= *Nowamycetaceae* Crous)

- 7- *Rivulata* Kohlm., Volkm.-Kohlm. & O.E. Erikss.

Dothideales Lindau (= *Neocelosporiales* Crous *fide* Hongsanan et al. 2020)

Dothideaceae Chevall.

- 8- *Scirrhia* Nitschke ex Fuckel

Sacotheciaceae Bonord.

- 9- *Aureobasidium* Viala & G. Boyer
- 10- *Pseudoseptoria* Speg

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

Mycosphaerellales genera *incertae sedis*

- 11- *Mucomycosphaerella* Quaedvl. & Crous

Pleosporales Luttr. ex M.E. Barr

Amniculicolaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde

- 12- *Neomassariosphaeria* Y. Zhang ter, J. Fourn. & K.D. Hyde

Camarosporiaceae Wanas., Wijayaw., K.D. Hyde & Crous

- 13- *Camarosporium* Schulzer

Cyclothyriellaceae Jaklitsch & Voglmayr

- 14- *Massariosphaeria* (E. Müll.) Crivelli

Dictyosporiaceae Boonmee & K.D. Hyde

- 15- *Dictyosporium* Corda
- 16- *Jalapriya* M.J. D'souza, Hong Y. Su, Z.L. Luo & K.D. Hyde

Didymellaceae Gruyter, Aveskamp & Verkley (= *Microsphaeropsidaceae*

Qian Chen et al.)

- 17- *Epicoccum* Link

- 18- *Chaetasbolisia* Speg.
- 19- *Paraboeremia* Qian Chen & L. Cai
- 20- *Phoma* Sacc. (= *Atracidymella* M.L. Davey & Currah)
- 21- *Stagonosporopsis* Died.

Didymosphaeriaceae Munk

- 22- *Julella* Fabre
- 23- *Paraphaeosphaeria* O.E. Erikss.
- 24- *Pseudopithomyces* Ariyaw. & K.D. Hyde
- 25- *Spegazzinia* Sacc.
- 26- *Tremateia* Kohlm., Volkm.-Kohlm. & O.E. Erikss.

Lentitheciaceae Y. Zhang ter, C.L. Schoch, J. Fourn., Crous & K.D. Hyde

- 27- *Halobyssothecium* Dayar., E.B.G. Jones & K.D. Hyde
- 28- *Keissleriella* Höhn.
- 29- *Lentithecium* K.D. Hyde, J. Fourn. & Ying Zhang
- 30- *Setoseptoria* Quaedvl., Verkley & Crous
- 31- *Towyspora* Wanas., E.B.G. Jones & K.D. Hyde

Leptosphaeriaceae M.E. Barr

- 32- *Leptosphaeria* Ces. & De Not.

Lindgomycetaceae K. Hiray., Kaz. Tanaka & Shearer

- 33- *Arundellina* Wanas., E.B.G. Jones & K.D. Hyde

Lophiostomataceae Sacc.

- 34- *Sigarispora* Thambug. & K.D. Hyde

Massarinaceae Munk

- 35- *Massarina* Sacc.
- 36- *Stagonospora* (Sacc.) Sacc.

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

- 37- *Bicrouania* Kohlm. & Volkm.-Kohlm.

Morosphaeriaceae Suetrong, Sakay., E.B.G. Jones & C.L. Schoch

- 38- *Helicascus* Kohlm.

Neocamarosporiaceae Wanas., Wijayaw., Crous & K.D. Hyde

- 39- *Neocamarosporium* Crous & M.J. Wingf.

Periconiaceae Nann.

- 40- *Periconia* Tode (= *Bambusistroma* D.Q. Dai & K.D. Hyde; = *Noosia* Crous, R.G. Shivas & McTaggart)

Phaeosphaeriaceae M.E. Barr

- 41- *Amarenographium* O.E. Erikss. (= *Amarenomyces* O.E. Erikss.)
 42- *Camarosporioides* W.J. Li & K.D. Hyde
 43- *Loratospora* Kohlm. & Volkm.-Kohlm.
 44- *Phaeosphaeria* I. Miyake
 45- *Sclerostagonospora* Höhn.
 46- *Septoriella* Oudem. (= *Poaceicola* W.J. Li, Camporesi, Bhat & K.D. Hyde Doth; = *Wojnowicia* Sacc.)

Pleomassariaceae M.E. Barr

- 47- *Splanchnonema* Corda (= *Myxocyclus* Riess; = *Pleomassaria* Speg.)

Pleosporaceae Nitschke

- 48- *Alternaria* Nees (= *Pseudoalternaria* D.P. Lawr., Gannibal, Dugan & B.M. Pryor)
 49- *Curvularia* Boedijn
 50- *Decorospora* Inderb., Kohlm. & Volkm.-Kohlm.
 51- *Exserohilum* K.J. Leonard & Suggs
 52- *Paradendryphiella* Woudenb. & Crous
 53- *Typhicola* Crous
 54- *Stemphylium* Wallr. (= *Pleospora* Rabenh. ex Ces. & De Not.)

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

- 55- *Cytoplea* Bizz. & Sacc.

Sporormiaceae Munk

- 56- *Preussia* Fuckel

57- *Sporormia* De Not.

58- *Sporormiella* Ellis & Everh.

Teichosporaceae M.E. Barr

59- *Teichospora* Fuckel

Pleosporales genera *incertae sedis*

60- *Phialophorophoma* Linder

Testudinaceae Arx

61- *Verruculina* Kohlm. & Volkm.-Kohlm.

Tetraplosphaeriaceae Kaz. Tanaka & K. Hiray

62- *Tetraploa* Berk. & Broome (= *Tetraplosphaeria* Kaz. Tanaka & K. Hiray.)

Trematosphaeriaceae K.D. Hyde, Y. Zhang ter, Suetrong & E.B.G. Jones

63- *Halomassarina* Suetrong, Sakay., E.B.G. Jones, Kohlm., Volkm.-Kohlm. & C.L. Schoch

Dothideomycetes orders *incertae sedis*

Acrospermales Minter, Peredo & A.T. Watson

Acrospormaceae Fuckel

64- *Acrospermum* Tode 1783

Asterinales M.E. Barr ex D. Hawksw. & O.E. Erikss. (= *Asterotexales* Firmino, O.L. Pereira & Crous)

Morenoinaceae Hongsanan & K.D. Hyde

65- *Morenoina* Theiss.

Botryosphaeriales C. L. Schoch, Crous & Shoemaker

Botryosphaeriaceae Theiss. & Syd. (= *Endomelanconiopsidaceae* Tao Yang & Crous)

66- *Macrophomina* Petr.

67- *Tiarosporella* Höhn.

Microthyriales G. Arnaud

Microthyriaceae Sacc.

68- *Microthyrium* Desm.

Monoblastiales Lücking, M.P. Nelsen & K.D. Hyde

Eriomycetaceae Huanraluek & K.D. Hyde

69- *Heleiosa* Kohlm., Volkm.-Kohlm. & O.E. Erikss.

Dothideomycetes families *incertae sedis*

Pseudorobillardaceae Crous

70- *Pseudorobillarda* M. Morelet

Venturiales Y. Zhang ter, C.L. Schoch & K.D. Hyde

Cylindrosympodiaceae Crous, M. Shen & Y. Zhang ter

71- *Septonema* Corda

Phaeotrichales Ariyaw., Jian K. Liu & K.D. Hyde

Phaeotrichaceae Cain

72- *Trichodelitschia* Munk

Dothideomycetes genera *incertae sedis*

73- *Monodictys* S. Hughes

74- *Neottiosporina* Subram.

75- *Otthia* Nitschke ex Fuckel

76- *Trichometasphaeria* Munk

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

Subclass *Chaetothyriomycetidae* Doweld

Chaetothyriales M.E. Barr

Eurotiales G.W. Martin ex Benny & Kimbr.

Aspergillaceae Link (= *Monascaceae* J. Schröt.)

77- *Monascus* Tiegh.

Herpotrichiellaceae Munk

78- *Rhinocladiella* Nannf

79- *Veronaea* Cif. & Montemart.

Thermoascaceae Apinis

80- *Paecilomyces* Bainier

Thermoascaceae Apinis

81- *Thermoascus* Miehe

Trichocomaceae E. Fisch.

82- *Thermomyces* Tsikl.

Onygenales Cif. ex Benny & Kimbr.

Neoarthropsidaceae Torres-García & Gené

83- *Albidomyces* Torres-García, Dania García, Cano & Gené

Class Lecanoromycetes O.E. Erikss. & Winka

Ostropales Nannf.

Stictidaceae Fr.

84- *Glomerobolus* Kohlm. & Volkm.-Kohlm.

Class Leotiomyces O.E. Erikss. & Winka

Helotiales Nannf. ex Korf & Lizoň (= *Cyttariales* Luttr. ex Gamundí; = *Medeolariales* Korf)

Amorphothecaceae Parbery

85- *Amorphotheca* Parbery

Helotiaceae Rehm

86- *Cyathicula* De Not. (= *Glarea* Bills & Paláez)

Lachnaceae Raitv.

87- *Brunnipila* Baral

Mollisiaceae Rehm (= *Loramycetaceae* Dennis ex Digby & Goos)

88- *Belonopsis* (Sacc.) Rehm

Tricladiaceae P.R. Johnst. & Baschien

89- *Halenospora* E.B.G. Jones

Sclerotiniaceae Whetzel

90- *Botrytis* P. Micheli ex Pers.

Helotiales genera *incertae sedis*

91- *Cadophora* Lagerb. & Melin

92- *Cejpia* Velen.

93- *Cistella* Quél.

Leotiales genera incertae sedis

94- *Flagellospora* Ingold

Thelebolales P.F. Cannon

Thelebolaceae (Brumm.) Eckblad

95- *Thelebolus* Tode (= *Pezizella* P. Karst.)

Class *Lichinomycetes* V. Reeb, Lutzoni & Cl. Roux (= *Candelariomycetes* Voglmayr & Jaklitsch; = *Coniocybomycetes* M. Prieto & Wedin; = *Geoglossomycetes* Zheng Wang, C.L. Schoch & Spatafora; *Sareomycetes* Beimforde, A.R. Schmidt, Rikkinen & J.K. Mitch.; *Xylonomycetes* Gazis & P. Chaverri)

Sareales Beimforde, A.R. Schmidt, Rikkinen & J.K. Mitch

Sareaceae Beimforde, A.R. Schmidt, Rikkinen & J.K. Mitch.

96- *Zythia* Fr.

Class *Orbiliomycetes* O.E. Erikss. & Baral

Orbiliales Baral, O.E. Erikss., G. Marson & E. Weber

Orbiliaceae Nannf.

97- *Orbilia* Fr. (= *Pseudotriporconidium* Z.F. Yu & K.Q. Zhang)

98- *Arthrobotrys* Corda

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

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

Diaporthales Nannf.

Gnomoniaceae G. Winter

99- *Gnomonia* Ces. & De Not.

Magnaporthales Thongk., Vijaykr. & K.D. Hyde

Ceratosphaeriaceae Z.L. Luo, H.Y. Su & K.D. Hyde*FWF

100- *Ceratosphaeria* Niessl (= *Tropohalonectria* R.H. Perera, E.B.G. Jones & K.D. Hyde)

Magnaporthaceae P.F. Cannon

- 101- *Buergenerula* Syd.
- 102- *Gaeumannomyces* Arx & D.L. Olivier
- 103- *Kohlmeyeriopsis* Klaubauf, M.-H. Lebrun & Crous
- 104- *Utrechtiana* Crous & Quaedvl.

Pseudohalonectriaceae Hongsanan & K.D. Hyde

- 105- *Pseudohalonectria* Minoura & T. Muroi

Myrmecridiales Crous

Myrmecridiaceae Crous

- 106- *Myrmecridium* Arzanlou, W. Gams & Crous

Phomatosporales Senan., Maharachch. & K.D. Hyde

Phomatosporaceae Senan. & K.D. Hyde

- 107- *Phomatospora* Sacc.

Diaporthomycetidae families *incertae sedis*

Papulosaceae Winka & O.E. Erikss.

- 108- *Papulosa* Kohlm. & Volkm.-Kohlm.

Trichosphaeriaceae G. Winter (= *Plectosphaerellaceae* W. Gams, Summerb. & Zare)

- 109- *Stachylidium* Link

Trichosphaeriaceae genera *incertae sedis*

- 110- *Koorchaloma* Subram. (= *Kananascus* Nag Raj)

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

Coronophorales Nannf. (= *Melanosporales* N. Zhang & M. Blackw.; = *Parasymptodiellales* Hern. Restr., Gené, R.F. Castañeda & Crous)

Ceratostomataceae G. Winter

- 111- *Microthecium* Corda (= *Pteridiosperma* J.C. Krug & Jeng)

Coronophorales genera *incertae sedis*

- 112- *Papulaspora* Preuss

Hypocreales Lindau*Bionectriaceae* Samuels & Rossman (= *Spicariaceae* Nann.)

- 113- *Acremonium* Link
- 114- *Fusariella* Sacc.
- 115- *Gliomastix* Guég.
- 116- *Hydropisphaera* Dumort. (= *Heleococcum* C.A. Jørg.)

Clavicipitaceae (Lindau) Earle ex Rogerson

- 117- *Atkinsonella* Diehl
- 118- *Claviceps* Tul.

Nectriaceae Tul. & C. Tul. (= *Tuberculariaceae* Fr.)

- 119- *Fusarium* Link
- 120- *Nectria* (Fr.) Fr. (= *Tubercularia* Tode)
- 121- *Volutella* Fr.

Sarocladiaceae L. Lombard

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

Stachybotryaceae L. Lombard & Crous

- 123- *Albifimbria* L. Lombard & Crous
- 124- *Paramyrothecium* L. Lombard & Crous
- 125- *Stachybotrys* Corda
- 126- *Striaticonidium* L. Lombard & Crous
- 127- *Xepicula* Nag Raj

Microascales Luttr. ex Benny & Kimbr.*Halosphaeriaceae* E. Müll & Arx ex Kohlm.

- 128- *Aniptodera* Shearer & Miller
- 129- *Ceriosporopsis* Linder
- 130- *Cirrenalia* Meyers & R.T. Moore
- 131- *Corollospora* Werderm. (= *Sigmoidea* J.L. Crane)
- 132- *Haligena* Kohlm.
- 133- *Halosarpheia* Kohlm. & E. Kohlm.
- 134- *Lautisporopsis* E.B.G. Jones, Yusoff & S.T. Moss

- 135- *Lignincola* Höhnk
- 136- *Magnisphaera* J. Campb., J.L. Anderson & Shearer
- 137- *Natantispora* J. Campb., J.L. Anderson & Shearer
- 138- *Nais* Kohlm.
- 139- *Oceanitis* Kohlm.
- 140- *Panorbis* J. Campb., J.L. Anderson & Shearer
- 141- *Remispora* Linder
- 142- *Tirispota* E.B.G. Jones & Vrijmoed

Torpedosporales E.B.G. Jones, Abdel-Wahab & K.L. Pang

Juncigenaceae E.B.G. Jones, Abdel-Wahab & K.L. Pang

- 143- *Juncigena* Kohlm., Volkm.-Kohlm. & O.E. Erikss.

Torpedosporaceae E.B.G. Jones & K.L. Pang

- 144- *Torpedospora* Meyers

Subclass *Lulworthiomycetidae* Dayar., E.B.G. Jones & K.D. Hyde

Lulworthiales Kohlm., Spatafora & Volkm.-Kohlm.

Lulworthiaceae Kohlm., Spatafora & Volkm.-Kohlm.

- 145- *Cumulospora* I. Schmidt
- 146- *Halazon* Abdel-Aziz, Abdel-Wahab & Nagah.
- 147- *Lulworthia* G.K. Sutherl.
- 148- *Moleospora* Abdel-Wahab, Abdel-Aziz & Nagahama

Subclass *Savoryellomycetidae* Hongsanan, K.D. Hyde & Maharachch .

Savoryellales Boonyuen, Suetrong, Sivichai, K.L. Pang & E.B.G. Jones

Savoryellaceae Jaklitsch & Réblová

- 149- *Bactrodesmium* Cooke
- 150- *Savoryella* E.B.G. Jones & R.A. Eaton

Subclass *Sordariomycetidae* O.E. Erikss. & Winka (= *Meliolomycetidae* P.M. Kirk & K.D. Hyde)

Chaetosphaeriales Huhndorf, A.N. Mill. & F.A. Fernández

Chaetosphaeriaceae Réblová, M.E. Barr & Samuels

- 151- *Minimidochium* B. Sutton

Phyllachorales M.E. Barr

Phyllachoraceae Theiss. & Syd.

152- *Phyllachora* Nitschke ex Fuckel

Sordariales Chadeff. ex D. Hawksw. & O.E. Erikss.

Chaetomiaceae G. Winter

153- *Achaetomium* J.N. Rai, Tewari & Mukerji

154- *Chaetomium* Kunze

155- *Corynascus* Arx, Proc. Kon. Ned. Akad. Wetensch.

156- *Dichotomopilus* X. Wei Wang, Samson & Crous

157- *Humicola* Traaen

158- *Thermothielavioides* X. Wei Wang & Houbraken

159- *Trichocladium* Harz

Lasiosphaeriaceae Nannf.

160- *Zopfiella* G. Winter

Schizotheciaceae Y. Marin & Stchigel (= *Neoschizotheciaceae* S.K. Huang & K.D. Hyde

161- *Schizothecium* Corda (= *Apiosordaria* Arx & W. Gams; = *Neoschizothecium* S.K. Huang & K.D. Hyde; = *Triangularia* Boedijn)

Sordariaceae G. Winter

162- *Neurospora* Shear & B.O. Dodge (= *Gelasinospora* Dowding)

163- *Sordaria* Ces. & De Not.

Sordariales genera *incertae sedis*

164- *Aropsiclus* Kohlm. & Volkm.-Kohlm.

Tracyllalales Crous

Tracyllaceae Crous

165- *Tracylla* (Sacc.) Tassi

Subclass *Xylariomycetidae* O.E. Erikss & Winka

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

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

166- *Apiospora* Sacc.

167- *Arthrinium* Kunze

168- *Nigrospora* Zimm.

Beltraniaceae Nann.

169- *Beltrania* Penz.

Hyponectriaceae Petr.

170- *Phragmitensis* M.K.M. Wong, Poon & K.D. Hyde

171- *Physalospora* Niessl

Sporocadaceae Corda

172- *Pestalotiopsis* Steyaert (= *Pestalopezia* Seaver)

Xylariales Nannf.

Cainiaceae J.C. Krug

173- *Atrotriquata* Kohlm. & Volkm.-Kohlm.

Clypeosphaeriaceae G. Winter

174- *Ommatomyces* Kohlm., Volkm.-Kohlm. & O.E. Erikss

Xylariales genera *incertae sedis*

175- *Anthostomella* Sacc.

Coniocessiaceae Asgari & Zare

176- *Circinotrichum* Nees

Diatrypaceae Nitschke

177- *Cryptovalsa* Ces. & De Not. ex Fuckel

178- *Halocryptovalsa* Dayar. & K.D. Hyde

Xylariaceae Tul. & C. Tul.

179- *Virgaria* Nees

Zygosporiaceae J.F. Li, Phookamsak & K.D. Hyde

180- *Zygosporium* Mont.

Sordariomycetes families *incertae sedis*

Lautosporaceae Kohlm., Volkm.-Kohlm. & O.E. Erikss

181- *Lautospora* K. D. Hyde & E.B.G. Jones

Pezizomycotina genera *incertae sedis*

182- *Psammia* Sacc. & M. Rousseau ex E. Bommer & M. Rousseau

Subphylum *SACCHAROMYCOTINA* O.E. Erikss. & Winka

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

Saccharomycetales Kudryavtsev

Saccharomycetaceae G. Winter

183- *Kluyveromyces* Van der Walt

Class *Pichiomycetes* M. Groenew., Hittinger, Opulente & A. Rokas

Serinales M. Groenew., Hittinger, Opulente & A. Rokas

Debaryomycetaceae Kurtzman & M. Suzuki

184- *Debaryomyces* Lodder & Kreger-van Rij

185- *Scheffersomyces* Kurtzman & M. Suzuki

Ascomycota genera *incertae sedis*

186- *Asteromyces* F. Moreau & V. Moreau

187- *Cytoplacosphaeria* Petr.

188- *Haplobasidion* Erikss.

189- *Hymenopsis* Sacc.

190- *Hyphopolynema* Nag Raj

191- *Kolletes* Kohlm. & Volkm.-Kohlm.

192- *Neottiospora* Desm.

193- *Octopodotus* Kohlm. & Volkm.-Kohlm.

194- *Pycnodallia* Kohlm. & Volkm.-Kohlm.

195- *Tetranacriella* Kohlm. & Volkm.-Kohlm.

196- *Tetranacrium* H.J. Huds. & B. Sutton

197- *Sphaeronaema* Fr.

198- *Stauronema* (Sacc.) Syd., P. Syd. & E.J. Butler

Phylum *BASIDIOMYCOTA* R.T. Moore

Subphylum *Agaricomycotina* Doweld

Class *Agaricomycetes* Doweld

Agaricales Underw

Suborder *Pleurotineae* Aime, Dentinger & Gaya

Cyphellopsidaceae Jülich (= *Niaceae* Jülich)

199- *Merismodes* Earle (= *Cyphellopsis* Donk; = *Maireina* W.B. Cooke)

200- *Nia* R.T. Moore & Meyers

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

Sebacinaceae K. Wells & Oberw.

201- *Chaetospermum* Sacc.

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

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

Agaricostilbales Oberw. & R. Bauer

Chionosphaeraceae Oberw. & Bandoni

202- *Stilbum* Tode

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

Sporidiobolales Doweld

Sporidiobolaceae R.T. Moore

203- *Sporobolomyces* Kluyver & C.B. Niel (= *Sporidiobolus* Nyland)

Subphylum *Ustilaginomycotina* Doweld

Class *Ustilaginomycetes* R. Bauer, Oberw. & Vánky

Urocystidales R. Bauer & Oberw.

Urocystidaceae Begerow, R. Bauer & Oberw.

204- *Flamingomyces* R. Bauer, M. Lutz, Piątek, Vánky & Oberw.

Ustilaginales G. Winter

Ustilaginaceae Tul. & C. Tul.

205- *Parvulago* R. Bauer, M. Lutz, Piątek, Vánky & Oberw.

206- *Tranzscheliella* Lavrov

Phylum *MUCOROMYCOTA* Doweld

Subphylum *Mucoromycotina* Benny

Class *Mucoromycetes* Doweld

Mucorales Dumort.

Mucoraceae Dumort.

207- *Blakeslea* Thaxt.

208- *Mucor* Fresen.

Syncephalastraceae Naumov ex R.K. Benj.

209- *Syncephalastrum* J. Schröt.

Rhizopodaceae K. Voigt & P.M. Kirk

210- *Rhizopus* Ehrenb.

4.2 Results

The taxa are listed according to their present classification as outlines of Hyde et al. (2024a) and Thiagaraja et al. (2025)

Cladosporium Link 1816

Classification: *Cladosporiaceae*, *Cladosporiales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

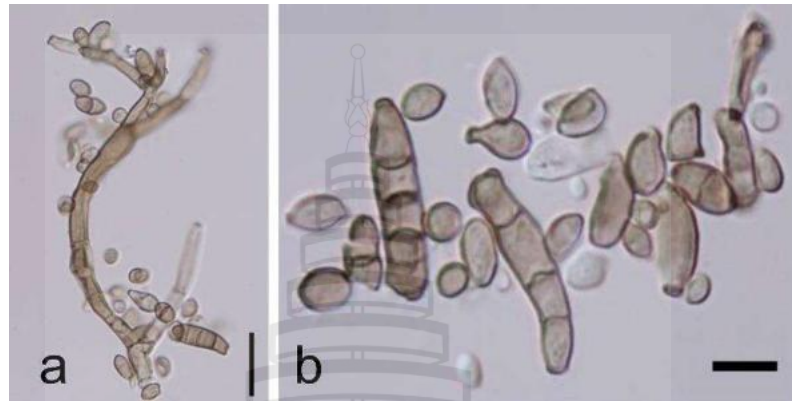
Cladosporium is a ubiquitous genus with diverse ecological roles as a saprobe, endophyte, plant pathogen, and lichenicolous fungus (Pem et al. 2024; Index Fungorum 2024). Species such as *Cladosporium algarum*, *C. allicinum*, *C. cladosporioides*, *C. herbarum*, *C. macrocarpum*, and *C. sphaerospermum* have been recorded on salt marsh hosts, mostly on *Spartina* species (Calabon et al. 2021b). *Cladosporium* is frequently isolated from marine environments and considered as marine-derived fungi (Jones et al. 2019). Jones et al. (2015) considered seven species as true marine fungi due to repeated isolation from marine hosts or substrates. The genus is known for its hyphomycetous asexual morph, with solitary conidiophores, coronate conidiogenous cells that proliferate sympodially, having intercalary ramoconidia and forming conidia in acropetal chains. Conidia vary in shape, color, and ornamentation (Bensch et al. 2012; Pem et al. 2019). Over 500 species are accepted in Species Fungorum (April 2026), divided into three major complexes: *C. cladosporioides*, *C. herbarum*, and *C.*

sphaerospermum. ITS, *tef1*, and *actin* gene sequences are important molecular barcodes for *Cladosporium* taxonomy (Pem et al. 2024).

Type species: *Cladosporium herbarum* (Pers.) Link. 1816

Basionym: *Dematium herbarum* Pers. 1794

Other accepted species: Species Fungorum (search *Cladosporium*)



Note a Conidiophores, conidiogenous cells and conidia. b Conidia. Scale bars: a = 10 μm , b = 5 μm

Source Jayasiri et al. (2019)

Figure 4.1 *Cladosporium aphidis*

Fulvia Cif. 1954

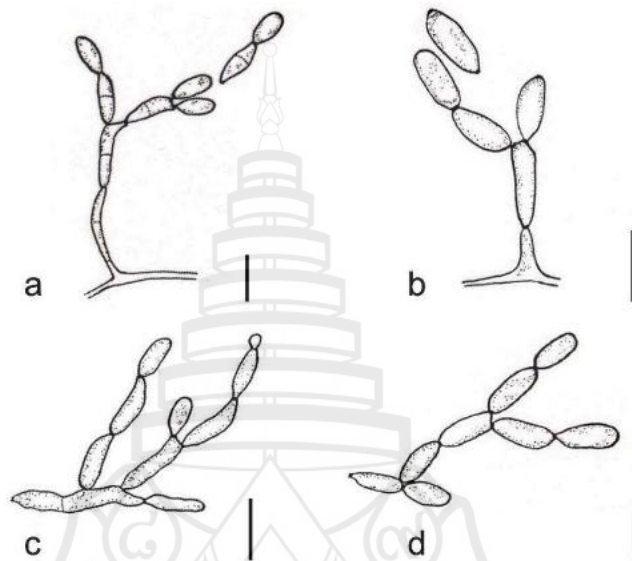
Classification: *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Fulvia belongs to the family *Mycosphaerellaceae* (*Mycosphaerellales*, *Dothideomycetidae*). The genus was introduced by Ciferri (1954) and typified with *Fulvia fulva* which was previously classified as *Cladosporium fulvum*. *F. fulva* is the only accepted species in this genus (Species fungorum 2026) that is known as a causal agent of tomato leaf mould and considered as a model for studying plant-pathogen interactions (Butler and Jones 1949; de Wit 1981, 1992; Jones et al. 1997). *Fulvia fulva* was also reported from stem and leaves of a salt marsh host; *Spartina* sp. in Canada (Miller and Whitney 1983). Based on Ellis (1971), colonies of *Fulvia* are effuse and stroma are present. Conidiophores are macronematous, mononematous, straight or flexuous, characterized by unilateral nodose swellings that may develop as short lateral branchlets. Conidiogenous cells are sympodial, clavate or cylindrical bearing branched

chains of smooth, 0–3-septate conidia. Videira et al. (2017) re-collected *F. fulva*, assigned as epitype, and showed that it is related to *Stromatoseptoria* phylogenetically. They also indicated that ITS, LSU and *rpb2* sequences can differentiate this species.

Type species: *Fulvia fulva* (Cooke) Cif. 1953

Other accepted species: None



Note a, b Conidiogenous cells and conidis. c, d Conidia. Scale bars: 10 µm

Source Redrawn from Videira et al. (2017)

Figure 4.2 *Fulvia fulva*

Micronectriella Höhn. 1906

Classification: *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Micronectriella is a saprobic genus within *Mycosphaerellaceae* (*Dothideomycetes*) (Hongsanant et al. 2020a). The genus was established by Höhnelt (1906) as a separate entity from *Micronectria* due to distinctive morphological features, including club-shaped asci and cylindrical to spindle-shaped ascospores, but the genus is treated as *Sphaerulina* in Species Fungorum. The absence of a type specimen and lack of molecular data has resulted in taxonomic confusion surrounding the genus. Fresh specimens need to be collected for a comprehensive revision of the phylogeny (Videira et al. 2017). *Micronectriella agropyri*, which is listed in Species Fungorum (December 2023), was described as a new species associated with upright grass debris

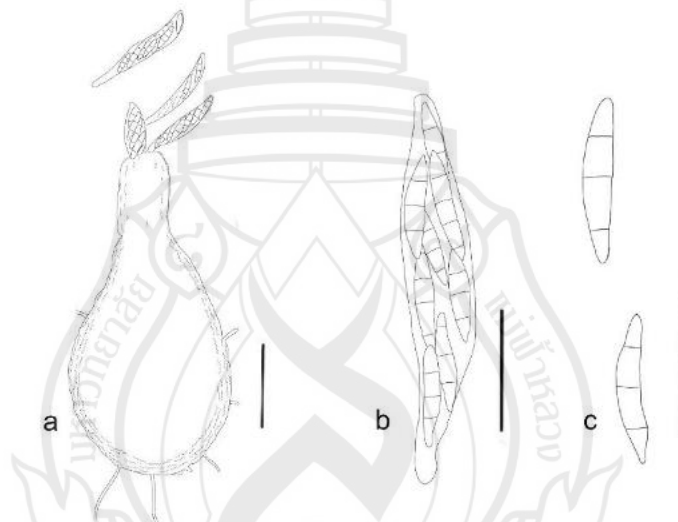
as well as in litter and fermentation layers in salt marsh habitats (Apinis and Chesters, 1964). This species has been documented on *Elymus pungens*, *Puccinellia maritima*, and *Spartina townsendii* in the United Kingdom (Apinis and Chesters 1964; Calabon et al. 2021b). *Micronectriella agropyri* is characterized by yellow-brown ascomata with a cylindrical neck. Asci are clavate-spindle-shaped containing eight fusiform, septate and hyaline to very pale yellow ascospores (Apinis and Chesters 1964).

Type species: *Micronectriella pterocarpi* (Racib.) Höhn. 1906

Synonyms: *Micronectria pterocarpi* Racib. 1900

Sphaerulina pterocarpi (Racib.) Arx & E. Müll. 1975

Other accepted species: *Micronectriella agropyri* Apinis & Chesters 1964



Note a Ascoma. b Ascus. c Ascospores. Scale bars: a, b = 20 µm, c = 10 µm

Source Redrawn from Apinis and Chesters (1964)

Figure 4.3 *Micronectriella agropyri*

Ramularia (= *Mycosphaerella*) Unger 1832

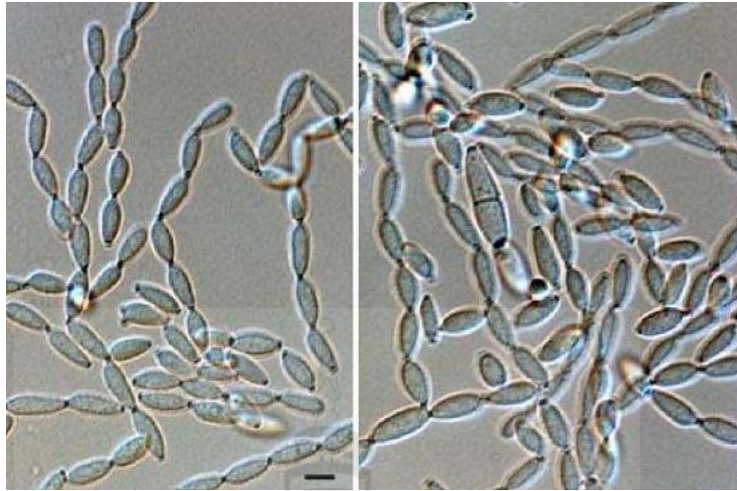
Classification: *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Ramularia was introduced by Unger (1833) to accommodate *R. pusilla* and *R. didyma*. The identification of *Ramularia* has mostly relied on morphology. Braun (1998) monographed the genus and, based on the morphology of solitary or catenated conidia, divided it into two subgenera. There has been long-standing confusion in the

taxonomy of *Ramularia* (Sutton and Waller 1988). Videira et al. (2016) studied *Ramularia* and allied genera based on morphology and multigene phylogenies, of combined LSU and *rpb2* and combined *rpb2*, ITS, *actA*, *gapdh*, *tef1* sequence data. They designated an epitype for the type species, *R. pusilla*, and transferred some species to novel genera within *Mycosphaerellaceae* or even outside the family, *Teratoramularia* in *Teratosphaeriaceae*, demonstrating the importance of molecular data in accurate taxonomy. *Ramularia* species are mostly hyphomycetous, forming hyaline, solitary, or synnematus conidiophores and polyblastic conidiogenous cells with thickened, darkened, and refractive conidiogenous loci. Conidia are hyaline with distinct hila, forming either solitary or catenated chains (Videira et al. 2016). The sexual morph of *Ramularia* is *Mycosphaerella*, characterized by globose to subglobose, black ascomata, cylindrical to cylindric-obclavate asci containing eight hyaline, uniseptate ascospores (Crous et al. 2009; Hongsanan et al. 2020b). The name *Ramularia* was selected over *Mycosphaerella* as it is the older name (Videira et al. 2015). *Ramularia* comprises approximately 400 species (Hyde et al. 2024a), with *Ramularia digitalis* (based on *Sphaeria digitalis* by Fuckel 1864) (Braun and Bensch 2020) and *Ramularia pararhabdospora* (Crous et al. 2021b) being recently introduced species. Many species are considered to be host-specific so the increase in the number of species is expected (Bhunjun et al. 2022). *Ramularia* species have been reported as saprobic, endophytic, hyperparasitic, and predominantly plant pathogens (Pem et al. 2024). They cause significant yield losses in important crops such as barley, sugar beet, and cotton (Videira et al. 2016; da Silva et al. 2019). *Ramularia collo-cygni* is an important plant pathogen that causes *Ramularia* leaf spot (RLS) in barley and is capable of producing phytotoxins such as rubellin D (Dussart et al. 2018). There are several reports of this genus occurring on salt marsh hosts under names such as *Mycosphaerella lineolata*, *Mycosphaerella salicorniae*, *Mycosphaerella staticicola*, and *Mycosphaerella suaedae-australis*, as well as several reports of undetermined *Mycosphaerella* species (Calabon et al. 2021b).

Type species: *Ramularia pusilla* Unger. 1832

Other accepted species: Species Fungorum (search *Ramularia*)



Note Conidia in chains. Scale bars: 6 μ m

Source Crous et al. (2007)

Figure 4.4 *Ramularia eucalypti*

Septoria Sacc. 1884

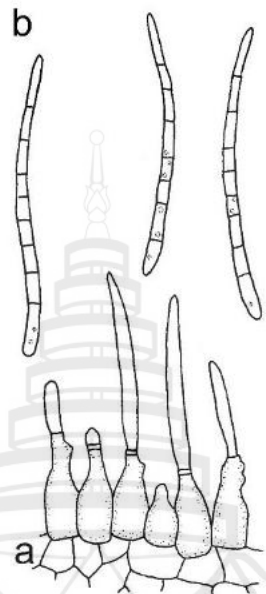
Classification: *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Septoria is a pathogenic genus causing field crop diseases reported from a wide range of hosts, mostly from leaf spots and stem cankers (Index Fungorum; Quaedvlieg et al. 2013). *Septoria* comprises more than 500 species with a *Mycosphaerella*-like sexual morph and coelomycetous asexual morph forming pycnidia. Conidiophores are reduced to holoblastic, proliferating conidiogenous cells. Conidia are filiform, multiseptate, and hyaline (Quaedvlieg et al. 2013; Pem et al. 2019). Providing molecular data has illuminated the identification and classification of the genus; Quaedvlieg et al. (2013) discussed the classification of *Septoria* based on morphology and molecular analyses of *rpb2* and LSU sequence data. *Septoria* species have been documented on living and decaying plant parts of halophytic hosts (Calabon et al. 2021b), including *Juncus roemerianus* (Fell and Hunter 1979; -Kohlmeyer et al. 1998) and *Spartina alterniflora* from USA (Gessner and Goos 1973b), as well as on *Phragmites australis* in the Netherlands (Van Ryckegem and Verbeken 2005b). *Septoria suaedae-australis* has been recorded on *Suaeda australis* in South Australia (Hansford 1954).

Type species: *Septoria cytisi* Desm. 1847

Basionym: *Neottiospora paludosa* Sacc. & Fiori, in Sydow 1899

Other accepted species: Species Fungorum (search *Septoria*)



Note a Conidiogenous cells. b Conidia. Scale bars = 10 μ m

Source Redrawn from Quaedvlieg et al. (2013)

Figure 4.5 *Septoria cytisi*

Sphaerulina Sacc. 1878

Classification: *Mycosphaerellaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

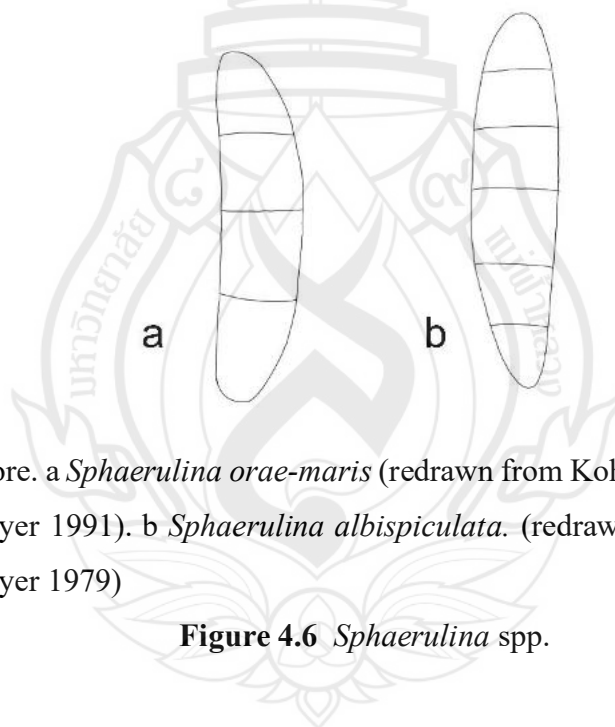
Sphaerulina is primarily a plant pathogenic genus introduced by Saccardo (1878) and typified with *S. myriadea* isolated from *Quercus petraea* (*Fagaceae*) in France. Several species, including *Sphaerulina* sp., *S. albispiculata*, *S. orae-maris*, and *S. pedicellate* (*nomen dubium*, confused with *Buergenerula spartinae*, Kohlmeyer and Kohlmeyer 1979), have been reported on salt marsh hosts, mostly as saprobes on *Spartina* species, with a few records on *Juncus roemerianus* and *Ammophila arenaria* (Calabon et al. 2021b). *Sphaerulina* is characterized by immersed, ostiolate, pseudothecial ascomata with a brown, 2–4 layered peridium and dissolving hamathecium at maturity. The asci are cylindrical to obclavate, containing eight hyalin, subcylindrical to fusiform, 1–3-septate ascospores. The asexual morph is septoria-like

(Videira et al. 2017; Pem et al. 2019). *Sphaerulina* was initially distinguished from *Mycosphaerella* based on the number of septa in the ascospores, but this is not a reliable feature for defining the genus (Crous et al. 2003, 2011c). Videira et al. (2017) studied *Mycosphaerellaceae* and demonstrated a close phylogenetic relationship between *Sphaerulina* and *Miuraea*. Ujat and Nakashima (2024) provided an updated phylogenetic tree based on analysis of ITS, LSU, *btub*, *rpb2*, *tef1*, *cal*, and *act* sequence data, and transferred several *Septoria* species to *Sphaerulina*, introducing seven new species in *Sphaerulina*.

Type species: *Sphaerulina myriadea* (DC.) Sacc. 1878

Basionym: *Sphaeria myriadea* DC. 1815

Other accepted species: Species Fungorum (search *Sphaerulina*)



Note Ascospore. a *Sphaerulina orae-maridis* (redrawn from Kohlmeyer and Volkmann-Kohlmeyer 1991). b *Sphaerulina albispiculata*. (redrawn from Kohlmeyer and Kohlmeyer 1979)

Figure 4.6 *Sphaerulina* spp.

Rivilata Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1998

Classification: *Phaeothecoidiaceae*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothidiomycete*, *Ascomycota*, *Fungi*

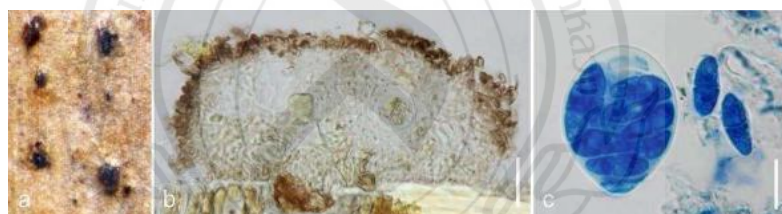
Rivilata is a saprobe in *Dothidiomycete*, described by Kohlmeyer et al. (1998) to accommodate *Rivilata ius*. *Rivilata ius* is the only species and it was isolated from a salt marsh host, *Juncus roemerianus*, in North Carolina, USA (Kohlmeyer et al. 1998). Asexual morph of *Rivilata* has not been determined and sexual morph is described by

having thyriotheacial ascomata which are flattened to slightly convex on top, forming beneath the cuticle and eventually peeling off, with an epithecium covering the hymenium. The epithecium consists of short dark brown hyphoid cells that open by irregular slits, exposing the hymenium when they are moistened. Hyaline pseudoparenchymatous tissue surrounds the asci. Asci are short pedicellate, clavate with an ellipsoidal to obovate shape in the upper part, dehiscence rostrate and with oculus containing eight hyaline, ellipsoidal, 1-septate, guttulate ascospores (Doilom et al. 2018).

Rivilata was previously assumed to be related to *Schizothyrium*; however, they are different in the morphology of ascomata which are epicuticular in *Rivilata* and subcuticular in *Schizothyrium* (Kohlmeyer et al. 1998). *Rivilata* was placed in *Saccardiaceae* based on similarity to the species in this family (Lumbsch and Huhndorf 2010a; Wijayawardene et al. 2018a), but later the holotype was re-examined by Doilom et al. (2018) and transferred to *Phaeothecoidiaceae* based on its morphological similarities to *Translucidithyrium*.

Type species: *Rivilata ius* Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1998

Other accepted species: None.



Note a Ascoma on substrate. b Vertical section through ascoma. c Ascus and ascospores stained in lactophenol cotton blue. Scale bars: d = 20 μ m, i = 10 μ m.

Source Doilom et al. (2018)

Figure 4.7 *Rivilata ius*

Scirrhia Nitschke ex Fuckel 1870

Classification: *Dothideaceae*, *Dothideales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

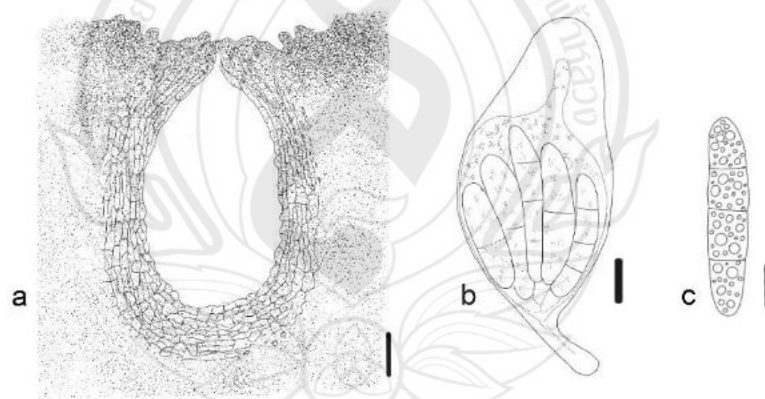
Scirrhia was introduced to accommodate four species; *Scirrhia castagnei*, *S. depauperata*, *S. poae* and *S. rimosa* (Fuckel 1870). *Scirrhia rimosa* is the type species of *Scirrhia*, collected on dry leaf sheaths of *Phragmites australis*, commonly found in

the spring (Fuckel 1870). Among the 26 species in *Scirrhia* (Species Fungorum, accessed April 2026), another species collected from a salt marsh host was *S. annulata*, isolated as a saprobe from *Juncus roemerianus* (Kohlmeyer and Volkmann-Kohlmeyer 1996a; Calabon et al. 2021b). Sexual morph of *Scirrhia* is characterized by pseudoparaphyses and elongated ascomata developing in multiple rows in hypostroma. Stromatic wall is composed of vertically oriented cells. Asci are bitunicate and contain eight bicellular, hyaline ascospores (Crous et al. 2011b; Videira et al. 2017). Based on morphology, the genus was placed in *Mycosphaerellaceae* (*Dothideales*) by Müller and von Arx (1962) and later transferred to *Dothideaceae* (*Dothideales*) (von Arx and Müller 1975). Based on molecular analyses of LSU sequence data, Crous et al. (2011b), placed the genus in *Mycosphaerellaceae* and suggested that *Scirrhia* is a potentially obligate plant pathogen. The placement of the genus remains doubtful, and further collections and sequence data are needed (Pem 2024).

Type species: *Scirrhia rimosa* (Alb. & Schwein.) Fuckel 1870

Basionym: *Sphaeria rimosa* Alb. & Schwein. 1805

Other accepted species: Species Fungorum (search *Scirrhia*)



Note a Ascoma. b Ascus. c Ascospore. Scale bar: a = 20 μ m, b, c = 10 μ m

Source Redrawn from redrawn from Kohlmeyer et al. (1996a)

Figure 4.8 *Scirrhia annulata*

Aureobasidium Viala & G. Boyer 1891

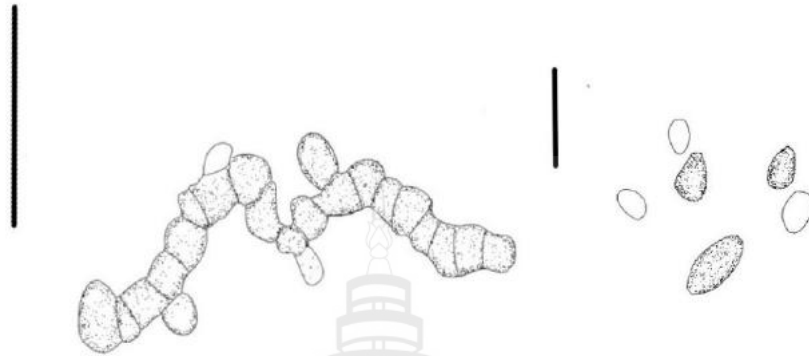
Classification: *Sacotheciaceae*, *Dothideales*, *Dothideomycetidae*,
Dothideomycetes, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Aureobasidium was established by Viala and Boyer (1891) and typified with *Aureobasidium vitis*. *Aureobasidium vitis* was considered the same species as *Dematium pullulans* (Arnaud 1910). As the type specimen of *Aureobasidium vitis* is lost, an ex-neotype of *A. pullulans* was designated as the oldest name for the type species by Hermanides-Nijhof (1977). *Aureobasidium* belongs to *Sacrotheciaceae* and comprises about 45 species (Hongsan et al. 2020a; Hyde et al. 2024a). *Aureobasidium* lives as a saprobe, endophyte, and plant or human pathogen (Martini et al. 2009, Pem et al. 2024). It is ubiquitous and has a worldwide distribution on various substrates, including soil, air, stone, glass, skin, nails, plant bark, roots, and fruits (Hermanides-Nijhof 1977; De Hoog and Yurlova 1994; Arzanlou 2014). Some species such as, *A. pullulans* are human opportunistic pathogen causing phaeohyphomycosis, keratomycosis, septicemia, peritoneal sepsis, and dermatological infections (Revankar et al. 2004; Chan et al. 2011). *Aureobasidium* species such as *A. pullulans*, *A. melanogenum* and *A. subglaciale*, have also been found in hypersaline marine habitats, such as seawater and the mud of salterns (Gunde-Cimerman et al. 2000; Nagahama 2006; Jones et al. 2019; Gostinčar and Gunde-Cimerman 2024). An unidentified species of *Aureobasidium* was reported on living and decaying leaves of the salt marsh host *Juncus roemerianus* (Calabon et al. 2021b). *Aureobasidium* species, particularly the well-known *A. pullulans*, can be utilized in the agricultural industry for their biocontrol activity against post-harvest plant pathogens, both in the field and during storage (Francesco et al. 2023). Additionally, *Aureobasidium* has potential applications in the food industry due to its ability to produce various enzymes, such as amylase, protease, lipase, cellulase, and xylanase (Francesco et al. 2023). *Aureobasidium pullulans* isolated from deep-sea sediments has been reported to produce extracellular amylase (Li et al. 2007). The sexual morph of the genus is not known. The asexual morph is characterized by acervular to sporodochial conidiomata, with hyaline to dark brown, unicellular conidia of various shapes, produced synchronously from holoblastic, polyblastic, terminal, lateral, or intercalary conidiogenous cells (Hermanides-Nijhof 1977; Arzanlou 2014; Hongsan et al. 2020a). ITS, LSU, SSU, *tub*, and *tef* are the available molecular markers for *Aureobasidium* in GenBank (Pem et al. 2024).

Type species: *Aureobasidium pullulans* (de Bary & Löwenthal) G. Arnaud 1918

Basionym: *Dematium pullulans* de Bary & Löwenthal 1884

Other accepted species: Species Fungorum (search *Aureobasidium*)



Note Conidiophore and conidia. Scale bar = 25 μ m

Source Redrawn from Abdelwehab et al. (2014)

Figure 4.9 *Aureobasidium pullulans*

Pseudoseptoria Speg. 1910

Classification: *Sacchettoeciaceae*, *Dothideales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Pseudoseptoria is a saprobic or pathogenic genus introduced by Spegazzini (1910). There are nine accepted species listed in Species Fungorum (Accessed April 2026). Sexual morph is undetermined. Asexual morph is coelomycetous, characterized by immersed pycnidial conidiomata with thin peridium. Conidiophores reduced to ampulliform, hyaline, smooth conidiogenous cells with a prominent cylindrical papilla and several percurrent proliferations at the apex. Conidia are hyaline, aseptate, guttulate and fusoid with rounded ends (Quaedvlieg et al. 2013; Pem et al. 2019).

Pseudoseptoria species are commonly collected on herbaceous plants and are found as plant pathogens on *Poaceae* (Quaedvlieg et al. 2013), causing halo spot, leaf blotch, and stem speckle (Jayawardena et al. 2020). Spores are dispersed in rain splash, and a wetness period is required for infection (Jayawardena et al. 2020). *Pseudoseptoria donacis* has been isolated from both living and decomposing *Phragmites australis* in the Netherlands (Van Ryckegem and Verbeken 2005b; Van Ryckegem et al. 2007; Calabon et al. 2021b). Quaedvlieg et al. (2013) placed *Pseudoseptoria* in *Dothioraceae*

based on molecular analyses of *tefl*, *btub*, *rpb2*, LSU and ITS sequence data. Crous et al. (2017) transferred *Pseudoseptoria* to *Sacchettoeciaceae* based on LSU sequence data, accepted by Wijayawardene et al. (2017a, b, 2018b, 2020).

Type species: *Pseudoseptoria donacicola* Speg. 1910

Other accepted species:

Pseudoseptoria bromigena (Sacc.) B. Sutton 1980

Pseudoseptoria collariana Quaedvl., Verkley & Crous 2013

Pseudoseptoria everhartii (Sacc. & P. Syd.) B. Sutton 1980

Pseudoseptoria obscura Quaedvl., Verkley & Crous 2013

Pseudoseptoria obtusa (R. Sprague & Aar.G. Johnson) B. Sutton 1980

Pseudoseptoria sorghi Lavrov 1948

Pseudoseptoria stomaticola (Bäumler) B. Sutton 1980

Pseudoseptoria usneae (Vouaux) D. Hawksw. 1981



Note Conidiophore (400×) and conidium (770×)

Source Redrawn from Frisullo (1984)

Figure 4.10 *Pseudoseptoria donacis*

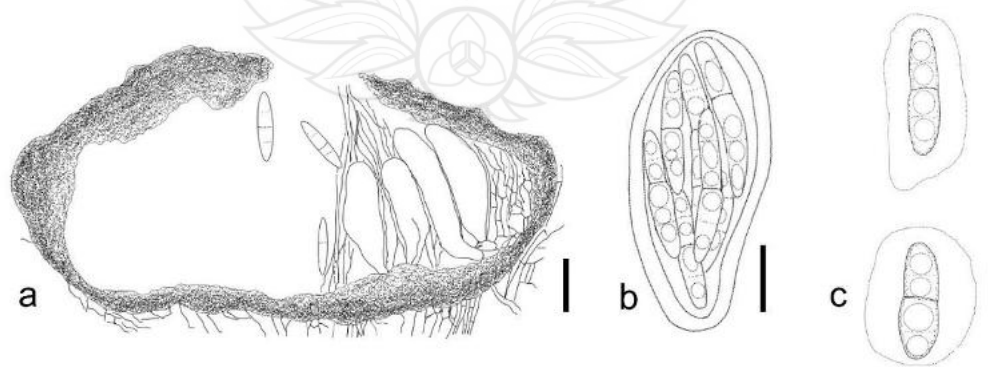
Mucomyosphaerella Quaedvl. & Crous 2014

Classification: *incertae sedis*, *Mycosphaerellales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Mucomyosphaerella was described as a novel genus belonging to the order *Capnodiales* (*Incertae sedis*) based on LSU and *rpb2* sequence data (Quaedvlieg et al. 2014). Quaedvlieg et al. (2014) suggested that the genus be placed in a separate family, sister to the *Schizothyriaceae*. Later, because of the classification of *Schizothyriaceae* under *Mycosphaerellales* (Abdollahzadeh et al. 2020), Wijayawardene et al. (2022) transferred *Mucomyosphaerella* to *Mycosphaerellales incertae sedis*. Wanasinghe et al. (2025) added *M. hongheensis* to this genus and transferred it to a novel family *Mycosphaerellaceae*. *Mucomyosphaerella* is characterized by pseudothecial, depressed, ostiolate, brown ascomata composed of 4–6 layers of peridium at the top and 2–3 layers at the sides and bottom. Pseudoparaphyses are branched and enclosed in a gelatinous matrix. Asci are bitunicate with a thin ectotunica and a thick gelatinous endotunica. Ascospores are elongate, ellipsoid, hyaline, septate, and embedded in a sheath (Quaedvlieg et al. 2014). The genus differs from *Mycosphaerella* in that it has well-developed sheaths surrounding its ascospores and lacks *Ramularia* asexual stages (Kohlmeyer et al. 1999). *Mucomyosphaerella* is typified by *M. eurypotami* that was first classified under *Mycosphaerella*. *M. eurypotami* is the only species in this taxon that was reported as a saprobe on *Juncus roemerianus* from USA (Kohlmeyer et al. 1999).

Type species: *Mucomyosphaerella eurypotami* (Kohlm., Volkm.-Kohlm. & O.E. Erikss.) Quaedvl. & Crous 2014

Other accepted species: *Mucomyosphaerella hongheensis* Wanas., Phookamsak, L.S. Dissan. & J.C. Xu 2025



Note a Ascoma. b Ascus. c Ascospores. Scale bars: 10 μ m

Source Redrawn from Kohlmeyer et al. (1999)

Figure 4.11 *Mucomyosphaerella eurypotami*

Neomassariosphaeria Y. Zhang ter, J. Fourn. & K.D. Hyde 2009

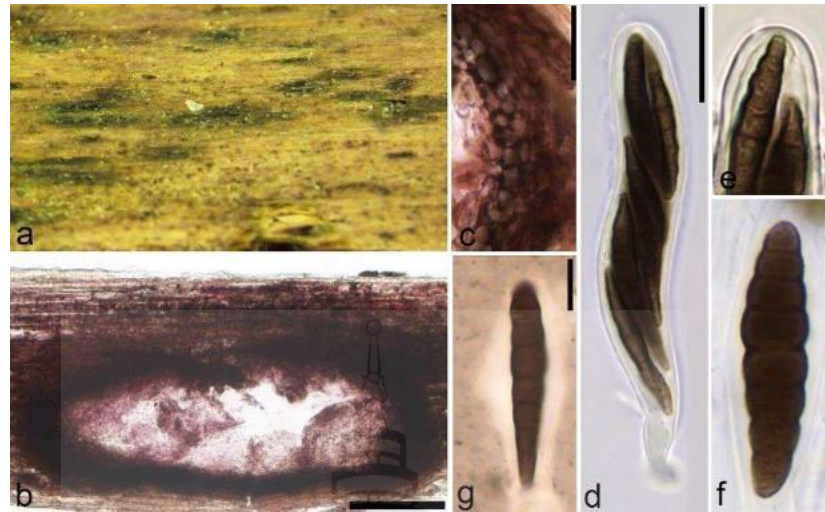
Classification: *Amniculicolaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Zhang et al. (2009a) conducted a taxonomic reassessment of *Pleosporales*, utilizing SSU, LSU, *tefl*, *rpb1*, and *rpb2* sequence data. Through a combination of molecular and morphological analyses, they established *Neomassariosphaeria* in *Amniculicolaceae*. This classification was subsequently affirmed by other researchers (Wijayawardene et al. 2018a, Jayasiri et al. 2019, Yang et al. 2023b). *Neomassariosphaeria* was introduced to accommodate two new combinations, of *Massariosphaeria grandispora* and *M. typhicola* and typified with *N. typhicola* (Zhang et al. 2009a). Subsequently, Ariyawansa et al. (2015a) excluded *N. grandispora* (= *Pseudomassariosphaeria grandispora*) from the genus, citing differences in morphology of asci and ascospores. The taxonomy of *N. typhicola* (= *Aquimassariosphaeria typhicola*) has undergone several transfers and discussions (Dong et al. 2020; Yang et al. 2023b). There are reports of *N. typhicola* isolation from salt marsh habitats on *Juncus roemerianus*, *Spartina densiflora*, and *Spartina* sp. (Kohlmeyer and Kohlmeyer 1979; Gessner and Kohlmeyer 1979; Peña and Arambarri 1998; Kohlmeyer and Volkmann-Kohlmeyer 2002; Walker 2012; Calabon et al. 2021b). With the introduction of *N. aquimucosa* as a new species from freshwater habitats in China, the genus now comprises two accepted species (Yang et al. 2023b). This saprobic genus exhibits immersed to erumpent ascomata with a thin peridium. Typically, the ascomata stain the host tissue purple. The asci are clavate to broadly clavate, featuring a short pedicle. Ascospores are fusiform, multi-septate, and surrounded by a gelatinous sheath, displaying a hyaline to reddish-brown color (Zhang et al. 2009a).

Type species: *Neomassariosphaeria typhicola* (P. Karst.) Y. Zhang ter, J. Fourn. & K.D. Hyde 2009

Basionym: *Leptosphaeria typhicola* P. Karst. 1873

Other accepted species: *Neomassariosphaeria aquimucosa* L.L. Liu, J. Yang, K.D. Hyde & Z.Y. Liu 2023



Note a Ascomata immersed in host tissue. b Vertical section of ascoma. c Peridium. d Ascus. e Ocular chamber in ascus. f Ascospore. g Ascospores' sheath. Scale bars: b = 100 μm , c, d = 20 μm , e–g = 10 μm

Source Dong et al. (2020)

Figure 4.12 *Aquimassariosphaeria typhicola* (= *Neomassariosphaeria typhicola*)

Camarosporium Schulzer 1870

Classification: *Camarosporiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

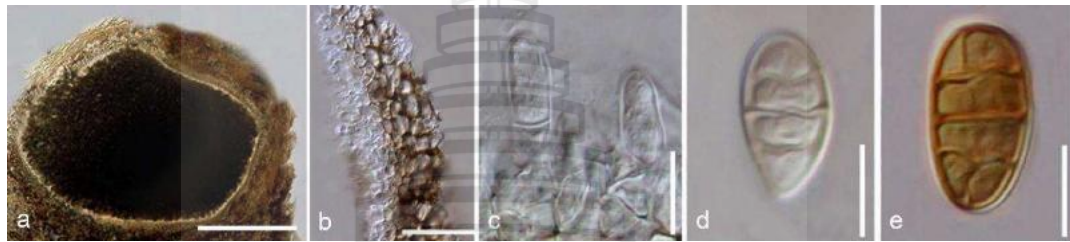
Camarosporium is generally a saprobic genus with more than 300 accepted species (Species Fungorum, April 2026). *Camarosporium feurichii*, *C. palliatum*, *C. roumeguerei*, *C. salicorniae*, and *C. suaedae-fruticosae* have been reported on various salt marsh plants such as *Phragmites australis*, *Spartina maritima*, *Sarcocornia* sp., *Salicornia* sp., *Atriplex* sp., *Suaeda* sp., and *Distichlis* species. Among these, *C. roumeguerei* is the most frequently recorded species in this ecosystem (Calabon et al. 2021b). Both sexual and asexual morphs of *Camarosporium* are known. The sexual morph features pseudothecial ascomata, cylindrical asci, and eight muriform ascospores (Crous and Groenewald 2017). The asexual morph is coelomycetous, with pycnidial conidiomata, doliiform annellidic conidiogenous cells, and muriform conidia. Synasexual morph has pycnidial conidiomata with ampulliform conidiogenous cells and subcylindrical conidia (Crous and Groenewald 2017). *Camarosporium* was introduced by Schulzer (1870) and has been linked to various families and orders in

different studies. Crous and Groenewald (2017) designated an epitype for the type species and restricted *Camarosporium sensu stricto* based on phoma-like synasexual and pleospora-like sexual morphs, placing it in *Coniothyriaceae*. While several species in *Camarosporium* lack molecular data, based on phylogenetic analyses of combined LSU, SSU, ITS, and *tef-1*, the genus' placement was confirmed in *Camarosporiaceae* (Wanasinghe et al. 2017; Pem et al. 2024).

Type species: *Camarosporium quaternatum* (Hazsl.) Schulzer 1870

Basionym: *Clinterium quaternatum* Hazsl. 1865

Other accepted species: Species Fungorum (search *Camarosporium*)



Note a Vertical section of conidioma. b Peridium. c Conidiogenous cells and developing conidia. d, e Conidia. scale bars: a = 200 µm, b = 50 µm, c–e = 10 µm

Source Liu et al. (2015)

Figure 4.13 *Camarosporium aborescentis*

Massariosphaeria (E. Müll.) Crivelli 1983

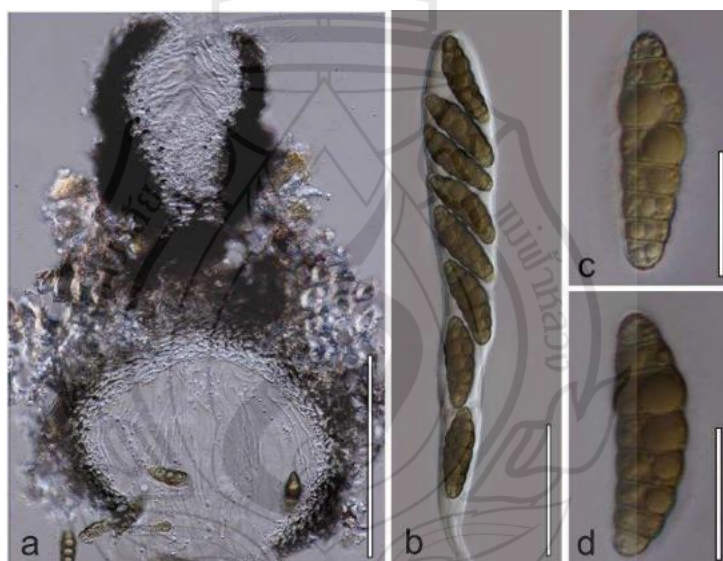
Classification: *Cyclothyriellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Müller in 1950 initially classified the genus as a section of *Leptosphaeria*. Subsequently, *Massariosphaeria* was established as a separate genus by Crivelli (1983). *Massariosphaeria* is identified by several distinct characteristics. These include immersed, black ascomata with a black to grayish peridium. Hamathecium are hyaline and septate. Asci are cylindrical to clavate and contain yellow to brown multi-septate ascospores. Ascospores are characterized by having a sheath and producing a red color on the host surface (Crivelli 1983; Leuchtman 1984; Wang et al. 2007). *Massariosphaeria* has a similar peridium to *Chaetomastia*, but they differ in the morphology of the ascomata and ascospores (Barr 1989; Phukhamsakda et al. 2020).

Molecular data has revealed that *Massariosphaeria* is polyphyletic (Wang et al. 2007; Zhang et al. 2012; Ariyawansa et al. 2015a; Phukhamsakda et al. 2016). Sequence data for the type species *M. phaeospora*, which clustered with *Cyclothyriella rubronotata*, has led to the inclusion of *Massariosphaeria* within the family *Cyclothyriellaceae* (Jaklitsch and Voglmayr 2016; Wijayawardene et al. 2018a). There are 21 epithets listed under *Massariosphaeria* in Index Fungorum. *Massariosphaeria erucacea*, *M. scirpina* and *Massariosphaeria* sp. were reported from salt marsh hosts; *Juncus roemerianus* and *Spartina* sp. in USA, and *Phragmites australis* in the Netherlands (Johnson and Sparrow 1961; Kohlmeyer et al. 1996a; Van Ryckegem and Verbeken 2005a).

Type species: *Massariosphaeria phaeospora* (E. Müll.) Crivelli 1983

Other accepted species: Species Fungorum (search *Massariosphaeria*)



Note a ascoma. b Ascus. c, d Ascospores. Scale bars: a = 200 µm, b = 50 µm, c, d = 20 µm

Source Phukhamsakda et al. (2020)

Figure 4.14 *Massariosphaeria clematidis*

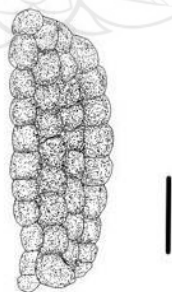
Dictyosporium Corda 1837

Classification: *Dictyosporiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Dictyosporium is a mostly saprobic genus distributed worldwide and is commonly collected as a saprobe on various host plants (Pem et al. 2024). Some species have been reported as pathogenic to pine wood nematodes and as potential biocontrol agents (Dong et al. 2004). *Dictyosporium* has 81 species found in both terrestrial and aquatic habitats (Specie Fungarum April 2026). *Dictyosporium oblongum* and *D. pelagicum* are species reported from salt marsh habitats. The former was found on *Phragmites australis*, while the latter was isolated from *Spartina* species (Jones 1963; Calabon et al. 2021b). There are few records of sexual morph in this genus, characterized by perithecial, superficial, ostiolate, darkly pigmented ascomata with numerous pseudoparaphyses. Asci are fissitunicate, clavate to cylindrical, or saccate. Ascospores vary in shape, being fusiform, elongated-ellipsoid, and with or without a sheath (Boonmee et al. 2016). Asexual morph has sporodochial hyphomycetous colonies and micronematous conidiophores if present. Conidiogenous cells vary from cylindrical or doliiform to spherical or subspherical, with multiseptated acrogenous conidia (Boonmee et al. 2016). The genus was introduced by Corda (in Witenweber, 1836) and typified with *D. elegans* isolated from decaying *Quercus* in Germany. Boonmee et al. (2016) introduced two new species based on molecular data and considered *Dictyosporium* as a heterogeneous genus. They formally introduced *Dictyosporiaceae* and designated *Dictyosporium* as the type genus (Pem et al. 2024). Zhang et al. (2024) introduced a novel species and performed the updated phylogenetic tree based on LSU, SSU, *tef1* and *rpb2* sequences data.

Type species: *Dictyosporium elegans* Corda 1837

Other accepted species: Species Fungorum (search *Dictyosporium*)



Note Conidium. Scale bar: 10 µm

Source Redrawn from Goh et al. (1999)

Figure 4.15 *Dictyosporium oblongum*

Jalapriya M.J. D'souza, Hong Y. Su, Z.L. Luo & K.D. Hyde 2016

Classification: *Dictyosporiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Boonmee et al. (2016) described *Jalapriya* to accommodate a novel species, *Jalapriya pulchra*, as the type species and two new combinations from *Dictyosporium*. Based on molecular analyses of ITS and combined LSU, SSU, and *tef* sequence data, the three species formed a monophyletic clade (Boonmee et al. 2016). The sexual morph of the genus has not been determined. The asexual morph is characterized by effuse and dark colonies on the substrate with micronematous, cylindrical, and unbranched conidiophores. Conidiogenous cells are holoblastic, integrated, determinate, and terminal, bearing solitary acrogenous conidia. Conidia are cheiroid and euseptate with 5–7 rows of cells, with or without appendages at the apex (Boonmee et al. 2016).

Jalapriya is a hyphomycetous genus with six accepted species (Species Fungorum, 2026), isolated from both terrestrial and aquatic habitats (Koch and Jones 1983, Fu et al. 2021). *Jalapriya toruloides* has been reported from marine sediment in Sweden, leading to its consideration as a euryhaline species (Tibell et al. 2020). The species has also been isolated from decaying stem of the saltmarsh plant *Spartina* sp. in the United Kingdom (Jones 1963; Calabon et al. 2021b).

Type species: *Jalapriya pulchra* D'souza, Su, Luo & K.D. Hyde 2016

Other accepted species:

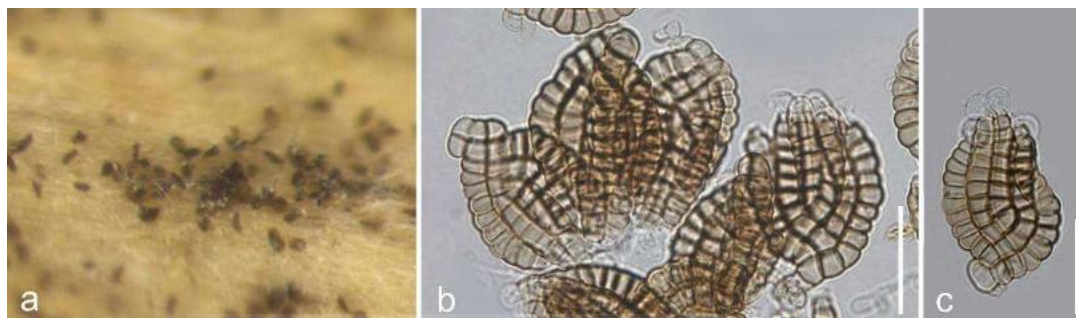
Jalapriya apicalivaginata D.F. Bao, Xi Fu, Hong Y. Su & Z.L. Luo 2021

Jalapriya aquatica D.F. Bao, X. Fu, H.Y. Su & Z.L. Luo 2021

Jalapriya cheirospora H.Z. Du & Jian K. Liu 2025

Jalapriya guttulata Y. Wang & Z.L. Luo 2025

Jalapriya toruloides (Corda) M.J. D'souza, Hong Y. Su, Z.L. Luo & K.D. Hyde 2016



Note a Colonies on the substrate. b, c Conidia. Scale bars: 15 μm

Source Boonmee et al. 2016

Figure 4.16 *Jalapriya pulchra*

Epicoccum Link 1816

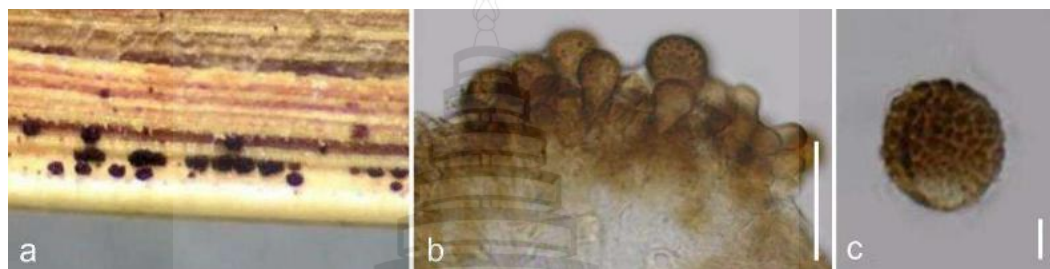
Classification: *Didymellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Link (1816) originally described *Epicoccum* as forming black spots on the host stem and black globose stroma. Initially, *Epicoccum* was identified by its epicoccoid conidia and placed in the family *Didymellaceae* (Aveskamp et al. 2010). Chen et al. (2015) later revised the genus, taking into account both morphology and phylogenetic analyses using combined ITS, LSU, *rpb2*, and *tub2* sequences. They introduced additional distinguishing characteristics, such as irregular pycnidial conidiomata and subcylindrical conidia. The asexual morph includes superficial or immersed pycnidial conidiomata in agar. Conidiogenous cells are hyaline, phialidic, and ampulliform, producing hyaline to brownish aseptate conidia in various shapes. The synasexual morph is defined by semi-immersed sporodochia, with multicellular-phragmosporous conidia and variable, irregular-shaped chlamydospores (Chen et al. 2015). There are currently about 100 species in this genus (Hyde et al. 2024). *Epicoccum* species have gained attention for their potential in biocontrol and production of biomaterial compounds (Chen et al. 2017; Del Frari et al. 2019). *Epicoccum* species are found worldwide, as saprobes, endophytes and plant pathogens (Dzoyem et al. 2017; Jayasiri et al. 2017; Raza et al. 2019; de Silva et al. 2021). These ubiquitous fungi have been isolated from diverse environments, such as soil, sand, decaying plants, crops, salt marshes, algae, cold water, air, and indoor settings (Schol-Schwarz 1959; Domsch et

al. 1980; Cole and Kendrick 1981; Flannigan et al. 2002). *Epicoccum nigrum* has been reported on decaying leaves and stems of halophytes, including *Distichlis spicata* in Argentina (Fell and Hunter 1979; Elíades et al. 2007), *Juncus roemerianus* and *Spartina alterniflora* in USA (Gessner and Goos 1973b; Gessner and Kohlmeyer 1976; Gessner 1977; Gessner 1980).

Type species: *Epicoccum nigrum* Link, Mag. 1816

Other accepted species: Species Fungorum (search *Epicoccum*)



Note a Synnemata on host. b Section of synnema. c Conidium. Scale bars: b = 50 µm, f = 10 µm

Source Hyde et al. (2018)

Figure 4.17 *Epicoccum nigrum*

Chaetasbolisia Speg. 1918

Classification: *Didymellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Chaetasbolisia was introduced by Spegazzini (1918) to accommodate *Chaetasbolisia erysiphoides*, which was formerly classified in *Chaetophoma*. The sexual morph of *Chaetasbolisia* has not been found. The asexual morph develops superficial, black, ostiolate pycnidia. The pycnidial wall has long, branched, septate, fuliginous hyphal outgrowths or is glabrous. conidiogenous cells are phialidic and globose, ampulliform, or lageniform in shape, bearing hyaline, unicellular conidia (Spegazzini 1918; Hou et al. 2020). Hou et al. (2020) added two new species and emended the generic circumscription of *Chaetasbolisia*. Based on a phylogenetic analysis of combined LSU, ITS, *rpb2*, and *tub2* data, Hou et al. (2020) demonstrated the distinct placement of *Chaetasbolisia* within *Didymellaceae*. Currently, *Chaetasbolisia* comprises nine species, which are mostly saprobic on plant material or soil (Hou et al. 2020; Hyde et al. 2024a; Pem et al. 2024). Some species, such as *C.*

microglobulosa and *C. falcata*, have been recorded as sooty molds (Khodaparast 2006; Byrami and Pedramfar 2013). An unidentified *Chaetasbolisia* species has been recorded on salt marsh host, *Phragmites australis* in China (Poon and Hyde 1998; Calabon et al. 2021b). Some species of *Chaetasbolisia* have potential medical applications, such as *C. erysiphoides*, which produces angiogenesis inhibitors (Otsuka et al. 1992).

Type species: *Chaetasbolisia erysiphoides* (Griffon & Maubl.) Griffon & Maubl. 1918

Basionym: *Chaetophoma erysiphoides* Griffon & Maubl. 1909

Other accepted species:

Chaetasbolisia argentina L.W. Hou, L. Cai & Crous 2020

Chaetasbolisia californiana Bat., Cif. & Nascim. 1963

Chaetasbolisia eupatorii (Died.) L.W. Hou, L. Cai & Crous 2020

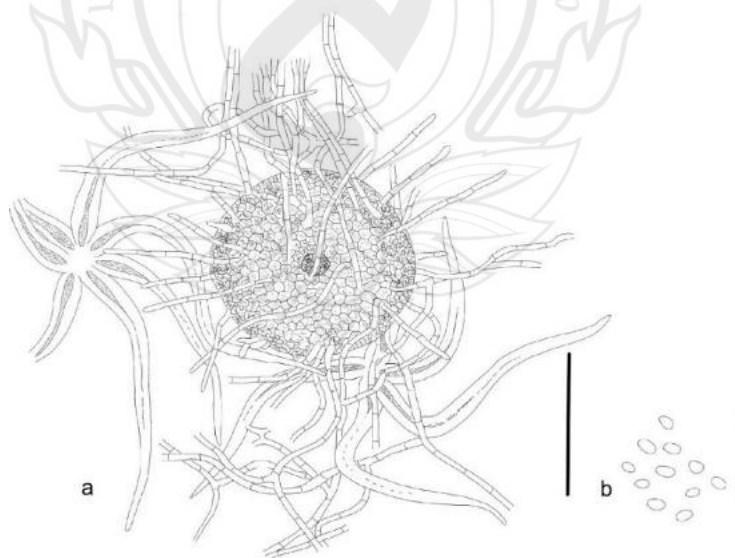
Chaetasbolisia falcata V.A.M. Mill. & Bonar 1941

Chaetasbolisia indica U.S. Patel, A.K. Pandey & R.C. Rajak 1997

Chaetasbolisia longiseta Cabral & Kerschen 1977

Chaetasbolisia raphiae Verpl. & R. Broecke 1936

Chaetasbolisia sapotae Bat. & Matta 1963



Note a Pycnidium. b Conidia. Scale bar: a = 100 μ m, b = 20 μ m (redrawn from Spegazzini 1918)

Figure 4.18 *Chaetasbolisia erysiphoides*

Paraboeremia Qian Chen & L. Cai 2015

Classification: *Didymellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Paraboeremia is a saprobic or pathogenic genus with 11 species listed in Index Fungorum. *P. putaminum* has been reported on the halophyte *Distichlis spicata* in Argentina (Eliades et al. 2007; Calabon et al. 2021b). *Paraboeremia* was introduced by Chen et al. (2015) to accommodate *P. adianticola*, *P. putaminum*, and *P. selaginellae* and *P. selaginellae* was designated as the type species. It was placed in *Didymellaceae* based on morphology and multigene phylogeny of combined LSU, ITS, *tub2*, and *rpb2* sequences. Sexual morph forms subglobose to pyriform ascomata. Asci are bitunicate, containing eight subcylindrical, hyaline, and 1-septate ascospores with a wider upper cell. Asexual morph is coelomycetous, with ostiolate, globose to subglobose or irregularly shaped pycnidia, sometimes with a short neck. The peridium is composed of 3–6 layers with a pigmented outer layer. Conidiogenous cells are phialidic, forming globose to flask-shaped structures bearing ellipsoidal or curved conidia. Conidia are mostly aseptate, guttulate, and hyaline or sometimes greenish. *Paraboeremia* has a similar morphology to *Boeremia* but is distinct based on phylogeny (Chen et al. 2015; Pem et al. 2019).

Type species: *Paraboeremia selaginellae* (Sacc.) Q. Chen & L. Cai 2015

Basionym: *Phyllosticta selaginellae* Sacc., in Bresadola & Saccardo 1897

Other accepted species: Species Fungorum (search *Phyllosticta*)



Note a Conidiogenous cells and conidia. b Conidia. Scale bars: a = 10 µm, b = 5 µm.
(redrawn from Pem et al. 2024)

Figure 4.19 *Paraboeremia selaginellae*

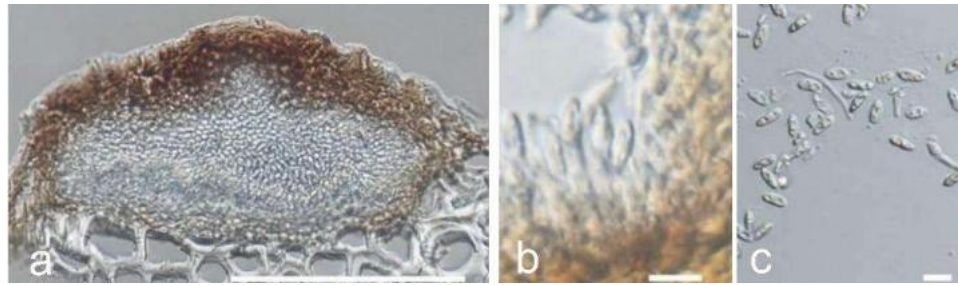
Phoma Sacc. 1880

Classification: *Didymellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Saccardo (1880) established the generic name *Phoma*, which was later emended by Boerema and Bollen (1975). *Phoma* is recognized by its coelomycetous asexual morph, forming globular pycnidia and hyaline conidia *in vivo* and *in vitro* (Boerema 1964, Hou et al. 2020). *Phoma* is a polyphyletic genus with uncertain taxonomic boundaries, as several species share similar morphology. Boerema et al. (1997) divided *Phoma* into nine sections, associating it with sexual morphs in *Mycosphaerella*, *Didymella*, *Pleospora*, and *Leptosphaeria*. The use of molecular data has provided greater resolution in the classification of phoma-like taxa (Hou et al. 2020; Pem et al. 2024). However, Aveskamp et al. (2010) suggested that ITS alone is insufficient, and researchers have used combinations of SSU, LSU, ITS, *tub2*, and *rpb2* sequences (Aveskamp et al. 2010; Chen et al. 2015). *Phoma* is one of the specious genera in *Pleosporales*, with more than 3,300 associated records in Index Fungorum, many of which have been transferred to other genera. Currently, there are about 50 species in this genus. *Phoma* species are ubiquitous, living as saprobes, endophytes, and pathogens on various substrates, including soil and plant material (Hyde et al. 2024a; Pem et al. 2024). Several *Phoma* species are important plant pathogens, causing diseases such as root rot, leaf spot, leaf blight, and stem rot, primarily in members of the family *Solanaceae* (Deb et al. 2020). Some species have also been found in marine habitats, such as *P. glomerata*, *P. herbarum*, and *P. putaminum*, which are listed as marine fungi by Jones et al. (2019). Additionally, there are more than ten reports of *Phoma* species associated with various salt marsh hosts, including *P. herbarum* and *P. leveillei* on *Distichlis spicata* and *P. suaedae* on *Suaeda maritima* (Calabon et al. 2021b). *Phoma* species have been investigated for their ability to produce various chemical compounds with antifungal and antibacterial properties (Rai et al. 2022). For example, the sponge-derived fungus *Phoma* sp. Q60596, isolated from marine habitat, exhibits strong antifungal and antibiotic activity (Jones 2019; Nagai et al. 2002).

Type species: *Phoma herbarum* Westend. 1852

Other accepted species: Species Fungorum (search *Phoma*)



Note a Conidioma. b Conidiogenous cells. c Conidia. Scale bars: a = 100 μm , b, c = 10 μm

Source Pem et al. (2024)

Figure 4.20 *Phoma herbarum*

***Stagonosporopsis* Died. 1912**

Classification: *Didymellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

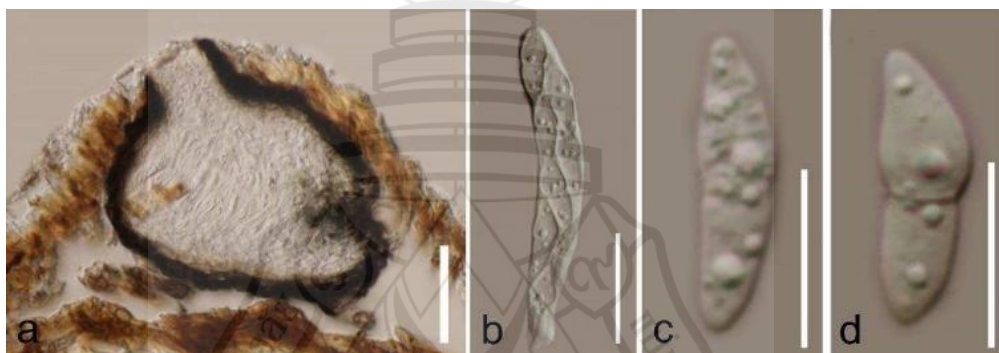
Diedicke (1912) divided the genera *Ascochyta* and *Diplodia* into seven genera, including the novel genus *Stagonosporopsis*, characterized by conidia that are sometimes divided into three cells. Aveskamp et al. (2010) emended the description of *Stagonosporopsis*, providing both asexual and sexual characteristics. The asexual morph is coelomycetous, forming pycnidial conidiomata with a pseudoparenchymatous peridium and phialidic, ampulliform, or doliiform conidiogenous cells bearing two types of conidia. The majority of conidia are aseptate, while the second type ranges from aseptate to 3-septate. The sexual morph forms pseudothecial ascomata with cylindrical or subclavate asci containing eight uniseptate, guttulate ascospores (Aveskamp et al. 2010). *Stagonosporopsis* comprises approximately 40 species, including plant pathogens, endophytes, and saprobes (Jayasiri et al. 2019; Chen et al. 2023; Hyde et al. 2024a; Ren et al. 2024). Plant pathogenic species of *Stagonosporopsis* cause various diseases, such as leaf spot, stem blight, dieback and fruit rot (Vaghefi et al. 2012; Shams et al. 2021; Dong et al. 2021). *Stagonosporopsis cucurbitacearum* has been recorded as a marine fungus and *St. salicorniae* is listed as a salt marsh fungus collected from *Salicornia europaea* and *Sa. patula* (Jones et al. 2019; Calabon et al. 2021b).

Stagonosporopsis cucurbitacearum, as a marine-derived fungus, produces chemical compounds with antifungal activity against *Candida albicans*, *C. glabrata*, and *Cryptococcus neoformans* (Haga et al. 2013). Recently introduced species include *St. lijiangensis*, *St. bungeiana*, *St. malaiana*, and *St. pedicularis-striatae*, which were collected in China (Chen et al. 2023; Ren et al. 2024). Ren et al. (2024) provided an updated phylogenetic tree for the genus based on molecular analyses of LSU, ITS, *rpb2*, and *tub2* sequence data.

Type species: *Stagonosporopsis boltshauseri* (Sacc.) Died. 1912

Basionym: *Ascochyta boltshauseri* Sacc. 1891

Other accepted species: Species Fungorum (search *Stagonosporopsis*)



Note a Ascoma. b Ascus. c,d Ascospores. Scale bars: a = 50 μm , b = 20 μm , c, d = 10 μm

Source Ren et al. (2024)

Figure 4.21 *Stagonosporopsis lijiangensis*

Julella Fabre 1879

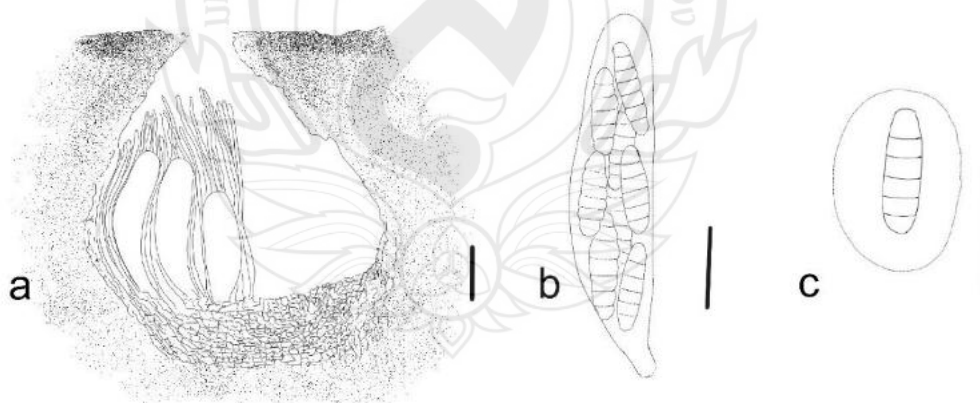
Classification: *Didymosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Julella is a saprobic or possibly lichenized genus introduced by Fabre (1879). Sexual characters of *Julella* include immersed ostiolate ascomata, which form under a clypeus with a short neck. Peridium is composed of a dark pigmented outer layer and a yellowish-brown inner layer. Hamathecium consists of pseudoparaphyses embedded in mucilage. Asci are fissitunicate, clavate to cylindrical, and short-pedicellate, containing two hyaline, muriform, guttulate, verruculose ascospores with a mucilaginous sheath. Asexual morph of the genus remains undetermined (Ariyawansa et al. 2014; Pem et al.

2024). The most common mangrove *Julella* is *Julella avicenniae* introduced by Borse (1987) as *Pleospora avicenniae*, referred by Hyde (1992a) to *Julella*. Subsequently based on a phylogenetic study it was transferred to a new genus *Halojulella* by Suetrong, K.D. Hyde and E.B.G. Jones (in Ariyawansa et al. 2013) and in new family *Halojulellaceae*. Among its six species, *Julella herbatilis* was isolated from the salt marsh host *Juncus roemerianus* (Kohlmeyer et al. 1997; Calabon et al. 2021b). *Julella herbatilis* has 3–5-layered peridium and eight-spored asci (Kohlmeyer et al. 1997). Aptroot and van den Boom (1995) accepted three species in *Julella* and considered them tropical bark saprobes. Zhang et al. (2012) reported that *Julella* is morphologically related to *Montagnulaceae* (currently *Didymosphaeriaceae*), but it differs by having hyaline ascospores. Upon re-examination of the type species *J. buxi*, *Julella* was transferred to *Didymosphaeriaceae* based on morphology (Ariyawansa et al. 2014). *Julella fallaciosa* and *J. avicenniae* were the only species with available sequence data and were transferred to *Arthopyrenia* (Thiyagaraja et al. 2021) and *Halojulella*, respectively (Ariyawansa et al. 2013). Fresh collections and molecular data are needed to confirm the accurate taxonomic placement of *Julella* (Pem et al. 2024).

Type species: *Julella buxi* Fabre 1879

Other accepted species: Species Fungorum (search *Julella*)



Note a Ascoma. b Ascus. c Ascospore. Scale bars = 20 µm

Source Redrawn from Kohlmeyer et al. (1997)

Figure 4.22 *Julella herbatilis*

Paraphaeosphaeria O.E. Erikss. 1967

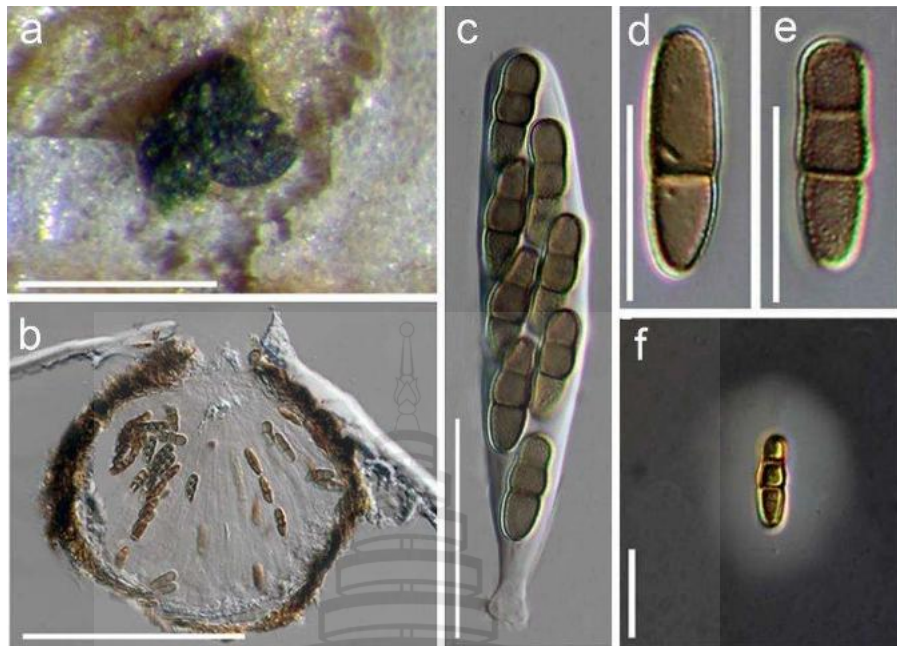
Classification: *Didymosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Paraphaeosphaeria, established by Eriksson (1967), has been reported as saprobes, endophytes, and pathogens (Chen et al. 2022b; de Paula et al. 2022). Species such as *P. apicicola* and *P. pilleata* have been found in salt marsh environments, particularly on *Juncus roemerianus*. The type species, *P. michotii*, has also been discovered on halophytes like *Elymus pungens* and *Phragmites australis* (Calabon et al. 2021b). *Paraphaeosphaeria* has gained attention due to its ability to produce natural metabolites (Carrieri et al. 2020; Su et al. 2023). Sexual morph of *Paraphaeosphaeria* has ostiolate ascomata with a 3-5 layered peridium. Asci are cylindrical and fissitunicate, containing eight multi-septate, broadly elliptical, yellowish-brown ascospores (Ariyawansa et al. 2014; Tennakoon et al. 2022; Pem et al. 2024). Asexual morph is coniothyrium-like, with aseptate or uniseptate conidia. *Paraphaeosphaeria* differs from *Phaeosphaeria* in the morphology of its ascospores and asexual morphs (Wanasinghe et al. 2018; Pem et al. 2024). Based on phylogenetic analyses of SSU, LSU, *tef-1*, *rpb1*, and *rpb2*, *Paraphaeosphaeria* was placed in *Montagnulaceae* (Zhang et al. 2009a). Ariyawansa et al. (2014) designated an epitype for *P. michotii* and synonymized *Montagnulaceae* under *Didymosphaeriaceae* based on ITS, LSU, SSU and *βtub* sequence data.

Type species: *Paraphaeosphaeria michotii* (Westend.) O.E. Erikss. 1967

Basionym: *Sphaeria michotii* Westend. 1859

Other accepted species: Species Fungorum (search *Paraphaeosphaeria*)



Note a Ascoma under host epidermal tissue. b Section of ascoma. c Ascus. d, e Ascospores. f Ascospore stained with Indian ink. Scale bar: a = 200 μm , b = 100 μm , c = 20 μm , d–f = 10 μm

Source Wanasinghe et al. (2018)

Figure 4.23 *Paraphaeosphaeria michotii*

Pseudopithomyces Ariyaw. & K.D. Hyde 2015

Classification: *Didymosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Pseudopithomyces is a saprobic or parasitic genus introduced by Ariyawansa et al. (2015a) and typified with *P. chartarum* (based on = *Sporidesmium chartarum* Berkeley 1874). *Pseudopithomyces* is hyphomycetous, characterized by brown to black colonies on the host with flexuous conidiophores and terminal monoblastic or blastic conidiogenous cells. The conidia are fusiform, dark, with verruculose to echinulate ornamented walls. Sexual morph has not been determined (Ariyawansa et al. 2015a; Hyde et al. 2017; Wanasinghe et al. 2018; Jayasiri et al. 2019; Pem et al. 2019; Tennakoon et al. 2021).

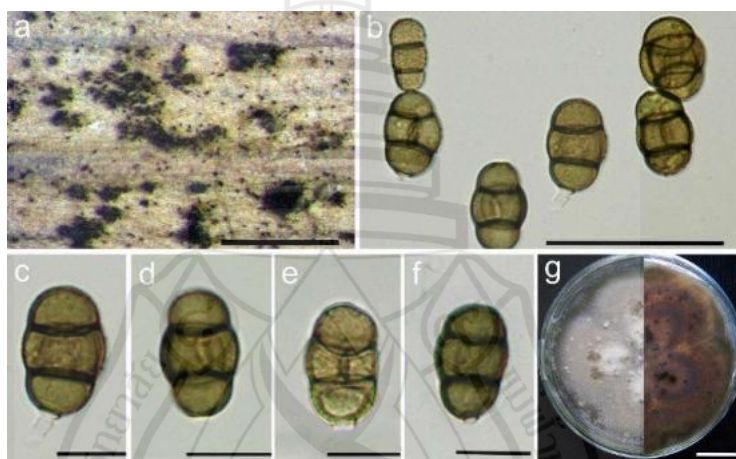
Pseudopithomyces is similar to *Pithomyces* but differs in the morphology of fusiform, verruculose dark conidia and forming brown to black colonies on the host (Ariyawansa et al. 2015a; Hongsanant et al. 2020b). With the introduction of a novel

species by Tennakoon et al. (2021) based on morphology and molecular analyses of LSU, SSU, ITS, and *tef1* sequence data, *Pseudopithomyces* currently comprises 15 species (Species Fungorum, April 2026). Three species (*P. atro-olivaceus*, *P. chartarum*, *P. maydicus*) have been reported as foliar saprobes on the salt marsh plant *Juncus roemerianus* from USA (Fell & Hunter 1979; Calabon et al. 2021b).

Type species: *Pseudopithomyces chartarum* (Berk. & M.A. Curtis) J.F. Li, Ariyawansa & K.D. Hyde 2015

Basionym: *Sporidesmium chartarum* Berk. & M.A. Curtis, in Berkeley 1874

Other accepted species: Species Fungorum (search *Pseudopithomyces*)



Note a Colonies on host. b–f Conidia g Upper and lower view of colony. Scale bars: a = 500 μ m, b = 50 μ m, c–f = 20 μ m, g = 3 cm.

Source Ariyawansa et al. (2015a)

Figure 4.24 *Pseudopithomyces maydicus*

Spegazzinia Sacc. 1879

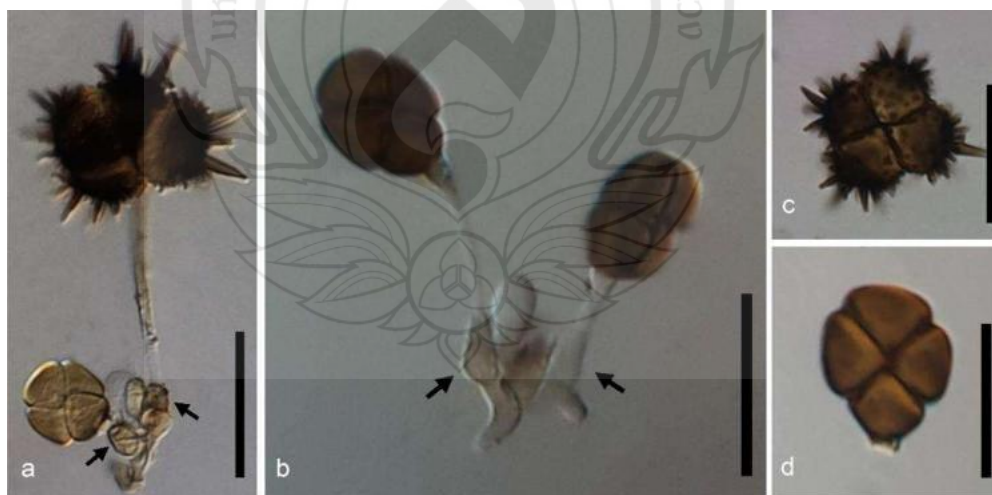
Classification: *Didymosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Spegazzinia was introduced by Saccardo (1880) to accommodate a single asexual species, *S. ornata*, collected from the leaves of *Andropogon gryllus* in Italy. The sexual morph remains undetermined. The asexual morph has micronematous conidiophores and basauxic, ampullate conidiogenous cells that develop two types of distinctive conidia. The conidia are holoblastic: α conidia have 4–8 stellate-shaped dark cells, while β conidia are pale brown and disc-shaped, with cross-septate or muriform

structures (Hongsanan et al. 2020a; Samarakoon et al. 2020). Hyde et al. (1998) considered *Spegazzinia* as a member of *Apiosporaceae* based on morphology. Later, Tanaka et al. (2015) transferred the genus to *Didymosphaeriaceae* based on phylogenetic analyses of SSU, LSU and *tef1* sequence data from *S. deightonii* and *S. tessarthra*. The genus comprises approximately 25 species, mostly saprobes on various plant parts (Hyde et al. 2024a; Pem et al. 2024). For example, *S. cryptica* was found on dead leaves of *Carex pumila* (Lu et al. 2024), *S. zhujiangyuanensis* on dead twigs (Zhang et al. 2024), *S. jinghaensis* on dead twigs of *Myristica yunnanensis* (Ren et al. 2022), *S. musae* on decaying leaf of *Musa* sp. (Samarakoon et al. 2020) and *S. camelliae* as endophyte from leaves of *Camellia sinensis* (Suwannarach et al. 2021). *Spegazzinia tessarthra* has been reported from living leaves of the salt marsh host *Juncus roemerianus* in the USA (Calabon et al. 2021b). Previously classified as *Sporidesmium tessarthrum*, *S. tessarthra* has also been reported on various hosts, such as endophytes in lichens collected from forests in India (Tripathi et al. 2014), as saprobes on leaves of *Brachypodium* sp. in Iran (Hashemlou et al. 2023), and on dead stem of *Acacia auriculiformis* in Thailand (Tennakoon et al. 2022).

Type species: *Spegazzinia ornata* Sacc. 1880

Other accepted species: Species Fungorum (search *Spegazzinia*)



Note a Conidiophores of α and β conidia with conidiophores mother cells (arrows). b Conidiophores of β conidia with conidiophore mother cells (arrows). c α conidia. d 4-celled β conidia. Scale bars: a, c = 20 μm , b, d = 15 μm

Source Hashemlou et al. (2023)

Figure 4.25 *Spegazzinia tessarthra*

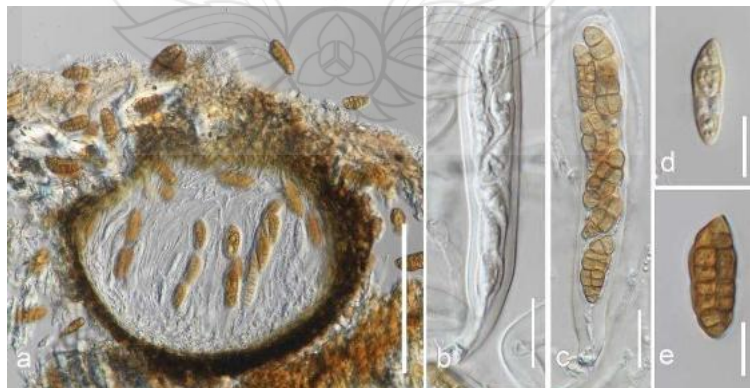
Tremateia Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1995

Classification: *Didymosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Tremateia was described by Kohlmeyer et al. (1995c) as a facultative marine genus isolated from senescent culms of *Juncus roemerianus* in USA. *Tremateia halophila*, the type species, was also reported on another salt marsh host, *Spartina maritima*, in Portugal (Barata 2002; Calabon et al. 2021b). There are ten species listed in Index Fungorum. *Tremateia phragmitis* was isolated on a salt marsh plant, *Phragmites australis* in the United Kingdom (Devadatha et al. 2023). Based on morphological characters, Kohlmeyer et al. (1995c) classified *Tremateia* in *Pleosporaceae*, suggesting its similarity to *Lewia* and *Diademosia*. Morphological and phylogenetic analysis of combined LSU, ITS, SSU, and *EFL-α* sequence data showed a distinct placement of *Tremateia* in *Montagnulaceae* (current name = *Didymosphaeriaceae*) (Ariyawansa et al. 2014), forming a sister clade to *Bimuria novae-zelandiae*. The sexual morph is characterized by immersed, globose to subglobose ascomata with a two-layered peridium and a dense hamathecium of cellular, septate pseudoparaphyses. Asci are clavate with short pedicels and a distinct ocular chamber. They contain 4–8 muriform ascospores with a large sheath. The asexual morph is phoma-like (Ariyawansa et al. 2014; Pem et al. 2019; Hongsanan et al. 2020b).

Type species: *Tremateia halophila* Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1995

Other accepted species: Species Fungorum (search *Tremateia*)



Note a Ascoma. b, c Asci. d, e Ascospores. Scale bar: a = 100 µm, b, c = 20 µm, d, e = 10 µm)

Figure 4.26 *Tremateia phragmitis*

Halobyssothecium Dayar., E.B.G. Jones & K.D. Hyde 2018

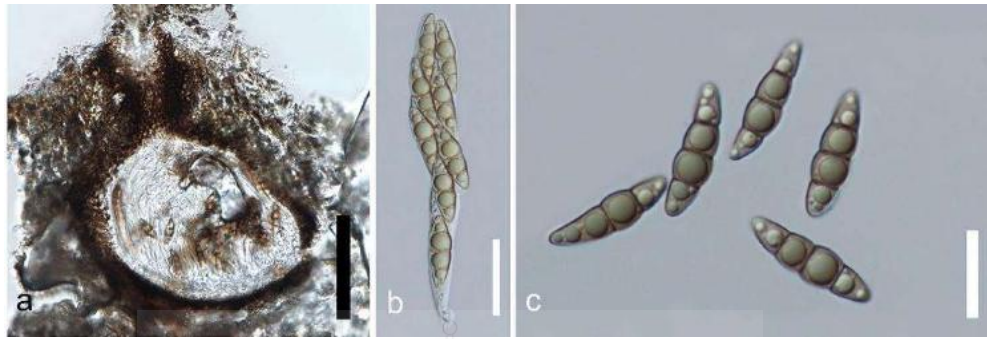
Classification: *Lentitheciaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Dayarathne et al. (2018) introduced *Halobyssothecium* to accommodate *H. obiones*, a frequently observed fungus on salt marsh halophytes, primarily recorded on *Spartina* species. *Halobyssothecium* is a saprobic genus found on salt marsh plants and submerged wood in aquatic habitats, with 13 accepted species (Calabon et al. 2021a; Hyde et al. 2024a). The second species, *H. estuariae*, was introduced by Devadatha et al. (2020) and was isolated from *Phragmites communis*. Calabon et al. (2021a) collected three new *Halobyssothecium* species and re-evaluated the taxonomy of *Halobyssothecium* and *Lentithecium*, incorporating morphological data and phylogenetic analyses based on LSU, SSU, ITS, and *tef1*- α sequence data. As a result, five species were transferred to *Halobyssothecium*. Yang et al. (2023) introduced a new species, and their phylogenetic analysis of LSU, ITS, SSU, and *tef1*- α showed that *Halobyssothecium* and *Lentithecium* formed a sister clade, except for *H. versicolor* and *L. aquaticum*. *Halobyssothecium phragmitis* and *H. versicolor* have also been reported from salt marsh plants, *Phragmites* sp. and *Atriplex portulacoides*, respectively (Calabon et al. 2021b). The sexual morph of *Halobyssothecium* is characterized by immersed, semi-immersed, or erumpent carbonaceous, dark brown to black ostiolate ascomata with cellular, branched pseudoparaphyses. Asci are fissitunicate, short-pedicellate, with or without an ocular chamber. Ascospores are 1–3-septate, versicolored with hyaline apical cells and brown central cells, slightly curved, and lack a mucilaginous sheath (Calabon et al. 2021a). The asexual morph is coelomycetous, forming pycnidial ostiolate conidiomata. Conidiophores are reduced to phialidic, hyaline, aseptate conidiogenous cells. Conidia are hyaline, unicellular, and straight to slightly curved. Chlamydospores are single or in chains, branched, with thickened septa (Calabon et al. 2021a).

Type species: *Halobyssothecium obiones* (M.E. Barr) Dayarathne, E.B.G. Jones & K.D. Hyde 2018

Basionym: *Pleospora obiones* P. Crouan & H. Crouan 1867

Other accepted species: Species Fungorum (search *Halobyssothecium*)



Note a Ascoma. b Ascus. c Ascospores. Scale bar: a = 100 µm, b = 30 µm, c = 20 µm.

Source Yang et al. (2023b)

Figure 4.27 *Halobyssothecium aquifusiforme*

Keissleriella Höhn. 1919

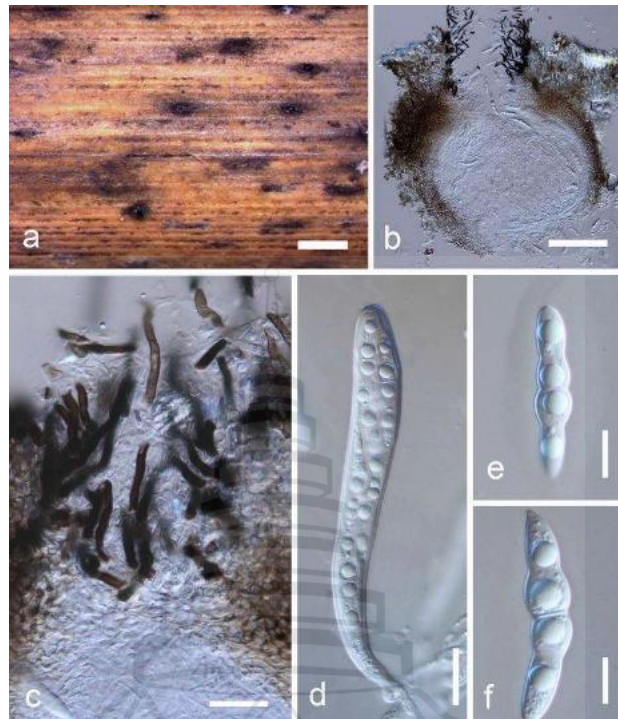
Classification: *Lentitheciaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Keissleriella is a saprobic genus established by Höhnelt (1919) and typified with *K. aesculin* and based on *Pyrenochaeta aesculi* Höhn. (1917). Phylogenetic analyses based on combined LSU, SSU, *rpb2*, and *tef1* sequence data have placed *Keissleriella* in the family *Lentitheciaceae* (Zhang et al. 2012). There are 45 accepted species listed in Species Fungorum (April 2026). *Keissleriella* species have been reported on various hosts, including halophytes (Calabon et al. 2021b). *Keissleriella linearis* and *K. phragmiticola* were reported on *Phragmites australis* (Van Ryckegem and Verbeken 2005a; Devadatha et al. 2020), *K. culmifida* on *Elymus pungens* (Apinis and Chesters 1964), and *K. rara* and *Keissleriella* sp. on *Juncus roemerianus* (Fell and Hunter 1979; Kohlmeyer et al. 1996b). The genus is characterized by papillate, ostiolate ascomata with short dark setae covering the necks. Asci are fissitunicate, cylindro-clavate, and contain 4-8 hyaline to pale brown septate ascospores (Barr 1990; Wanasinghe et al. 2018; Pem et al. 2019). The genus also has a *Dendrophoma* asexual morph (Bose 1961). *Keissleriella* is similar to *Trichometasphaeria* but differs in the nature of woody substrates and the morphology of the peridium and pseudoparaphyses (Barr 1990; Pem et al. 2019).

Type species: *Keissleriella aesculi* (Höhn.) Höhn. 1919

Basionym: *Pyrenochaeta aesculi* Höhn. 1917

Other accepted species: Species Fungorum (search *Keissleriella*)



Note a Ascomata on host. b Vertical section of ascoma. c Apical setae of ascoma. d Ascus. e, f Ascospores. Scale bars: a = 1 mm, b = 100 μ m, c, d = 20 μ m, e, f = 10 μ m

Source Wanasinghe et al. (2018)

Figure 4.28 *Keissleriella phragmiticola*

Lentithecium K.D. Hyde, J. Fourn. & Ying Zhang 2009

Classification: *Lentitheciaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Lentithecium, the type genus of *Lentitheciaceae*, was established by Zhang et al. (2009b) to accommodate a novel species, *L. aquaticum*, and three new combinations: *L. arundinaceum*, *L. lineare*, and *L. fluviatile*. The genus is saprobic and is typified by *L. fluviatile*, isolated from dead leaf sheaths of *Phragmites australis* in Belgium. *Lentithecium fluviatile* has also been recorded on *P. australis* from the Netherlands (Ryckegem and Verbeken 2005a, b; Calabon et al. 2021b). The genus is distributed in aquatic and terrestrial habitats, mostly from freshwater and marine environments on submerged wood and herbaceous plants (Ryckegem and Aptroot 2001; Zhang et al.

2009b; Tanaka et al. 2015; Hongsanant et al. 2020b; Lu et al. 2022). *Lentithecium* species have undergone various taxonomic changes. *Lentithecium arundinaceum* was transferred to *Setoseptoria* (Tanaka et al. 2015), and *L. lineare* moved between *Keissleriella* and *Lentithecium* before being subsequently transferred to *Keissleriella* (Tibell et al. 2020). Based on molecular analysis of LSU, SSU, ITS, and *tef1-α* sequence data, Calabon et al. (2021a) transferred five *Lentithecium* species to *Halobyssothecium* and accepted four species in *Lentithecium*. Additionally, *L. aquaticum* did not cluster within the *Lentithecium* clade, and fresh material is required for its precise classification (Calabon et al. 2021a). With the introduction of *L. yunnanense* from China, the genus comprises five species (Lu et al. 2022). Sexual morph of *Lentithecium* is characterized by immersed to semi-immersed ostiolate ascomata with a thin peridium and numerous pseudoparaphyses. Asci are 8-spored, short-pedicellate, containing hyaline or brown septate ascospores with or without a sheath (Calabon et al. 2021a; Lu et al. 2022).

Type species: *Lentithecium fluviatile* (Aptroot & Van Ryck.) K.D. Hyde, J. Fourn. & Ying Zhang 2009

Basionym: *Massarina fluviatilis* Aptroot & Van Ryck., 2001

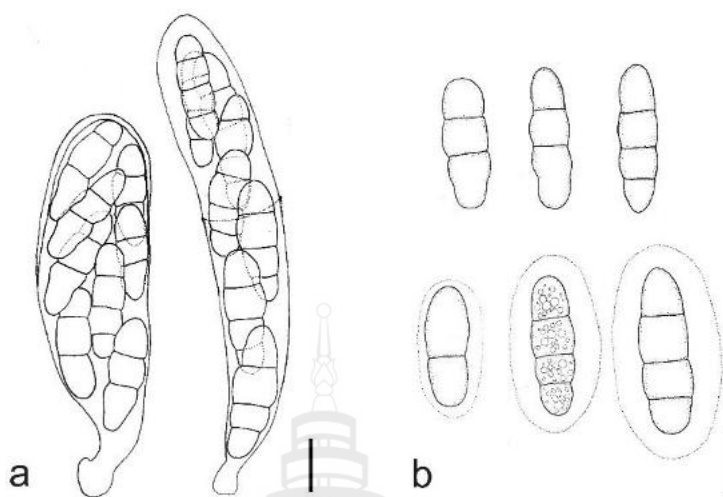
Other accepted species:

Lentithecium clioninum (Kaz. Tanaka, Sat. Hatak. & Y. Harada) Kaz. Tanaka & K. Hiray. 2015

Lentithecium lineare (E. Müll. ex Dennis) K.D. Hyde, J. Fourn. & Ying Zhang 2009

Lentithecium pseudoclioninum Kaz. Tanaka & K. Hiray. 2015

Lentithecium yunnanense W.H. Lu, Karun. & Tibpromma 2022



Note a Asci. b Ascospores. Scale bars: 10 μ m

Source Redrawn from Ryckegem and Aptroot (2001)

Figure 4.29 *Lentithecium fluviatile*

Setoseptoria Quaedvl., Verkley & Crous 2013

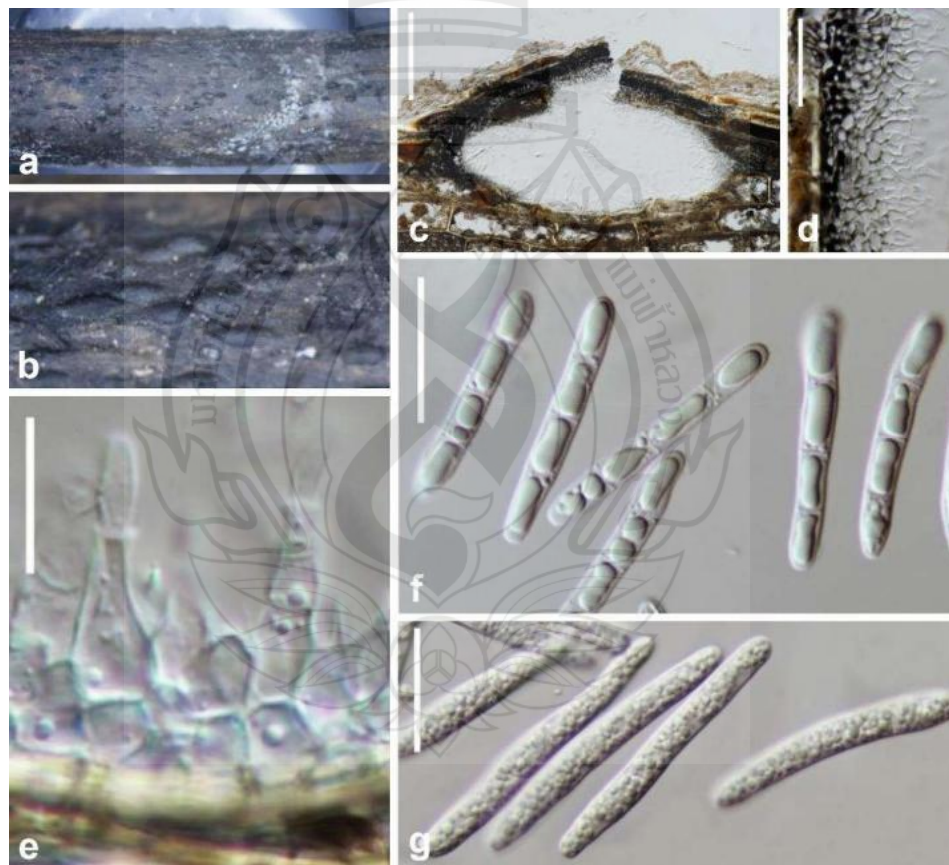
Classification: *Lentitheciaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Setoseptoria was introduced by Quaedvlieg et al. (2013) to accommodate *S. phragmitis* isolated from *Phragmites australis* in Hong Kong, China. There is another record of *S. phragmitis* on the halophyte *Phragmites* sp. from Sweden (Tibell et al. 2020; Calabon et al. 2021b). *Setoseptoria* comprises nine species, mostly saprobes collected from *Phragmites* and herbaceous plants (Yang et al. 2023b). *Setoseptoria arundinacea* was recorded on *Ph. australis*, *Elymus pungens*, and *Spartina* sp. from the Netherlands, UK, and USA, respectively (Johnson and Sparrow 1961; Apinis and Chesters 1964; Van Ryckegem and Verbeken 2005a, 2005b; Van Ryckegem et al. 2007; Calabon et al. 2021b). *Setoseptoria arundelensis* and *S. lulworthcoviensis* were isolated from *Ph. australis* in the UK (Wanasinghe et al. 2018). *Setoseptoria bambusae* and *S. suae* were recorded from *Phragmites* sp. in China (Shen et al. 2023). Sexual morph has immersed to superficial, uniloculate to multi-loculate, ostiolate ascomata with a multi-layered peridium. The hamathecium is composed of abundant septate pseudoparaphyses. Asci are fissitunicate, cylindrical to clavate, comprising 8-septate, guttulate, narrowly fusiform ascospores surrounded by a mucilaginous sheath

(Wanasinghe et al. 2018; Yang et al. 2023b). Asexual morph is coelomycetous, characterized by immersed, ostiolate, setose conidiomata. Conidiophores are reduced to hyaline conidiogenous cells with inconspicuous percurrent proliferations or periclinal thickening. Conidia are hyaline, cylindrical to subcylindrical, straight, or slightly curved, septate, and guttulate, mostly with one large central guttule (Quaedvlieg et al. 2013; Pem et al. 2019; Yang et al. 2023b). The sexual-aseexual connections of *Setoseptoria* species have not yet been confirmed (Wanasinghe et al. 2018). There is an updated phylogenetic tree (Shen et al. 2023) based on LSU, SSU, ITS, and *tefl* sequence data.

Type species: *Setoseptoria phragmitis* Quaedvl., Verkley & Crous 2013

Other accepted species: Species Fungorum (search *Setoseptoria*)



Note a, b Conidiomata on host. c Section of conidioma. d Section of peridium. e Conidiogenous cells. f, g Conidia. Scale bar: c = 100 μm ; d = 30 μm ; e–g = 10 μm

Source Shen et al. (2023)

Figure 4.30 *Setoseptoria suae*

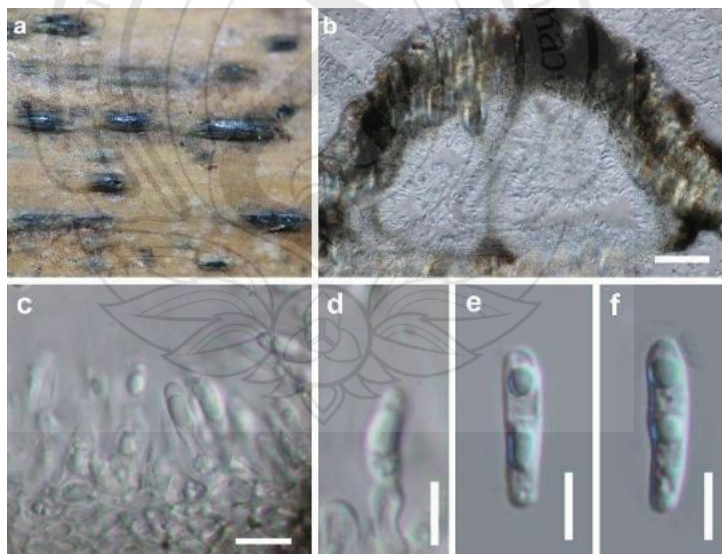
Towyspora Wanas., E.B.G. Jones & K.D. Hyde 2016

Classification: *Lentitheciaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Towyspora is a monotypic saprobe genus, introduced to accommodate *Towyspora aestuari* from estuarine habitat in the United Kingdom (Li et al. 2016). It was isolated from halophyte host *Phragmites communis*, established based on morphology and molecular analyses of catenated LSU, SSU, *tef* and ITS sequences. The sexual morph is unknown. The asexual morph has pycnidial, uni- to multi-loculate conidiomata with 2-3 layers of textura angularis and dark brown pigmented peridium. Conidiogenous cells are phialidic, hyaline and aseptate with ampulliform to cylindric-clavate shape. Conidia are hyaline, aseptate, guttulate, and oblong to cylindrical with round or obtuse ends (Li et al. 2016). Morphologically, *Towyspora* closely resembles *Setoseptoria* but it has smaller conidia. Phylogenetic analyses have confirmed the distinctiveness of *Towyspora* from *Setoseptoria* (Li et al. 2016).

Type species: *Towyspora aestuari* Wanasinghe, E.B.G. Jones & K.D. Hyde 2016

Other accepted species: None



Note a Conidiomata on host. b Vertical section through conidioma. c Conidia attached to conidiogenous cells. d–f Conidia. Scale bars: b = 50 μm , c = 20 μm , d–f = 5 μm

Source Li et al. (2016)

Figure 4.31 *Towyspora aestuari*

Leptosphaeria Ces. & De Not. 1863

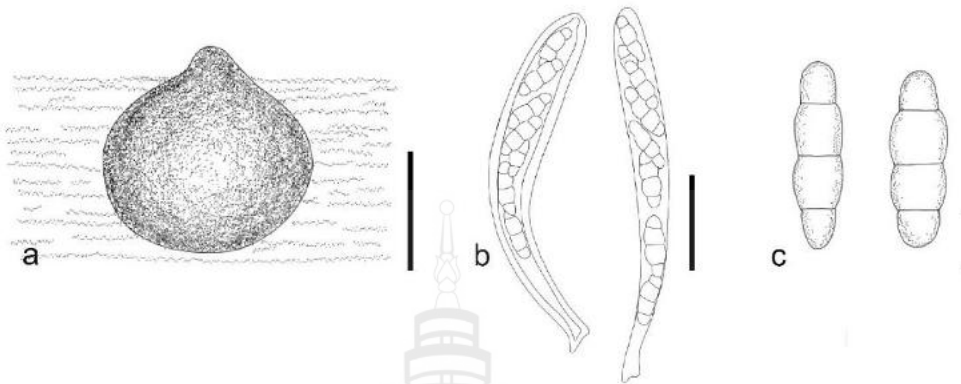
Classification: *Leptosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Leptosphaeria, the type genus of *Leptosphaeriaceae*, was introduced by Cesati and de Notaris (1863) and is typified by *L. doliolum*, which formerly belonged to *Sphaeria* (Person 1800). *Leptosphaeria* species are saprobes or phytopathogens on herbaceous or woody plants such as members of the *Asteraceae* and *Mercurialis perennis* (Ariyawansa et al. 2015b). Recently, saprobic species such as *L. chatkalica*, *L. regiae*, and *L. urticae* have been introduced from Uzbekistan, Turkey, and the UK, respectively (Phookamsak et al. 2019; Pem et al. 2020; Lestari et al. 2021). Several species have also been reported on halophytes, including *L. albopunctata*, *L. australiensis* (based on *Metasphaeria australiensis* Cribb and Cribb 1955), *L. culmifraga*, *L. littoralis*, *L. marina*, *L. pelagica*, *L. peruviana*, and *L. suaedae*, mostly as saprobes on *Spartina* species (Calabon et al. 2021b). The sexual morph of *Leptosphaeria* has erumpent to superficial, ostiolate ascomata with a shiny papilla. Asci are fissitunicate and cylindrical, containing eight reddish to yellowish-brown, 3-septate, fusoid ascospores (Ariyawansa et al. 2015b). The asexual morph is coelomycetous, with depressed globose conidiomata and ellipsoidal to subcylindrical conidia (Hyde et al. 2011, Ariyawansa et al. 2015b). *Leptosphaeria* was considered one of the genera with *Phoma* asexual morphs. *Leptosphaeria maculans* is an important pathogen and the causal agent of blackleg disease in *Brassica* crops, with a *Phoma lingam* asexual morph (Sivasithamparan et al. 2005; Hyde et al. 2024a). Based on phylogenetic analyses, Reddy et al. (1998) showed that *Phoma lingam* is related to *Plenodomus*. Subsequently, De Gruyter et al. (2013) resurrected the genus *Plenodomus* to accommodate the phoma-like taxa classified in *Leptosphaeriaceae* and transferred *Leptosphaeria maculans* to *Plenodomus*. Hyde et al. (2024a) proposed using *Leptosphaeria maculans* over *Plenodomus maculans*, as the former is the widely used name, for the stability of nomenclature. Ariyawansa et al. (2015b) studied *Leptosphaeriaceae* based on morphological and phylogenetic data of ITS, SSU, LSU, *rpb2*, *tef1*, and *act* sequences and introduced three novel genera related to *Leptosphaeria*: *Alloleptosphaeria*, *Neoleptosphaeria*, and *Pseudoleptosphaeria*.

Type species: *Leptosphaeria doliolum* (Pers.) Ces. & De Not. 1863

Basionym: *Sphaeria doliolum* Pers. 1800

Other accepted species: Species Fungorum (search *Leptosphaeria*)



Note a Ascoma. b Asci. c Ascospores. Scale bar: a = 150 µm, b = 50 µm, c = 10 µm

Source Redrawn from Jones (1962b)

Figure 4.32 *Leptosphaeria pelagica*

Arundellina Wanas., E.B.G. Jones & K.D. Hyde 2016

Classification: *Lindgomycetaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Arundellina is a facultative marine genus isolated from decaying stem of *Typha* sp. in the United Kingdom (Hyde et al. 2016; Calabon et al. 2021b). The genus is monotypic with *A. typhae* as the type species (Jones et al. 2019, Hongsan et al. 2020a). Hyde et al. (2016) placed *Arundellina* in *Lindgomycetaceae* based on phylogenetic analysis of combined LSU and SSU genes. The sexual morph has immersed, black, ostiolate ascomata with reddish to dark brown outer layers in the peridium. Asci are 8-spored, fissitunicate, bitinicate, and become thicker around the ocular chamber at the apex. Ascospores are fusiform, with 3–4 transverse septa and cone-shaped ends. Immature ascospores are hyaline, and mature ascospores become golden-pale brown (Hyde et al. 2016; Pem et al. 2019).

Type species: *Arundellina typhae* Wanasinghe, E.B.G. Jones & K.D. Hyde

Other accepted species: None.



Note a Ascomata on host. b Section of ascoma. c Pseudoparaphyses. d Ascus. e, f Ascospores. Scale bars: b = 50 μm , c, e, f = 10 μm , d = 20 μm

Source Hyde et al. (2016)

Figure 4.33 *Arundellina typhae*

Sigarispora Thambug. & K.D. Hyde 2015

Classification: *Lophiostomataceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Liu et al. (2015) introduced *Lophiostoma ravennicum* in *Lophiostomataceae* based on phylogenetic analysis. However, its morphology differs from *Lophiostoma sensu stricto* in having cigar-shaped, 6-septate, brown ascospores with a mucilaginous sheath. Thambugala et al. (2015) studied *Lophiostomataceae* and introduced *Sigarispora* based on morphology and phylogenetic analyses of combined LSU, SSU, ITS, and *tefl* α sequence data. They placed four lophiostoma-like species in the genus: *S. arundinis*, *S. caudata*, *S. caulium*, and the type species *S. ravennica* (Thambugala et al. 2015). With the introduction of *S. rosicola*, the genus comprises five species, which are saprobic on grasses and herbaceous stems (Wanasinghe et al. 2018; Pem et al. 2024). *Sigarispora arundinis* was reported on the salt marsh host *Phragmites australis* from the Netherlands (Calabon et al. 2021b). Morphologically, the sexual morph has immersed, ostiolate ascomata with erumpent papillae. Asci are cylindric-clavate,

fissitunicate, with an ocular chamber and long pedicel. Ascospores are ellipsoidal-fusiform or cigar-shaped, yellowish brown to dark brown, with 2–4 vertical septa and 5–6 transversely septate or muriform. Ascospores may be surrounded by a mucilaginous sheath and may also have terminal appendages. The asexual morph is undetermined (Thambugala et al. 2015).

Type species: *Sigarispora ravennica* (Tibpromma, Camporesi & K.D. Hyde) Thambugala & K.D. Hyde 2015

Basionym: *Lophiostoma ravennicum* Tibpromma, Camporesi & K.D. Hyde 2015

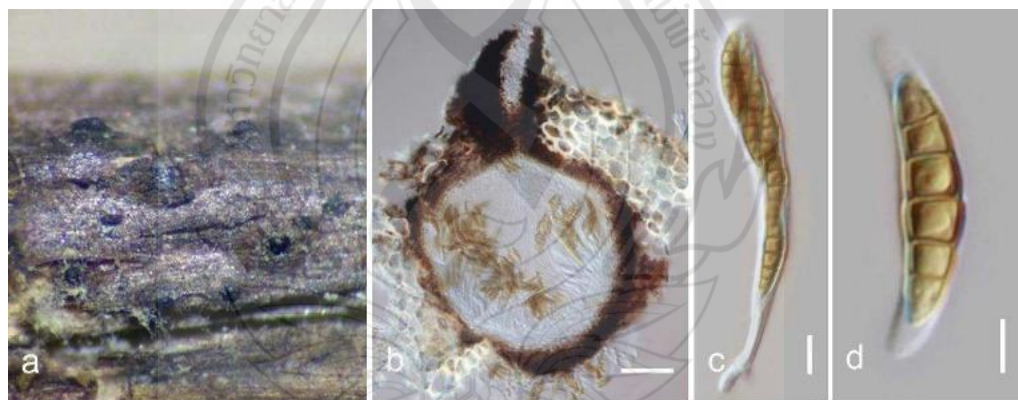
Other accepted species:

Sigarispora arundinis (Pers.) Thambug., Qing Tian, Kaz. Tanaka & K.D. Hyde 2015

Sigarispora caudata (Fabre) Thambug., Qing Tian, Kaz. Tanaka & K.D. Hyde 2015

Sigarispora caulium (Fr.) Thambug., Wanas., Kaz. Tanaka & K.D. Hyde 2015

Sigarispora rosicola Wanas., Bulgakov, E.B.G. Jones & K.D. Hyde 2018



Note a Ascomata on host. b. Section through an ascoma. c Ascus. d Ascospore. Scale bars: b=50 μ m, c=10 μ m, d=5 μ m

Source Thambugala et al. (2015)

Figure 4.34 *Sigarispora caulium*

Massarina Sacc. 1883

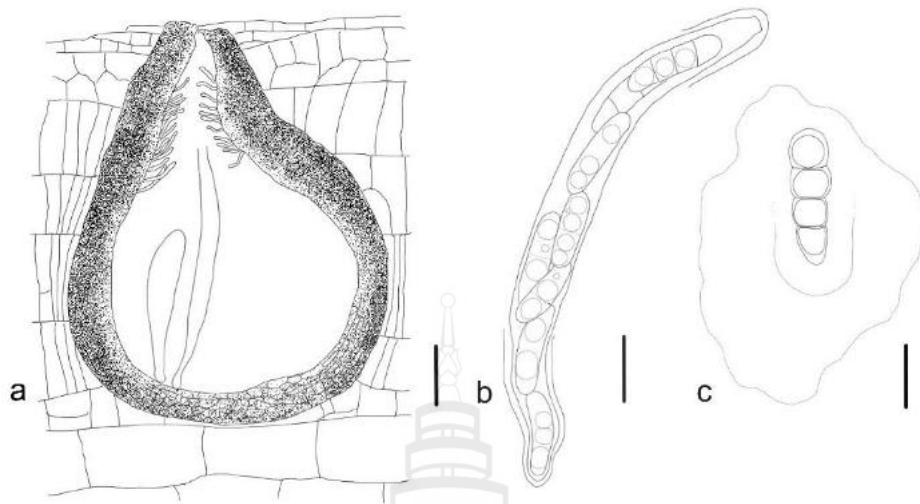
Classification: *Massarinaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Saccardo (1883) established *Massarina* to encompass a group of species formerly belonging to *Massaria*, including *Massarina eburnea*, without designating a type species. *Massarina eburnea* was designated as the lectotype of *Massarina* by Clements and Shear (1931) and the genus was placed in *Massarinaceae* by Munk (1956). Hyde (1995) provided a detailed description of *M. eburnea* and listed 160 epithets. Hyde and Aptroot (1998) later accepted only 43 species. *Massarina* has undergone various taxonomic changes, mostly based on morphological characteristics (Bose 1961, Pem et al. 2024). There are 94 accepted species listed in Species Fungorum (accessed April 2026), but only five of them have been confirmed with molecular data. Tibpromma et al. (2018) introduced a new endophytic species, *Massarina pandanicola*, based on morphology and phylogenetic analyses of ITS, *tef1*, SSU, LSU, and *rpb2* sequence data, confirming the placement of the genus in *Massarinaceae*. The species of *Massarina* are mostly saprobic (Pem et al. 2024). *Massarina beaurivagea*, *M. cystophorae*, *M. lacertensis*, *M. mauritiana*, *M. phragmiticola*, and *M. ricifera* were listed as marine fungi (Jones et al. 2019). *Massarina phragmiticola* has been collected from the salt marsh host *Phragmites australis*, while *Massarina carolinensis*, *Massarina igniaria*, and *Massarina ricifera* are reported on *Juncus roemerianus* (Calabon et al. 2021b). Tan and Shivas (2022) introduced *Massarina tangneyae* from necrotic leaf spots of *Pandanus tectorius* in a coastal area of Australia. Several chemical compounds have been reported from *Massarina* species (Pem et al. 2024). Abdel-Wahab et al. (2007) described two new secondary metabolites, spiromassaritone and massariphenone, from a marine-derived fungus *Massarina* sp. (strain CNT-019). The sexual morph of *Massarina* has clypeate, immersed ascomata. Asci are 8-spored, cylindric-clavate, fissitunicate with an ocular chamber. Ascospores are 1–multiseptate, hyaline, and most are surrounded by a mucilaginous sheath (Hyde 1995). The asexual morph is ceratophoma-like, with enteroblastic conidiogenous cells and hyaline, aseptate conidia (Tibpromma et al. 2018).

Type species: *Massarina eburnea* (Tul. & C. Tul.) Sacc. 1883

Basionym: *Massaria eburnea* Tul. & C. Tul. 1863

Other accepted species: Species Fungorum (Search *Massarina*)



Note a Ascoma. b Ascus. c Ascospore. Scale bar: a, b = 20 µm, c = 10 µm

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer 1995b)

Figure 4.35 *Massarina ricifera*

Stagonospora (Sacc.) Sacc. 1884

Basionym: *Hendersonia* subgen. *Stagonospora* Sacc.

Classification: *Massarinaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

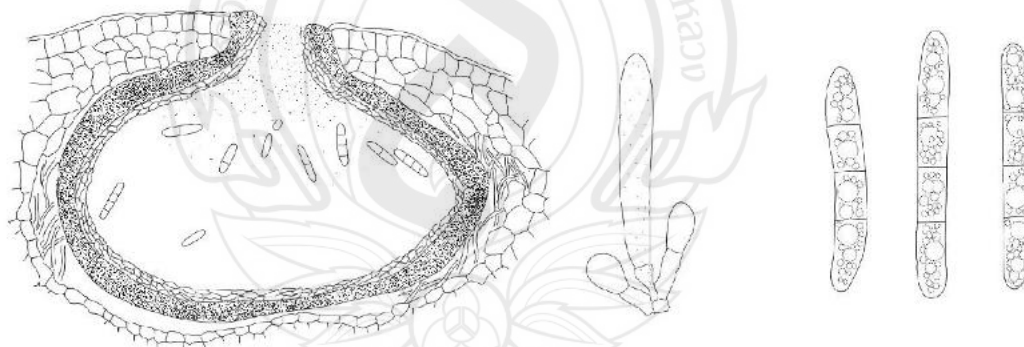
Saccardo (1884b) introduced *Stagonospora*, listing 55 species with monocotyledonous and dicotyledonous plant hosts. *Stagonospora* is primarily described based on its coelomycetous asexual morph. Pycnidial, globose, ostiolate conidiomata develop immersed. Conidiophores are reduced to doliiform conidiogenous cells with several percurrent proliferations at the apex. Conidia are cylindrical or fusoid-ellipsoidal, hyaline, and uni- to multiseptated (Quaedvlieg et al. 2013). The sexual morph of *Stagonospora* is didymella-like, with *S. perfecta* being the first species in the genus confirmed to have a sexual state. It forms globose, brown ascomata on sterile *Carex* leaves on SNA. Asci are bitunicate containing eight hyaline, smooth ascospores with guttules in each cell (Quaedvlieg et al. 2013). *Stagonospora* was previously distinguished from *Septoria* by its morphology and percurrent proliferation of conidiogenous cells, with *Septoria* showing sympodial proliferation (Quaedvlieg et al. 2013). Quaedvlieg et al. (2013) designated an epitype for the type species, *S. paludosa*,

and demonstrated the separation of these two genera based on a multigene phylogeny using *rpb2* and LSU sequences. There are more than 50 species in *Stagonospora* (Hyde et al. 2024a). *Stagonospora* species are saprobic or pathogenic on various plants, mostly grasses and grass-like hosts (Quaedvlieg et al. 2013; Thambugala et al. 2017; Bhagya et al. 2024). Jones et al. (2019) listed *S. abundata*, *S. cylindrica*, *S. elegans*, and *S. haliclysta* as marine species. Calabon et al. (2021b) recorded *S. abundata*, *S. cylindrica*, *S. elegans*, *S. epicalamias*, *S. haliclysta*, *S. suaedae*, and several unidentified species as salt marsh fungi. Recently, Bhagya et al. (2024) introduced a new species, *Stagonospora samroiensis*, from coastal wetlands on *Typha* species, based on morphology and a phylogenetic analysis of LSU, ITS, SSU, and *tef1-α* sequence datasets. *Stagonospora* can also produce various chemical compounds, such as sorbicillinoid pigments with anti-inflammatory activity, isolated from the sponge-derived fungus *Stagonospora* sp. SYSU-MS7888 (Chen s. et al. 2022; Pem et al. 2024).

Type species: *Stagonospora paludosa* (Sacc. & Speg.) Sacc. 1884

Basionym: *Hendersonia paludosa* Sacc. & Speg. 1878

Other accepted species: Species Fungorum (Search *Stagonospora*)



Note a Conidioma (150 ×), conidiogenous cells and conidia (555 ×).

Source Redrawn from Cunnell (1957)

Figure 4.36 *Stagonospora cylindrica*

Bicrouania Kohlm. & Volkm.-Kohlm 1990

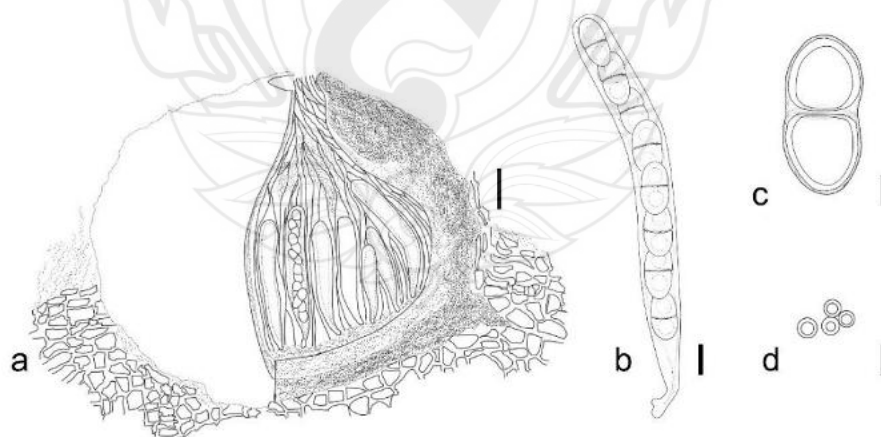
Classification: *Melanommataceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Bicrouania is an obligate marine saprobe classified under the family *Melanommataceae* due to its trabeculate pseudoparaphyses and melanommataceous features (Kohlmeyer and Volkmann-Kohlmeyer 1990; Hongsanan et al. 2020a). In a revision of marine species belonging to *Didymosphaeria*, Kohlmeyer and Volkmann-Kohlmeyer (1990) introduced *Bicrouania* to accommodate *Sphaeria maritima*, which was isolated from *Atriplex portulacoides*, probably in France. The species was also reported on the same host in India (Borse et al. 2012; Calabon et al. 2021b). There is no molecular data available for this genus, and sequence data is essential for confirming its classification (Jones et al. 2009; Hyde et al. 2013; Wijayawardene et al. 2014b; 2017a; Hongsanan et al. 2020a). The sexual morph displays dark, ostiolate, rough ascomata, mostly superficial and erumpent on the host substrate. The outer layers of the peridium are dark brown, becoming hyaline toward the inside. The hamathecium consists of trabeculate pseudoparaphyses. Asci are cylindrical, short-pedicellate, fissitunicate, bitunicate, without ocular chamber or apical apparatus. Asci contain eight ellipsoidal ascospores that are one septate and reddish-brown.

Type species: *Bicrouania maritima* (P. Crouan & H. Crouan) Kohlm. & Volkm.-Kohlm. 1990

Basionym: *Sphaeria maritima* P. Crouan & H. Crouan 1867

Other accepted species: None.



Note a Ascoma. b Ascus. c Ascospores. d Phycobiont. Scale bars: a = 50 μ m, b = 15 μ m, c, d = 5 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (1990)

Figure 4.37 *Bicrouania maritima*

***Helicascus* Kohlm. 1969**

Classification: *Morosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Kohlmeyer (1969) introduced *Helicascus* as a saprobic marine genus from decaying *Rhizophora mangle* in the Hawaiian Islands. The genus comprises four species commonly reported in tropical mangrove areas (Preedanon et al. 2017; Jones et al. 2019; www.marinefungi.org), while seven have been referred to *Neohelicascus*, and *Helicascus thalassioideus* to *Aquihelicascus*. *Helicascus* is typified by *H. kanaloanus*, which has also been reported from a salt marsh host, *Spartina* species (Kohlmeyer and Volkmann-Kohlmeyer 2002; Calabon et al. 2021b). Based on the phylogeny of LSU, SSU, *tef1*, and *rpb2*, the genus was classified in *Morosphaeriaceae* (Suetrong et al. 2009), a classification confirmed by Hyde et al. (2013) and Jones et al. (2015). A key to marine *Helicascus* species is provided on the Marine Fungi website (www.marinefungi.org). Sexual morph is characterized by immersed carbonaceous ascostromata with 3-4(-5) loculi. Ascomata are ostiolate with a neck, forming a depressed ampulliform shape arranged under a black pseudoclypeus. The hamathecium is composed of numerous hyphae-like filaments. Asci are 8-spored and fissitunicate, forming in a subcylindrical to oblong clavate shape with a thick wall and multilayered apex. Ascospores are obovoid, brown, uniseptate, and constricted at the septum with a deliquescing sheath (Hyde 1991; Pem et al. 2019).

Type species: *Helicascus kanaloanus* Kohlm. 1969

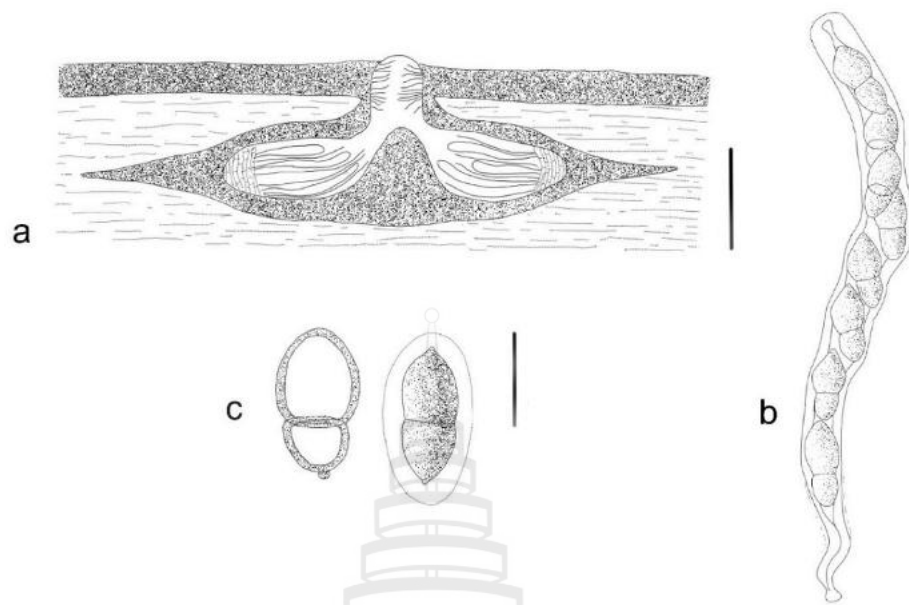
Other accepted species:

Helicascus alatus M. Zeng, S.K. Huang, Q. Zhao & K.D. Hyde 2018

Helicascus mangrovei Preedanon, Suetrong & Sakay. 2017

Helicascus nypae K.D. Hyde 1991

Helicascus satunensis Preedanon, Suetrong & Sakay. 2024



Note a Section through stroma with pseudoclypeus, neck, and two loculi with asci. b Ascus. c Ascospores. Scale bars: a = 300 μm , b = 40 μm , c = 25 μm

Source Redrawn from Kohlmeyer (1969)

Figure 4.38 *Helicascus kanaloanus*

Neocamarosporium Crous & M.J. Wingf. 2014

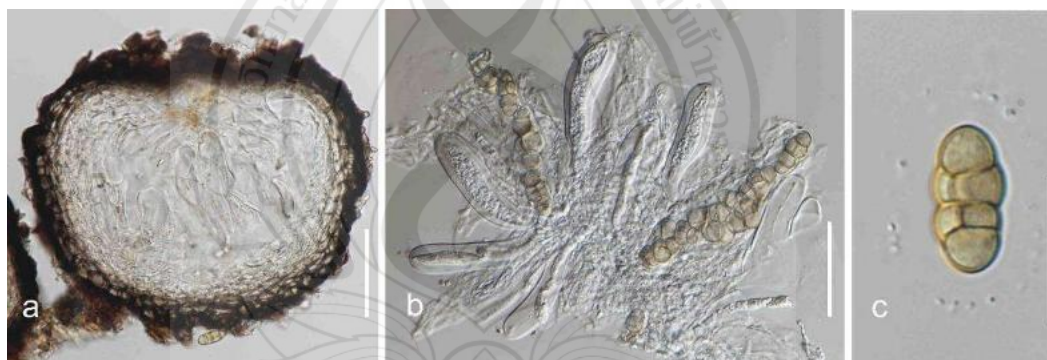
Classification: *Neocamarosporiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Neocamarosporium is a halotolerant genus introduced by Crous et al. (2014b), reported on various substrates such as wood, soils, water, and seagrasses (Calabon et al. 2021b, Dayarathne et al. 2020a, Gonçalves et al. 2019, Yin et al. 2020, Papizadeh et al. 2017). The genus includes 26 species (Species Fungorum, accessed April 2026), mostly isolated as endophytes, saprophytes, and pathogens in salt marshes and mangroves (Prematunga et al. 2023; www.marinefungi.org). *Neocamarosporium salicorniicola* was introduced on dead *Salicornia* sp. in Thailand (Wanasinghe et al. 2017), and *N. artemisiae* and *N. maritimae* were described as saprobes on *Artemisia maritima* in Sweden (Dayarathne et al. 2020a). *Neocamarosporium phragmitis* was isolated on decaying *Phragmites australis* in the UK in its sexual morph (Hyde et al. 2018), and *N. obiones* was found on *Atriplex portulacoides* (Kohlmeyer and Kohlmeyer 1979). *Neocamarosporium calvescens* was reported from marine drift wood in Sweden

(Tibell et al. 2019, 2020). Prematunga et al. (2023) provided an updated phylogenetic tree of *Neocamarosporium* based on ITS, LSU, SSU, and *tef1* gene sequence data and introduced *N. aquaticum* on decaying halophyte (probably *Halimione portulacoides*). Sexual morph is characterized by semi-immersed papillate ascomata with a short ostiole, 4–5 layered peridium, and filamentous, branched pseudoparaphyses. Asci are 8-spored, fissitunicate, cylindrical-clavate to cylindrical with an ocular chamber. Ascospores are hyaline to pale brown and muriform with a wider upper part (Hyde et al. 2018, www.marinefungi.org). The genus is mostly described with a coelomycetous asexual morph with globose papillate conidiomata with a 3–6 layered peridium. Conidiophores are reduced to ampulliform conidiogenous cells, proliferating several times percurrently near the apex. Conidia are initially hyaline and aseptate, becoming muriform and golden brown with maturity. Morphologically, it is similar to *Camarosporium* but distinct based on molecular data (Crous et al. 2014b; Pem et al. 2019).

Type species: *Neocamarosporium goegapense* Crous & M.J. Wingf. 2014

Other accepted species: Species Fungorum (search *Neocamarosporium*)



Note a Ascoma. b Asci. c Ascospore. Scale bars: a, b = 50 μ m, c = 20 μ m

Figure 4.39 *Neocamarosporium* sp.

***Periconia* Tode 1791**

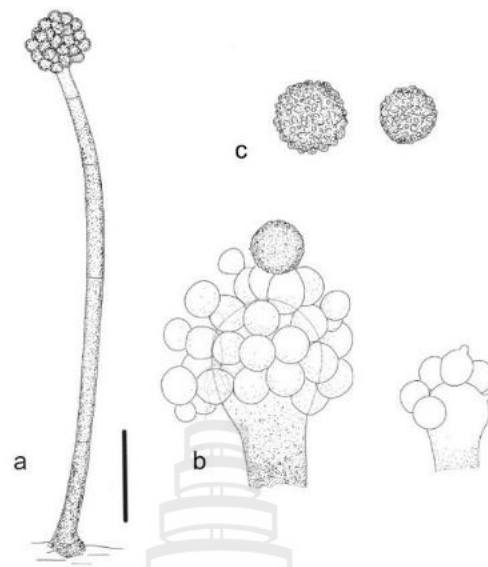
Classification: *Periconiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Tode (1791) introduced *Periconia* based on a collection of *Periconia lichenoides* found on decaying stems of various plants on the ground in Germany. *Periconia* is primarily known for its asexual morph, which develops macronematous,

mononematous, branched or unbranched conidiophores. Conidiogenous cells are blastic, and conidia are verruculose to echinulate, unicellular, brown, and typically catenate in a spherical head (Ellis 1971; Tanaka et al. 2015). The sexual morph is known for a few species and has been linked to *Didymosphaeria*, *Massarina*, or *Okeanomyces* (Booth 1968; Kohlmeyer 1969; Pang et al. 2004; Tanaka et al. 2015; Hyde et al. 2020b). Based on Tanaka et al. (2015), the sexual morph features globose, ostiolate ascomata, fissitunicate asci, and hyaline, fusiform, 1-septate ascospores surrounded by a sheath. Tanaka et al. (2015) suggested that the genus is polyphyletic based on SSU, LSU and *tefl* phylogenetic analyses. *Periconia* is the type genus of *Periconiaceae* and comprises about 170 species, which live as saprobes, endophytes, or pathogens on various hosts and diverse habitats (Hyde et al. 2024a, Pem et al. 2024, Zhang et al. 2024, Kim et al. 2025). Kohlmeyer (1969) observed *P. prolifica* as the asexual morph of *Okeanomyces cucullatus* in culture, a relationship later confirmed by molecular data (Pang et al. 2004). Kohlmeyer and Kohlmeyer (1979) listed *P. abyssa* recovered from the deep sea. Jones et al. (2019) listed *P. byssoides*, *P. cookei*, *P. digitata*, *P. echinochloae*, and *P. minutissima* as marine species. Hyde et al. (2020b) discussed *Periconia* species from marine and freshwater habitats. Another marine species, *P. salina*, was described by Dayarathne et al. (2020a) from buried bark in a sand dune. Calabon et al. (2021b) listed *P. cookei*, *P. digitata*, *P. echinochloae*, *P. minutissima*, and *Periconia* sp. as salt marsh fungi, mostly recorded on *Juncus roemerianus* and *Phragmites australis*. Salimi et al. (2023) isolated endophytic *P. igniaria* from root, stem and leaves of *Ph. australis*, from a salty lake in Iran. Kim et al. (2025) identified the endophytic *P. chimonanthi* from marine macroalgae in Korea. *Periconia* species produce a wide range of natural compounds with medicinal properties (Azhari and Supratman 2021). Endophytic *P. macrospinosa*, isolated from plants in a salty lake, has been shown to enhance the growth of tomato, cucumber, and barley under drought and salinity stress (Moghaddam et al. 2021, 2022).

Type species: *Periconia lichenoides* Tode. 1791

Other accepted species: Species Fungorum (search *Periconia*)



Note a Conidiophore. b Development of conidia. c Conidia. Scale bars: a = 100 μm , b, c (500 $\times$)

Source Redrawn from Mason and Ellis (1953)

Figure 4.40 *Periconia cookei*

Amarenographium O.E. Erikss. 1982

Classification: *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Eriksson (1982) introduced *Amarenographium* to accommodate *Camarosporium metableticum* based on morphological data (Hodhod et al. 2012). The genus was typified with *A. metableticum* as the asexual morph of *Amarenomyces*. *Amarenographium* was excluded from *Phaeosphaeriaceae* (Hodhod et al. 2012; Hyde et al. 2013) based on molecular evidence, while *Amarenomyces* was transferred to *Phaeosphaeriaceae* (Zhang et al. 2009, 2012). Although *A. metableticum* could not be included in the phylogenetic analysis due to a lack of molecular data, Phookamsak et al. (2014) accepted *Amarenographium* in *Phaeosphaeriaceae*. The sexual morph is characterized by ostiolate, papillate ascomata with dark brown peridium cells. Pseudoparaphyses are abundant, filiform, and septate. Asci are fissitunicate and cylindrical, with a minute knob-like pedicel and a distinct ocular chamber. Asci contain 1–3 series of fusiform, 6-septate, yellowish-brown ascospores (Eriksson 1981; Phookamsak et al. 2014). The asexual morph has papillate conidiomata with a brown

peridium. Conidiophores, if present, are septate and branched but generally reduced to ampulliform, phialidic conidiogenous cells. Macroconidia are blastic-phialidic, brown, muriform, bearing appendage. Microconidia are blastic-phialidic and hyaline (Eriksson 1982, Phookamsak et al. 2014). The sexual morph was isolated from the halophyte host, *Ammophila arenaria* (Eriksson 1981; Jones et al. 2015; Calabon et al. 2021b). The asexual species *A. ammophilae* and *A. ammophilicola* were also isolated from *Ammophila arenaria* in Italy (Wijayawardene et al. 2016) and the United Kingdom (Dayarathne et al. 2020a), respectively. *Amarenographium solium* was also isolated from marine habitats on mangroves (Hodhod et al. 2012).

Type species: *Amarenographium metableticum* (Trail) O.E. Erikss. 1982

Basionym: *Camarosporium metableticum* Trail 1886

Other accepted species:

Amarenographium ammophilae Wanas., Camporesi, Wijayaw. & K.D. Hyde 2016

Amarenographium metableticum (Trail) O.E. Erikss. 1982

Amarenographium sinense Joanne E. Taylor, K.D. Hyde & E.B.G. Jones 2003

Amarenographium solium Abdel-Wahab, Hodhod, Bahkali & K.D. Hyde 2012



Note a Conidiomata on host. b Vertical section through a conidioma. c conidium attached to conidiogenous cell. d conidium. Scale bar: b = 50 µm, c, d = 10 µm

Source Wijayawardene et al. (2016)

Figure 4.41 *Amarenographium ammophilae*

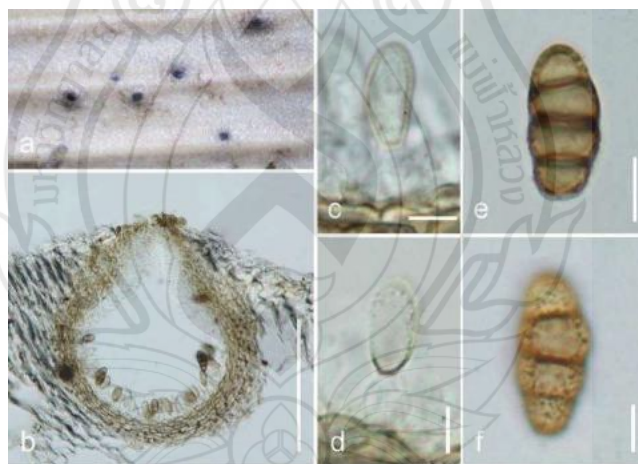
Camarosporioides W.J. Li & K.D. Hyde 2016

Classification: *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Hyde et al. (2016) introduced *Camarosporioides* based on a fungus isolated from dead stem of halophyte macrophyte *Phragmites australis* from Germany. *Camarosporioides* shares similar morphology with *Camarosporium* and together form a distinct clade in phylogenetic analyses (Hyde et al. 2016). Sexual morph of *Camarosporioides* is unknown. Asexual morph is coelomycetous with immersed, ostiolate, obpyriform conidiomata. Peridium is thick and brown with textura angularis. Conidiophores are reduced to hyaline to pale brown conidiogenous cells that are long lageniform and inflated at the base. Conidia are brownish rough cells with primary transverse septa, with a longitudinal septum (Hyde et al. 2016). Based on molecular analyses of combined dataset of ITS, LSU and SSU partial sequences, the genus was placed in *Phaeosphaeriaceae* (Hyde et al. 2016), which was confirmed by Hongsanan et al. (2020a).

Type species: *Camarosporioides phragmitis* W.J. Li & K.D. Hyde 2016

Other accepted species: *Camarosporioides kunmingensis* Y. Gao, H. Gui & K.D. Hyde 2025



Note a Conidiomata on host. b Vertical section of conidioma. c, d conidiogenous cells and developing conidia. e, f conidia. Scale bar: b = 100 μ m, c–f = 5 μ m

Source Hyde et al. (2016)

Figure 4.42 *Camarosporioides phragmitis*

Loratospora Kohlm. & Volkm.-Kohlm. 1993

Classification: *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

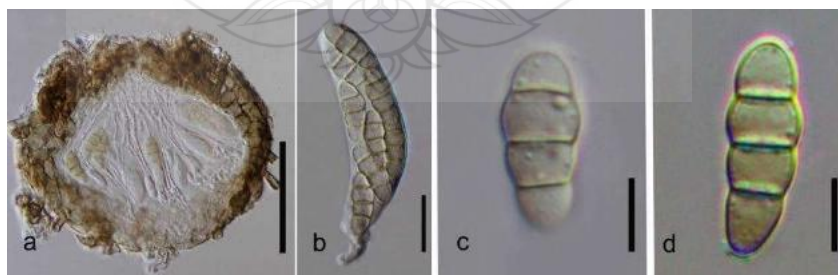
Loratospora was first described based on the isolation of *L. aestuarii* from dead culms of black needlerush (*Juncus roemerianus*) in USA (Kohlmeyer and Volkmann-Kohlmeyer 1993). There is another report of the type species on an unidentified saltmarsh host in USA (Walker 2012; Calabon et al. 2021b). *Loratospora* comprises two more species introduced on *Juncaceae* from Italy (Ariyawansa et al. 2015c; Hyde et al. 2020a), and sequence data are available for all three species (Pem et al. 2019, Hongsanan et al. 2020a). The genus was classified in *Planistromellaceae* based on morphology of the ostiole (Barr 1996; Jones et al. 2009; Monkai et al. 2013). By combining phylogenetic analyses with morphological data, the genus was accepted in *Planistromellaceae* (Schoch et al. 2009; Zhang et al. 2012; Hyde et al. 2013). Phookamsak et al. 2014 confirmed its classification in *Planistromellaceae* by a re-examination of the type material and combined ITS, LSU, SSU, and *rpb2* sequence analysis. However, it was later placed in *Phaeosphaeriaceae* (Wanasinghe and Maharachchikumbura 2023).

The sexual morph is characterized by immersed to erumpent ascomata with periphyses ostiole. The peridium is composed of several layers of pseudoparenchymatous cells. Asci are fissitunicate, ovoid to ampulliform with an indistinct ocular chamber. They contain 8 cylindrical or fusiform and 3-septate ascospores, which are hyaline when immature and become pale brown at maturity (Pem et al. 2019; Phookamsak et al. 2014).

Type species: *Loratospora aestuarii* Kohlm. & Volkm.-Kohlm. 1993

Other accepted species:

Loratospora arezzoensis Bundhun, Wanas., R. Jeewon & K.D. Hyde 2020



Note a Section through ascoma. b Ascus. c, d Ascospores. Scale bars: a = 50 μ m, b = 30 μ m, c, d = 5 μ m

Source Ariyawansa et al. (2015a)

Figure 4.43 *Loratospora luzulae*

Phaeosphaeria I. Miyake 1909

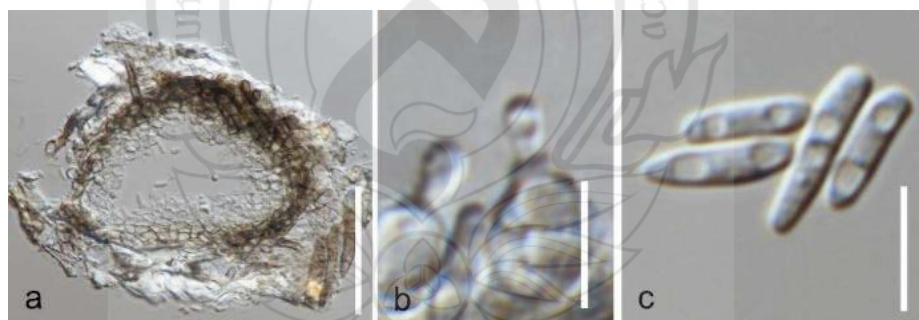
Classification: *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Phaeosphaeria, the type genus of *Phaeosphaeriaceae*, was first isolated from *Oryza sativa* in Japan and is characterized by perithecial ascomata (Miyake 1990). The ascomata form scattered or clustered structures with fissitunicate asci. The asci contain ellipsoidal or fusiform, phragmosporous pale brown to brown ascospores (Pem et al. 2019). The asexual morph is septoria-like and coelomycetous, producing cylindrical to subcylindrical conidia (Quaedvlieg et al. 2013; Phookamsak et al. 2014; Hyde et al. 2017). ITS, LSU, SSU and *tef1* are the available molecular markers for *Phaeosphaeria* in GenBank.

Eighteen species of *Phaeosphaeria* have been reported from dead salt marsh plants. *Phragmites australis*, *Elymus pungens*, *Spartina alterniflora*, *S. densiflora*, *S. foliosa*, *S. maritima*, *S. patens*, *S. townsendii*, *S. densiflor*, *Juncus roemerianus* and *J. maritimus*, are recorded as salt marsh hosts for *Phaeosphaeria* species (Calabon et al. 2021b).

Type species: *Phaeosphaeria oryzae* I. Miyake 1909

Other accepted species: Species Fungorum (search *Phaeosphaeria*)



Note a Section of a conidioma. b Conidiogenous cells and developing conidia. c Conidia. Scale bars: c = 50 μ m, b = 5 μ m, c = 10 μ m

Figure 4.44 *Phaeosphaeria* sp.

Sclerostagonospora Höhn. 1917

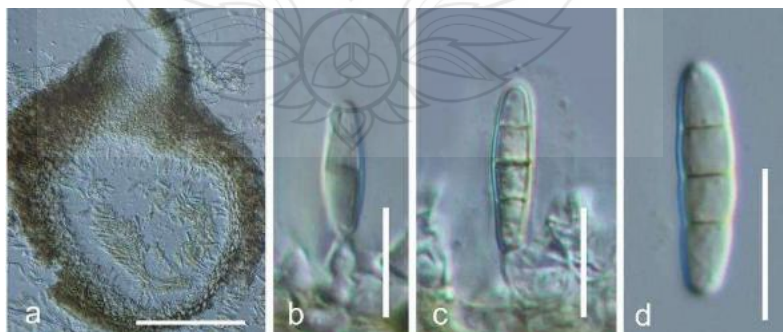
Classification: *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Sclerostagonospora was introduced by Höhnelt (1917) to accommodate the single species *S. heraclei*, which lacks molecular data. The genus comprises 18 species recorded as endophytes or saprobes on various plant materials (Wijayawardene et al. 2016; Jam Ashkezari and Fotouhifar 2017). *Sclerostagonospora* was also identified as the causal agent of necrotic leaf and stem spots on *Salsola kali* in Europe (Schwarczinger et al. 2000). Recently, *S. lathyri*, *S. rosae*, and *S. rosicola* have been introduced as new species from herbaceous plants, with providing molecular data and species synopsis table (Wanasinghe et al. 2018). Quaedvlieg et al. (2013) introduced *S. phragmiticola* from the salt marsh host *Phragmites australis* and, based on molecular analyses of ITS, LSU, *tef-1*, *rpb2*, and *tub2* sequence data, confirmed the placement of *Sclerostagonospora* in the family *Phaeosphaeriaceae*. They also suggested that *Sclerostagonospora* may have a phaeosphaeria-like sexual morph. The asexual morph of *Sclerostagonospora* is coelomycetous, characterized by immersed, ostiolate, papillate pycnidia. Conidiophores are reduced to holoblastic, ampulliform to irregular, hyaline conidiogenous cells that produce phragmosporous, pale brown, verruculose conidia (Quaedvlieg et al. 2013; Phookamsak et al. 2014). Morphologically, *Sclerostagonospora* is similar to *Stagonospora* but differs by having pigmented conidia. Phylogenetically, it is distinct from *Stagonospora* (Sutton 1980; Quaedvlieg et al. 2013).

Type species: *Sclerostagonospora heraclei* (Sacc.) Höhn. 1917

Basionym: *Hendersonia heraclei* Sacc. 1878

Other accepted species: Species Fungorum (search *Sclerostagonospora*)



Note a Conidioma. b,c Conidiogenous cells and conidia. d Conidium. Scale bars: a = 100 µm, b–d = 10 µm

Source Wanasinghe et al. (2018)

Figure 4.45 *Sclerostagonospora lathyri*

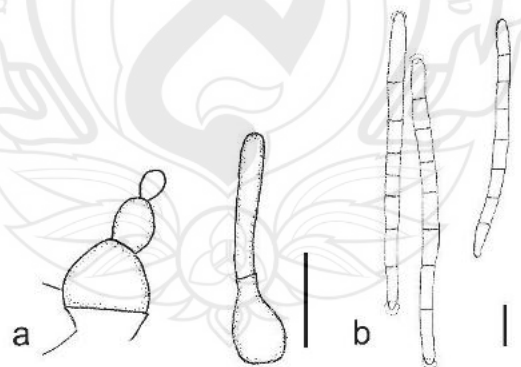
Septoriella Oudem. 1889

Classification: *Phaeosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Septoriella was introduced by Oudemans (1889) and typified by *Septoriella phragmitis*, a saprobic fungus isolated from *Phragmites australis*. Crous et al. (2015a) designated an epitype for *S. phragmitis* and confirmed the genus' placement in *Phaeosphaeriaceae* based on LSU and ITS molecular analyses. In addition to the type species, *S. thalassica*, *S. unigalerita*, and *S. vagans* have also been reported from salt marsh ecosystems on various hosts (Calabon et al. 2021b). Devadatha et al. (2023) transferred *Phaeosphaeria spartinae* to *Septoriella* due to its phylogenetic affinity. This species has been isolated from marsh plants, *Spartina densiflora*, *Spartina maritima*, and *Spartina* spp. (Calabon et al. 2021b). *Septoriella* forms a coelomycetous asexual morph with pycnidial, ostiolate conidiomata. The conidiophores are reduced to ampulliform to lageniform, proliferating conidiogenous cells. The conidia are pale brown, septate, with a truncate base and appendages at both ends (Crous et al. 2015a, Pem et al. 2024).

Type species: *Septoriella phragmitis* Oudem. 1889

Other accepted species: Species Fungorum (search *Septoriella*)



Note a Conidiogenous cells. b Conidia. Scale bars = 10 µm

Source Redrawn from Crous et al. (2015)

Figure 4.46 *Septoriella phragmitis*

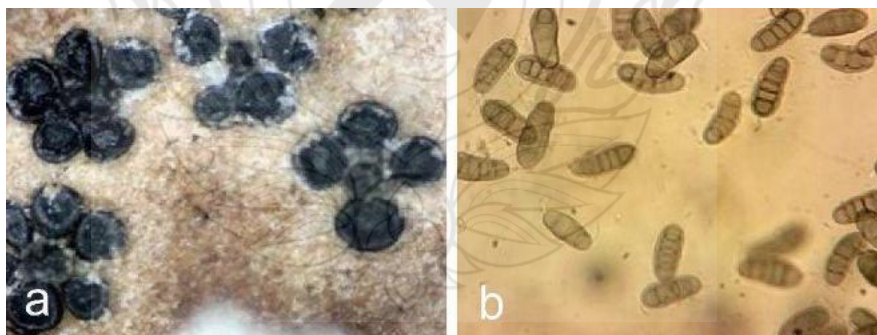
Splanchnonema Corda 1829

Classification: *Pleomassariaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Splanchnonema was introduced by Corda (1829) to accommodate its saprobic sexual type species, *S. pustulatum*. The sexual morph develops immersed, subglobose, ostiolate ascomata with a thin ascomatal wall. Pseudoparaphyses are embedded in mucilage, and asci are fissitunicate, clavate to broadly cylindrical, with a short, furcate pedicel. Ascospores are clavate, acute-based, reddish-brown, septate, and constricted at the septa. The sexual morph of *Splanchnonema* has been linked to *Myxocyclus* or *Steganosporium* (Zhang et al. 2012; Chethana et al. 2015). *Splanchnonema* belongs to *Pleomassariaceae* and comprises approximately 50 species, most of which are saprobic in terrestrial habitats (Zhang et al. 2012; Hyde et al. 2024a). *Splanchnonema platani* is a plant-pathogenic species that causes Massaria disease in the branches of plane trees (Hristova et al. 2025). In addition to its terrestrial occurrence, *S. britzelmayrianum* was the first species of the genus, and also the first representative of *Pleomassariaceae*, reported from a marine environment (Calabon et al. 2023). Previously, an unidentified *Splanchnonema* species was recorded on the salt marsh host *Juncus roemerianus* (Fell and Hunter 1979; Calabon et al. 2021b).

Type species: *Splanchnonema pustulatum* Corda 1829

Other accepted species: Species Fungorum (search *Splanchnonema*)



Note a Ascomata on host. b Ascospore

Source Hristova et al. (2025)

Figure 4.47 *Splanchnonema platani*

Alternaria Nees 1816

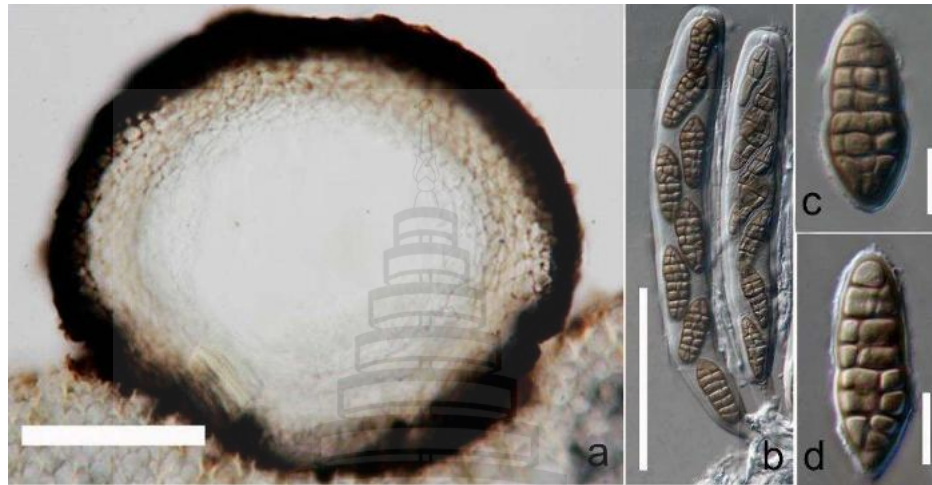
Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Alternaria, introduced by Nees von Esenbeck (1816), is a well-known ubiquitous genus, distributed globally as a saprobe, endophyte, and pathogen (Jayawardena et al. 2025). It has been found on various substrates, including plant material, soil, dust, old buildings, and food (Salo et al. 2005, Escrivá et al. 2017, Li et al. 2023). *Alternaria* species are important plant pathogens that infect a wide range of hosts, including economically significant crops, causing varying symptoms (Chethana et al. 2019; Fekrikohan et al. 2022; Bhunjun et al. 2024). A characteristic symptom is necrotic leaf spots with concentric zonation (Mac Kinon et al. 1999). *Alternaria* is also recognized as a human opportunistic pathogen and has frequently been associated with allergic respiratory diseases (Abel-Fernández et al. 2023). The asexual morph of *Alternaria* is commonly observed and is characterized by dematiaceous hyphomycetes with pale brown to brown conidiophores. The conidiogenous cells are monotretic to polytretic and sympodial. Conidia are mostly catenated in chains or solitary, olivaceous-brown to brown, multi-celled, and typically dictyosporous, though some may be phragmosporous (Lawrence et al. 2013, 2014; Ariyawansa et al. 2015a). The sexual morph of *Alternaria* is less frequently reported and is characterized by erumpent to superficial ascomata with papillate ostioles and thin walls. The asci are fissitunicate and contain (4–6–)8 muriform, yellow-brown ascospores (Ariyawansa et al. 2015a). *Alternaria* comprises approximately 400 species, taxonomically classified into more than 20 sections (Hyde et al. 2024a; Jayawardena et al. 2025). Woudenberg et al. (2013) conducted phylogenetic analyses using SSU, LSU, ITS, *gapdh*, *rpb2*, and *tef-1* for *Alternaria* and related genera, transferring thirteen genera under *Alternaria* and introducing 16 new sections. Lawrence et al. (2016) conducted a comprehensive taxonomic study of *Alternaria*, recognizing 27 sections, with subsequent modifications in later studies increasing this number to 29 (Ghafri et al. 2019, Gannibal et al. 2022). More recently, Li et al. (2023) conducted evolutionary analyses and multigene phylogenetic studies, leading to the introduction of 18 new *Alternaria* species. In addition to various terrestrial habitats, *Alternaria* species have also been reported from marine environments, such as sea foam samples, sponge and alga (Jones et al. 2019). *Alternaria alternata*, *A. infectoria*, *A. longissima*, *A. maritima*, and several unidentified

Alternaria species have been recorded from salt marsh halophytes (Calabon et al. 2021b).

Type species: *Alternaria tenuis* Nees 1816

Other accepted species: Species Fungorum (search *Alternaria*)



Note a Section of ascoma. b asci. c, d Ascospores. Scale bars: a = 80 µm, b = 20 µm, c, d = 5 µm

Source Ariyawansa et al. (2015a)

Figure 4.48 *Alternaria alternata*

Curvularia Boedijn 1933

Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

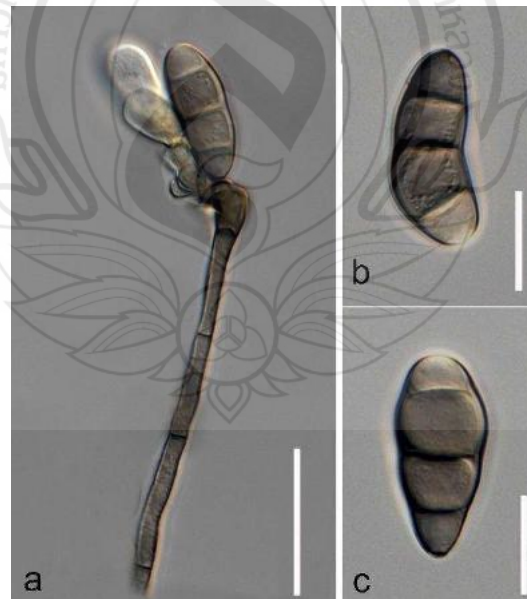
Curvularia was introduced by Boedijn (1933), with *Curvularia lunata* (previously classified under *Acrothecium*) designated as the type species. It was collected from dead leaves of *Saccharum officinarum* in Java. The genus is primarily known for its asexual morph, characterized by simple or unbranched conidiophores, which are often geniculate. Conidiogenous cells are polytretic and integrated. Conidia are brown, 3–10-distoseptate, and vary in shape, oblong, ellipsoidal, clavate, fusiform, subcylindrical, or lunate, and are often curved (Manamgoda et al. 2012; Pem et al. 2024). The sexual morph produces superficial, ostiolate, globose to ellipsoidal ascomata with a carbonaceous peridium. Asci are fissitunicate, short-pedicellate, and contain 1–8 ascospores. The ascospores are fasciculate, filamentous, filiform to flagelliform, 3–20-septate, and hyaline or somewhat pigmented at maturity

(Manamgoda et al. 2012; Pem et al. 2024). *Curvularia* and *Bipolaris* share many morphological similarities, which has led to taxonomic confusion in the past. However, molecular phylogenetic studies, particularly those incorporating ITS, *gapdh*, *tef1*, and *rpb2* gene regions, have clarified their boundaries and confirmed their separation as distinct genera (Manamgoda et al. 2014; Ferreira and Barreto 2020). The genus *Curvularia* comprises around 200 species (Hyde et al. 2024a), including important plant pathogens such as *C. lunata*, which causes Curvularia leaf spot in maize (Wang et al. 2022). Several *Curvularia* species have also been reported from clinical samples as opportunistic pathogens, causing infections in humans and animals, including diseases of the eye, skin, nails, and respiratory tract (Robson and Craver 1994, Krizsán et al. 2015). In addition, *Curvularia* species have been recorded from marine ecosystems, with six species listed as marine fungi (Jones et al. 2019). Calabon et al. (2021b) reported seven occurrences of *Curvularia* on salt marsh plants, mostly on *Juncus roemerianus*, including *C. hawaiiensis*, *C. protuberata*, and *C. tuberculata*.

Type species: *Curvularia lunata* (Wakker) Boedijn 1933

Basionym: *Acrothecium lunatum* Wakker, in Wakker & Went 1898

Other accepted species: Species Fungorum (search *Curvularia*)



Note a Conidiophores. b, c Conidia. Scale bars: 10 µm

Source Ariyawansa et al. (2015c)

Figure 4.49 *Curvularia lunata*

Decorospora Inderb., Kohlm. & Volkm.-Kohlm. 2002

Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Decorospora, a saprobic marine *Dothideomycetes*, was initially described as *Pleospora gaudefroyi* by Patouillard (1887). Inderbitzin et al. (2002) used SSU and ITS sequence data to confirm the placement of *P. gaudefroyi* in *Pleosporaceae*, but because it formed a distinct clade with other genera, they introduced *Decorospora* to accommodate this species. *Decorospora* is identified by its black, erumpent ascomata and fissitunicate, clavate asci. The ascospores have both transverse and longitudinal septa, are yellow to brown and surrounded by a quadri-cornute sheath, a distinctive feature of this genus (Inderbitzin et al. 2002; Hongsanan et al. 2020a; Jones 2023). The asexual morph of *Decorospora* remains unknown. *Decorospora* is commonly found in marine and salt marsh environments (Calabon et al. 2021b, Jones 2023). It has been isolated from various salt marsh plant species, including *Atriplex* sp., *Atriplex portulacoides*, *Sarcocornia perennis*, *Sarcoconia fruticosa*, *Salicornia europaea*, *Salicornia* sp., *Spartina maritima*, and *Suaeda maritima* (Yusoff et al. 1994b; Kohlmeyer and Kohlmeyer 1979; Calado et al. 2015; Calabon et al. 2021b).

Type species: *Decorospora gaudefroyi* (Pat.) Inderb., Kohlm. & Volkm.-Kohlm. 2002

Basionym: *Pleospora gaudefroyi* Pat. 1886

Other accepted species: None



Note a Ascomata on host. b Section of ascoma. c Asci. d, e Ascospores. Scale bars: a = 300 μm , b = 50 μm , c = 30 μm , d, e = 10 μm

Source Ariyawansa et al. (2015c)

Figure 4.50 *Decorospora gaudefroyi*

Exserohilum K.J. Leonard & Suggs 1974

Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Leonard and Suggs (1974) established *Exserohilum* to accommodate bipolaris-like species with the distinct characteristic of having a conspicuously protuberant conidial hilum. They also introduced *Setosphaeria* to accommodate the sexual morphs of *Exserohilum*. According to the one fungus-one name principle, *Exserohilum* has priority over *Setosphaeria* (Wijayawardene et al. 2014b). *Exserohilum* species have been recorded as saprobes, plant pathogens, and clinically relevant species (Hernández-Restrepo et al. 2018). *Exserohilum rostratum* has been isolated from salt marsh hosts such as *Distichlis spicata* (Kohlmeyer and Kohlmeyer 1979), *Juncus roemerianus* (Fell and Hunter 1979), *Spartina alterniflora* (Kohlmeyer and Kohlmeyer 1979; Gessner and Kohlmeyer 1976; Gessner 1977) and *Spartina* spp. (Kohlmeyer and Volkmann-Kohlmeyer 2002), primarily as a saprobe (Calabon et al. 2021b). The sexual morph consists of superficial *ascomata* with coriaceous-carbonaceous *peridium* that has hairs

over the surface. Asci are cylindrical to cylindrical-clavate, containing 1–8 fusoid, septate ascospores with a sheath. Asexual morph is characterized by cylindrical, olivaceous brown to brown *conidiophores*. Conidia are olivaceous to brown, porogenous, acrogenous or pseudopleurogenous, distoseptate with a protruding hilum (Ariyawansa et al. 2015c; Pem et al. 2019). Both morphological and molecular data are important in fungal classification. Tian et al. (2024) provided an updated phylogenetic tree of the genus using combined ITS, LSU, *tef1*, and *gapdh* sequence data.

Type species: *Exserohilum turcicum* (Pass.) K.J. Leonard & Suggs 1974

Basionym: *Helminthosporium turcicum* Pass. 1876

Other accepted species: Species Fungorum (search *Exserohilum*)



Note a Conidia on host. b, c Conidia. Scale bars: a = 100 μ m, b, c = 50 μ m)

Figure 4.51 *Exserohilum rostratum*

Paradendryphiella Woudenb. & Crous 2013

Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

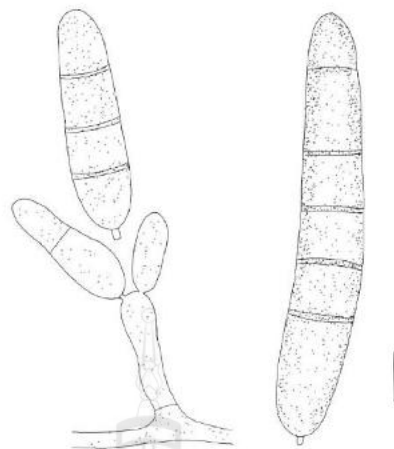
Woudenberg et al. (2013) introduced *Paradendryphiella*, utilizing both morphological features and molecular data from SSU, LSU, and *rpb2*. The genus includes two species, *Paradendryphiella salina* and *P. arenariae*, which were formerly classified as *Dendryphiella salina* (based on *Cercospora salina*, (Sutherland 1916b) and *D. arenariae*, respectively (Nicot 1958; Woudenberg et al. 2013). Earlier, Jones et

al. (2008) demonstrated the classification of these two species within *Pleosporaceae*, as supported by ITS, SSU, and LSU sequence data. This placement was confirmed by Woudenberg et al. (2013) and Jones et al. (2015). Jones et al. (2008) proposed the possibility of transferring these species to a new genus. *Paradendryphiella* is typified by *P. salina*, which has been extensively employed in salinity experiments and is recognized for the production of biomaterial compounds such as dendryphiellin A (Guerriero et al. 1988). *Paradendryphiella* is hyphomycetous and characterized by straight or flexuous subhyaline conidiophores with brown pigments at the apex. Conidiogenous cells exhibit denticles at the apical region, sometimes proliferating. Scars are visible on conidiogenous cells after conidia release. The conidia are septate, pale brown to medium brown, with a thickened hilum (Woudenberg et al. 2013; Hongsanan et al. 2020a). A sexual morph is undetermined. *Paradendryphiella arenariae* has been isolated from the low marsh plant *Spartina alterniflora* in USA (Gessner and Goos 1973b; Kohlmeyer and Kohlmeyer 1979). *Paradendryphiella salina* has been reported from *Spartina* sp., *S. alterniflora*, *S. townsendii*, *Suaeda maritima*, *Atriplex portulacoides*, *Juncus roemerianus*, *Puccinellia maritima*, and *Salicornia europaea* (Gessner and Goos 1973b; Kohlmeyer and Kohlmeyer 1979; Calabon et al. 2021b; Fell and Hunter 1979; Miller and Whitney 1983; Kohlmeyer and Volkmann-Kohlmeyer 2002).

Type species: *Paradendryphiella salina* (G.K. Sutherl.) Woudenb. & Crous 2013

Basionym: *Cercospora salina* G.K. Sutherl. 1916

Other accepted species: *Paradendryphiella arenariae* (Nicot) Woudenb. & Crous



Note Conidiogenous cells and conidia. Scale bar = 5 μ m

Source Redrawn from Ellis (1971)

Figure 4.52 *Paradendryphiella salina*

Typhicola Crous 2019

Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

The monotypic genus *Typhicola*, characterized as a facultative marine saprobe, was established by Crous et al. (2019) through a combination of morphological and molecular data, including ITS, LSU, *act*, *rpb2*, *tefl*, and *tub2*. Initially identified as *Sphaeria scirpicola*, *Typhicola* is notably recognized as the earliest documented facultative marine fungus on *Typha*, as indicated by Desmazières (1849) and later acknowledged by Jones (2023). The sexual morph of *Typhicola* exhibits immersed, globose, and ostiolate ascomata, accompanied by numerous branched hyaline pseudoparaphyses. The asci are fissitunicate with a thick wall, featuring an ocular chamber and a short papillate structure. Each ascus contains eight brown ascospores with a thick wall and septa, surrounded by a sheath. There are no reports of an asexual morph for this genus (Crous et al. 2019). Morphologically, *Typhicola* bears resemblance to *Juncaceicola*, but they are well-distinguished through molecular analyses (Crous et al. 2019). The genus has been consistently reported from salt marsh plants in various locations, including Canada, USA (New Jersey, Virginia, North Carolina, Florida), the United Kingdom, and Argentina, indicating a probable global

distribution (Calabon et al. 2021b). There are documented records of *Typhicola* occurring on the halophyte genus *Spartina*, encompassing *S. alterniflora*, *S. patens*, and *S. townsendii* (Goodman 1959; Jones 1962b; Apinis and Chesters 1964; Gessner and Goos 1973b; Gessner and Kohlmeyer 1976; Gessner 1977, 1980; Kohlmeyer and Kohlmeyer 1979; Calabon et al. 2021b).

Type species: *Typhicola typharum* (Desm.) Crous. 2019

Basionym: *Sphaeria scirpicola* var. *typharum* Desm. 1848

Other accepted species: None

Note Ascus and ascospore

Source Redrawn from Fuckel (1870)

Figure 4.53 *Typhicola typharum*

Stemphylium Wallr. 1833

Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Stemphylium was introduced by Wallroth (1833) and typified by the hyphomycetous species *Stemphylium botryosum*. It is a saprobic, endophytic, and pathogenic genus known for both its sexual and asexual morphs (Mirjalili et al. 2012; Woudenberg et al. 2017; Brahmanage et al. 2019; Karimzadeh and Fotouhifar 2021; 2022; Pem et al. 2024). The asexual morph of *Stemphylium* is a dematiaceous hyphomycete, producing solitary, muriform conidia. It is characterized by macronematous, mononematous conidiophores with percurrent proliferation and apically swollen conidiogenous cells. These morphological characters distinguish *Stemphylium* from related genera such as *Alternaria* (Simmons 1969; Woudenberg et

al. 2017; Marin-Felix et al. 2019a). The sexual morph of *Stemphylium* is linked to *Pleospora*, forming solitary, black, ostiolate, papillate ascomata with a two-layered peridium and cellular pseudoparaphyses. The asci are fissitunicate and contain eight muriform brown ascospores with a sheath (Simmons 1969; Brahmanage et al. 2019). While *Stemphylium* is considered a monophyletic genus, *Pleospora* is polyphyletic (Inderbitzin et al. 2009; Hongsanant et al. 2020a). Following the "one fungus, one name" rule, *Stemphylium* was recommended over *Pleospora* (Rossman et al. 2015). In addition to morphological data, ITS, *cmdA*, *gapdh*, *tub2*, *act*, *rpb2*, and *tef1* sequence data have been used for species delimitation within *Stemphylium* (Inderbitzin et al. 2009; Woudenberg et al. 2017; Marin-Felix et al. 2019a; Ahmadpour et al. 2024). *Stemphylium* is a speciose genus with approximately 100 species, including important plant pathogens that cause diseases in various economically significant crops such as wheat, barley, garlic, onion, pear, potato, and tomato (Wang et al. 2021; Ahmadpour et al. 2024; Hyde et al. 2024a). *Stemphylium gracilariae*, *S. lycopersici*, *S. maritimum*, *S. triglochonicola*, and *S. vesicarium* are listed as marine fungi (Jones et al. 2019). Additionally, *Stemphylium botryosum*, *S. lycopersici*, *S. maritimum*, and *S. vesicarium* have been reported on salt marsh plants (Calabon et al. 2021b).

Type species: *Stemphylium botryosum* Wallr. 1833

Basionym: *Cucurbitaria spiraeae* Fuckel 1864

Other accepted species: Species Fungorum (search *Stemphylium*)



Note a Conidiophores and conidia. b Conidia. Scale bars: a = 50 μ m, b = 10 μ m

Source Redrawn from Johnson 1956)

Figure 4.54 *Stemphylium maritimum*

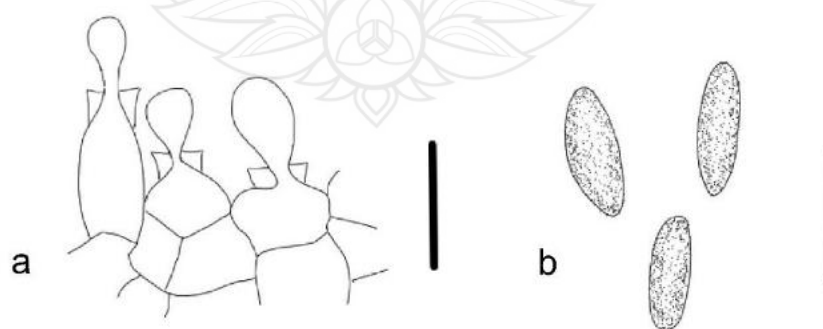
Cytoplea Bizz. & Sacc. 1885

Classification: *Roussoellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cytoplea was introduced by Bizzozero (1885) to accommodate a saprobic asexual species, *Cytoplea arundinicola*. The asexual morph of *Cytoplea* is coelomycetous, developing stromatic, superficial, pulvinate, multi-loculate conidiomata with filiform paraphyses. The conidiogenous cells are phialidic, ampulliform, or short cylindrical, producing aseptate, brown, guttulate conidia (Sutton 1980; Bizzozero 1885). Hyde et al. (1996) introduced a new species, *Cytoplea hysterioides*, based on the observation of a cytoplea-like asexual morph in media culture of *Roussoella hysterioides*. They suggested a possible link between the sexual and asexual morphs of *Cytoplea*. Subsequent phylogenetic analyses by Verkley et al. (2004) confirmed a close relationship between *Roussoella hysterioides* and *Cytoplea hysterioides*. *Cytoplea* and *Roussoella* were considered congeneric by Liu et al. (2014). However, due to the lack of molecular data for *Cytoplea*, Wijayawardene et al. (2014a) treated them as separate genera. *Cytoplea* currently comprises 19 species, but only three sequences are available for *Cytoplea hysterioides* and *Cytoplea hederæ* (Hyde et al. 2024a). Species of *Cytoplea* are either endophytic or saprobic on various host plants (Pem et al. 2024). An unidentified species was recorded from decaying stems and leaf sheaths of the salt marsh host *Phragmites australis* in China (Poon and Hyde 1998; Calabon et al. 2021b).

Type species: *Cytoplea arundinicola* Bizz. & Sacc. 1885

Other accepted species: Species Fungorum (search *Cytoplea*)



Note a Conidiogenous cells and conidia. b Conidia. Scale bars: 10 µm

Source Redrawn from Pem et al. (2024)

Figure 4.55 *Cytoplea orientalis*

***Preussia* Fuckel 1867**

Classification: *Sporormiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Preussia was established by Fuckel (1866) to accommodate a saprobic sexual species, *Preussia funiculata*, characterized by long pedicellate asci and splitting ascospores. The ascomata of the sexual morph are globose, cleistothecial or perithecial, with brown cylindrical ascospores that break easily into separate parts and have a germ slit in each part. The asexual morph of the genus has been linked to *Phoma* (Fuckel 1866; Cain 1961; Malloch and Cain 1972). Currently, *Preussia* comprises approximately 60 species, found as saprobes or endophytes in various substrates, including plant material, lichen, air, soil, and dung (Sandberg et al. 2022; Tan et al. 2022; 2024; Hyde et al. 2024a; Noh et al. 2025). Recently, four new species, *P. crataegi*, *P. iranica*, *P. pianica*, and *P. pistaciae*, were described from symptomatic forest trees in Iran, based on morphological characteristics and phylogenetic analyses using combined ITS, LSU, *tub2*, and *tefl* sequences (Eisvand and Mehrabi Koushki, 2025). *Preussia* species have also been reported from aquatic environments. *Preussia cylindricalis* and *Preussia sedimenticola* were isolated from freshwater sediment in a lake in China (Phurbu et al. 2024). Additionally, *Preussia funiculata* and *Preussia terricola* have been recorded from salt marsh hosts, *Spartina townsendii* and *Elymus pungens*, in the United Kingdom (Apinis and Chesters 1969; Calabon et al. 2021b). A newly described species, *Preussia aseelix*, was discovered in coastal sediment in Iraq with a salinity of 51.3 ppt; however, no holotype was designated in the protologue (Al-Musa et al. 2024). *Preussia* has been investigated for its natural products, demonstrating antifungal, antimicrobial and anti-inflammatory activities (Weber et al. 1991; Mapperson et al. 2014; Youn et al. 2018; Pem et al. 2024).

Type species: *Preussia funiculata* (Preuss) Fuckel 1867

Basionym: *Perisporium funiculatum* Preuss 1851

Other accepted species: Species Fungorum (search *Preussia*)



Note a Section of an ascoma. b Ascus. c Ascospore. Scale bars: a = 200 μm , b = 40 μm , c = 20 μm)

Figure 4.56 *Preussia* sp.

Sporormia De Not. 1849

Classification: *Sporormiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

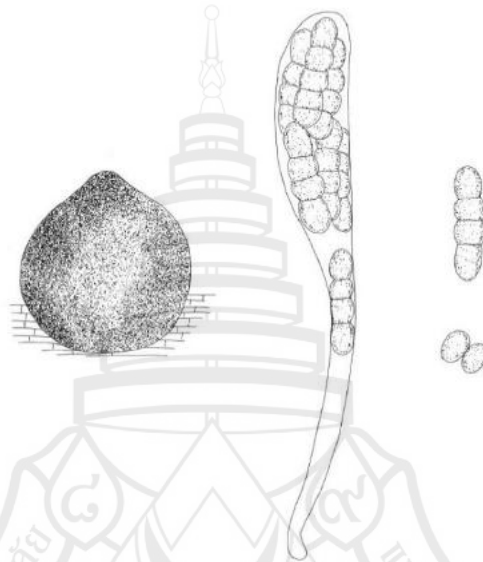
Sporormia was introduced by De Notaris (1849) to accommodate *Sporormia fimetaria*, which was isolated from cow dung. The genus is characterized by its sexual morph, featuring globose to subglobose, black ascomata, a thin peridium, and cylindrical asci with a short furcate pedicel. The ascospores are cylindrical, brown, and multiseptate with 15–32 cells, easily separating into part-spores, and usually lacking a germ slit. Its asexual morph has not yet been determined (Hyde et al. 2013; Pem et al. 2024). *Sporormia* comprises approximately 50 species, most of which are coprophilous and saprobic on dung (Hyde et al. 2024a; Pem et al. 2024). However, *Sporormia longipes* and an unidentified *Sporormia* species have been recorded from salt marsh plants, *Elymus pungens* and *Juncus roemerianus*, respectively (Calabon et al. 2021b). Morphologically, *Sporormia* is similar to *Preussia* but differs in having ostiolate ascomata and a predominantly coprophilous habitat (Fuckel 1866; Kruys and Wedin 2009). Kruys and Wedin (2009) investigated the phylogenetic relationships within *Sporormiaceae* using ITS, mtSSU, and β -tubulin sequences. They concluded that substrate choice, presence or absence of an ostiole, and presence or absence of germ

slits are homoplastic traits, making them ineffective for defining monophyletic groups. Consequently, they treated *Sporormia* and *Preussia* as separate genera.

Type species: *Sporormia fimetaria* (Rabenh) De Not. 1849

Basionym: *Sphaeria fimetaria* Rabenh. 1845

Other accepted species: Species Fungorum (search *Sporormia*)



Note Ascoma, ascus and ascospores

Source Redrawn from Masee and Salmon (1901)

Figure 4.57 *Sporormia longipes*

Sporormiella Ellis & Everh. 1892

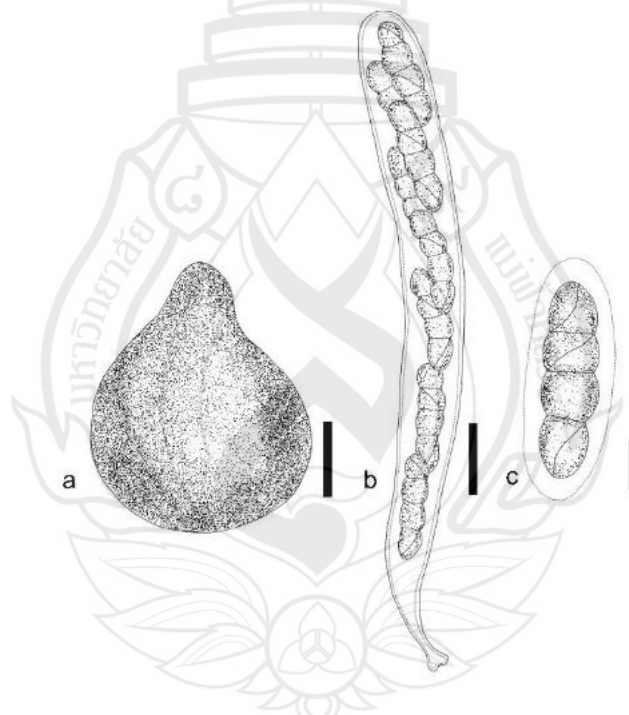
Classification: *Sporormiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Sporormiella was introduced based on a collection of sporormia-like species, with *Sporormiella nigropurpurea* isolated from cow dung as the type species (Ellis and Everhart 1892). The sexual morph of *Sporormiella* develops immersed to semi-immersed, papillate perithecial ascomata, with a smooth wall or covered with hairs in the upper part. The asci are eight-spored, with a short to relatively long stipe. Ascospores are dark brown at maturity, three- to multi-septate, and break into part-spores with a germ slit. The asexual morph is unknown (Ahmed and Cain 1972). *Sporormiella* was considered a synonym of *Preussia* by some researchers (Kruys and

Wedin 2009); however, Hongsanan et al. (2020a) retained it as a separate genus due to the lack of molecular data for the type species of *Sporormiella*. Recently, Jakob et al. (2024) introduced a new species, *Sporormiella tela*, based on morphology and phylogenetic analysis of ITS and LSU sequences. They suggested that fresh material and additional sequence data are needed to clarify the taxonomic placement of both genera. The genus comprises approximately 60 species, most of which are coprophilous (Hyde et al. 2024a; Pem et al. 2024). Calabon et al. (2021b) listed *S. intermedia*, *S. lageniformis*, and *S. minima* as salt marsh fungi, isolated from *Elymus pungens* *Spartina townsendii*, and *Elymus pungens*, respectively.

Type species: *Sporormiella nigropurpurea* Ellis & Everh. 1892

Other accepted species: Species Fungorum (search *Sporormiella*)



Note a Ascoma. b Ascus. c Ascospores. Scale bars: a = 100 µm, b = 10 µm, c = 5 µm

Source Redrawn from Ahmed and Cain (1972)

Figure 4.58 *Sporormiella nigropurpurea*

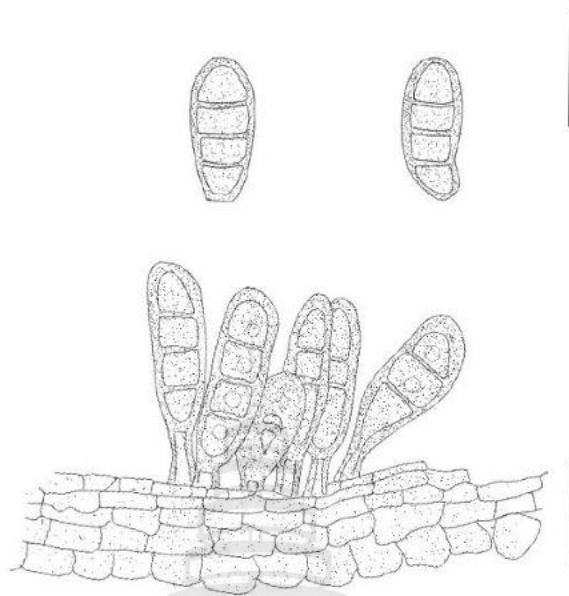
Teichospora Fuckel 1870

Classification: *Teichosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Fuckel (1870) introduced *Teichospora* to accommodate wood-saprobic species, including *Teichospora morthieri*, *T. obducens*, *T. brevirostris*, *T. dura*, and the type species *T. trabicola*. The sexual morph of *Teichospora* is characterized by ostiolate, globose to pyriform, dark brown ascomata with a complex peridium and numerous paraphyses and pseudoparaphyses. The asci are 4–8-spored, cylindrical to subclavate, and fissitunicate. Ascospores are ellipsoid to oblong, muriform, with 3(–4–5) transverse septa, 1–3 longitudinal septa, and 123 V- or Y-shaped septa in the terminal cells. They are usually brown and lack a sheath. The asexual morph is coelomycetous, developing pycnidia with conidiophores reduced to conidiogenous cells. These bear brown, aseptate coniothyrium-like conidia or hyaline, aseptate aposphaeria-like conidia. In some species, the asexual morph is characterized by multicellular brown conidia (Jaklitsch et al. 2016; Wijayawardene et al. 2017a). Based on phylogenetic similarities between *Teichospora* and *Misturatosphaeria*, Jaklitsch et al. (2016) transferred several species of *Misturatosphaeria* to *Teichospora*. However, this classification was not accepted by Hongsanan et al. (2020a) and Tennakoon et al. (2020). Hongsanan et al. (2020a) demonstrated the distinct placement of *Teichospora* within *Teichosporaceae* through phylogenetic analyses of ITS, LSU, and *tef1* sequence data. However, *T. kingiae*, *T. nephelii*, and *T. quercus* formed a separate clade from other *Teichospora* species, suggesting that further research is needed to clarify their taxonomic placement. The genus *Teichospora* comprises approximately 50 species, including *T. striata* and *T. suaedae*, which have been reported from salt marsh plants *Juncus roemerianus* and *Suaeda divaricata*, respectively (Calabon et al. 2021b; Hyde et al. 2024a).

Type species: *Teichospora trabicola* Fuckel 1870

Other accepted species: Species Fungorum (search *Teichospora*)



Note Conidioma, conidiogenous cells and conidia. Scale bars = 10 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (2000)

Figure 4.59 *Teichospora striata*

Phialophorophoma Linder 1944

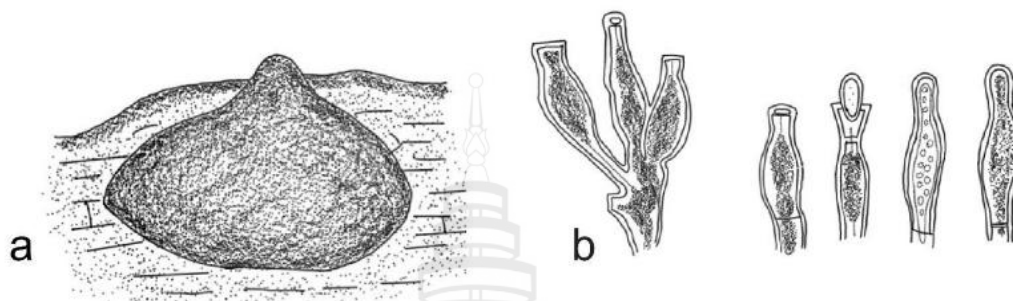
Classification: *Incertae sedis*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Phialophorophoma was introduced by Barghoorn and Linder (1944) on oak bark in a marine habitat. The genus is monotypic and has been reported on decaying salt marsh plants, *Spartina maritima* in Portugal (Barata 2002, 2006, Calabon et al. 2021b), and *Phragmites australis* in the Netherlands (Van Ryckegem and Verbeken 2005a, 2005b; Calabon et al. 2021b). The sexual morph of *Phialophorophoma* has not been determined. The asexual morph is coelomycetous, characterized by immersed, ovoid or ellipsoid, and ostiolate pycnidia. Conidiophores are hyaline, phialidic, elongated, filiform, tapering to the apex, with a short cylindrical neck. Conidia are hyaline, ellipsoid to slipper or pear-shaped, mostly with two guttules (Barghoorn and Linder 1944; De Gruyter et al. 2009; Pem et al. 2019). De Gruyter et al. (2009) provided LSU and SSU sequence data of two strains of the type species and showed its placement in *Pleosporales*. There is no certain family assigned for *Phialophorophoma*, and it is

suggested that more samples and molecular data are needed to solve its taxonomic placement (Pem et al. 2019).

Type species: *Phialophorophoma litoralis* Linder 1944

Other accepted species: None.



Note a Pycnidium (25×). b Phialides (1000×)

Source Redrawn from Barghoorn and Linder (1944)

Figure 4.60 *Phialophorophoma litoralis*

Verruculina Kohlm. & Volkm.-Kohlm. 1990

Classification: *Testudinaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

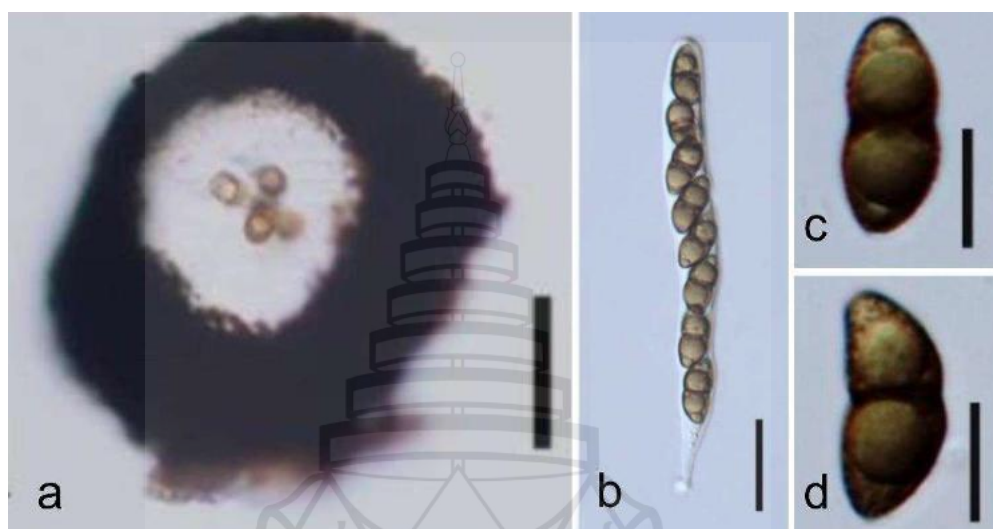
Kohlmeyer and Volkmann-Kohlmeyer (1990) introduced the novel saprobic monotypic genus, *Verruculina*, to accommodate *V. enalia*, initially classified as *Didymosphaeria enalia* (Kohlmeyer 1966), isolated from a marine ecosystem and later referred to a new genus *Lojkania* as *L. enalia* by Barr (1990). *Verruculina enalia* has been isolated from mangroves in Liberia and India (Kohlmeyer and Volkmann-Kohlmeyer 1990; Hongsan et al. 2020a) and from the salt marsh plant *Phragmites australis* in China (Poo and Hyde 1998; Jones et al. 2019; Calabon et al. 2021b). Based on phylogenetic analyses of combined LSU, SSU, *tefl*, and *rpb2* sequence data, the genus was transferred to *Testudinaceae* from *Didymosphaeriaceae* (Schoch et al. 2006b; Suetrong et al. 2009; Hongsan et al. 2020a). The sexual morph is characterized by papillate ascomata that are subglobose, ampulliform, or depressed ellipsoid. Asci are cylindrical with an indistinct apical apparatus containing 8 uniseptate dark brown ascospores (Pem et al. 2019; Hongsan et al. 2020a). The key characteristics of having verrucose or verruculose ascospores, papillate ascomata, and

living in marine habitats distinguish this genus from other taxa in *Testudinaceae* (Suetrong et al. 2009).

Type species: *Verruculina enalia* (Kohlm.) Kohlm. & Volkm.-Kohlm. 1990

Basionym: *Didymosphaeria enalia* Kohlm. 1966

Other accepted species: None.



Note a Section of ascoma. b Ascus. c, d Ascospores. Scale bars: a = 100 μm , b = 30 μm , c, d = 10 μm

Source Redrawn from Jayasiri et al. (2019)

Figure 4.61 *Verruculina enalia*

Tetraploa Berk. & Broome 1850

Classification: *Tetraplosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Tetraploa is a dothideomycetous fungus, described by Berkeley and Broome (1850) to accommodate *T. aristata* as type species. Tanaka et al. (2009) introduced a sexual morph genus, *Tetraplosphaeria* with a tetraploa-like asexual morph. They placed *Tetraplosphaeria* in the novel family *Tetraplosphaeriaceae* based on morphology and molecular analyses of combined ITS, *tef* and β -*tubulin*. Due to nomenclatural priority, *Tetraplosphaeria* was considered synonymous with *Tetraploa* (Hongsanan et al. 2020a).

There are 46 accepted species for *Tetraploa* in Species Fungorum (2026). They have been recorded from various substrates (Hyde et al. 2013) mostly herbaceous plants

and decaying wood (Ellis 1949; Révay 1993). *Tetraploa aristata* has been isolated from decaying stems and leaves and leaf sheaths on salt marsh hosts including *Distichlis spicata* from Argentina, *Juncus roemerianus* from USA and *Phragmites australis* from China (Eliades et al. 2007; Fell and Hunter 1979; Poon and Hyde 1998).

The sexual morph is distinguished by globose to subglobose ascomata that may feature a short-papillate to cylindrical beak. Asci are fissitunicate containing fusiform and hyaline ascospores with have a mucilaginous appendage-like sheath (Tanaka et al. 2009). The asexual morph is characterized by micronematous conidiophores with monoblastic conidiogenous cells. Conidia are composed of four columns each with an apical appendages and short cylindrical in shape with pigmented wall (Tanaka et al. 2009; Li et al. 2021).

Type species: *Tetraploa aristata* Berk. & Broome 1850

Other accepted species: Species Fungorum (search *Tetraploa*)



Note Conidia. Scale bars: a, b = 10 μ m, c, f = 20 μ m

Source Asghari et al. (2025)

Figure 4.62 *Tetraploa maritima*

Halomassarina Suetrong, Sakay., E.B.G. Jones, Kohlm., Volkm.-Kohlm. & C.L. Schoch 2009

Classification: *Trematosphaeriaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

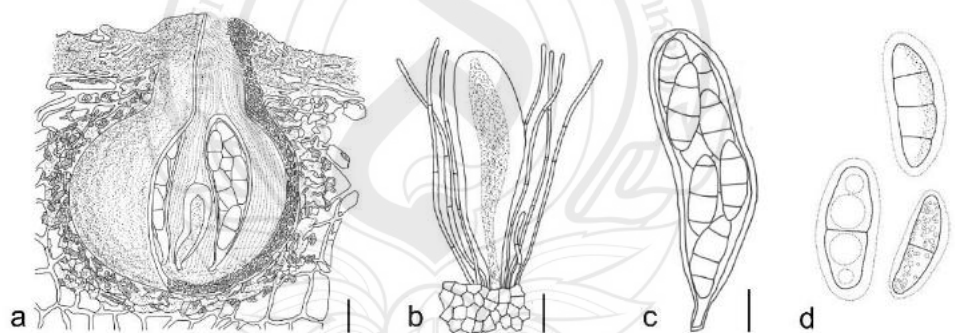
Halomassarina was established to accommodate *H. thalassiae*, which was initially introduced as *Massarina thalassiae* by Kohlmeyer and Volkmann-Kohlmeyer (1987). *Halomassarina* is a marine saprobic genus widely collected from mangrove wood and fishing craft in tropical areas (Suetrong et al. 2009). The type species, *H. thalassiae*, was reported on decaying *Phragmites australis* in China (Poon and Hyde 1998; Calabon et al. 2021b). Molecular analyses of SSU, LSU, *rpb2*, and *tef1*, showed that *H. thalassiae* forms a distinct clade in *Trematosphaeriaceae*, separate from *Massarina eburnea*. Sexual morph is characterized by ostiolate, subglobose to pyriform ascomata, which are immersed or erumpent in host tissue. Asci are fissitunicate, short pedicellate, cylindrical to clavate, with a distinct ocular chamber lacking an apical apparatus. Ascospores are ellipsoidal, hyaline, and 1 to 3-septate with a gelatinous sheath. Asexual morph is unknown (Kohlmeyer and Volkmann-Kohlmeyer 1987; Pem et al. 2019; Suetrong et al. 2009).

Type species: *Halomassarina thalassiae* (Kohlm. & Volkm.-Kohlm.)

Suetrong, Sakay., E.B.G. Jones, Kohlm., Volkm.-Kohlm. & C.L. Schoch 2009

Basionym: *Massarina thalassiae* Kohlm. & Volkm.-Kohlm. 1987

Other accepted species: None.



Note a Ascoma. b Immature ascus and pseudoparaphyses. c Mature ascus. d Ascospores. Scale bars: a = 25 μ m, b, c = 15 μ m, d = 10 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (1987)

Figure 4.63 *Halomassarina thalassiae*

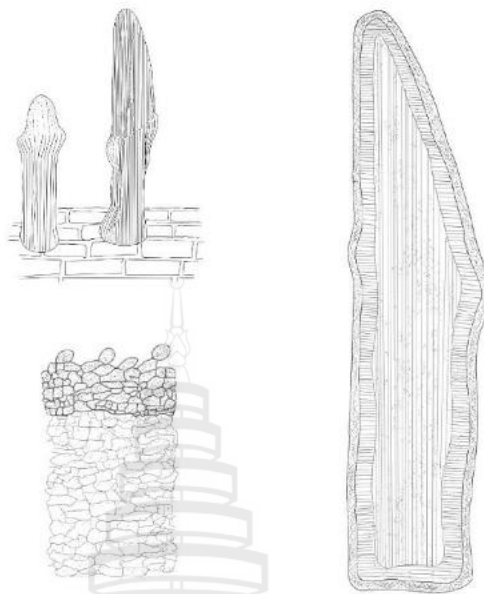
Acrospermum Tode 1783

Classification: *Acrospermaceae*, *Acrospermales*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Acrospermum was introduced by Tode (1790b) to accommodate *A. unguinosum*, *A. pyramidale*, *A. lichenoides*, and *A. compressum*. The genus *Acrospermum* includes 44 species, which are epibiotic, rarely lichenicolous, and mostly saprobic (Species Fungorum accessed April 2026; Hyde et al. 2018; Hudson et al. 2019; Darmostuk and Flakus 2024). *Acrospermum* is globally distributed and found on various host families such as *Asteraceae*, *Apiaceae*, *Poaceae*, *Betulaceae*, *Rosaceae*, *Urticaceae*, *Moraceae*, and *Polypodiaceae* (ferns) (Hudson et al. 2019; Pem et al. 2024). *Acrospermum graminum*, found on grass and with available molecular markers ITS, LSU, SSU, and *rpb2*, has been reported on the salt marsh host *Elymus pungens* in the United Kingdom (Apinis and Chesters 1964, Hongsanan et al. 2020b, Calabon et al. 2021b). The sexual morph of *Acrospermum* has superficial, erect and club-like ascomata. Asci are narrowly cylindrical and contain eight filiform, hyaline, multi-septate ascospores (Hyde et al. 2013; Wijayawardene et al. 2018a; Hongsanan et al. 2020b). The asexual morph is hyphomycetous, with pale brown conidiophores, holoblastic, sympodial conidiogenous cells bearing denticles with cylindrical, pale-yellow conidia (Riddle 1920; Pem et al. 2024). *Acrospermum* was placed in the novel family *Acrospermaceae* by Fuckel (1870). The genus has been considered in various orders, such as *Hysteriales*, *Hypocreales*, and *Sphaeriales* (Ellis and Everhart 1892; Lindau 1897; von Höhnelt 1917; Riddle 1920; Hyde et al. 2013), before being assigned to the novel order *Acrospermales* by Minter et al. (2007). Phylogenetic analyses and ancestral state reconstructions indicate that the saprotrophic lifestyle is ancestral in *Acrospermales*.

Type species: *Acrospermum compressum* Tode 1790

Other accepted species: Species Fungorum (search *Acrospermum*)



Note Ascomata and ascomatal wall

Source Redrawn from Libert (1830)

Figure 4.64 *Acrospermum graminum*

Morenoina Theiss. 1913

Classification: *Morenoinaceae.*, *Asterinales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Morenoina was established by Theissen in 1913 and typified with *M. antarctica*. The taxonomic placement of this taxon has changed over time and has been previously classified in both *Leptopeltidaceae* and *Asterinaceae* (von Arx and Müller 1950; Lumbsch and Huhndorf 2010). Hongsanan et al. (2014) introduced an epitype and assigned this genus to *Aulographaceae* based on morphological characters and molecular data. Later, Hongsanan et al. (2020b) introduced the family *Morenoinaceae* to accommodate this genus. *Morenoina* is similar to *Aulographum* and differs only in the morphology of the scutellum (Ellis 1980). The sexual morph is characterized by black, solitary, or gregarious thyriothecia. Their shape is generally ellipsoid, oblong, or curved, and they open via X- or Y-shaped or linear fissures. Thyriothecia usually lack free hyphae and appressoria at the margin. Asci are 8-spored, subglobose to oblong or saccate to globose and apedicellate. The ascospores are typically arranged in an

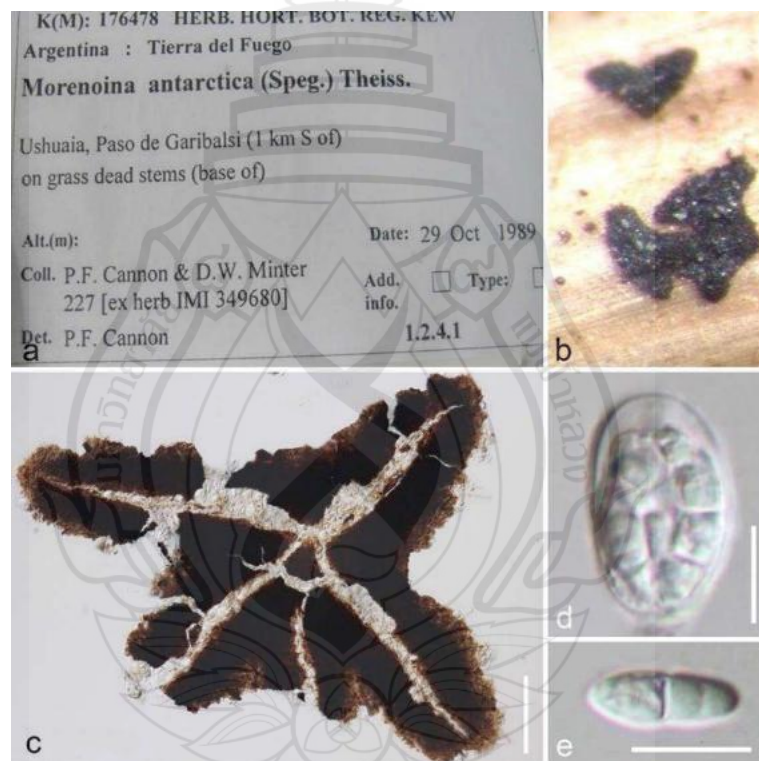
overlapping 2–3-seriate pattern. They are hyaline, 1-septate, and can be oblong, obovoid, or fusiform (Hongsanant et al. 2014; Tibpromma et al. 2017). The asexual morph is coelomycetous with circular pycnothyria. Conidiogenous cells are hyaline and holoblastic bearing cylindrical, hyaline conidia (Sivanesan 1984).

There are 26 species listed in Species Fungorum. *Morenoina phragmitis* was recorded on decomposing leaf sheaths and stems of *Phragmites australis* in the Netherlands (Van Ryckegem and Verbeken 2005a, 2005b).

Type species: *Morenoina antarctica* (Speg.) Theiss. 1913

Basionym: *Morenoella antarctica* Speg. 1887

Other accepted species: Species Fungorum (search *Morenoina*)



Note a Herbarium and specimen. b Appearance of thyriothecia on surface of plant. c Squash mount of thyriothecium. d Immature ascus. E Ascospore. Scale bars: c = 100 μ m, d, e = 20 μ m

Source Hongsanant et al. (2020b)

Figure 4.65 *Morenoina antarctica*

Macrophomina Petr. 1923

Classification: *Botryosphaeriaceae*, *Botryosphaeriales*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Petrak (1923) introduced *Macrophomina* based on an asexual species, *M. philippinensis*, from *Sesamum indicum* in the Philippines. *Macrophomina* is a plant pathogen causing charcoal rot and dry root rot on various hosts worldwide (Poudel and Vaghefi 2023). *Macrophomina* sp. has been isolated from decaying stems and leaf sheaths of *Phragmites australis* in salt marsh habitats in China (Poon and Hyde 1998; Calabon et al. 2021b). The sexual morph of the genus is unknown. Characteristics of *Macrophomina* species include brown, septate mycelium with prolific production of black microsclerotia. Conidiomata are pycnidial, with aseptate, hyaline conidia that have apical appendages. These conidia may sometimes become dark and septate with maturity (Crous et al. 2006; Machado et al. 2019; Poudel et al. 2021). This necrotrophic fungus has changed taxonomically several times (Poudel and Vaghefi 2023). Several investigations have shown substantial genetic diversity within the type species, *M. phaseolina*, suggesting the potential existence of cryptic species (Poudel et al. 2021). Currently, *Macrophomina* is classified under *Botryosphaeriaceae* (Crous et al. 2006; Hongsanan et al. 2020b), comprising five accepted cryptic species using multigene phylogeny of combined *act*, *cmd*, ITS, *tefl-α* and *tub2* sequence data (Zhao et al. 2019; Poudel et al. 2021; Species Fungorum 2026).

Type species: *Macrophomina phaseolina* (Tassi) Goid. 1947

Basionym: *Macrophoma phaseolina* Tassi 1901

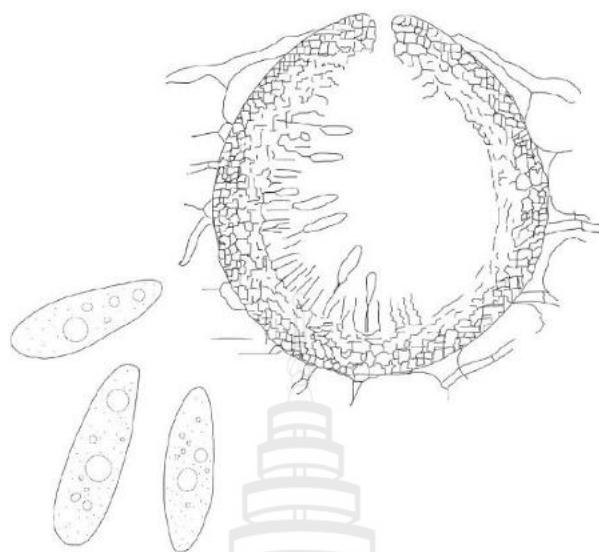
Other accepted species:

Macrophomina euphorbiicola A.R. Machado, D.J. Soares & O.L. Pereira 2018

Macrophomina pseudophaseolina Crous, M.P. Sarr & Ndiaye 2014

Macrophomina tecta Vaghefi, B. Poudel & R.G. Shivas 2021

Macrophomina vaccinii Y. Zhang ter & L. Zhao 2019



Note Pycnidium and conidia

Source Redrawn from Tassi (1901)

Figure 4.66 *Macrophomina phaseolina*

Tiarosporella Höhn. 1919

Classification: *Botryosphaeriaceae*, *Botryosphaeriales*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Tiarosporella is saprobic or endophytic on various woody and herbaceous plants, mostly recorded in terrestrial habitats (Index Fungorum, Pem et al. 2019). Kohlmeyer and Volkmann-Kohlmeyer (1996b) described *T. halmyra* on the halophyte *Juncus roemerianus* from USA (Calabon et al. 2021b). There are eight species of *Tiarosporella* in Species Fungorum (Accessed April 2026) with an unknown sexual morph. Asexual morph is coelomycetous with thick-walled, immersed, and ostiolate pycnidia. Conidiophores are short, septate, and smooth-walled with cylindrical to ampulliform macroconidiogenous cells, which are with or without proliferations, or ampulliform microconidiogenous cells. Macroconidia are hyaline, unicellular, and fusiform or long clavate with irregular mucoid appendages. Microconidia, if present, are hyaline, aseptate, and globose to ovoid (Pem et al. 2019; Li et al., 2020). ITS, LSU, SSU, *btub*, *rpb2*, and *tefl* are available markers for *Tiarosporella* species in GenBank (Pem et al. 2019).

Type species: *Tiarosporella paludosa* (Sacc. & Fiori) Höhn. 1919

Basionym: *Neottiospora paludosa* Sacc. & Fiori, in Sydow 1899

Other accepted species:

Tiarosporella azadirachtae Abbas, Iftikhar, Niaz, I. Ali, N. Iftikhar & Al. Abbas 2012

Tiarosporella corymbiae Crous & P.A. Barber 2017

Tiarosporella graminis (Piroz. & Shoemaker) Nag Raj 1974

Tiarosporella halmyra Kohlm. & Volkm.-Kohlm. 1996

Tiarosporella madreya (Subram. & K. Ramakr.) Nag Raj 1974

Tiarosporella proteae Crous, Marinc. & M.J. Wingf. 2008

Tiarosporella schizochlamys (Ferd. & Winge) Höhn. 1919



Note Conidiogenous cells and conidia. Scale bars = 20 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (1996b)

Figure 4.67 *Tiarosporella halmyra*

Microthyrium Desm. 1841

Classification: *Microthyriaceae*, *Microthyriales*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Microthyrium was described by Desmazières (1814) to accommodate *Microthyrium microscopicum*, which was reported from the upper surface of dry leaves of *Castanea vulgaris* in France. The genus is characterized by superficial, membranous, shield-like ascomata on the host surface (Desmazières 1814). The outer layer of the peridium is darkly pigmented, while the inner layer is light brown. The upper peridial cells are arranged in a parallel fashion around a central ostiole. Asci are fissitunicate,

with or without a short pedicel, and contain eight hyaline, fusiform to ellipsoidal, bicellular ascospores, sometimes bearing appendages (Wu et al. 2011). *Microthyrium* is the type genus of both *Microthyriaceae* and *Microthyriales*. Wu et al. (2011) indicated the polyphyletic nature of *Microthyrium* and its family in their phylogenetic analysis based on SSU and LSU sequences. Available molecular data for *Microthyrium* in GenBank include ITS, LSU, SSU, *tef1*, and *rpb2*. However, many species still lack sequence data, and fresh collections are needed to establish a more precise taxonomy for the genus (Pem et al. 2024). The genus includes approximately 90 species and is widely distributed on various plant hosts (Hyde et al. 2024a). Most species are saprobic and occur on the upper surfaces of leaves (Wu et al. 2011). *Microthyrium microscopicum* and *M. gramineum* have been reported from salt marsh plants, specifically *Spartina patens* and *Elymus pungens*, respectively (Calabon et al. 2021b).

Type species: *Microthyrium microscopicum* Desm. 1841

Other accepted species: Species Fungorum (search *Microthyrium*)



Note a Section of ascoma. b Ascus. c Ascospores. Scale bars: a = 100 µm, b, c = 20 µm

Source Wu et al. (2011)

Figure 4.68 *Microthyrium microscopicum*

Heleiosa Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1996

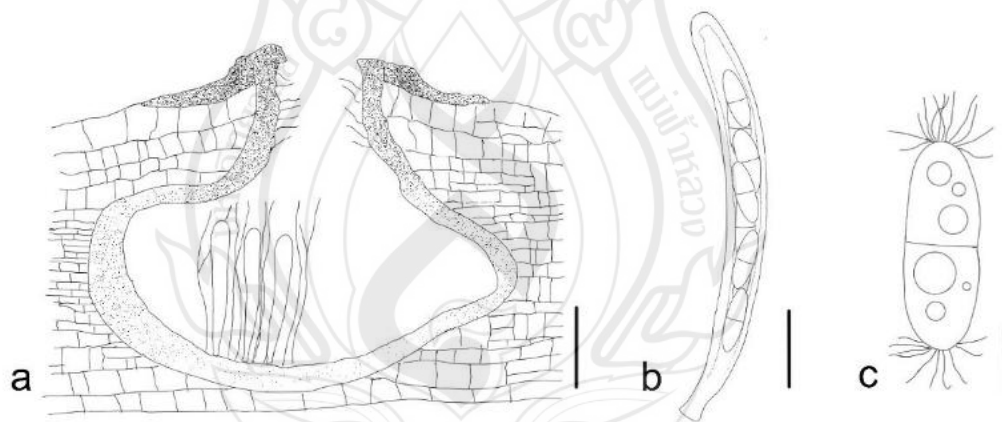
Classification: *Eriomycetaceae*, *Monoblastiales*, *Dothideomycetes*, *Ascomycota*, *Fungi*.

Heleiosa was introduced by Kohlmeyer et al. (1996a) to accommodate *Heleiosa barbatula* which was isolated as a saprobe on *Juncus roemerianus* from salt marshes in USA. *Heleiosa* is characterized by papillate, clypeate ascomata without neck and a thin, *textura angularis* peridium. Pseudoparaphyses are branched and anastomose above the

asci. Asci are cylindrical and short pedicellate containing four-to-eight ascospores. Ascospores are pale brown, 1-septate, smooth with 10 or more short and curved bipolar appendages. Kohlmeyer et al. (1996a) did not assign the genus to any family but suggested that it may be related to the *Dothideales*. Later, Jones et al. (2009) placed the genus in *Pleosporales incertae sedis*. Suetrong et al. (2009) conducted a study on *Heleiosa* and, using molecular data, determined that the taxonomic position of this taxon remains unresolved. Nelsen et al. (2011) proposed that *H. barbatula* and *Funbolia dimorpha*, as non-lichen-forming taxa, have a close relationship within *Monoblastiaceae*. *Heleiosa* forms a sister clade with *Neoheliosia*, which differs in peridium and ascospore morphology (Mortimer et al. 2021). Currently the genus is accepted in *Eriomycetaceae* (Hyde et al. 2024). Sun et al. (2025), expanded the genus with introducing one new species and two new combinations.

Type species: *Heleiosa barbatula* Kohlm., Volkm.-Kohlm. & O.E. Erikss 1996

Other species: None



Note a Ascoma. b Ascus. c Ascospores. Scale bars: a = 50 µm, b = 20 µm, c = 5 µm

Source Redrawn from Kohlmeyer et al. 1996)

Figure 4.69 *Heleiosa barbatula*

Pseudorobillarda M. Morelet 1968

Classification: *Pseudorobillardaceae*, *Incertae sedis*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

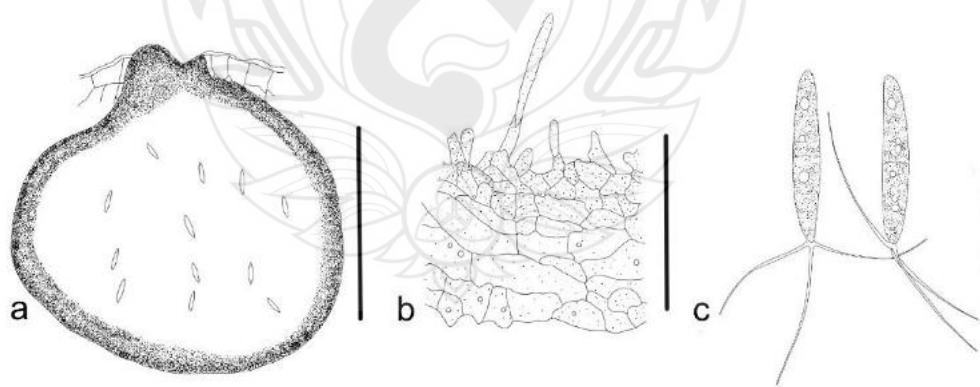
The genus *Pseudorobillarda* can be found as saprobes, endophytes, and pathogens, mostly in temperate and tropical regions. *Pseudorobillarda* species have

been isolated from terrestrial and freshwater habitats on various host plants and soil (Hongsan et al. 2020b, Li et al. 2020). The type species, *P. phragmitis* (based on *Robillarda phragmitis*, Cunnell 1958) was isolated from the halophyte *Phragmites australis* in the United Kingdom (Morelet 1968), with other records on *P. australis* in China (Poon and Hyde 1998, Johnson, and Hughes 1960, Calabon et al. 2021b). Another species of *Pseudorobillarda* was documented on *Spartina alterniflora* in Canada (Gessner and Kohlmeyer 1976; Calabon et al. 2021b). The genus has a coelomycetous asexual morph without a known sexual morph. The conidiomata are pycnidial, thick-walled, and ostiolate, containing filiform paraphyses. Conidiophores are present or reduced to phialidic or annellidic, enteroblastic, and hyaline conidiogenous cells. Conidia are hyaline, septate, or aseptate with flexuous, divergent appendages (Pem et al. 2019; Li et al. 2020). The presence of paraphyses and morphology of conidia are key characteristics for distinguishing species (Nag Raj, 1993). Twenty species are listed in Index Fungorum. The genus was placed in a novel family, *Pseudorobillardaceae*, based on morphology and molecular analyses of LSU sequence data (Crous et al. 2018a).

Type species: *Pseudorobillarda phragmitis* (Cunnell) M. Morelet 1968

Basionym: *Robillarda phragmitis* Cunnell 1958

Other accepted species: Species Fungorum (search *Pseudorobillarda*)



Note a Pycnidium. b Developing conidia. c Conidia. Scale bars: a = 200 µm, b, c = 20 µm

Source Redrawn from Cunnell (1958)

Figure 4.70 *Pseudorobillarda phragmitis*

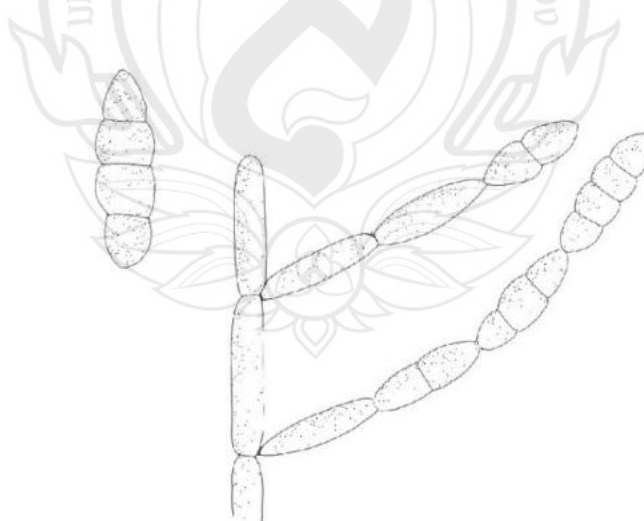
***Septonema* Corda 1837**

Classification: *Cylindrosympodiaceae*, *Venturiales*, *incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Septonema was introduced by Corda (1837) and was first isolated on *Betula alba* in the Czech Republic. The genus was typified with *S. secedens*, and there are 64 species recorded for this genus in Species Fungorum (accessed April 2026). *Septonema secedens* has been reported as a saprobe on the salt marsh plant *Juncus roemerianus* in the United States (Calabon et al. 2021b; Fell and Hunter 1979). *Septonema* develops as a hyphomycetous asexual morph, and sexual morph has not been determined yet. Conidiophores are brown, single or crowded, unbranched or with short branches. Conidiogenous cells are monoblastic or sympodial, bearing ramoconidia in branched chains (Pem et al. 2019; Hongsanant et al. 2020b). *Septonema* is classified within *Mytilinidiaceae* (*Mytilinidiales*) (Hyde et al. 2013; Hongsanant et al. 2020b). ITS, LSU, *rpb2*, and *tef1* are the available markers for some *Septonema* species on GenBank. It is suggested that further collections and sequence data are needed to confirm the certain taxonomic position of *Septonema* (Pem et al. 2019; Hongsanant et al. 2020b).

Type species: *Septonema secedens* Corda 1837

Other accepted species: Species Fungorum (search *Septonema*)



Note Conidiophore and conidia

Source Redrawn from Corda (1837)

Figure 4.71 *Septonema secedens*

***Trichodelitschia* Munk 1953**

Classification: *Phaeotrichaceae*, *Phaeotrichales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Trichodelitschia was established by Munk (1953) and typified with *T. bisporula*, which was initially classified as *Hormospora bisporula*, isolated from the dung of domestic cattle in France. There are five species listed in Index Fungorum, all introduced as saprobes on dung. There are two records of *T. bisporula* on salt marsh hosts, *Elymus pungens* and *Spartina townsendii*, from the United Kingdom (Apinis and Chesters 1964; Calabon et al. 2021b). Munk (1957) placed *Trichodelitschia* in *Sporormiaceae*, but later it was suggested to be placed in *Phaeotrichaceae* by Lundqvist (1964). Based on combined ITS and LSU and combined LSU and SSU sequence data, *Trichodelitschia* showed a close relationship with *Phaeotrichum* in *Phaeotrichaceae* (Hongsanan et al. 2020b). The morphology of *Trichodelitschia* is characterized by pseudothecial ascomata and 1-septate ascospores with hyaline to subhyaline terminal apophyses and circular germ pores at the spore apices (Ebersohn and Eicker 1992; Hongsanan et al. 2020b).

Type species: *Trichodelitschia bisporula* (P. Crouan & H. Crouan) Munk 1953

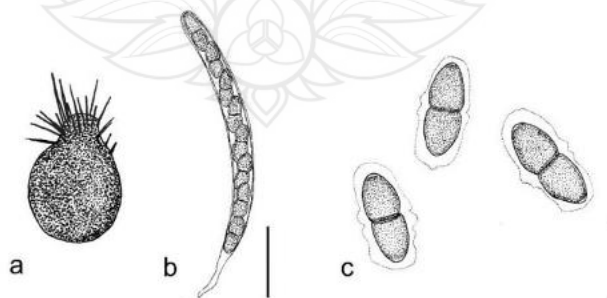
Basionym: *Hormospora bisporula* P. Crouan & H. Crouan 1867

Other accepted species: *Trichodelitschia adelphica* Luck-Allen 1970

Trichodelitschia lundqvistii N. Heine & P. Welt 2007

Trichodelitschia microspora Ebersohn & Eicker 1992

Trichodelitschia munkii N. Lundq. 1964



Note a Ascoma. b Ascus. c Ascospores. Scale bars: b = 50 μ m, c = 50 μ m

Source Redrawn from <https://www.centrodeestudiosmicologicosasturianos.org>, photo taken by Enrique Rubio

Figure 4.72 *Trichodelitschia bisporula*

Monodictys S. Hughes 1958

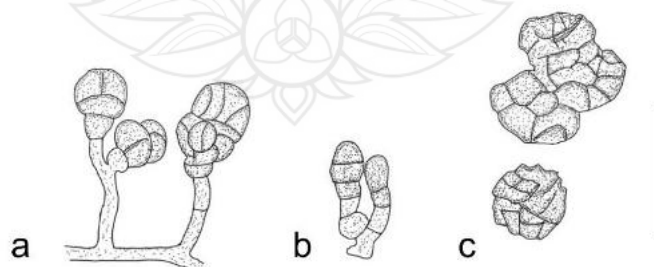
Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Hughes (1958) established the genus *Monodictys* in *Moniliales*, based on a new combination of *Melanconium putredinis*. There are over 58 accepted species of *Monodictys* listed in Species Fungorum (accessed April 2026), with a few species having available ITS, LSU, SSU, and *tef-1* sequence data. *Monodictys* is a polyphyletic genus, with its species positioned variably within *Leotiomycetes*, *Sordariomycetes* and *Dothideomycetes* in different phylogenetic analyses (Tanaka et al. 2015; Yeh and Kirschner 2019). Due to the lack of reliable DNA data for the type species, *M. putredinis*, the accurate taxonomic placement of this genus remains undetermined. The genus is characterized by its hyphomycetous asexual morph, with brown or olivaceous brown conidiophores. Conidiogenous cells are monoblastic and terminal, bearing acrogenous, dark brown, septate conidia with verrucose or echinulate surfaces (Pem et al. 2019). *Monodictys* species are saprobic on various substrates, with *M. austrina* recorded on *Juncus roemerianus* and *M. castaneae* on *Spartina* sp. as halophyte hosts (Fell and Hunter 1979; Miller and Whitney 1983; Calabon et al. 2021b). *Monodictys austrina* was first introduced from soil in Antarctica by Tubaki and Asano (1965), while *M. castaneae* was originally described from rotten wood in Germany (Wallroth 1833).

Type species: *Monodictys putredinis* (Wallr.) S. Hughes 1958

Basionym: *Melanconium putredinis* Wallr. 1833

Other accepted species: Species Fungorum (search *Monodictys*)



Note a Conidiophores. b Developing immature conidia. c Mature conidia. Scale bar: 25 µm

Source Redrawn from Gharizadeh et al. (2004)

Figure 4.73 *Monodictys castaneae*

Neottiosporina Subram. 1961

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

The saprobic genus *Neottiosporina* was introduced based on *Cryptostictis apoda* (Spegzanni 1910) on decaying *Achyrocline saturejoides* from Argentina, with other saprobic records on various plants (Index Fungorum). *Neottiosporina* has been documented on halophytes from China (Poon and Hyde, 1998). *Neottiosporina australiensis* was described on *Phragmites australis* by Sutton and Alcorn (1974), as well as other records from the Netherlands (Van Ryckegem and Verbeken 2005a, b; Van Ryckegem et al. 2007; Calabon et al. 2021b). There are ten species characterized by their asexual stage with thin-walled pycnidial and ostiolate conidiomata. Conidiophores are reduced to holoblastic, doliiiform conidiogenous cells. Conidia are cylindrical, navicular to obovoid, septate, and hyaline to brown, with a gelatinous sheath or appendage (Pem et al. 2019). Molecular data of ITS, LSU, SSU, *rpb2* and *tef1* are available for a few species of *Neottiosporina* in GenBank.

Type species: *Neottiosporina apoda* (Speg.) Subram. 1961

Basionym: *Cryptostictis apoda* Speg. 1910

Other accepted species: Species Fungorum (search *Neottiosporina*)



Note Developing conidia and conidia

Source Redrawn from Sutton and Alcorn (1974)

Figure 4.74 *Neottiosporina phragmiticola*

Otthia Nitschke ex Fuckel 1870

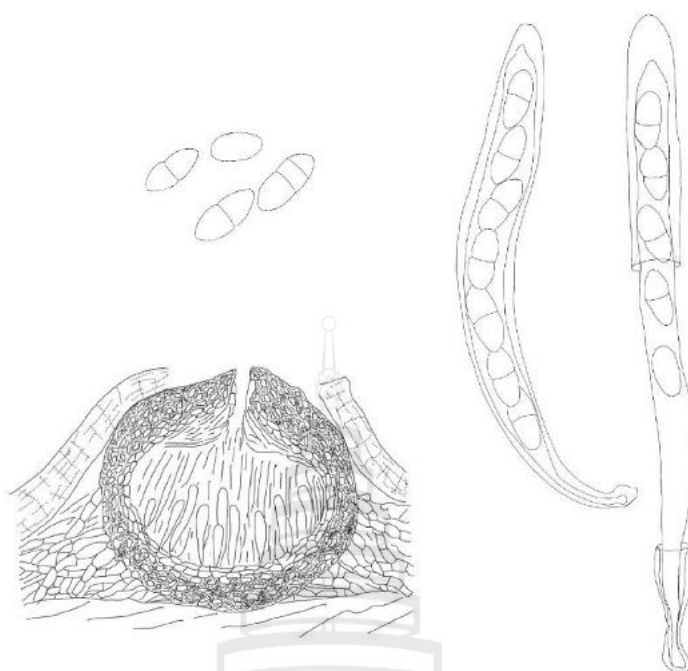
Classification: *incertae sedis*, *incertae sedis*, *incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Otthia was established by (Fuckel 1870) to accommodate plant-saprobic species, including *Otthia rosae*, *O. populina*, *O. spiraeae*, *O. urceolata*, and *O. quercus*. The genus is described based on its sexual morph, while the asexual morph remains undetermined (Pem et al. 2024). The ascostromata of *Otthia* develop gregariously to densely crowded, immersed in the host tissue or becoming erumpent through bark fissures. Ostioles, if present, are central and inconspicuous on the surface. The pseudoparaphyses are numerous and hypha-like. The asci are eight-spored, cylindrical, and have a short pedicle. Ascospores are uniseptate, initially hyaline but becoming dark brown at maturity, ovoid to broadly ellipsoidal, and arranged in overlapping row within the asci (Doilom et al. 2018). *Otthia* was historically linked to *Botryosphaeria* and *Botryosphaeriaceae* by some taxonomists based on morphology or a combination of morphology and LSU and SSU sequence data (Phillips et al. 2005; Kirk et al. 2008; Hu 2010). However, Doilom et al. (2018) placed it within *Dothideomycetes* genera *incertae sedis*, a classification later followed by Lumbsch and Huhndorf (2010b), Wijayawardene et al. (2017a, 2020), and Hyde et al. (2024a). The genus comprises approximately 50 species, but its precise taxonomic placement requires further studies and additional molecular data (Hyde et al. 2024a; Pem et al. 2024). One unidentified species of *Otthia* has been reported on the halophyte *Juncus roemerianus* (Calabon et al. 2021b).

Type species: *Otthia spiraeae* (Fuckel) Fuckel 1870

Basionym: *Cucurbitaria spiraeae* Fuckel 1864

Other accepted species: Species Fungorum (search *Otthia*)



Note a Ascoma, asci and ascospores (500×)

Source Redrawn from Booth (1958)

Figure 4.75 *Otthia spiraeae*

Trichometasphaeria Munk 1953

Classification: *incertae sedis*, *incertae sedis*, *incertae sedis*, Dothideomycetes, Pezizomycotina, Ascomycota, Fungi.

Munk (1953) introduced *Trichometasphaeria*, typified by *T. dianthi*. This genus is characterized by superficial ascomata with a papilla composed of dark brown setae. Asci are clavate, containing eight verrucose, septate ascospores that are hyaline to pale brown. The asexual morph has not been determined (Yuan and Barr 1994; Pem et al. 2019). *Trichometasphaeria* is similar to *Keissleriella* in having setae within the ascomata neck, and it has been considered synonymous with *Keissleriella* (Bose 1961). However, they differ in the structure of the ascoma centrum, and both are regarded as distinct genera (Barr 1990). *Trichometasphaeria* comprises six accepted species listed in Index Fungorum, most of which are isolated as saprobes on herbaceous plants. *Trichometasphaeria* sp. has been recorded on the halophyte *Elymus pungens* in the United Kingdom (Apinis and Chesters 1964; Calabon et al. 2021b).

Type species: *Trichometasphaeria dianthi* (Rostr.) Munk 1953

Basionym: *Metasphaeria dianthi* Rostr. 1905

Other accepted species:

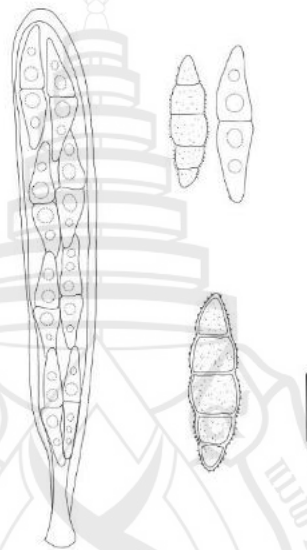
Trichometasphaeria barriae Chleb. 2009

Trichometasphaeria fuispora (Scheuer) Scheuer 1999

Trichometasphaeria papillisetosa Z.Q. Yuan & M.E. Barr 1994

Trichometasphaeria pentamera Munk 1957

Trichometasphaeria populi (Ellis & Everh.) M.E. Barr 1992



Note Ascus and ascospores. Scale bar = 20 µm

Source Redrawn from Yuan and Barr (1994)

Figure 4.76 *Trichometasphaeria papillisetosa*

Monascus Tiegh. 1884

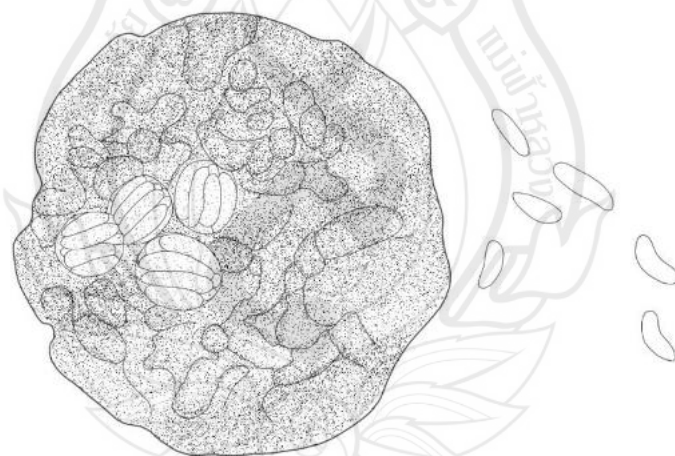
Classification: *Aspergillaceae*, *Eurotiales*, *Eurotiomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Tieghem (1884) established the genus *Monascus* to accommodate two species, *Monascus ruber* and *M. mucoroides*, characterized by stiped cleistothecial ascomata. Subsequent studies introduced additional species to the genus, and *Basipetospora* was considered its asexual morph. *Basipetospora* produces truncate-based aleurioconidia in a basipetal manner (Cole and Samson 1979; Barbosa et al. 2017). The taxonomic placement of the genus at higher ranks was previously unclear, but molecular studies later placed it in the family *Aspergillaceae* (*Eurotiales*) (Berbee et al. 1995; Ogawa and

Sugiyama 2000; Barbosa et al. 2017). Barbosa et al. (2017) investigated the phylogenetic relationships in *Monascus* using a polyphasic approach, incorporating ITS, LSU, β -tubulin, calmodulin, and *rpb2* sequences for their phylogenetic analyses, and accepted nine species. *Monascus* species have been collected from various substrates, including plants, soil, honey, pollen, and nests of stingless bees (Tieghem 1884; Stchigel et al. 2004; Barbosa et al. 2017). *Monascus purpureus* is the only species reported from a salt marsh plant, *Elymus pungens*, in the United Kingdom (Calabon et al. 2021b). *Monascus* species, including *M. purpureus*, are economically important, particularly for their use as yellow and red food colorants in fermented Asian foods and for producing compounds with potential medicinal applications (Pattanagul et al. 2007; Shi and Pan. 2011; Vendruscolo et al. 2014; Moradi and Mortazavi 2024). The results of a study by Safari et al. (2025) showed that a diet containing *M. purpureus* pigments had a positive effect on growth, fillet color quality, and immune responses of crayfish.

Type species: *Monascus ruber* Tiegh. 1884

Other accepted species: Species Fungorum (search *Monascus*)



Note Ascoma, asci and ascospores. Scale bar = 10 μ m

Source Redrawn from Stchigel et al. (2004)

Figure 4.77 *Monascus lunisporas*

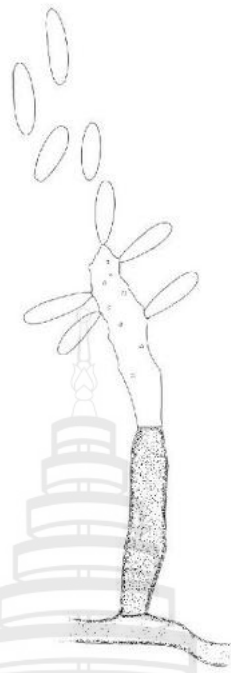
Rhinocladiella Nannf. 1934

Classification: *Herpotrichiellaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Nannfeldt introduced *Rhinocladiella*, typified by *Rhinocladiella atrovirens*, which was collected from wood of *Pinus* in Sweden (Melin and Nannfeldt 1934). Members of *Rhinocladiella* are black yeast-like fungi that produce exophiala-type budding cells in culture. The conidial apparatus is typically branched and olivaceous-brown. Conidiogenous cells are polyblastic, occurring intercalarily or terminally, and with a sympodially proliferating subdenticulate rachis. Conidia are unicellular, subglobose with a slightly pigmented hilum (Arzanlou et al. 2007). The sexual morph is currently unknown. The genus comprises approximately 20 species (Hyde et al. 2024a), found as saprobes or as pathogens of plants and humans (Agarwal 1969, Arzanlou et al. 2007; Mohammadi et al. 2017; Roeun et al. 2022). Several species are known to cause human diseases; for example, *R. aquaspersa* is associated with verrucous skin infections (Badali et al. 2010), and *R. mackenziei* is a known agent of cerebral phaeohyphomycosis (Arzanlou et al. 2007; Mohammadi et al. 2017). Two unidentified species of *Rhinocladiella* have been recorded as saprobes on salt marsh plants, *Juncus roemerianus* and *Phragmites australis*, from the USA and China, respectively (Calabon et al. 2021b). Morphological characteristics, along with ITS and LSU sequence data, are useful for species delineation (Arzanlou et al. 2007; Roeun et al. 2022).

Type species: *Rhinocladiella atrovirens* Nannf. 1934

Other accepted species: Species Fungorum (search *Rhinocladiella*)



Note Conidiophore and conidia

Source Redrawn from Seifert et al. (2011a)

Figure 4.78 *Rhinocladiella atrovirens*

Veronaea Cif. & Montemart. 1957

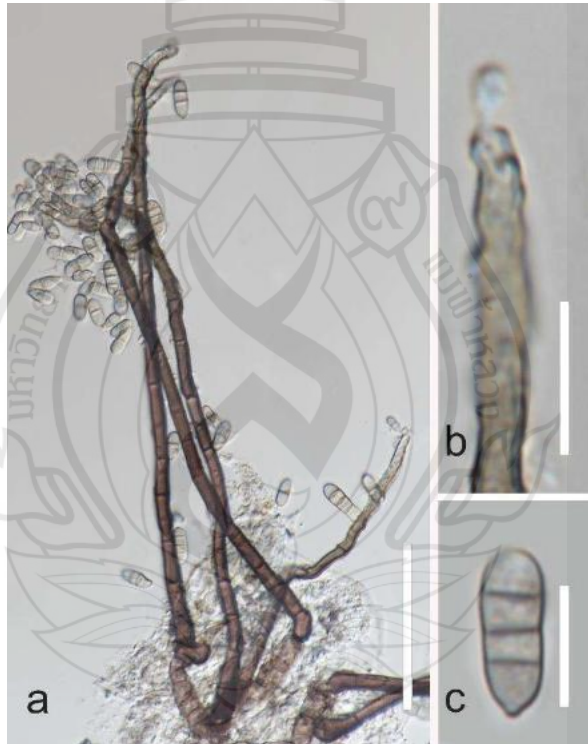
Classification: *Herpotrichiellaceae*, *Chaetothyriales*, *Chaetothyriomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cifferi and Montemartini (1958) introduced the genus *Veronaea* to accommodate its type species, *Veronaea botryosa*, which was isolated from olive slag in Italy. Species of *Veronaea* have been reported from a variety of substrates, including dung, soil, and dead plant material (Arzanlou et al. 2007). One unidentified *Veronaea* species has been recorded as a saprobe on the halophyte *Juncus roemerianus* from the USA (Calabon et al. 2021b). *Veronaea botryosa* has been identified as a causal agent of human diseases such as phaeohyphomycosis and chromoblastomycosis (Bonifaz et al. 2013, Zhu et al. 2015). The genus currently includes 21 species, although sequence data are available for only six of them (Chandrasiri et al. 2021; Su et al. 2023; Hyde et al. 2024a). Su et al. (2023) introduced a novel species, *V. polyconidia*, based on morphological features and phylogenetic analyses of SSU, ITS, LSU, and Btub

sequence data. The sexual morph of *Veronaea* remains unknown, while the asexual morph is hyphomycetous, characterized by erect, pale to medium- or olivaceous-brown conidiophores, polyblastic cylindrical conidiogenous cells, a rachis with unthickened scars, and cylindrical to pyriform, pale brown to brown conidia. *Veronaea* does not produce Exophiala-type budding cells in culture (Arzanlou et al. 2007; Chandrasiri et al. 2021). Previously, there was taxonomic confusion among *Ramichloridium*, *Veronaea*, and *Rhinocladiella*; however, Arzanlou et al. (2007) showed the placement of *Veronaea* and *Rhinocladiella* in *Chaetothyriales*, while *Ramichloridium* is placed in the *Capnodiales*.

Type species: *Veronaea botryosa* Cif. & Montemart. 1957

Other accepted species: Species Fungorum (search *Veronaea*)



Note a Conidiophores. b Conidiogenous cells. c Conidium. Scale bars: a = 50 μm , b = 20 μm , c = 5 μm .

Figure 4.79 *Veronaea botryose*

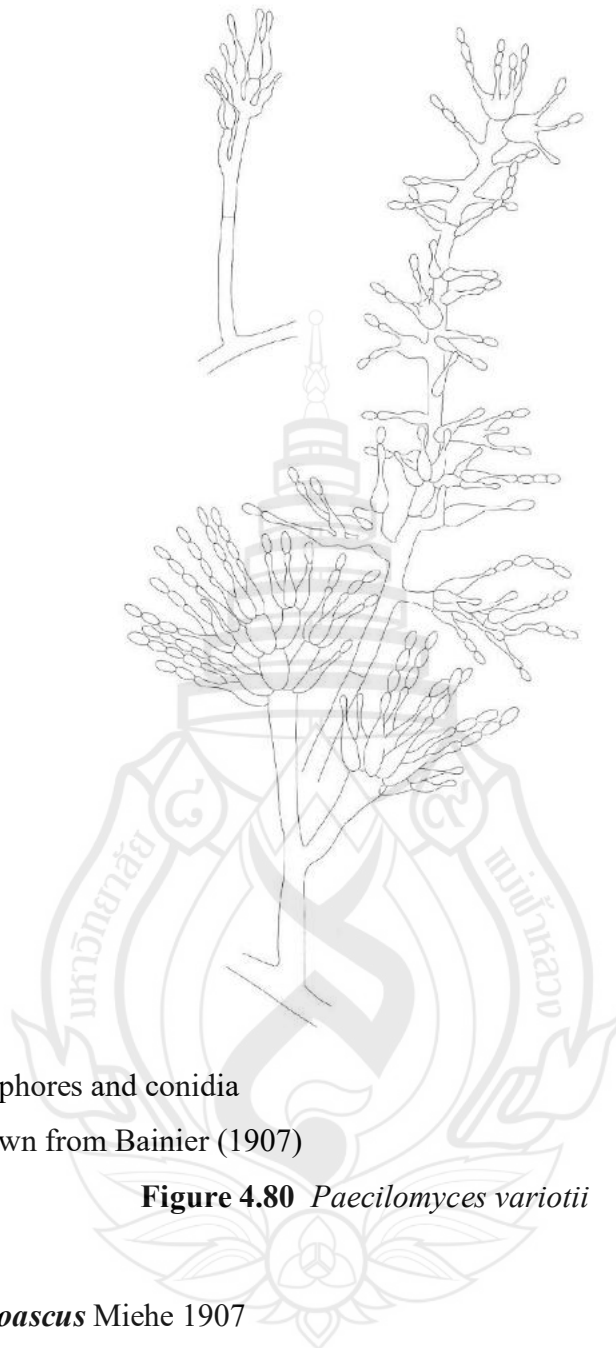
Paecilomyces Bainier 1907

Classification: *Thermoascaceae*, *Eurotiales*, *Eurotiomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Paecilomyces was established by Bainier (1907) as a *Penicillium*- and *aspergillus*-like genus. The asexual morph of *Paecilomyces* is characterized by irregularly branched conidiophores and phialides with an inflated base that taper abruptly into long cylindrical necks, producing catenate, olive-brown conidia (Samson et al. 2009; Houbraken et al. 2020). Phylogenetic analysis of SSU sequence data revealed the polyphyletic placement of *Paecilomyces* within both Sordariomycetidae and Eurotiomycetidae (Samson 1974), with the type species, *Paecilomyces variotii*, placed in the order *Eurotiales* (Luangsa-Ard et al. 2004). The sexual morph of *Paecilomyces* is linked to *Byssosclamyces*, a thermotolerant genus that produces smooth-walled, ellipsoidal ascospores (Samson et al. 2009; Houbraken et al. 2020). The use of the name *Paecilomyces* was proposed over *Byssosclamyces* (Rossman et al. 2016, Houbraken et al. 2020). Houbraken et al. (2020) reviewed several taxa within Eurotiales and accepted the family *Thermoascaceae*, which comprises two genera: *Paecilomyces* and *Thermoascus*. These genera cluster together in their phylogenetic analyses based on combined datasets of *rpb1*, *rpb2*, *Cct8*, *Tsr1*, *cam*, *benA*, SSU, LSU, and ITS. *Paecilomyces* species have been recorded from various substrates, including plants, soil, human tissue, and food. They have also been reported from salt marsh plants, with three undetermined species identified as saprobes (Calabon et al. 2021b). *Paecilomyces* is one of the frequently reported genera of marine-derived fungi, and *P. variotii* has been listed as a marine species (Jones et al. 2019). *Paecilomyces* species are highly heat-resistant and are considered very important spoilage fungi, particularly in heat-processed foods (Samson et al. 2009). In addition, they have been investigated for their beneficial applications, such as biological control agents against pests and diseases.

Type species: *Paecilomyces variotii* Bainier 1907

Other accepted species: Species Fungorum (search *Paecilomyces*)



Note Conidiophores and conidia

Source Redrawn from Bainier (1907)

Figure 4.80 *Paecilomyces variotii*

Thermoascus Miehe 1907

Classification: *Thermoascaceae*, *Eurotiales*, *Eurotiomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Thermoascus was described by Hugo Miehe (1907) to accommodate *Thermoascus aurantiacus* as the type species. Species of *Thermoascus* are thermophilic and have been isolated on different substrate such as soil, bird nest and dead plant material (Apinis and Chesters 1964; Samson and Tansey 1975; Houbroken et al. 2020). Although *Thermoascus* species have been reported as food spoilage agents, the type

species has gained attention due to its ability to produce thermostable enzymes (Hosoya et al. 2014; McClendon et al. 2012). *Thermoascus egyptiacus* was isolated from marine sludge in Egypt, and *Thermoascus crustaceus* was reported from the halophyte *Elymus pungens* in the United Kingdom (Calabon et al. 2021b). The taxonomic placement of *Thermoascus* has changed over time. Houbraken et al. (2020) restudied this genus and accepted seven species based on phylogenetic analyses of nine loci: *rpb1*, *rpb2*, *cct8*, *tsr1*, *cam*, *benA*, SSU, LSU, and ITS. Sexual morph of *Thermoascus* includes orange-yellow, brown, or red-brown cleistothecia. When present, asexual morph is paecilomyces-like or polypaecilum-like (Houbraken et al. 2020).

Type species: *Thermoascus aurantiacus* Miehe 1907

Other accepted species:

Thermoascus crustaceus (Apinis & Chesters) Stolk 1965

Thermoascus egyptiacus S. Ueda & Udagawa 1983

Thermoascus endophyticus T.M. Silva, C.S. Oliveira & J.D.P. Bezerra 2024

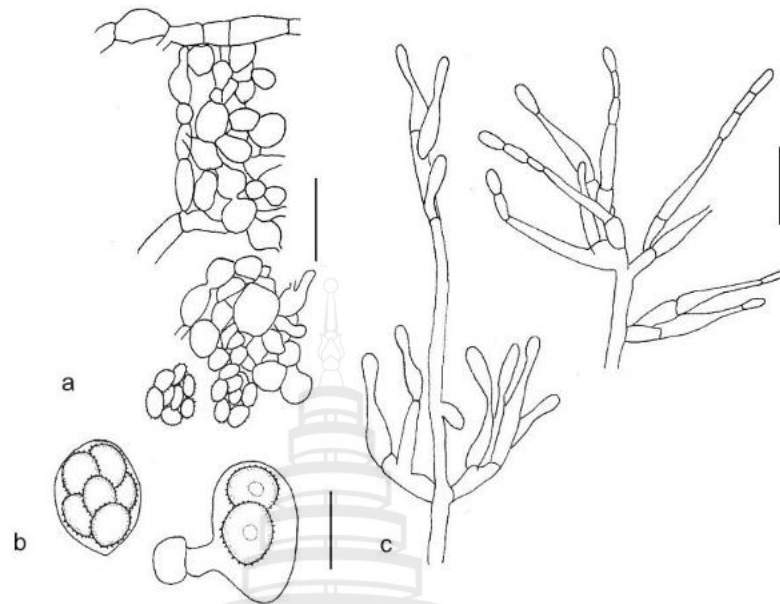
Thermoascus simplicissimus Sastoque, Stchigel & Cano 2026

Thermoascus taitungiacus K.Y. Chen & Z.C. Chen 1996

Thermoascus thermophilus (Sopp) Arx 1970

Thermoascus verrucosus (Samson & Tansey) Houbraken, Frisvad & Samson
2020

Thermoascus yaguchii Houbraken, Frisvad & Samson 2020



Note a Structure of the peridium with clusters of asci, b Asci and ascospores. c Conidiophores. Scale bars: a, c = 20 µm, b = 10 µm

Source Redrawn from Apinis and Chesters (1964)

Figure 4.81 *Thermoascus crustaceus*

Thermomyces Tsikl. 1899

Classification: *Trichocomaceae*, *Eurotiales*, *Eurotiomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Thermomyces was introduced based on the thermophilic fungus *T. lanuginosus*, which can be cultivated at temperatures between 42°C and 60°C (Tsiklinsky 1899). To eliminate thermophilic associated bacteria and obtain a pure culture, the fungus was first grown on white bread, where it grows abundantly, and then the spores were transferred to media plates (Tsiklinsky 1899). Phylogenetically, *Thermomyces* is closely related to *Ascospirella*, but *Ascospirella* species are mesophilic. Additionally, *Ascospirella* differs in its penicillium-like conidiophores and the production of yellow to orange ascomata (Wijayawardene et al. 2022). Five species of *Thermomyces* are listed in Species Fungorum (Accessed April 2026). *Thermomyces dupontii* was reported on the halophyte *Elymus pungens* in the United Kingdom (Apinis and Chesters 1964; Calabon et al. 2021b). This species, formerly classified under *Penicillium*, was

synonymized as a *Thermomyces* species by Houbraken et al (2014) based on phylogenetic analyses of a combined data *cct8*, *tsr1*, *rpb1*, and *rpb2* sequence data. It is characterized by hyaline, branched hyphae with a short fertile part and globose-ovoid conidia developing in chains (Griffon and Maublanc 1911). *Thermomyces dupontii* has recently gained attention for producing highly thermostable enzymes (Wang et al 2019, Li et al. 2022).

Type species: *Thermomyces lanuginosus* Tsikl. 1899

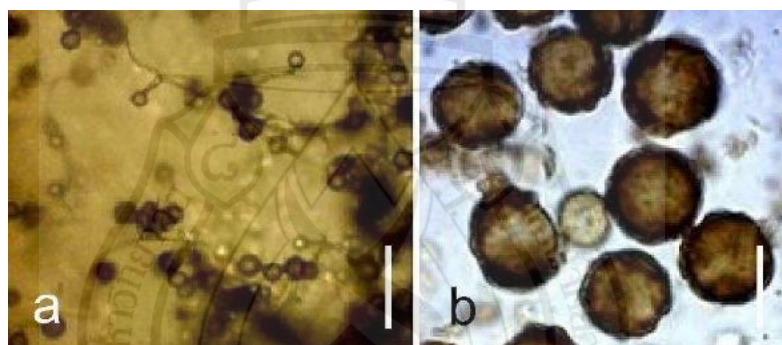
Other accepted species:

Thermomyces dupontii (Griffon & Maubl.) Houbraken & Samson 2014

Thermomyces ibadanensis Apinis & Eggins 1966

Thermomyces stellatus (Bunce) Apinis 1963

Thermomyces thermophilus (Stolk) P.M. Kirk 2014



Note a Conidiophores. b Conidia. Scale bars: a = 10 μ m, b= 5 μ m

Source Redrawn from Yousofvand et al. (2020)

Figure 4.82 *Thermomyces lanuginosus*

Albidomyces Torres-Garcia, Dania García, Cano & Gené 2023

Classification: *Nearthropsidaceae*, *Onygenales*, *Eurotiomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

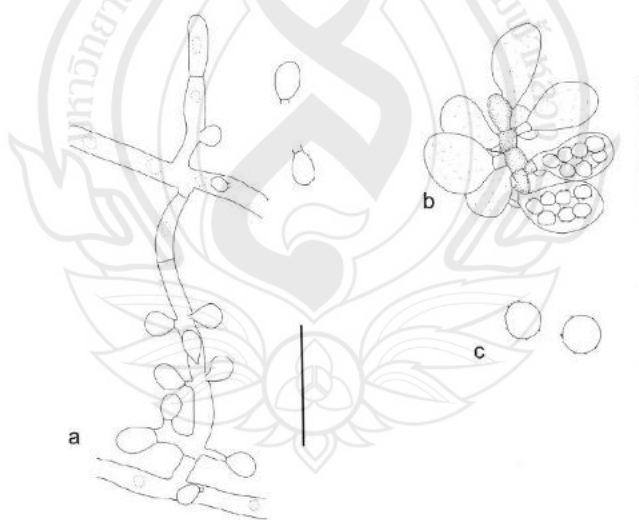
Albidomyces was established by Torres-Garcia et al. (2023) to accommodate its only species, *Albidomyces albicans* and based on *Arachniotus albicans* (Apinis 1964). The genus is characterized by whitish colonies on culture media, with a chrysosporium-like asexual morph. Conidiophores are indistinguishable, and fertile hyphae are straight to flexuous, septate, and branched. Conidia form terminally or laterally, are aseptate, subglobose or pyriform, and hyaline. Sexual morph has white gymnothecial ascomata

with a peridium made of loosely interwoven hyaline hyphae. Ascomata initials form on a side branch spirally twisted around the ascogonium. Asci are oval, form in clusters on short stalks, and contain eight aseptate, hyaline, slightly punctate ascospores (Apinis 1964; Torres-Garcia et al. 2023). The taxonomic placement of *Arachnietus albicans* has shifted between different genera such as *Arachnietus*, *Amauroascus*, and *Arachnotheca*. However, Torres-Garcia et al. (2023), based on phylogenetic analyses of combined ITS and LSU data, showed that this species is distinct from others in *Onygenales*. Thus, based on both morphological and molecular evidence, they introduced a new monotypic genus in *Neoarthropsidaceae*. *Albidomyces albicans* has been isolated from various habitats such as freshwater sediments, soil, and rhizosphere soil (Torres-Garcia et al. 2023). It has also been reported on salt marsh plants *Elymus pungens* and *Spartina townsendii* in the United Kingdom (Calabon et al. 2021b).

Type species: *Albidomyces albicans* (Apinis) Torres-Garcia, Dania García, Cano & Gené 2023

Basionym: *Arachnietus albicans* Apinis 1964

Other accepted species: None.



Note a Conidiophores and conidia. b, c Asci and ascospores. Scale bars: 20 µm

Source Redrawn from Apinis (1964)

Figure 4.83 *Albidomyces albicans*

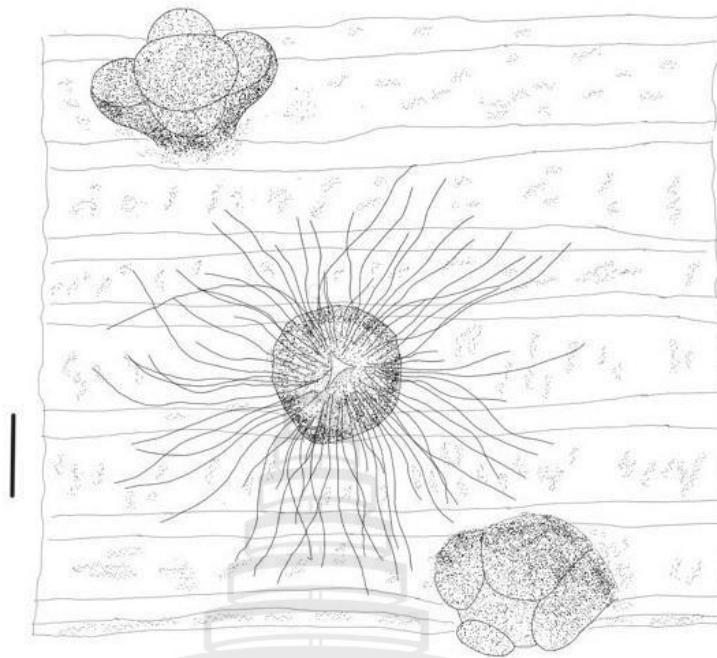
Glomerobolus Kohlm. & Volkm.-Kohlm. 1996

Classification: *Stictidaceae*, *Ostropales*, *Ostropomycetidae*, *Lecanoromycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Kohlmeyer and Volkmann-Kohlmeyer (1996a) established *Glomerobolus* to accommodate *G. gelineus* collected from senescent culms of *Juncus roemerianus* in salt marshes in North Carolina, USA (Calabon et al. 2021b). They introduced it as the first ballistic member of *Agonomycetales*. *Glomerobolus gelineus* has a unique reproductive structure called a hyphoma, made up solely of sterile hyphae embedded in a gelatinous matrix and it produces a ballistic propagule. This propagule is forcefully ejected due to water absorption by the gelatinous matrix and forms new mycelium in the host tissue. The hyphoma in *Glomerobolus* forms a tap root-like base without gel and a superficial 'calyx' of several ellipsoidal lobes with crystals in the outer lobes. These lobes become horny with dryness and dilate with moisture, surrounding a central ball. The propagule is composed of branched hyphae in a gelatinous matrix, dehiscing at maturity and forcefully ejected by the squeezing action of the 'calyx' (Kohlmeyer and Volkmann-Kohlmeyer 1996a; Schoch et al. 2006a). Schoch et al. (2006a) placed *Glomerobolus* in *Ostropales* based on morphological features such as crystal presence and the absence of sexual and asexual spores. Additionally, their molecular analyses of combined SSU, LSU, and *rpb2* confirmed its placement and relationship with *Stictidaceae*. The second other species in this genus is *Glomerobolus poacearum*, isolated from *Poaceae* in china (Gao et al. 2024).

Type species: *Glomerobolus gelineus* Kohlm. & Volkm.-Kohlm. 1996

Other accepted species: *Glomerobolus poacearum* Ying Gao & H. Gui 2024



Note Hyphoma on host. Scale bar =150 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (1996a)

Figure 4.84 *Glomerobolus gelineus*

Amorphotheca Parbery 1969

Classification: *Amorphothecaceae*, *Helotiales*, *Leotiomyetidae*, *Leotiomyetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Amorphotheca was established by Parbery (1969) to accommodate *A. resinae*, which was isolated from soil in Australia. This species has also been recorded as saprobic on the roots of *Spartina* sp. in Canada (Miller and Whitney 1983; Calabon et al. 2021b). The genus is characterized by immersed to superficial, globose to irregular ascomata in culture with a non-hyphal peridium. The asci are 8-spored, pyriform to globose, unitunicate, evanescent, and develop among radiating hyphae. The ascospores are hyaline to brown, unicellular, biguttulate, with a constricted inner membrane. Asexual morph is cladosporium-like (Parbery 1969). *Amorphotheca resinae* is the only species in this genus and has gained significant attention due to its ability to absorb hydrocarbon fuel in some of its strains. This ability can cause problems for aviation

equipment, such as deteriorating aviation fuel and corroding metal elements (Krivushina et al. 2023).

Type species: *Amorphotheca resinae* Parbery 1969

Other accepted species: None



Note Asexual morph (at the top) a Conidiophores. b Conidiogenous cells and conidia. Sexual morph (below). c Ascoma. d Asci and ascospores. Scale bar = 10 μ m

Source Redrawn from Parbery (1969)

Figure 4.85 *Amorphotheca resinae*

Cyathicula De Not. 1863

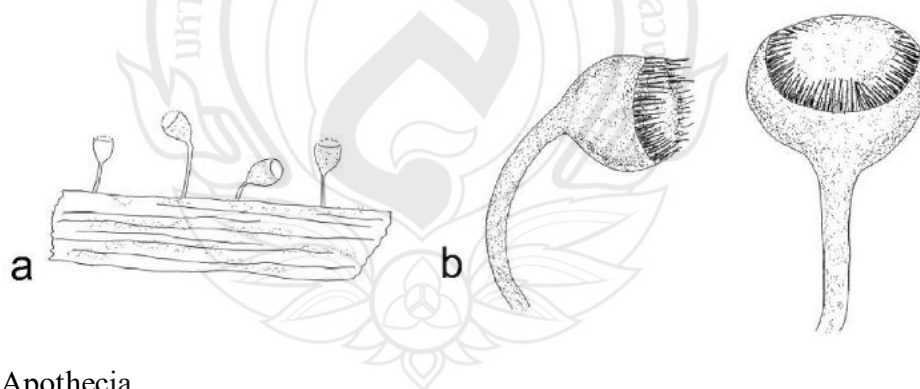
Classification: *Helotiaceae*, *Helotiales*, *Leotiomyetidae*, *Leotiomyetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cyathicula belongs to the class *Leotiomyces* (Hyde et al. 2024b) and is characterized by cup-shaped apothecia that are initially closed and later open, with a distinct fringe of bristly teeth along the margin. The genus produces filamentous, hyaline paraphyses and cylindrical to clavate asci, which contain hyaline, aseptate to 1-septate ascospores (Rehm 1995). *Cyathicula* was typified with *C. coronata*, originally collected from dry stems of various plants such as *Clematis*, *Urtica*, *Atropa*, and *Cirsium* (Rehm 1995). According to Index Fungorum (April 2026), 93 epithets have been published under *Cyathicula*, although many have since been transferred to other genera, including *Crocicreas*, *Leptopeltis*, and *Brunnipila*. The genus currently includes around 25 accepted species (Hyde et al. 2024a). Among them, *Cy. culmicola* has been reported from the salt marsh plant *Elymus pungens* in the United Kingdom (Calabon et al. 2021b). Hyde et al. (2024b) conducted a phylogenetic analysis based on combined ITS and LSU sequence data of *Helotiaceae*, including *Cyathicula*, and introduced two new species: *C. dioscoreae* and *C. rusci*.

Type species: *Cyathicula coronata* (Bull.) Rehm 1893

Basionym: *Peziza coronata* Bull. 1789

Other accepted species: Species Fungorum (search *Cyathicula*)



Note Apothecia

Source Redrawn from Batsch (1783)

Figure 4.86 *Cyathicula coronata*

Brunnipila Baral 1985

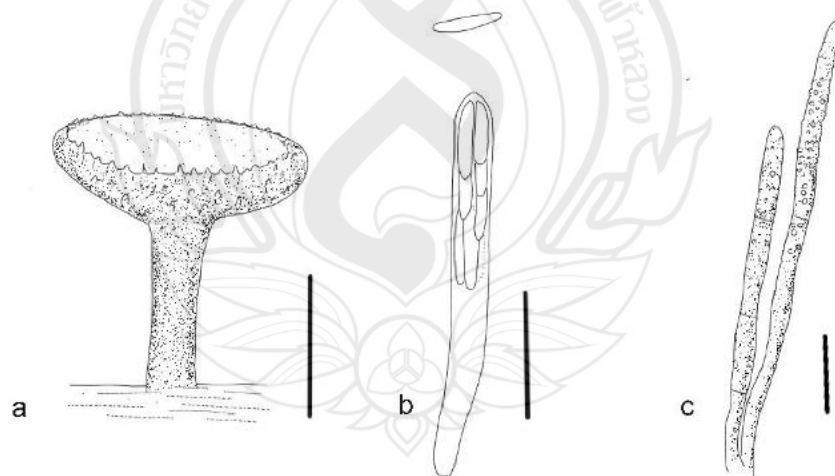
Classification: *Lachnaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Baral (1985) introduced the genus *Brunnipila* to accommodate six species: *B. calycioides*, *B. calyculiformis*, *B. clandestina*, *B. fagicola*, *B. fuscescens*, and *B. palearum*, which were previously classified under *Peziza* or *Trichopeziza* or *Lachnella*. The genus currently comprises 12 species, primarily saprobic on dead plant material (Species Fungorum, April 2026). Notably, *Brunnipila palearum* has been recorded on salt marsh hosts *Elymus pungens* and *Spartina townsendii* from the United Kingdom (Apinis and Chesters 1964; Calabon et al. 2021b). *Brunnipila* is characterized by stipitate apothecia covered with hyaline to brown hairs, with hair apices either naked or bearing octahedral-shaped crystals. Asci are cylindrical to clavate, containing ellipsoid to fusiform unicellular ascospores (Suková 2005; Šandová et al. 2018). Suková (2005) examined selected lignicolous species of *Brunnipila* and noted that the hair crystals of this genus are less sharp compared to *Incrucipulum*. ITS, LSU, SSU and *rpb2* sequences are available for this genus on NCBI (accessed on September 2024).

Type species: *Brunnipila clandestina* (Bull.) Baral 1985

Basionym: *Peziza clandestina* Bull. 1791

Other accepted species: Species Fungorum (search *Brunnipila*)



Note a Apothecia on dead culms. b Ascus and ascospore. c Excipular hairs. Scale bars: a = 20 µm, b, c = 10 µm

Source Redrawn from Koukol et al. (2020)

Figure 4.87 *Brunnipila palearum*

Belonopsis (Sacc.) Rehm 1891

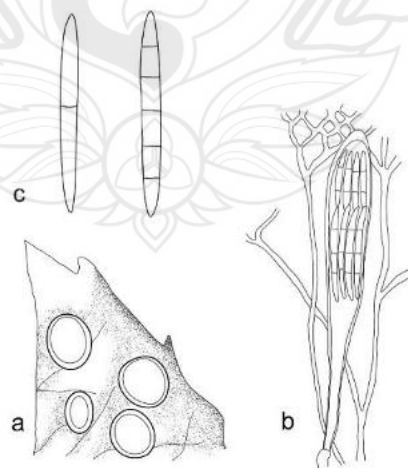
Classification: *Mollisiaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Belonopsis was established by Rehm (1981) to accommodate *Belonopsis excelsior* and *B. decolorans*, which were previously classified under *Peziza* and *Helotium*, respectively. The genus is placed in the order *Helotiales* and is characterized by the formation of apothecia in small clusters, with ascospores that are elongated, spindle- to needle-shaped, aseptate and becoming multiseptated with maturity (Rehm 1981). Morphologically, *Belonopsis* is similar to *Neobelonopsis*; however, the latter can be distinguished by its apothecia arising from a dark-hued hyphal mass on the substrate surface, a brownish receptacle, and the absence of crystals in the medullary excipulum (Hyde et al. 2024a). ITS, SSU, LSU and *rpb1* are available molecular barcode for *Belonopsis* on GenBank (May 2025). Approximately 20 species are currently recognized within *Belonopsis*, most of which are saprobic on dead plant material (Rehm 1981; Hyde et al. 2024a). Several species have also been reported from salt marsh vegetation, including *B. atriella* on *Spartina cynosuroides* (Calabon et al. 2021b), *B. excelsior* on *Phragmites australis* (Rehm 1981), *B. ebudensis* on *Phragmites* sp. (Dennis 1990), and *B. juncicola* on *Juncus* sp. (Graddon 1991).

Type species: *Belonopsis excelsior* (P. Karst.) Rehm 1891

Basionym: *Peziza excelsior* P. Karst. 1869

Other accepted species: Species Fungorum (search *Belonopsis*)



Note a Ascomata on host. b Ascus. c Ascospores

Source Redrawn from Engler and Prantl (1900)

Figure 4.88 *Belonopsis uredo*

Halenospora E.B.G. Jones 2009

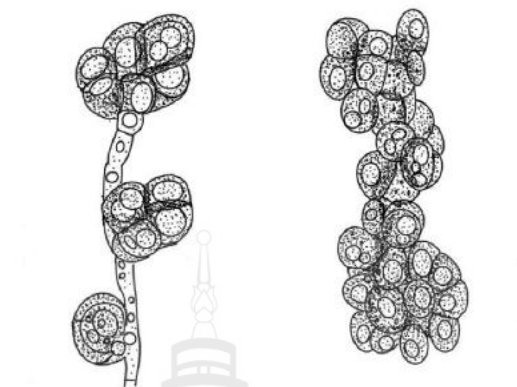
Classification: *Tricladiaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Halenospora is a saprobic genus widely distributed on intertidal submerged leaves and wood, mostly on mangroves (Jones et al. 2009, Pang et al. 2011). It has also been isolated from halophytes such as *Juncus roemerianus*, *Spartina* spp., and *Spartina densiflora* (Calabon et al. 2021b). Molecular analyses of ITS sequences showed that *Zalerion varia* formed a distinct clade with *Z. maritima*, the type species of *Zalerion* (Bills et al. 1999). *Zalerion varia* was positioned in *Leotiaceae*, while *Z. maritima* is a member of the *Lulworthiales* (Campbell et al. 2005). Subsequently, Jones et al. (2009) established a new genus to accommodate *Halenospora varia*. *Halenospora* and *Zalerion* also differ in the morphology of their spiral conidia (Anastasiou 1963; Jones et al. 2009). Sexual morph of *Halenospora* is unknown. Asexual morph is hyphomycetous, characterized by simple, cylindrical, hyaline to pale olivaceous conidiophores with irregular helicoid or coiled conidia forming a knot or ball. The conidia are brown to dark brown with a smooth, thick wall. Complex conidia, comprising several hundred cells, can also form within the substrate (Pang et al. 2011; <https://www.marinefungi.org/>). The genus includes the type species, *H. varia*, which was formerly classified under *Zalerion* (Jones et al. 2009) and *H. multiseptata*, formerly classified as *Scytalidium* (Li et al. 2026).

Type species: *Halenospora varia* (Anastasiou) E.B.G. Jones 2009

Basionym: *Zalerion varia* Anastasiou 1963

Other accepted species: *Halenospora multiseptata* (Hol.-Jech.) D.W. Li & N.P. Schultes 2025



Note Highly convoluted, knot like conidia. Scale bar = 10 μ m

Source Redrawn from Jones et al. (2009)

Figure 4.89 *Halenospora varia*

Botrytis P. Micheli ex Pers. 1794

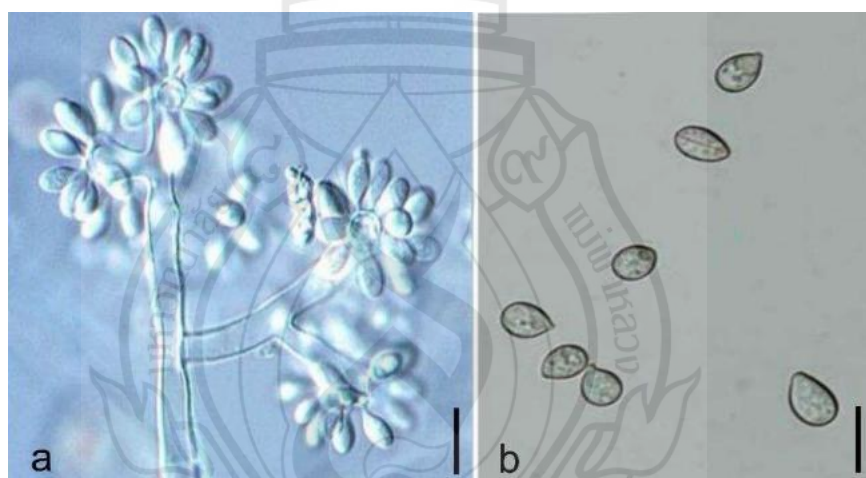
Classification: *Sclerotiniaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Botrytis, commonly known as gray mold, is an economically important plant pathogen, with *B. cinerea* recognized as its type species (Bautista-Baños 2014). *Botrytis* infects over 1,400 plant species (Elad et al. 2016) and is a major pre- and post-harvest pathogen in various crops such as grapes, strawberries, tomatoes, apples, and peaches (Bautista-Baños 2014, Jayawardena et al. 2018), causing significant yield and quality losses estimated at 10 to 100 billion USD annually worldwide (Boddy 2015). Interestingly, *Botrytis cinerea* has also been reported from marine habitats (Jones et al. 2019) and salt marsh ecosystems, including associations with *Spartina townsendii* and as a saprobe on *Spartina* sp. (Calabon et al. 2021b). *Botrytis cinerea* is considered an important model organism for studying plant-pathogen interactions and the development of fungicide resistance (Staats et al. 2005; Hahn 2014; Valero-Jiménez et al. 2019). The genus *Botrytis* was first established by Micheli in 1729 to accommodate 26 species and now includes approximately 70 species, and is one of the ten most cited fungal genera globally (Bhunjun et al. 2024; Hyde et al. 2024a). Both sexual and asexual morphs are recognized, but the asexual name *Botrytis* is recommended for use

over the sexual morph *Botryotinia*, as it is older and more commonly used (Kirk et al. 2013; Hyde et al. 2014). The asexual morph is characterized by branched, septate mycelia with conidiophores arising from them. Macroconidia are ellipsoidal to obovoid and pale brown. Microconidia are sphaerical and smaller than macroconidia. Sclerotia, which serve as survival structures, are commonly formed and germinate under favorable conditions. Sclerotia are considered as maternal parent in the production of sexual morph and developing apothecia (Hyde et al. 2014). Genetic markers such as *g3pdh*, *rpb2*, and *hsp60* are valuable for taxonomic placement within the *Sclerotiniaceae* and broader ascomycetes, while *nep1* and *nep2* offer higher resolution within the genus *Botrytis* (Hyde et al. 2014).

Type species: *Botrytis cinerea* Pers. 1801

Other accepted species: Species Fungorum (search *Botrytis*)



Note a Conidiophores. b Conidia. Scale bars: 20 μ m

Source Redrawn from Jayawardena et al. (2018)

Figure 4.90 *Botrytis cinerea*

Cadophora Lagerb. & Melin 1927

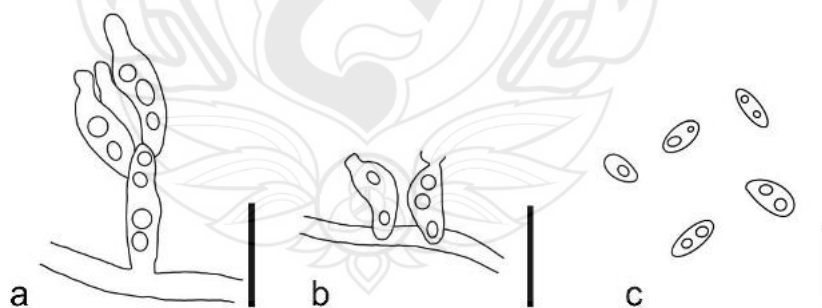
Classification: *incertae sedis*, *Helotiales*, *Leotiomyetidae*, *Leotiomyetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cadophora was introduced by Lagerberg et al. (1927), with *Cadophora fastigiata* designated as the type species, originally collected from dead wood of *Pinus sylvestris* and *Picea excelsa* in Sweden. The genus is primarily known for its hyphomycetous asexual morph, producing conidiophores bearing phialides singly or in

groups of two or three, with flask-shaped, hyaline collarettes (Lagerberg et al. 1927, Chen et al. 2022a; Travadon et al. 2015). Due to morphological overlap among species, phylogenetic analyses are essential for accurate identification (Chen et al. 2022a). Commonly used molecular markers for species delimitation in *Cadophora* include the internal transcribed spacer (ITS) region, translation elongation factor 1- α (*tef1*), and beta-tubulin (*tub2*) gene sequences (Chen et al. 2022a). The genus currently comprises approximately 30 species isolated from diverse environments, including soil, decaying plant material, and as pathogens of economically important crops (Chen et al. 2022a; Hyde et al. 2024a). For instance, *Cadophora* species have been reported as the causal agents of several plant diseases, including brown stem rot in soybean (Allington and Chamberlain 1948), wood decay in kiwifruit (Di Marco et al. 2004), Petri disease and esca in grapevines (Travadon et al. 2015; Díaz et al. 2023), and trunk disease in citrus (Espargham et al. 2020). Additionally, *Cadophora* species have been reported from a range of environments, including Antarctic extreme habitats, as well as coastal ecosystems (Jones et al. 2019; Iliushin et al. 2024). *Cadophora malorum* has been isolated from marine substrates (Jones et al. 2019), and *C. melinii* has been recorded as a saprobic fungus on *Spartina* species in salt marsh ecosystems (Calabon et al. 2021b).

Type species: *Cadophora fastigiata* Lagerb. & Melin 1927

Other accepted species: Species Fungorum (search *Cadophora*)



Note a Conidiophores and conidiogenous cells. b Phialides and conidia. c Conidia.

Scale bars = 10 μm

Source Redrawn from Zhang et al. (2022a)

Figure 4.91 *Cadophora caespitosa*

Classification: *incertae sedis*, *Helotiales*, *Leotiomycetidae*, *Leotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

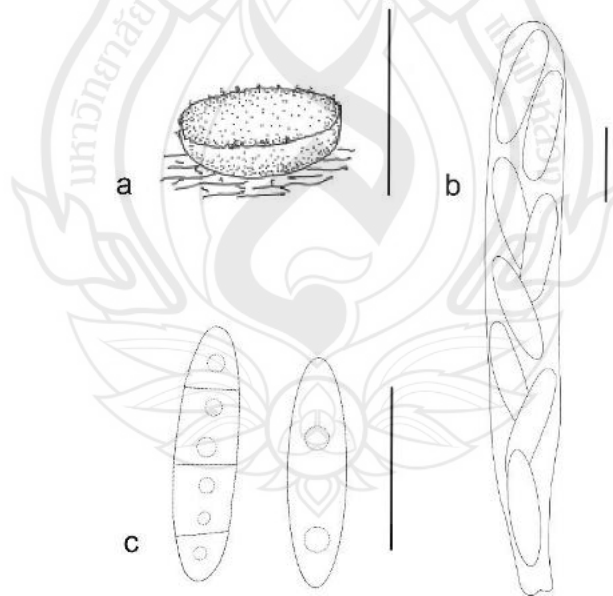
Cejpia was introduced by Velenovský (1934) as a discomycete genus and typified by *C. coerulea*, which was isolated from a leaf of *Scirpus sylvaticus* in the Czech Republic. Two other species are *C. amaena*, isolated from soil and rotten leaves of *Carex* in France, and *C. hystrix*, isolated from dead culms of *Molina* in Italy. *Cejpia hystrix* was also reported from the salt marsh plant *Elymus pungens* in the United Kingdom (Apinis and Chesters 1964; Calabon et al., 2021). *Cejpia hystrix* was initially described in *Belonidium* and transferred to *Cejpia* by Baral (1994). This species is listed among marine fungi in European waters (Landy and Jones 2006) and is characterized by hyaline, smooth, 4-celled sporidia with obtuse ends (De Notaris 1864).

Type species: *Cejpia coerulea* Velen. 1934

Other accepted species:

Cejpia amaena (Boud.) Svrček 1976

Cejpia hystrix (De Not.) Baral 1994



Note a Apothecia. B Ascus. c Ascospores. Scale bar: a = 5 mm, b, c = 10 μm

Source Redrawn from De Meulder et al. (2006)

Figure 4.92 *Cejpia hystrix*

Cistella Quél. 1886

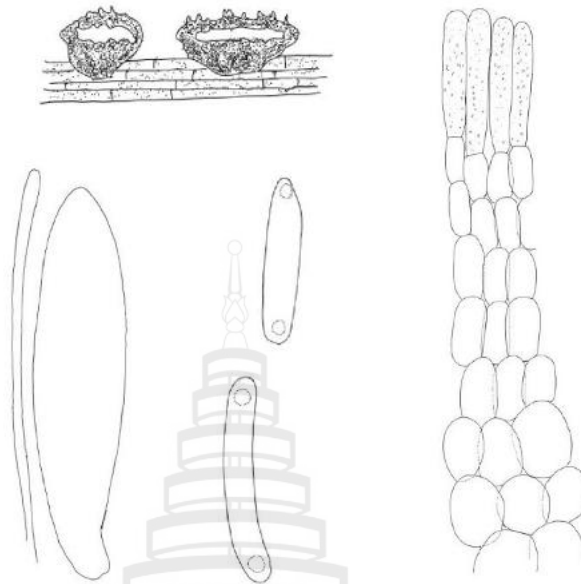
Classification: *incertae sedis*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cistella was introduced by Quélet (1886) to accommodate eight species: *Cistella crystallina*, *C. dentata*, *C. leucostigma*, *C. serrata*, *C. succinea*, *C. typharum*, *C. versicolor*, and *C. opalina*. The genus currently comprises approximately 50 species (Hyde et al. 2024a), all described as sexual morphs characterized by cup- or plate-shaped ascomata, fusiform to linear ascospores, and a non-gelatinized excipulum with a *textura prismatica* to *textura angularis* (Quélet 1886; Raitviir 2004). *Cistella blauvikensis* is a hyphomycetous species and the only known asexual morph associated with this genus, based on phylogenetic analyses. It is characterized by conidiophores reduced to hyphal pegs or conidiogenous loci, with hyaline conidia formed in branched chains (Crous et al. 2023a). *Cistella* is morphologically similar to *Hyphodiscus*, but they can be distinguished by differences in hair structure and ectal excipulum: *Hyphodiscus* has a gelatinized ectal excipulum with a parallel to intricate texture (Raitviir 2004; Quijada et al. 2015). Species of *Cistella* have been collected from various substrates, mostly soil and decaying plant material. *Cistella fugiens* has been reported as a saprobe on salt marsh plant, *Phragmites australis* (Calabon et al. 2021b). In addition to saprobic record of *Cistella*, *C. japonica* is a plant-pathogenic species and the causal agent of resinous stem canker in Japanese cypress (*Chamaecyparis obtusa*) (Suto 1997).

Type species: *Cistella dentata* (Pers.) Quél. 1886

Basionym: *Peziza dentata* Pers. 1800

Other accepted species: Species fungorum (search *Cistella*)



Note Apothecia, marginal part of the ectal excipulum with hairs, asci, paraphysis, and ascospores

Source Redrawn from Svrček (1988)

Figure 4.93 *Cistella typhae*

Flagellospora Ingold 1942

Classification: *Incertae sedis*, *Leotiales*, *Leotiomyetidae*, *Leotiomyetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Flagellospora is an aquatic fungal genus comprising six species (Ingold 1942, Hyde et al. 2024a). It was established for its type species, *Flagellospora curvula*, which was originally found on decaying leaves of *Alnus glutinosa* and *Salix* in Great Britain (Ingold 1942). The genus was described based on its asexual morph, characterized by branched, septate mycelia; hyaline, septate conidiophores with phialidic conidiogenous cells; and filiform, hyaline conidia (Ingold 1942). Subsequently, five additional species have been added to *Flagellospora*, described from substrates such as submerged decaying leaves, freshwater foam, and river spume (Nilsson 1962; Iqbal 1974; Iqbal and Bhatti 1980; Marvanová 1986; Marvanová and Bärlocher 1989). These fungi function primarily as saprobes and endophytes (Altaf and Bisht 2025). There is also a report of an unidentified *Flagellospora* species isolated from living leaves of the

halophytic plant *Juncus roemerianus* (Calabon et al. 2021b). *Flagellospora* species are frequently recorded in freshwater habitats (Tejaswi et al. 2025), and some have demonstrated sensitivity to environmental disturbances, making them potential indicators of water quality (Fernández et al. 2017). Phylogenetic analysis using combined ITS and LSU sequences by Baschien et al. (2013) revealed that *Flagellospora* is polyphyletic, indicating that the genus, as currently defined, does not form a single evolutionary lineage.

Type species: *Flagellospora curvula* Ingold 1942

Other accepted species:

Flagellospora fusarioides S.H. Iqbal 1974

Flagellospora leucorhynchos Marvanová 1987

Flagellospora minuta S.H. Iqbal & Bhatta 1980

Flagellospora saccata Marvanová & Bärli. 1989

Flagellospora stricta Sv. Nilsson 1962



Note Conidiophores and conidia. (486×), developing conidia on phialides (740×)

Source Redrawn from Ingold (1942)

Figure 4.94 *Flagellospora curvula*

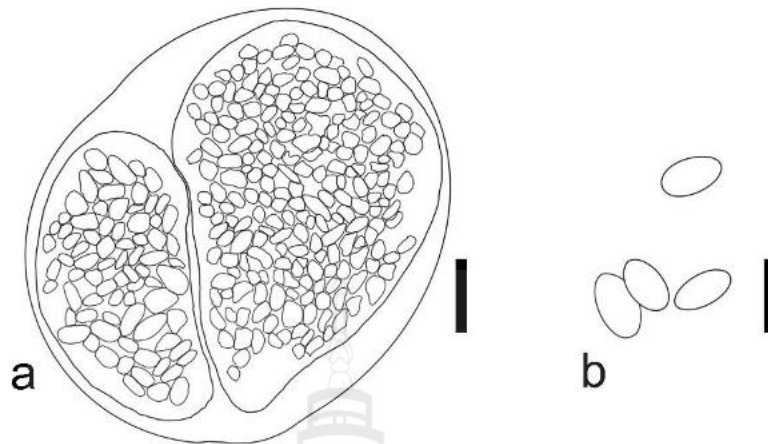
Thelebolus Tode 1790

Classification: *Thelebolaceae*, *Thelebolales*, *Leotiomyetidae*, *Leotiomyetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Thelebolus was introduced by Tode (1790a) and typified with *Thelebolus stercoreus*. The genus comprises 16 species, most of which were described based on morphology, with no available sequence data (Bovio et al. 2015; Hyde et al. 2024a). Morphologically, species in this genus produce ascomata with variable shapes—globose, subglobose, ovoid to ellipsoid, hemispheric, or subcylindrical. They contain one to numerous asci, each producing from 8 up to 3,000 ovoid to oblong-ellipsoidal ascospores. The number of ascospores has been considered a key characteristic for species identification (de Hoog et al. 2005; Bovio et al. 2015). Bovio et al. (2015) provided sequence data for species available in culture collections and presented a synopsis of all known species. They also introduced two new species—*Thelebolus spongiae* and *Thelebolus balaustiformis*—based on morphology and phylogeny using combined ITS and β -tubulin data. *Thelebolus* species have been reported from diverse environments, ranging from terrestrial to aquatic habitats, and across climatic zones from tropical to Arctic regions (de Hoog et al. 2005). They have been associated with various substrates, including plant material, animal dung, soil, marine sponges, and algae (Bovio et al. 2015, Durán et al. 2019). *Thelebolus microsporus*, *Th. balaustiformis*, and *Th. spongiae* have been reported as marine species (Jones et al. 2019). *Thelebolus microsporus* has been found in both freshwater and hypersaline environments, particularly in low-temperature conditions (de Hoog et al. 2005). *Thelebolus balaustiformis* and *Th. spongiae* were isolated from the marine sponge *Dysidea fragilis* (Bovio et al. 2015). Additionally, *Th. crustaceus* has been reported from salt marsh plants such as *Elymus pungens*, *Puccinellia maritima*, and *Spartina townsendii* in the United Kingdom (Calabon et al. 2021b).

Type species: *Thelebolus stercoreus* Tode 1790

Other accepted species: Species Fungorum (search *Thelebolus*)



Note a Ascoma with two asci. b Ascospores. Scale bars: a = 30 µm, b = 10 µm

Source Redrawn from Bovio et al. (2018)

Figure 4.95 *Thelebolus spongiae*

Zythia Fr. 1825

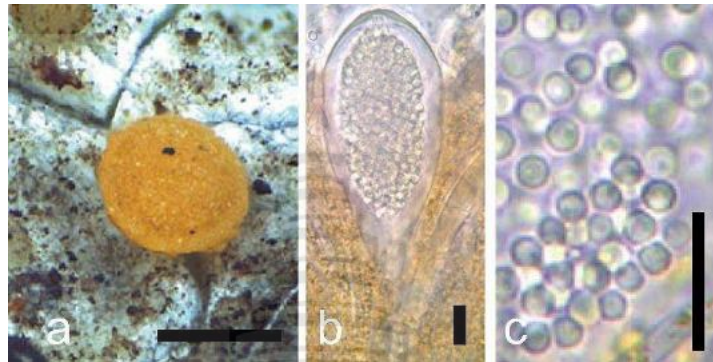
Classification: *Sareaceae*, *Sareales*, *Lichinomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

The fungal genus *Zythia* was originally introduced by Fries (Fr.) in 1825. In the protologue, Fries cited "*Sphaeronæmata priora in S. M., forsan & Sphaeria resinae &c.*" without designating a type species or making a formal combination of *Sphaeria resinae* under *Zythia*. As a result, the type species of *Zythia* has been a subject of discussion (Mitchell and Quijada 2020). Clements and Shear (1931) later cited "*Z. resinae* (Ehrb.) Fr." as the type. To clarify the historical confusion, Mitchell and Quijada (2020) reviewed the relationship between the similarly introduced species *Lecidea resinae* and *Sphaeria resinae*, along with the putative synonym *Cytospora resinae*. They proposed to conserve the name *Cytospora resinae* using the same type specimen selected for *Sphaeria resinae*, thereby making the two names homotypic. *Zythia resinae* is a highly variable species and the only currently accepted species in the genus *Zythia* (Mitchell and Quijada 2020, Mitchell et al. 2021, Hyde et al. 2024a). Its sexual morph is characterized by orange-yellow to deep orange apothecial ascomata, which are erumpent from resin. The paraphyses contain numerous orange lipid guttules, and the medullary excipulum is composed of *textura intricata* and is hyaline. The asexual

morph is coelomycetous (Mitchell et al. 2021). There is one record of *Zythia* as a saprobe on the salt marsh plant *Juncus roemerianus*, cited as *Zythia* spp. (Calabon et al. 2021b).

Type species: *Zythia resinae* (Fr.) P. Karst. 1890

Other accepted species: Species Fungorum (search *Zythia*)



Note a Ascoma on host. b Asci. c Ascospores. Scale bars: a = 500 μ m, b, c = 10 μ m

Source Photo adapted from Mitchell 2021, licensed under Creative Commons Attribution 4.0 (CC BY 4.0)

Figure 4.96 *Zythia resinae*

Orbilia Fr. 1836

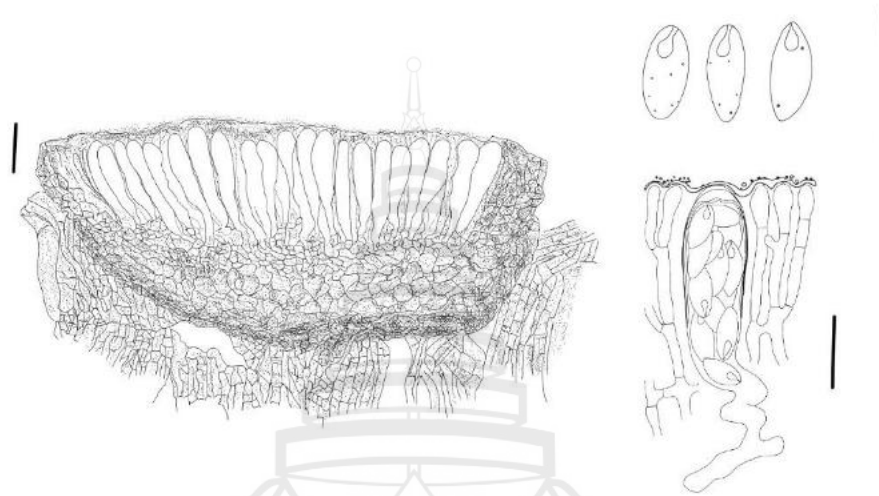
Classification: *Orbiliaceae*, *Orbiliales*, *Orbiliomycetidae*, *Orbiliomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Orbilia is a discomycetous genus typified by *O. xanthostigma* (Fries 1836). There are more than 600 records in Species Fungorum (2026), collected from a variety of hosts. *Orbilia junci* was described on the tips of aging leaves of *Juncus roemerianus* in USA (Kohlmeyer et al. 1998, Calabon et al. 2021b). This species endures harsh environmental conditions such as drought, saturation from rain or dew, temperature changes in winter and summer, and exposure to salt spray. *Orbilia junci* is characterized by light orange to rose-colored apothecial ascomata (Kohlmeyer et al. 1998). Asci are cylindrical to clavate, with a thickened apex and contain sixteen spores. Ascospores are ellipsoidal to clavate, aseptate, and hyaline. The hyphomycetous asexual morph forms in culture and is characterized by conidia branched at the apex consisting of a main axis and four upward and downward curved arms (Kohlmeyer et al. 1998). Kohlmeyer and

Volkman-Kohlmeier (2001b) recorded the asexual morph of this species in nature on *Juncus roemerianus* for the first time.

Type species: *Orbilia xanthostigma* (Fr.) Fr. 1849

Other accepted species: Species Fungorum (search *Orbilia*)



Note Ascoma, ascus and ascospores. Scale bars 10 μ m

Source Redrawn from Kohlmeier et al. (1998)

Figure 4.97 *Orbilia junci*

Arthrobotrys Corda 1839

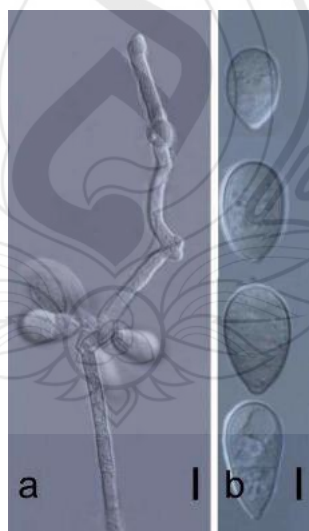
Classification: *Orbiliaceae*, *Orbiliales*, *Orbiliomycetidae*, *Orbiliomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Arthrobotrys, established by Corda (1839) based on the type species *A. superbus* collected in the Czech Republic, is a large genus comprising approximately 100 species (Hyde et al. 2024a). It is characterized by hyphomycetous asexual morphs, with branched or unbranched conidiophores that bear denticles or nodes producing obovoid, elliptic to pyriform conidia, which are aseptate to three-septate (Zhang et al. 2025). Species of *Arthrobotrys* are known as nematode-trapping fungi and have potential applications in agriculture as biological control agents against parasitic nematodes. In particular, *A. oligospora* has been studied as a model organism to understand the interactions between nematodes and nematophagous fungi (Liou and Tzean 1997; Niu and Zhang 2011; Soliman et al. 2021). Members of this genus are

commonly isolated from soil or sediment in a wide range of habitats, including mangroves, freshwater, indoor environments, and agricultural lands. They have also been found on various substrates such as animal dung and plant material. (Corda 1839; Duddington 1954; Swe et al. 2008; Kim et al. 2001; Kumar et al. 2011; Masigol et al. 2022; Zhang et al. 2025). *Arthrobotrys* is one of the diverse genera occurring in marine environments. According to Jones et al. (2019), fifteen species of *Arthrobotrys* are listed as marine fungi. *A. conoides* and an unidentified *Arthrobotrys* species have been reported as saprobes on the salt marsh plant *Phragmites australis* in China (Calabon et al. 2021b). Several new species have recently been described, including *A. cibiensis*, *A. heihuiensis*, and *A. jinshaensis* from freshwater lake sediments (Zhang et al. 2024), *A. chinensis* from bamboo (Jin et al. 2024), and *A. angiopteridis* from dead ferns (Zhang et al. 2025). For accurate species identification within the genus, morphological features should be used in combination with molecular data. DNA sequences from the ITS, *tef1*, and *rpb2* gene regions are effective molecular barcodes for distinguishing species in *Arthrobotrys* (Zhang et al. 2025).

Type species: *Arthrobotrys superbus* Corda 1839

Other accepted species: Species Fungorum (search *Arthrobotrys*)



Note a Conidiophore. b Conidia. Scale bars = 10 μ m.

Source Zhang et al. (2022b)

Figure 4.98 *Arthrobotrys jinpingensis*

Gnomonia Ces. & De Not. 1863

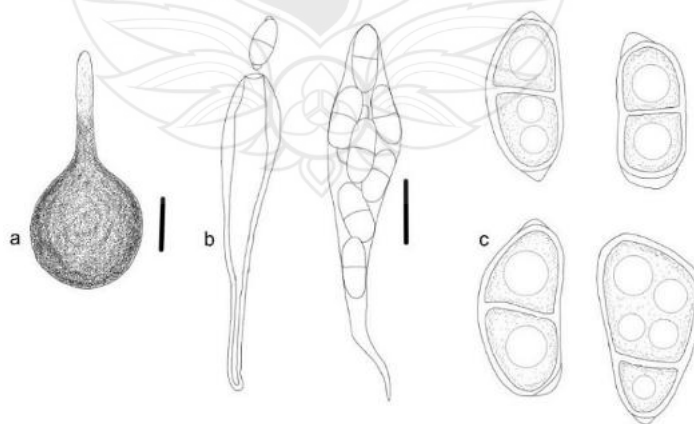
Classification: *Gnomoniaceae*, *Diaporthales*, *Diaporthomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Gnomonia was introduced by Cesati & Notaris (1863) and is the type genus of *Gnomoniaceae* (Hyde et al. 2020c). *Gnomonia* comprises approximately 100 species, which are mostly saprobic, epiphyllous, or rarely hypophyllous on plant material, primarily on *Betulaceae* (Sogonov et al. 2008; Hyde et al. 2024a). Some *Gnomonia* species are plant pathogens, such as *Gnomoniopsis fructicola*, which causing leaf spot in strawberry (Pugliese et al. 2023). *Gnomonia salina*, introduced by Jones (1962b), is recorded on the salt marsh halophyte *Spartina* species (Calabon et al. 2021b). The sexual morph develops immersed to erumpent perithecial ascomata with 1–3 necks, occasionally featuring a wide opening with a white or pink powdery collar around the neck. The powdery substance does not dissolve in water or 3% KOH. Asci are oval to fusiform, with a J– apical ring, containing eight fusiform to acerose, uniseptate, appendaged ascospores. The asexual morph remains undetermined (Sogonov et al. 2008; Maharachchikumbura et al. 2016). Sogonov et al. (2008) studied the taxonomy of leaf-inhabiting genera of *Gnomoniaceae* using morphology and multigene phylogeny of *tefl-a*, *nrLSU*, and *rpb2* sequences. They introduced eight novel species in *Gnomonia* and provided a key for leaf-inhabiting genera of *Gnomoniaceae*.

Type species: *Gnomonia gnomon* (Tode) J. Schröt. 1866

Basionym: *Sphaeria gnomon* Tode 1791

Other accepted species: Species Fungorum (search *Gnomonia*)



Note a Ascoma. b Asci. c Ascospores. Scale bars: a = 250 µm, b = 50 µm, c = 10 µm

Source Redrawn from Jones (1962b)

Figure 4.99 *Gnomonia salina*

***Ceratosphaeria* Niessl 1876**

Classification: *Ceratosphaeriaceae*, *Magnaporthales*, *Diaporthomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Ceratosphaeria was introduced by Niessl (1876) to accommodate its type species, *Ceratosphaeria lampadophora*, which was formerly classified under *Sphaeria*. In its sexual morph, *Ceratosphaeria* forms deeply immersed to superficial carbonaceous ascomata with thick-walled necks, long cylindrical black or yellow crystals, and a multilayered peridium. Asci are cylindrical, with a J- apical ring, containing eight cylindric-fusiform to filiform, hyaline, guttulate ascospores. The asexual morph of *Ceratosphaeria* is harpophora-like, characterized by aerial hyphae and slimy conidial heads. Conidiogenous cells are hyaline and phialidic, producing hyaline, cylindrical, unicellular conidia (Luo et al. 2019). The genus comprises 27 species, mostly saprobic on plant material, with limited available sequence data for type strains (Yang et al. 2023b, Hyde et al. 2024a). Although most *Ceratosphaeria* species are saprobic, some can act as plant pathogens. For example, *C. phyllostachydis* has been reported to cause disease on bamboo (Xu et al. 2022). One unidentified species has been recorded on the salt marsh halophyte *Juncus roemerianus* in the USA (Calabon et al. 2021b). Yang et al. (2023) introduced two new species, *C. fava* and *C. suthepensis*, from freshwater submerged wood in Thailand and leaves of *Magnolia liliifera*, respectively, based on morphology and phylogenetic analysis of LSU, SSU, and TEF1 α sequences. They suggested that the taxonomy of *Ceratosphaeria* species needs revision, as many older species differ from the type species in having short ellipsoidal to fusiform ascospores, including *C. bicellula*, *C. caespitosa*, *C. mycophila*, and *C. pusilla*.

Type species: *Ceratosphaeria lampadophora* (Berk. & Broome) Niessl 1876.

Basionym: *Sphaeria lampadophora* Berk. & Broome 1859

Other accepted species: Species Fungorum (search *Ceratosphaeria*)



Note a Ascoma on wood. b Section of an ascoma. c Ascus. d, e Ascospores. Scale bars: a = 200 μm , b = 100 μm , c = 40 μm , d, e = 30 μm

Source Yang et al. (2023b)

Figure 4.100 *Ceratosphaeria flava*

***Buergenerula* Syd. 1936**

Classification: *Magnaporthaceae*, *Magnaporthales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Buergenerula was introduced to accommodate its type species *Buergenerula biseptata*, which formerly belonged to *Metasphaeria* (Sydow 1936). The genus was considered a member of *Pleosporaceae* (Müller 1950; Dennis 1968; von Arx and Müller 1975), but Barr (1976) suggested its placement in *Physosporrellaceae* (*Phyllachorales*). Subsequently, based on phylogenetic analyses, its taxonomic placement was confirmed as *Magnaporthaceae* (*Magnaporthales*) (Yuan et al. 2010; Luo and Zhang 2013; Maharachchikumbura et al. 2015, 2016). *Buergenerula* has six species, from which *Buergenerula spartinae* has been frequently reported on the

halophyte *Spartina alterniflora* as a saprobe or parasite (Barata et al. 2002; Calabon et al. 2021b; www.marinefungi.org). The species was considered a marine fungus by Jones et al. (2015). *Buergenerula spartinae* has morphological similarities with *Buergenerula biseptata*, in having coriaceous, papillate ascomata, and pseudoparaphyses attached at the top to a pseudoparenchyma. Asci are cylindrical, thick-walled, with a non-amyloid apical apparatus that stains faintly blue in ink. However, *B. spartinae* differs in having thick-walled ascomata, hyphopodia, long periphyses, and clavate, three-septate ascospores, in addition to its marine nature (Kohlmeyer and Gessner 1976).

Type species: *Buergenerula biseptata* (Rostr.) Syd. 1936

Basionym: *Metasphaeria biseptata* Rostr. 1904

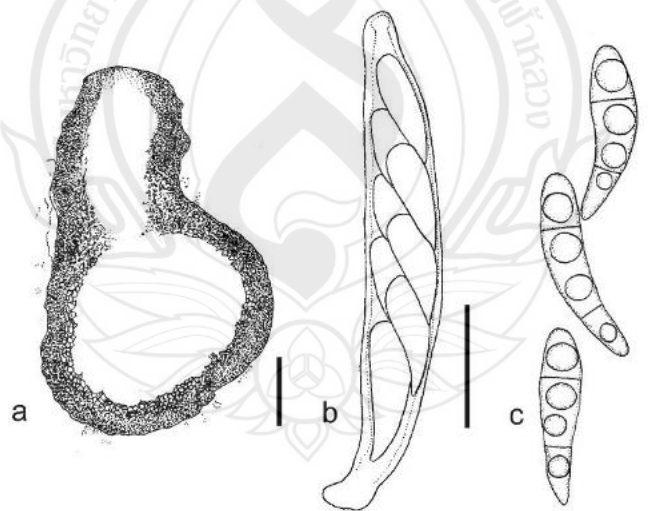
Other accepted species:

Buergenerula caricis (R. Sprague) Arx 1977

Buergenerula spartinae Kohlm. & R.V. Gessner 1976

Buergenerula typhae (Fabre) Arx 1977

Buergenerula zelandica McKenzie 1991



Note a Longitudinal section through ascoma. b Ascus. c Ascospores. Scale bars: a = 75 µm, b, c = 30 µm

Source Redrawn from Kohlmeyer and Gessner (1976)

Figure 4.101 *Buergenerula spartinae*

Gaeumannomyces Arx & D.L. Olivier 1952

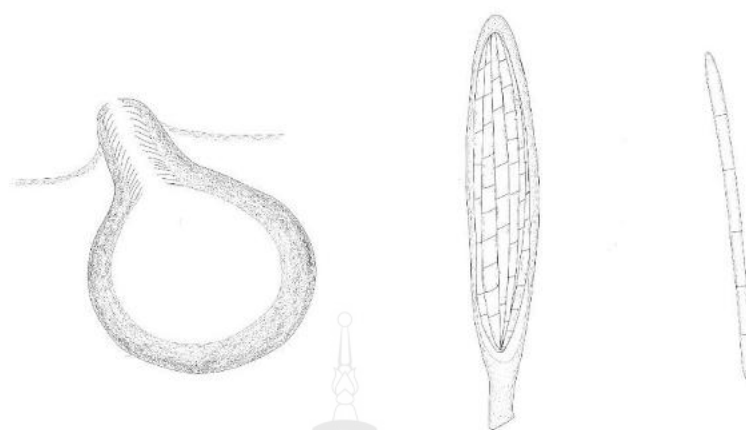
Classification: *Magnaporthaceae*, *Magnaporthales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Gaeumannomyces was introduced by Arx and Olivier (1952) to accommodate an important cereal pathogen, *Gaeumannomyces graminis*. The sexual morph of *Gaeumannomyces* develops immersed, globose to pyriform ascomata with a conical to cylindrical neck and hyaline, multiseptate ascospores. The asexual morph is characterized by phialidic conidiogenous cells with refractive collarettes, producing lunate or phialophora-like conidia (Hyde et al. 2020c). Arx and Olivier (1952) noted that *Gaeumannomyces* is morphologically similar to *Plagiosphaera* but differs in having globose perithecia, a thicker peridium, and differences in the neck angle. Hernández-Restrepo et al. (2016a) restudied the genus and recognized 19 species, classifying them into four groups: *Graminis*, *Orzinus*, *Radicolica*, and *Tritici*. Subsequently, additional studies by Feng et al. (2024) identified four endophytic *Gaeumannomyces* strains that clustered separately from these groups, forming a lineage basal to the *Tritici* group within *Magnaporthaceae*, based on a multigene phylogeny using six loci (ITS, LSU, *act*, *mcm7*, *rpb1*, and *tef1*). Consequently, they introduced a new species, *G. yunnanensis*, to accommodate this clade, representing a fifth group in the genus. Currently, Species Fungorum (April 2026) listed 23 species of *Gaeumannomyces*, which are broadly distributed on grasses in the family *Poaceae* (Hernández-Restrepo et al. 2016a). Important plant pathogenic species, such as *G. tritici* and *G. graminis*, cause the serious take-all disease in wheat roots. One unidentified species has been reported as a saprobe on the salt marsh plant *Phragmites australis* (Calabon et al. 2021b).

Type species: *Gaeumannomyces graminis* (Sacc.) Arx & D.L. Olivier 1952

Basionym: *Rhaphidophora graminis* Sacc. 1875

Other accepted species: Species Fungorum (search *Gaeumannomyces*)



Note Ascoma (60×), ascus and ascospore. (500×)

Source Redrawn from Arx and Olivier (1952)

Figure 4.102 *Gaeumannomyces graminis*

Kohlmeyeriopsis Klaubauf, M.-H. Lebrun & Crous 2014

Classification: *Magnaporthaceae*, *Magnaporthales*, *Diaporthomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Kohlmeyer et al. (1995b) described *Gaeumannomyces medullaris* on *Juncus roemerianus* while Klaubauf et al. (2014) referred it to *Kohlmeyeriopsis* based on molecular analyses of combined *act*, ITS and *rpb1*. The type species, *K. medullaris*, was initially described by Kohlmeyer et al. (1995b) isolated as a saprobic marine fungus, on *Juncus roemerianus* in North Carolina (Calabon et al. 2021b). However, phylogenetically, *G. medullaris* is distinct from *G. graminis*, the type species of *Gaeumannomyces*. Morphologically, *Kohlmeyeriopsis* differs from *Gaeumannomyces* in having a trichocladium-like asexual morph that is heterogeneous (Seifert et al. 2011a). Classification of *Kohlmeyeriopsis* under *Magnaporthaceae* (*Magnaporthales*) was accepted by Jones et al. (2015, 2019) and Maharachchikumbura et al. (2015). The sexual morph is characterized by immersed, ostiolate ascomata with long cylindrical periphysate necks, fusoid to cylindrical asci with a large apical ring containing filamentous, coiled, hyaline ascospores, producing appressoria at germination. The asexual morph is trichocladium-like with pale brown, septate mycelium. Conidiophores are reduced to short, conidiogenous cells with lateral branches. Conidia have a brown,

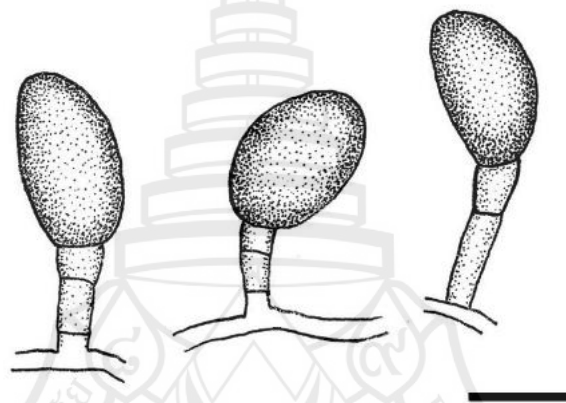
large ellipsoidal apical cell and one or two pale brown, small, cylindrical or doliiform basal cells (Kohlmeyer et al. 1995b; Klaubauf et al. 2014).

Type species: *Kohlmeyeriopsis medullaris* (Kohlm., Volkm.-Kohlm. & O.E. Erikss.) Klaubauf, Lebrun & Crous 2014

Synonymy: *Gaeumannomyces medullaris* Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1995

Trichocladium medullare Kohlm. & Volkm.-Kohlm. 1995

Other accepted species: None



Note Conidiogenous cells and conidia. Scale bar = 10 μ m

Source Redrawn from Goh and Hyde (1999)

Figure 4.103 *Kohlmeyeriopsis medullaris*

Utrechtiana Crous & Quaedvl. 2011

Classification: *Magnaporthaceae*, *Magnaporthales*, *Diaporthomycetidae*, *Sordariomycetes*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Utrechtiana was introduced by Crous et al. (2011a) to accommodate the type species *U. cibiessia*, isolated from leaves of *Phragmites australis* in the Netherlands. Based on morphology, the genus was considered synonymous with *Deightoniella* (Seifert et al. 2011a), and *U. cibiessia* was regarded as synonymous with *Deightoniella roumeguerei* (basionym: *Scolicotrichum roumeguerei*) isolated from *Phragmites australis* in France (Briosi and Cavara 1890; Videira et al. 2017). However, Videira et al. (2017) restudied type material of *Utrechtiana* and *Deightoniella* and considered them to be morphologically distinct genera, suggesting that fresh material is needed for

the type species of *Deightoniella* to confirm classification. *Utrechtiana* has a hyphomycetous asexual morph, with solitary, unbranched brown conidiophores emerging through the host surface with a swollen basal cell. The conidiogenous cell is terminal, subcylindrical with a bluntly rounded apex, bearing solitary ellipsoidal, guttulate to granular conidia with a smooth to finely roughened surface. Conidia are 1–2-septate with a prominent darkened and thickened hilum (Crous et al. 2011a; Videira et al. 2017). *Utrechtiana* is similar to *Polytrincium*, *Polythrinciopsis*, and *Passalora* but differs by lacking stromata and having solitary conidiophores and conidiogenous cells (Crous et al. 2011a). ITS, *act*, *cal*, and *rpb1* are important barcodes for species identification in *Utrechtiana* (Marin-Felix et al. 2019b).

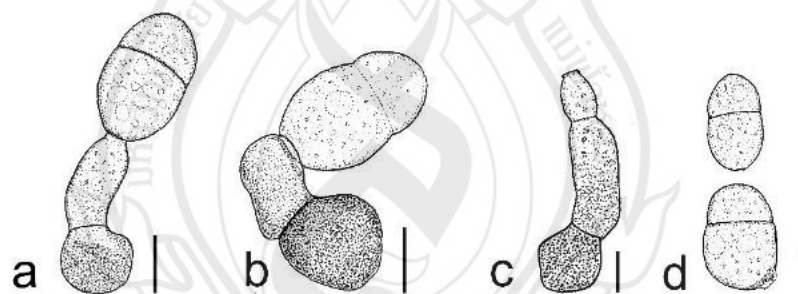
Type species: *Utrechtiana roumeguerei* (Cavara) Videira & Crous 2017

Basionym: *Scolicotrichum roumeguerei* Cavara 1890

Other accepted species:

Utrechtiana arundinacea (Corda) Crous, Quaedvl. & Y. Marín 2018

Utrechtiana constantinescui (Melnik & Shabunin) Crous & Y. Marín 2018



Note a–c Conidiophores bearing conidia. d Conidia. Scale bars: 10 µm

Source Redrawn from Marin-Felix et al. (2019b)

Figure 4.104 *Utrechtiana roumeguerei*

Pseudohalonectria Minoura & T. Muroi. 1978

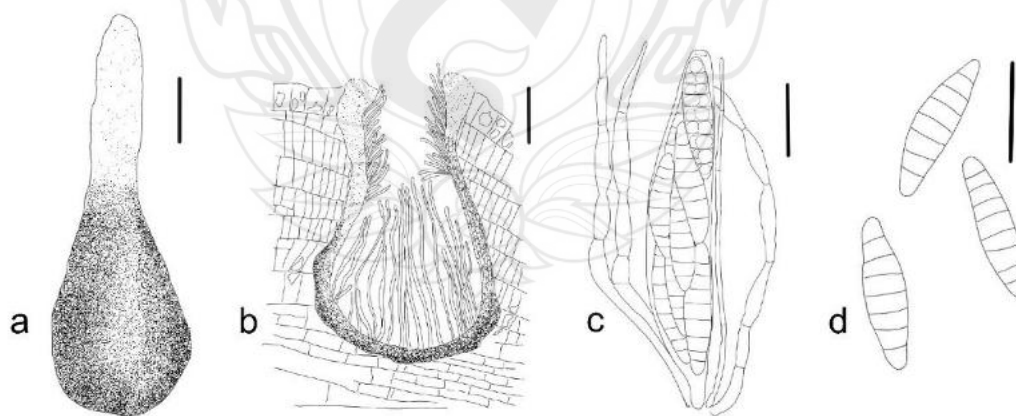
Classification: *Pseudohalonectriaceae*, *Magnaporthales*, *Diaporthomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Minoura and Muroi (1978) established *Pseudohalonectria* when they isolated a new aquatic saprobic fungus, *P. lignicola* from submerged wood in freshwater in Japan. However, Minoura and Muroi (1978) did not assign any family and order for the genus.

Hongsanan et al. (2017) restudied the genus based on the molecular clock analysis and a phylogenetic analysis of combined LSU, SSU, *tef1* and *rpb2*. They introduced the novel family *Pseudohalonectriaceae* within the *Magnaporthales*. The genus is distinguished by its bright yellow to brown ascomata, featuring elongated cylindrical necks with periphyses. It also has unitunicate, cylindrical to clavate asci with a J-thimble-shaped, refractive apical ring. The ascospores are typically cylindrical, hyaline to slightly pigmented and septate (Shearer 1989b; Hyde et al. 2020). A hyphomycetous asexual morph was documented for *P. aomoriensis*, with phialides producing hyaline, allantoid, and aseptate conidia (Ono and Kobayashi 2001). There are 15 species recorded for *Pseudohalonectria* in Species Fungorum (April 2026), with some species showing potential antagonistic activity by producing azaphilone compounds (Asthana and Shearer 1990; Dong et al. 2004, 2006; Yang et al. 2023b). *Pseudohalonectria* species have been collected from both terrestrial and aquatic habitats (Perera et al. 2016). *Pseudohalonectria falcata* and *P. halophila* have been isolated from decaying salt marsh plant, *Phragmites australis* in China and *Juncus roemerianus* in USA, respectively (Poon and Hyde 1998; Kohlmeyer and Kohlmeyer 2005; Calabon et al. 2021b).

Type species: *Pseudohalonectria lignicola* Minoura & T. Muroi. 1978

Other accepted species: Species Fungorum (search *Pseudohalonectria*)



Note a, b Ascomata. c Ascus. d Ascospores. Scale bars: a, b = 50 µm, c, d = 20 µm

Source Redrawn from Kohlmeyer et al. (2005)

Figure 4.105 *Pseudohalonectria halophila*

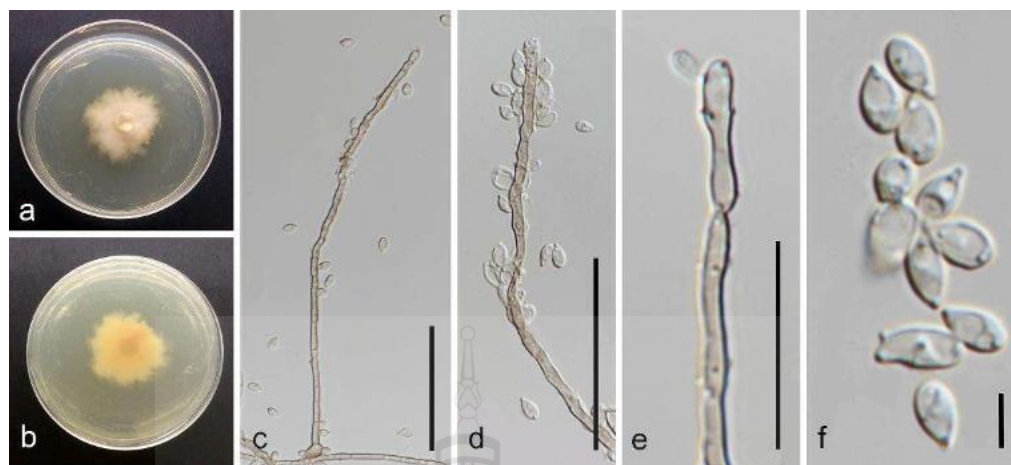
Myrmecridium Arzanlou, W. Gams & Crous 2007

Classification: *Myrmecridiaceae*, *Myrmecridiales*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Myrmecridium was established by Arzanlou et al. (2007) to encompass *M. schulzeri* (initially introduced as *Psilobotrys schulzeri* by Saccardo in Schulzer and Saccardo 1884) and its varieties, previously classified under *Ramichloridium*. The key features distinguishing *Myrmecridium* from other ramichloridium-like species include hyaline vegetative hyphae and conidiophores adorned with pimple-shaped denticles (Arzanlou et al. 2007). It is mostly known for its asexual morph, characterized by straight or flexuous conidiophores arising from hyaline mycelium. Cylindrical, hyaline to light brown conidiogenous cells bear pimple-like denticles, producing septate or aseptate, smooth or ornamented conidia, mostly with wing-like sheath (Arzanlou et al. 2007; Tibpromma et al. 2017). *Myrmecridium montsegurinum*, the sole identified sexual species, is characterized by ostiolate ascumata with dark pigmented clypeus. Asci are unitunicate featuring an elongated pedicel and containing eight hyaline, 3-septate ascospores (Réblová et al. 2016a). *Myrmecridium* was placed under family *Myrmecridiaceae* and the order *Myrmecridiales*, based on LSU molecular data (Crous et al. 2015b). The genus comprises 24 species listed in Species Fungorum (April 2026). The genus has been documented in diverse habitats and on various substrates, with a global distribution (Arzanlou et al. 2007; Tibpromma et al. 2017; Yang et al. 2023b). Species have also been reported in marine habitats, e.g., *M. hydei* found on a decaying submerged branch in the sea in Thailand (Asghari et al. 2023) and *M. schulzeri* from salt marsh host *Distichlis spicata* in Argentina (Eliades et al. 2007; Calabon et al. 2021b, 2023).

Type species: *Myrmecridium schulzeri* (Sacc.) Arzanlou, W. Gams & Crous 2007

Other accepted species: Species Fungorum (search *Myrmecridium*)



Note a Colonies on PDA after two weeks (above). b Colonies on PDA after two weeks (below). c Conidiophores. d, e. Conidiogenous cells. f. Conidia. Scale bars: c, d = 50 μm , e = 20 μm , f = 5 μm

Source Asghari et al. (2023)

Figure 4.106 *Myrmecridium hydei*

Phomatospora Sacc. 1875

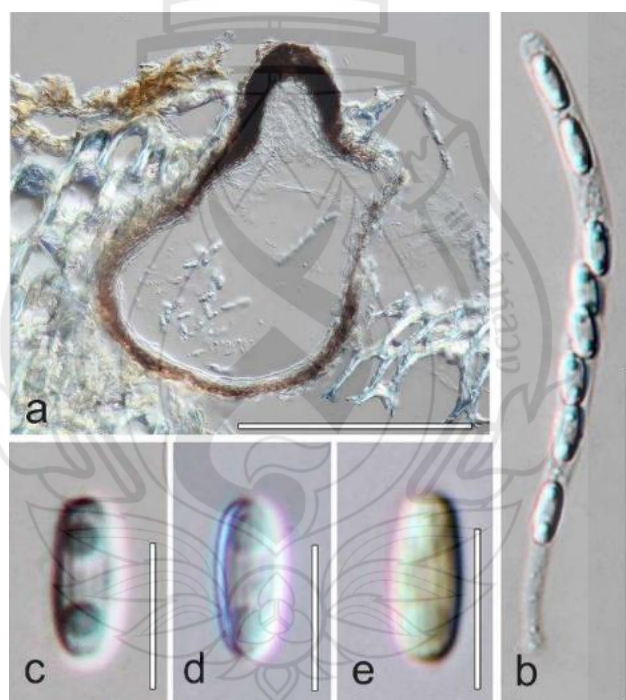
Classification: *Phomatosporaceae*, *Phomatosporales*, *Incertae sedis*, *Sordariomycetes*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Phomatospora, with 84 species (Species Fungorum, accessed April 2026), is an endophyte or saprobe found in both terrestrial and aquatic habitats. It is the type genus of *Phomatosporaceae* (Hyde et al. 2020c; Phukhamsakda et al. 2020). In aquatic environments, *Phomatospora* ascospores may produce appendages or sheaths for adaptation (Hyde 1993; Raja and Shearer 2008). For example, *P. bellaminuta*, isolated from halophyte *Juncus roemerianus* in marine habitats, presents a gelatinous cap (Kohlmeyer et al. 1995a). There are other records of salt marsh plants hosting this genus (Calabon et al. 2021b), mostly of *P. berkeleyi* on *Phragmites australis* (Van Ryckegem and Verbeken 2005a, 2005b; Van Ryckegem et al. 2007), *P. dinemasporium* (Van Ryckegem and Verbeken 2005a; Poon and Hyde 1998), and *P. phragmiticola* (Poon and Hyde 1998), on *J. roemerianus* (Kohlmeyer et al. 1995a; Fell and Hunter 1979) and one record of *P. dinemasporium* on *Spartina townsendii* (Apinis and Chesters 1964). *Phomatospora* is typified by *P. berkeleyi*, which produces a *Sporothrix* asexual morph in culture. This characteristic led to its classification in *Xylariales* (Rappaz

1992), although this was not confirmed by further phylogenetic analyses (Lumbsch and Huhndorf 2007), and the genus was treated as Sordariomycetes genera *incertae sedis*. Molecular analyses by Réblová et al. (2016a) and Senanayake et al. (2016) demonstrated a relationship between *Phomatospora* and *Lanspora*, leading to the establishment of *Phomatosporaceae*. Sexual morph is characterized by globose or subglobose ascomata and filamentous paraphyses. The asci are cylindrical or oblong-fusiform with a J-apical ring containing hyaline, ellipsoidal to fusiform ascospores with bipolar gelatinous caps (Raja and Shearer 2008, Phukhamsakda et al. 2020). Combined LSU, SSU, and ITS sequences can be used for species identification in this genus (Phukhamsakda et al. 2020).

Type species: *Phomatospora berkeleyi* Sacc 1875

Other accepted species: Species Fungorum (search *Phomatospora*)



Note a Vertical section through ascoma. b Ascus. c – e Ascospores. Scale bars: a, b = 50 μ m, c–e = 5 μ m.

Source Phukhamsakda et al. (2020)

Figure 4.107 *Phomatospora uniseriate*

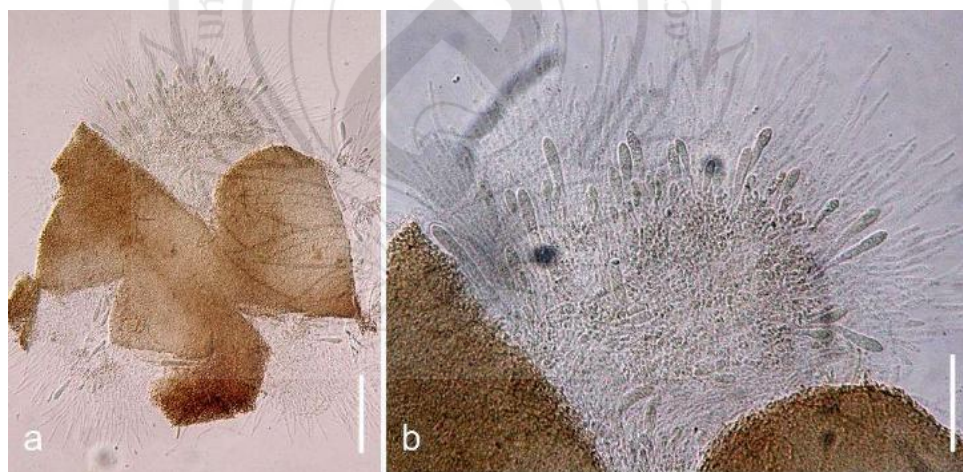
Papulosa Kohlm. & Volkm.-Kohlm. 1993

Classification: *Papulosaceae*, *incertae sedis*, *Diaporthomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Papulosa was established by Kohlmeyer and Volkmann-Kohlmeyer (1993b), isolated from dead culms of the halophyte *Juncus roemerianus* in USA (Calabon et al. 2021b) with *Papulosa amerospora* as the type species. The sexual morph is characterized by immersed, subglobose, ostiolate ascomata with a long periphysate neck and septate, hyaline paraphyses. Asci are cylindrical with a bipartite, IKI+, apical ring and contain eight hyaline, ellipsoid, and verrucose ascospores. The asexual morph is unknown (Maharachchikumbura et al. 2016; Bundhun et al. 2020). This monotypic genus is typified by *P. amerospora* without a certain classification into any order or family (Kohlmeyer and Volkmann-Kohlmeyer 1993b). Winka and Eriksson (2000) classified the genus in a novel family, *Papulosaceae*, based on morphological and SSU molecular data. They suggested that the placement of *Papulosa* in *Sordariomycetidae* is not certain. Maharachchikumbura et al. (2016) showed the placement of *Papulosa* in *Diaporthomycetidae* based on LSU, SSU, *tef*, and *rpb2*, which was confirmed by Hyde et al. (2020c) and Wijayawardene et al. (2020).

Type species: *Papulosa amerospora* Kohlm. & Volkm.-Kohlm. 1993

Other accepted species: None.



Note a Squash mount of ascoma. b Developing asci with paraphyses. Scale bars: a = c = 100 μ m, b = c = 50 μ m

Source Maharachchikumbura et al. (2016)

Figure 4.108 *Papulosa amerospora*

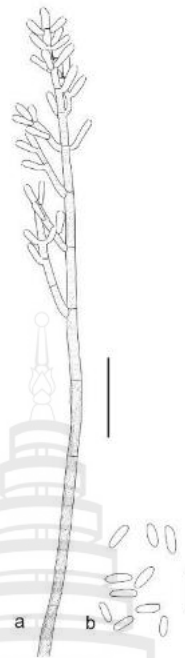
***Stachylidium* Link 1809**

Classification: *Trichosphaeriaceae, incertae sedis, Diaporthomycetidae, Sordariomycetes, Pezizomycotina, Ascomycota, Fungi.*

Link (1809) introduced *Stachylidium* to accommodate *Stachylidium bicolor* and *S. terrestre* without designating a type species. After several attempts to designate *S. bicolor* as the lectotype (Hughes 1951; Gams 2017), Giraldo and Crous (2019) reexamined the authentic material of Link and proposed the specimen with code B700016303 as the most suitable lectotype. Currently, *Stachylidium* comprises seven species, mostly reported as saprobes on herbaceous and woody plants worldwide (Giraldo and Crous 2019; Hyde et al. 2024a). *Stachylidium bicolor* is the most frequently reported species and has also been documented in marine environments and salt marsh habitats, with one report on *Juncus roemerianus* (Jones et al. 2019, Calabon et al. 2021b).s. Chemical investigations of a *Stachylidium* species derived from a marine sponge led to the discovery of compounds with potent inhibitory activity against human leukocyte elastase (Almeida et al. 2012). *Stachylidium* is a hyphomycetous genus characterized by septate, verticillate, roughened conidiophores arising from hyphae, monophialidic hyaline or pale brown conidiogenous cells, and aseptate, pale brown to brown conidia produced in slimy heads (Giraldo and Crous 2019). LSU, ITS, *tef1*, and *rpb2* sequences are available for two *Stachylidium* species (Giraldo and Crous 2019).

Type species: *Stachylidium bicolor* Link 1809

Other accepted species: Species Fungorum (search *Stachylidium*)



Note a Conidiophore. b. Conidia. Scale bar: a=50 μ m, b= 10 μ m

Source Redrawn from Dewi (2006)

Figure 4.109 *Stachylidium bicolor*

Koorchaloma Subram. 1953

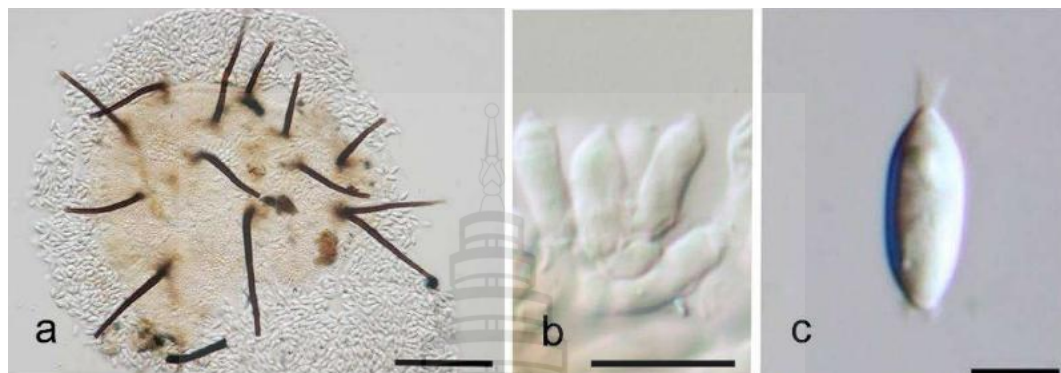
Classification: *Trichosphaeriaceae*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Koorchaloma was described as a saprobic fungus on *Oryza sativa* in India (Subramanian 1953). There are 13 accepted species listed in Index Fungorum. *Spartina alterniflora* (Buchan et al. 2002) and *Juncus roemerianus* (Kohlmeyer and Volkmann-Kohlmeyer 2001a) are reported salt marsh hosts for *Koorchaloma spartinicola* and *K. galateae*, respectively (Sarma et al. 2001; Kohlmeyer and Volkmann-Kohlmeyer 2001a; Calabon et al. 2021b). Sexual morph has globose to pyriform, setose ascomata. Asci are clavate, with J-, and apical rings, with eight hyaline, fusiform, and septate ascospores (Nag Raj 1984; Treigene, 2006). Asexual morph has sporodochioid to acervular, setose conidiomata. If present, conidiophores are hyaline, branched, and septate. Conidiogenous cells are phialidic, bearing fusiform conidia with appendages at both ends or only at the apex (Nag Raj 1984; Treigene 2006). Tian et al. (2021b)

introduced a new species provided a key to *Koorchaloma* species and an updated phylogenetic tree based on ITS, LSU, and *rpb2*.

Type species: *Koorchaloma madreya* Subram. 1953

Other accepted species: Species Fungorum (search *Koorchaloma*)



Note a Conidioma. b Conidiophores, conidiogenous cells and developing conidia. c conidium. Scale bars: a = 100 μm , b = 10 μm , c = 5 μm

Source Wen-Jing et al. (2020)

Figure 4.110 *Koorchaloma bambusae*

Microthecium Corda 1842

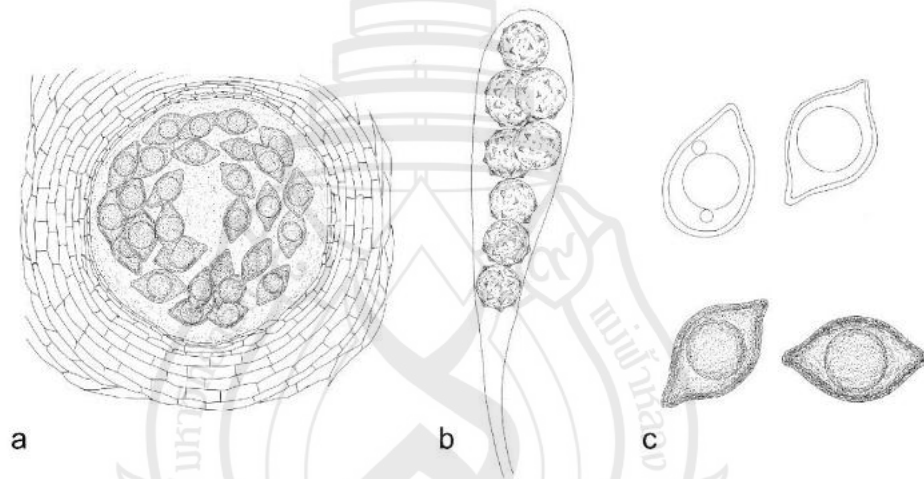
Classification: *Ceratostomataceae*, *Coronophorales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Microthecium was established by Corda (1842) and typified with *Microthecium zobellii*, isolated from truffle (*Rhizopogon albus*). Marin-Felix et al. (2018) reexamined the phylogeny of several genera within *Ceratostomataceae* based on fresh material, reference strains, and type specimens. They re-established *Microthecium* and provided a key for the accepted species. Currently, *Microthecium* comprises approximately 25 species, most of which are soil-borne (Marin-Felix et al. 2018; Hyde et al. 2024a). However, *M. fimicola* and *M. levitum* have been reported as saprobes on salt marsh plants, *Elymus pungens* and *Spartina alterniflora*, respectively (Calabon et al. 2021b). The most recently introduced species, *M. inferius*, was established based on its phylogenetic placement within *Microthecium*, supported by ITS and LSU sequences (Li et al. 2020). The sexual morph of *Microthecium* is characterized by superficial or immersed, translucent yellowish to reddish ascomata, with or without a short neck. The ascomata typically have a crown of hyaline, septate setae around the ostiole and a

peridium of *textura angularis*. Asci are 8-spored, clavate, and evanescent, while ascospores are unicellular, hyaline to dark brown, and have a variety of shapes, including fusiform, navicular, citriform, plataniform, or spindle-shaped. The ascospores are ornamented and have a terminal apiculate or depressed germ pore at each end. The asexual morph is phialidic, typically producing bulbils with pale orange to reddish-orange conidia (Marin-Felix et al. 2018). Morphologically, *Microthecium* is similar to *Dactylidispora*, *Pustulipora*, and *Pseudomicrothecium* in having similar ascomata but differs in the morphology of asci and ascospores (Marin-Felix et al. 2018).

Type species: *Microthecium zobellii* Corda 1842

Other accepted species: Species Fungorum (search *Microthecium*)



Note a Section through ascomata, inside truffle. b Ascus. c Ascospores

Source Redrawn from Corda (1842)

Figure 4.111 *Microthecium zobellii*

Papulaspora Preuss 1851

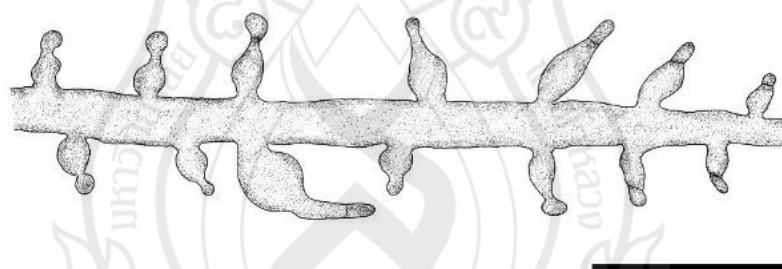
Classification: *incertae sedis*, *Coronophorales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Papulaspora was introduced based on a hyphomycetous species with globose, solitary, pigmented conidia, *Papulaspora sepedonioides* (Preuss 1851). This species was isolated as a saprobe from *Brassica oleracea* in Germany and designated as the type species (Preuss 1851).

The genus *Papulaspora* includes 34 species, which have been isolated as saprobes, endophytes, and parasites from various substrates (Hyde et al. 2024a; Species Fungorum 2026). They have been reported from soil, dung, and plant materials such as roots, rhizosphere, bark, and leaves, as well as from animals (Hotson 1912, 1917, 1929; Warren 1948; Tubaki et al. 1991). *Papulaspora halima* is a saprobic species isolated from the salt marsh host *Juncus roemerianus* (Calabon et al. 2021b). Some species in this genus are parasitic, such as *Papulaspora equi*, which was isolated from an infected horse eye and has also been associated with keratomycosis in humans (Shadomy et al. 1989; Selvin et al. 2014). The investigation of metabolites from an endophytic strain of *Papulaspora immersa* demonstrated antimicrobial activity (Ramos et al. 2010). ITS, LSU, *tub*, *rpb2*, and *tef1* sequences are available for a few *Papulaspora* species in GenBank.

Type species: *Papulaspora sepedonioides* Preuss 1851

Other accepted species: Species Fungorum (search *Papulaspora*)



Note Developing conidia. Scale bar: 30 µm

Source Redrawn from Hotson (1942)

Figure 4.112 *Papulaspora appendicularis*

Acremonium Link 1809

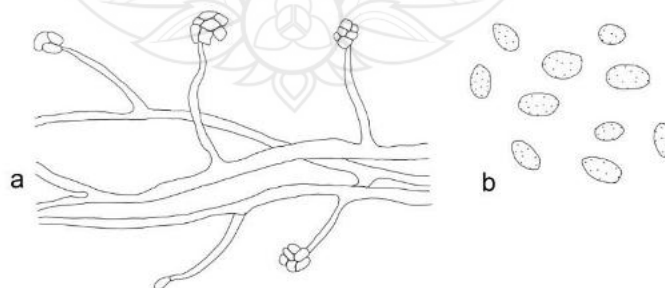
Classification: *Bionectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Acremonium was introduced by Link (1809) to accommodate the hyphomycetous species *A. alternatum* and *A. verticillatum*. The genus comprises approximately 100 species, which are ubiquitously distributed across various habitats as saprobes, endophytes, or parasites of plants, fungi, animals, and humans (Yang et al. 2019; Hou et al. 2023; Hyde et al. 2024a). *Acremonium* species are also frequently

isolated from marine environments, with 16 species recognized as marine fungi by Jones et al. (2019). Additionally, three unidentified species have been reported as saprobes on salt marsh plants, including *Distichlis spicata*, *Juncus roemerianus*, and *Phragmites australis* (Calabon et al. 2021b). *Acremonium* has been extensively studied for its bioactive metabolites, making it a valuable source of over 350 known compounds with industrial, medicinal, and agricultural applications (Hou et al. 2023). One of the most significant metabolites is cephalosporin C, a broad-spectrum antibiotic derived from the marine fungus *A. chrysogenum* (Abraham 1979; Jones et al. 2019). Taxonomically, *Acremonium* has long been considered a highly polyphyletic genus. Hou et al. (2023) reexamined its taxonomy using 633 *acremonium*-like cultures, applying a polyphasic approach that integrated morphology, host associations, ecology, and phylogenetic analyses. The study utilized ITS, LSU, and *rpb2* sequences for higher-level classification and ITS, LSU, *rpb2*, and *tef-1* for species delimitation at generic and family levels. Morphologically, *Acremonium* is characterized by its hyphomycetous asexual morph, with no confirmed sexual morph. Conidiophores are solitary, hyaline, smooth-walled, and either simple or branched. Conidiogenous cells are mono- or polyphialidic, often with a distinct or inconspicuous collarette and periclinal thickening at the conidiogenous loci. Conidia vary in shape, are smooth-walled, hyaline or slightly pigmented, and are arranged in slimy heads or long chains. Crystals and chlamydospores are present in some species (Hou et al. 2023).

Type species: *Acremonium alternatum* Link 1809

Other accepted species: Species Fungorum (search *Acremonium*)



Note Conidiogenous cells and conidia

Source Redrawn from Sukapure and Thirumalachar (1963)

Figure 4.113 *Acremonium chrysogenum*

***Fusariella* Sacc. 1884**

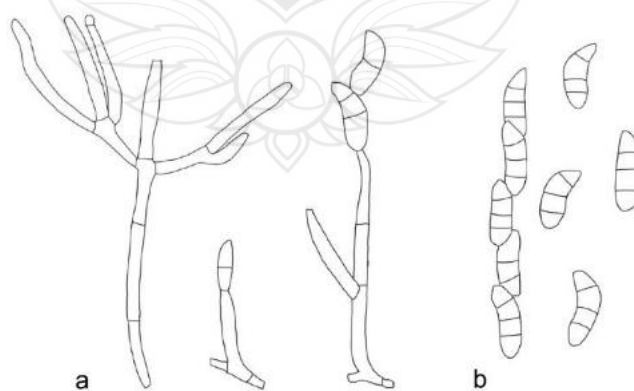
Classification: *Bionectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Fusariella was introduced by Saccardo (1884a) with *Fusariella atrovirens* as the type species (based on *Fusisporium atrovirens*, Berkley 1836). There are 17 species listed in this genus in Species Fungorum (Accessed October 2024), though few have available sequence data (Hou et al. 2023). The lack of molecular data and comprehensive taxonomic studies has led to its uncertain placement. Lin et al. (2016) revised the genus and, based on morphology and phylogenetic analyses of SSU, LSU, *tefl-α*, and *rpb2* sequences, placed the genus in *Bionectriaceae*. The asexual morph of *Fusariella* is characterized by semi- to macronematous, mononematous, unbranched or variously branched conidiophores, which are flexuous, and hyaline to pale brown. Conidiogenous cells are monophialidic, integrated or discrete, with collarettes. Conidia are catenate, subhyaline to brown, 1–3-septate, curved to straight, often fusiform, and frequently form in chains (Ellis 1971; Hou et al. 2023). *Fusariella obstipa*, which has obclavate and mostly 3-septate conidia, has been reported as a foliar saprobe on the halophyte *Juncus roemerianus* from the USA (Fell and Hunter 1979; Lin et al. 2016; Calabon et al. 2021b).

Type species: *Fusariella atrovirens* (Berk.) Sacc. 1884

Basionym: *Fusisporium atrovirens* Berk., in Smith 1836

Other accepted species: Species Fungorum (search *Fusariella*)



Note a Conidiophores, conidiogenous cells and developing conidia. b Conidia

Source Redrawn from Lin et al. (2016)

Figure 4.114 *Fusariella obstipa*

***Gliomastix* Guég. 1905**

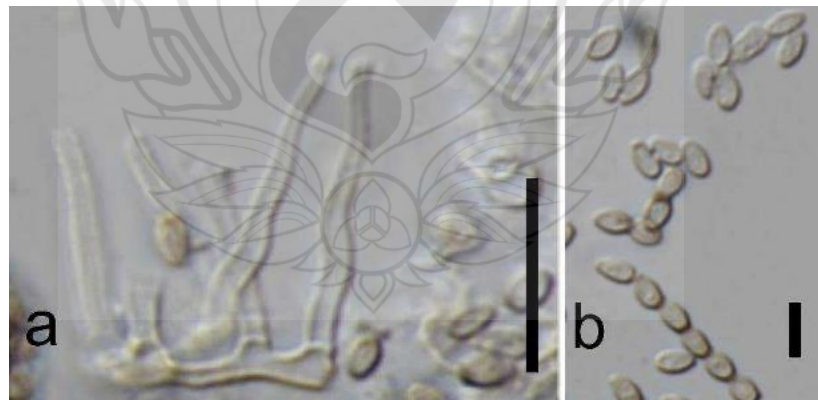
Classification: *Bionectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Guéguen (1905) introduced *Gliomastix* to accommodate *G. chartarum* (syn. *G. murorum*). Gams (1971) considered it a section of *Acremonium*, and Gams (1978) proposed that it might be connected to a sphaeriaceous sexual morph. Summerbell et al. (2011) revised the genus and resurrected it as a separate genus. Among *Gliomastix* species, *G. fusigera* was linked to a sexual morph in *Hydropisphaera*, but Hou et al. (2023) reclassified *G. fusigera* as *Monohydropisphaera fusigera* based on phylogenetic analyses of combined LSU, ITS, *rpb2*, and *tef-1 α* sequence data. Asexual morph of *Gliomastix* produces white mycelia in culture with green, brown, or black conidia, which are darkly pigmented in mass. Conidia are unicellular and develop in chains or slimy heads on phialides. Chlamydospores are absent (Hou et al. 2023). *Gliomastix* has been isolated from soil, plants, or as airborne fungi. There is one record of an unconfirmed species of *Gliomastix* as a saprobe on the salt marsh plant *Juncus roemerianus* from the USA (Calabon et al. 2021b).

Type species: *Gliomastix murorum* (Corda) S. Hughes 1958

Basionym: *Torula murorum* Corda 1838

Other accepted species: Species Fungorum (search *Gliomastix*)



Note a Conidiophores and conidia. b Conidia. Scale bars: a = 30 µm, b = 2.5 µm

Source Samaradiwakara et al. (2025)

Figure 4.115 *Gliomastix musae*

***Hydropisphaera* Dumort. 1822**

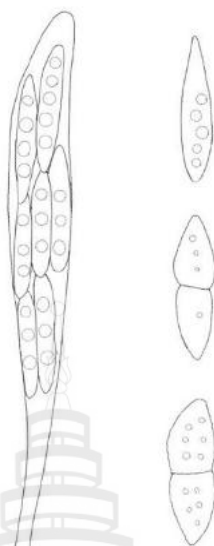
Classification: *Bionectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Dumortier (1822) introduced *Hydropisphaera*, with *H. peziza* as the type species (based on *Sphaeria peziza* by Tode 1791). The genus comprises 29 species in Species Fungorum (April 2026), including *H. arenula* and *H. erubescens*, which have been reported as saprobes on salt marsh hosts. *Hydropisphaera arenula* has been found on *Phragmites australis* in China and the Netherlands, while *H. erubescens* has been hosted by *Spartina alterniflora* in the USA (Calabon et al. 2021b). This genus includes several species with nectria-like sexual morphs and various asexual morphs such as acremonium-like, cylindrocarpon-like, *Cephalosporium*, or *Gliomastix*. *Hydropisphaera* was previously considered synonymous with the genus *Nectria* (Hou et al. 2023). However, Rossman et al. (1999) reinstated *Hydropisphaera* as a distinct genus within the Bionectriaceae family. Hou et al. (2023), based on phylogenetic analyses of combined ITS, LSU, *rpb2*, and *tef-1α* sequences, showed that *Hydropisphaera* is polyphyletic in at least eight clades. They suggested that the genus can be separated based on phylogeny and morphology, restricting *Hydropisphaera* to taxa related to the type species *H. peziza*, with only an acremonium-like asexual morph. The sexual morph of *Hydropisphaera* has superficial perithecia and, rarely, cleistothecia. Ascomata are pale yellow to orange, with thick walls generally over 25 µm. Clavate asci contain ellipsoid, hyaline ascospores that are typically uniseptate and striate (Rossman et al. 1999; Hou et al. (2023)).

Type species: *Hydropisphaera peziza* (Tode) Dumort. 1822

Basionym: *Sphaeria peziza* Tode 1791

Other accepted species: Species Fungorum (search *Hydropisphaera*)



Note Ascus and ascospores

Source Redrawn from Berkeley and Broome (1852)

Figure 4.116 *Hydropisphaera arenula*

Atkinsonella Diehl 1950

Classification: *Clavicipitaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Ascomycota*, *Fungi*.

Atkinsonella hypoxylon, the type species of *Atkinsonella*, was initially placed in *Epichloe* and later separated as a novel genus by Diehl (1950) based on morphology. *Atkinsonella hypoxylon* was first isolated as a pathogenic fungus from a living *Poaceae* host. Subsequently, *A. hypoxylon* var. *texensis*, isolated from another grass host, *Stipa leucotricha*, was elevated to species level as *A. texensis* (Leuchtmann and Clay 1989). The genus has two species. *Atkinsonella hypoxylon* was reported on the salt marsh host *Spartina cynosuroides* (Seymour 1929; Calabon et al. 2021b). *Atkinsonella* species are characterized by immersed, cylindrical spores. The asexual morph is acremonium-like, developing both micro- and macroconidia (Ginns 2011; Ambrose et al. 2014; Hyde et al. 2020c). ITS, SSU, *tub*, *tef1-α*, *tubP*, *rpb1*, *rpb2*, *atp6*, and whole genome sequences are available for *Atkinsonella* in GenBank.

Type species: *Atkinsonella hypoxylon* (Peck) Diehl 1950

Basionym: *Epichloe hypoxylon* Peck 1875

Other accepted species: *Atkinsonella texensis* (Diehl) Leuchtm. & Clay 1989



Note a Stromata on host. b Stromata. c Ascus. d, e Ascospores. Scale bar: a = 1 mm, b = 500 μ m. c = 50 μ m, d, e = 20 μ m

Source Hyde et al. (2020c)

Figure 4.117 *Atkinsonella hypoxylon*

Claviceps Tul. 1853

Classification: *Clavicipitaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

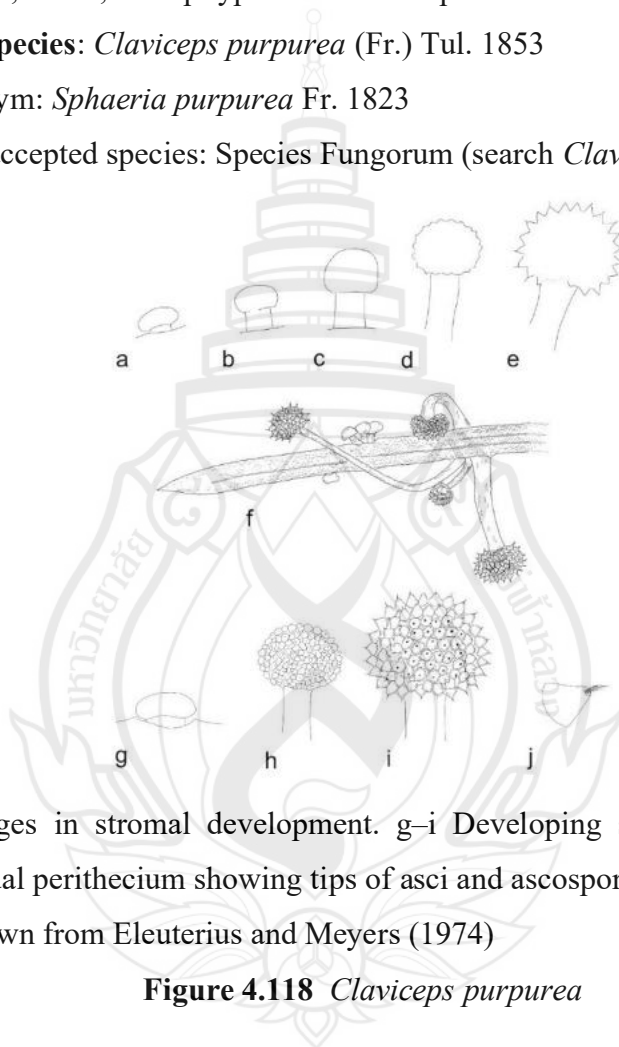
Claviceps, introduced by Tulasne (1853), comprises approximately 70 species and is an important parasite of *Poaceae*, *Cyperaceae*, and *Juncaceae*, leading to significant crop losses in cereals such as wheat and rye (Menzies and Turkington 2015; Tanaka et al. 2023; Hyde et al. 2024a). A characteristic symptom of *Claviceps* infection is the production of sclerotia, which vary in color and contain ephelidial conidia. Under favorable environmental conditions of cool damp weather, these sclerotia germinate and develop stipitate ascostromata (White et al. 2003). Following infection, the florets of the host exude a sticky, sugar-rich honey dew containing numerous conidia (White et al. 2003). *Sphacelia* is recognized as the asexual morph of *Claviceps*, growing on honeydew (Tulasne 1853; Hyde et al. 2020c). The sclerotia of *C. purpurea*, when present in infected crops, can cause ergotism in humans and other animals due to toxicity of alkaloids in the ergot (Menzies and Turkington 2015). This species is frequently reported as a saprobe or pathogen on salt marsh hosts, particularly *Spartina* species (Calabon et al. 2021b). Phylogenetic analyses have clarified the taxonomy of

the genus within *Clavicipitaceae* (White et al. 2000; Tanaka et al. 2008). *Claviceps* consists of four distinct lineages, each classified into separate sections, differing in morphology, host range, geographical distribution, and secondary metabolites (van der Linde et al. 2022). Recently, Tanaka et al. (2023) re-examined the phylogeny of the genus using LSU, *tef1*, *tub2*, *Mcm7*, and *rpb2* with a focus on species from Japan, and designated neo-, lecto-, and epitypes for several species.

Type species: *Claviceps purpurea* (Fr.) Tul. 1853

Basionym: *Sphaeria purpurea* Fr. 1823

Other accepted species: Species Fungorum (search *Claviceps*)



Note a–e Stages in stromal development. g–i Developing stages of capitulum. j Individual perithecium showing tips of asci and ascospores

Source Redrawn from Eleuterius and Meyers (1974)

Figure 4.118 *Claviceps purpurea*

Fusarium Link 1809

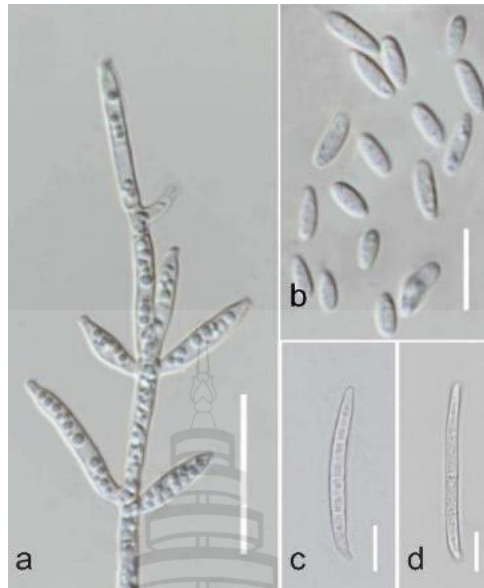
Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Fusarium was introduced based on a single species, *Fusarium roseum*, by Link (1809), using morphological characteristics. The genus comprises about 400 species, with both sexual and asexual forms recognized (Hyde et al. 2024a). The sexual morph produces ascomata that are non-stromatic or develop on a thin stroma, bluish-purple to

black, and lack papillae, hairs, or appendages. The asci are clavate, containing eight ellipsoidal to cylindrical, 1–3-septate ascospores. In the asexual morph, conidiophores can be aerial or grouped in sporodochia. Aerial conidiophores are unbranched, sympodial, or irregularly branched, bearing phialides terminally or laterally. They produce hyaline aerial conidia of three types: microconidia, macroconidia, and occasionally mesoconidia. Sporodochial conidiophores are verticillately branched, with apical monophialides producing falcate (macro)conidia (Crous et al. 2021). There are differing views on the taxonomy of *Fusarium* and its allied genera, with some proposing to retain it as a single genus and others suggesting segregation into multiple genera (Lombard et al. 2015; Crous et al. 2021; Yilmaz et al. 2021). Morphological characteristics of both sexual and asexual morphs, culture features, host preference, and molecular phylogeny (useful markers: *tef1* and *rpb2*) can be used for species identification (Leslie and Summerell 2006, Crous et al. 2021, Bhunjun et al. 2024). *Fusarium* species are ubiquitous, occurring as saprobes, endophytes, and pathogens (Bhunjun et al. 2024). Some species, such as *F. graminearum* and *F. oxysporum*, are important plant pathogens (Dean et al. 2012). They can cause diseases in economically important crops, threatening agricultural productivity, including cereals, potatoes, tomatoes, sugarcane, bananas, and palms (Bhunjun et al. 2024; Gomdola et al. in prep.). Additionally, some species are opportunistic pathogens in animals and humans, causing infections such as skin diseases (Al-Hatmi et al. 2019; Song et al. 2023). These fungi are also known to produce various compounds, including harmful mycotoxins and beneficial metabolites with antimicrobial and antiparasitic activity (Crous et al. 2021). For example, *F. moniliforme* is known to produce gibberellic acid (Puyam et al. 2017). *Fusarium sensu lato* is one of the common genera found among marine-derived fungi, with six species listed as true marine fungi (Jones et al. 2019). Seven known species, along with several unidentified *Fusarium* taxa, have been reported from salt marsh habitats on plants such as *Suaeda australis*, *Phragmites australis*, *Spartina* spp., *Distichlis* spp., and *Juncus roemerianus* (Calabon et al. 2021b).

Type species: *Fusarium sambucinum* Fuckel, 1863

Other accepted species: Species Fungorum (search *Fusarium*)



Note a Conidiophores and conidia. b Microconidia. c, d Macroconidia. Scale bars: 10 μm

Source Absalan et al. (2025)

Figure 4.119 *Fusarium chiangraiense*

Nectria (Fr.) Fr. 1849

Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

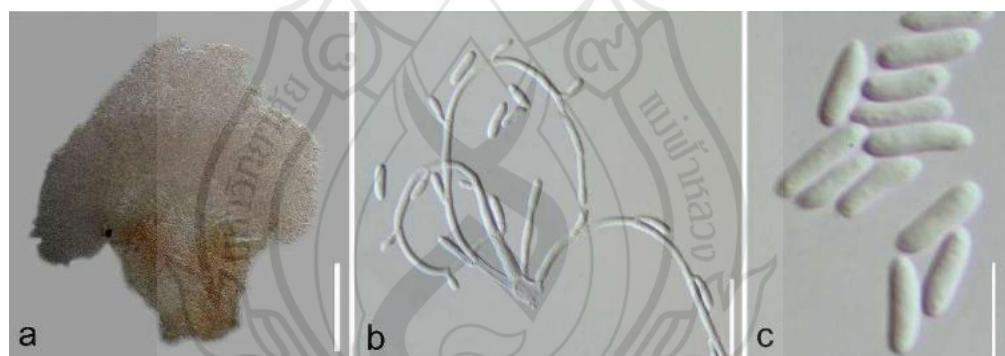
Nectria is the type genus of the family *Nectriaceae*, erected by Fries (1849) based on its basionym *Hypocrea* sect. *Nectria*. However, Fries did not designate a type species. The legitimate type species, *Nectria cinnabarina*, was later designated by Clements and Shear (1931). The sexual morph of *Nectria* is characterized by red, fleshy, globose to subglobose ascomata, with filamentous paraphyses. The asci are clavate to cylindrical, containing eight hyaline ascospores, which may have up to four septa. The asexual morph is pycnidial, sporodochial, and phialidic, producing hyaline microconidia and macroconidia (Lombard et al. 2015; Maharachchikumbura et al. 2016). Morphological characteristics combined with phylogenetic analyses of ITS, LSU, *tub2*, and *tef1* gene regions are useful for accurate species identification (Perera et al. 2023). *Nectria* comprises about 300 species, recorded primarily as saprobes on decaying wood (Perera et al. 2023; Hyde et al. 2024a). However, several species are known pathogens, causing dieback and canker diseases on a wide range of woody plant

hosts, such as apple and sweet cherry (Gutiérrez et al. 2005; Yang et al. 2018; Grinbergs et al. 2025). *Nectria pulverulenta* and *N. marina* are marine species within the genus (Jones et al. 2019; Dayarathne et al. 2020a). Additionally, *Tubercularia pulverulenta*, which belongs to the genus *Tubercularia*—a genus considered congeneric with *Nectria*—is also reported as a marine fungus (Jones et al. 2019; Hyde et al. 2024a). One unidentified species of *Nectria* has been reported from the salt marsh plant *Juncus roemerianus*. Moreover, four additional records under the name *T. pulverulenta* have been found on *Sarcocornia* sp. and *Salicornia europaea* (Calabon et al. 2021b). Saprobic, pathogenic, and endophytic species of *Nectria* have been shown to produce natural bioactive compounds in various studies (Gutiérrez et al. 2005; Kawahara et al. 2013; Cui et al. 2016).

Type species: *Nectria cinnabarina* (Tode) Fr. 1849

Basionym: *Sphaeria cinnabarina* Tode 1791

Other accepted species: Species Fungorum (search *Nectria*)



Note a Vertical section through sporodochium. b Conidiophores and conidia. c Conidia. Scale bars: a = 200 μ m, b = 20 μ m, c = 10 μ m

Source Perera et al. (2023)

Figure 4.120 *Nectria cinnabarina*

Volutella Tode 1790

Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

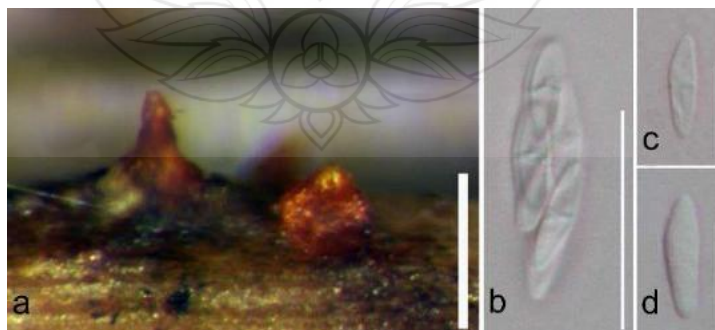
Volutella is a genus in *Nectriaceae*, introduced by Tode (1790a). The genus comprises approximately 30 species, which are plant pathogens or saprobes found on plant material and in soil (Ghosh et al. 2020; Perera et al. 2020, 2023; Hyde et al.

2024a). Zhang et al. (2024a) suggested that the increase in pathogenic fungi, such as *Volutella*, may be an important reason for continuous cropping challenges in sweet potatoes. However, one strain of *V. citronella*, isolated from the cysts of potato cyst nematodes, has demonstrated nematocidal activity, making it potentially useful for agricultural purposes (Zhang et al. 2021). *Volutella ciliata* is the only species recorded from a salt marsh habitat, identified as a saprobe on *Distichlis spicata* in Argentina (Calabon et al. 2021b). Both sexual and asexual morphs of *Volutella* have been described. The sexual morph develops perithecial, superficial, orange to red ascomata with a smooth or hairy surface. Asci are subcylindrical to clavate, containing eight hyaline, bicellular ascospores. The asexual morph is hyphomycetous, forming sporodochial or synnematal setose conidiomata with branching conidiophores. Conidiogenous cells are monophialidic, mostly with a conspicuous periclinal thickening, producing hyaline, aseptate conidia that form slimy white, yellow, orange, or pink masses (Gräfenhan et al. 2011; Lombard et al. 2015). Recently, *V. sinensis*, isolated from soil, and *V. leucaenae*, collected from decaying stems of *Leucaena leucocephala*, were added to the genus (Perera et al. 2023; Zhang et al. 2024b). Perera et al. (2023) utilized morphological and phylogenetic analyses of LSU, ITS, *tub2*, and *tef1* sequences for species identification in *Volutella* and suggested that a comprehensive revision of the genus is needed.

Type species: *Volutella ciliata* (Alb. & Schwein.) Fr. 1832

Basionym: *Tubercularia ciliata* Alb. & Schwein. 1805

Other accepted species: Species Fungorum (search *Volutella*)



Note a Ascomata on host. b Ascus. c, d Ascospores. Scale bar: a = 200 μ m, b = 50 μ m, c, d = 10 μ m

Source Perera et al. (2023)

Figure 4.121 *Volutella consors*

Sarocladium W. Gams & D. Hawksw. 1976

Classification: *Sarocladiaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Sarocladium oryzae was initially described as *Acrocylindrium oryzae*, associated with sheath rot on rice (Sawada 1922; Sakthivel et al. 2002) but Gams and Hawksworth (1976) transferred it to *Sarocladium* based on Sawada's holotype collection. The *Sarocladium* clade was further examined by Giraldo et al. (2012), who included seven species. Subsequent research by Giraldo et al. (2015) clarified the phylogenetic relationships within *Sarocladium*, encompassing a total of 18 species. Crous et al. (2018a) established family *Sarocladiaceae* comprising *Sarocladium* and *Parasarocladium*. Crous et al. (2018a) based on an LSU sequence analysis and Hyde et al. (2020c) based on combined LSU, ITS, *cmdA*, *rpb2*, *tef1* and *tub2* sequence analyses confirmed the phylogenetic distinction between *Acremonium* and *Sarocladium*. With the introduction of additional species (Phukhamsakda et al. 2020; Hou et al. 2023), sequence data is available for 25 species in GenBank (Hou et al. 2023). *Sarocladium* is hyphomycetous, with conidiophores or conidiophore-like structures, erect from septate mycelium, with or without branching. Conidiogenous cells are phialidic forming hyaline or subhyaline conidia in chains or mucoid heads (Hou et al. 2023). *Sarocladium* species have been isolated as plant pathogens, plant saprobes, soil-associated fungi and human pathogens (Gams and Hawksworth 1976; Crous et al. 2018a; Phukhamsakda et al. 2020; Giraldo et al. 2015; Hou et al. 2023). *Sarocladium* sp. was reported from decaying stems and leaf sheaths of salt marsh host, *Phragmites australis* from China (Poon and Hyde 1998) and *S. implicatum* was reported from decaying leaves of *Distichlis spicata* from Argentina (Eliades et al. 2007). *Sarocladium spinificis* was isolated as an endophyte from coastal grass, *Spinifex littoreus* (Yeh and Kirschner 2014). Garzoli et al. (2016) reported *S. glaucum* associated with the alga *Padina pavonica*. Jones et al. (2019) have listed other species of *Sarocladium* isolated from marine habitats, including *S. strictum* and *S. kiliense*. *Sarocladium kiliense* isolated from mangroves and marine water has been shown to produce cyclic depsipeptides, Saroclides A and B (Guo et al. 2018), as well as the anticancer enzyme L-asparaginase (Bhargavi and Madhuri 2022).

Type species: *Sarocladium oryzae* (Sawada) W. Gams & D. Hawksw. 1976

Other accepted species: Species Fungorum (search *Sarocladium*)



Note a, b Colonies on PDA after two months. c, d Conidiophores, conidiogenous cells and conidia. Scale bars: 20 µm

Source Asghari et al. (2025)

Figure 4.122 *Sarocladium gamsii*

Albifimbria L. Lombard & Crous 2016

Classification: *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Lombard et al. (2016) introduced *Albifimbria* to accommodate a new combination, *A. verrucaria*, and three novel species: *A. lateralis*, *A. terrestris*, and *A. viridis*. Based on phylogenetic analysis of combined LSU and *rpb2* and combined *cmdA*, ITS, *rpb2*, and *tub2* sequence data, the type species, *A. verrucaria*, formerly classified as *Myrothecium verrucaria* (= *Peziza verrucaria*), formed a distinct clade separate from *Myrothecium* (Lombard et al. 2016). The sexual morph of *Albifimbria* is unknown. The asexual morph is characterized by stromatic sporodochia or absent conidiomata, reduced to simple hyaline conidiophores. Sporodochial conidiophores are hyaline and branched irregularly, verticillate, or penicillate. Conidiogenous cells are phialidic, bearing unicellular conidia sometimes with a funnel-shaped mucoid apical appendage. *Albifimbria* differs from *Myrothecium* in having verrucose setae surrounding the sporodochia and conidia sometimes with a mucoid appendage (Lombard et al. 2016). *Albifimbria verrucaria* was reported as saprobic on the salt marsh host *Distichlis spicata* in Argentina (Eliades et al. 2007; Calabon et al. 2021b).

Type species: *Albifimbria verrucaria* (Alb. & Schwein.) L. Lombard & Crous 2016

Basionym: *Peziza verrucaria* Alb. & Schwein. 1805

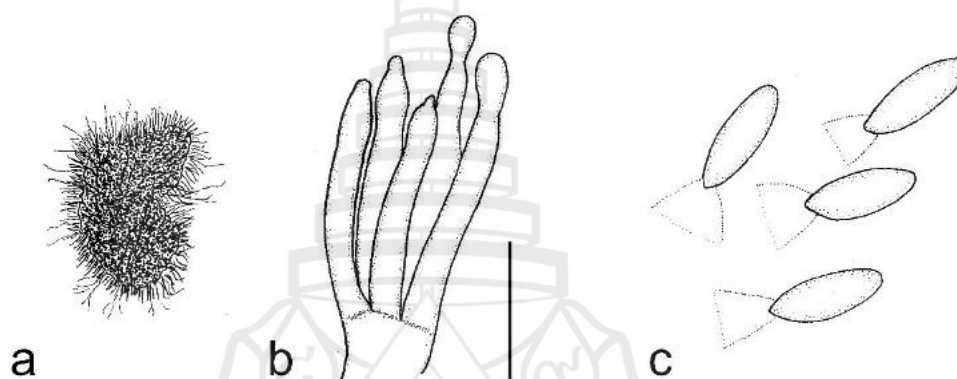
Other accepted species:

Albifimbria bidentis Htet, A. Mapook, K.W.T. Chethana & K.D. Hyde 2025

Albifimbria lateralis L. Lombard & Crous 2016

Albifimbria terrestris L. Lombard & Crous 2016

Albifimbria viridis L. Lombard & Crous 2016



Note a Sporodochial conidioma. b Conidiogenous cells. c Conidia. Scale bars: b, c = 20 μ m

Source Redrawn from Lombard et al. (2016)

Figure 4.123 *Albifimbria verrucaria*

Paramyrothecium L. Lombard & Crous 2016

Classification: *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

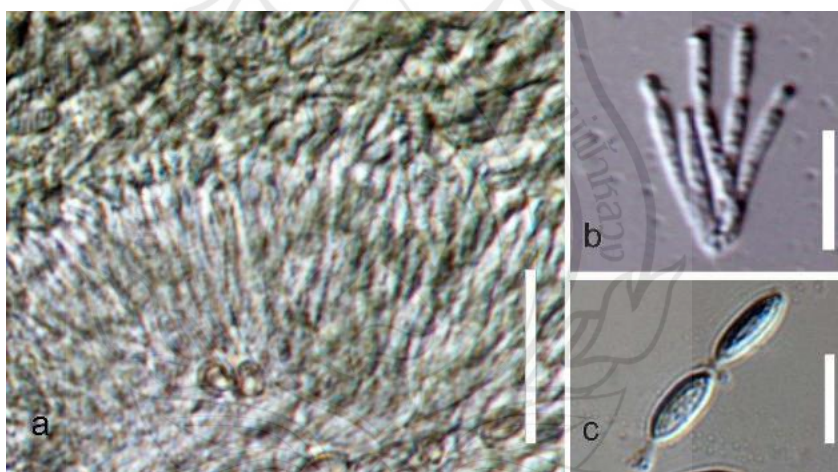
Paramyrothecium was established by Lombard et al. (2016) to accommodate a group of species that formed a distinct clade separate from *Myrothecium*, based on phylogenetic analyses of combined *cmdA*, ITS, *rpb2*, and *tub2* sequences. The sexual morph of *Paramyrothecium* is unknown, while the asexual morph produces sporodochial, superficial conidiomata, with or without a surrounding setose fringe. Conidiophores are phialidic, hyaline, and penicillately branched, with conspicuous collarettes and periclinal thickenings. Conidia are unicellular to bicellular, hyaline to pale green, and smooth. Morphologically, *Paramyrothecium* differs from *Myrothecium*

by the presence of “1–3-septate, thin-walled setae surrounding the sporodochia” (Lombard et al. 2016). The genus *Paramyrothecium* comprises approximately 20 species, most of which are plant pathogens causing symptoms such as leaf spots and cankers on various hosts, including melon, eggplant, and apple trees (Azizi et al. 2020; Aumentado and Balendres 2022; Sabahi et al. 2022; Armand et al. 2023; Hyde et al. 2024a). Recently, *P. kamalii* was identified as a foliar pathogen on *Matourea azurea*, *P. amorphophalli* was reported as the causal agent of leaf blight in *Amorphophallus* species, and *P. travancorensis* was found to cause leaf spots and blight on *Coffea travancorensis* (Armand et al. 2023). The type species, *P. roridum*, has been reported on both decaying and living leaves of salt marsh halophyte, *Juncus roemerianus* (Calabon et al. 2021b).

Type species: *Paramyrothecium roridum* (Tode) L. Lombard & Crous 2016

Basionym: *Myrothecium roridum* Tode 1790

Other accepted species: Species Fungorum (search *Paramyrothecium*)



Note a Sporodochium. b Conidiogenous cells and conidia. c Conidia. Scale bars: 10 μm)

Figure 4.124 *Paramyrothecium* sp.

Stachybotrys Corda 1837

Classification: *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Stachybotrys is a saprobe belonging to *Stachybotryaceae*, *Hypocreales* (*Sordariomycetes*, *Ascomycota*) (Hyde et al. 2020c). The genus was established by

Corda (1837) from the Czech Republic and typified with *Stachybotrys atrus* (current name *Stachybotrys chartarum*). Based on Species Fungorum (2026) there are 95 accepted species, of which about 30 have molecular data in GenBank (Hyde et al. 2020c). A lack of living ex-type material and molecular data for many species complicates taxonomic studies for this genus. Nuclear rDNA species-specific primers were first created by Haugland and Heckman (1998) for the purpose of identifying toxigenic strains of *S. chartarum*. Lombard et al. (2016) revised the genus based on the phylogenetic study of ITS, LSU, *rpb2*, *cmdA*, *tef1*, and *tub2* and transferred many species to other genera.

The asexual morph of *Stachybotrys* is hyphomycetous with erect, branched or unbranched conidiophores with terminal phialidic conidiogenous cells. Conidia are one-celled, smooth to rough forming in chains or slimy masses (Wang et al. 2015; Lombard et al. 2016). *Stachybotrys* is similar to *Memnoniella* and they were considered as synonym by Smith (1962) and Wang et al. (2015) but *Memnoniella* was reinstated as a separate genus by Lombard et al. (2016).

Stachybotrys oleronensis was described as the sexual morph and is characterized by immersed ascomata with erect hairs on the peridium. Paraphyses are branched with oily orange drops. Asci are clavate and 8-spored, containing ellipsoidal to fusiform, 1-septate ascospores (Lechat et al. 2013). Other genera, *Melanopsamma* and *Ornatispora* are related to *Stachybotrys* as sexual stages (Wang et al. 2015; Hyde et al. 1999b).

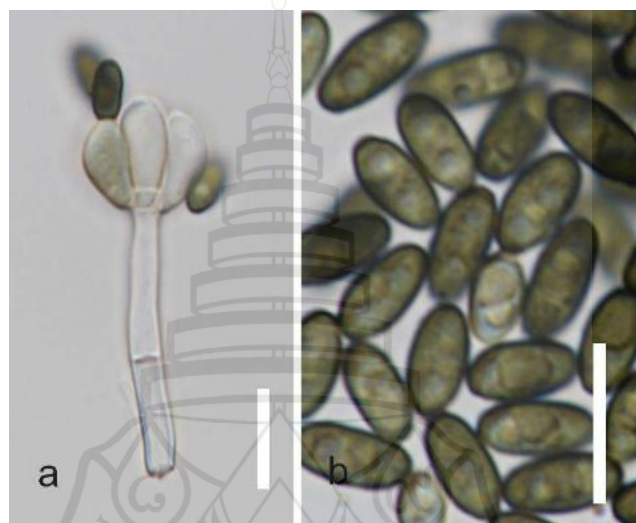
Stachybotrys is widespread in both terrestrial and aquatic habitats. It is frequently found in air, soil, plant litter, marine environments, water-damaged buildings and also damped paper, cotton and cellulolytic material (Ellis et al. 1971; Lombard et al. 2016; Hyde et al. 2020c; Samarakoon et al. 2021). Some species have been recorded on salt marsh plants: *Stachybotrys chartarum*, *S. cylindrosporus*, *S. echinatus*, *S. kampalensis*, *S. nephrosporus* on *Juncus roemerianus* from USA (Fell and Hunter 1979) and a few undetermined *Stachybotrys* on *Phragmites australis*, *Spartina alterniflora*, and *Juncus roemerianus* from China and USA (Poon and Hyde 1998).

Stachybotrys can produce mycotoxins that have been linked to agricultural damage and health problems in humans and animals (Johanning et al. 1996; Page and Trout 2001; Hyde et al. 2020c). *Stachybotrys chartarum* (formerly known as *S. atra*)

and *S. chlorohalonata* are known as black mold and are associated with water-damaged buildings and assumed to be associated with health problems (Nielsen 2003). However, there is disagreement regarding the connection between *Stachybotrys* mold and particular health issues (Rudert 2017; Chang and Gershwin 2019).

Type species: *Stachybotrys chartarum* (Ehrenb.) S. Hughes 1958

Other accepted species: Species Fungorum (search *Stachybotrys*)



Note a Conidiophores, conidiogenous cells and conidia. b Conidia. Scale bars: 10 μ m

Figure 4.125 *Stachybotrys* sp.

Striaticonidium L. Lombard & Crous. 2016

Classification: *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Lombard et al. (2016) introduced *Striaticonidium* for several myrothecium-like species including *Myrothecium brachysporum*, *Fusarium cinctum*, *Striaticonidium humicola* and *S. synnematum*. The genus is distinguishable with striate conidia and phylogenetic analyses of combined LSU and *rpb2* sequence and combined *cmdA*, ITS, *rpb2* and *tub2* sequence data, confirmed its placement within the myrothecium-like taxa (Lombard et al. 2016). The genus is known for its asexual morph and is typified by *Striaticonidium cinctum*. Conidiomata are synnematus, sporodochial or mononematous with hyaline and branched conidiophores. Hyaline, phialidic, cylindrical to subcylindrical conidiogenous cells bear fusiform to ellipsoidal, olivaceous green to brown conidia ornamented by longitudinal striate with an apical

hilum (Lombard et al. 2016). There are ten species under *Striaticonidium* in Species Fungorum (April 2026), mostly isolated from soil (Lombard et al. 2016). *Striaticonidium brachysporum* has been found in coastal sand dunes in Iran (Nicot and Olivry 1961, Lombard et al. 2016) and *S. cinctum* was collected from decaying *Phragmites australis* in the Netherlands (Ryckegem and Verbeken 2005b; Calabon et al. 2021b).

Type species: *Striaticonidium cinctum* (Corda) L. Lombard & Crous 2016

Basionym: *Fusarium cinctum* Corda 1842

Other accepted species:

Striaticonidium brachysporum (Nicot) L. Lombard & Crous 2016

Striaticonidium chiangraiense N. Afshari, Lumyong & K.D. Hyde 2025

Striaticonidium dekljnearum L. Lombard 2017

Striaticonidium humicola L. Lombard & Crous 2016

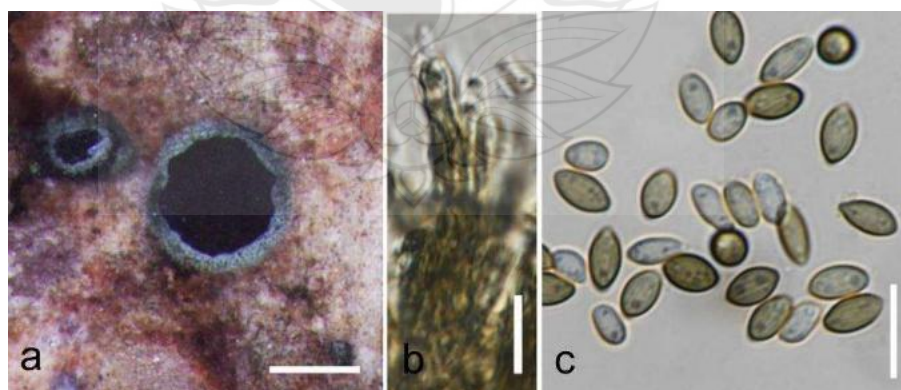
Striaticonidium kfriense Rajeshk., O.P. Sruthi, S.K. Ashtamoorthy & K.V. Sankaran 2024

Striaticonidium olivaceobrunneum Y.R. Sun, Yong Wang bis & K.D. Hyde 2025

Striaticonidium panamaense Crous 2024

Striaticonidium synnematum L. Lombard & Crous 2016

Striaticonidium xishuangbannaense S.C. He, K.D. Hyde & R.S Jayawardena 2025



Note a Conidiomata on host. b Conidiophore and conidiogenous cells. c Conidia. Scale bars: a = 200 μ m, b, c = 10 μ m

Source Afshari et al. (2025)

Figure 4.126 *Striaticonidium chiangraiense*

Xepicula Nag Raj 1993

Classification: *Stachybotryaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Xepicula is an asexual genus introduced by Nag Raj (1993) to accommodate *X. leucotricha*, which was formerly classified in *Myrothecium*. Nag Raj also synonymized both *M. indicum* and *M. jollymannii* with *X. leucotricha*. However, Lombard et al. (2016) resurrected *M. jollymannii* as *X. jollymannii* based on phylogenetic analyses of combined LSU and *rpb2* sequences, as well as combined *cmdA*, ITS, *rpb2*, and *tub2* sequence data. *Xepicula jollymannii* has been recorded as a saprobe on *Juncus roemerianus* from USA (Fell and Hunter 1979; Calabon et al. 2021b). It is characterized by cup-shaped sporodochia with septate hyaline setae. The conidiophores are composed of olivaceous brown, branched, septate fertile hyphae, and sub-hyaline, straight or slightly curved, slightly clavate phialides. The conidia are greenish-brown, biguttulate, cylindrical, or slightly tapering with blunt ends (Preston 1948).

Type species: *Xepicula leucotricha* (Peck) Nag Raj 1993

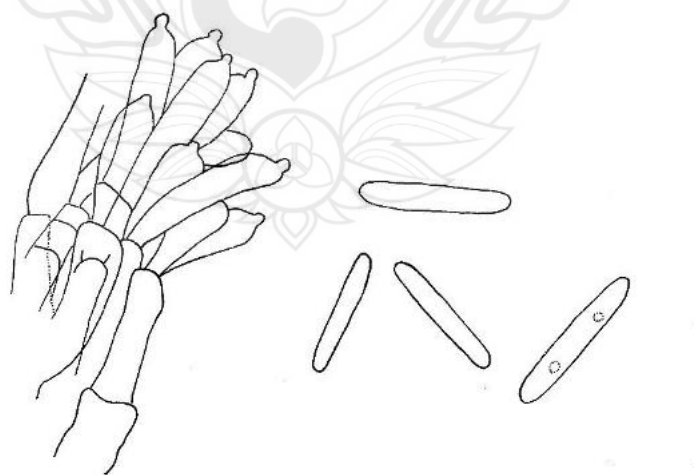
Basionym: *Excipula leucotricha* Peck 1878

Other accepted species:

Xepicula crassiseta L. Lombard & Crous 2016

Xepicula jollymannii (N.C. Preston) L. Lombard & Crous 2016

Xepicula yifeiae Qian Zhang, Yong Wang bis & K.D. Hyde 2020



Note Phialides from PDA culture and conidia. Scale bar = 10 µm

Source Redrawn from Preston (1948)

Figure 4.127 *Xepicula jollymannii*

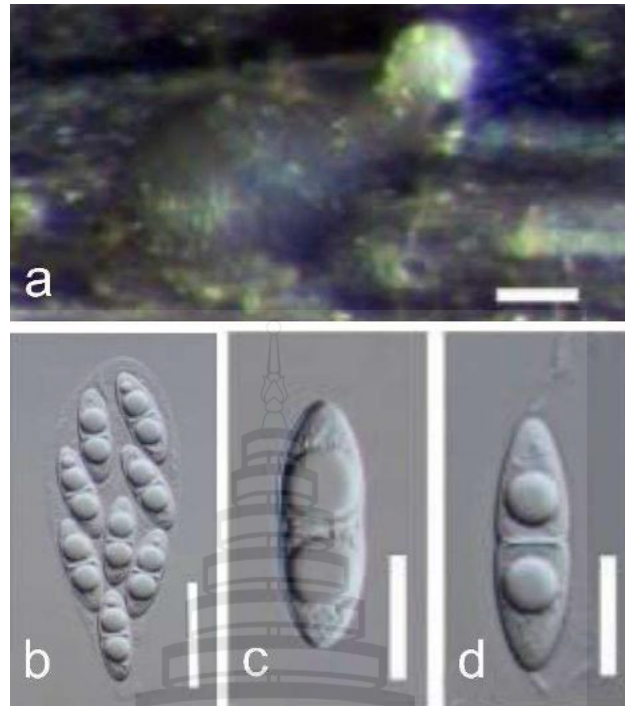
Aniptodera Shearer & M.A. Mill. 1977

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Aniptodera was established by Shearer and Miller (1977) based on collections of the novel species *Aniptodera chesapeakeensis*, found on balsa wood submerged in the Patauxen river, USA. The genus was originally described as having superficial to semi-immersed, hyaline, ostiolate ascomata with elongated necks; clavate asci with an apical pore that deliquesces at maturity, and retraction of apical plasmalemma; no paraphyses; and 1-septate, hyaline, thick-walled ascospores without appendages. Shearer and Miller (1977) also discussed the similarity of *A. chesapeakeensis* to *Lignincola laevis* and *Nais inornata*, but noted that the latter two species differ in having blackish ascomata, thin-walled ascospores, and asci that lack an apical pore. Later, Shearer (1989a) emended the description of *A. chesapeakeensis* to include ascospores that are either without appendages or with bipolar unfurling appendages. *Aniptodera* comprises 17 species (Hyde et al. 2024a) isolated from both freshwater and marine habitats, occurring on various plant substrates such as decaying wood, leaves, and fern rachises (Pang et al. 2011, Jones et al. 2017). *Aniptodera nypae* and *A. intermedia* are host-specific to the mangrove palm *Nypa fruticans* (Jones et al. 2019). Ten species are listed as marine fungi by Jones et al. (2019). *A. chesapeakeensis*, *A. juncicola*, and *A. phragmiticola* have been reported as saprobes on salt marsh hosts, including *Phragmites australis*, *Juncus roemerianus*, and *Spartina* species (Calabon et al. 2021b). Based on SSU and LSU phylogenetic data, *A. chesapeakeensis* is placed in the family *Halosphaeriaceae* (Jones et al. 2017). Most *Aniptodera* species lack molecular data, while other have been referred to other genera: *Aniptodera lignatilis* = *Aniptosporopsis lignatilis* and *Aniptodera longispora* = *Paraaniptodera longispora*. However, the genus is suggested to require revision based on new collections and molecular data (Marine Fungi).

Type species: *Aniptodera chesapeakeensis* Shearer & M.A. Mill. 1977

Other accepted species: Species Fungorum (search *Aniptodera*)



Note a Ascoma in host. b Ascus. c, d Ascospores. Scale bars: a = 50 μm , b = 30 μm , c, d = 10 μm

Source Li et al. (2016)

Figure 4.128 *Aniptodera aquibella*

Ceriosporopsis Linder 1944

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Ceriosporopsis is a marine genus established by Linder (1944) based on its type species, *Ceriosporopsis halima* (Barghoorn and Linder 1944). The genus is characterized by immersed or superficial, ostiolate ascomata; eight-spored, early deliquescing asci; and 1-septate, hyaline ascospores with gelatinous polar appendages that uncoil in water to form long, filamentous structures (Johnson et al. 1984; Barghoorn and Linder 1944; Pang et al. 2011; Sakayaroj et al. 2011). Chlamydospores can also be observed in culture (Pang et al. 2011). All *Ceriosporopsis* species are known as marine fungi, commonly isolated from decaying wood and widely distributed across marine habitats (Jones et al. 2019). *Ceriosporopsis halima* has also been reported from salt marsh plants, including *Arundo donax* and several *Spartina* species, such as *S. alterniflora*, *S. townsendii*, and *S. maritima* (Calabon et al. 2021b). Sequence data are

currently available only for *Ceriosporopsis halima* and *Ceriosporopsis capillacea*. Sakayaroj et al. (2011) showed that the genus is polyphyletic based on phylogenetic analyses of combined SSU, LSU, and *rpb2* data. As a result, *Bovicornua intricata* was transferred to *Ceriosporopsis*, while *C. tubulifera* was excluded and reassigned to the genus *Toriella*. Currently, there are five *Ceriosporopsis* species, while *C. halima* has demonstrated demonstrated antimicrobial activity against certain Gram-positive bacteria, which highlights its potential for biotechnological applications (Kalyuzhnaya 2015).

Type species: *Ceriosporopsis halima* Linder 1944

Other accepted species:

Ceriosporopsis barbata Höhnk 1955

Ceriosporopsis caduca E.B.G. Jones & Zainal 1988

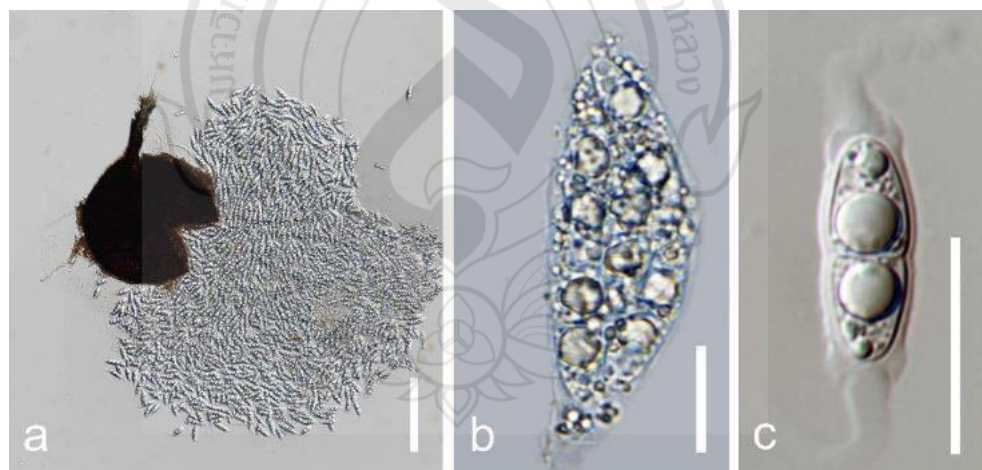
Ceriosporopsis calyptrata Kohlm. 1960

Ceriosporopsis cambrensis I.M. Wilson 1954

Ceriosporopsis capillacea Kohlm. 1981

Ceriosporopsis longissima Kohlm. 1962

Ceriosporopsis minuta Abdel-Wahab, Nagah. & E.B.G. Jones 2017



Note a Ascoma. b Ascus. c Ascospore. Scale bar: a 150 μ m, b, c = 25 μ m

Figure 4.129 *Ceriosporopsis halima*

Cirrenalia Meyers & R.T. Moore 1960

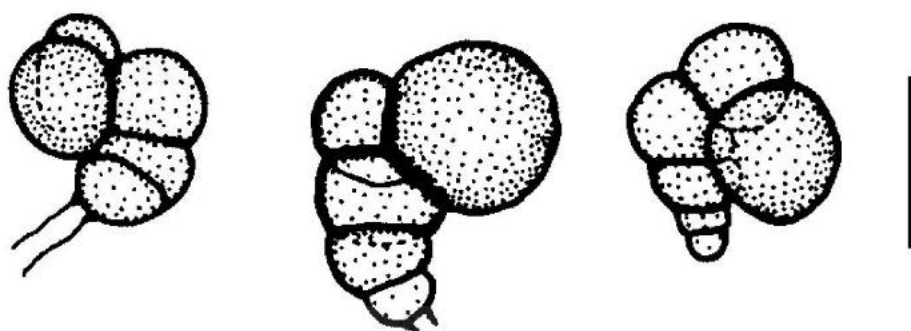
Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cirrenalia was established by Meyers and Moore (1960) based on its marine type species, *Cirrenalia macrocephala*, which was formerly classified in *Helicoma*. The genus was described as a saprobic marine dematiaceous hyphomycete, characterized by helicosporous conidia with non-congruent cells that are constricted at the septa, and a larger, darker terminal cell (Meyers and Moore 1960). The first terrestrial species, *C. donnae*, was introduced by Sutton (1973). Since then, several marine and terrestrial species have been added to *Cirrenalia*, leading to its recognition as a polyphyletic genus. Zhao et al. (2007) provided a synopsis of *Cirrenalia* species and included notes and illustrations for those found in China. Abdel-Wahab et al. (2010) revised cirrenalia-like genera through a phylogenetic study based on SSU and LSU rDNA sequences, introducing eight new genera in the *Lulworthiales* (Dayarathne et al. 2025a). They noted that since the type species clusters with marine fungi, other species forming distinct clades require revision. Jones, in Hyde et al. (2024a), also mentioned that although *Cirrenalia* is polyphyletic, the correct concept of the genus is marine. Currently, *Cirrenalia* comprises 12 species (of which two are marine) isolated from diverse substrates such as soil, dead mangroves, decaying wood, and leaves (Zhao et al. 2007; Abdel-Wahab et al. 2010; Zhang et al. 2014). *Cirrenalia macrocephala* has been referred to *Remisporopsis* as *R. macrocephala* a genus in the *Halosphaeriaceae* (Dayarathne et al. 2026). *Cirrenalia lichenicola* and *C. pertusariicola* have been recorded as lichenicolous fungi (Diederich et al. 2024). *Cirrenalia macrocephala* has been reported from salt marsh plants including *Ammophila arenaria*, *Juncus roemerianus*, and species of *Spartina*, and *C. pseudomacrocephala* has also been recorded on *J. roemerianus* (Calabon et al. 2021b). Other *Cirrenalia* species need to be recollected, isolated and sequenced to determine their taxonomic identity.

Type species: *Cirrenalia macrocephala* (Kohlm.) Meyers & R.T. Moore 1960

Basionym: *Helicoma macrocephalum* Kohlm. [as '*macrocephala*'] 1958

Other accepted species: Species Fungorum (search *Cirrenalia*)



Note Conidiophores and conidia. Scale bar = 12 μm

Source Zhao & Liu (2005)

Figure 4.130 *Cirrenalia macrocephala*

Corollospora Werderm. 1922

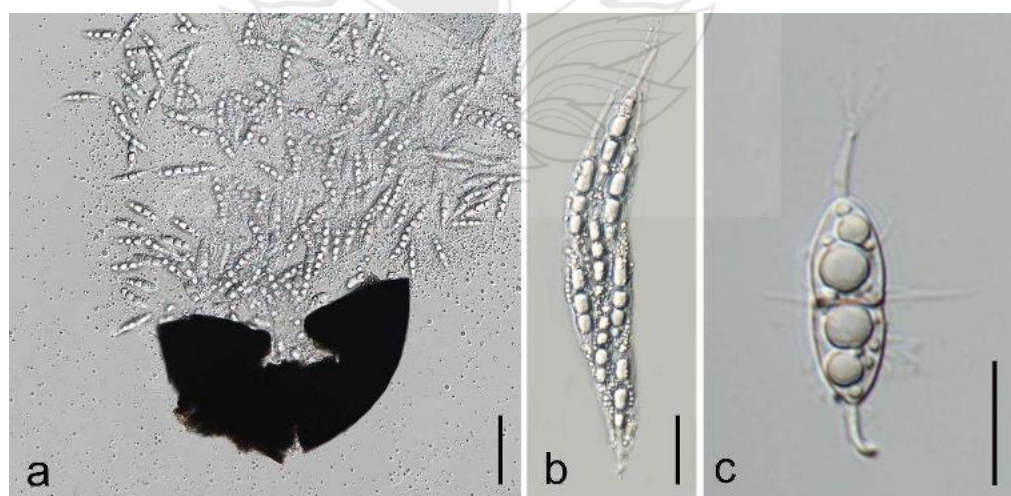
Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Corollospora was introduced by Werdermann (1922) to accommodate a single species, *Corollospora maritima*, collected from maritime wood in Germany. It was originally described as a coelomycetous asexual morph, producing pycnidia and pycnidiospores (Werdermann 1922). Later, Kohlmeyer (1962a) examined the type species of *Peritrichospora*, *P. integra*, and synonymized it with *C. maritima*, subsequently transferring four additional species to *Corollospora*. These included *C. comata* (now classified as *Nereiospora comata*), *C. cristata*, and *C. lacera* from *Peritrichospora*, and *C. trifurcata* from *Arenariomyces*. *Corollospora* is considered a large marine genus, with 33 epithets currently listed in Species Fungorum (accessed April 2026), although several species have been reassigned to other genera. Most *Corollospora* species are described based on their sexual morphs, which typically form globose to subglobose, superficial, carbonaceous ascomata. The asci are deliquescent, fusiform to subclavate, and lack an apical apparatus. Ascospore morphology is a key character for species delimitation within the genus, showing variation in shape (fusiform to subellipsoidal), septation (1–14-septate or muriform), pigmentation (hyaline to brown), and the presence of distinctive spine- or hair-like appendages (Jones et al. 2009). Three species of *Corollospora* are known only from their asexual morphs, while four species have both sexual and asexual morphs; the asexual morphs of these

species correspond to three genera: *Clavatospora*, *Halosigmoidea*, and *Varicosporina* (Nakagiri et al. 2025). Among them, *C. intermedia* was once regarded as the sexual morph of *Varicosporina prolifera*. However, Nakagiri et al. (2025) re-evaluated this relationship and, by inducing the sexual morph of *V. prolifera* in culture, concluded they were distinct species. As a result, a new combination, *C. prolifera*, was proposed. Correia et al. (2023) investigated cryptic diversity within *C. maritima* using multilocus sequence data (ITS, LSU, and SSU), leading to the description of ten new genera and thirteen new combinations. However, subsequent studies retained *Corollospora* as a single genus (Nakagiri et al. 2025; Dayarathne et al. 2026). *Corollospora* forms a distinct and robust clade within the *Halosphaeriaceae* (Jones et al. 2015). A monograph of the *Halosphaeriaceae* is in preparation to resolve the taxonomy of corollospora-like genera (Dayarathne et al. 2026). Ecologically, *Corollospora* species are saprobic in marine habitats, particularly on driftwood, mangroves, seaweeds, and seagrasses, often associated with sandy substrates (Pang et al. 2011). *Corollospora maritima* and *C. ramulosa* have also been recorded on salt marsh plants such as *Spartina* spp. and *Zostera marina*, respectively (Calabon et al. 2021b). In addition to their ecological significance, some species have been studied for their bioactive compounds. Notably, the antibacterial metabolite corollosporine was isolated and synthesized from *C. maritima* (Ohzeki and Mori 2001).

Type species: *Corollospora maritima* Werderm. 1922

Other accepted species: Species Fungorum (search *Corollospora*)



Note a Ascoma. b Ascus. c Ascospore. Scale bar: a = 50 μ m, b, c = 20 μ m

Figure 4.131 *Corollospora portsaidica*

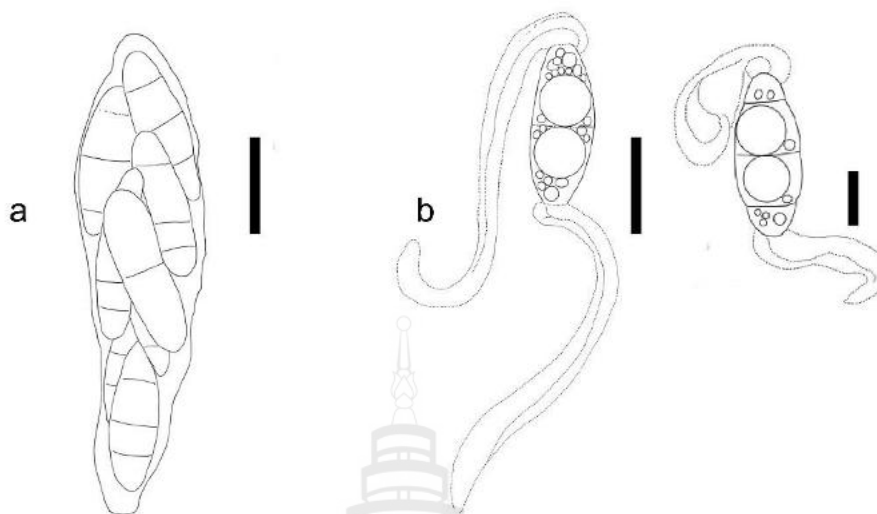
***Haligena* Kohlm. 1961**

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Haligena was established by Kohlmeyer (1961), based on the saprobic marine fungus *Haligena elaterophora*, which was designated as the type species. The sexual morph of *Haligena* is characterized by globose to ovoid, ostiolate black ascomata, with or without a papilla, asci are early deliquescing, clavate to somewhat apiculate in shape, typically containing eight ascospores, though occasionally only four, and ascospores are oblong to ellipsoidal, 3–5-septate, with bipolar, strap-like appendages. Immature ascospores are surrounded by a gelatinous sheath that expands at maturity, unfolds to form long “elator-like” appendages and remain attached at both ends with protrusions (Kohlmeyer 1961). Subsequently, five additional species were assigned to *Haligena* (Jones 1962a, Kohlmeyer and Kohlmeyer 1965, Jones and Le Campion-Alsumard 1970; Farrant and Jones 1986), but these were later transferred to other genera: *Haligena amicta* to *Appendichordella* (Johnson et al. 1987), *H. salina* to *Morakotiella* (Sakayaroj et al. 2005b), *H. spartinae* to *Magnisphaera* (Campbell et al. 2003), and *H. unicaudata* and *H. viscidula* to *Oceanitis* (Doupé et al. 2009). Currently, *Haligena elaterophora* remains the only accepted species in the genus, and has been reported from intertidal and drifting wood, submerged test panels, submerged polyurethane panels, and salt marsh plants including *Spartina* species (Kohlmeyer 1961; Jones and Le Campion-Alsumard 1970; Sakayaroj et al. 2005b; Calabon et al. 2021b; Hyde et al. 2024a). Sequence data available for *Haligena* include LSU, SSU, and *rpb2* regions.

Type species: *Haligena elaterophora* Kohlm. 1961

Other accepted species: None



Note a Ascus, b Ascospores. Scale bars = 20 μ m

Source Redrawn from Sakayaroj et al. (2005b)

Figure 4.132 *Haligena elaterophora*

Halosarpheia Kohlm. & E. Kohlm. 1977

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Halosarpheia is a saprobic marine ascomycete genus belonging to the family *Halosphaeriaceae* (*Microascales*, *Sordariomycetes*) (Jones et al. 2015; Maharachchikumbura et al. 2015). *Halosarpheia* was established by Kohlmeyer and Kohlmeyer (1977) to accommodate *H. fibrosa*, a marine fungus, based on the specific morphological characteristics of hyaline ascospores with cap-like appendages that unravel to form long threads in water. Other species were placed in *Halosarpheia* based on the similarity of ascospore appendages, which led to the inclusion of diverse fungi in the genus with divergent morphologies emphasizing ascospore appendage morphology (Campbell et al. 2003; Abdel-Wahab and Nagahama 2012). Molecular investigations have aided in resolving the phylogeny of the genus (Chen et al 1999; Kong et al. 2000). Phylogenetic analysis using the SSU and LSU rDNA sequences revealed that *Halosarpheia* is a polyphyletic genus (Kong et al. 2000; Abdel-Wahab et al. 2001; Anderson et al. 2001; Pang et al. 2003a). Based on morphological and molecular analyses *Halosarpheia abbonis* and *H. ratnagiriensis* were transferred to *Saagaromyces*, a new genus (Pang et al. 2003a), and more *Halosarpheia* species were

assigned to new genera: *Ascosacculus*, *Ascosalsum*, *Magnisphaera*, *Natantispora*, *Oceanitis*, *Panorbis* and *Praelongicaulis*, while *H. aquadulcis* was reclassified to the genus *Aniptodera* (Campbell et al. 2003; Pang et al. 2003b; Jones et al. 2015).

Halosarpheia is characterized by ostiolate, papillate, obpyriform to sub-globose ascomata. Ascomata are coriaceous, brown to black with catenophyses hamathecia. Asci are eight-spored, clavate, thin-walled, unitunicate, containing 0–1 septate, hyaline ascospores with coiled apical appendages that unfold in water (Abdel-Wahab and Nagahama 2012). The asexual morph of *Halosarpheia* is characterized by helicoidal conidia that are frequently associated in marine habitats (Abdel-Wahab and Nagahama 2012). There are eight epithets in Species Fungorum (2026) that have been introduced from Australia, China, Egypt, Japan, Singapore, Sri Lanka, and USA on unidentified rotting wood or decaying plants of the *Acanthaceae*, *Poaceae*, and *Juncaceae* families. Some *Halosarpheia* species, including *H. culmiperda* and *H. viscosa* were discovered as salt marsh fungi on halophytes including *Juncus roemerianus*, *Spartina alterniflora*, and *Spartina maritima* from USA and Portugal (Kohlmeyer et al. 1995b, Buchan et al. 2002, Barata 2006).

Type species: *Halosarpheia fibrosa* Kohlm. & E. Kohlm. 1977

Other accepted species:

Halosarpheia bentotensis Jørg. Koch 1982

Halosarpheia culmiperda Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1995

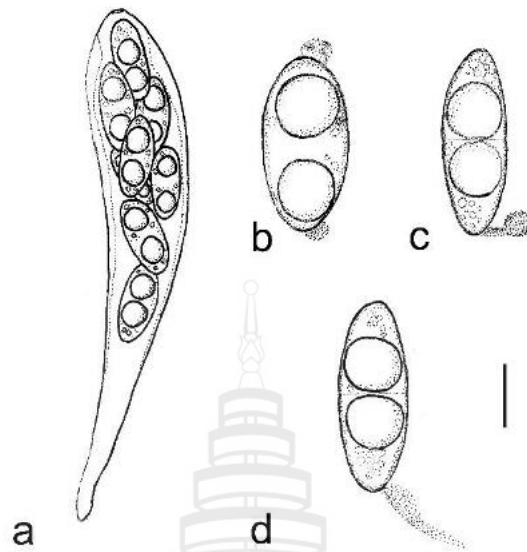
Halosarpheia japonica Abdel-Wahab & Nagah. 2012

Halosarpheia marina (Cribb & J.W. Cribb) Kohlm. 1984

Halosarpheia minuta W.F. Leong 1991

Halosarpheia phragmiticola Poon & K.D. Hyde 1998

Halosarpheia unicellularis Abdel-Wahab & E.B.G. Jones 2001



Note a Ascus. b–d Ascospores. Scale bar = 10 μ m

Source Redrawn from Kohlmeyer et al. (1995b)

Figure 4.133 *Halosarpheia culmiperda*

Lautisporopsis E.B.G. Jones, Yusoff & S.T. Moss 1994

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Yusoff et al. (1994a) restudied the taxonomy of *Ceriosporopsis* and, based on morphological differences in the appendages, excluded *C. circumvestita* from the genus, transferring it to a novel genus, *Lautisporopsis*. Later, Jones (1998) formally established *Lautisporopsis* in accordance with the International Code of Botanical Nomenclature. *Lautisporopsis* is characterized by its sexual morph, producing brown to black ascomata, clavate to elongate or broadly clavate asci, and hyaline ascospores with appendages and a chambered sheath of mesosporial origin. The species lacks a collar at the base of the appendage and lacks an exosporium (Yusoff et al. 1994a; Sarma and Hyde 2000a). *Lautisporopsis* is a marine, monotypic genus with no available sequence data (Hyde et al. 2024a). In *L. circumvestita* ascospores are enveloped in a mucilaginous sheath, which is mesosporial in origin, and forming irregular polar and equatorial appendages (Yusoff et al. 1994a). *Ceriosporopsis* species have only polar appendages (Johnson et al. 1987). *Lautisporopsis circumvestita* is a lignicolous marine

fungus reported from various countries, including the USA, Chile, Portugal, and Sweden (Jones 1998; Azevedo et al. 2010; Tibell et al. 2020). Tibell et al. (2020) reported the species for the first time from the Baltic Sea and Södermanland, and due to its tolerance of the low salinity in Södermanland, considered it a euryhaline species. This species has also been recorded as a salt marsh fungus, found on *Arundo donax* (Calabon et al. 2021b).

Type species: *Lautisporopsis circumvestita* (Kohlm.) E.B.G. Jones, Yusoff & S.T. Moss 1998

Basionym: *Halosphaeria circumvestita* Kohlm. 1960

Other accepted species: None

Note Ascospore. Scale bar: 10 µm

Source Redrawn from Tibell et al. (2019)

Figure 4.134 *Lautisporopsis circumvestita*

Lignincola Höhnk 1955

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Lignincola was introduced by Höhnk (1955) to accommodate a saprobic marine species, *L. laevis*, found on wood submerged in seawater in Germany. *Lignincola laevis* has also been reported on salt marsh plants, including *Elymus pungens* and *Spartina* species (Calabon et al. 2021b). The genus was described based on its sexual morph,

which develops perithecial ascomata. The asci are clavate to fusiform, with a persistent, thin wall, lacking an apical apparatus. The ascospores are hyaline, 1-septate, and without appendages (Höhnk 1955). The absence of appendages in the ascospores is a key feature that distinguishes *Lignincola* from related genera such as *Aniptodera*, *Halosarpheia*, and *Phaeonectriella* (Pang et al. 2003a,b; Jones et al. 2009). Currently, *Lignincola* comprises four species (Hyde et al. 2024a). *Lignincola tropica* was originally isolated from submerged mangrove wood, however molecular studies show it does not belong in *Lignincola* and should be assigned to a different genus (Kohlmeyer 1984). *Lignincola nypae* was collected from the petiole of intertidal *Nypa fruticans*, but differs from the generic concept by having asci with a refractive apical thickening and a pore (Hyde et al. 1999a). *Lignincola conchicola* was introduced by Liu et al. (2011) from the adhesive disc of an invertebrate on submerged fronds of the palm *Phoenix paludosa* in Thailand, and a key to the species of *Lignincola* was provided. Although molecular data are available for the type species, sequence data for the other species are still needed to confirm their taxonomic placement. Pang et al. (2013) investigated the genetic variation within *L. laevis* and suggested that it is highly diverse and likely represents a species complex comprising several closely related taxa. *Lignincola* has also been investigated for its bioactive compounds. A methylene chloride:methanol (2:1 v/v) extract from *L. laevis* showed inhibitory effects on the growth of murine leukemia cells (Abraham et al. 1994).

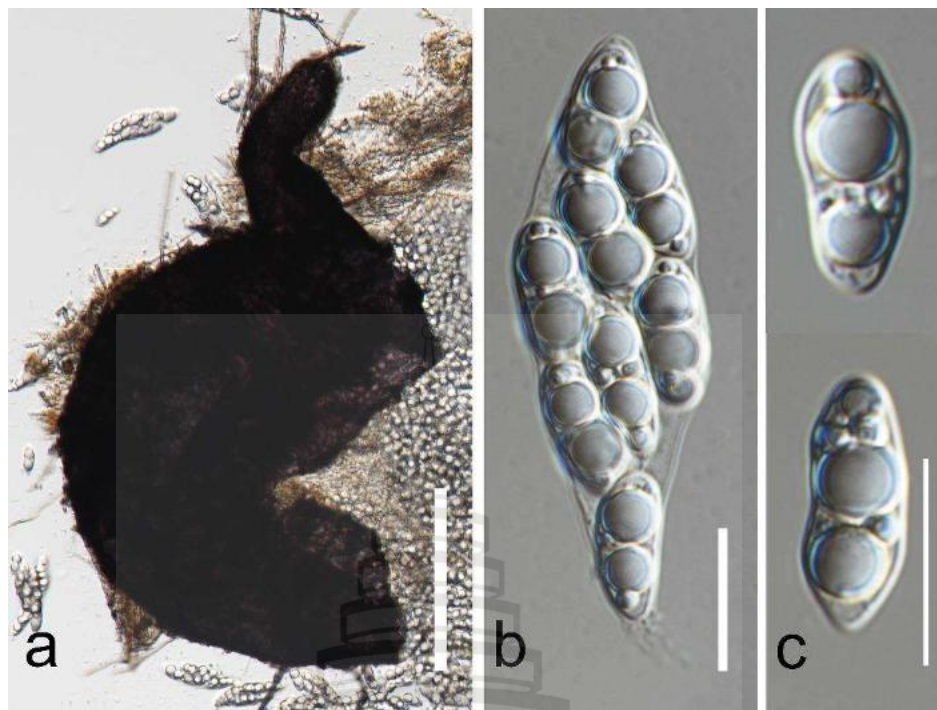
Type species: *Lignincola laevis* Höhnk 1955

Other accepted species:

Lignincola conchicola Jian K. Liu, E.B.G. Jones & K.D. Hyde 2011

Lignincola nypae K.D. Hyde & Alias 1999

Lignincola tropica Kohlm. 1984



Note a Ascoma. b a Acus. c A scospore. Scale bar: a = 100 μ m, b = 15 μ m, c = 10 μ m

Figure 4.135 *Lignicola laevis*

Magnisphaera J. Campb., J.L. Anderson & Shearer 2003

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Ascomycota*, *Fungi*.

Magnisphaera in the family *Halosphaeriaceae* (*Microascales*, *Sordariomycetes*) has been recorded from both marine and freshwater habitats (Campbell et al. 2003). *Magnisphaera spartinae*, the type species of the genus was initially described as *Haligena spartinae* by Jones (1962). However, it has been transferred to different genera, driven by either morphological observations or sequencing data. These reclassifications included *Halosarpheia spartinae* (Shearer and Crane 1980) and *Magnisphaera spartinae* (Campbell et al. 2003). Campbell et al. (2003) also introduced *Magnisphaera stevemossago* as a novel species based on differences in morphology of the septa and size of the ascospores. The type species was collected from marine habitats while *M. stevemossago* was collected from freshwater habitats. *Magnisphaera spartinae* was reported from various salt marsh hosts: *Elymus farctus*, *E. pungens*, *Phragmites australis*, *Spartina alterniflora*, *S. patens*, *S. townsendii* and *Typha* sp. from the Netherland, United Kingdom and USA (Ryckegem

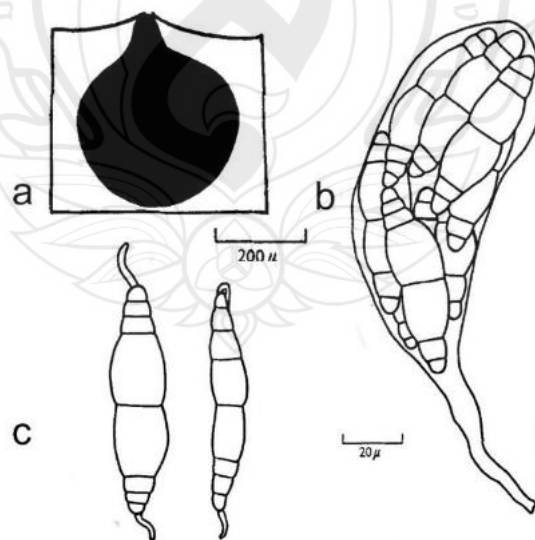
and Verbeken 2005a; Gessner and Goos 1973a; Gessner and Kohlmeyer 1976; Kohlmeyer and Kohlmeyer 1979; Jones 1962a).

The genus *Magnisphaera* is distinguished by its large, black, globose to flattened globose ascomata. These ascomata feature a central neck that is relatively short in relation to the overall length of the ascoma. The peridium consists of two layers made up of approximately 8 to 10 large cells. The cell walls become darkened and filled with brown amorphous material toward the outer region. The asci are ellipsoidal and early deliquescent. Ascospores are broadly acerose in shape, phragmoseptate with warted wall and each of the central cells contains a large guttule. There is a pattern of lipid droplets present around the mid-septum and at the apices of the ascospores. Initially, the ascospores are hyaline to pale reddish-gold in color, later transitioning to subhyaline to gray-brown. The ascospores have bipolar appendages that are coiled into short, flat, hamate structures, which unfurl to form long, threadlike structures in water (Campbell et al. 2003).

Type species: *Magnisphaera spartinae* (E.B.G. Jones) J. Campb., J.L. Anderson & Shearer 2003

Other accepted species:

Magnisphaera stevemossago J. Campb., J.L. Anderson & Shearer 2003



Note a Ascoma. b Ascus. c Ascospores. Scale bars: a = 200 µm, b, c = 20 µm

Source Jones (1962a)

Figure 4.136 *Magnisphaera spartinae*

Natantispora J. Campbell, J.L. Anderson & Shearer 2003

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

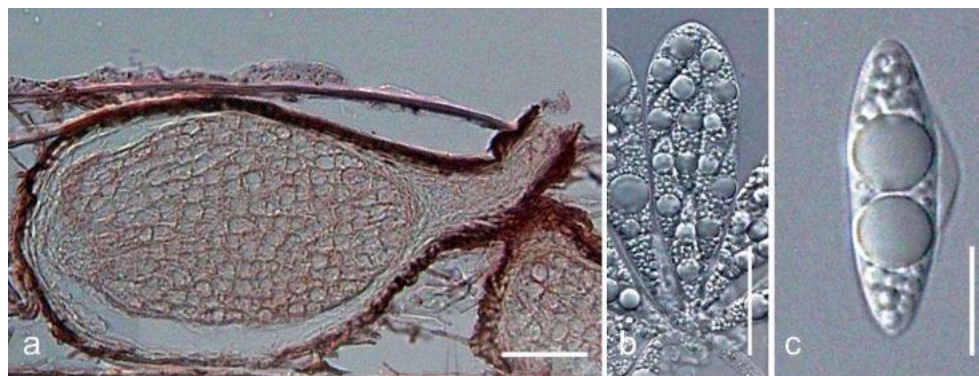
Natantispora is an ascomycetous genus belonging to the family *Halosphaeriaceae* (*Microascales*) in *Sordariomycetes*. Based on the phenotypic and phylogenetic data, Campbell et al. (2003) introduced *Natantispora* to accommodate *Halosarpheia lotica* and *H. retorquens* which were described as saprobes on submerged wood in freshwater from USA (Shearer and Crane 1980; Shearer 1984). *Natantispora* formed a distinct clade with *Halosarpheia* species with high bootstrap support based on ITS, SSU and LSU sequence data (Liu et al. 2015). *Natantispora* species have different shapes of ascomata and peridium, deliquescing asci and different ascospores when compared to *Halosarpheia* (Campbell et al. 2003). *Natantispora* is characterized by ostiolate, membranous, black ascomata with dark cylindrical, periphysate necks that become lighter toward the apex. Asci are thin-walled and early deliquescing with hyaline, septate ascospores. There is a single coiled, threadlike appendage, into a hamate structure at both apexes of ascospores which uncoil in water to form a long sticky filamentous structure (Campbell et al. 2003). The asexual morph has not been determined. The third species, *Natantispora unipolaris* was reported from Taiwan on a dead stem of *Phragmites australis* (Liu et al. 2015). *Natantispora retorquens* has also been reported from the salt marsh host *Spartina maritima* from Portugal (Calado et al. 2019, Barata 2002).

Type species: *Natantispora lotica* (Shearer) J. Campb., J.L. Anderson & Shearer 2003

Other accepted species:

Natantispora retorquens (Shearer & J.L. Crane) J. Campb., J.L. Anderson & Shearer 2003

Natantispora unipolaris K.L. Pang, S.Y. Guo & E.B.G. Jones 2015



Note a Ascoma. b Asci. c Ascospore. Scale bars: a = 30 μm , b = 20 μm , c = 10 μm

Source Liu et al. (2015)

Figure 4.137 *Natantispora unipolaris*

Nais Kohlm. 1962

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Nais was introduced by Kohlmeyer (1962b) to accommodate the saprobic marine species *Nais inornata*, which was designated as the type species. *Nais* develops immersed to superficial, coriaceous, ostiolate, papillate ascomata with a long neck and thick peridium. The asci are clavate, thin-walled, early deliquescing, and lack an apical apparatus. Ascospores are broadly ellipsoidal, hyaline, bicellular, and guttulate, with one large oil globule in each cell and many small oil globules near the septum, without sheath or appendages (Kohlmeyer 1962b; Jones et al. 2009). *Nais inornata* was originally collected from rotten wood submerged in salt water along the Mediterranean coast in France (Kohlmeyer 1962b). It has been considered a late-appearing species on decorticated wood in fresh, brackish, and seawater environments (Zare-Maivan 1987). The species has been widely reported from various substrates, including driftwood, intertidal wood, test blocks, mangrove wood, herbaceous materials, and freshwater woody substrata. It has also been found on salt marsh plants, such as *Spartina alterniflora* and *Spartina* sp. (Calabon et al. 2021b). *Nais* contains two additional species (Species Fungorum, April 2025). *Nais aquatica* was collected from freshwater habitats, on submerged wood in a river in Queensland, Australia (Hyde 1992b). Hyde et al. (1999c) provided a synopsis of *Nais* and freshwater species of *Aniptodera*, *Haloarphaea*, and *Phaeonectriella*. The third species, *N. submersa*, was described from

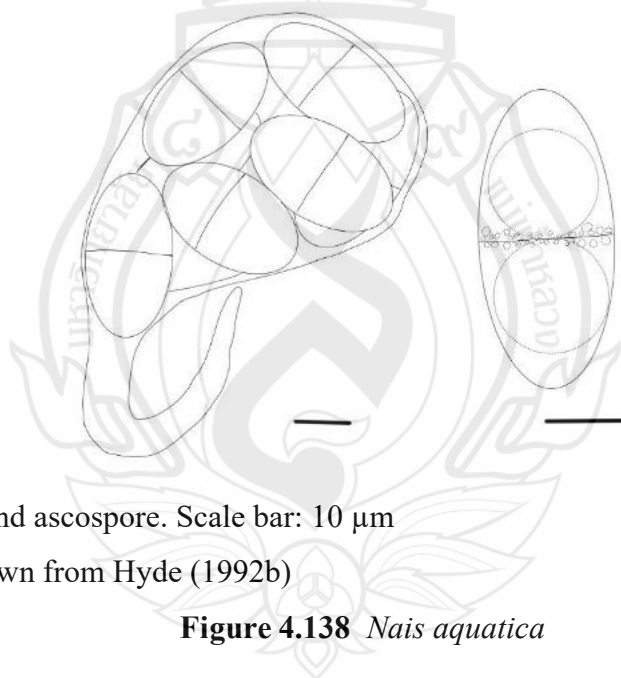
decaying wood submerged in freshwater in Yunnan, China (Yang et al. 2024). Phylogenetic analyses of LSU sequences showed that *Nais* is closely related to *Aniptodera* (Pang et al. 2003a; Jones et al. 2009), a placement further supported by analyses of SSU, LSU rDNA, and *rpb2* sequences (Sakayaroj et al. 2011). In the phylogeny of *Halosphaeriaceae* by Jones et al. (2017), based on SSU and LSU data, *Nais* forms a sister group to *Nantantisporea retorquens* with strong support. Further collections and sequence data are needed to clarify the accurate taxonomic placement of the genus.

Type species: *Nais inornata* Kohlm. 1962

Other accepted species:

Nais aquatica K.D. Hyde 1992

Nais submersa Huang Zhang & Rang Yang 2024



Note Ascus and ascospore. Scale bar: 10 µm

Source Redrawn from Hyde (1992b)

Figure 4.138 *Nais aquatica*

Oceanitis Kohlm. 1977

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Oceanitis was established by Kohlmeyer (1977) and initially placed in the order *Sphaeriales*, though its familial placement remained uncertain, possibly resembling *Halosphaeriaceae* or *Hypocreaceae*. The type species, *O. scuticella*, is a saprobic

fungus collected from submerged wood at a depth of 3,975 meters in the Gulf of Angola, Atlantic Ocean (Kohlmeyer 1977). It produces subglobose to ellipsoidal, brown to dull orange ostiolate ascomata on a thin hypostroma, with a thick peridium and no paraphyses. The asci are clavate, unitunicate, thin-walled, and deliquescent. Ascospores were originally described as filiform, hyaline, and 1-septate, with a single apical appendage (Kohlmeyer 1977). Later collections led to an expanded features of the genus to include drop-shaped ascomata and filiform to elongate fusiform, hyaline ascospores with 0–11 septa and appendages at one or both ends (Jones et al. 2009, Nagano et al. 2024). *Oceanitis* species have been variously assigned from *Haligena* (Jones et al. 1971), *Halosarpheia* (Johnson, et al. 1987), *Ascosalsum* (Campbell et al. 2003) and *Falcatispora* (Pang et al. 2003a). Dupont et al. (2009) listed four species (*O. cincinnatula*, *O. unicaudata*, *O. scuticella* and *O. viscidula*). A fifth species, *O. abyssalis*, was later introduced from deep-sea sunken wood (depth 5,707 m) by Nagano et al. (2024). Their taxonomic revisions also indicated that what was previously identified as *O. scuticella* likely includes several cryptic, undescribed species (Nagano et al. 2024). All *Oceanitis* species are marine fungi (Jones et al. 2019), with *O. scuticella* also reported from salt marsh plants such as *Phragmites australis* and *Spartina maritima* (Calabon et al. 2021b). Notably, *O. cincinnatula* has shown potential as a feed additive for disease prevention in shrimp, demonstrating protective effects against acute hepatopancreatic necrosis disease (AHPND) (Soowannayan et al. 2019).

Type species: *Oceanitis scuticella* Kohlm. 1977

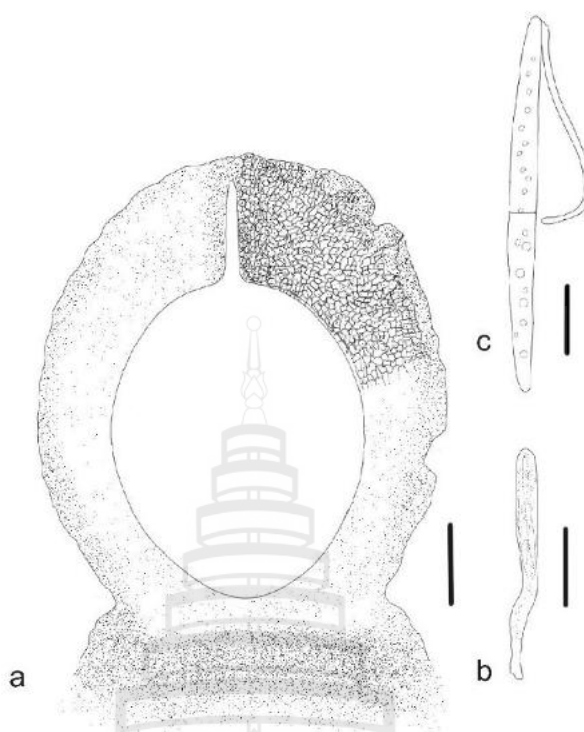
Other accepted species:

Oceanitis abyssalis Y. Nagano & Abdel-Wahab 2024

Oceanitis cincinnatula (Shearer & J.L. Crane) J. Dupont & E.B.G. Jones 2009

Oceanitis unicaudata (E.B.G. Jones & Camp.-Als.) J. Dupont & E.B.G. Jones 2009

Oceanitis viscidula (Kohlm. & E. Kohlm.) J. Dupont & E.B.G. Jones 2009



Note a Ascoma. b Immature ascus. c Ascospore. Scale bars: a = 0.3 mm, b = 30 μm , c = 15 μm

Source Redrawn from Kohlmeyer (1977)

Figure 4.139 *Oceanitis scuticella*

Panorbis J. Campb., J.L. Anderson & Shearer 2003

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Ascomycota*, *Fungi*.

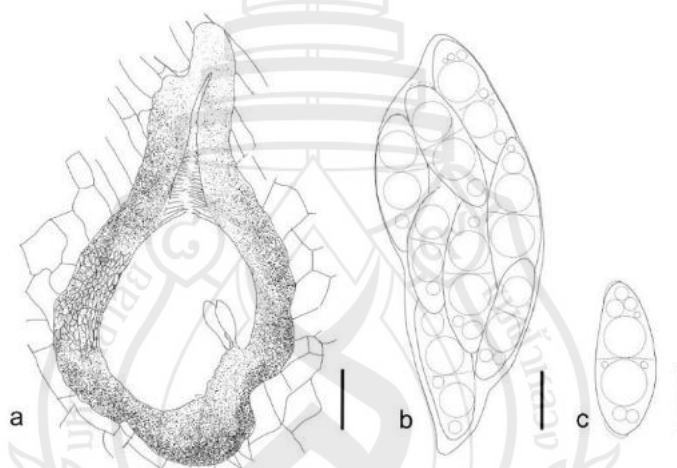
Panorbis is a marine genus belonging to the family *Halosphaeriaceae* (*Microascales*, *Sordariomycetes*) (Campbell et al. 2003). Based on morphology and molecular data of combined LSU and SSU sequences, Campbell et al. (2003) introduced *Panorbis* to accommodate *P. viscosus* (= *Halosphaeria viscosa*) which was formerly under *Halosarpheia*. Sexual morph of the genus is characterized by hyaline, ostiolate ascomata that turn black in maturity with cylindrical periphysate necks with a hyaline apex and a pigmented base. Hamathecia in this genus are either missing or present in the form of catenophyses. Asci are ellipsoid to clavate with or without a persistent wall and contain hyaline, 1-septate ascospores with apical appendages.

Appendages are short and unroll in water to create long, sticky, threadlike filaments (Campbell et al. 2003). The asexual morph has not been found.

Panorbis has been reported from freshwater, brackish and marine habitats on wood and herbaceous substrates. It was first reported on submerged decaying wood in seawater in the Baltic Sea, Germany (Schmidt 1985). *Panorbis viscosus* has been found on leaf sheaths and blades and stem of salt marsh host (*Spartina maritima*) from Portugal (Barata 2006; Calado et al. 2015; Calabon et al. 2021b)

Type species: *Panorbis viscosus* (I. Schmidt) J. Campb., J.L. Anderson & Shearer 2003

Other accepted species: None



Note a Ascoma. b Ascus. c Ascospore. Scale bars = ascoma 50 µm, ascus and ascospore 10 µm

Source Redrawn from Pang et al. (2011)

Figure 4.140 *Panorbis viscosus*

***Remispora* Linder 1944**

Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Remispora was established to accommodate its type species, *Remispora maritima*, which was isolated from driftwood in a marine habitat in USA (Barghoorn and Linder 1944). Paratype specimens were collected from submerged test blocks and the jetty bulkhead of a breakwall in Maine and Massachusetts, USA, respectively. The

genus was originally described as forming light-colored, membranous ascomata with an eccentric ostiole and lacking paraphyses (Barghoorn and Linder 1944). Asci are clavate broadly fusoid, without an apical apparatus, deliquescing and contain hyaline, uniseptate ascospores, which are characterized by polar appendages (Jones et al. 2009). *Remispora* can be distinguished from *Massarinula* by differences in the morphology of ascospore appendages and the membranous ascomatal wall (Barghoorn and Linder 1944). *Remispora* is a lignicolous, saprobic marine genus comprising two species (*R. maritima*, *R. pileata*), most of which have been described based on their sexual morphs (Jones et al. 2019; Gonçalves et al. 2021). Gonçalves et al. (2021) introduced a novel species, *R. submersa*, based on its asexual morph, which is characterized by thick-walled hyphae and conidiophores reduced to hyaline, aseptate conidiogenous cells bearing aseptate, hyaline, cylindrical to narrowly ellipsoidal conidia. The authors also provided a synopsis for selected *Remispora* species and conducted a phylogenetic analysis of *Halosphaeriaceae* based on LSU sequence data. Jones et al. (2009) discussed the polyphyletic nature of *Remispora* and provided a key for species identification. Several reports exist of *R. hamata* occurring on salt marsh plants, including *Juncus roemerianus*, *Phragmites*, *Spartina*, and *Typha* species. *Remispora trullifera* has also been recorded on *Spartina maritima* (Calabon et al. 2021b). Notably, *R. maritima* is capable of producing polyketide metabolites, including remisporine A, which is unstable and dimerizes to form remisporone B (Hill 2004; Sherer et al. 2012). However, this isolate has been shown to be a separate fungus: grouping within the *Sarocladium* clade and the species *S. kiliense*, with high statistical support (Calabon et al. 2023). *Remispora* is polyphyletic with *R. submersa*, *R. stellata*, *R. maritima*, *R. pileata*, *R. hamata* and *R. spitsbergenensis* referred to the new genus *Remisporiopsis*.

Type species: *Remispora maritima* Linder 1944

Other accepted species:

Remispora hamata (Höhnk) Kohlm. 1961

Remispora lobata Höhnk 1955

Remispora minuta E.B.G. Jones, K.L. Pang & Vrijmoed 2004

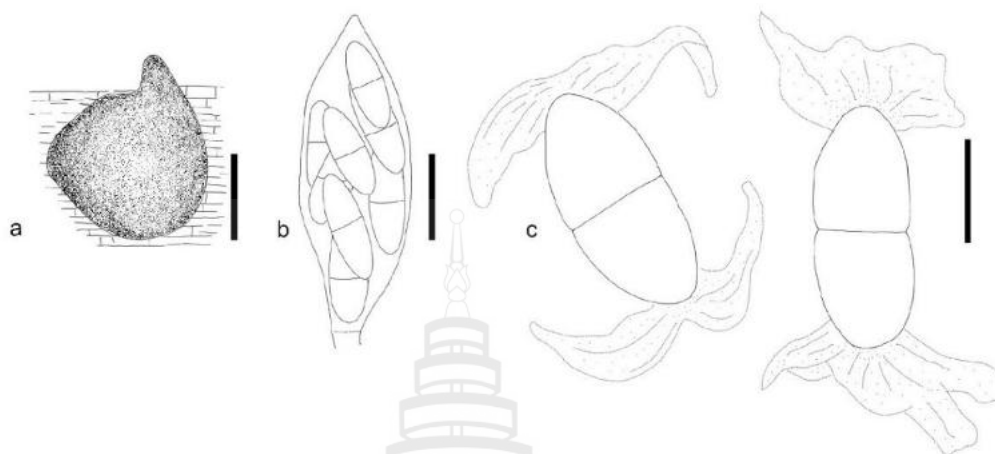
Remispora ornata T.W. Johnson & A.R. Caval. 1963

Remispora spitsbergensis K.L. Pang & Vrijmoed 2009

Remispora stellata Kohlm. 1960

Remispora submersa M. Gonç., A. Abreu & A. Alves 2021

Remispora trullifera Kohlm. 1963



Note a Ascoma (25×). b Ascus (425×). c Ascospores (1000×)

Source Redrawn from Barghoorn and Linder (1944)

Figure 4.141 *Remispora maritima*

Tirispora E.B.G. Jones & Vrijmoed 1994

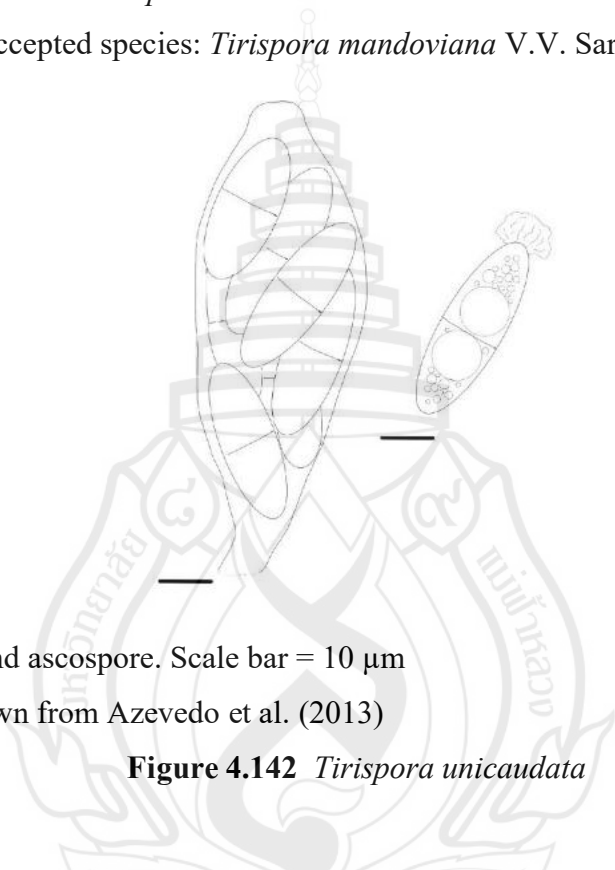
Classification: *Halosphaeriaceae*, *Microascales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Tirispora was introduced to accommodate its type species, *Tirispora unicaudata*, collected from intertidal stems of *Acanthus ilicifolius* in Hong Kong (Jones et al. 1994). This species has a worldwide distribution but is considered to be restricted to mangrove habitats (Pang et al. 2011). With the introduction of *T. mandoviana*, the genus now comprises two species (Sarma and Hyde 2000b, Hyde et al. 2024a). Although *T. mandoviana* was initially collected from freshwater habitats (Sarma and Hyde 2000b), it was later reported from Indian saline mangroves by Maria and Sridhar (2002). Additionally, *T. unicaudata* has been reported from salt marsh plants, including *Spartina maritima* in Portugal (Calabon et al. 2021b) and *Phragmites australis* in Egypt (Voronin et al. 2021). The sexual morph of *Tirispora* develops superficial ascomata on the host surface, typically with an ostiole and papilla. Catenophyses are present in the type species but absent in *T. mandoviana*. The asci are persistent, clavate, and short-pedicellate, with an apical ring or pore, and a thickened apex, sometimes showing retraction of the plasmalemma. Ascospores are ellipsoidal, uniseptate, constricted at the

septum, and possess a unipolar unfurling appendage (Jones et al. 2009). *Tirispora* is morphologically related to *Aniptodera*, and Jones et al. (2009) considered *Aniptodera indica* a synonym of *T. unicaudata*. However, in a phylogenetic analysis of the *Halosphaeriaceae* based on combined SSU and LSU sequences, *T. unicaudata* grouped with *Nimbospora* and was distinct from *Aniptodera* (Sakayaroj et al. 2011).

Type species: *Tirispora unicaudata* E.B.G. Jones & Vrijmoed 1994

Other accepted species: *Tirispora mandoviana* V.V. Sarma & K.D. Hyde 2000



Note Ascus and ascospore. Scale bar = 10 µm

Source Redrawn from Azevedo et al. (2013)

Figure 4.142 *Tirispora unicaudata*

Juncigena Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1997

Classification: *Juncigeaceae*, *Torpedosporales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Kohlmeyer et al. (1997) introduced *Juncigena* as a novel genus, typified by *Juncigena adarca*, and also described *Cirrenalia adarca* as its asexual morph in culture. Based on morphological characteristics, they placed *Juncigena* in the family *Magnaporthaceae*. However, the genus was later transferred to the family *Juncigenaceae* (*Torpedosporales*) (Jones et al. 2014) and this was followed in Wijayawardene et al. (2022). The genus was classified with other marine fungi in the TBM (*Torpedospora/Bertia/Melanospora*) clade based on phylogenetic analysis of LSU and SSU rDNA sequences (Jones et al. 2014). Kohlmeyer et al. (1997) considered

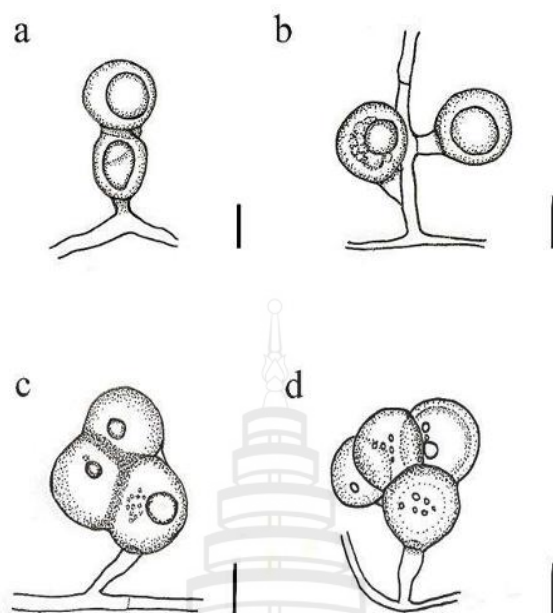
Cirrenalia adarca as the asexual morph of *J. adarca*. Abdel-Wahab et al. (2010) introduced a new genus, *Moheitospora*, and transferred *C. adarca* to *Moheitospora*, based on the phylogenetic and morphological data. Réblová et al. (2016b) reclassified *Moheitospora* under *Juncigena*, in accordance with the one name, one fungus protocol.

Sexual morph is characterized by subglobose to pyriform, papillate ascomata. The asci are fusiform to cylindrical, short pedicellate with a J- apical ring. Ascospores are fusiform to elongate-ellipsoidal. They are hyaline, 3-septate, and constricted at the septa (Jones et al. 2009). In asexual morph conidiophores, if present, form acrogenous or laterally on the hyphae, with monoblastic, integrated, terminal conidiogenous cells. Conidia are irregularly helicoid, with densely attached yellow-brown to brown, muriform cells (Kohlmeyer et al. 1997; Abdel-Wahab et al. 2010). *Juncigena fruticosa* differs from asexual morph of *J. adarca* in that it has small conidial cells that are comparable in size and colour. *Juncigena* comprises two species and is typified by *J. adarca* which was first reported on *Juncus roemerianus* from USA (Kohlmeyer et al. 1997). *Juncigena fruticosa* was also reported on *Suaeda fruticosa*, from Egypt (Abdel-Wahab et al. 2010).

Type species: *Juncigena adarca* Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1997

Other accepted species:

Juncigena fruticosa (Abdel-Wahab, Abdel-Aziz & Nagah.) A.N. Mill. & Shearer 2016



Note a–d Various shapes of mature conidia, with a sheath surrounding the conidia and conidial cells attached to each other by connective bands. Scale bars: 5 μ m

Source Redrawn from Abdel-Wahab et al. (2010)

Figure 4.143 *Juncigena fruticosae*

Torpedospora Meyers 1957

Classification: *Torpedosporaceae*, *Torpedosporales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Torpedospora was introduced by Meyers (1957) and typified by *T. radiata*. It was isolated from yellow pine panels in seawater from Florida. *Torpedospora* is a marine genus that is characterized by perithicoid, ostiolate ascomata containing thin-walled, clavate to ellipsoidal, short pedicellate asci (Jones et al. 2015). Ascospores are cylindrical to ellipsoidal, guttulate, 3-septate with radiating appendages at one or both ends. The asexual morph is hyphomycetous and characterized by irregularly helicoid, muriform conidia (Jones et al. 2015). *Torpedospora radiata* was also found on a salt marsh host from Mississippi (Walker 2012). *Torpedospora ambispinosa* the second species in the genus was isolated by Kohlmeyer (1960) from marine driftwood in California. *Torpedospora mangrovei* was previously described as *Glomerulispora*

mangrovis from marine drift wood from Nansei-shoto and is the only species with an asexual morph (Abdel-Wahab et al. 2010). Multigene analyses of LSU and SSU showed that *Torpedospora mangrovei* formed a close clade with two other species, so *Glomerulispora* and *Torpedospora* were considered synonyms (Sakayaroj et al. 2005a; Abdel-Wahab et al. 2010; Jones et al. 2015). Réblová et al. (2016) suggested *Torpedospora* instead of *Glomerulispora*. Different higher taxa have been used for the classification of *Torpedospora* but subsequently the genus was classified under *Torpedosporaceae* (Jones et al. 2014), order *Torpedosporales* (Jones et al. 2015) within *Hypocreomycetidae* based on molecular analyses.

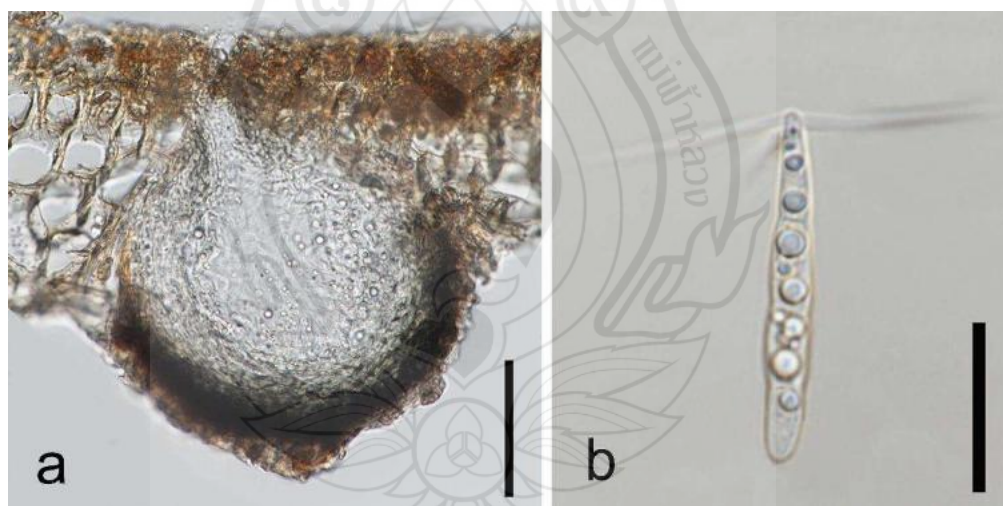
Type species: *Torpedospora radiata* Meyers 1957

Other accepted species:

Torpedospora ambispinosa Kohlm. 1960

Torpedospora mangrovei (Abdel-Wahab & Nagah.) E.B.G. Jones & Abdel-Wahab 2016

Torpedospora yanbuensis Abdel-Wahab & E.B.G. Jones 2022



Note a Ascoma. b Ascospore. Scale bar: a = 50 μ m, b = 20 μ m

Figure 4.144 *Torpedospora radiata*

Cumulospora I. Schmidt 1985

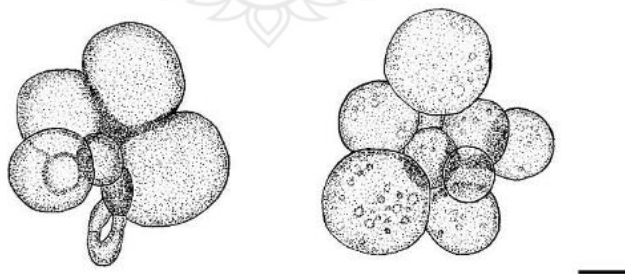
Classification: *Lulworthiaceae*, *Lulworthiales*, *Lulworthiomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Schmidt (1974) introduced the genus *Vesicularia*, a name already occupied and therefore proposed *Cumulospora* (Schmidt 1985). *Cumulospora* is a saprobic hyphomycetous marine genus and was first isolated from decaying submerged wood in seawater from the Baltic Sea, Germany (Schmidt 1985) and has been frequently found on mangrove substrates. Abdullah et al. (1989) reported the *C. marina* as *Basramyces marinus* from *Phragmites australis* in the marshes of Iraq. *Cumulospora marina* has also been reported on this host from Egypt, Germany, and Thailand (Calabon et al. 2021b). Kohlmeyer and Volkmann-Kohlmeyer (2002) listed *Cumulospora marina* as a reported fungus on *Spartina* spp. The genus was shown to belong to *Lulworthiaceae* (*Lulworthiales*) by Jones et al. (2008). Subsequently, Abdel-Wahab et al. (2010) demonstrated that it is a polyphyletic genus based on phylogenetic analysis of SSU and LSU sequence data. They proposed that it can be classified within the *Lulworthiales*, and indicated the need for further studies to link it with its sexual morph. Two additional species have been associated with this genus: *Cumulospora mangrovei*, which was isolated from dead sedge (*Cyperus malaccensis*) (Karamchand and Sridhar 2009), and *C. varia*, which was later transferred to *Moromyces varius* by Abdel-Wahab et al. (2010). *Cumulospora* is a helicosporous hyphomycete, with helicoid conidia in their early stages and a mass of cells at maturity. The conidiogenous cells are poorly developed or absent (Abdel-Wahab et al. 2010).

Type species: *Cumulospora marina* Schmidt 1985

Basionym: *Vesicularia marina* I. Schmidt 1974.

Other accepted species: *Cumulospora mangrovei* Karamchand & K.R. Sridhar 2009



Note Mature conidia. Scale bar: 10 µm

Source Redrawn from Abdel-Wahab et al. (2010)

Figure 4.145 *Cumulospora marina*

Halazon Abdel-Aziz, Abdel-Wahab & Nagah.

Classification: *Lulworthiaceae*, *Lulworthiales*, *Lulworthiomycetidae*, *Sordariomycetes*, *Ascomycota*, *Fungi*.

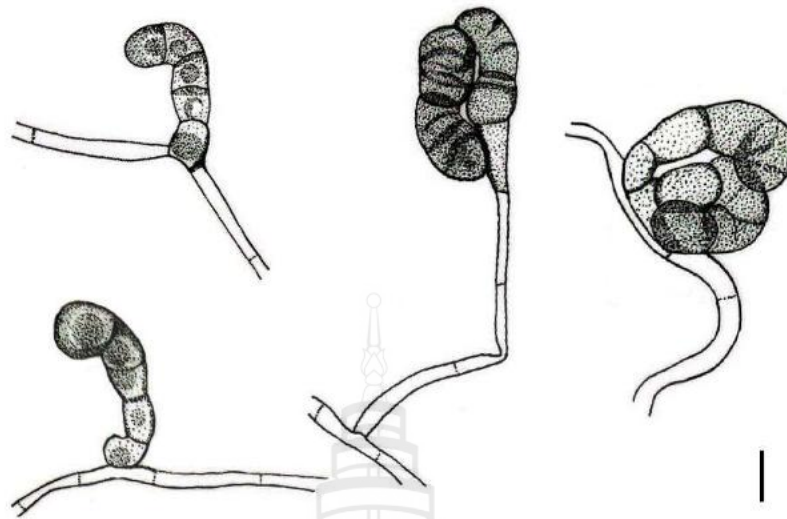
Halazon is an asexual marine genus belonging to the family *Lulworthiaceae* (*Lulworthiales*, *Sordariomycetes*) (Jones et al. 2015; Maharachchikumbura et al. 2015). Abdel-Wahab et al. (2010) introduced *Halazon*, grouped in *Lulworthiales*, based on the morphological and molecular analyses of LSU and SSU loci. The genus is typified with *Halazon melhae*, isolated from decaying stem of *Phragmites australis* in coastal area in Egypt. Abdel-Wahab et al. (2010) transferred *Cirrenalia fusca* to *Halazon* based on phylogenetical data and morphology of coiled conidia. *Halazon fusca* was first isolated from dead rhizome of *Phragmites communis* from Baltic Sea in Germany (Schmidt 1985). Asexual morph is hyphomycetous with conidiophores. when present, micronematous, septate and cylindrical and hyaline to yellow-brown. Conidiogenous cells are holoblastic terminal or lateral conidia. Conidia form single or branched coils in two or three dimensions. From the base toward the apex, conidial cells grow in size and pigments.

Recent studies have shown that *Halazon* has a sexual morph with typical *lulworthia*-like filiform ascospores with an apical chamber (Dayarathne et al. 2025) when *Lulworthia purpurea* was found to group in the *Halazon* clade. *Halazon melhae* is similar to *Zalerion maritima*, but it differs in having reddish brown larger conidia forming more coils. *Halazon fuscus* is also similar to *Cirrenalia pygmea* in apical cell morphology but its conidia are dark colored (Abdel-Wahab et al. 2010).

Type species: *Halazon melhae* Abdel-Aziz, Abdel-Wahab & Nagah. 2010

Other accepted species:

Halazon fuscus (I. Schmidt) Abdel-Wahab, K.L. Pang, Nagah., Abdel-Aziz & E.B.G. Jones 2010



Note Conidiophores and coiled conidia in a variety of shapes. Scale bar: 10 µm

Source Redrawn from Abdel-Wahab et al. (2010)

Figure 4.146 *Halazon melhae*

Lulworthia G.K. Sutherl. 1916

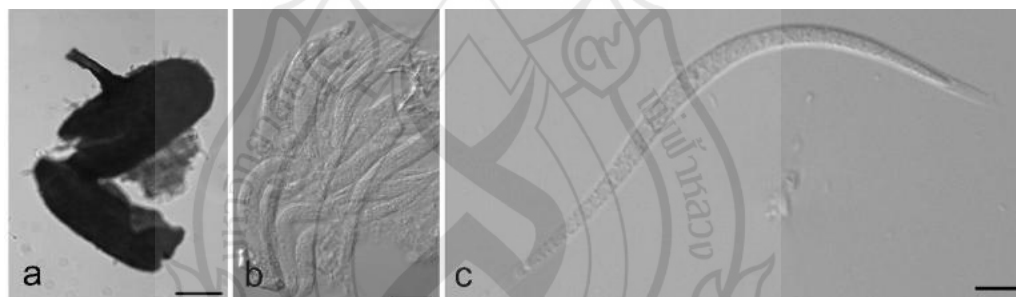
Classification: *Lulworthiaceae*, *Lulworthiales*, *Lulworthiomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Lulworthia is a marine saprobe that thrives on a range of substrates in marine habitats (Azevedo et al. 2017). The genus was introduced to accommodate *L. fucicola*, isolated from the seaweed *Fucus vesiculosus* in United Kingdom, although no type material was designated (Sutherland 1916a). *Lulworthia* species have been frequently reported on halophytes, mostly on *Spartina* species, including *S. alterniflora*, *S. cynosuroides*, *S. townsendii*, and *S. maritima*, which are distributed in USA, United Kingdom, Argentina, and Portugal (Azevedo et al. 2017, Calabon et al. 2021b). There are also a few records on *Juncus roemerianus* and *Elymus pungens* (Calabon et al. 2021b). Kohlmeyer et al. (2000) classified the genus in a novel family and order, *Lulworthiaceae* and *Lulworthiales*. Based on morphology and phylogenetic analyses of SSU and LSU sequence data, Campbell (2005) transferred species that did not group with *Lulworthia sensu stricto* to the new genera *Lulwoidea* and *Lulwoana*. Campbell (2005) designated a neotype for *Lulworthia fucicola* from a collection of wood made in Chile by C.A. Shearer in 1984 (Shearer and Burgos 1987). Currently six species with

sequence data are accepted in *Lulworthia*: *L. atlantica*, *L. fucicola*, *L. floridana*, *L. fundyensis*, *L. opaca* and *L. norwegica*, while *L. bulgariae*, *L. calcicola*, *L. curalii*, *L. halima*, *L. kniepii*, *L. lindroidea* and *L. longirostris* lack sequence data (Dayarathne et al. 2025). *Lulworthia* species are characterized by superficial, immersed, or deeply immersed ascomata with elongated hyaline ascospores that have conical end chambers (Sutherland 1916a; Azevedo et al. 2017). Worldwide in distribution and found on a wide range substrata, including polyurethane panels in sea (Dayarathne et al. 2025). A dichotomous key to the genus was provided by Jones et al. (2009) and Azevedo et al. (2017). An unidentified *lulworthia*-like species produced lulworthinone (a dimeric biaryllic naphtho α -pyrone substituted with a sulfate group) and showed antibacterial activity against reference strains of *Staphylococcus aureus* and *Streptococcus agalactiae*, as well as several clinical MRSA isolates (Jenssen et al. 2021).

Type species: *Lulworthia fucicola* G.K. Sutherl. 1916

Other accepted species: Species Fungorum (search *Lulworthia*)



Note a Ascoma. b Asci. c Ascospore. Scale bar: a = 30 μ m, b, c = 10 μ m

Source Dayarathne et al. (2025)

Figure 4.147 *Lulworthia fucicola*

Moleospora Abdel-Wahab, Abdel-Aziz & Nagah. 2010

Classification: *Lulworthiaceae*, *Lulworthiales*, *Lulworthiomycetidae*, *Sordariomycetes*, *Ascomycota*, *Fungi*.

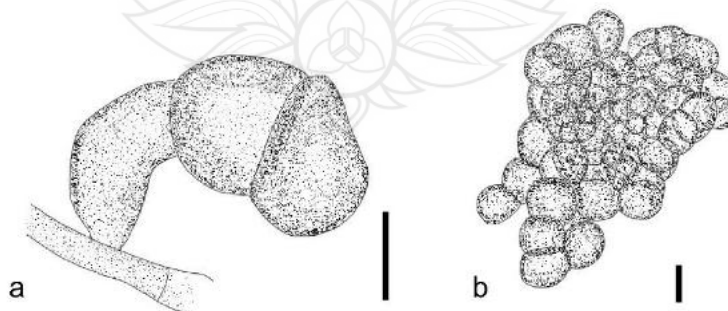
Moleospora was introduced by Abdel-Wahab et al. (2010) based on morphology and molecular data of LSU and SSU sequences. The genus is typified by *Moleospora maritima* collected from decaying stems of *Phragmites australis*, in coastal Egypt.

Moleospora is characterized by branched, immersed to superficial hyphae. Conidiophores may be present or obsolete. When present, they are macronematous, septate, and typically range in color from hyaline to light brown. They have a cylindrical to clavate shape with holoblastic conidiogenous cells. Conidia initially adopt a helicoid structure but rapidly transition into a cluster of cells. They are dark brown to black, lateral in placement, single, and have a determinate arrangement. Cells of conidia typically are globose to subglobose, round or with a truncate base, brown to dark brown (Abdel-Wahab et al. 2010).

Several hyphomycetous marine fungi like *Halenospora varia* and *Cumulospora marina* have been identified with characteristic conidia forming a mass of cells at maturity, but with a helical structure in their juvenile stage. *Moleospora maritima* distinguishes itself by producing notably larger, solid black conidia consisting of a substantial number of smaller-sized conidial cells. *Moleospora maritima* shares a resemblance with *Halenospora varia* in having intricate conidia that consist of numerous small cells. However, *M. maritima* produces larger conidia. Phylogenetically, they are placed in different families; *M. maritima* is categorized as a member of the *Lulworthiaceae* (*Lulworthiales*, *Sordariomycetes*) while *H. varia* belongs to family *Leotiaceae* (Bills et al. 1999; Abdel-Wahab et al. 2010; Jones et al. 2015).

Type species: *Moleospora maritima* Abdel-Wahab, Abdel-Aziz & Nagah. 2010

Other accepted species: None



Note a Young helicoid conidia, b Contorted conidia. Scale bar: 10 μm

Source Abdel-Wahab et al. (2010)

Figure 4.148 *Moleospora maritima*

***Bactrodesmium* Cooke 1883**

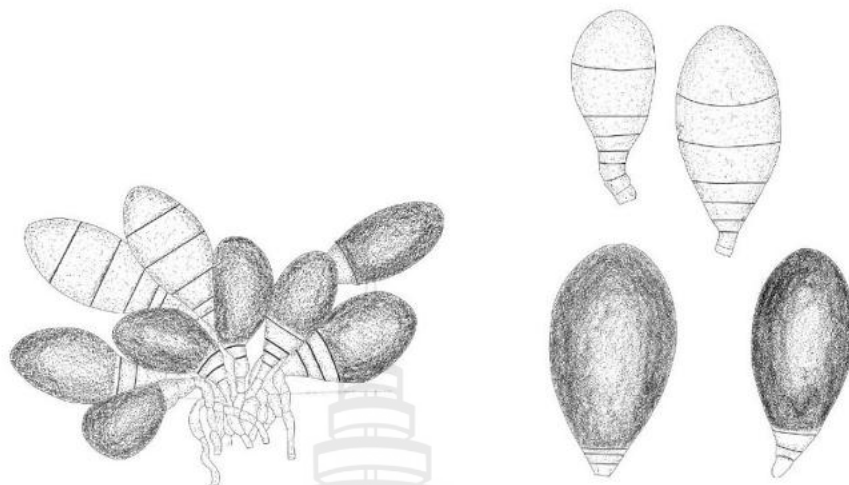
Classification: *Savoryellaceae*, *Savoryellales*, *Savoryellomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Bactrodesmium was established by Cooke (1883) to accommodate species with clavate, multiseptate spores, including novel species such as *B. abruptum* and *B. spilomeum*, which were previously classified under *Sporidesmium*. Later, *B. abruptum* was designated as the type species by Hughes (1958). The asexual morph of *Bactrodesmium* was traditionally described as hyphomycetous, forming punctiform, dark sporodochial, or sometimes synnematal conidiomata that are scattered or clustered on the substrate. Conidiophores are inconspicuous, fasciculate, hyaline to brown, with monoblastic, integrated, terminal conidiogenous cells. Conidia are euseptate and variable in shape (Ellis 1959, 1971; Seifert et al. 2011a). Further studies added species with polyblastic conidiogenous cells and distoseptate conidia, as well as both euseptate and distoseptate conidia, highlighting the need for a taxonomic reassessment of *Bactrodesmium* (Shi et al. 2020). Réblová et al. (2020) re-examined the genus using fresh material, axenic cultures and sequence data from ITS, SSU, LSU, *rpb2*, and *tef1*. Their phylogenetic analysis strongly placed the genus within *Savoryellales*. They amended the generic description, defining *Bactrodesmium* as having sporodochial conidiomata; mononematous, macronematous to semi-macronematous, simple or branched, often fasciculate, hyaline to brown conidiophores; terminal, integrated, mono- or polyblastic conidiogenous cells; and rhexolytic conidial secession. The conidia are brown, variable in shape, euseptate, sometimes with longitudinal or oblique septa, and occasionally having banded transverse septa, with thickening at the septa (Réblová et al. 2020). *Bactrodesmium* comprises 47 accepted species, mostly recorded as saprobic on dead plants in terrestrial and freshwater habitats (Réblová et al. 2020; Hyde et al. 2024a). *Bactrodesmium amazonicum* was recently introduced from decaying twigs in the intertidal zone of fluvial beaches in Brazil. There are three records of *Bactrodesmium atrum* occurring on salt marsh hosts; *Phragmites australis*, *Elymus pungens*, and *Puccinellia maritima* (Calabon et al. 2021b).

Type species: *Bactrodesmium abruptum* (Berk. & Broome) E.W. Mason & S. Hughes 1958

Basionym: *Sporidesmium abruptum* Berk. & Broome 1865

Other accepted species: Species Fungorum (search *Bactrodesmium*)



Note Conidiogenous cells and conidia. $\times 500$

Source Redrawn from Ellis (1959)

Figure 4.149 *Bactrodesmium atrum*

Savoryella E.B.G. Jones & R.A. Eaton 1969

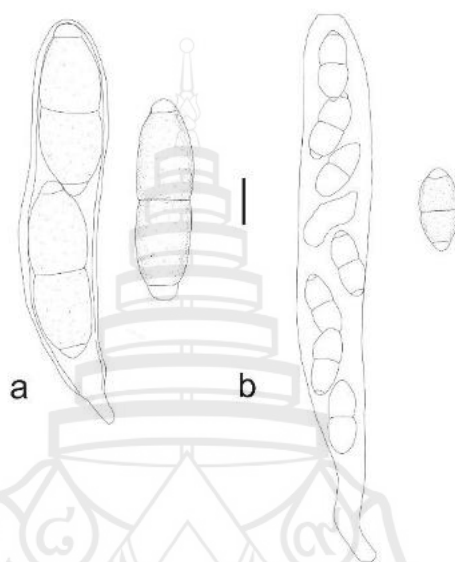
Classification: *Savoryellaceae*, *Savoryellales*, *Savoryellomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Jones and Eaton (1969) introduced *Savoryella*, typified by *Savoryella lignicola*, which was isolated from pine test blocks in a water-cooling tower run with brackish water in the United Kingdom. The taxonomic placement of *Savoryella* has changed across different orders and families (Jones et al. 2016). The genus *Savoryella* formed a monophyletic clade together with *Ascotaiwania*, *Ascothailandia*, and *Canalisporium* (the asexual morph of *Ascothailandia*) based on SSU, LSU, *rpb2* and *tef1* phylogenetic data (Boonyuen et al. 2011). Based on that data, Boonyuen et al. (2011) established *Savoryellales* to accommodate these genera, and later, *Savoryellaceae* was introduced by Jaklitsch (2015) as the sole family in this order. *Savoryella* has been reported from terrestrial, freshwater, and marine environments, with *S. paucispora* being found on various salt marsh hosts such as *Elymus pungens*, *Juncus roemerianus*, and *Spartina* species (Kohlmeyer and Kohlmeyer 1979; www.marinefungi.org; Calabon et al. 2021b). Sexual morph of *Savoryella* has papillate ascomata, clavate to cylindrical asci, and 3-septate brown ascospores with hyaline polar cells. Asexual morph is

hyphomycetous, with hyaline to pale brown conidiophores and holoblastic conidiogenous cells producing septate conidia. Conidia are brown in the central cells and paler in the basal cell (Boonyuen et al. 2011; Tian et al. 2024).

Type species: *Savoryella lignicola* E.B.G. Jones & R.A. Eaton 1969

Other accepted species: Species Fungorum (search *Savoryella*)



Note Asci and ascospores. Scale bars = 10 μ m

Source Redrawn from Koch (1982)

Figure 4.150 *Savoryella paucispora* and *S. lignicola*

Minimidochium B. Sutton 1970

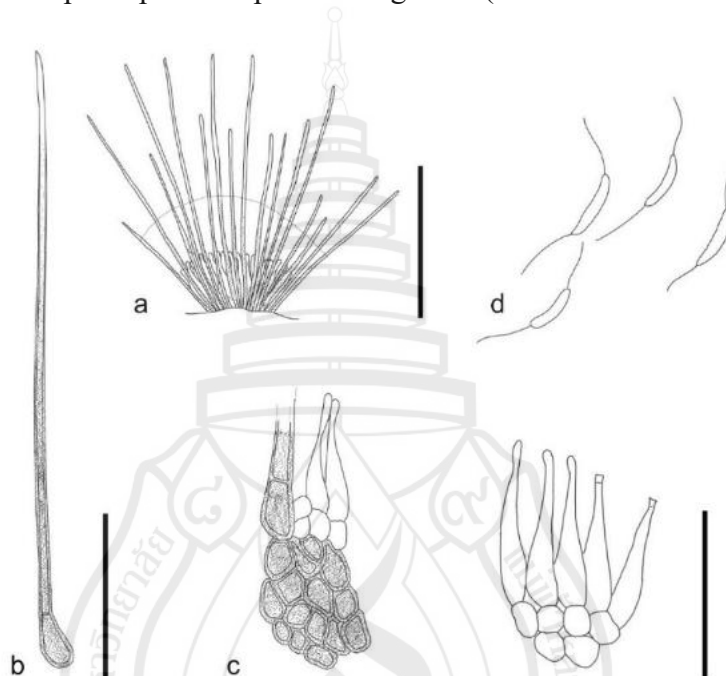
Classification: *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Minimidochium is a saprobic fungus on plant material, introduced by Sutton (1969), with the genus typified by *M. setosum*, though molecular data for this species is not available. Wu and Diao (2022) introduced two novel species, including *M. dictyochaetum*, providing ITS and LSU sequences, and classified *Minimidochium* within *Chaetosphaeriaceae*. They also developed a key for species identification and suggested that further studies with molecular data are needed for the accurate placement of the genus, particularly for the type species. Asexual morph is a sporodochial hyphomycete, characterized by sterile setae emerging from the lower cells of the stroma. Conidiophores, either straight or flexuous, form a palisade over the stroma.

Conidiogenous cells are monophialidic, with a small apical collarette, producing falcate, hyaline conidia with polar appendages (Sutton 1970; Wu and Diao 2022). *Minimidochium parvum* has been recorded as a foliar saprobe on salt grass (*Distichlis spicata*) in Argentina (Eliades et al. 2007; Calabon et al. 2021b).

Type species: *Minimidochium setosum* B. Sutton 1970

Other accepted species: Species Fungorum (search *Minimidochium*)



Note a Sporodochium. b Setae. c Conidiogenous cells. d Conidia. Scale bars: a = 100 μm, b = 160 μm, c, d = 25 μm

Source Cabello et al. (1998)

Figure 4.151 *Minimidochium parvum*

Phyllachora Nitschke ex Fuckel 1870

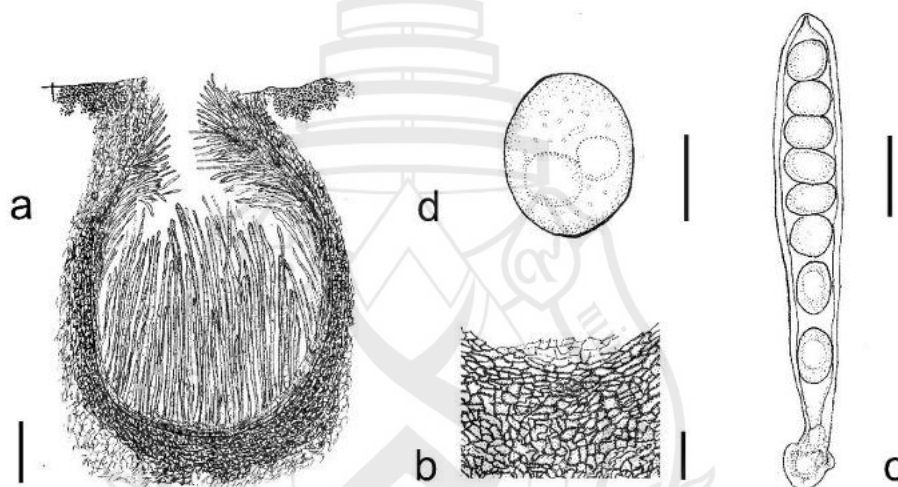
Classification: *Phyllachoraceae*, *Phyllachorales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Phyllachora, the type genus of *Phyllachoraceae*, is an obligate plant parasitic fungal genus with 1518 records in Index Fungorum (Accessed May 2024). *Phyllachora* species are mostly found in clypeate pseudostromata on host leaves of various hosts with a global distribution (Li et al. 2022). Li et al. (2022) introduced four novel species based on morphology, host relationships, and combined molecular data of LSU, SSU,

and ITS. They showed the occurrence of the ancestral *Phyllachora* to be about 194 million years ago. Kohlmeyer and Volkmann-Kohlmeyer (2003) introduced a new species, *P. paludicola*, isolated from decomposing leaves of salt marsh plant, *Spartina alterniflora* in USA (Kohlmeyer and Volkmann-Kohlmeyer 2003; Calabon et al. 2021b). *Phyllachora paludicola* is characterized by ostiolate ascomata enclosed in distinct stromata with a dark brown peridium. Asci are cylindrical with a conical tip and thick-walled. Ascospores are subglobose to ellipsoidal, aseptate, hyaline, with 1-2 large and many small guttules (Kohlmeyer and Volkmann-Kohlmeyer 2003).

Type species: *Phyllachora graminis* (Pers.) Fuckel 1870

Other accepted species: Species Fungorum (search *Phyllachora*)



Note a Section through ascoma. b Peridium. c Ascus. d Ascospore. Scale bars: a = 50 μm , b = 4 μm , c = 20 μm , d = 10 μm

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (2003)

Figure 4.152 *Phyllachora paludicola*

Achaetomium J.N. Rai, J.P. Tewari & Mukerji 1964

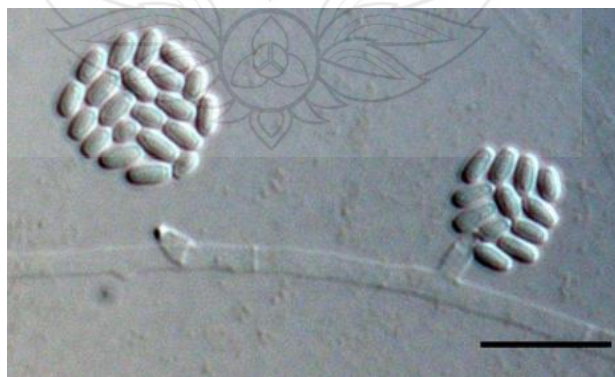
Classification: *Chaetomiaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Rai et al. (1964) established *Achaetomium* based on three new species: *A. luteum*, *A. strumarium*, and the type species *A. globosum*. The genus was originally classified in the invalidly published family *Achaetomiaceae*, which was later validated by Mukerji (1978). Rodríguez et al. (2004) suggested that *Achaetomium* and

Chaetomium share a common ancestor within *Chaetomiaceae*, based on LSU sequence analyses. Subsequent studies confirmed these two as distinct genera in *Chaetomiaceae* (Maharachchikumbura et al. 2015, 2016; Wang et al. 2016a, 2019; Wijayawardene et al. 2018a). *Achaetomium* species have been found as saprobes or endophytes and are primarily known for their sexual morph (Rai et al. 1964; Mehrabi et al. 2020; Qian et al. 2024). They form ostiolate, globose to pyriform perithecia, covered with yellowish hypha-like hairs, with a peridium composed of *textura intricata* cells. The asci are cylindrical, and ascospores are dark brown, with an apical germ pore. Colonies typically produce a reddish-brown exudate (Rodríguez et al. 2004). Recently, Qian et al. (2024) introduced a new species, *Achaetomium astragali*, which solely forms a hyphomycetous asexual morph. This species is characterized by phialidic conidiogenous cells and hyaline, unicellular, ovate to elliptic conidia arranged in false heads. Phylogenetic analyses based on *rpb2*, *tub2*, ITS, and LSU confirmed its placement within *Achaetomium*. The authors recommended further studies to explore the sexual-asexual link in *Achaetomium*. Currently, about 15 accepted species are recognized in *Achaetomium*, with one unidentified species recorded from the halophyte *Juncus roemerianus* and *A. marinum* reported from mangrove swamp soil (Chowdhery and Rai 1980; Calabon et al. 2021b; Hyde et al. 2024a). *Achaetomium* species have demonstrated bioactive potential, showing hepatoprotective, antimicrobial, and antioxidant activities (Anitha and Mythili 2017).

Type species: *Achaetomium globosum* J.N. Rai & J.P. Tewari 1964

Other accepted species: Species Fungorum (search *Achaetomium*)



Note Conidiophore and conidia. Scale bar: 10 µm

Source Qian et al. (2024), under CC BY license

Figure 4.153 *Achaetomium astragali*

***Chaetomium* Kunze 1817**

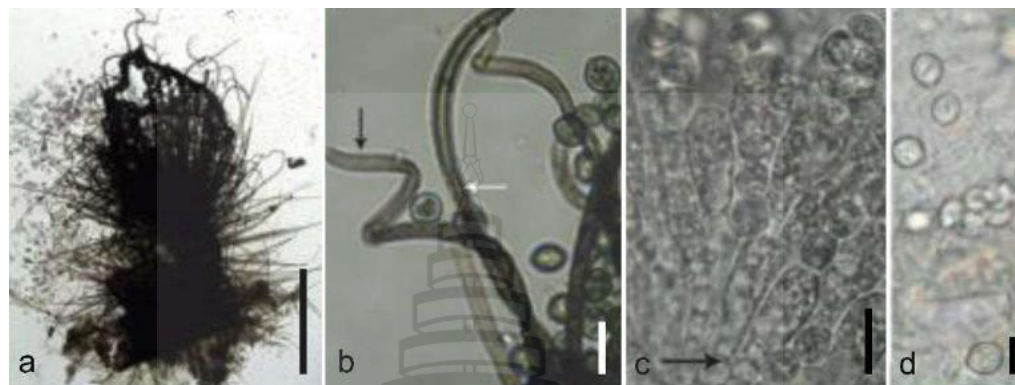
Classification: *Chaetomiaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Chaetomium was introduced by Kunze and Schmidt (1817) to accommodate its type species, *Chaetomium globosum*. It is the type genus and the largest genus within *Chaetomiaceae* (Wang et al. 2022), comprising approximately 200 accepted species found in a variety of substrates and habitats worldwide (Hyde et al. 2020c; Hyde et al. 2024a). Members of this genus function as endophytes, parasites, or saprobes on plant materials, soil, paper, dung, textiles, indoor environments and even humans (Ahmed et al. 2016; Wang et al. 2016a; Zhang et al. 2017; Bundhun et al. 2020; Manawasinghe et al. 2021; Mehrabi-Koushki and Safi 2023). The taxonomy of *Chaetomium* has been extensively reviewed to ensure accurate classification (Maharachchikumbura et al. 2016; Wang et al. (2016a, b). Wang et al. (2022) presented an updated classification and phylogeny of *Chaetomiaceae* based on morphology, molecular dating, multigene phylogenetic analysis (ITS, LSU, *rpb2*, and *tub2*), and temperature-growth characteristics. Wang et al. (2022) accepted 43 species within *Chaetomium* and transferred several species to other genera. For example, the thermophilic fungus *Chaetomium thermophilum*, which thrives at temperatures up to 60 °C, was reclassified into two separate species: *Thermochaetoides dissita* and *Th. thermophila*. Morphologically, *Chaetomium sensu stricto* is characterized by globose, ellipsoid to ovate, or obovate ascomata, typically with an ostiole and a surface composed of *textura intricata* or *textura epidermoidea*. The ascomata bear distinctive hypha-like ascomatal hairs, which may be undulate, coiled, or simply to dichotomously branched. The asci are 8-spored, clavate, or fusiform, and the ascospores are limoniform to globose, arranged in a biserial or irregular pattern. When present, the asexual morph is acremonium-like (Wang et al. 2022). Seven *Chaetomium* species have been reported as marine fungi (Jones et al. 2019). Calabon et al. (2021b) listed *Chaetomium elatum*, *Chaetomium globosum*, *Chaetomium spirale*, *Chaetomium thermophilum*, and an unidentified *Chaetomium* species from salt marsh plants, all recorded from the United Kingdom, with an additional record of *Chaetomium globosum* from China. *Chaetomium* species have been extensively studied for their secondary metabolites, with more than 100 bioactive compounds identified. These compounds have diverse

medicinal and agricultural properties, including antifungal, antitumor, cytotoxic, antimalarial, and enzyme inhibitory activities (Dwibedi et al. 2023).

Type species: *Chaetomium globosum* Kunze 1817

Other accepted species: Species Fungorum (search *Chaetomium*)



Note a Ascoma. b Terminal hairs. c Asci. d Ascospores. Scale bars: a = 200 μ m, b–d = 20 μ m

Source Mungai et al. (2012a)

Figure 4.154 *Chaetomium globosum*

Corynascus Arx 1973

Classification: *Chaetomiaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Corynascus was initially proposed by von Arx in 1973 to include *Thielavia novoguineensis* and *T. sepedonium*. However, later Van den Brink et al. (2012) merged *Corynascus* into the genus *Myceliophthora*. A subsequent re-evaluation of *Myceliophthora* by Marin-Felix et al. (2015), using molecular analyses of combined ITS, *tef1*, and *rpb2* sequence data, resulted in the reinstatement of *Corynascus*. Additionally, a new species, *C. fumimontanus*, was introduced as part of this revision.

Corynascus species are homothallic and mesophilic fungi, characterized by development of cleistothecial ascomata with a textura epidermoidea on the surface and mostly ornamented ascospores. The key characteristic that sets them apart from *Myceliophthora* is having ascospores with two germ pores at each end. If present, the asexual morph of *Corynascus* is myceliophthora-like (Marin Felix et al. 2015; Crous et al. 2016b). *Corynascus* species have mostly been collected from soil (Crous et al.

2016b). *Corynascus sepedonium* has been isolated from salt marsh habitat in the United Kingdom on *Elymus pungens*, *Puccinellia maritima*, and *Spartina townsendii* (Apinis and Chesters 1964; Calabon et al. 2021b).

Type species: *Corynascus sepedonium* (C.W. Emmons) Arx. 1973

Other accepted species:

Corynascus citrinus A. Giraldo & Crous 2016

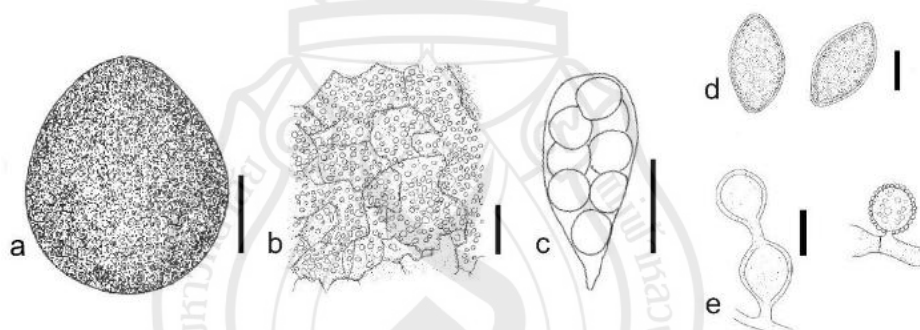
Corynascus fumimontanus Y. Marín, Stchigel, A.N. Mill., J. Guarro & Cano 2015

Corynascus novoguineensis (Udagawa & Y. Horie) Arx 1973

Corynascus sexualis Stchigel, Cano & Guarro 2000

Corynascus similis Stchigel, Cano & Guarro 2000

Corynascus verrucosus Stchigel, Cano & Guarro



Note a ascoma, b peridium. c ascus. d ascospores. e developing conidia. Scale bars: a = 50 μm , b, d, e = 5 μm , c = 15 μm

Source Marin-Felix et al. (2015)

Figure 4.155 *Corynascus fumimontanus*

Dichotomopilus X. Wei Wang, Samson & Crous 2016

Classification: *Chaetomiaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

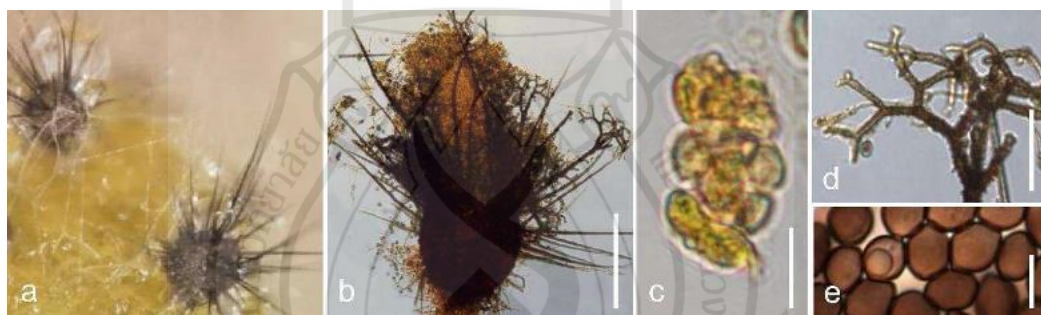
Wang et al. (2016a) established *Dichotomopilus* to accommodate two new species and ten other species that formerly belonged to *Chaetomium*. *Dichotomopilus* species have been found on plants, air, dust, feathers, paper, and textiles, with widespread distribution (Phukhamsakda et al. 2020; Bundhun et al. 2020). *Dichotomopilus funicola* was hosted by salt marsh plants *Elymus pungens*, *Spartina*

alterniflora, and *S. townsendii* (Apinis and Chesters 1964, Gessner and Goos 1973b, Calabon et al. 2021b). *Dichotomopilus indicus*, the type species of the genus, was also reported on *E. pungens* (Apinis and Chesters 1964; Calabon et al. 2021b). With the introduction of *D. finlandicus*, based on morphology and phylogenetic analysis of *tef1*, ITS, *rpb2*, and *tub2*, there are 13 species in the genus. The sexual morph has superficial ostiolate ascomata with dichotomously branched terminal hairs forming a net structure to hold ascospores. Asci are fasciculate, evanescent, pedicellate, clavate to ovate, containing eight biseriate or irregularly arranged ascospores. Ascospores are brown at maturity, narrow to broadly ovate, with flattened apices and a germ pore at one end. The asexual morph is not yet determined (Wang et al. 2016a).

Type species: *Dichotomopilus indicus* (Corda) X. Wei Wang & Samson 2016

Basionym: *Chaetomium indicum* Corda 1840

Other accepted species: Species Fungorum (search *Dichotomopilus*)



Note a, b Ascomata. c Ascus, d Terminal hair. e Ascospores. Scale bars: b = 150 μm , c, e = 10 μm , d = 20 μm

Source Yang et al. (2023a)

Figure 4.156 *Dichotomopilus finlandicus*

Humicola Traaen 1914

Classification: *Chaetomiaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Humicola was established by Traaen (1914) to accommodate two species, *Humicola fuscoatra* and *H. grisea*, isolated from soil in Norway. Among these, *Humicola fuscoatra* was designated as the type species, while *Humicola grisea* and its varieties were later transferred to other genera. Wang et al. (2019) conducted a comprehensive study and revised the phylogenetic status of the genus. Later, Wang et

al. (2022) introduced a new species, *H. hirsuta*, using a polyphasic approach that included morphology, molecular dating, and phylogenetic analyses based on *rpb2*, *tub2*, ITS, and LSU genes. They also segregated *Humicola sensu* into two genera, *Humicola* and *Pseudohumicola*, and emended the generic description of *Humicola*. The sexual morph, has ostiolate ascomata with flexuous, seta-like terminal hairs. Ascomata might be present or absent. Asci are clavate, eight-spored, and evanescent before ascospore maturity. Ascospores are limoniform to quadrangular, bilaterally flattened, with an apical germ pore. The asexual morph is humicola-like, producing aleurioconidia-like conidia, with some species also producing an acremonium-like morph. In the humicola-like morph, conidiophores are absent, and aleurioconidia-like conidia arise laterally, intercalarily, or terminally from hyphal cells, forming solitary onidia or, rarely, short chains. In the acremonium-like morph, hyaline conidia form in basipetal chains on lateral (Hyde et al. 2020c; Wang et al. 2022) or terminal phialides. *Humicola* species have been reported from various substrates, including dead plant material, soil, indoor environments, and the fur of cats, with some species being mycoparasitic or thermophilic (Wang et al. 2019; Ibrahim et al. 2021). The genus comprises approximately 75 species, with two unidentified *Humicola* species recorded from salt marsh hosts (*Juncus roemerianus* and *Phragmites australis*) (Calabon et al. 2021b; Hyde et al. 2024a). *Humicola* species are reservoirs of thermostable enzymes and produce various bioactive metabolites, such as terpenoids, xanthonenes, xanthoquinones, and benzenediol lactones, with significant biotechnological and industrial potential (Ibrahim et al. 2021).

Type species: *Humicola fuscoatra* Traaen 1914

Other accepted species: Species Fungorum (search *Humicola*)



Note Phialide and conidia

Source Redrawn from Traaen (1914)

Figure 4.157 *Humicola fuscoatra*

Thermothielavioides X. Wei Wang & Houbraken 2019

Classification: *Chaetomiaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Thermothielavioides is a thermophilic genus with optimal growth at 45°C or higher. In culture media, ascomata of *Thermothielavioides* are globose or subglobose, superficial or surrounded by aerial mycelium with flexuous and verrucose ascomatal hairs. Asci are fasciculate with eight aseptate olivaceous-brown ascospores with a germ pore at the end. In the asexual stage, phialidic conidiogenous cells arise from aerial hyphae bearing hyaline, aseptate conidia in basipetal chains. Conidia are truncate at the base and rounded at the apex (Wang et al. 2019). The genus was introduced based on morphology and phylogenetic analyses of *rpb2* sequence data. Phylogenetically, *Floropilus* is closely related to *Thermothielavioides* but differs in mesophilic growth and having chaetomium-like ascomata, (Wang et al. 2019). *Thermothielavioides* comprises two species isolated from soil (Wang et al. 2019; Tan and Shivas 2023). *Thermothielavioides terrestris* has been reported from salt marsh hosts *Elymus pungens* and *Puccinellia maritima* in the United Kingdom (Apiñes and Chesters 1964; Calabon et al. 2021b).

Type species: *Thermothielavioides terrestris* (Apinis) X. Wei Wang & Houbraken 2019

Basionym: *Allescheria terrestris* Apinis 1963

Other accepted species: *Thermothielavioides maryleeae* Y.P. Tan 2023

Trichocladium Harz 1871

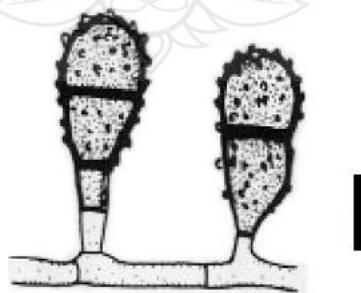
Classification: *Chaetomiaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Harz (1871) introduced *Trichocladium* to accommodate three saprobic species: *Trichocladium asperum*, *T. fuscum*, and *T. tenellum*. The asexual morph of *Trichocladium* has branched mycelia with poorly distinguished conidiophores, conidiogenous cells are monoblastic or polyblastic, integrated and terminal, with clavate, obovoid, pyriform or cylindrical shape bearing septate thick-walled, pale to dark brown to black conidia (Jones et al. 2001). Jones et al. (2009) revised the taxonomy of *Trichocladium*, accepting seven species and highlighting that the genus is

polyphyletic, with various sexual morphs connected to it. *Trichocladium* comprises approximately 40 species, mostly found as saprobes in soil and on dead plant material in both terrestrial and aquatic environments (Goh and Hyde 1999; Jones et al. 2001; Wang et al. 2019; Hyde et al. 2024a). Wang et al. (2022) introduced *T. tomentosum* from soil near a lake, forming a sexual morph. Recently, *T. solani* was described as a plant pathogen causing yellow rot in potato tubers (Belosokhov et al. 2022). Goh and Hyde (1999) introduced two new species from submerged wood and provided a key for *Trichocladium*, accepting 18 species. Jones et al. (2019) listed *T. alopallonellum*, *T. griseum*, *T. lignicola*, *T. melhae* and *T. nypae* as marine species, but the genus is polyphyletic, with Zhang et al. (2019) transferring *T. nypae* to *Savoryella*, and Calabon et al. (2023) transferring *T. alopallonellum* to *Halosphaeriopsis* based on sequence data from the type collection by Meyers and Moore (1960). Calabon et al. (2023) based on phylogenetic analysis of combined LSU and SSU sequence data, showed a close relationship between *Trichocladium* and *Humicola*. Likewise, *Trichocladium acharospora* is the asexual morph of *Halosphaeriopsis mediosetigera* in the *Halosphaeriaceae* (Jones et al. 2009). A few *Trichocladium* species have been reported in salt marsh habitats, including *T. constrictum* and *T. crispatum* (Calabon et al. 2021b). *Trichocladium* is capable of producing bioactive compounds. In a study by Simons et al. (2024), the OSMAC (One Strain Many Compounds) approach was applied to an endophytic *Trichocladium* species, resulting in the discovery of five new and five known compounds.

Type species: *Trichocladium asperum* Harz 1871

Other accepted species: Species Fungorum (search *Trichocladium*)



Note Conidiogenous cells and conidia. Scale bar = 10 µm

Source Goh and Hyde (1999)

Figure 4.158 *Trichocladium asperum*

Zopfiella G. Winter 1884

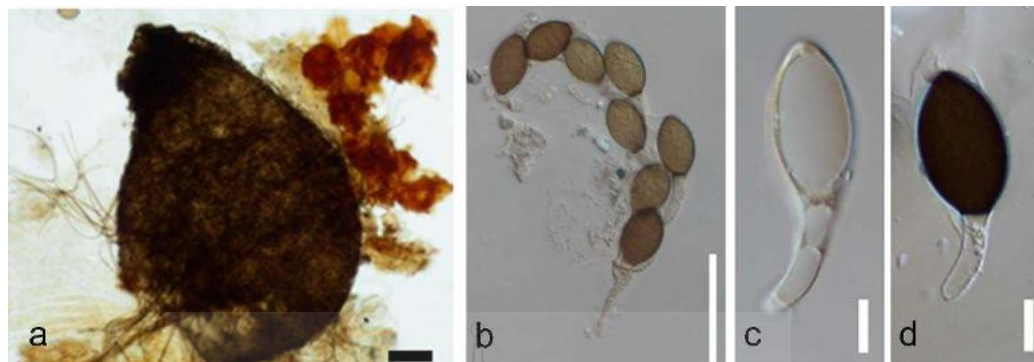
Classification: *Lasiosphaeriaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Zopfiella was established by Winter (1884) to accommodate *Zopfiella tabulata* and *Z. curvata*, which were previously classified under *Cephalotheca*. These species were originally isolated from rabbit and sheep dung. Winter (1884) described *Zopfiella* based on its sexual morph, which has superficial perithecia covered with olive to yellow-green, long, thin hairs. The asci are clavate, evanescent, and pedicellate, while the ascospores are ellipsoidal, truncated at one end, and have a hyaline cylindrical appendage that often collapses upon maturity. The asexual morph of *Zopfiella* remains unknown, though a humicola-like anamorph has been observed in *Z. latipes* in culture (Guarro et al. 1991). *Zopfiella* is considered a polyphyletic genus, and its taxonomy has been a subject of confusion (Hyde et al. 2020c). Cai et al. (2006) reviewed *Zopfiella* and its related genera and, based on phylogenetic analyses of LSU, ITS, and *tub* sequences, transferred this polyphyletic genus to *Lasiosphaeriaceae*. They proposed that *Zopfiella* should be restricted to species with ascospores with a septum in the dark cell. Jones et al. (2019) listed *Z. latipes* and *Z. marina* as marine fungi, with *Z. latipes* recorded on the salt marsh plant *Phragmites australis* (Calabon et al. 2021b). *Zopfiella indica* was described from the bark of intertidal mangrove wood and, based on phylogeny, morphology, and host association, was placed in *Zopfiella* (Phookamsak et al. 2019). Unlike the related genus *Podospora*, which is predominantly coprophilous, *Zopfiella* species are more commonly found in soil or on plant substrates, with fewer records from dung (Phookamsak et al. 2019). The marine species, *Z. latipes* is capable of producing antimicrobial metabolites, zopfiellamides A and B (Daferner et al. 2002).

Type species: *Zopfiella tabulata* Zopf ex G. Winter 1884

Basionym: *Cephalotheca tabulata* Zopf 1880

Other accepted species: Species Fungorum (search *Zopfiella*)



Note a Ascoma. b Ascus. c, d Ascospores. Scale bars: a = 100 µm, b = 50 µm, c, d = 10 µm

Source Phookamsak et al. (2019)

Figure 4.159 *Zopfiella indica*

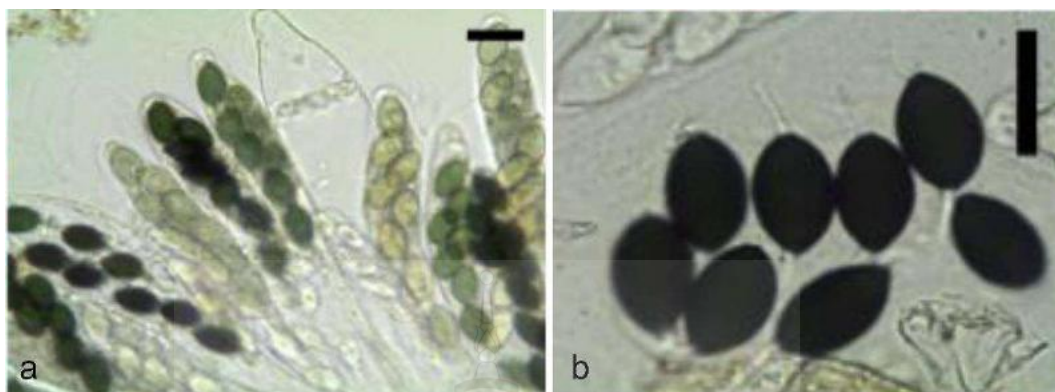
***Schizothecium* Corda 1838**

Classification: *Schizotheciaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Corda (1838) introduced *Schizothecium*, based on *Schizothecium fimicola*, which was collected from dried cattle dung in the Czech Republic. The genus was described as forming superficial, membranous perithecia and dark-colored ascospores with a short stalk (Corda 1838). Due to the loss of the original type material, Wang et al. (2019) designated the original illustration as the lectotype and also designated an epitype for *S. fimicola*. However, later studies showed that the epitype is morphologically and phylogenetically related to *Podospora* and does not match the lectotype. As a result, the generic name *Schizothecium* was resurrected as distinct from *Podospora* (Marin-Felix and Miller 2022). The placement of *Schizothecium* in the order *Sordariales* was confirmed by Cai et al. (2005) based on morphology and a multi-gene phylogenetic analysis using ITS, LSU, and *tub2* sequences. The genus includes about 20 species, generally isolated as saprobes on dung, dead plants, and soil (Mouchacca 1986; Stchigel et al. 2002; Cai et al. 2005; Hyde et al. 2024a). There are no known records of *Schizothecium* in marine habitats (Jones et al. 2019); however, *S. hispidulum* has been reported from a salt marsh plant, *Phragmites australis*, in the Netherlands (Calabon et al. 2021b).

Type species: *Schizothecium fimicola* Corda 1838

Other accepted species: Species Fungorum (search *Schizothecium*)



Note a Asci. b Ascospores. Scale bars: a = 50 μm , b = 20 μm

Source Mungai et al. (2012a)

Figure 4.160 *Schizothecium conicum*

Neurospora Shear & B.O. Dodge 1927

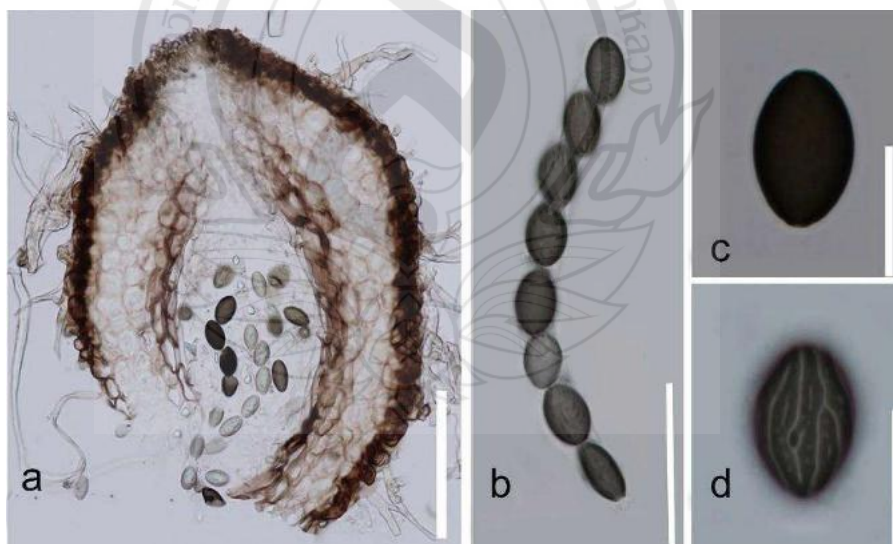
Classification: *Sordariaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Neurospora, established by Shear and Dodge (1927), mainly is a saprobic genus comprising approximately 50 species that are commonly isolated from dung, soil, and both burned and unburned plant material in terrestrial environments (Huang et al. 2021, Hyde et al. 2024a). *Neurospora calospora* has been reported on the salt marsh plant *Elymus pungens* in the United Kingdom (Calabon et al. 2021b). Some species of *Neurospora* have significant economic and ecological importance (Hasanzadeh et al. 2022; Toghiani et al. 2025). For instance, *N. intermedia* is an edible fungus that has been frequently studied for its ability to produce enzymes that facilitate the degradation of agricultural waste (Shahryari et al. 2019; Maini Rekdal et al. 2024; Toghiani et al. 2025). This species is also capable of generating valuable metabolites, including ethanol and organic acids, from plant-based waste materials (Ghasemian et al. 2018). However, *N. intermedia* has been reported as potential causative agents of human infections, such as endobronchial masses (Wu et al. 2024). The genus *Neurospora* forms both sexual and asexual morphs. The sexual morph is characterized by the formation of perithecial or cleistothecial ascomata, which are brown to black, ostiolate, and vary in structure from carbonaceous to membranous. The asci are cylindrical to

clavate, with a J- apical ring, and contain four to eight oval to ellipsoidal, aseptate, hyaline, or brown to black ascospores. The ascospores are characterized by an ornamented surface, which may have longitudinal ribs or irregular to circular pits of varying depth (Huang et al. 2021). The asexual morph of *Neurospora* is chrysonilia-like and has been reported from both natural substrates and culture. The genus has three mating strategies: homothallism, pseudohomothallism, and heterothallism (Huang et al. 2021). Taxonomic studies by García et al. (2004) led to the synonymization of the genus *Gelasinospora* with *Neurospora*. García et al. (2004) proposed that ascospore ornamentation and mating strategy are important characteristics for understanding the relationship between morphology and phylogeny within the genus. However, Huang et al. (2021) did not find consistent correlation between these morphological traits and phylogenetic results. In their phylogenetic analyses based on LSU, ITS, and *tub* sequences, *Neurospora* segregated into four clades within *Sordariaceae*, with species grouped according to mating type, ascomatal morphology, ascospore appearance, and episporium structure.

Type species: *Neurospora sitophila* Shear & B.O. Dodge 1927

Other accepted species: Species Fungorum (search *Neurospora*)



Note a Vertical section of ascoma. b Ascus. c, d Ascospores. Scale bars: a = 100 μ m, b = 50 μ m, c, d = 20 μ m

Source Huang et al. (2021)

Figure 4.161 *Neurospora sitophila*

Sordaria Ces. & De Not. 1863

Classification: *Sordariaceae*, *Sordariales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

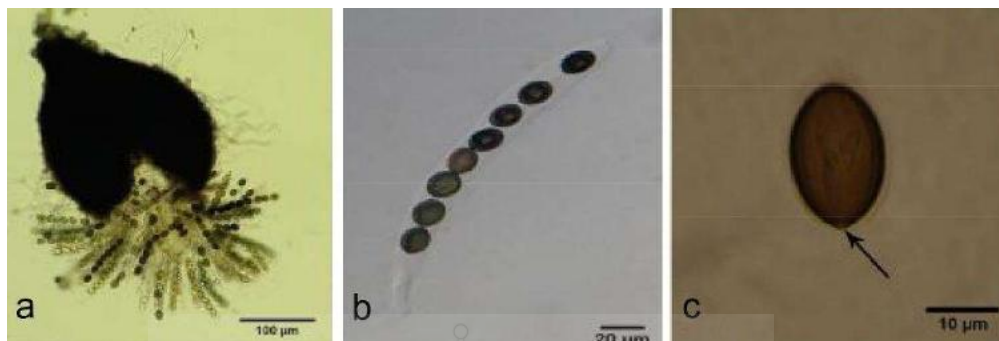
Cesati and De Notaris (1863) introduced *Sordaria* and typified it with *S. fimicola*. Later, Winter (1885) established family *Sordariaceae* based on morphological characters and transferred *Sordaria* to this family as the type genus. There are 51 species listed under this saprobic genus in Species Fungorum (2023), but only 17 species have sequence data with different barcodes, such as ITS, LSU, SSU, *tef1*, *rpb2*, *tub2*, *act1* (Phukhamsakda et al. 2020; Crous et al. 2021a). *Sordaria* species are mostly coprophilous, associated with faeces or dung, and have also been reported from soil, seeds, or plants (Furtado 1969, Watanabe 1989; Mungai et al. 2012b; Kavak 2012; Phukhamsakda et al. 2020). Some species e.g., *S. fimicola* and *S. macrospora*, serve as important models for studying fungal development (Mai 1977; Teichert et al. 2014). *Sordaria fimicola* has been found in salt marsh habitats associated with *Elymus pungens*, *Spartina townsendii*, and *Puccinellia maritima* in the United Kingdom (Apinis and Chesters 1964) and *Distichlis spicata* in Argentina (Eliades et al. 2007).

The sexual morph of *Sordaria* is recognized by the production of perithecioid, coriaceous ascomata. The asci are cylindrical, with a prominent apical ring containing 8 ellipsoidal to ovoid, dark brown to black ascospores with appendages or a gelatinous sheath (Crous et al. 2021a; Phukhamsakda et al. 2020). *Sordaria equicola* is the only known asexual morph species, characterized by erect conidiophores arising from pale brown, branched hyphae with phialidic conidiogenous cells with an inconspicuous collarete, forming terminally or intercalary. The conidia are hyaline, pyriform, and have smooth walls with a truncate base (Crous et al. 2021a).

Type species: *Sordaria fimicola* (Roberge ex Desm.) Ces. & De Not. 1863

Basionym: *Sphaeria fimicola* Roberge ex Desm. 1849

Other accepted species: Species Fungorum (search *Sordaria*)



Note a Ascoma. b Ascus. c Ascospore

Source Hashemloo et al. (2014)

Figure 4.162 *Sordaria fimicola*

Aropsiclus Kohlm. & Volkm.-Kohlm. 1994

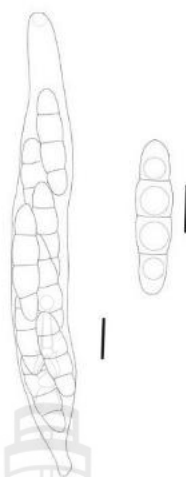
Classification: *incertae sedis*, *incertae sedis*, *incertae sedis*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Aropsiclus was introduced to accommodate *A. junci*, which was previously classified in *Sulcospora*. It was isolated from dead culms of *Juncus roemerianus* in USA by Kohlmeyer and Volkmann-Kohlmeyer (1994) during their investigation of salt marsh fungi in North Carolina. They did not assign any family or order to *Aropsiclus*. Ascomata are cream coloured and are embedded in the outer tissue of the host. Ascomatal necks, are periphysate, and periphysoids are present. Ascospores are hyaline, 3-septate, with a striated wall (Jones et al. 2009). Fresh collections and sequence data are needed for certain classification.

Type species: *Aropsiclus junci* (Kohlm. & Volkm.-Kohlm.) Kohlm. & Volkm.-Kohlm. 1994

Basionym: *Sulcospora junci* Kohlm. & Volkm.-Kohlm. 1993

Other accepted species: None.



Note Ascus and ascospores

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer B. (1994)

Figure 4.163 *Aropsichus junci*

Tracylla (Sacc.) Tassi 1904

Classification: *Tracyllaceae*, *Tracyllales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Saccardo (1895) described *Tracylla* as a subgenus and Tassi (1904) introduced it as a genus to accommodate *T. spartinae* and *T. aristata* which formerly belonged to *Leptothyrium*. Crous et al. (2018a) described *T. eucalypti* and introduced *Tracyllaceae* and *Tracyllales* to accommodate these three species based on multigene phylogenetic study of ITS, LSU and SSU data. *Tracylla* is a sordariomycetous genus that has been found as a saprobe and pathogen (Nag Raj 1993; Hernández-Restrepo et al. 2016b; Crous et al. 2018a). Its sexual morph has not been determined. The asexual morph is coelomycetous with pycnothyrial, superficial, brown conidiomata lacking an ostiole (Crous et al. 2018a). Conidiophores are reduced to doliiform to ellipsoid conidiogenous cells, which are hyaline, smooth and phialidic. Conidia are hyaline, aseptate, falcate to naviculate or ellipsoid with or without polar appendages (Crous et al. 2018a).

The type species, *Tracylla spartinae* (based on *Leptothyrium spartinae* Peck 1894) was isolated from *Spartina patens* and other grass hosts, mostly from tropical and subtropical regions (Nag Raj 1993; Seymour 1929). *Tracylla aristata* was found on *Eucalyptus* and *Hakea dactyloides* (Cooke 1891; Crous and Van der Linde 1993;

Nag Raj 1993) and *T. eucalypti* was isolated from *Eucalyptus urophylla* (Crous et al. 2018a).

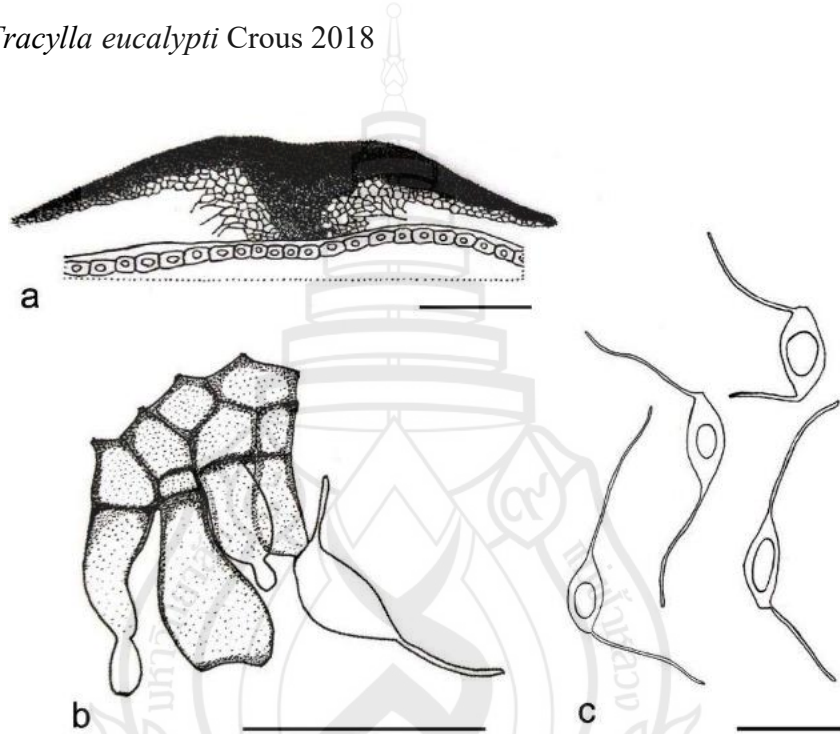
Type species: *Tracylla spartinae* (Peck) Tassi 1904

Other accepted species:

Tracylla andrasovzkyi Moesz 1914

Tracylla aristata (Cooke) Tassi 1904

Tracylla eucalypti Crous 2018



Note a Vertical section of conidiomata. b Conidiogenous cells with developing conidia. c Conidia. Scale bars: a=50 µm, b–c= 20 µm

Source Redrawn from Nag Raj (1993)

Figure 4.164 *Tracylla spartinae*

Apiospora Sacc. 1875

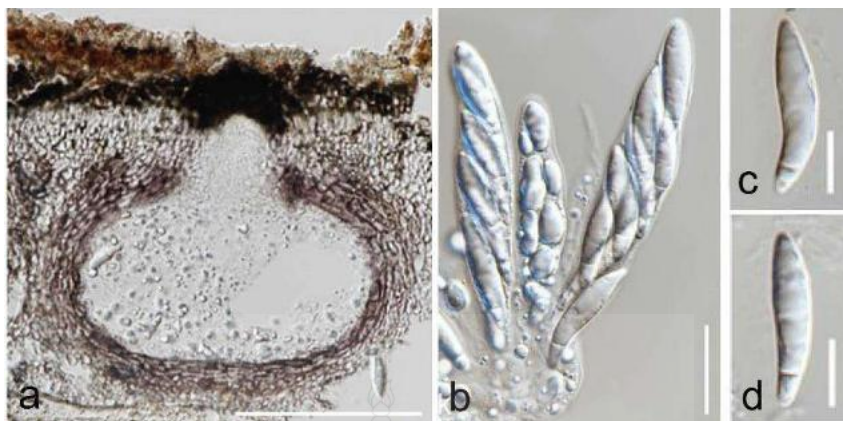
Classification: *Apiosporaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Apiospora was introduced by Saccardo (1875b) and typified with *Ap. montagnei*. Although previously considered synonymous with *Arthrinium*, phylogenetic analyses by Pintos and Alvarado (2021) confirmed their distinction.

Apiospora is a diverse genus comprising approximately 100 species distributed worldwide as endophytes, saprobes, or pathogens (Tian et al. 2021a; Hyde et al. 2024a). These fungi have been isolated from various sources, including air, animal tissues, lichens, soil, and numerous host plants, particularly bamboo (Wang et al. 2017a; Tang et al. 2020; Tian et al. 2021a; Bashiri and Abdollahzadeh 2024). Some species, including *Apiospora arundinis*, can cause human infections like onychomycosis (Dyląg et al. 2017). Pathogenic species have also been reported on economically important plants like olive, peach, rosemary, and barley, causing leaf necrosis, leaf spot, blight, brown culm streak, and kernel blight (Chen et al. 2014; Piccolo et al. 2014; Ji et al. 2020; Yin et al. 2021). Interestingly, *Ap. arundinis*, which causes kernel blight in barley, has been studied for its potential as an antifungal agent (Hyde et al. 2020c). This species has also been reported as a saprobe on salt marsh plants like *Phragmites australis* and an unidentified *Phragmites* species (Calabon et al. 2021b). Both sexual and asexual morphs of *Apiospora* have been documented. The sexual morph form multi-locular perithecial stromata, with hyaline ascospores surrounded by a thick gelatinous sheath (Dai et al. 2016, 2017). Conidiophores in the asexual morph are present or reduced to basauxic conidiogenous cells. conidia are globose to subglobose, nearly spherical in the frontal view and lenticular in the side view, pale brown to brown (Dai et al. 2016; Liu et al. 2024). Kwon et al. (2022) reported two new records of *Apiospora* from marine substrates in South Korea: *Apiospora piptatheri* from *Sargassum fulvellum* and *Apiospora rasikravindrae* from egg masses of *Arctoscopus japonicus* (Japanese sandfish). Additionally, they expanded the genus by introducing eight new combinations of marine species based on morphological, ecological, and phylogenetic analyses of ITS, LSU, *tef1*, and *tub2* sequences: *Apiospora agari*, *Apiospora arctoscopi*, *Apiospora fermenti*, *Apiospora koreana*, *Apiospora marina*, *Apiospora pusillisperma*, *Apiospora sargassi*, and *Apiospora taeianensis*.

Type species: *Apiospora montagnei* Sacc. 1875

Other accepted species: Species Fungorum (search *Apiospora*)



Note a Ascoma. b Asci. c, d Ascospores. Scale bars: a = 100 μm , b = 20 μm , c, d = 10 μm

Source Samarakoon et al. (2022)

Figure 4.165 *Apiospora guiyangensis*

Arthrinium Kunze 1817

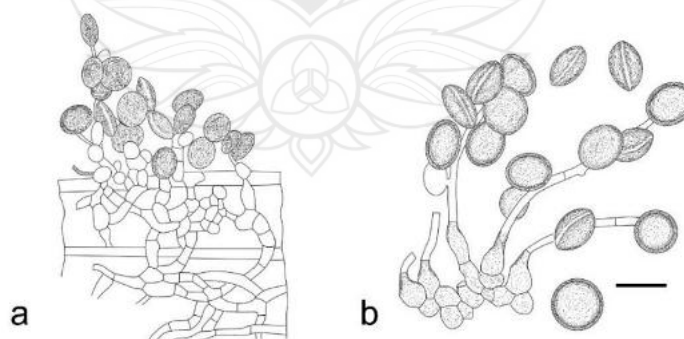
Classification: *Apiosporaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Arthrinium was introduced by Kunze (1817) and has been placed in various higher taxa. Subsequently, Hyde et al. (1998) assigned it to the novel family *Apiosporaceae* based on morphological characteristics of both sexual and asexual morphs. *Apiosporaceae* belongs to the order *Amphisphaeriales* (Samarakoon et al. 2022; Hyde et al. 2024a), having been previously classified in *Xylariales* (Smith et al. 2003; Crous and Groenewald 2013; Jiang et al. 2019). *Arthrinium* is the type genus of *Apiosporaceae* and comprises around 30 species that have been reported as endophytes, pathogens, or saprobes (Hyde et al. 2024a; Hyde et al. 2020c). Some species are plant pathogens, causing scabs, spots, or damping-off, and some are human pathogens (Rai 1989; Martínez-Cano et al. 1992; Mavagani et al. 2007). *Arthrinium phaeospermum* has been reported as human pathogens, causing superficial infections (Dyląg et al. 2017). *Arthrinium* has been collected on *Cyperaceae*, *Juncaceae* and *Poaceae* plant hosts, including salt marsh plants. For example, *A. phaeospermum* has been reported on *Phragmites australis*, *Spartina patens*, and *S. alterniflora* in *Poaceae* (Calabon et al. 2021b). In addition to salt marshes, it is also recorded as an endophyte from algae in marine habitats (Suryanarayanan 2012). In fact, as this is usually the first saprobe to

appear on many recently dead grasses, it is likely to occupy both endophytic, saprobic and pathogenic lifestyles (Bhunjun et al. 2024). The asexual morph of *Arthrinium* is distinguished by its basauxic conidiophores, doliiform to ampulliform to subcylindrical polyblastic conidiogenous cells, which bear unicellular conidia terminally and intercalarily (Hyde et al. 1998; Crous and Groenewald 2013; Mapook et al. 2020). The sexual morph is characterized by immersed to erumpent stromata and globose, papillate, ostiolate ascomata. Asci are clavate to broadly cylindrical and contain eight hyaline, ellipsoidal, inequilateral ascospores with one septum near the lower end, with or without a sheath (Crous and Groenewald 2013). *Apiospora* was considered the sexual morph of *Arthrinium* and synonymous with *Arthrinium*, as the latter name is older and more frequently encountered (Crous and Groenewald 2013). Pintos and Alvarado (2021) introduced a new species *Arthrinium crenatum*, and based on 5.8S-ITS2, LSU, *tef1* and *tub2* exons showed that the *Arthrinium* and *Apiospora* are separate phylogenetically and they were considered as sperate genera. However, they are very similar morphologically, conidia in *Apiospora* are nearly spherical in the front and lenticular at the side, while various conidial shape is *Arthrinium* (Tian et al. 2021a, Liu et al. 2024). Several species of *Arthrinium* have been transferred to *Apiospora*, including the reclassification of eight species collected from marine habitats (Kwon et al. 2022).

Type species: *Arthrinium caricicola* Kunze & J.C. Schmidt 1817

Other accepted species: Species Fungorum (search *Arthrinium*)



Note a Mycelia, conidiophores (650×). b Conidiogenous cells and conidia. Scale bar:
b = 10 μ m

Source Redrawn from Ellis (1965)

Figure 4.166 *Arthrinium phaeospermum*

***Nigrospora* Zimm. 1902**

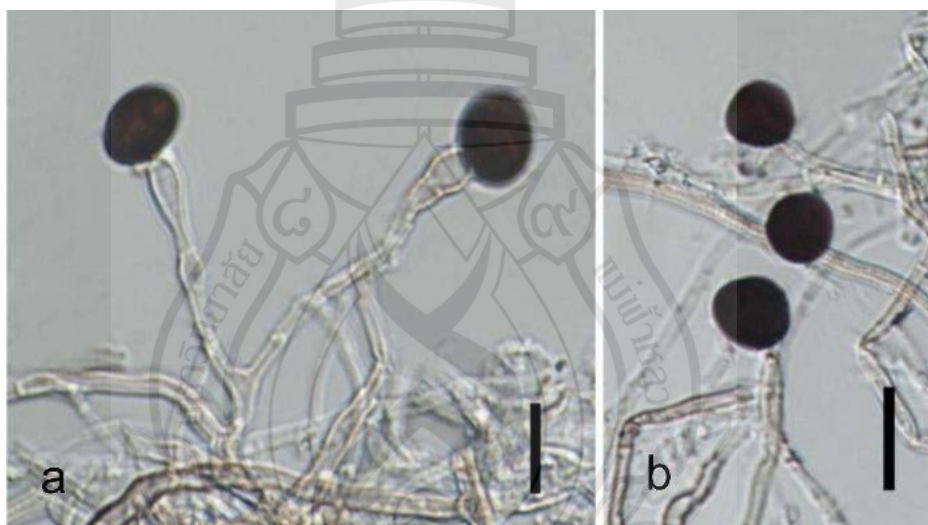
Classification: *Apiosporaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Nigrospora was established by Zimmerman (1902) and typified with an endophytic species, *Nigrospora panici*. Wang et al. (2017c) employed a polyphasic approach, integrating morphology, ecology, host associations, and multi-locus phylogenies based on ITS, *tef1*, and *tub2* genes, for species delimitation in *Nigrospora*. This study added 13 new taxa to the genus and, based on morphology and phylogenetic analyses of LSU sequence data, placed the genus in *Apiosporaceae*. *Nigrospora* comprises approximately 54 species (Species Fungorum, accessed April 2026) and has diverse ecological roles as saprobes, endophytes, and pathogens (Wang et al. 2017c; Hao et al. 2020; Jayawardena et al. 2020; Maharachchikumbura et al. 2021; de Silva et al. 2021; Karimi et al. 2025). The genus includes pathogens of various economically important plants. For example, *Nigrospora oryzae* causes leaf spot on pearl millet (Kalati et al. 2014), while *N. gorlenkoana*, *N. osmanthi*, and *N. philosophiae-doctoris* have been reported as causing leaf spot on olive (*Olea europaea* L.) (Petrović et al. 2023). *Nigrospora sphaerica* is known to cause leaf blight on blueberry, sugarcane, sesame, and tea (Cui et al. 2018), and *N. musae* is the causative agent of ‘squirter’ disease in banana (Jones and Stover 2000). *Nigrospora* species have also been reported as human pathogens. *N. sphaerica* has been reported to cause human infections, including corneal ulcers, respiratory allergies, and onychomycosis (Fan et al. 2009, Ananya et al. 2014), while *N. oryzae* has been isolated from superficial skin scrapings and pulmonary infections (Yew et al. 2014; Vanam et al. 2020). *Nigrospora* species have been reported from various habitats, including marine environments. *Nigrospora oryzae*, *N. sphaerica*, and *N. camelliaesinensis* have been collected from mangroves (Jones et al. 2019; Ukwatta et al. 2019; Ola et al. 2021). *Nigrospora aurantiaca* has been isolated from sponges (Said Hassane et al. 2020), while *N. cooperae*, *N. covidalis*, *N. guilinensis*, *N. lacticolonina*, *N. osmanthi*, *N. pyriformis*, and *N. rubi* have been isolated from macroalgae (Lee et al. 2023). *Nigrospora oryzae* was isolated as a saprobe from halophytes such as *Distichlis spicata* and *Juncus roemerianus* (Calabon et al. 2021b). Some species have also been reported as endophytes, including *N. pernambucoensis* from *Allenrolfea occidentalis*, *N. shadeganensis* from *Phragmites*

australis and *Seidlitzia rosmarinus*, and both *N. oryzae* and *N. osmanthi* from *Suaeda vermiculata* (Safi et al. 2024). *Nigrospora* species, such as *N. sphaerica*, have been shown inflammatory, antimicrobial, and anti-cancer activity (Ukwatta et al. 2019). *Nigrospora* is characterized by a hyphomycetous asexual morph, with conidiophores that are micronematous, semi-macronematous, or reduced to subspherical, doliiform, ampulliform, subcylindrical, or clavate conidiogenous cells. The asexual morph produces distinctive black, shiny, spherical conidia. The sexual morph, referred to as *Khusia*, forms perithecial ascomata, short-stalked asci, and hyaline, granular, aseptate or uniseptate ascospores (Wang et al. 2017c).

Type species: *Nigrospora panici* Zimm. 1902

Other accepted species: Species Fungorum (search *Nigrospora*)



Note a, b Conidiophores, Conidiogenous cells and conidia. Scale bars: 10 μ m

Source Karimi et al. (2025)

Figure 4.167 *Nigrospora chinensis*

Beltrania Penz. 1882

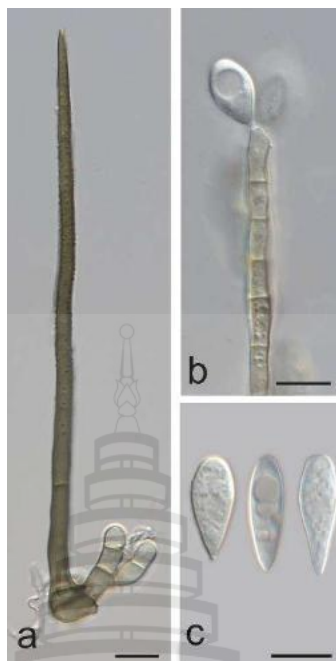
Classification: *Beltraniaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Penzig (1882) introduced *Beltrania* based on the collection of its type species, *Beltrania rhombica*, from leaves of *Citrus limon* in Italy. Two years later, a second species, *B. querna*, was added to the genus, isolated from decaying leaves of *Quercus agrifolia* (Harkness 1884). *Beltrania querna* has also been reported as saprobic on

Juncus roemerianus in salt marsh habitats (Calabon et al. 2021b). With the availability of sequence data for the type species, the taxonomy of *Beltrania* has been better resolved (Shirouzu et al. 2010; Rajeshkumar et al. 2016; Lin et al. 2017; Phukhamsakda et al. 2022). Currently, about 20 species are accepted in this genus, most of which are saprobic on plant material, commonly found in leaf litter (Phukhamsakda et al. 2022; Hyde et al. 2024a). Recent additions to the genus include *B. shenzhenica*, isolated from dead leaves in the Futian Mangrove Nature Reserve in China (Zhang et al. 2022a); *B. aquatica*, found on submerged wood in freshwater habitats in Thailand (Phukhamsakda et al. 2022); and *B. liliiferae*, identified on dead leaves of *Magnolia liliifera* in Thailand (Liu et al. 2024). These studies utilized morphological characteristics and phylogenetic analysis based on combined LSU and ITS sequence data for species identification. The sexual morph of *Beltrania* has not yet been determined. The asexual morph is hyphomycetous, characterized by dark, typically unbranched setae with radially lobed basal cells. The conidiophores are unbranched, arising from basal cells of the setae or from separate radially lobed basal cells. Conidiogenous cells are polyblastic, sympodial, and denticulate, producing biconic, spicate, or apiculate conidia (Seifert et al. 2011b; Hyde et al. 2020c). Some *Beltrania* species have been reported to produce enzymes with industrial applications, as well as bioactive compounds with antitumor, anticancer, and antimicrobial properties (Elkhateeb et al. 2019).

Type species: *Beltrania rhombica* Penz. 1882

Other accepted species: Species Fungorum (search *Beltrania*)



Note a Seta and conidiophore. b Conidiophores, conidiogenous cells, and conidia. c Conidia. Scale bars: 10 μ m

Source Liu et al. (2025)

Figure 4.168 *Beltraniella danzhouensis*

Phragmitensis M.K.M. Wong, Poon & K.D. Hyde 1998

Classification: *Hyponectriaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

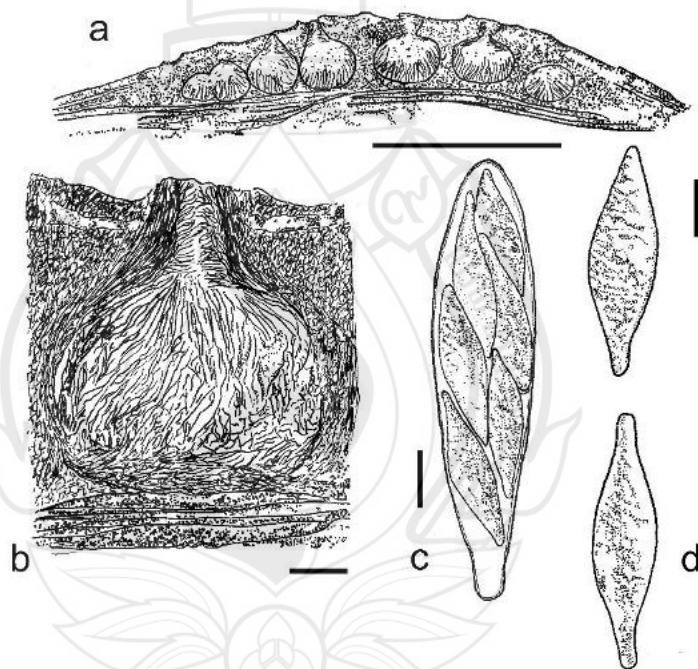
Wong et al. (1998) described *Phragmitensis* to accommodate *P. marina* which was found on decaying culms of *Phragmites australis* in Hong Kong. *Phragmitensis* has immersed, pseudostromata containing several ascomata. The ascomata are immersed, ostiolate, obpyriform containing straight to flexuous septate paraphyses and clavate, unitunicate asci, lacking an apical ring (Wong et al. 1998, 1999). The ascospores are hyaline, guttulate, unicellular, cymbiform, ellipsoidal to reniform, and surrounded by a mucilaginous sheath (Wong et al. 1998, 1999). A second species, *Phragmitensis ellipsoidea*, was isolated from the same host in Hong Kong (Wong et al. 1999). However, *P. ellipsoidea* was discovered in freshwater while *P. marina* was from saline environments. The two species are similar despite their different habitat and

ascospore shape; spindle-shaped in *P. marina* and widely ellipsoidal in *P. ellipsoidea* (Wong et al. 1999).

Wong et al. (1998) classified the genus based on morphological features in *Xylariales* based on the key in Barr (1990). However, due to the absence of an apical ring, they classified it as *Ascomycetes incertae sedis*. There is no molecular data for the genus and it belongs to *Hyponectriaceae* (*Amphisphaeriales*, *Xylariomycetidae*) (Hyde et al. 2020c; Wijayawardene et al. 2022).

Type species: *Phragmitensis marina* M.K.M. Wong, Poon & K.D. Hyde 1998

Other accepted species: *Phragmitensis ellipsoidea* M.K.M. Wong, Goh & K.D. Hyde 1999



Note a Section of pseudostroma. b Section through mature ascoma. c Asci. d Ascospores. Scale bars: a = 1 mm, b = 50 μ m, c = 20 μ m, d = 10 μ m

Source Redrawn from Wong et al. (1998)

Figure 4.169 *Phragmitensis marina*

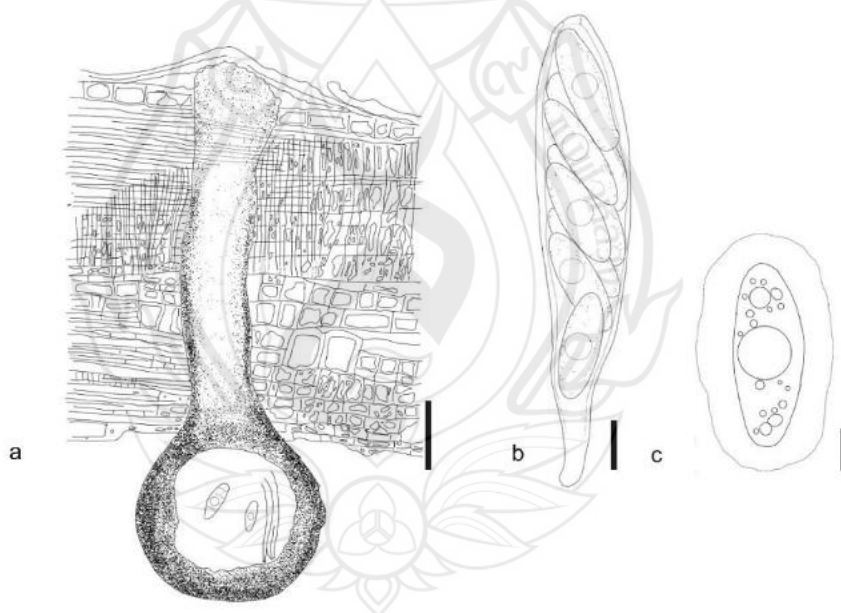
Physalospora Niessl 1876

Classification: *Hyponectriaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Physalospora was established by Mayendorf (1876) to accommodate its type species, *P. alpestris*. *Physalospora* species are distributed worldwide on a variety of hosts. *Physalospora citogermians* was described by Kohlmeyer et al. (1995a) as a saprobe on *Juncus roemerianus* in USA (Calabon et al. 2021b). As the fungus appeared on both upper and lower parts of the host, they treated it as a facultative marine fungus. *Physalospora* is characterized by immersed clypeate ascomata. Asci contain hyaline to pale brown ascospores, with or without a sheath (Wang and Hyde 1999; Sivanesan and Shivas 2002). *Physalospora citogermians* is characterized by deeply immersed ascomata with a long neck. It differs from the type species in having hyaline ascospores (Kohlmeyer et al. 1995a). Two other species are reported on *Juncus*, *P. antarctica* on *J. scheuchzerioides* and *P. moutonii* on *Juncus* sp. (Kohlmeyer et al. 1995a).

Type species: *Physalospora alpestris* Niessl 1876

Other accepted species: Species Fungorum (search *Physalospora*)



Note a Ascoma. b Ascus. c Ascospore. Scale bars: a = 50 µm, b = 10 µm, c = 5 µm

Source Redrawn from Kohlmeyer et al. (1995a)

Figure 4.170 *Physalospora citogermians*

Pestalotiopsis Steyaert 1949

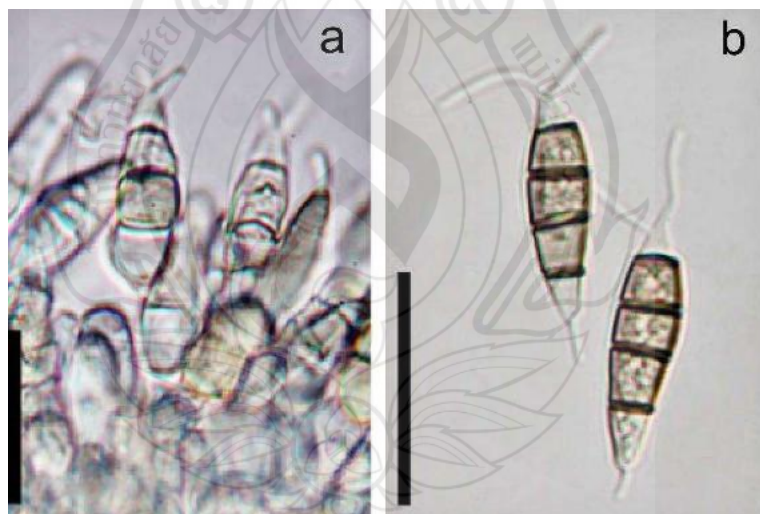
Classification: *Sporocadaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Pestalotiopsis species are well-known as endophytes and pathogens on economically important plants. There are also records of saprobic species on decaying plants (Jeewon et al., 2003, 2004; Maharachchikumbura et al., 2011, 2014). *Pestalotiopsis planimi* has been isolated from the salt marsh plant *Spartina alterniflora* in USA (Gessner and Goos 1973b). *Pestalotiopsis* sp. and *P. juncestris* were reported as saprobes on *Phragmites australis* (Poon and Hyde 1998) and *Juncus roemerianus*, respectively (Kohlmeyer and Volkmann-Kohlmeyer 2001a, Calabon et al. 2021b). There are 414 records listed in Index Fungorum (May 2024), characterized by appendage-bearing conidia, mostly with similar morphology. Some studies have investigated classification of *Pestalotiopsis* (Maharachchikumbura et al. 2011, 2012, 2014; Peng et al. 2022). Phylogenetic analyses of ITS, *tef1*, and *tub2* sequence data are commonly used markers for molecular classification (Dong et al. 2023).

Type species: *Pestalotiopsis guepinii* (Desm.) Steyaert 1949

Basionym: *Pestalotia guepinii* Desm. 1840

Other accepted species: Species Fungorum (search *Pestalotiopsis*)



Note a Conidiogenous cells. b Conidia. Scale bars: 20 μ m

Source Maharachchikumbura et al. (2012)

Figure 4.171 *Pestalotiopsis adusta*

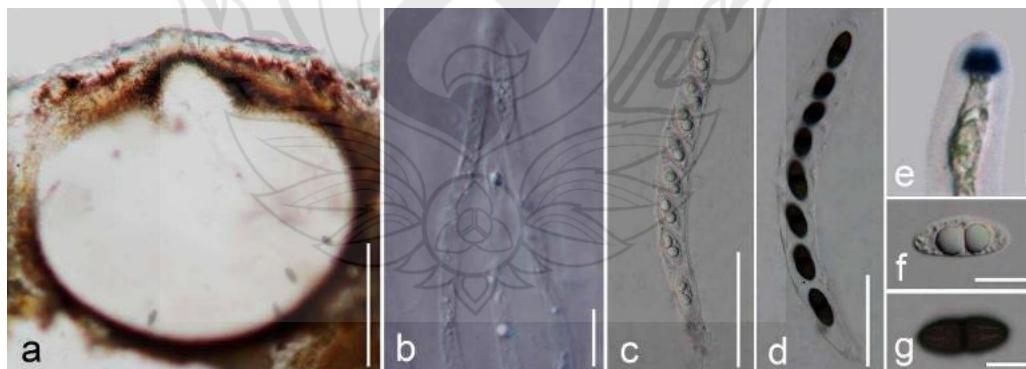
Atrotriquata Kohlm. & Volkm.-Kohlm. 1993

Classification: *Cainiaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Atrotriquata was established by Kohlmeyer and Volkmann-Kohlmeyer (1993) based on a saprobic fungus, *A. lineata*, isolated from dead culms of the halophyte *Juncus roemerianus* in USA. This species has also been recorded on an unknown salt marsh plant in USA (Walker 2012; Calabon et al. 2021b). This genus is characterized by immersed ascomata beneath a clypeus, cylindrical unitunicate asci with a J+ apical ring, and brown, 1-septate ascospores. The ascospores have 5–7 longitudinal striations at each apex and are surrounded by a sheath (Kang et al. 1999a, b; Hyde et al. 2020c). Morphologically, it is similar to *Cainia* but differs in having a wedge-shaped apical apparatus and longitudinal striations in the ascospores (Kohlmeyer and Volkmann-Kohlmeyer 1993a; Maharachchikumbura et al. 2015). Based on morphology, *Atrotriquata* was placed in *Cainiaceae* (Kang et al. 1999a, b). However, Liu et al. (2015) introduced a novel species, *Atrotriquata spartii*, from dead *Spartium junceum* in Italy. Based on LSU phylogenetic analyses, *A. spartii* was placed outside of *Cainiaceae*. Senanayake et al. (2015) confirmed the placement of *Atrotriquata* in *Cainiaceae* based on morphology and phylogenetic analyses of combined LSU and ITS sequences.

Type species: *Atrotriquata lineata* Kohlm. & Volkm.-Kohlm. 1993

Other accepted species: *Atrotriquata spartii* Thambug., Camporesi & K.D. Hyde 2015



Note a Section through ascoma. b Pseudoparaphyses. c, d Asci. e Ascus in Melzer's reagent. f, g Ascospores. Scale bars: a = 150 μ m, c, d = 50 μ m, e = 20 μ m, b, f, g = 10 μ m

Source Liu et al. (2015)

Figure 4.172 *Atrotriquata spartii*

Ommatomyces Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1995

Classification: *Clypeosphaeriaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Ascomycota*, *Fungi*.

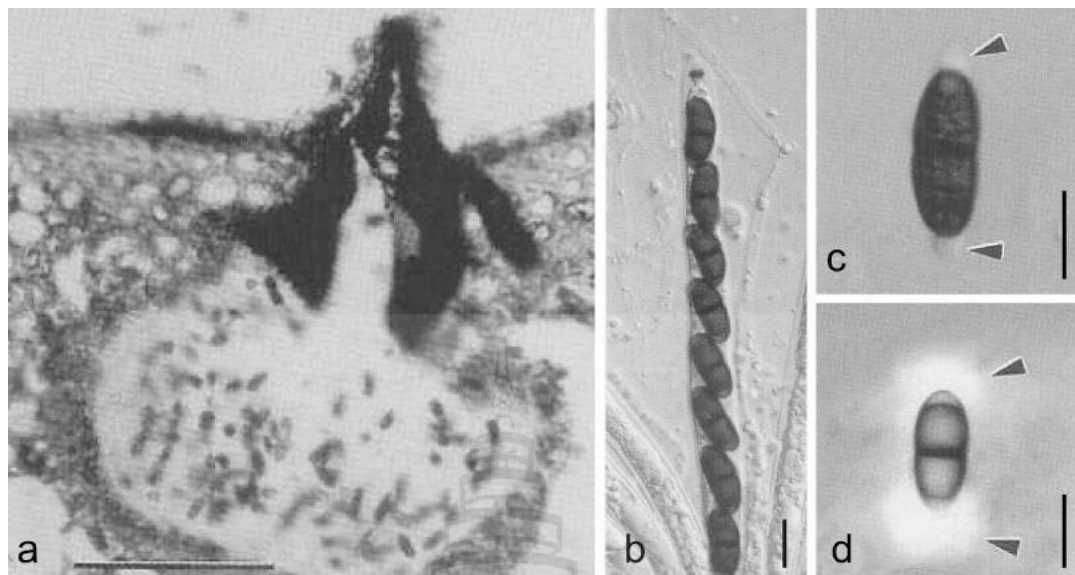
Ommatomyces was described by Kohlmeyer et al. (1995b) to accommodate the type species, *O. coronatus*, which was isolated from the lower part of *Juncus roemerianus* as a saprobic obligate marine fungus. With the introduction of a new species and combination by Wang et al. (2000), there are currently three species. *Ommatomyces* was initially classified in *Amphisphaeriaceae* based on morphology (Kohlmeyer et al. 1995b), but later it was transferred to *Cainiaceae* (Kang et al. 1999a, Wang et al. 2000). Kirk et al. (2001) placed it in *Xylariaceae*, but subsequently, it was accepted in *Clypeosphaeriaceae* (*Xylariales*) (Jones et al. 2009; Wijayawardene et al. 2022). The genus is characterized by clypeate, immersed, papillate ostiolate ascomata with septate periphyses and paraphyses. The asci are cylindrical with a J+ layered subapical ring, containing broadly ellipsoidal, brown, 1-septate ascospores with gelatinous spore caps and sheaths and lacerate germ slits at each end (Kohlmeyer et al. 1995b; Jones et al. 2009). There is no molecular data available for this genus and recollection of the species is required to resolve their taxonomic relationship.

Type species: *Ommatomyces coronatus* Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1995

Other accepted species:

Ommatomyces pardalinus (Ellis & Everh.) You Z. Wang, M.K.M. Wong & K.D. Hyde 2000

Ommatomyces terrestris You Z. Wang, M.K.M. Wong & K.D. Hyde 2000



Note a Ascoma. b Asci. c Ascospores. Scale bars: a = 50 μm , b = 10 μm , c, d = 5 μm

Source Wang et al. (2000)

Figure 4.173 *Ommatomyces terrestris*

Anthostomella Sacc. 1875

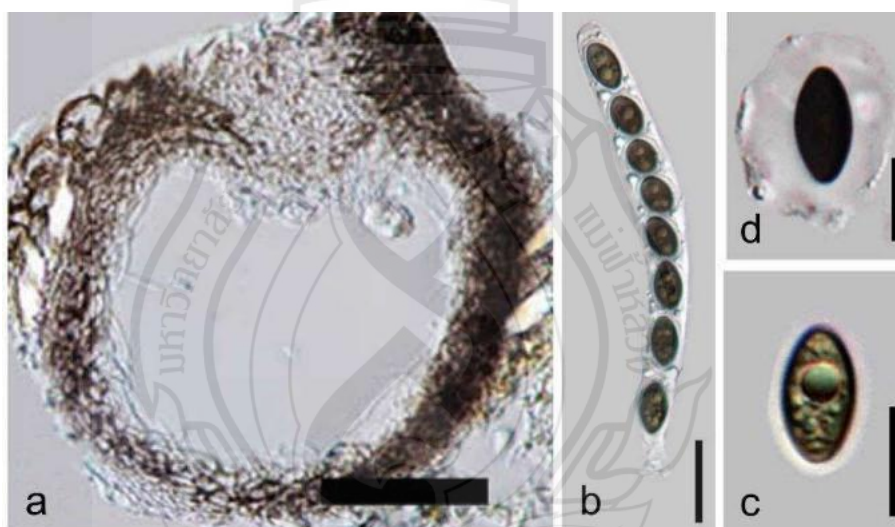
Classification: *Gyrotrichaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Anthostomella was introduced by Saccardo (1875a) to include *A. limitata*, *A. tomicoides*, and *A. perfidiosa*. Species in *Anthostomella* develop immersed, ostiolate ascomata with a dark clypeus, cylindrical asci, and generally brown, aseptate ascospores, which may or may not have a dwarf cell or appendages (Lu and Hyde 2000; Daranagama et al. 2015). Saccardo (1875a) did not designate a type species, which led to subsequent debates over whether *A. limitata* or *A. tomicoides* should be selected as the type. *Anthostomella limitata* was accepted as the type species based on its non-appendiculate ascospores (Eriksson 1966) and the presence of a dark clypeus (Lu and Hyde 2000). However, Daranagama et al. (2015) accepted *A. tomicoides* as the generic type and clarified the taxonomic placement of *Anthostomella sensu stricto*. Phylogenetic analyses of ITS, LSU, *rpb2*, *tub2*, and *tef1* sequence data by Samarakoon et al. (2022) placed anthostomella-like taxa within the order *Xylariales*, but in a clade distinct from *Xylariaceae*. Although there are over 300 epithets under *Anthostomella* in Species Fungorum (April 2026), many of them have been transferred to other genera.

Approximately 100 species are currently accepted (Hyde et al. 2024a), known to occur as saprobes, endophytes, or pathogens (Iacovelli et al. 2024). Nine species are listed as marine fungi, and *Anthostomella* has also been reported from salt marsh hosts, with over ten records, including *A. atroalba*, *A. lugubris*, *A. phaeosticta*, *A. poecila*, *A. punctulata*, *A. semitecta*, *A. spissitecta*, and *A. torosa* (Jones et al. 2019; Calabon et al. 2021b). Future studies are needed to obtain fresh collections, sequence more species, and confirm the accurate placement and type designation of the genus. A few studies have explored the metabolite production of *Anthostomella*; for instance, Iacovelli et al. (2024) investigated *A. pinea* and revealed a rich secondary metabolism, particularly sesquiterpenoids and sesquiterpene lactones, with notable anti-Gram-positive activity.

Type species: *Anthostomella limitata* Sacc. 1875

Other accepted species: Species Fungorum (search *Anthostomella*)



Note a Ascoma. b Ascus. c, d Ascospores. Scale bars: a = 50 µm, b–d = 10 µm

Source Daranagama et al. (2015)

Figure 4.174 *Anthostomella forlicesenica*

Circinotrichum Nees 1816

Classification: *Coniocessiaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Circinotrichum, introduced by Nees von Esenbeck (1817), comprises approximately 16 species, most of which are saprobic on plant material, particularly decaying leaves (Hyde et al. 2024a). *Circinotrichum maculiforme* is the only species in

Circinotrichum recorded from salt marsh habitats, found on *Juncus roemerianus* (Calabon et al. 2021b). The genus is typified by *C. maculiforme* and is characterized by a hyphomycetous asexual morph, producing unbranched, circinate, or flexuous setae, with conidiogenous cells aggregating around the bases of the setae. Morphologically, *Circinotrichum* is similar to *Gyrothrix*; however, the latter differs by having branched setae, whereas *Circinotrichum* has simple setae. The two genera are also phylogenetically distinct (Hernández-Restrepo et al. 2022). A recently introduced species, *C. podocarpi*, was described based on morphological characteristics and phylogenetic analysis using combined ITS, LSU, and *rpb2* sequences (Tian et al. 2024). *Circinotrichum* was previously classified as *Xylariales* genera *incertae sedis* but was later transferred to the newly established family *Coniooeciaceae* by Asgari & Zare (2011).

Type species: *Circinotrichum maculiforme* Nees 1816

Other accepted species: Species Fungorum (search *Circinotrichum*)



Note Conidiogenous cells and conidia. Scale bar 10 μ m

Source Redrawn from Hernández-Restrepo et al. (2022)

Figure 4.175 *Circinotrichum maculiforme*

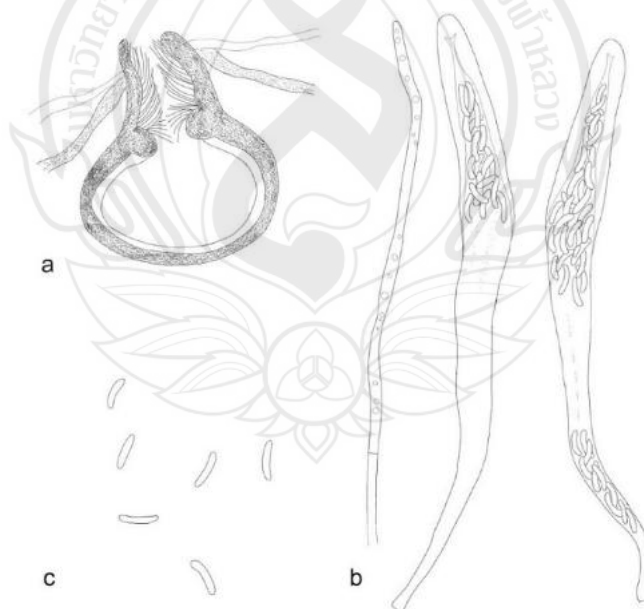
Cryptovalsa Ces. & De Not. ex Fuckel 1870

Classification: *Diatrypaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cryptovalsa was introduced to accommodate four species: *C. protracta*, *C. ampelina*, *C. nitschkei*, and *C. effusa* (Fuckel 1870). According to Index Fungorum (March 2025), there are 71 epithets associated with *Cryptovalsa*, many of which have been transferred to other genera, including *Halocryptovalsa*, *Annulohypoxylon*, *Diatrypella*, *Allocryptovalsa*, and *Cryptovalsaria*. Currently, *Cryptovalsa* comprises approximately 25 accepted species (Hyde et al. 2024a). *Cryptovalsa suaedicola* was introduced based on a collection from twigs of *Suaeda fruticosa*, found among lichens in a salt marsh habitat (Spooner 1981; Calabon et al. 2021b). In addition to *Cryptovalsa suaedicola*, *C. halosarceicola* and *C. mangrovei* are also considered marine fungi (Jones et al. 2019). Besides their saprobic lifestyle, some *Cryptovalsa* species are known pathogens, such as *C. ampelina*, which is associated with grapevine disease (Díaz et al. 2011). Morphologically, *Cryptovalsa* species produce effuse stromata containing one or multiple ostiolate perithecia. The asci are polysporous, with crowded, allantoid, and yellowish ascospores (Spooner 1981; Hyde et al. 2020c).

Type species: *Cryptovalsa protracta* (Pers.) De Not. 1863

Other accepted species: Species Fungorum (search *Cryptovalsa*)



Note a Diagrammatic vertical section (120×). b Asci and paraphyses (1200×). c Ascospores (1200×)

Source Redrawn from Spooner (1981)

Figure 4.176 *Cryptovalsa suaedicola*

***Halocryptovalsa* Dayar. & K.D. Hyde 2020**

Classification: *Diatrypaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Dayarathne et al. (2020b) introduced *Halocryptovalsa* to accommodate two marine species, *H. avicenniae* (= *Cryptovalsa avicenniae*) and *H. salicorniae*. The type species *H. avicenniae* was isolated from a decaying mangrove tree, *Avicennia marina*, in Saudi Arabia, and *H. salicorniae* was collected from the salt marsh host *Salicornia* sp. in Thailand (Dayarathne et al. 2020b; Calabon et al. 2021b). In addition to these two saprobic species, a third species, *H. endophytica*, was collected as an endophyte in the roots of the salt marsh plant *Salicornia patula* in Spain (Crous et al. 2023b). Poorly developed stromata with long ascomatal necks and being deeply immersed in the host tissue are distinct characters of *Halocryptovalsa*. Asci are cylindrical and poly-spored, with hyaline or yellowish-brown to brown allantoid spores (Dayarathne et al. 2020b). Sequence data of LSU, ITS, SSU, and *btub* are available for the genus in GenBank.

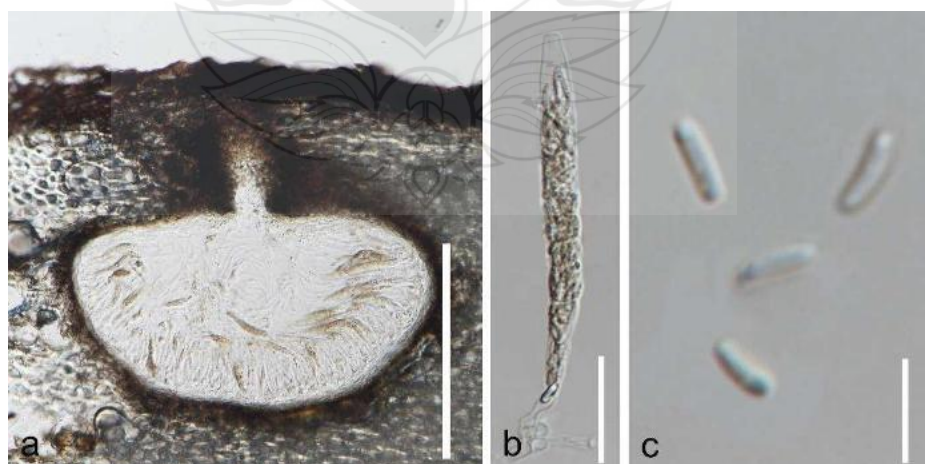
Type species: *Halocryptovalsa avicenniae* (Abdel-Wahab, Bahkali & E.B.G. Jones) Dayar. & K.D. Hyde 2020

Basionym: *Cryptovalsa avicenniae* Abdel-Wahab, Bahkali & E.B.G. Jones, in Abdel-Wahab et al., (2017)

Other accepted species:

Halocryptovalsa endophytica G. Delgado, T. Nau & Maciá-Vicente 2023

Halocryptovalsa salicorniae Dayar. & K.D. Hyde 2020



Note a Ascoma. b Ascus. c Ascospores. Scale bars: a = 150 μ m, b = 20 μ m, c = 5 μ m

Figure 4.177 *Halocryptovalsa* sp.

***Virgaria* Nees 1816**

Classification: *Xylariaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Nees (1817) established *Virgaria* to accommodate its type species, *Virgaria nigra*, which was previously classified in *Botrytis*. *Virgaria* is characterized by a geniculosporium-like asexual morph and has been linked to *Ascovirgaria* as its sexual morph (Réblová et al. 2016). The sexual morph has stromatic ascomata with cylindrical asci that have long pedicels and a J+ apical ring, containing aseptate, ellipsoid, brown ascospores (Hyde et al. 2020). The use of *Virgaria* over *Ascovirgaria* has been recommended (Réblová et al. 2016). According to the latest outline of fungi and fungus-like taxa, *Virgaria* comprises three species, though only two have available sequence data (Hyde et al. 2020c; Hyde et al. 2024a). The genus was confirmed to belong to *Xylariaceae* (Nonaka et al. 2013; Hyde et al. 2020c). However, Zhang et al. (2024) introduced a new asexual species, *V. palmae*, isolated from a dead palm branch, based on morphology and phylogeny. Their phylogenetic analysis, using combined LSU, SSU, *tef1*, and *rpb2* sequence data, revealed that *Virgaria* did not group within *Xylariaceae sensu stricto*. There is one record of the genus from salt marsh plants: *V. nigra*, which was found as a saprobe on *Juncus roemerianus* (Calabon et al. 2021b).

Type species: *Virgaria nigra* (Link) Nees

Basionym: *Botrytis nigra* Link 1809

Other accepted species:

Virgaria boninensis Nonaka & Masuma 2013

Virgaria cardiospora Bres. 1896

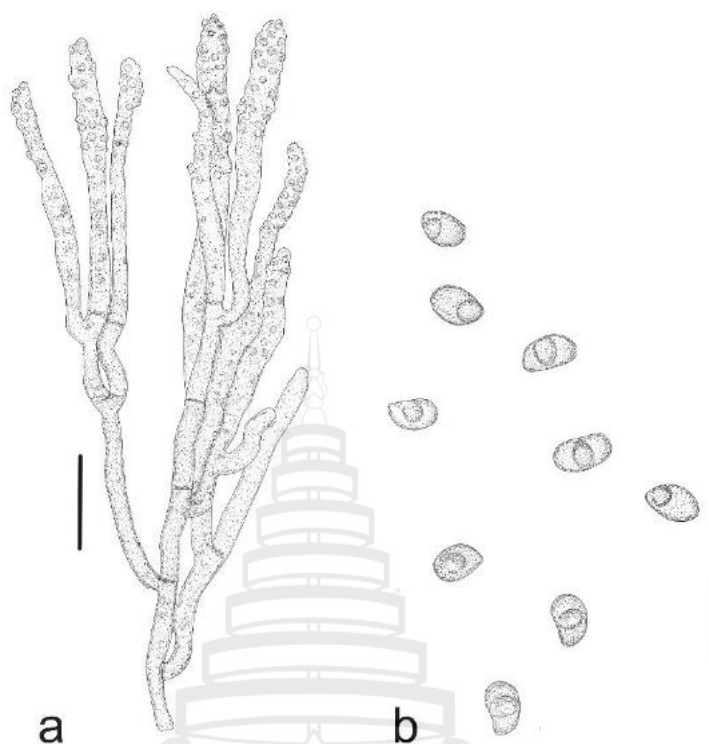
Virgaria coffeospora Sacc., E. Bommer & M. Rousseau 1884

Virgaria guizhouensis J. Ma, K.D. Hyde & Y.Z. Lu 2025

Virgaria lignatilis (Schwein.) S. Hughes 1953

Virgaria macrospora P. Karst. 1888

Virgaria palmae S.N. Zhang, K.D. Hyde & Jian K. Liu 2024



Note a Conidiophores. b Conidia. Scale bar: a = 10 μ m, b = 5 μ m

Source Redrawn from Prasher and Verma (2016)

Figure 4.178 *Virgaria nigra*

Zygosporium Mont. 1842

Classification: *Zygosporiaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

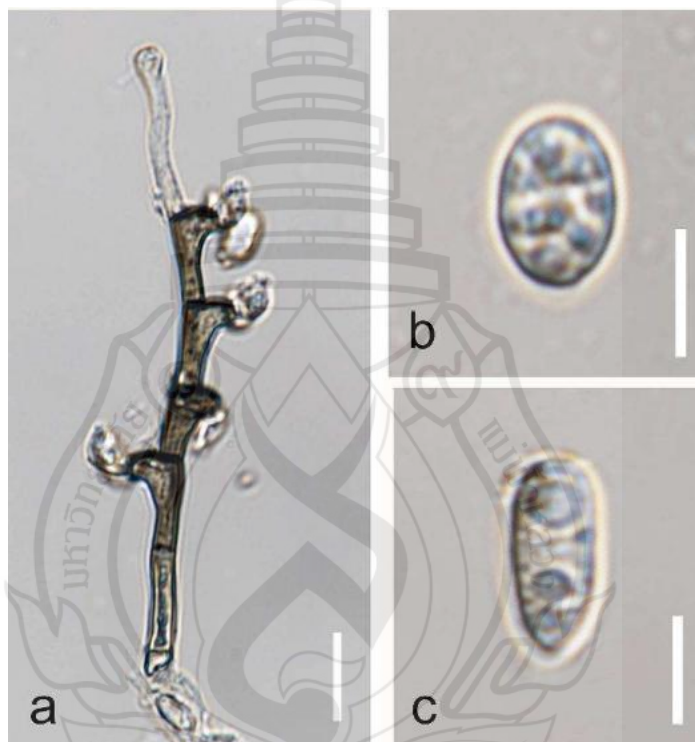
Zygosporium is a saprobe genus in Sordariomycetes, described by Montagne (1842) to accommodate *Z. oscheoides*. Li et al. (2017) classified *Zygosporium* under the novel family Zygosporiaceae (Xylariales) based on phylogenetic results from combined LSU and ITS sequence data. *Zygosporium* species are hyphomycetous, mainly reported from temperate to tropical regions (Photita et al. 2001; McKenzie et al. 2007; Taheriyani et al. 2014). There are accepted species listed in Species Fungorum (2026), collected from various hosts (Hyde et al. 2020c). *Zygosporium gibbum* and *Z. masonii* were reported from salt marsh habitats on decaying leaves of *Juncus roemerianus* in Florida (Fell and Hunter 1979). *Zygosporium* species can produce

biologically active secondary metabolites, e.g. *Z. masonii* is a producer of cytochalasins (Hayakawa et al. 1968).

The genus is characterized by dark colonies, unbranched, septate conidiophores with swollen dark brown vesicles, bearing conidiogenous cells developing in groups of two to four cells. Conidia are globose or ellipsoidal, with a smooth or ornamented wall (Li et al. 2017; Hyde et al. 2020c).

Type species: *Zygosporium oscheoides* Mont. 1842

Other accepted species: Species Fungorum (search *Zygosporium*)



Note a Conidiophores, conidiogenous cells and conidia. b, c Conidia. Scale bars: a = 20 µm, b, c = 10 µm

Figure 4.179 *Zygosporium masonii*

Lautospora K. D. Hyde & E.B.G. Jones 1989

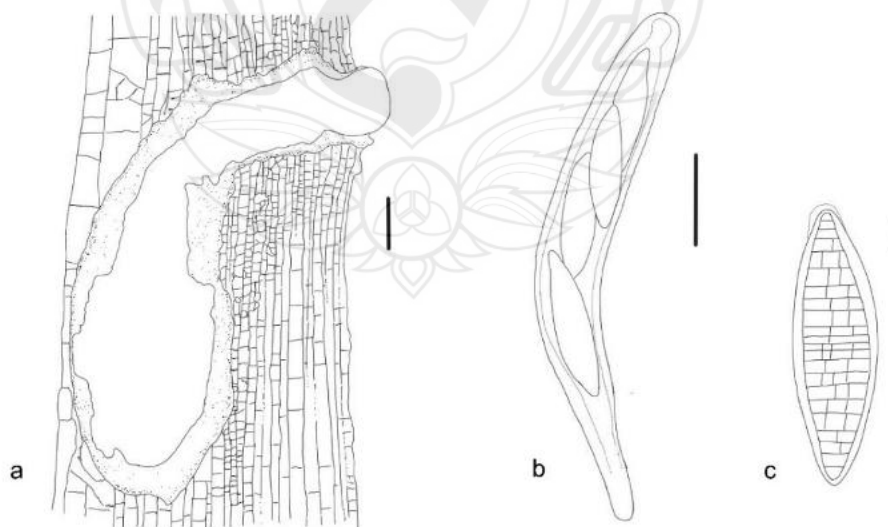
Classification: *Lautosporaceae*, *Incertae sedis*, *Incertae sedis*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Hyde and Jones (1989) introduced *Lautospora*, to accommodate *L. gigantea*, a novel saprobic species from decaying intertidal mangrove sediments. The genus develops immersed ascomata in the host tissue with cellular and hyaline paraphyses.

Asci are unitunicate with a thick wall, initially considered bitunicate by Hyde and Jones (1989). The asci have an ocular chamber and an apical ring containing four large, hyaline, and muriform ascospores with a very thick wall (Hyde and Jones 1989; Hyde et al. 2020c). Initially, *Lautospora* was placed in *Pleosporales*, as suggested by Hyde and Jones (1989). Subsequently, Kohlmeyer et al. (1995a) introduced a new species, *L. simillima*, isolated from a halophyte plant *Juncus roemerianus*, and established a new family, *Lautosporaceae*, to accommodate the genus. The family was not allocated to a specific order because of insufficient molecular data, and the genus was referred to *Ascomycotina incertae sedis* (Kohlmeyer et al. 1995a). Considering the thick ascus wall, Jones et al. (2009) categorized the family within *Dothideomycetidae incertae sedis*. It was subsequently excluded from class *Dothideomycetes* by Hyde et al. (2013). Analysis of LSU sequence data (Suetrong, unpublished data) placed *L. simillima* within an unnamed clade in *Sordariomycetes*, positioned as a basal clade to *Diaporthales* (Jones et al. 2015, [www/marinefungi.org](http://www.marinefungi.org)). Additional taxon sampling and molecular data are needed to confirm the phylogenetic placement of this genus (Hyde et al. 2020c).

Type species: *Lautospora gigantea* K.D. Hyde & E.B.G. Jones 1989

Other accepted species: *Lautospora simillima* Kohlm., Volkm.-Kohlm. & O.E. Erikss. 1995



Note a Ascoma. b Ascus. c Ascospore. Scale bars: a, b = 100 µm, c = 20 µm

Source Redrawn from Kohlmeyer et al. (1995a)

Figure 4.180 *Lautospora simillima*

Psammia Sacc. & M. Rousseau ex E. Bommer & M. Rousseau 1890

Classification: *incertae sedis*, *incertae sedis*, *incertae sedis*, *incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Psammia is a genus in *Ascomycota* without a defined family, order, or class. It was introduced by Bommer and Rousseau (1890) and currently comprises 11 species (Hyde et al. 2024a). *Psammia* species can be lichenized or saprophytic and also can be found on lichens and algae, often on the dry surfaces of trees and stones (Earland-Bennett and Hawksworth 2005; Cáceres and Aptroot 2016; van Der Kolk et al. 2020). One unidentified species has been recorded as a saprobe from the salt marsh halophyte *Juncus roemerianus* (Calabon et al. 2021b). van Der Kolk et al. (2020) provided a key for *Psammia* species and introduced a new species collected from green algae and lichens. This species was pathogenic to its host, causing bleaching. *Psammia* species produce dark brown to black spots on their hosts and are characterized by their palm-like conidia, which may have more or fewer than 20 arms. The number and size of the arms, their septation, as well as the host and ecological habitat, are important characteristics for species identification in this genus (van Der Kolk et al. 2020).

Type species: *Psammia bommerae* Sacc. & M. Rousseau 1890

Other accepted species: Species Fungorum (search *Psammia*)



Note Conidium. Scale bar: 10 µm

Source Redrawn from Cáceres and Aptroot (2016)

Figure 4.181 *Psammia tropica*

Kluyveromyces Van der Walt 1956

Classification: *Saccharomycetaceae*, *Saccharomycetales*, *Saccharomycetidae*, *Saccharomycetes*, *Saccharomycotina*, *Ascomycota*, *Fungi*.

Kluyveromyces is a budding yeast introduced by Van der Walt (1956) as a new genus, which isolated from a sample soil of uncultivated earth. The genus characterized by oval to long oval cells which vegetative reproduction occurs through multilateral budding, and pseudomycelium formation may also be observed. Ascus formation is generally preceded by isogamous or heterogamous conjugation, although asci may also develop without an immediately preceding conjugation event with large asci contain multiple spores. A pellicle may develop in liquid media. Fermentation occurs, but nitrate is not assimilated (Van der Walt 1956). There are eight species in this genus listed in Species Fungorum (accessed on 14 June 2025). Jones et al. (2019) listed three species of *Kluyveromyces* as marine fungi, including *K. aestuarii*, *K. marxianus*, and *K. nonfermentans*. *Kluyveromyces lactis* has also been reported from salt marsh on *Spartina alterniflora* (Calabon et al. 2021b). Sequence data are currently available for *K. aestuarii*, *K. dobzhanskii*, *K. marxianus*, *K. nonfermentans*, *K. lactis*, and *K. starmeri*. Members of this genus play a significant role in the biotechnology industry due to the enzymes and other biomolecules they produce, as well as their capacity to serve as hosts for the expression of recombinant enzymes (Batt 2014).

Type species: *Kluyveromyces marxianus* (E.C. Hansen) Van der Walt 1971

Other accepted species:

Kluyveromyces aestuarii (Fell) Van der Walt 1965

Kluyveromyces dobzhanskii (Shehata, Mrak & Phaff) Van der Walt 1971

Kluyveromyces hubeiensis M.X. Li, X.H. Fu & R.G. Tang 1992

Kluyveromyces lactis (Stell.-Dekk.) Van der Walt 1971

Kluyveromyces marxianus (E.C. Hansen) Van der Walt 1971

Kluyveromyces nonfermentans Nagah., Hamam., Nakase & Horikoshi 1999

Kluyveromyces shennongjiaensis Y.J. Qiu, H.Y. Zhu & F.Y. Bai 2025

Kluyveromyces starmeri A.O.S. Santos, Mafra, P.B. Morais, Lachance & C.A. Rosa 2020

Debaryomyces Lodder & Kreger-van Rij 1909

Classification: *Debaryomycetaceae*, *Serinales*, *Pichiomycetes*,
Saccharomycotina, *Ascomycota*, *Fungi*.

Debaryomyces was introduced by Lodder and Kreger-van Rij (Kreger-van Rij 1984) and typified by *D. hansenii*, which formerly belonged to *Saccharomyces*. The sexual morph is characterized by the formation of asci through conjugation, either between a mother cell and its bud or between separate cells. Ascospores are globose, ovoid, or lenticular in shape, with smooth, warty, or occasionally spirally ridged walls. They generally remain enclosed within the ascus, except in *D. udonii*. Typically, one to two ascospores are produced per ascus, though some species may form up to four. Asexual reproduction occurs through cell division by multilateral budding, and pseudohyphae may be absent or present but are usually poorly developed. Currently, 19 species are listed in this genus (Species Fungorum, accessed on 15 June 2025). Jones et al. (2019) listed two species of *Debaryomyces* as marine fungi, including *D. nepalensis* and *D. hansenii*. *Debaryomyces hansenii* has also been reported from salt marshes as a saprobe on decaying leaf blades of *Spartina alterniflora* (Calabon et al. 2021b). *Debaryomyces* species, especially *D. hansenii*, has significant biotechnological potential across a wide range of applications (Breuer and Harms 2006). *Debaryomyces hansenii* is particularly efficient at producing xylitol from D-xylose in wood hydrolysates, yielding high xylitol-to-ethanol ratios (Breuer and Harms 2006). This trait is especially valuable for biomass conversion, where one of the main challenges is the efficient bioconversion of pentose sugars to ethanol (Hahn-Hägerdahl et al. 2007).

Type species: *Debaryomyces hansenii* (Zopf) Lodder and Kreger-van Rij 1984

Basionym: *Saccharomyces hansenii* Zopf 1889

Other accepted species: Species Fungorum (search *Debaryomyces*)

Scheffersomyces Kurtzman & M. Suzuki 2010

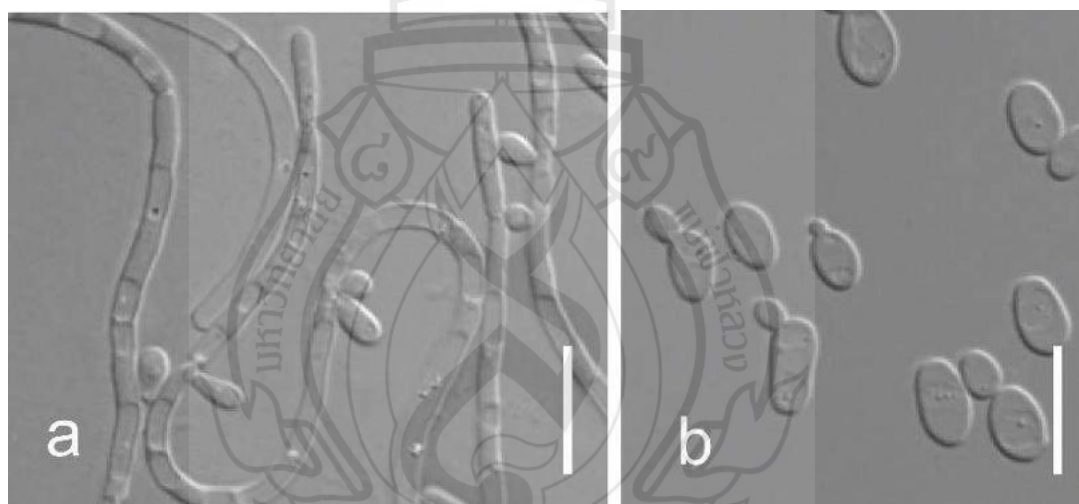
Classification: *Debaryomycetaceae*, *Serinales*, *Pichiomycetes*, *Saccharomycotina*, *Ascomycota*, *Fungi*.

Scheffersomyces was established by Kurtzman and Suzuki (2010), with *S. stipitis* as the type species, to accommodate D-xylose-fermenting species in the *Pichia stipitis* clade (viz., *P. segobiensis*, *P. spartinae*, and *P. stipitis*), based on combined phylogenetic analyses of LSU (D1/D2) and SSU sequences. Subsequently, the genus was expanded with the discovery of new species on rotting wood and wood-ingesting insects (Urbina and Blackwell 2012; Suh et al. 2013; Urbina et al. 2013; Liu et al. 2016).

The genus is characterized by evanescent conjugate asci containing 1–4 petal-shaped ascospores. Vegetative cells are either globose or elongated. Pseudohyphae are formed, while true septate hyphae are absent. D-xylose (variably) and other sugars are fermented. The coenzyme Q-9 system is present. There is no reaction with diazonium blue B (Kurtzman and Suzuki 2010). Currently, 24 species are accepted in this genus (Species Fungorum, April 2026). Jones et al. (2019) listed *Scheffersomyces spartinae* as marine fungi. *Scheffersomyces spartinae* has also been reported from salt marshes as a saprobe on decaying leaf blades of *Spartina alterniflora* (Calabon et al. 2021b). Sequence data are available for all species, and combined phylogenetic analysis (ITS, LSU) shows that the genus *Candida* is closely related to this genus (Jia et al. 2020).

Type species: *Scheffersomyces stipitis* (Pignal) Kurtzman & M. Suzuki 2010

Other accepted species: Species Fungorum (search *Scheffersomyces*)



Note a Pseudohyphae. b Budding cells. Scale bars: 10 μm

Source Jia et al. (2020)

Figure 4.182 *Scheffersomyces jinghongensi*

Asteromyces Moreau & M. Moreau ex Hennebert 1962

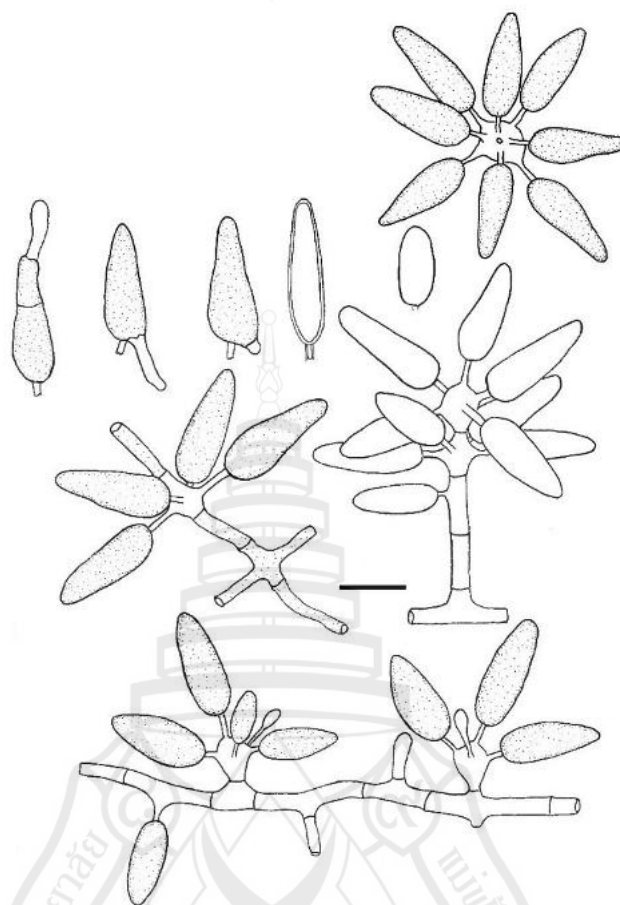
Classification: *Pleosporaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Asteromyces, with a single species, *A. cruciatus*, is a marine hyphomycete isolated from soil of sand dunes in association with halophytes such as *Agropyron* sp., *Ammophila arenaria*, *Spartina* sp., and *Zostera* sp. (Hennebert, 1962; Calabon et al.

2021b). The genus and species were first described and illustrated by Moreau and Moreau (1941), but they did not designate any type material, and their description lacked a Latin diagnosis, which was required at the time for formal validation. Later, Hennebert in 1962, designated a dried culture as the type and provided a Latin diagnosis for both the genus and species, thereby formally introducing them. Torres-Garcia et al. (2022) placed *A. cruciatus* in the *Pleosporaceae* based on a phylogenetic analysis of five gene markers (ITS, LSU, *gapdh*, *rpb2*, and *tef1*). *Asteromyces* is characterized by hyaline, septate, and branched hyphae. Conidiogenous cells arise singly and laterally, initially hyaline and narrow, becoming globose as conidia develop. The conidia, which form on long denticles are ovoid to pyriform, dark brown, thin-walled, and produced apically or laterally (Hennebert 1962). *Asteromyces* is similar to *Wardomyces* but differs in several key aspects. *Asteromyces* has unbranched conidiophores, conidiogenous cells that swell due to the successive development of conidia, it forms long denticles, has a different conidial arrangement, and lacks a germ slit (Hennebert 1962). Jones and Ward (1973) noted that conidia of *A. cruciatus* became septate when grown at high salinity and different light intensity. Conidia become 1-6 septate when subjected to black light (fluorescent lamp with a continuous spectrum maximum at 360 nm, 18 in. above plates), depending on the growth media (Jones and Ward 1973). It can tolerate concentrations of up to 2.0 M NaCl in liquid media (Jones and Jennings 1965), with tolerance increased to 2.5 M NaCl with the addition of 0.05 M CaCl₂.

Type species: *Asteromyces cruciatus* Moreau & M. Moreau ex Hennebert 1962

Other accepted species: None.



Note Hyphae, conidiophores, and conidia. Scale bar = 10 μ m

Source Redrawn from Hennebert (1962)

Figure 4.183 *Asteromyces cruciatus*

Cytoplacosphaeria Petr. 1920

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Cytoplacosphaeria was established by Petrak (1919) and typified by *C. rimosa*, which was isolated from senescent *Phragmites communis*. *Cytoplacosphaeria rimosa* has also been reported on *Phragmites australis* and *Phragmites* sp. in Latvia, Czechoslovakia, and England (Sutton 1980, Poon and Hyde 1998). The genus is known for its asexual coelomycetous form, characterized by scattered, immersed stromata with a black to brown peridium containing hyaline inner layers, typically with one, and rarely with 2-3 cavities. The conidiogenous cells, which bear a collarete, produce cylindrical or narrowly elongated, hyaline, septate, guttulate spores that are straight or curved.

Poon and Hyde (1998) introduced a second species, *C. phragmiticola*, which was isolated from *P. australis* in marshes in Hong Kong. This species shares similar morphology with the type species, featuring immersed stromatic conidiomata with dark outer layers and paler inner layers. The conidiophores are reduced to enteroblastic, phialidic, ampulliform to doliiform conidiogenous cells with apical or lateral apertures and collarettes. The conidia are straight, curved, or irregular, with 0–5 septa. However, *C. rimosa* has distinct collarette and shorter guttulate conidia (Poon and Hyde 1998). There are two species listed in Index Fungorum (accessed August 2024) without available sequence data. Fresh material and molecular data are needed to confirm the classification of this marine genus (Jones et al. 2019).

Type species: *Cytoplacosphaeria rimosa* (Oudem.) Petr. 1920

Basionym: *Placosphaeria rimosa* Oudem. 1889

Other accepted species: *Cytoplacosphaeria phragmiticola* Poon & K.D. Hyde 1998



Note a Conidioma. b Conidiogenous cells and developing conidia. c Conidia. Scale bars: a = 100 μ m, b, c = 10 μ m

Source Redrawn from Sutton (1980)

Figure 4.184 *Cytoplacosphaeria rimosa*

Haplobasidium Erikss. 1889

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Haplobasidion is an ascomycetous genus with an uncertain taxonomic placement (Wijayawardene et al. 2022). The genus was established by Eriksson in 1889 based on *H. thalictri*, which was isolated from living leaves of *Thalictrum flavum* in Sweden. According to Species Fungorum (April 2026), there are five species accepted. *Haplobasidion lelebae* was reported as a saprobe on *Juncus roemerianus* in the United Kingdom (Fell and Hunter 1979; Calabon et al. 2021b). This hyphomycetous species is characterized by solitary or small groups of structures emerging from the host epidermis and cuticle, with septate, brown hyphae that have a swollen apical cell. The conidiogenous cells are hyaline and smooth, becoming brown and verruculose. The conidia are simple or form in branched chains, and are brown and verruculose (Ellis 1957).

Type species: *Haplobasidion thalictri* Erikss. 1889

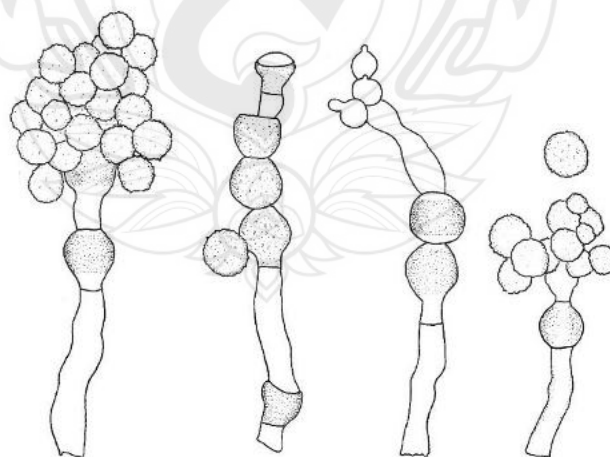
Other accepted species:

Haplobasidion himalayense J.N. Kapoor & Munjal 1968

Haplobasidion indicum V.G. Rao & D. Rao 1970

Haplobasidion lelebae Sawada ex M.B. Ellis 1957

Haplobasidion musae M.B. Ellis 1957



Note Conidiogenous cells and conidia (500×)

Source Redrawn from Ellis (1957)

Figure 4.185 *Haplobasidion lelebae*

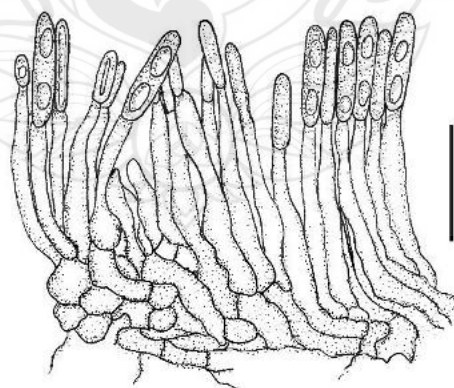
***Hymenopsis* Sacc. 1886**

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Hymenopsis is a coelomycetous saprobic genus typified by *H. trochiloides* (Kohlmeyer and Volkmann-Kohlmeyer 2001). The genus has been isolated from dead plant material from various hosts, mostly herbaceous plants (Index Fungorum 2024). Kohlmeyer and Volkmann-Kohlmeyer (2001) introduced a novel species, *Hymenopsis chlorothrix*, from *Juncus roemerianus* in USA. The species was collected 16–43 cm above the rhizome and thus classified as an obligate marine fungus. *Hymenopsis chlorothrix* has acervular conidiomata, which are initially immersed and become superficial with maturity. When dry, the conidiomata appear black, and when wet, they turn dark green, sometimes with or without setae. When setae are present, they are usually in small numbers, straight or slightly curved, mostly 1-septate, thick-walled, greenish, bulbous at the base, with a lightly colored tapered apex. Conidiophores are hyaline and cylindrical with 1–2 cells. Conidiogenous cells are hyaline, greenish at the apex, cylindrical. Conidia are elongate ellipsoidal or cylindrical, aseptate, green, smooth, and guttulate (Kohlmeyer and Volkmann-Kohlmeyer 2001b). Only one ITS sequence data is available for the genus in GenBank.

Type species: *Hymenopsis trochiloides* (Sacc.) Sacc. 1886

Other accepted species: Species Fungorum (search *Hymenopsis*)



Note Conidiophores and conidia. Scale Bars = 10 µm

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (2001b)

Figure 4.186 *Hymenopsis chlorothrix*

Hyphopolynema Nag Raj 1977

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Hyphopolynema was introduced by Raj (1977), with *H. tropicale* as the type species, collected from fruits of *Inga spectabilis* in Colombia. The genus was described based on its asexual morph, characterised by effuse, waxy, ivory-white colonies; superficial sporodochia often arising from immersed mycelium aggregated into pseudostromata within ruptured host tissue; and branched, septate, subhyaline to pale brown conidiophores. Phialides are clavate, subhyaline, and arranged in a compact hymenium. Conidia are solitary, terminal, unicellular or 1–2-septate, hyaline, and bear apical and basal appendages that are simple or rarely branched and flexuous (Raj 1977). Morphologically, *Hyphopolynema* resembles *Thozetella* in conidiophore structure, mode of proliferation, and conidial ontogeny; however, it differs by lacking synnemata and microawns, and by exhibiting distinct conidial morphology. The genus currently comprises six accepted species (Species Fungorum, April 2026). *Hyphopolynema juncatil* has been reported from salt marshes as a saprobe on senescent leaves of *Juncus roemerianus* (Calabon et al. 2021b).

Type species: *Hyphopolynema tropicale* Nag Raj 1977

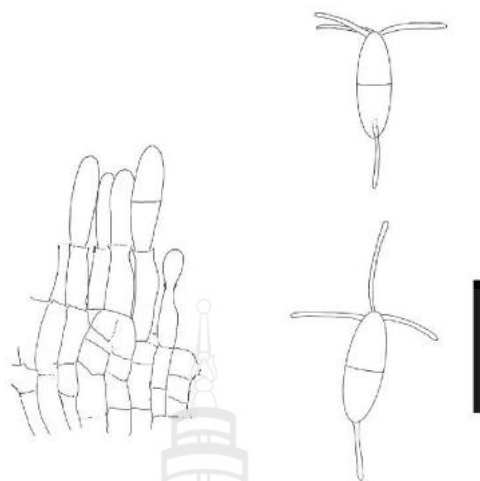
Other accepted species: *Hyphopolynema australe* B. Sutton & Alcorn 1948

Hyphopolynema ellisiorum B. Sutton & Alcorn 1984

Hyphopolynema ingae Pinho & O.L. Pereira 2011

Hyphopolynema juncatile Kohlm. & Volkm.-Kohlm 1999

Hyphopolynema stilboideum Bhat & W.B. Kendr 1993



Note Conidiogenous cells and conidia. Scale bars: 20 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (1999)

Figure 4.187 *Hyphopolynema juncatile*

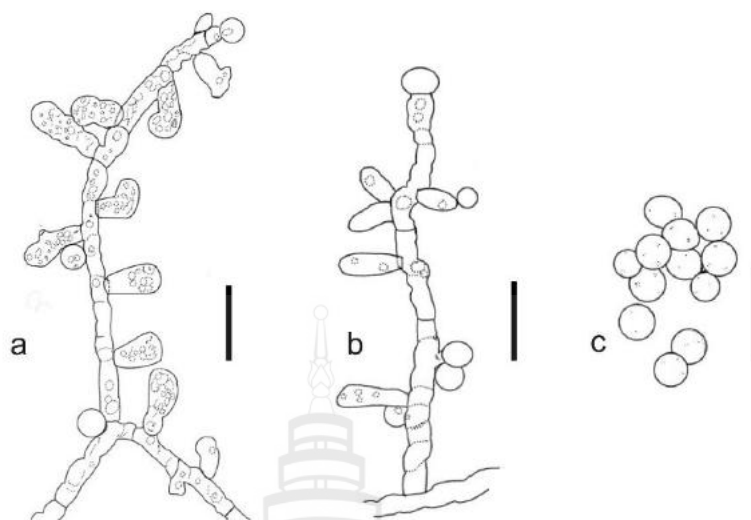
Kolletes Kohlm. & Volkm.-Kohlm. 2005

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Kolletes was described from *Juncus roemerianus*, forming cottony and pulvinate hyphomycetous colonies on dead leaves (Kohlmeyer et al. 2005, Calabon et al. 2021b). Fungal colonies are easily found on completely discolored dead host leaves and culms, which are often bent or broken by storms and rain (Kohlmeyer et al. 2005). The colonies may fuse leaves of the same plants or adjoining vegetation together. Conidiophores are reduced to ellipsoidal to clavate conidiogenous cells. Conidia are aseptate, hyaline to light brown with a scar, developing on small denticles on hypha. The type species, *K. undulatus*, was considered a halotolerant terrestrial species as it has never been found on submerged parts of the host (Kohlmeyer et al. 2005).

Type species: *Kolletes undulatus* Kohlm. & Volkm.-Kohlm. 2005

Other accepted species: None



Note a Hyphae with club-shaped conidiogenous cells. b Developing conidia. c Conidia. Bars = 20 μ m

Source Redrawn from Kohlmeyer et al. (2005)

Figure 4.188 *Kolletes undulatus*

Neottiospora Desm. 1843

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Neottiospora was introduced based on a saprobic fungus collected on dead leaves of *Carex varia* in France (Desmazières 1843). The genus is coelomycetous and was initially characterized by appendaged conidia (Desmazières 1843). Later, Grove (1935) suggested that the appendage was mucoid. Subsequently, Subramanian and Ramakrishnan (1953) reexamined the type material nearly a century later and reported that the conidia have a single apical appendage, which is mucoid and evanescent, taking the form of an inverted hollow cone with thin, hyaline walls.

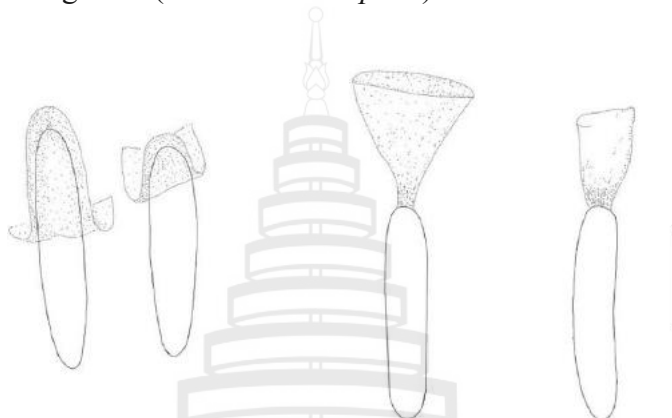
Currently, 12 species are accepted in *Neottiospora* in Species Fungorum (April 2026), several of which have been transferred to other genera such as *Libartania*, *Ciliochora*, *Allantophomopsis*, *Tiarosporella*, and *Alpakesa*. Eleven species are currently accepted in the genus, mostly described from dead leaves (Desmazières 1843; Sydow and Sydow 1912; Index Fungorum, June 2025). *Neottiospora* has not been recorded as a marine fungus (Jones et al. 2019); however, there is one report of an

unidentified *Neottiospora* species from the leaves of the salt marsh plant *Juncus roemerianus* in the USA (Calabon et al. 2021b). All species in the genus were described prior to 1960, and molecular sequence data are needed to clarify its taxonomy.

Type species: *Neottiospora caricum* Desm. 1843

Other accepted species:

Species Fungorum (search *Neottiospora*)



Note Ascospores. Scale bar = 10 μ m

Source Redrawn from Subramanian and Ramakrishnan (1953)

Figure 4.189 *Neottiospora* sp.

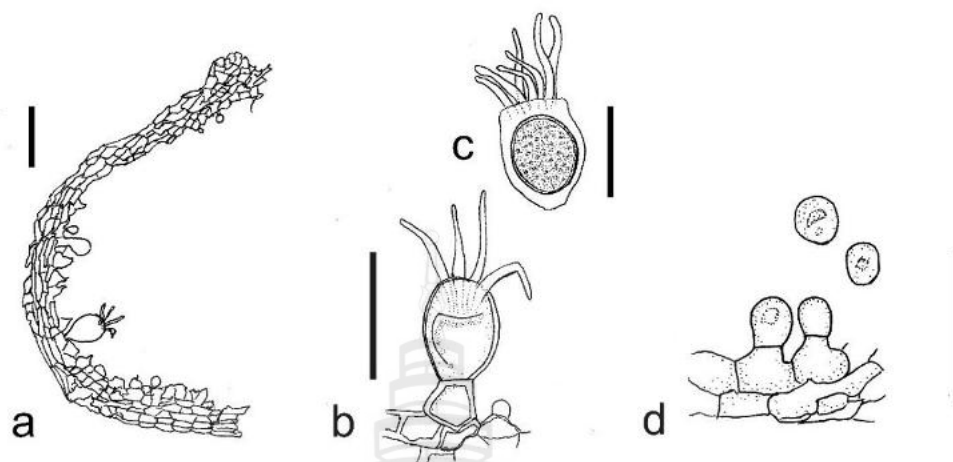
Octopodotus Kohlm. & Volkm.-Kohlm. 2003

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Octopodotus is a coelomycetous obligate marine genus introduced and typified by *O. stupendus* collected from decaying *Spartina alterniflora* in USA (Kohlmeyer and Volkmann-Kohlmeyer 2003; Calabon et al. 2021b). Pycnidia of *Octopodotus* are papillate, ostiolate, and brown with a *textura angularis* thin-walled peridium. Conidiophores are reduced to polygonal macroconidiogenous cells and microconidiogenous cells. Macroconidia are brown, aseptate, thick-walled, and verrucose with a gelatinous sheath and tentaculiform appendages. Microconidia are hyaline, aseptate, and have one oil globule, originating at the base of the ostiolar canal (Kohlmeyer and Volkmann-Kohlmeyer 2003). Needs to be recollected, and sequences to determine its taxonomic position.

Type species: *Octopodotus stupendus* Kohlm. & Volkm.-Kohlm. 2003

Other accepted species: None



Note a Sections through pycnidium. b Conidiogenous cell and developing conidium. c Mature conidium. d Section through peridium with two microconidiogenous cells and conidia. Scale bars: a = 25 μ m. b–d = 20 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (2003)

Figure 4.190 *Octopodotus stupendous*

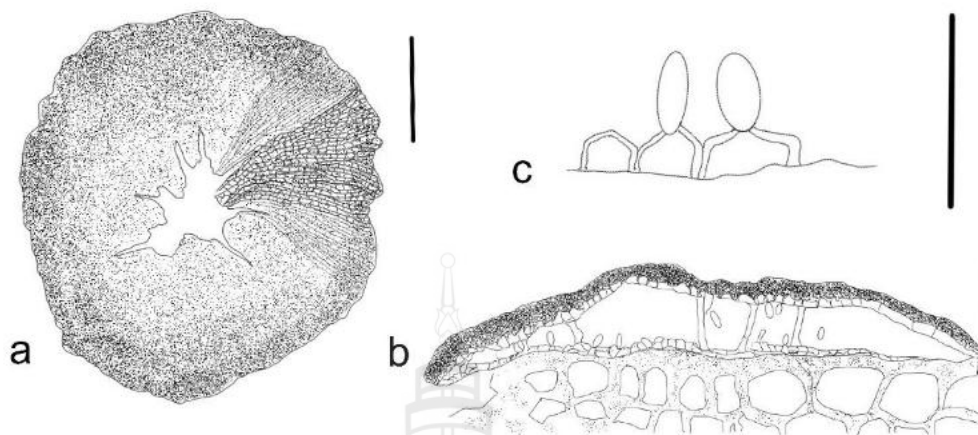
Pycnodallia Kohlm. & Volkm.-Kohlm. 2001

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Pycnodallia was described by Kohlmeyer and Volkmann-Kohlmeyer (2001b) and typified by *P. dupla*. *Pycnodallia* was isolated from needlerush, *Juncus roemerianus*, in USA (Kohlmeyer and Volkmann-Kohlmeyer 2001b; Calabon et al. 2021b). As *Pycnodallia* was found between 40 and 60 cm above the root, it was considered a facultative marine fungus. The genus is coelomycetous with shield-shaped conidiomata (pynothyria) which lack ostioles, opening instead through the development of radiating fissures at the center of the upper wall as they mature. The basal wall and the upper wall are connected with columns of short hyaline hyphae. Conidiophores are reduced to holoblastic conidiogenous cells with percurrent enteroblastic proliferation. Conidia are schizolytic with an ellipsoidal shape, aseptate, hyaline, and smooth-walled (Kohlmeyer and Volkmann-Kohlmeyer 2001b).

Type species: *Pycnodallia dupla* Kohlm. & Volkm.-Kohlm. 2001

Other accepted species: None



Note a Face view of upper wall. b Superficial conidioma. c Conidium attached to conidiogenous cell. Scale bar: a = 50 µm, b = 20 µm, c = 10 µm

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (2001b)

Figure 4.191 *Pycnodallia dupla*

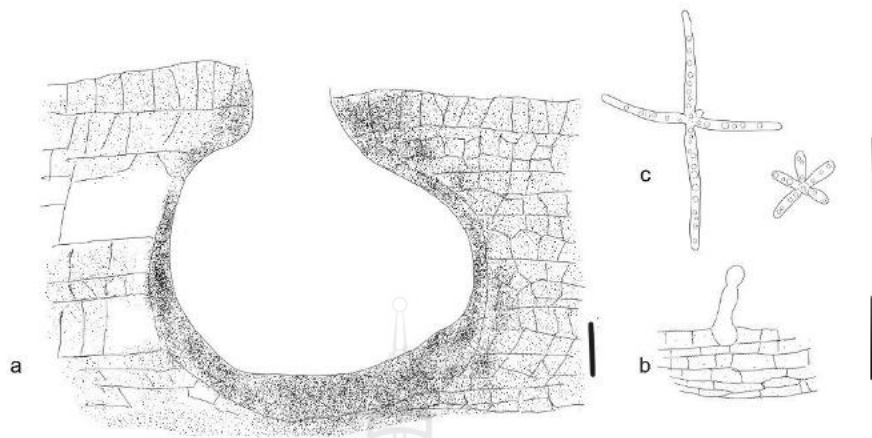
Tetranacriella Kohlm. & Volkm.-Kohlm. 2001

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Tetranacriella is a halotolerant terrestrial fungus isolated from dead leaves of *Juncus roemerianus* in USA (Kohlmeyer and Volkmann-Kohlmeyer 2001a, Calabon et al. 2021b). The genus is typified by *T. papillata*, which is the only species in the genus without available sequence data. *Tetranacriella* is coelomycetous, with ostiolate, papillate, subglobose to ellipsoidal pycnidia. Conidiomata are brown with a thin peridium. Conidiophores are reduced to discrete conidiogenous cells. Conidia are hyaline and star-shaped (staurosporous) with 4–5 filamentous, cylindrical arms radiating from a basal ellipsoidal cell. Arms taper toward the apex and are indistinctly septate (Kohlmeyer and Volkmann-Kohlmeyer 2001a).

Type species: *Tetranacriella papillata* Kohlm. & Volkm.-Kohlm. 2001

Other accepted species: None



Note a Conidioma. b Conidiogenous cell and developing conidium. c Conidia. Scale bars = 10 μ m

Source Redrawn from Kohlmeyer and Volkmann-Kohlmeyer (2001a)

Figure 4.192 *Tetranaeriella papillata*

Tetranaerium H.J. Huds. & B. Sutton 1964

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

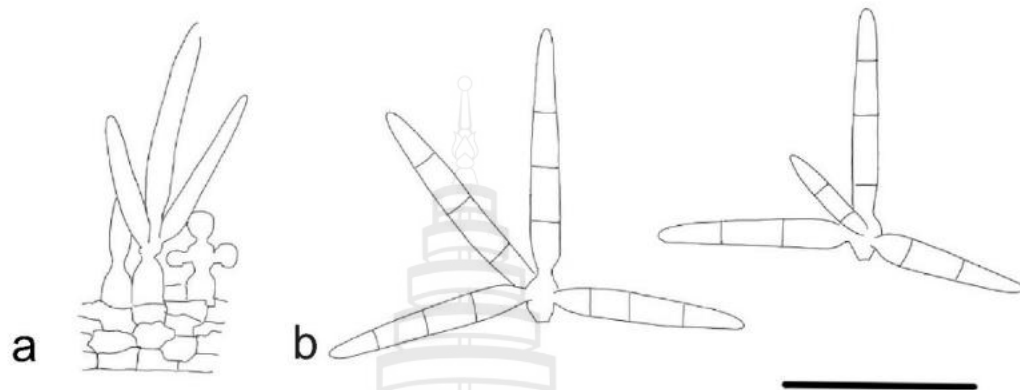
Tetranaerium was first introduced by Hudson and Sutton (1964) and later re-described and re-illustrated by Morgan-Jones et al. (1972e) and Sutton (1980). The genus was described based on its asexual morph (Coelomycetes). It is distinguished by having stromatic, pycnidial conidiomata that are blackish brown to black, occurring either solitarily or in groups, and lacking an ostiole. The conidiomatal wall is composed of thick-walled, dark brown cells forming a *textura angularis* structure on the exterior, gradually becoming pale brown to hyaline toward the hymenial layer. Conidiophores arise from the inner wall of the conidiomata. Conidiogenous cells are hyaline, holoblastic, and cylindrical to doliiform. The conidia are hyaline and tetradiate, consisting of a central vertical arm and three to four equidistant horizontal arms (Morgan-Jones et al. 1972; Sutton 1980). The genus currently comprises three accepted species (Species Fungorum, April 2025). *Tetranaerium* sp. has been reported from salt marshes as a saprobe on decaying stems and leaf sheaths of *Phragmites australis* (Calabon et al. 2021b). Currently, there are no available sequence records for this genus in NCBI, and its taxonomic placement remains uncertain (Hyde et al. 2024a).

Type species: *Tetranacrium gramineum* H.J. Huds. & B. Sutton 1964

Other accepted species:

Tetranacrium eugeniae Subhedar & V.G. Rao 1978

Tetranacrium malpighiacearum J.L. Bezerra & Poroca 1969



Note a Conidiogenous cells and conidia. b Conidia. Scale bar = 20 μ m

Source Redrawn from Hudson and Sutton (1964)

Figure 4.193 *Tetranacrium gramineum*

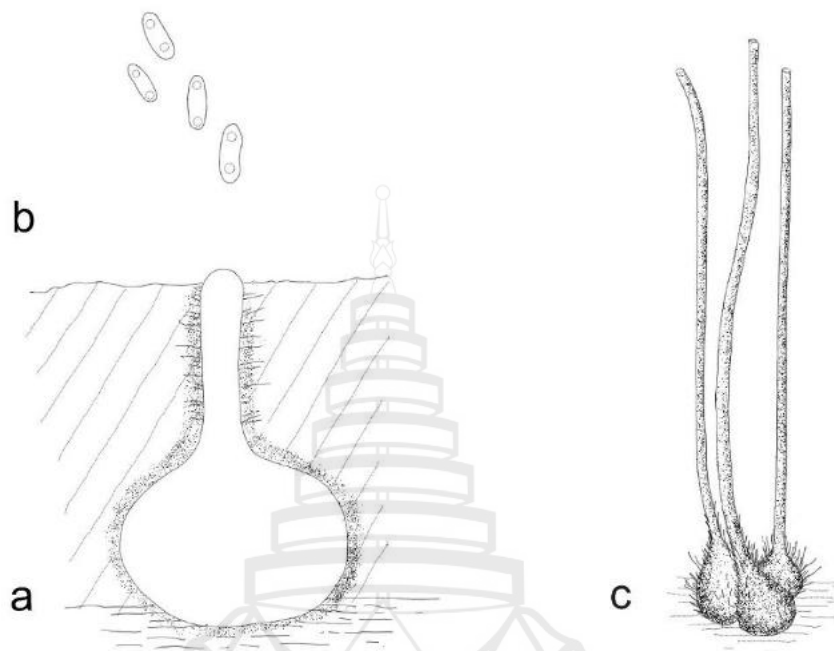
Sphaeronaema Fr. 1815

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Fries (1815) introduced the genus *Sphaeronaema*, including 15 species, without designating a type species. The species included in this genus were: *S. subulatum* (*Eleutheromyces subulatus*), *S. rufum* (*Dacryonaema rufum*), *S. aciculare* (*Sphaeronaemella acicularis*), *S. acrospermum*, *S. ventricosum* (*Caliciopsis ventricosa*), *S. cladoniscum*, *S. cylindricum*, *S. parabolicum*, *S. conicum*, *S. pyriforme* (*Rhamphoria pyriformis*), *S. truncatum*, *S. subtile*, *S. hemisphaericum*, *S. colliculosum*, and *S. pteridis*. Later, the genus was typified by *S. cylindricum*, but it has never been well studied (Rossman and Castlebury 2019). Currently, 113 species are accepted in this genus (Species Fungorum, April 2026). There is only one record of an unidentified species of this genus from salt marshes, reported as a saprobe on senescent leaves of *Juncus roemerianus*. (Calabon et al. 2021b). Currently, there are no available sequence records for this genus in NCBI, and its taxonomic placement remains uncertain, listed as *Ascomycota* genera *incertae sedis* (Hyde et al. 2024a).

Type species: *Sphaeronaema cylindricum* (Tode) Fr. 1815

Other accepted species: Species Fungorum (search *Sphaeronaema*)



Note *Sphaeronaema floccosum*. a Conidioma and ascospores. c Conidiomata of *S. comatum*

Source Redrawn from Grove (1935)

Figure 4.194 *Sphaeronaema floccosum* and *S. comatum*

Stauroinema (Sacc.) Syd., P. Syd. & E.J. Butler 1916

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Pezizomycotina*, *Ascomycota*, *Fungi*.

Dinemasporium subdiv. *Stauroinema* Sacc. was elevated to generic level as *Stauroinema*, characterized by cruciate-aristate spores (Sydow et al. 1916). The genus currently includes four saprobic species: *Stauroinema cruciferum*, collected on decaying culms and leaves of *Poaceae*; *S. platense*, on rotten culms of *Scirpus*; *S. sacchari*, on rotten culms of *Saccharum officinarum* (Sydow et al. 1916); and *S. indicum*, on dead culms of *Lawsonia alba* (Kalani 1964). All species were introduced before 1970, and no sequence data are currently available for them. *Stauroinema* belongs to the phylum *Ascomycota*, subphylum *Pezizomycotina*, but its lower taxonomic placement remains

unresolved (Hyde et al. 2024a). Therefore, fresh collections and molecular data are essential for clarifying its phylogenetic position. Additionally, one unidentified *Stauronema* species has been reported from the salt marsh plant *Phragmites australis* in Hong Kong, China (Calabon et al. 2021b).

Type species: *Stauronema cruciferum* (Ellis) Syd., P. Syd. & E.J. Butler 1916

Basionym: *Dinemasporium cruciferum* Ellis 1882

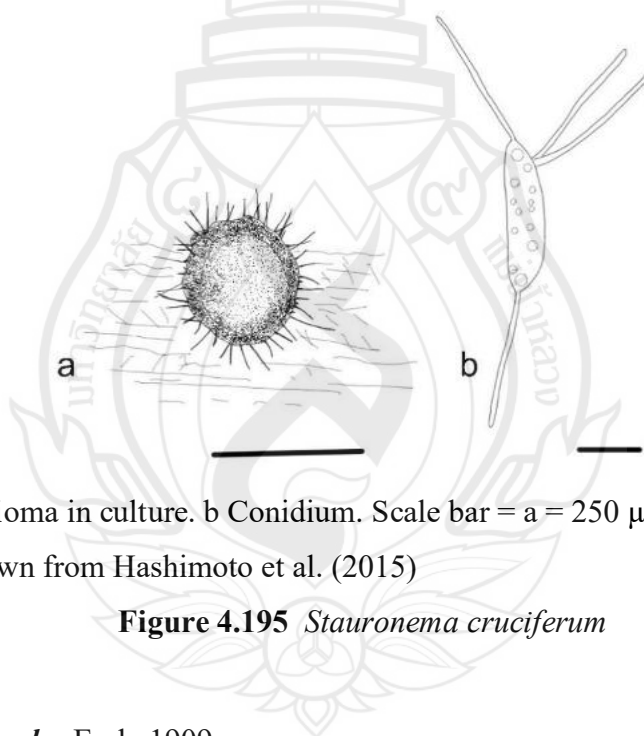
Other accepted species:

Stauronema indicum Kalani 1964

Stauronema platense (Speg.) Syd., P. Syd. & E.J. Butler 1916

Stauronema sacchari Syd., P. Syd. & E.J. Butler 1916

Stauronematopsis sojæ (Uecker & Kulik) Abbas, B. Sutton & Ghaffar 2002



Note a Conidioma in culture. b Conidium. Scale bar = a = 250 μ m, b= 5 μ m

Source Redrawn from Hashimoto et al. (2015)

Figure 4.195 *Stauronema cruciferum*

Merismodes Earle 1909

Classification: *Cyphellopsidaceae*, *Agaricales*, *Agaricomycetidae*, *Agaricomycetes*, *Agaricomycotina*, *Basidiomycota*, *Fungi*.

Merismodes was introduced by Earle in 1909 as a genus equal to *Cantharellus*, and was typified with *Cantharellus fasciculatus*, originally described in 1832 (Schweinitz 1832). Its current name is *Merismodes fasciculata*. *Merismodes* belongs to the phylum *Basidiomycota* and is characterized by cupulate to tubular basidiomata with yellow-brown to brown hairs. The basidiospores vary in shape, being subglobose,

ellipsoid, cylindrical, allantoid, or subfusiform (Silva-Filho et al. 2023). The genus comprises 12 species, mostly saprobic on dead plant material. The most recently described species are *M. yunnanensis* and *M. wumengshanensis*, introduced from China based on morphology and multigene phylogenetic analyses of combined ITS, nLSU, mtSSU, *rpb1*, *rpb2*, and *tef1* gene regions (Yang et al. 2025). There are no known records of this genus from marine habitats (Jones et al. 2019), and only a single report from a salt marsh ecosystem: *Merismodes bresadolae* on *Phragmites australis* in the Netherlands (Calabon et al. 2021b). Additionally, *Merismodes* has attracted interest for its production of natural compounds. For instance, *M. anomala* has been reported to produce strobilurins D and F, compounds with antifungal properties capable of inhibiting a range of fungal species (Sivanandhan et al. 2017).

Type species: *Merismodes fasciculata* (Schwein.) Donk, in Singer 1951

Other accepted species: Species Fungorum (search *Merismodes*)



Note Basidiomata and microscopic structures. Scale bars: a = 1 cm, b = 1 mm

Source Yang et al. (2025)

Figure 4.196 *Merismodes wumengshanensi*

Nia R.T. Moore & Meyers 1961

Classification: *Cyphellopsidaceae*, *Agaricales*, *Agaricomycetidae*, *Agaricomycetes*, *Agaricomycotina*, *Basidiomycota*, *Fungi*.

Moore and Meyers (1959) introduced the marine genus *Nia* to accommodate *Nia vibrissa*, which was collected from *Fagus sylvatica* wood submerged in seawater in Florida. This genus belongs to the *Basidiomycota* and is characterized by the formation of relatively large, orange basidiomata and globose to oval conidia with appendages (Moore and Meyers 1959). The basidiomycetous nature of *Nia vibrissa* was

indicated by the presence of clamp connections, as observed by Doguet (1967, 1968, 1969). The adaptation of *N. vibrissa* to the marine environment, as a basidiomycete, is associated with a reduction in basidiocarp size (Hibbett and Binder 2001; Jones et al. 2022). The genus includes seven saprobic species from marine environments. *Nia epidermoidea* was found on wet sand along the foreshore (Roselló et al. 1993), while *N. globispora* was described from a salt marsh host, *Spartina maritima* (Barata and Basilio 1997). *Nia lenicarpa* was introduced based on morphological and phylogenetic analyses (SSU and LSU sequences) of specimens collected from submerged intertidal wood of *Avicennia marina* in Saudi Arabia (Abdel-Wahab et al. 2019). Recently, Nakagiri et al. (2024) introduced three new species: *Nia furcatipilosa* and *N. sphaerocystis*, both isolated from sea foam samples, and *N. singaporensis*, collected from plant debris buried in maritime sand. In addition to *N. globispora*, *N. vibrissa* has also been reported from salt marsh hosts, particularly on species of *Spartina* (Calabon et al. 2021b).

Type species: *Nia vibrissa* R.T. Moore & Meyers 1961

Other accepted species:

Nia epidermoidea M.A. Roselló & Descals 1993

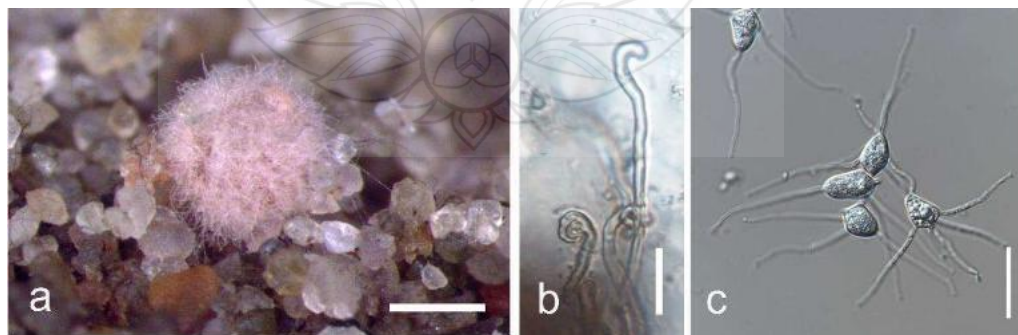
Nia furcatipilosa Hakotani & Nakagiri 2024

Nia globispora Barata & Basilio 1997

Nia lenicarpa Abdel-Wahab & E.B.G. Jones 2023

Nia singaporensis Hakotani & Nakagiri 2024

Nia sphaerocystis Hakotani & Nakagiri 2024



Note a Conidioma with peridial hairs. b Peridial hyphae. c Conidia bearing apical appendages. Scale bars: a = 500 μm , b = 10 μm , c = 20 μm

Source Qian et al. (2026)

Figure 4.197 *Nia singaporensis*

***Chaetospermum* Sacc. 1892**

Classification: *Sebacinaceae*, *Sebacinales*, *Incertae sedis*, *Agaricomycetes*, *Agaricomycotina*, *Basidiomycota*, *Fungi*.

Chaetospermum was originally described by Patouillard (1888) as *Tubercularia chaetospora* from decaying grass. Due to its unique morphological features, Saccardo (1892) reassigned it to a newly established genus as *Chaetospermum tubercularioides*, designating it as the type species. The name was later corrected to *Chaetospermum chaetosporum* by Smith and Ramsbottom (1914) to align with naming conventions. Wells and Bandoni (2001) observed a chaetospermum morph in cultures of *Efibulobasidium albescens*. Later, Rungjindamai et al. (2008) demonstrated that *Chaetospermum* species are related to the order of *Sebacinales* within *Agaricomycetes* (*Basidiomycota*) based on LSU and SSU sequence data. Kirschner and Oberwinkler (2009) also reported both sexual and asexual morphs in a single specimen. Later, Crous et al. (2014a) designated a neotype for *C. chaetosporum* and confirmed its placement within *Sebacinales* (*Agaricomycetes*, *Basidiomycota*). Additionally, ITS sequence data supported the connection between *C. chaetosporum* and its sexual morph, *Efibulobasidium albescens*, and they recommended the use of the older generic name *Chaetospermum* over *Efibulobasidium*. The genus is characterized by a coelomycetous asexual morph and a basidiomycetous sexual morph. Its asexual form features pycnidial conidiomata that are off-white, pearl white, or yellowish-brown and waxy when moist or dry. Conidiomata may be solitary, gregarious, or confluent, with heavily gelatinized walls composed of hyaline, thick-walled cells in a *textura intricata* to *textura oblita* arrangement. Conidiophores are hyaline, branched, loosely aggregated, and septate at the base, arising from the inner conidiomatal cells. Conidiogenous cells are hyaline, subcylindrical to irregular. Conidia are hyaline, cylindrical to broadly ellipsoidal, aseptate, smooth, straight or slightly curved, with rounded ends, and bear polar or subpolar, filiform to attenuated, flexuous, unbranched appendages. For the sexual morph, see Wells and Bandoni (2001). Currently, 10 species are listed in this genus (Species Fungorum, accessed April 2026). *Chaetospermum camelliae* has been reported from salt marshes as a saprobe on decaying stems and leaf sheaths of *Phragmites australis* from China (Calabon et al. 2021b). Currently, sequence data for *Chaetospermum artocarp*, *Chaetospermum camelliae*, and *Chaetospermum*

chaetosporum are available in NCBI. Additionally, Crous et al. (2014a) showed through their analysis that *Chaetospermum* is placed in *Sebacinales*.

Type species: *Chaetospermum chaetosporum* (Pat.) A.L. Sm. & Ramsb. 1914

Other accepted species:

Chaetospermum artocarpi (Nag Raj) Nag Raj 1993

Chaetospermum camelliae Agnihothr 1962

Chaetospermum carneum Tassi 1990

Chaetospermum elasticae Koord 1907

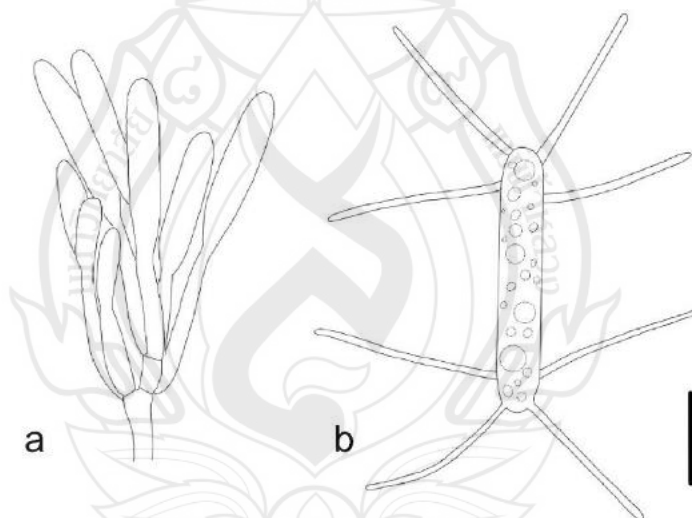
Chaetospermum gelatinosum Petch 1917

Chaetospermum gossypinum (G.F. Atk.) Nag Raj 1993

Chaetospermum indicum Talde 1982

Chaetospermum malipoense X.M. Tan & S.X. Guo 2014

Chaetospermum setosum Rajeshk., S.K. Singh & P.N. Singh 2010



Note Conidiophore and Conidium. Scale bar = 10 μ m

Source Redrawn from Tangthirasunun et al. (2014)

Figure 4.198 *Chaetospermum camelliae*

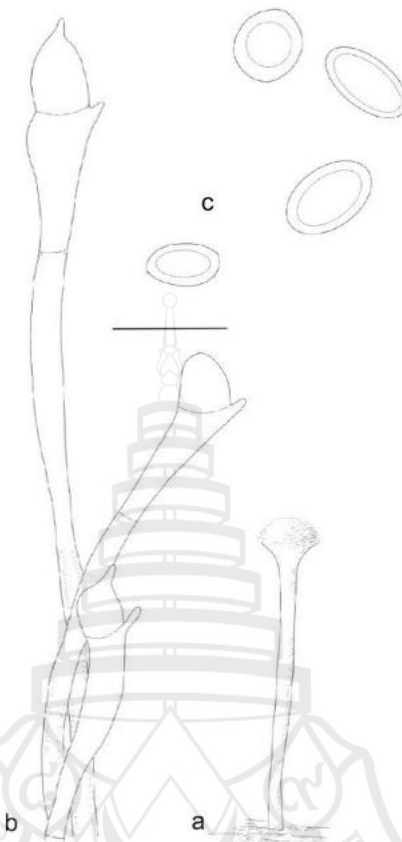
Stilbum Tode 1790

Classification: *Chionosphaeraceae*, *Agaricostilbales*, *Agaricostilbomycetidae*, *Agaricostilbomycetes*, *Pucciniomycotina*, *Basidiomycota*, *Fungi*.

Stilbum was introduced to accommodate six saprobic species from Germany (Tode 1790a). *Stilbum vulgare* is the type species of the genus, characterized by stipitate, synnema-like basidiomata with parallel hyphae forming the stipe. Clusters of 2 to 3 hyphae bear the basidia. The basidiospores are hyaline, subglobose to ellipsoidal, and give rise to secondary yeast cells through multiple budding (Seifert et al. 1992; Kirschner and Chen 2008). There are 198 epithets listed for this genus in Species Fungorum (April 2026); however, many of these species have been transferred to other genera, and some were even found to belong to *Ascomycota*. *Stilbum* was initially considered a hyphomycetous asexual fungus until Juel (1898) designated *S. vulgare* as the lectotype and discovered that it belongs to *Basidiomycota*. Currently, about 15 species are accepted in this genus, which is placed in the family *Chionosphaeraceae*, *Basidiomycota* (Bauer et al. 2006; Hyde et al. 2024a). These species are mostly recorded as saprobes on dead plant material (Tode 1790, Kirschner and Chen 2008). One unidentified species was recorded on leaf litter of the salt marsh plant *Juncus roemerianus* from the USA by Fell and Hunter (1979) (Calabon et al. 2021b). However, as the species name was not provided and it was listed among Ascomycetous fungi, it is unclear whether it was correctly identified as *Stilbum*. From 81 accepted species (Species Fungorum, April 2026), sequence data (ITS and SSU) are only available for the type species. Further molecular data are needed to clarify the phylogenetic relationships of species within this genus.

Type species: *Stilbum vulgare* Tode 1790

Other accepted species: Species Fungorum (search *Stilbum*)



Note a Habitat of basidiocarps. b Mature basidia. c Basidiospores. Scale bar: b, c = 10 μm

Source Redrawn from Seifert et al. (1992)

Figure 4.199 *Stilbum vulgare*

Sporobolomyces Kluyver & C.B. Niel 1924

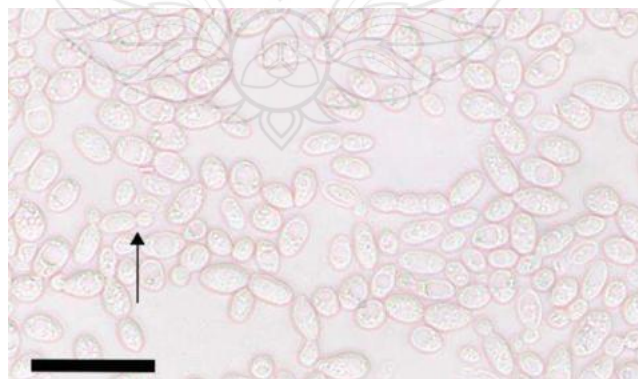
Classification: *Sporidiobolaceae*, *Sporidiobolales*, *Incertae sedis*, *Microbotryomycetes*, *Pucciniomycotina*, *Basidiomycota*, *Fungi*.

Sporobolomyces is a basidiomycetous yeast genus introduced to accommodate its type species, *Sporobolomyces salmonicolor* (Kluyver and van Niel 1924). The asexual morph produces ballistoconidia from ellipsoidal, subglobose, fusiform, or cylindroidal cells, mostly through polar budding. Colonies are brightly pigmented, typically red, orange, pink, or yellowish, when grown on agar media. Physiologically and chemically, these yeasts are incapable of fermenting sugars (Hong et al. 2000). The taxonomic placement of *Sporobolomyces* has been re-evaluated based on D1/D2

regions along with physiological data by Hong et al. (2000). These studies indicated that the taxonomy of *Sporobolomyces* and related genera such as *Leucosporidium*, *Rhodospordium* and *Rhodotorula* would require major revision (Hong et al. 2000). Li et al. (2020) further examined basidiomycetous yeasts using both physiological traits and multigene phylogeny (LSU, SSU, ITS, *rpb1*, *rpb2*, *tef1*, and CYTB), leading to the introduction of four new *Sporobolomyces* species from plant leaves. A recently described species, *Sporobolomyces lactucae*, was found to frequently colonize romaine lettuce (*Lactuca sativa*) (Fatemi et al. 2022). The genus comprises about 30 species, isolated from diverse terrestrial and aquatic habitats, including plants and soil (Fatemi et al. 2022, Hyde et al. 2024a). One species, *S. salmonicolor*, is known to be opportunistically pathogenic to humans (Sharma et al. 2006). Five species—*S. blumea*, *S. carnicolor*, *S. johnsonii*, *S. pararoseus*, and *S. salmonicolor*—have been listed as marine fungi (Jones et al. 2019). Additionally, *S. roseus* and an unidentified species have been reported from salt marsh plants such as *Spartina* spp. and *Phragmites australis* (Calabon et al. 2021b). *Sporobolomyces* has been investigated for its potential applications in biotechnology. *S. roseus* exhibits antimicrobial activity against human and plant pathogens (McCormack et al. 1994; Bashir and Fokkema 1977). Moreover, carotenoid pigments produced by various *Sporobolomyces* have attracted interest due to their industrial and pharmaceutical potential (Mannazzu et al. 2015).

Type species: *Sporobolomyces salmonicolor* (B. Fisch. & Brebeck) Kluyver & C.B. Niel 1924

Other accepted species: Species Fungorum (search *Sporobolomyces*)



Note Cells of *S. lactucae*. Scale bar = 20 μ m

Source Fatemi et al. (2022)

Figure 4.200 *Sporobolomyces lactucae*

Flamingomyces R. Bauer, M. Lutz, Piątek, Vánky & Oberw. 2007

Classification: *Urocystidaceae*, *Urocystidales*, *Ustilaginomycetidae*, *Ustilaginomycetes*, *Ustilaginomycotina*, *Basidiomycota*, *Fungi*.

Bauer et al. (2007) introduced the marine smut genus, *Flamingomyces* (*Urocystaceae*), to accommodate *Melanotaenium ruppiae* (introduced by Feldmann 1959), based on morphology and LSU phylogenetic analyses. *Flamingomyces ruppiae* was collected from the halophyte *Ruppia maritima* in France and is the only known smut fungus on *Ruppia* (Bauer et al. 2007; Calabon et al. 2021b). Sori form in the intercellular spaces of the rhizomes, stems, and basal parts of the leaves, containing single pigmented smooth teliospores. The soral hyphae have simple pores with more or less rounded pore lips, enclosed by two outer membrane caps and two inner non-membranous plates. *Flamingomyces ruppiae* forms intracellular aseptate haustoria that terminate within the host cell and are morphologically distinct from intercellular hyphae. The genus shares similar morphology with *Melanustilospora* and *Vankya*, but it is distinguished by molecular data and its parasitism on *Ruppiaceae* (Bauer et al. 2007).

Type species: *Flamingomyces ruppiae* (Feldmann) R. Bauer, M. Lutz, Piątek, Vánky & Oberw. 2007

Basionym: *Melanotaenium ruppiae* Feldmann 1959

Other accepted species: None



Note Germinating teliospores. Scale bar: 10 µm

Source Redrawn from Bauer et al. (2007)

Figure 4.201 *Flamingomyces ruppiae*

Parvulago R. Bauer, M. Lutz, Piątek, Vánky & Oberw. 2007

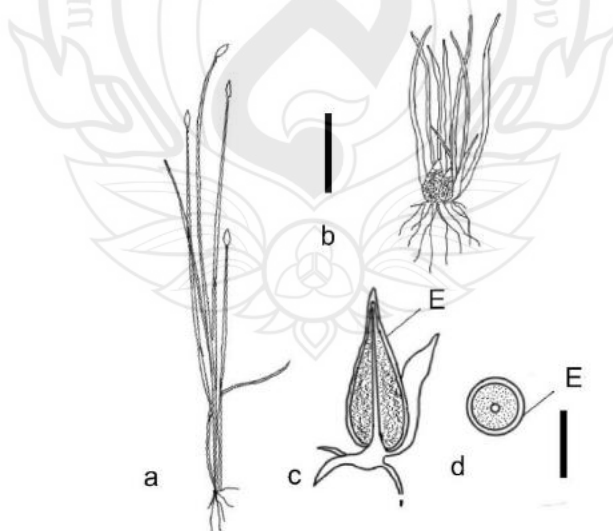
Classification: *Ustilaginaceae*, *Ustilaginales*, *Ustilaginomycetidae*, *Ustilaginomycetes*, *Ustilaginomycotina*, *Basidiomycota*, *Fungi*.

Parvulago was introduced by Bauer et al. (2007) as a new genus of marine smut fungi based on morphology and molecular analyses of LSU sequence data. It is typified by *P. marina* and synonymized with *Ustilago marina* (Durieu 1866) within *Ustilaginaceae*. The sori of *Parvulago* are situated at the base of host culms, appearing as bullate or onion-shaped swellings covered by a two-layered epidermis. Soral hyphae within these sori lack pores in their septa. The sori are composed of masses of black, agglutinated single spores. *Parvulago* forms a distinct clade with other members of the *Ustilaginaceae* family, and morphologically differs by exclusively forming sori at the base of the host plant culms (Bauer et al. 2007). *Parvulago marina* has been reported on *Eleocharis parvula* in several European countries including Finland, France, Germany, Great Britain, Norway, and Sweden (Bauer et al. 2007; Calabon et al. 2021b)

Type species: *Parvulago marina* (Durieu) R. Bauer, M. Lutz, Piątek, Vánky & Oberw. 2007

Basionym: *Ustilago marina* Durieu 1866

Other accepted species: None



Note a Healthy host plants. b Infected plant. c–e Sections through very young sori of *Parvulago marina*. Scale bars: a, b = 1 cm, c–e = 2 mm

Source Redrawn from Bauer et al. (2007)

Figure 4.202 *Parvulago marina* and its host

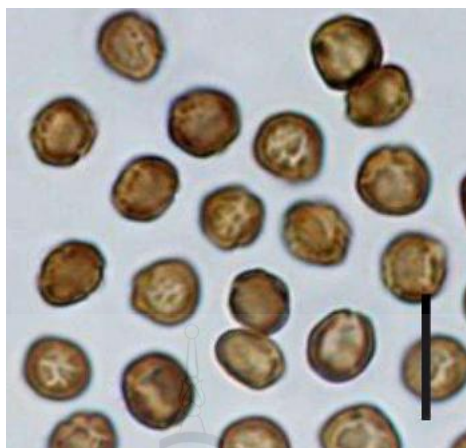
***Tranzscheliella* Lavrov 1936**

Classification: *Ustilaginaceae*, *Ustilaginales*, *Ustilaginomycetidae*, *Ustilaginomycetes*, *Ustilaginomycotina*, *Basidiomycota*, *Fungi*.

Tranzscheliella was introduced by Lavrov (1936), with *T. otophora*, collected from *Stipa pennata* in Turkmenistan, designated as the type species. The genus is characterized morphologically by the formation of sori on the surface of the host's stems or floral axis, which may be naked or enclosed in a peridium. The teliospores are generally small, dark, and have either smooth or ornamented walls (Vánky 2003; Vánky and Abbasi 2013; Savchenko and Mahmood 2023). *Tranzscheliella* is a cosmopolitan genus comprising about 25 species (Hyde et al. 2024a). These are smut fungi that infect the stems of grasses (*Poaceae*), and have been recorded on more than 30 plant genera (Vánky 2012, 2013; Li et al. 2017). Li et al. (2017) investigated cryptic diversity in *Tranzscheliella* using morphological data and phylogenetic analyses based on ITS and LSU sequences. They introduced four new species and conducted cophylogenetic analyses, which suggested that host switching is the primary driver of speciation in the genus. Species identification in *Tranzscheliella* relies on morphology, phylogenetic data, and host association. However, there are some challenges: certain species have been reported from multiple hosts, many lack sequence data, and the available morphological features are limited (Vánky 2012; Savchenko and Mahmood 2023). *Tranzscheliella distichlidis* is the only known species from a salt marsh plant. It represents one of the few reports of a pathogenic fungus on a halophyte and was recorded on *Distichlis spicata* in Australia (Calabon et al. 2021b).

Type species: *Tranzscheliella otophora* Lavrov 1936

Other accepted species: Species Fungorum (search *Tranzscheliella*)



Note Teliospores. Scale bar: 10 μm

Source Vánky and Abbasi (2013)

Figure 4.203 *Tranzscheliella iranica*

Blakeslea Thaxt. 1914

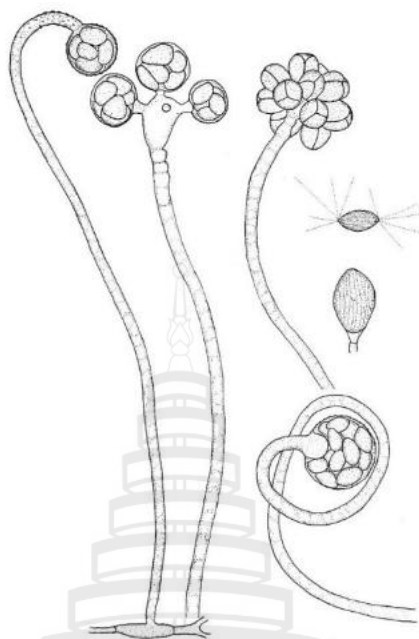
Classification: *Mucoraceae*, *Mucorales*, *Incertae sedis*, *Mucoromycetes*, *Mucoromycotina*, *Mucoromycota*, *Fungi*.

Blakeslea was introduced by Thaxter in 1914 and is typified by *B. trispora*. The genus is characterized by branched, rhizoidal hyphae that produce numerous intercalary chlamydospores. It has two types of sporangia; larger, solitary, choanephora-like sporangia with columella and dark sporangiospores with appendages, and sporangiola without columella containing a few dark, appendiculate spores (Thaxter 1914). There was some doubt in earlier studies about the similarity between *Blakeslea* and *Choanephora* (Sinha 1940), but Mehrotra and Baijal (1968) introduced a new species, *B. monospora*, and confirmed *Blakeslea* as a distinct genus (Mehrotra and Baijal 1968). *Blakeslea* has sporangiola, while *Choanephora* has conidia. *Blakeslea trispora* was first isolated from *Vigna unguiculata* in Florida, USA. It has also been reported as a saprobe on the decaying halophyte *Juncus roemerianus* from Florida (Fell and Hunter 1979, Calabon et al. 2021b). The zygomycete *B. trispora* has gained attention due to its high production of carotenoids, which are beneficial in reducing the risk of cancer and heart disease (Luo et al. 2020).

Type species: *Blakeslea trispora* Thaxt. 1914

Other accepted species:

Blakeslea monospora B.S. Mehrotra & Baijal 1968



Note Fertile hyphae, sporangia, sporangial spore

Source Redrawn from Thaxter (1914)

Figure 4.204 *Blakeslea trispora*

Mucor Fresen. 1850

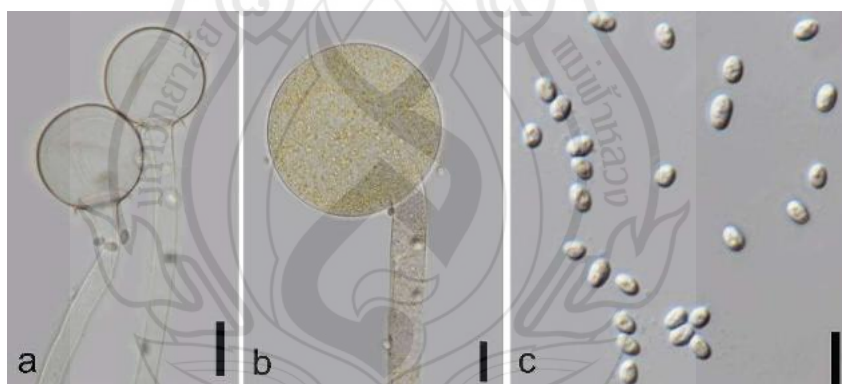
Classification: *Mucoraceae*, *Mucorales*, *Incertae sedis*, *Mucoromycetes*, *Mucoromycotina*, *Mucoromycota*, *Fungi*.

Mucor is a large genus comprising approximately 110 species and is the type genus of the phylum *Mucoromycota* (Hyde et al. 2024a; Zhao et al. 2023). It was established by Fresenius in 1850 to accommodate two filamentous species, *M. racemosus* and *M. bifidus*. Species of *Mucor* are characterized by fast-growing colonies and by producing branched or unbranched sporangiophores and round or slightly elongated sporangiospores. Basal rhizoids and apophyses are generally absent. Zygosporangia are formed with opposed or tongue-like suspensors (Schipper 1978; Hurdeal et al. 2021; Jayawardena et al. 2020). *Mucor* species have a cosmopolitan distribution and occur in a wide range of habitats, commonly found as saprobes in soil and dung (Walther et al. 2013). While they primarily function as saprobes, several species have also been reported as endophytes, plant pathogens, crop postharvest pathogens, or opportunistic human pathogens causing mucormycosis (Vaezi et al. 2016;

Domka et al. 2017; Nguyen et al. 2017; Jayawardena et al. 2020; Hurdeal et al. 2021). Some species are industrially significant due to their ability to ferment food (Cheng et al. 2009) and their medicinal properties (Huang et al. 2014). Additionally, certain *Mucor* species can grow at elevated temperatures up to 42 °C (Walther et al. 2019). Two *Mucor* species, *M. hiemalis* and *M. racemosus*, have been reported from marine habitats (Jones et al. 2019). Furthermore, two unidentified species have been isolated as saprobes from salt marsh plants (*Juncus roemerianus* and *Spartina* sp.) in the USA and Canada, respectively (Calabon et al. 2021b). Zhao et al. (2023) conducted a phylogenetic analysis based on ITS sequences and introduced 20 new *Mucor* species along with 16 new records from China, highlighting the genus's high diversity and taxonomic complexity. LSU and SSU are recommended markers for genus-level identification, while ITS and *rpb1* are recommended for species-level identification (Jayawardena et al. 2020).

Type species: *Mucor mucedo* Fresen. 1763

Other accepted species: Species Fungorum (search *Mucor*)



Note a Columella with collar. b Developing sporangium. c Sporangiospores. Scale bar: 10 μm

Source Hurdeal et al. (2021)

Figure 4.205 *Mucor aseptatophorus*

Syncephalastrum J. Schröt. 1886

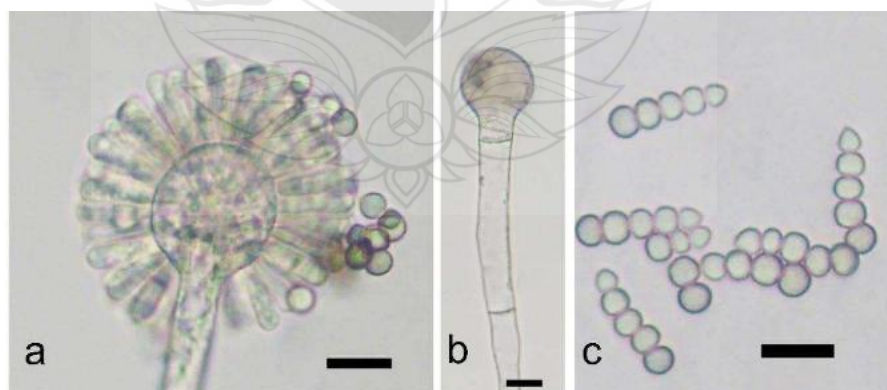
Classification: *Syncephalastraceae*, *Mucorales*, *Incertae sedis*, *Mucoromycetes*, *Mucoromycotina*, *Mucoromycota*, *Fungi*.

Syncephalastrum was introduced by Schröter (1886) to accommodate a single species, *Syncephalastrum racemosum*, which was first observed on rice and bread in

association with *Aspergillus oryzae*. The genus belongs to the order *Mucorales* and is the type genus of the family *Syncephalastraceae*, which is characterized by cylindrical merosporangia borne on fertile vesicles. *Syncephalastrum* species typically have cylindrical merosporangia, zygosporangia with rough or dark walls, and opposed suspensors (Benjamin 1959). Currently, the genus comprises about 12 species (Hyde et al. 2024a), including opportunistic human pathogens known to cause infections, particularly in immunocompromised individuals, affecting various organs and tissues such as the skin, nails, lungs, and central nervous system (Irshad et al. 2020). *Syncephalastrum* species have also been reported from soil, paper samples, plants, and as laboratory contaminants. Recently, Kabtani et al. (2024) introduced two new species, *S. massiliense* and *S. timoneanum*, from human clinical samples. Due to the morphological similarity among species, a polyphasic approach was employed for species identification, incorporating morphology, antifungal susceptibility testing, phylogenetic analyses (ITS, and combined datasets of ITS, *tub2*, *tef1*, and D1/D2), Biolog™ system, MALDI-TOF MS (matrix-assisted laser desorption/ionization time-of-flight mass spectrometry), and EDX (energy-dispersive X-ray spectroscopy). Although there are no confirmed marine records for the genus (Jones et al. 2019), *S. racemosum* has been reported as a saprobe on the salt marsh plant *Juncus roemerianus* in the USA (Calabon et al. 2021b).

Type species: *Syncephalastrum racemosum* Cohn ex J. Schröt. 1886

Other accepted species: Species Fungorum (search *Syncephalastrum*)



Note a Merosporangia. b Sporangiophore with vesicle. c Sporangiospores. Scale bars: 10 µm

Source Redrawn from Zhao et al. (2023)

Figure 4.206 *Syncephalastrum breviphorum*

Rhizopus Ehrenb. 1821

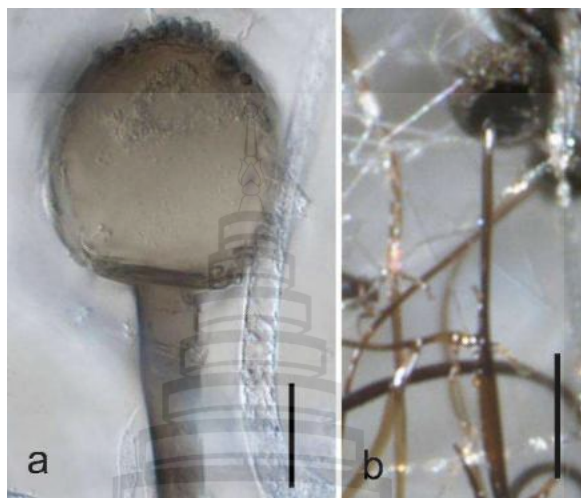
Classification: *Rhizopodaceae*, *Mucorales*, *Incertae sedis*, *Mucoromycetes*, *Mucoromycotina*, *Mucoromycota*, *Fungi*.

Rhizopus is a genus in the class *Mucoromycetes*, characterized by its asexual morph that produces root-like rhizoids and erect sporangiophores bearing sporangia, within which spores are formed (Bautista-Baños et al. 2014). The genus comprises approximately 12 species (Hyde et al. 2024a) and is well-known for its significant roles in human life. *Rhizopus* species are widely used in industry, particularly in the fermentation of foods such as tempeh, and in the production of metabolites and enzymes (Abe et al. 2003; Handoyo and Morita 2006; Gryganskyi et al. 2018). However, some species are also important plant pathogens, causing postharvest diseases in various crops such as strawberries and sweet potato (Tournas 2005; Hanson 2010; Abeywickrama et al. 2020). In addition, *Rhizopus* is considered an opportunistic pathogen of animals and humans, notably causing mucormycosis (Dolatabadi et al. 2018; Tabarsi et al. 2021). The genus was first described by Ehrenberg in 1821, based on the type species, *Rhizopus nigricans*, from fruit and the calyx of *Cornus mas* and *Morus alba* in Germany (Index fungorum June 2025). Subsequently, the type species changed as *Rh. stolonifer* (Inui et al. 1965; Zheng et al. 2007). Species of *Rhizopus* can grow on a wide range of substrates, including soil, food, leather, and rotten fruits and vegetables (Gryganskyi et al. 2018; Ghaderi and Abdollahzadeh 2024). *Rhizopus microsporus* and *Rh. stolonifer* have also been reported as marine fungi (Jones et al. 2019), with *Rh. stolonifer* recorded as a saprobe on the halophyte *Spartina townsendii* (Calabon et al. 2021b). Zheng et al. (2007) provided a monograph of *Rhizopus*, highlighting the difficulties in classification due to morphological variability under different conditions. They suggested that a combination of morphology and physiological traits, such as maximum growth temperature, acid production, and the Voges-Proskauer test, are useful for species identification. Using molecular data, enhanced the species identification and classification (Abe et al. 2006, 2010; Zheng et al. 2007; Jayawardena et al. 2020). Later, Gryganskyi et al. (2018) applied phylogenomic approaches to study the genus, showing that *Rhizopus* species cluster into three main clades: *Rh. microsporus*, *Rh. stolonifer*, and a group containing the closely related *Rh. arrhizus* and *Rh. delemar*. The most recently described species, *Rh.*

koreanus, was introduced by Li et al. (2016) based on morphological features and phylogenetic analyses using combined SSU, LSU, actin, and EF-1 α gene sequences.

Type species: *Rhizopus nigricans* Ehrenb. 1821

Other accepted species: Species Fungorum (search *Rhizopus*)



Note a Columella. b Sporangophore, rhizoids, and hyphae. Scale bars = 10 mm

Source Gryganskyi et al. (2018)

Figure 4.207 *Rhizopus arrhizus*

4.3 Discussion

Fungi in salt marshes act as essential decomposers, transforming halophytic plant material into nutrients that support coastal food webs. They occupy a wide range of ecological niches, functioning as saprobes, endophytes, and pathogens. Some taxa, such as *Bicrouania* and *Octopodotus*, were classified as obligate marine fungi (Kohlmeyer and Volkmann-Kohlmeyer 1990; Kohlmeyer and Volkmann-Kohlmeyer 2003), having adapted to high-salinity environments. Others, such as *Arundellina*, were considered as facultative marine fungi (Hyde et al. 2016), capable of thriving in both terrestrial and aquatic habitats.

Beyond their ecological importance, many salt marsh fungal genera are reservoirs of bioactive metabolites. These genera have been documented to produce broad-spectrum antibiotics (e.g., cephalosporin C from *Acremonium*) (Abraham 1979, Jones et al. 2019), medicinal pigments (e.g., from *Stagonospora*) (Chen s. et al. 2022,

Pem et al. 2024), and enzymes with industrial applications. Genera such as *Aureobasidium* and *Humicola* are particularly noted for producing thermostable enzymes (e.g., amylases and cellulases), which are highly valued in the agricultural and food industries (Ibrahim et al. 2021; Francesco et al. 2023). Furthermore, endophytes such as *Periconia macrospinosa* have demonstrated the ability to enhance crop tolerance to salinity and drought stress, suggesting potential applications in sustainable agriculture (Moghaddam et al. 2021, 2022).

This study, following by the checklist of salt marsh genera by Calabon et al. (2021b), represents a comprehensive documentation of fungal genera inhabiting salt marsh ecosystems, providing a curated reference database through the Fungalpedia platform. By detailing the taxonomic and morphological characteristics of these genera, this resource facilitates a more unified approach to marine related mycological research and provides a diagnostic-based reference. This level of detail is critical for researchers who require reference materials for identifying saprobic fungi in complex coastal habitats.

Historically, fungal classification relied on morphological traits, such as spore septation and colour. In view of the taxonomic and morphological information presented in this resource, it is important to emphasize that fungal taxonomy is undergoing continuous revision across many taxa, particularly as molecular phylogenetic data become available to clarify evolutionary relationships. A prominent example of this ongoing systematic revision is observed in the family *Halosphaeriaceae*, for which a monograph is currently in progress (Dayarathne et al. 2026). This work is expected to result in changes to the taxonomic status of several species and genera within the family. To maintain unified documentation, the classification adopted in this study primarily follows the most recent outline of fungi by Hyde et al. (2024).

The documented fungal diversity in these habitats is primarily dominated by the phylum *Ascomycota*. Within this phylum, the order *Pleosporales*, and families such as *Phaeosphaeriaceae* and *Pleosporaceae*, showed the greatest richness (Calabon et al. 2021b).

Among the dominant *Pleosporales* genera, *Phaeosphaeria* (*Phaeosphaeriaceae*) stands out as one of the most diverse and frequently recorded

genera in salt marsh ecosystems, with approximately 20 species documented. Species such as *Phaeosphaeria halima*, *P. neomaritima*, and *P. spartinicola* are commonly associated with *Juncus* and *Spartina* hosts. Similarly, *Leptosphaeria* (*Leptosphaeriaceae*) and *Stagonospora* (*Massarinaceae*) also show high record counts and have been documented across multiple host plants, indicating their broad distribution in salt marsh habitats (Calabon et al. 2021b).

Several additional genera demonstrate frequent occurrence across halophytic hosts. *Anthostomella* (*Xylariaceae*), for example, is well represented with at least nine taxa recorded, primarily associated with *Juncus roemerianus* and *Spartina* species. Another notable example is *Halobyssothecium*, which, although not highly species-rich, includes *Halobyssothecium obiones*, one of the most frequently recorded taxa in salt marsh systems, reported from six species of *Spartina* as well as several additional halophytes (Calabon et al. 2021b).

In addition to these dominant genera, some historically reported taxa remain taxonomically uncertain. One such example is *Phoma*, which has been documented from approximately ten different host plants. Notably, several records identified as *Phoma* sp. originate from earlier studies conducted prior to the widespread use of molecular phylogenetic methods (Calabon et al. 2021b). Given that *Phoma sensu lato* has been shown to be highly polyphyletic, with many species reassigned to other genera following molecular revision (Aveskamp et al. 2010; Chen et al. 2015), these historical records introduce uncertainty regarding their true taxonomic placement.

Notably, several other salt marsh genera, such as *Plenodomus*, *Camarosporium*, *Leptosphaeria*, *Preussia*, and *Tremateia*, are reported to produce phoma-like asexual morphs characterized by coelomycetous structures. This morphology may represent an adaptive feature that enables the production of conidia within protected pycnidia (Sutton 1980), potentially serving as a functional response to intertidal stress conditions in salt marsh environments.

This study documents approximately 80 genera for which both sexual and asexual morphs have been identified. In many cases, these morphs were historically classified as separate genera before being linked through morphological observations or molecular phylogenetic analyses. Examples include *Ramularia* (linked to *Mycosphaerella*), *Stemphylium* (linked to *Pleospora*), and *Juncigena* (linked to

Moheitospora), highlighting the successful implementation of the "one fungus–one name" principle in resolving historical systematic confusion (Simmons 1969; Crous et al. 2009; Rossman et al. 2015; Réblová et al. 2016b; Brahmanage et al. 2019; Hongsanan et al. 2020b).

Despite these advances, many genera still lack molecular data, particularly those described more than 100 years ago. Although morphological descriptions are available, the absence of modern molecular markers often leaves these genera in a state of taxonomic uncertainty or classified as *incertae sedis*, such as *Stauroinema*, *Sphaeronaema*, *Hyphopolynema*, *Tetranacrium*, *Tetranacriella*, *Octopodotus*, *Aropsichus*, and *Cytoplacosphaeria*. Several of these genera, including *Sphaeronaema*, *Stauroinema*, and *Cytoplacosphaeria*, were described from salt marsh fungi over a century ago and still lack the molecular data necessary for accurate classification. This taxonomic uncertainty underscores the essential need for fresh collections and molecular sequencing to confirm the systematic positions of many taxa.

Patterns of species richness also reveal a substantial number of monotypic genera. From the documented genera in this resource, 25 are monotypic, such as *Arundellina*, *Decorospora*, *Verruculina*, and *Lautisporopsis*, each containing only a single accepted species.

Genera such as *Mucomyosphaerella*, *Heleiosa*, *Camarosporioides*, *Halenospora*, and *Glomerobolus* were also previously considered monotypic; however, recent studies have expanded these genera by introducing additional species. *Mucomyosphaerella* was first introduced from the salt marsh host *Juncus roemerianus* in the USA by Kohlmeyer et al. (1999). However, a recent study by Wanasinghe et al. (2025) added *M. hongheensis* as the second species in the genus, collected from dry-hot valleys in China. Their study also led to the introduction of a new family, *Mucomyosphaerellaceae*, to accommodate this genus, highlighting the importance of continued research and fresh collections for improving higher-level taxonomic resolution.

Similarly, *Heleiosa* was established based on *H. barbatula*, first collected from *J. roemerianus* Kohlmeyer et al. (1996a). However, the genus now includes three additional species described in 2025: *H. brunnea*, *H. guizhouensis*, and *H. lincangensis* (Sun et al. 2025).

The occurrence of these genera on non-halophyte hosts and in different ecosystems suggests broader ecological plasticity and underscores the need for further collections to better understand the ecological preferences of these often poorly known taxa. For instance, recent studies on fungi associated with grasses by Gao et al. (2024, 2025) reported several genera that are also known from salt marsh plants, including *Phaeosphaeria*, *Leptosphaeria*, *Stagonospora*, *Septoriella*, *Keissleriella*, *Epicoccum*, *Periconia*, *Apiospora*, *Nigrospora*, *Massarina*, *Camarosporioides*, *Pseudopithomyces*, *Tremateia*, *Schizothecium*, *Sclerostagonospora*, and *Paraphaeosphaeria*.

In these studies, the second species of *Glomerobolus*, *G. poacearum*, was introduced from *Poaceae* in grasslands in China (Gao et al. 2024), about 30 years after *Glomerobolus* was first described from the salt marsh host *J. roemerianus*. They also introduced *Camarosporioides kunmingensis*, thereby expanding the previously monotypic genus *Camarosporioides*, for which *C. phragmitis* had been the only known species, originally described from *Phragmites australis* (Gao et al. 2025).

This Fungalpedia compilation provides a critical foundation for the study of coastal mycota in salt marsh ecosystems. However, significant gaps remain. Current records are largely concentrated in the United States, China, and the United Kingdom, highlighting the need to expand research into under-sampled salt marsh regions to achieve a truly global understanding of fungal diversity (Calabon et al. 2021b). Future efforts should focus on applying phylogenomic approaches to place poorly understood genera into a natural classification framework.

CHAPTER 5

TAXONOMY AND PHYLOGENY OF MICROFUNGI FROM MARINE BASED HABITATS IN THAILAND

5.1 Introduction

Fungi live in a variety of ecosystems from terrestrial to aquatic habitats on various substrate such as plant materials (Hyde et al. 2019, 2020; Bhunjun et al. 2022). Fungi have a high diversity in coastal environments significantly known with their important role and also with potential use in medicine, bioremediation, biotechnology and industry (Hyde et al. 1998; Bonugli-Santos et al. 2015; Pang et al. 2016; Jones et al. 2019). This chapter provides saprobic fungi associated with submerged wood trapped between rocks in seawater and seashore plants, particularly on *Suaeda maritima* and *Sesuvium portulacastrum* in Thailand, with detailed descriptions, illustrations, and a phylogenetic tree.

5.2 Results

5.2.1 Taxonomy and Phylogeny

Ascomycota Caval.-Sm

Pezizomycotina O. E. Erikss. & K. Winka

Dothideomycetes O.E. Erikss & Winka

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

Mycosphaerellales (Nannf.) P.F. Canno

Teratosphaeriaceae Crous & U. Braun

Teratosphaeriaceae was established by Crous et al. (2007) and typified by *Teratosphaeria* as the type genus. The family comprises 72 genera and is morphologically and ecologically diverse (Hyde et al. 2024). The sexual morph of *Teratosphaeria* has papillate, ostiolate ascomata, bitunicate, fasciculate asci, and

ellipsoid to fusoid or obovoid ascospores, with or without a mucoid sheath. The asexual morph is either coelomycetous or hyphomycetous (Crous et al. 2009; Hongsanan et al. 2020a). Members of *Teratosphaeriaceae* are cosmopolitan fungi within *Dothideomycetes*, with diverse life strategies, including saprobic, endophytic, rock-inhabiting, and pathogenic lifestyles on plants and humans (Crous et al. 2009, Hongsanan et al. 2020a, Quaedvlieg et al. 2014). *Hortaea* is a frequently reported genus from marine habitats within this family (Calabon et al. 2023).

Hortaea Nishim. & Miyaji

Hortaea was introduced by Nishimura and Miyaji (1989) and typified by *Hortaea werneckii*. The genus is known as a black yeast and is characterized only by its asexual morph, producing both filamentous structures and yeast-like cells. It has a mycelial structure, pseudomycelia formed by concatenated conidia, and sympodial to annellidic conidiogenous cells. Conidia are 0–1-septate, ellipsoidal to cylindrical, pale brown to black, with unipolar or bipolar budding (Nishimura and Miyaji 1989, Zalar et al. 2019). *Hortaea werneckii* is distributed globally and is an extremely halotolerant species, reported from a wide range of substrates including rocks, corals, salterns, seawater, salt marshes, and decaying plants (Formoso et al. 2015, Marchetta et al. 2018, Zalar et al. 2019). In this study, we report *Hortaea werneckii* as a new host record from *Suaeda maritima* and *Sesuvium portulacastrum* in Thailand.

Hortaea werneckii (Horta) Nishim. & Miyaji, Fig. 5.2

Index Fungorum number: IF 106184; Facesoffungi number: FoF 11381

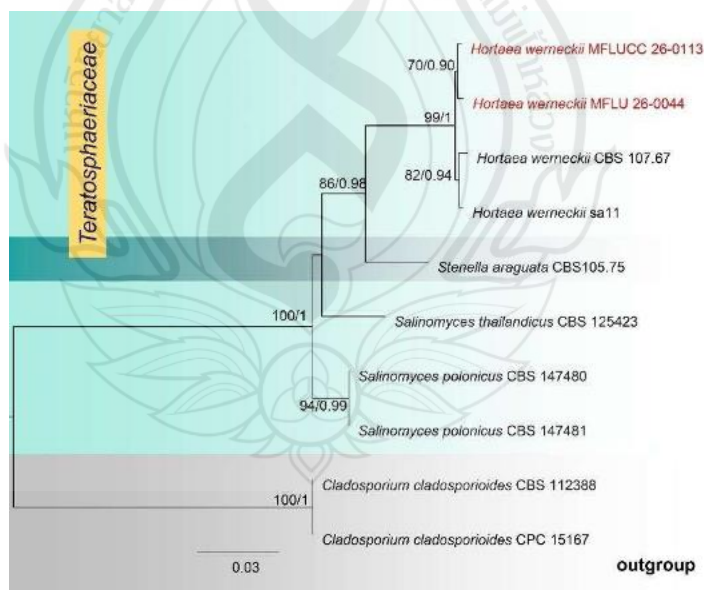
Saprobic on dead stems of *Suaeda maritima* and *Sesuvium portulacastrum*.

Asexual morph: Hyphomycetous *Colonies* on natural substrates flat, catenated, black. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–13 × 4–10 µm ($\bar{x}$ = 7.5 × 6 µm, n = 20), integrated, annellidic, subglobose, doliiform, ampulliform, subhyaline, pale brown to brown. *Conidia* 4–14.5 × 2.5–6 µm ($\bar{x}$ = 9 × 4 µm, n = 30), aseptate to 1-septate, ellipsoidal to cylindrical, subhyaline, pale brown to brown, smooth-walled, thick-walled, with bi-polar budding. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diam. after one month at $25\pm 2^{\circ}\text{C}$, flat, lobate margin, initially shiny and moist, becoming dry or moist; from above, surface and reverse, greenish black.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on margin of a dry saltern, on dry dead stems of *Sesuvium portulacastrum*, 6 April 2024, R. Asghari, S6a11 (MFLU 26-0044); living culture (MFLUCC 26-0150); *ibid.*, Phetchaburi Province, on margin of a saltern (water salinity 50 ppt (parts per thousand), on dead dry stems of *Suaeda maritima*, 6 February 2023, C2-1 (MFLU 26-0045); living culture (MFLUCC 26-0113).

Notes – Based on the multi-gene phylogenetic analyses from ITS and LSU sequence data, our strains grouped with *Hortaea werneckii* (CBS 107.67) (ex-neotype), with 99% ML/1.00 BPP support. Morphologically, our collections are similar to *H. werneckii* in having mycelial structure and yeast-like budding conidia, and greenish black shiny colonies in culture media (Nishimura and Miyaji 1989, Zalar et al. 2019). Our collections are introduced as new host records of *H. werneckii* on *Sesuvium portulacastrum* and *Suaeda maritima* in Thailand.



Note The tree is rooted to *Cladosporium cladosporioides* (CBS 112388 and CPC 15167). Bootstrap values for ML equal to or greater than 70% and BPP greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.1 Phylogram generated from the ML analysis based on the combined ITS and LSU sequence data of *Teratosphaeriaceae*



Note a Colonies on natural substrate. b Conidiogenous cells and developing conidia. c, d Conidia. e, f Colonies on PDA (front and below). Scale bars: a = 1 mm, b–d = 10 μ m.

Figure 5.2 *Hortaea werneckii* (MFLU 26-0044, new host record)

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

Hysteriales Lindau

Hysteriaceae Chevall.

Hysteriaceae is a well-defined family in the *Dothideomycetes*, introduced by Chevallier (1826) with *Hysterium* as the type genus. The family is characterized by distinctive hysterothecial or apothecioid, carbonaceous, navicular ascomata with a pronounced longitudinal slit (Chevallier 1826, Hongsanan et al. 2020a). Pseudoparaphyses may be cellular or trabeculate, varying among genera (Hongsanan et al. 2020a). *Hysteriaceae* comprises 13 genera, whose members are lignicolous or corticolous, mainly occurring on decorticated hardwoods substrates (Hongsanan et al. 2020a, Pem et al. 2020, Ren et al. 2022, Hyde et al. 2024).

Rhytidhysterion Speg.

Rhytidhysterion was introduced by Spegazzini (1881) based on *R. brasiliense* and *R. viride*, and was later typified with *R. brasiliense* by Clements and Shear (1931). *Rhytidhysterion* belongs to the family *Hysteriaceae* and produces dark, pigmented, boat-shaped ascomata that open by a longitudinal slit (Thambugala et al. 2016). The genus comprises about 40 species, among which *R. mangrovei* and *R. bruguierae* have been reported from mangrove habitats (Kumar et al. 2019, Dayarathne et al. 2020a, Hyde et al. 2024). In this study, two strains of *R. bruguierae* collected from a seashore plant (*Leucaena leucocephala*) and from submerged decaying wood are identified.

Rhytidhysterion bruguierae Dayar., Fig. 5.4

Index Fungorum number: IF556574

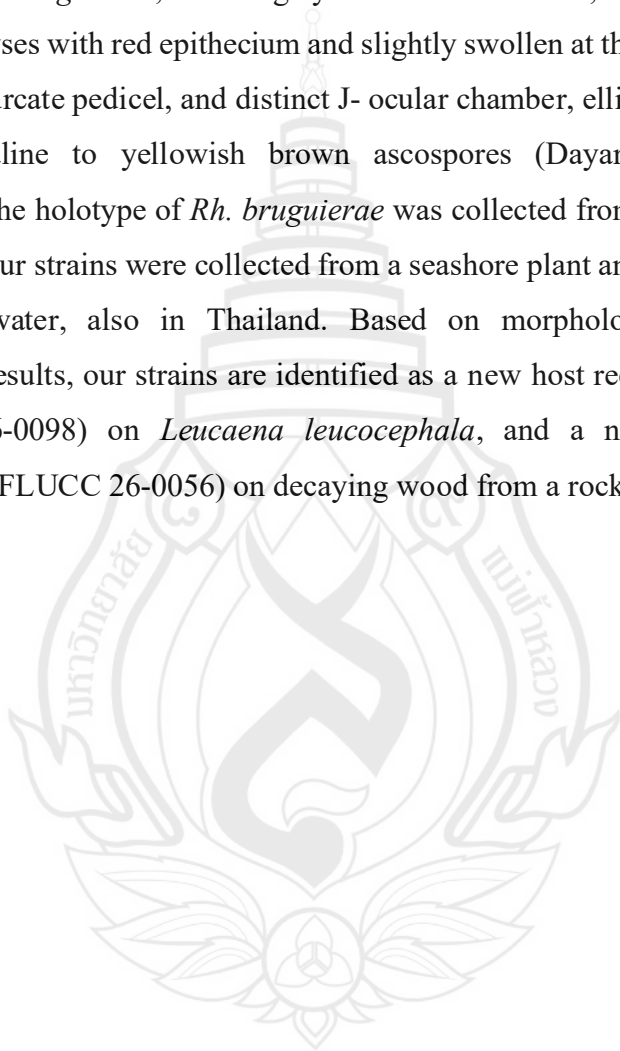
Saprobic on dead stems of *Leucaena leucocephala* and unknown submerged wood. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* hysterothecial 320–625 µm long × 125–525 µm wide ($\bar{x}$ = 435 × 290, n = 10), solitary or in groups, erumpent to superficial, black. *Ectal excipulum* 25–77 µm ($\bar{x}$ = 46.5 µm, n = 15), thick, black, compact *textura angularis* cells. *Medullary excipulum* 20–54 µm ($\bar{x}$ = 35 µm, n = 15), compact cells *textura epidermoidea*, hyaline to pale brown. *Hamathecium* 1–2.3 µm wide ($\bar{x}$ = 1.6 µm, n = 20), numerous pseudoparaphyses, filiform, branched, septate, hyaline with swollen and reddish apex. *Asci* 72–140 × 7.5–10.5 µm ($\bar{x}$ = 120 × 9 µm, n = 15), 8-spored, short pedicellate, furcate pedicel, cylindric, round apex, with distinct J-ocular chamber. *Ascospores* 16–23 × 6–8.5 µm ($\bar{x}$ = 19 × 7.5 µm, n = 20), ellipsoidal to fusiform, round or pointed ends, 1–3-septate, slightly constricted at the septa, smooth-walled, hyaline when immature, yellowish-brown to brown with maturity, guttulate.

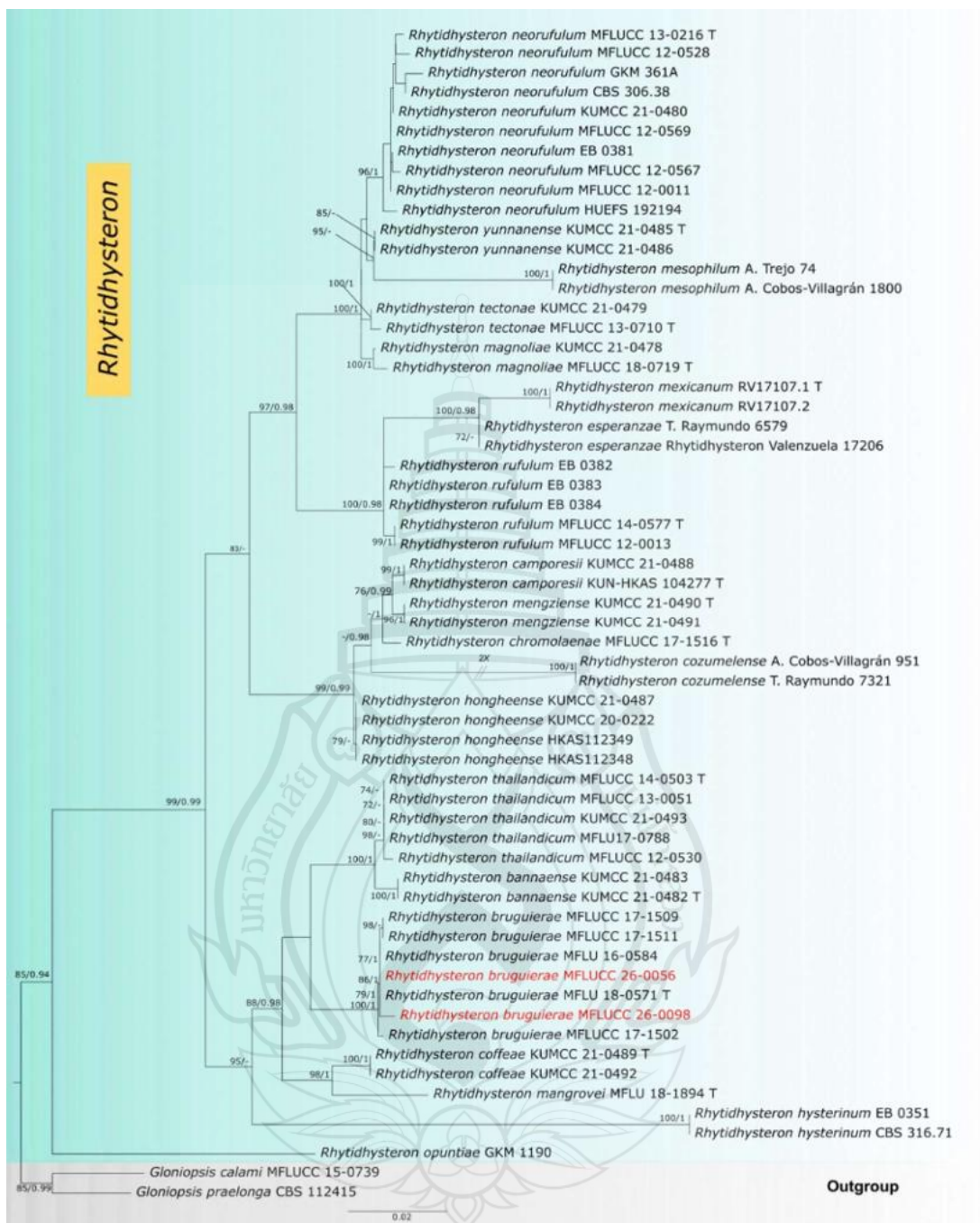
Culture characteristics – Colonies on PDA reaching 4 cm diam. after one month at 25±2°C, flat, circular, entire margin; from surface, brownish gray and brownish red; from reverse, brownish red.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on dead dry stems of *Leucaena leucocephala*, 23 May 2023, R. Asghari, LL11 (MFLU 26-0042); living culture (MFLUCC 26-0098); *ibid.*, on submerged decaying

wood in rocky shore (water salinity 19 ppt), 25 October 2022, KD Hyde, R5B (MFLU 26-0043); living culture (MFLUCC 26-0056).

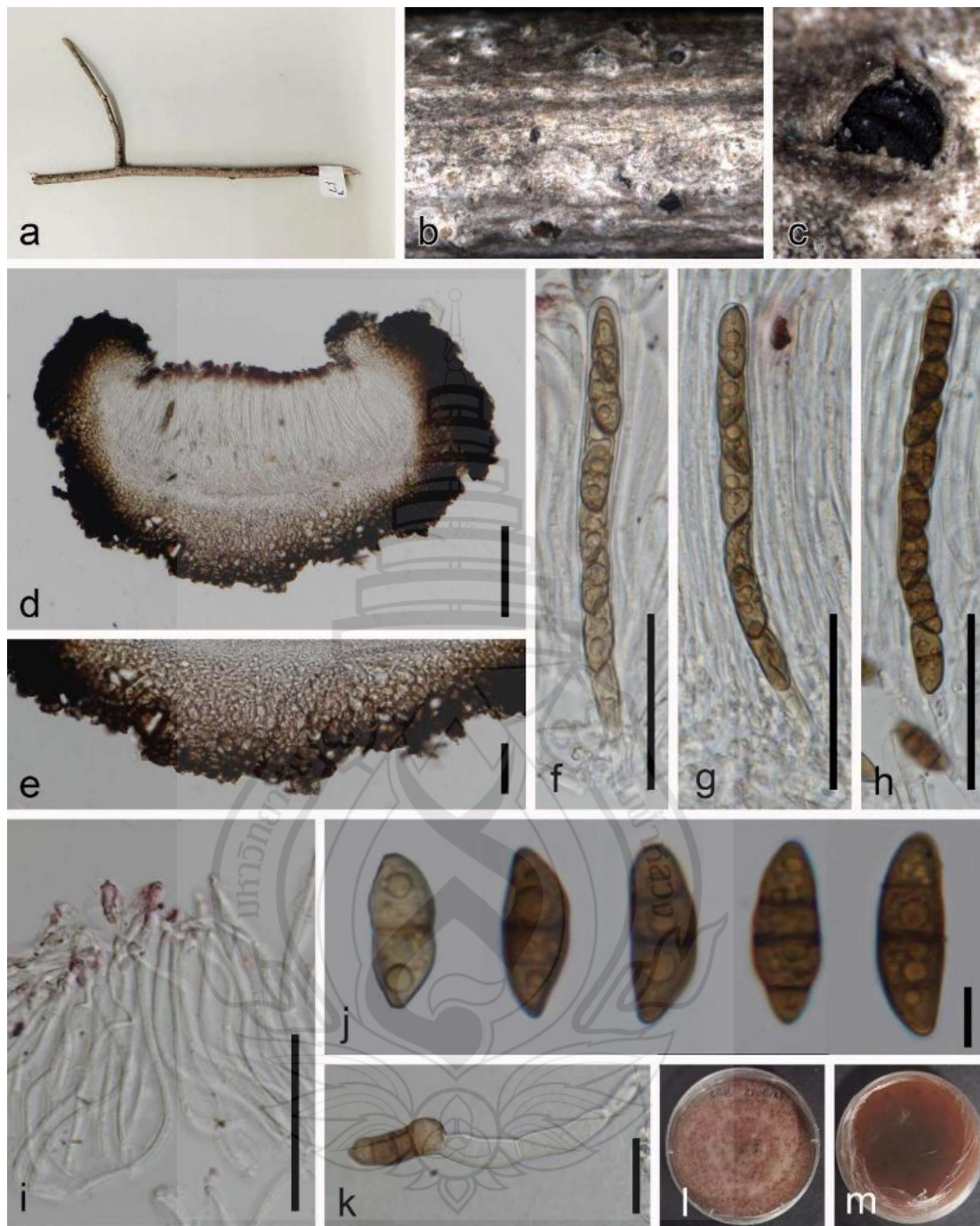
Notes – In our multi-gene phylogenetic analyses, our collections (MFLUCC 26-0098, MFLUCC 26-0056) grouped with *Rhytidhysterium bruguierae* (MFLU 18-0571) (holotype), with 79% ML support. Morphologically, our collections are similar to the holotype of *Rh. bruguierae*, in having hysterothecial acomata, dense, branched, septate pseudoparaphyses with red epithecium and slightly swollen at the apex, cylindrical asci with a short, furcate pedicel, and distinct J-ocular chamber, ellipsoidal to fusiform, 1–3-septate, hyaline to yellowish brown ascospores (Dayarathne et al. 2020a). Ecologically, the holotype of *Rh. bruguierae* was collected from mangrove habitats in Thailand and our strains were collected from a seashore plant and submerged decaying wood in seawater, also in Thailand. Based on morphological, ecological and phylogenetic results, our strains are identified as a new host record of *Rh. bruguierae* (MFLUCC 26-0098) on *Leucaena leucocephala*, and a new collection of *Rh. bruguierae* (MFLUCC 26-0056) on decaying wood from a rocky shore in Thailand.





Note The tree is rooted to *Glioniopsis calami* (MFLUCC 15-0739) and *G. praelonga* (CBS 112415). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red, while type strains are indicated with T.

Figure 5.3 Phylogram generated from the ML analysis based on the combined LSU, ITS, SSU, and *tef1* sequence data of *Rhytidhysterion*



Note a Decaying twig of host. b, c Colonies on natural substrate. d Section of an ascoma. e Peridium. f–h Asci and paraphyses. i Paraphyses. j Ascospores. k Germinated ascospore. l, m Colony on PDA (front and below). Scale bars: b = 1000 μ m, c = 200 μ m, d = 100 μ m, e–i = 50 μ m, j = 10 μ m, k = 20 μ m.

Figure 5.4 *Rhytidhysterium bruguierae* (MFLU 26-0042, new host record)

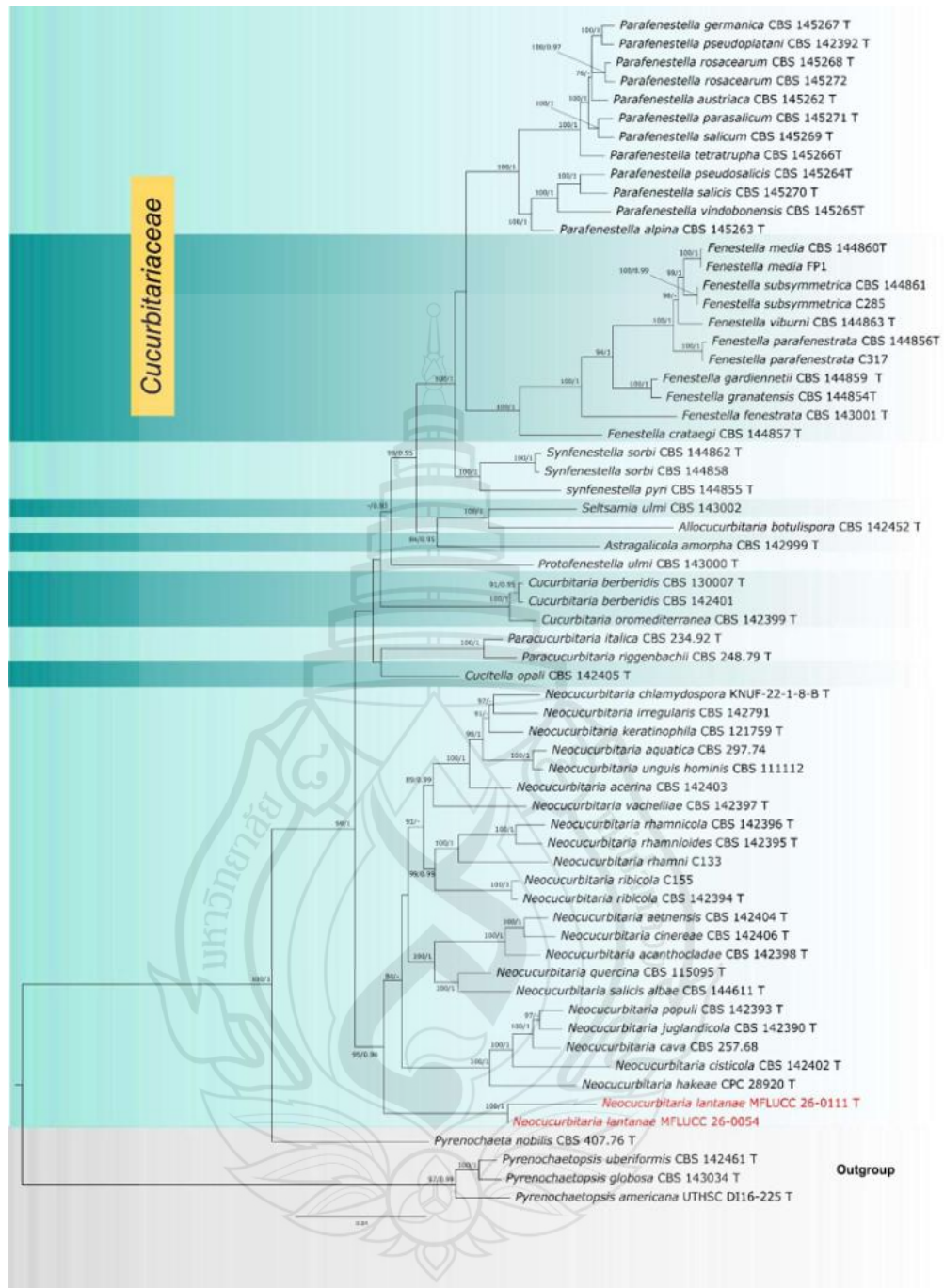
Pleosporales Luttr. ex M.E. Barr

Cucurbitariaceae Lueress.

Cucurbitariaceae was introduced by Winter (1885) and is typified by *Cucurbitaria* as the type genus. Traditionally, the classification of genera in *Cucurbitariaceae* was based on morphological characters, which led to taxonomic confusion and inconsistent generic boundaries. Subsequent molecular phylogenetic studies demonstrated that the family is heterogeneous, resulting in the exclusion and reassignment of several genera (Doilom et al. 2013, Valenzuela-Lopez et al. 2018, Hongsanan et al. 2020a). *Cucurbitariaceae* currently comprises 15 genera, mostly distributed in temperate and Mediterranean regions (Jaklitsch et al. 2018, Wijayawardene et al. 2020). Species of *Cucurbitariaceae* have been reported as plant saprobes and endophytes, as well as plant pathogens and opportunistic pathogens of animals and humans (Wanasinghe et al. 2017b, Jaklitsch et al. 2018, Hill et al. 2023, Eisvand et al. 2024). Here, a phylogenetic tree of the family is provided.

Neocucurbitaria Wanas., E.B.G. Jones & K.D. Hyde

Neocucurbitaria is a well-supported genus in *Cucurbitariaceae*, introduced by Wanasinghe et al. (2017) based on *Neocucurbitaria acerina*, *N. quercina* (*Pyrenochaeta quercina*), and *N. unguis-hominis* (*P. unguis-hominis*). The sexual morph has ostiolate, globose ascomata, short-pedicellate asci with a minute ocular chamber, and pale brown, muriform ascospores. The asexual morph is coelomycetous, with papillate ostiolate conidiomata, doliiiform to cylindrical conidiogenous cells, and hyaline, aseptate conidia (Wanasinghe et al. 2017b). The genus comprises 29 species (Index Fungorum, November 2025), isolated from various substrates, including decaying and symptomatic plants and soil (Wanasinghe et al. 2017b; Tan et al. 2024; Xu et al. 2024). Among them, *N. aquatica* was collected from a marine habitat in Montenegro and *N. hakeae* was collected from a seashore plant in Australia (Crous et al. 2016; Valenzuela-López et al. 2018; Jones et al. 2019). Here, a new species of *Neocucurbitaria* is introduced, isolated from a seashore plant in Thailand.



Note The tree is rooted to *Bipolaris austrostipae* (BRIP 12490), *B. peregrinaensis* (BRIP12790) and *B. microstegii* (CBS 132550). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red, while type strains are indicated with T.

Figure 5.5 Phylogram generated from the ML analysis based on the combined ITS, LSU, *rpb2*, *tef1* and TUB sequence data of *Cucurbitariaceae*

Neocucurbitaria lantanae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.6

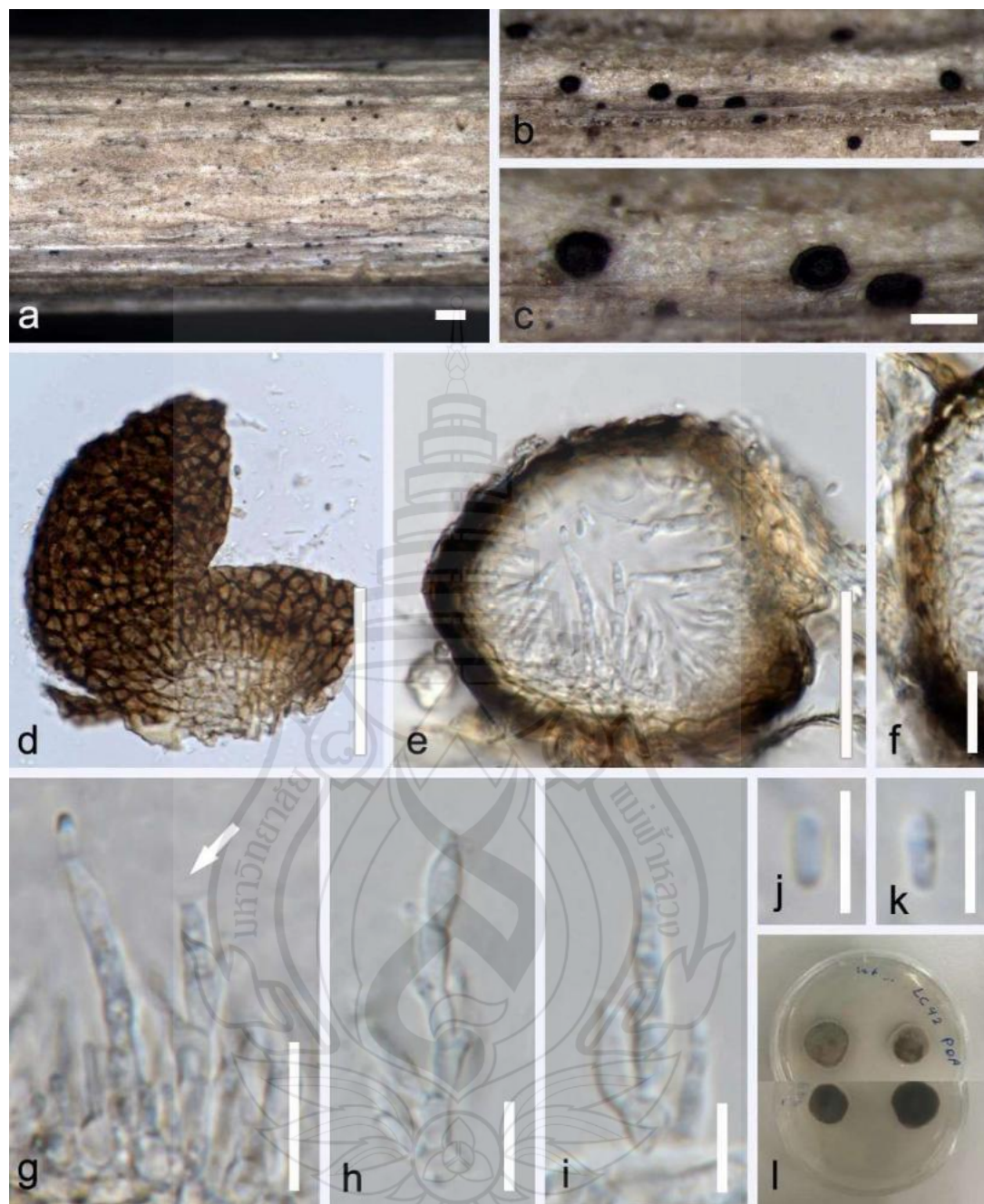
Etymology – Referring to the isolation of the fungus from *Lantana camara*.

Saprobic on dead stems of *Lantana camara*. Asexual morph: *Conidiomata* pycnidial $55\text{--}81 \times 67\text{--}131 \mu\text{m}$ ($\bar{x} = 65.5 \times 94.5$, $n = 10$), solitary, or in small group, semi-immersed, subglobose, oval, discoid, black. *Peridium* $4\text{--}8 \mu\text{m}$ ($\bar{x} = 5.5 \mu\text{m}$, $n = 20$), thick-walled, brown, *textura angularis*. *Conidiophores* $7.5\text{--}24 \times 1.5\text{--}3 \mu\text{m}$ ($\bar{x} = 14 \times 2$, $n = 15$), cylindrical, subcylindrical, straight or curved, branched, 1–5 septate, hyaline. *Conidiogenous cells* $3\text{--}7.5 \times 1\text{--}1.5 \mu\text{m}$ ($\bar{x} = 4.5 \times 1.2 \mu\text{m}$, $n = 20$), phialidic, subcylindrical, integrated, terminal and intercalary, hyaline, with a wide collarette. *Conidia* $3.5\text{--}6.5 \times 1\text{--}2 \mu\text{m}$ ($\bar{x} = 4.5 \times 1.5 \mu\text{m}$, $n = 20$), oblong, smooth-walled, guttulate, aseptate, hyaline, round apex. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 1.5 cm diam. after two weeks at $25\pm 2^\circ\text{C}$, umbonate, entire margin; from surface, greenish gray; from reverse, dark gray.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on dead dry stems of *Lantana camara*, 23 May 2023, R. Asghari, LC42 (MFLU 26-0038, holotype); ex-type culture (MFLUCC 26-0111); *ibid.*, LC42b (MFLU 26-0039, isotype); ex-isotype culture (MFLUCC 26-0054).

Notes – Based on the multi-gene phylogenetic analyses from five loci, *Neocucurbitaria lantanae* formed a distinct clade from other *Neocucurbitaria* species, basal to *N. hakeae*, *N. cisticola*, *N. cava*, *N. juglandicola*, and *N. populi* with 95% ML/0.96 BPP support. Morphologically, *N. lantanae* is similar to these five species in having phialidic conidiogenous cells and aseptate conidia. However, it differs in having discoid pycnidia, wide distinct collarette at the apex of conidiogenous cells (Crous et al. 2016, Valenzuela-Lopez et al. 2018, Jaklitsch and Voglmayr 2020). The ITS base pair differences between *N. lantanae* (MFLUCC 26-0111) and the compared taxa were 7% (36/519) for *N. hakeae* (CPC 28920), 7.9% (42/532) for *N. cisticola* (CBS 142402), 7.3% (36/488) for *N. cava* (CBS 257.68), 7.3% (39/532) for *N. juglandicola* (CBS 142390), and 7.5% (40/533) for *N. populi* (CBS 142393), including gaps. Based on morphological and molecular results, *N. lantanae* is introduced as a novel species.



Note a–c Colonies on natural substrate. d Conidioma. e Section of a conidioma. f Peridium. g–i Conidiophores, conidiogenous cells and developing conidia (wide collarette indicated with arrow). j, k Conidia. l Colonies on PDA (front and below). Scale bars: a = 500 μm , b = 200 μm , c = 100 μm , d = 50 μm , e = 50 μm , f–i = 10 μm , j, k = 5 μm .

Figure 5.6 *Neocucurbitaria lantanae* (MFLU 26-0038, holotype)

Didymellaceae Gruyter, Aveskamp & Verkley

Didymellaceae was introduced by De Gruyter et al. (2009) and is typified by *Didymella*. Members of *Didymellaceae* are cosmopolitan and occur as saprobes, endophytes, and pathogens on a wide range of plant hosts (Chen et al. 2015, 2022a; Samaradiwakara et al. 2025). The circumscription of *Didymellaceae* has been repeatedly revised based on multigene phylogenetic evidence (Aveskamp et al. 2010; Chen et al. 2015). Currently, the family comprises approximately 50 genera and represents one of the largest families within *Pleosporales* (*Dothideomycetes*) (Hyde et al. 2024).

Didymella Sacc. 1880

Didymella was introduced by Saccardo (1880) and typified with *D. exigua*. The genus comprises more than 400 species and is the type genus of *Didymellaceae* (De Gruyter et al. 2009; Hyde et al. 2024). The sexual morph has ostiolate ascomata with a multi-layered peridium and hyaline or brownish ascospores, while the asexual morph is coelomycetous, with conidiomata having a multi-layered peridium, phialidic conidiogenous cells, and mainly aseptate conidia (De Gruyter et al. 2009; Chen et al. 2015). *Didymella* species have been reported as saprobes and plant pathogens from various habitats, with *D. avicenniae*, *D. fucicola*, *D. gloiopeltidis*, and *D. magnei* listed as marine fungi (Chen et al. 2015; Jones et al. 2019; Luo et al. 2024). Here, we introduce one new species of *Didymella* from a coastal plant in Thailand based on its asexual morph.

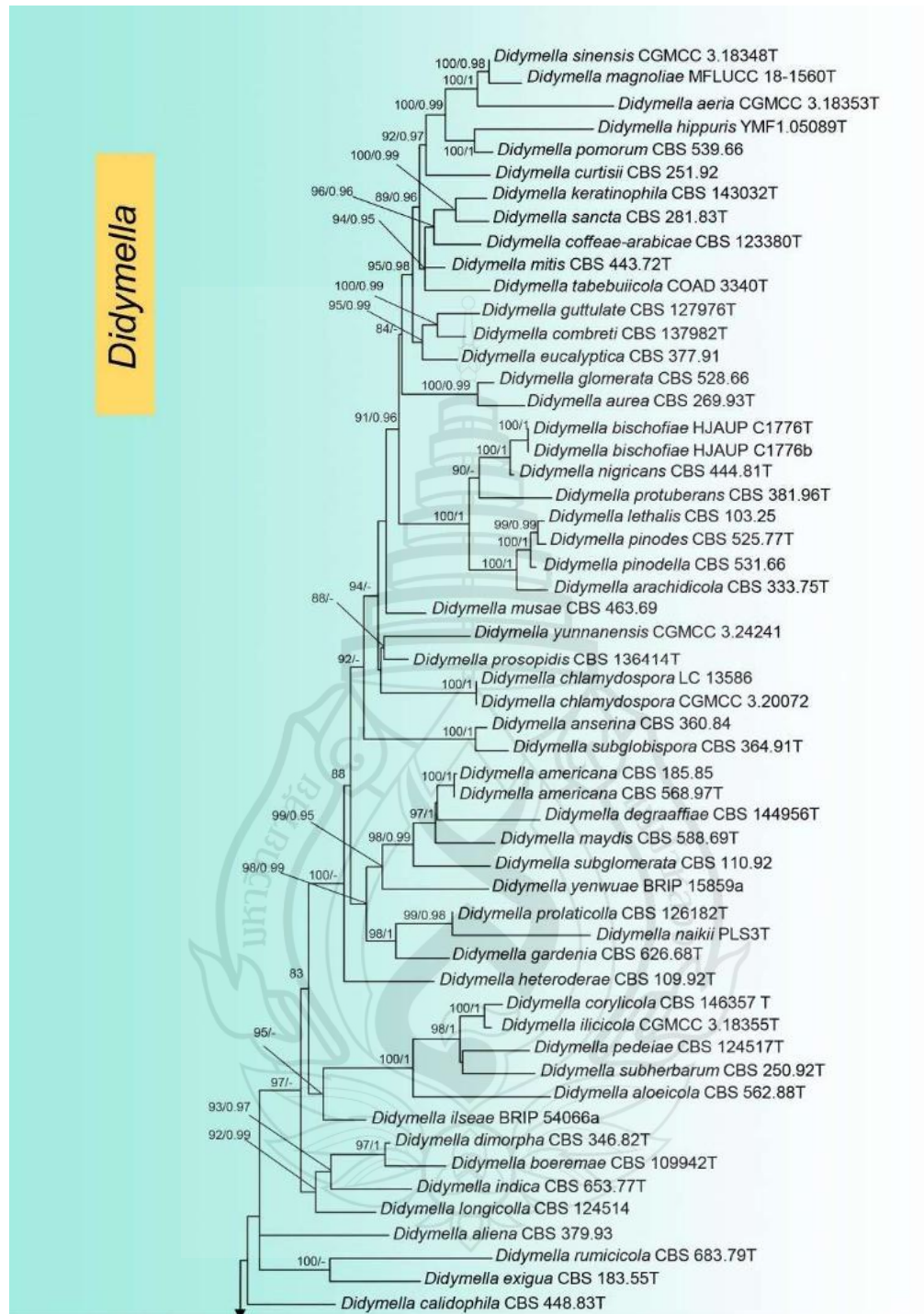
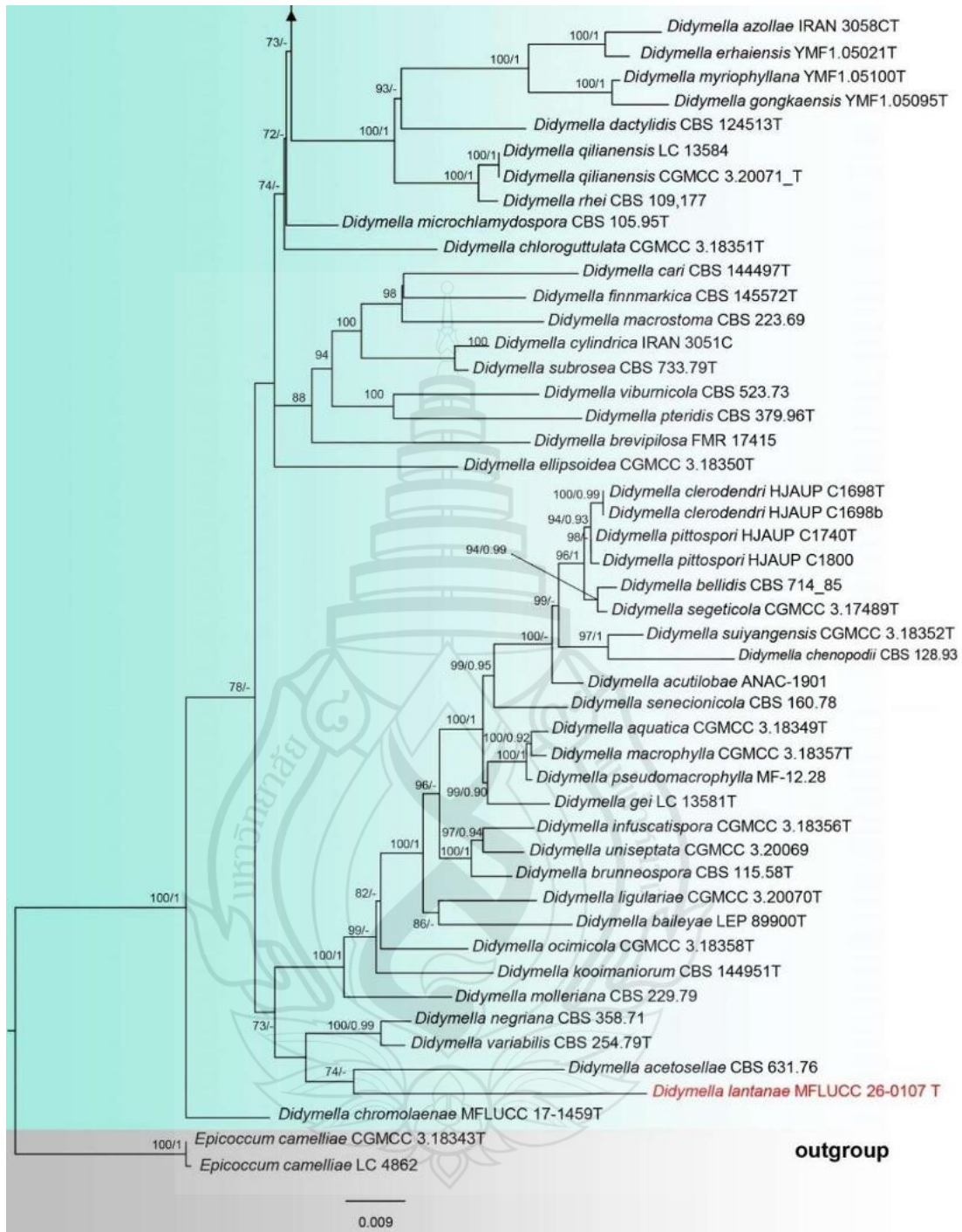


Figure 5.7 Phylogram generated from the ML analysis based on the combined ITS, LSU, TUB and *rpb2* sequence data of *Didymella*



Note The tree is rooted to *Epicoccum camelliae* (CGMCC 3.18343, LC 4862). Bootstrap values for ML equal to or greater than 70% and BYPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red, while type strains are indicated with T.

Figure 5.7 (continued)

Didymella lantanae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov., Fig. 5.8

Etymology – Referring to the isolation of the fungus from a *Lantana camara*.

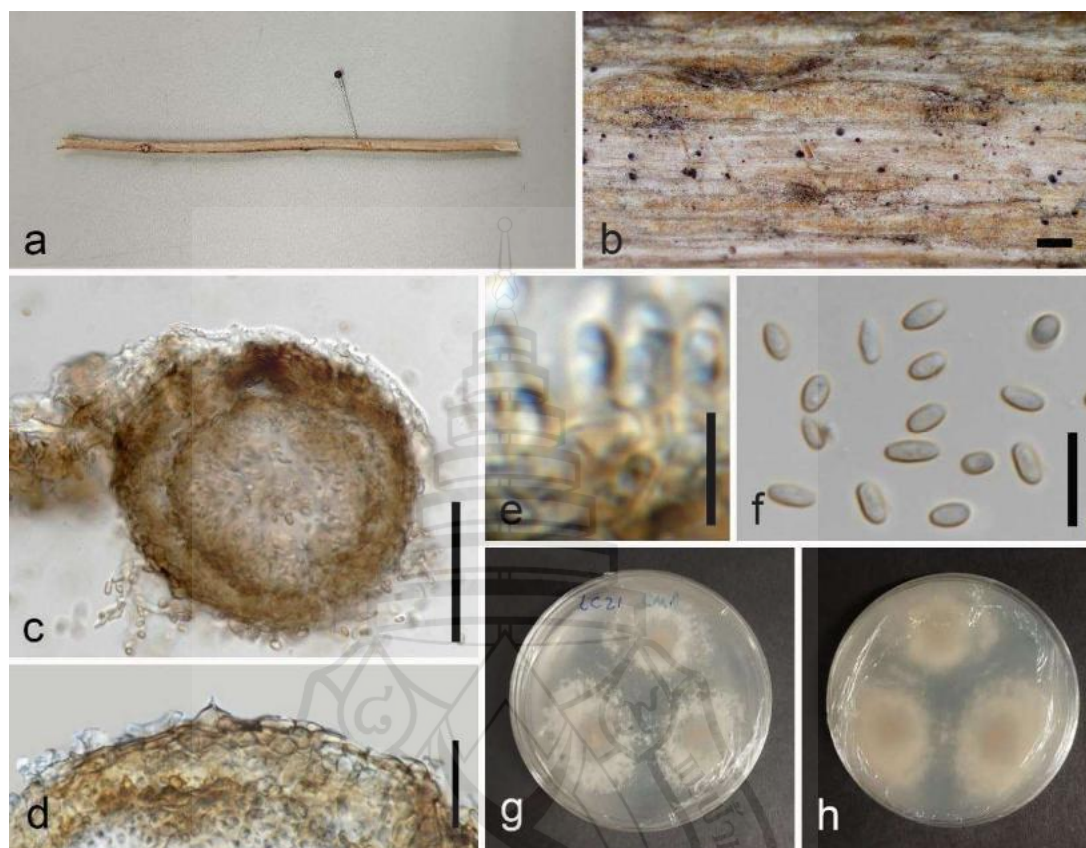
Saprobic on dead stems of *Lantana camara*. Asexual morph: *Conidiomata* pycnidial, 100–130 µm diam. ($\bar{x}$ = 115, n = 10), solitary or confluent, immersed to semi-immersed, globose to subglobose, black, ostiolate, with a short papilla. *Peridium* 9–17 µm ($\bar{x}$ = 12 µm, n = 20), thick-walled, honey to citrine, dark brown at the papilla, *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–4.5 × 2–4.5 µm ($\bar{x}$ = 3.2 × 3 µm, n = 20), holoblastic, phialidic, dolliiform, hyaline, originating from the inner layer of pycnidium wall. *Conidia* 2.5–5.5 × 1.5–3 µm ($\bar{x}$ = 4.5 × 2.5 µm, n = 20), ellipsoidal, guttulate, mostly with two guttules at each end, aseptate, rarely 1-septate, subhyaline to pale brown, round apex. Sexual morph: Undetermined.

Culture characteristics – Colonies on PDA reaching 4 cm diam. after one month at 25±2°C, flat, medium dense, entire margin; from surface, white; from reverse, pale orange, yellowish brown at the margin. Colonies on CMA reaching 5 cm diam. after one month at 25±2°C, crateriform, fluffy, entire margin; from surface, white, pale orange at the center; from reverse, orange white.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on dead dry stems of *Lantana camara*, 23 May 2023, R. Asghari, LC21 (MFLU 26-0040, holotype); ex-type culture (MFLUCC 26-0107).

Notes – In our phylogenetic analyses from four loci (Fig 9), *Didymella lantanae* formed a sister clade to *D. acetosellae* with 74% ML support. The two species share globose, ostiolate, honey to citrine colored conidiomata and ellipsoidal 0–1-septate conidia (De Gruyter et al. 2002). However, *D. lantanae* differs by its smaller conidiomata (100–130 vs. 90–350 µm), smaller conidiogenous cells (2.5–4.5 × 2–4.5 vs. 5–13 × 6–12 µm) and smaller conidia (4.5 × 2.5 vs. 8.5–2.7 µm). Additionally, conidiogenous cells in *D. lantanae* are doliiform, and in *D. acetosellae*, globose to bottle-shaped (De Gruyter et al. 2002). The base pair differences between *Didymella lantanae* (MFLUCC 26-0107) and *D. acetosellae* (CBS 631.76), are recorded as, 2% (10/450, with gap), 0.6% (5/870, without gaps), 12.4% (73/590, with gaps), in ITS,

LSU, and *rpb2* respectively. Based on the morphological and molecular data, *D. lantanae* is introduced as a novel species.

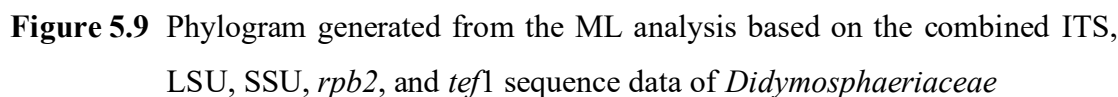


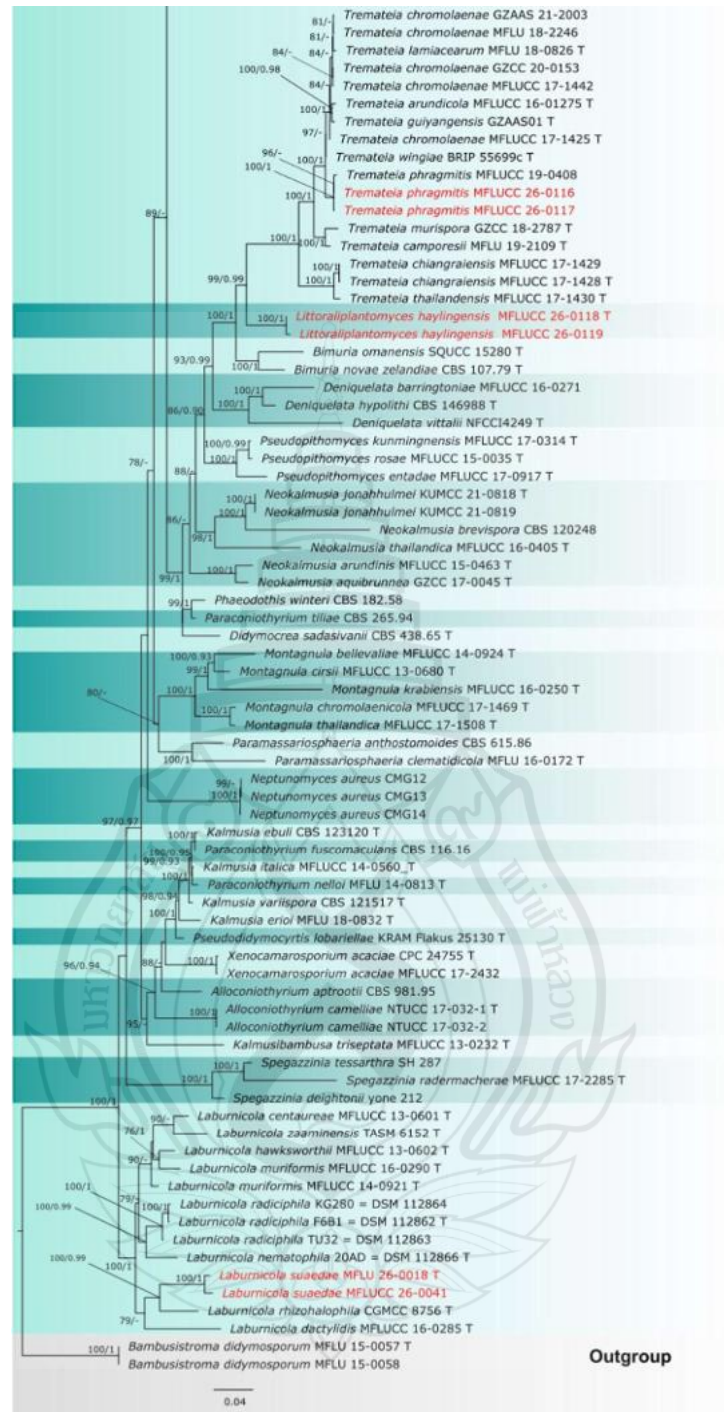
Note a Dead twig of the host. b Colonies on natural substrate. c Section of a conidioma. d Peridium. e Conidiogenous cells and developing conidia. f Conidia. g, h Colonies on CMA (front and back). Scale bars: a = 500 μ m, c = 50 μ m, d = 20 μ m, e, f = 10 μ m.

Figure 5.8 *Didymella lantanae* (MFLU 26-0040, holotype)

Didymosphaeriaceae Munk, Dansk Bot. Ark. 15 (2): 128 (1953)

Didymosphaeriaceae was established by Munk (1953) to accommodate the type genus *Didymosphaeria*. Members of *Didymosphaeriaceae* have diverse morphologies and the sexual morphs generally produce 1-septate, brown ascospores and trabeculate pseudoparaphyses (Ariyawansa et al. 2014; Wanasinghe et al. 2016; Hongsanant et al. 2020a). Ariyawansa et al. (2014) studied the family based on both morphological and molecular data and synonymized *Montagnulaceae* under *Didymosphaeriaceae*. The family currently comprises 39 genera, mostly reported as saprobes from various





Note The tree is rooted to *Bambusistroma didymosporum* (MFLU 15-0057, MFLU 15-0058). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red, while type strains are indicated with T.

Figure 5.9 (continued)

Chromolaenicola Mapook & K.D. Hyde

Chromolaenicola is a saprobic genus on plant materials in *Didymosphaeriaceae* (Tian et al. 2024b; Du et al. 2025), introduced by Mapook et al. (2020). The genus currently comprises ten species, with *C. nanensis* as the type species. Both sexual and asexual morphs have been reported. The sexual morph is characterized by cylindrical asci and ellipsoidal, muriform ascospores, while the asexual morph is coelomycetous, with enteroblastic, phialidic conidiogenous cells and conidia of variable shapes (Jayasiri et al. 2019; Mapook et al. 2020). In this study, we introduce a new species in this genus from decaying *Leucaena leucocephala* collected in the Thai coastal region.

Chromolaenicola leucaenae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.10

Etymology – Referring to the isolation of the fungus from *Leucaena leucocephala*.

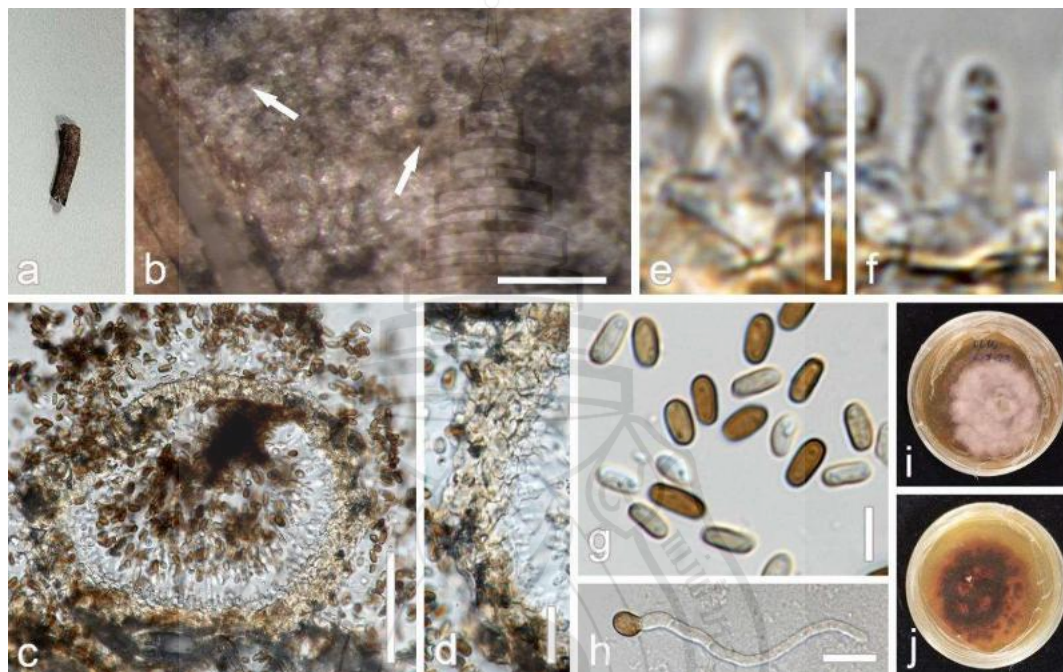
Saprobic on dead stems of *Leucaena leucocephala*. **Asexual morph:** *Conidiomata* pycnidial 130–320 × 160–400 µm ($\bar{x}$ = 230 × 280 µm, n = 10), solitary or gregarious, immersed, becoming erumpent, subglobose, obpyriform to cordate, black, ostiole central. *Peridium* 11–20 µm ($\bar{x}$ = 15 µm, n = 10), thick walled, brown, *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–7 × 3–6 µm ($\bar{x}$ = 5 × 4.5 µm, n = 15), enteroblastic, phialidic, ampulliform, smooth-walled, hyaline, originated from the inner layer of the pycnidium wall. *Conidia* 4–7 × 2.2–3.5 µm ($\bar{x}$ = 6 × 2.5 µm, n = 20), ellipsoidal, smooth-walled, thick-walled, guttulate, aseptate, initially hyaline, becoming brown. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 4 cm diam. after one month at 25±2°C, low convex, floccose, irregular lobate margin; from surface, dull red; from reverse, dark brown and grayish red.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on dead dry stems of *Leucaena leucocephala*, 23 May 2023, R. Asghari, LL15 (MFLU 26-0015, holotype); ex-type culture (MFLUCC 26-0108).

Notes – *Chromolaenicola leucaenae* formed a sister clade to *Ch. ananasi* with strong support (100% ML/0.99 BPP). Morphologically, *Ch. leucaenae* is similar to the holotype of *Ch. ananasi* by its ellipsoid, aseptate, pale brown to brown, guttulate, thick-

walled conidia; however, it differs in having a coelomycetous asexual morph, whereas *Ch. ananasi* has hyphomycetous characteristics (Tian et al. 2024b). *Chromolaenicola leucaenae* (MFLUCC 26-0108) showed 1.9% (11/581), 0.9% (7/811), and 1.1% (10/888) base pair differences with *Ch. ananasi* (MFLU 23-0167), in ITS, LSU, and *tef1* respectively, with gaps. *Chromolaenicola leucaenae* is introduced as a novel species, based on morphological differences and molecular data.



Note a Decaying twig of host. b Colonies on natural substrate. c Section of conidioma. d Peridium. e, f Conidiogenous cells and developing conidia. g Conidia. h Germinating conidium. i, j Colonies on PDA (front and below). Scale bars: b = 200 μ m, c = 50 μ m, d = 20 μ m, e–g = 5 μ m, h = 10 μ m.

Figure 5.10 *Chromolaenicola leucaenae* (MFLU 26-0015, holotype)

Laburnicola Wanas., Camporesi, E.B.G. Jones & K.D. Hyde

Laburnicola was introduced by Wanasinghe et al. (2016) to accommodate four novel saprobic species, from *Centaurea*, *Dactylis* and *Laburnum anagyroides* in Italy. The sexual morph of *Laburnicola* is characterized by immersed to semi-erumpent, ostiolate ascomata, a peridium that is wider at the apex and thinner at the base, numerous filamentous pseudoparaphyses, bitunicate, fissitunicate asci with a minute ocular chamber, and muriform, hyaline to dark brown ascospores with a rugged surface

(Wanasinghe et al. 2016). The genus currently comprises eight species (Index Fungorum, accessed November 2025). *Laburnicola rhizohalophila* was isolated as a root endophyte from the coastal halophyte *Suaeda salsa* in China (Yuan et al. 2020). In this study, we introduce a novel saprobic species of *Laburnicola* collected from a coastal halophyte in Thailand.

Laburnicola suaedae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.11

Etymology – Referring to the isolation of the fungus from a coastal plant.

Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** Undetermined.

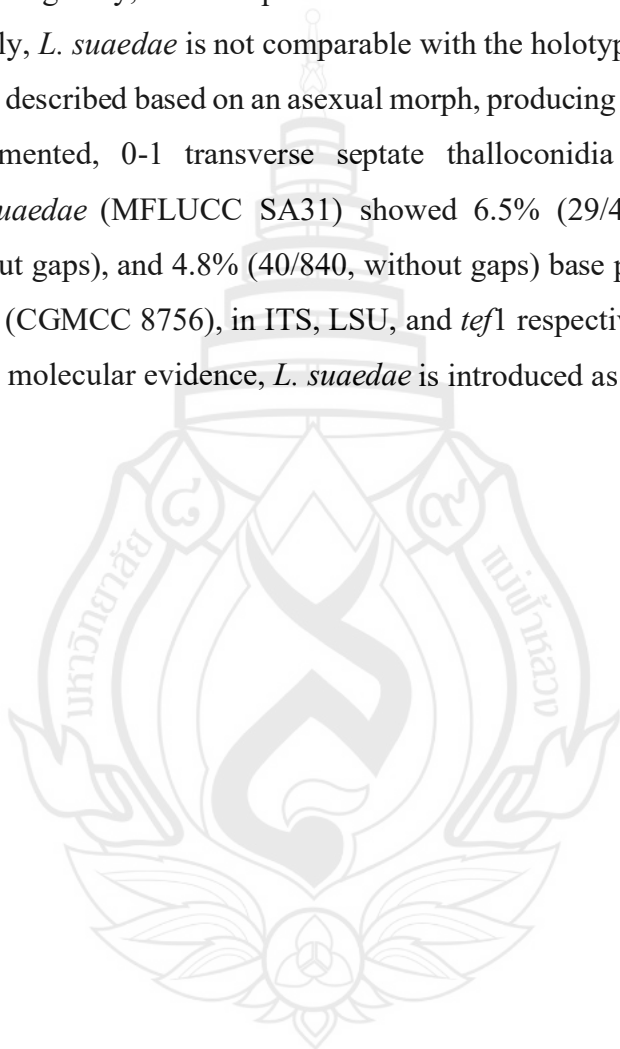
Asexual morph: *Ascomata* 150–350 × 165–280 µm ($\bar{x}$ = 250 × 210 µm, n = 10), solitary, immersed, becoming semi-erumpent and raising host tissue, globose to subglobose, black. *Ostiole* central, if distinguished, filled with hyaline cells, without a discernable neck. *Peridium* 14–54 µm ($\bar{x}$ = 19 µm, n = 15) at the base, 26–53 µm ($\bar{x}$ = 35 µm, n = 15) at the sides and apex, thinner at the base, becoming thicker at the sides and apex, brown, becoming dark pigmented at the apex, outer layer darker than inner layers and fusing with the host tissues, *textura angularis*. *Hamathecium* 1.7–4.5 µm diam. ($\bar{x}$ = 3 µm, n = 20), numerous, filamentous, branched, septate pseudoparaphyses, constricted at septa or not, anastomosing, hyaline. *Asci* 82–180 × 14–23 µm ($\bar{x}$ = 123 × 18 µm, n = 15), 8-spored, clavate, cylindric-clavate, to elongate-cylindrical, bitunicate, fissitunicate, short pedicellate, becoming long pedicellate with elongation, thick-walled at the apex, with a minute ocular chamber. *Ascospores* 19–28 × 8–11 µm ($\bar{x}$ = 25 × 10 µm, n = 20), overlapping 1–2-seriate, clavate, asymmetrical, wider at the upper part, muriform, (2)3–5-transversely septate, 0–2 irregular longitudinal septa, constricted at the septa, rounded at the ends, golden brown to brown, guttulate, with rugged surface.

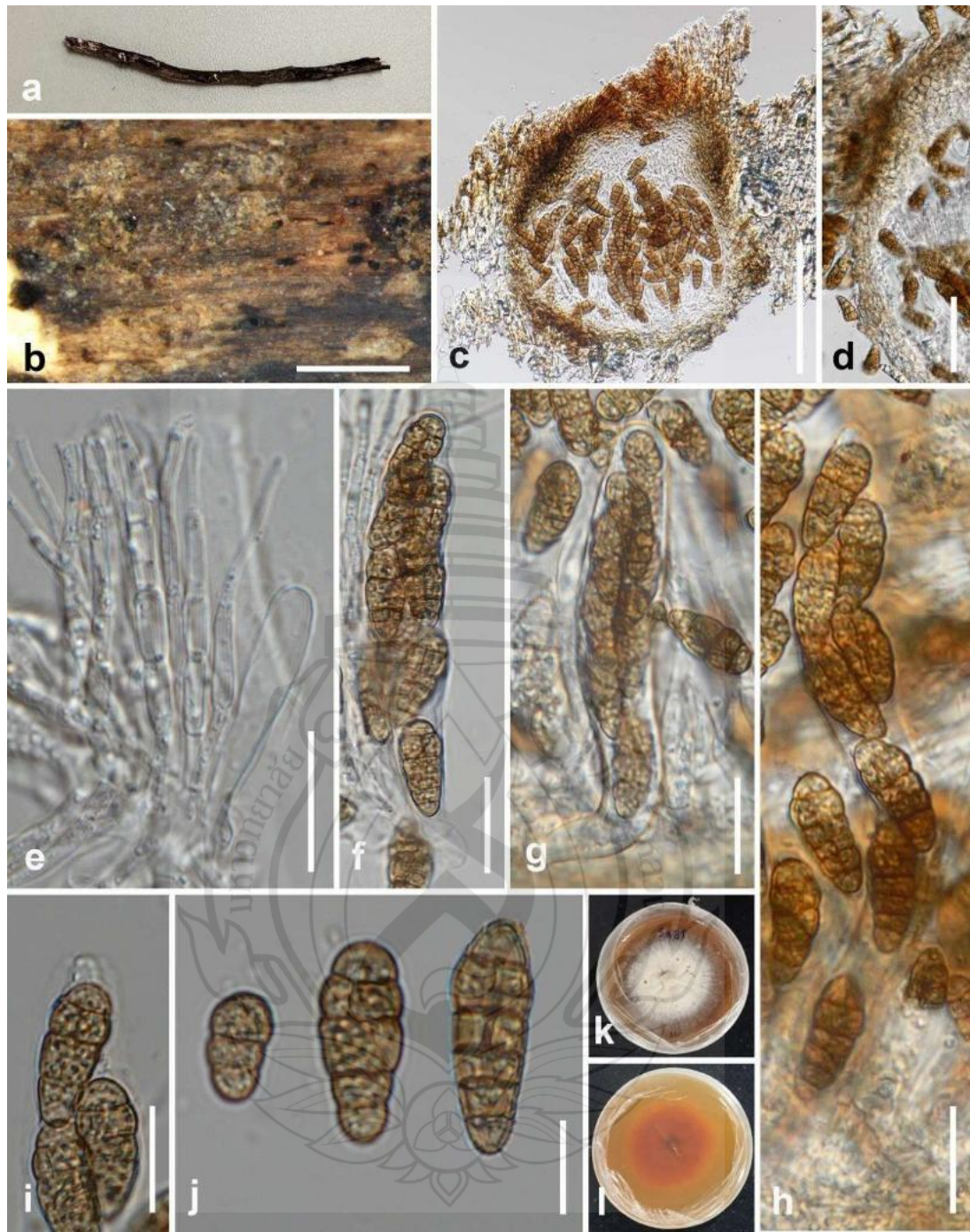
Culture characteristics – Colonies on PDA reaching 4 cm diam. after one month at 25±2°C, flat, entire margin, fimbriate, slightly radiating; from surface, orange white; from reverse, brownish orange at the center, light orange at the margin.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park (water salinity 28 ppt), on dead stems of submerged *Suaeda maritima*, 30 November 2023, R. Asghari, SA31 (MFLU 26-0018, holotype); ex-type

culture (MFLUCC 26-0163); *ibid.*, SA31b (MFLU 26-0019, isotype); ex-isotype living culture (MFLUCC 26-0041).

Notes – Multi-gene phylogenetic analyses based on ITS, LSU, SSU, *rpb2*, and *tef1* sequence data showed that our collections of *Laburnicola suaedae* form a sister clade to *L. rhizohalophila* (CGMCC 8756, ex-type), with 100% ML/0.99 BPP support (Fig 11). Ecologically, both species were found on a coastal halophyte. Morphologically, *L. suaedae* is not comparable with the holotype of *L. rhizohalophila*, as the later was described based on an asexual morph, producing peanut-shaped, hyaline to darkly pigmented, 0-1 transverse septate thalloconidia (Yuan et al. 2020). *Laburnicola suaedae* (MFLUCC SA31) showed 6.5% (29/440, with gaps), 1.8% (14/794, without gaps), and 4.8% (40/840, without gaps) base pair differences with *L. rhizohalophila* (CGMCC 8756), in ITS, LSU, and *tef1* respectively, without including gaps. Based on molecular evidence, *L. suaedae* is introduced as a novel species.





Note a Decaying twig of host. b Colonies on natural substrate. c Section of ascoma. d Peridium. e Paraphyses. f–h Asci. i Ascus with an ocular chamber. j Ascospores. k, l Colony on PDA (front and below). Scale bars: b = 500 μ m, c = 100 μ m, d = 50 μ m, e–i = 20 μ m, j = 10 μ m.

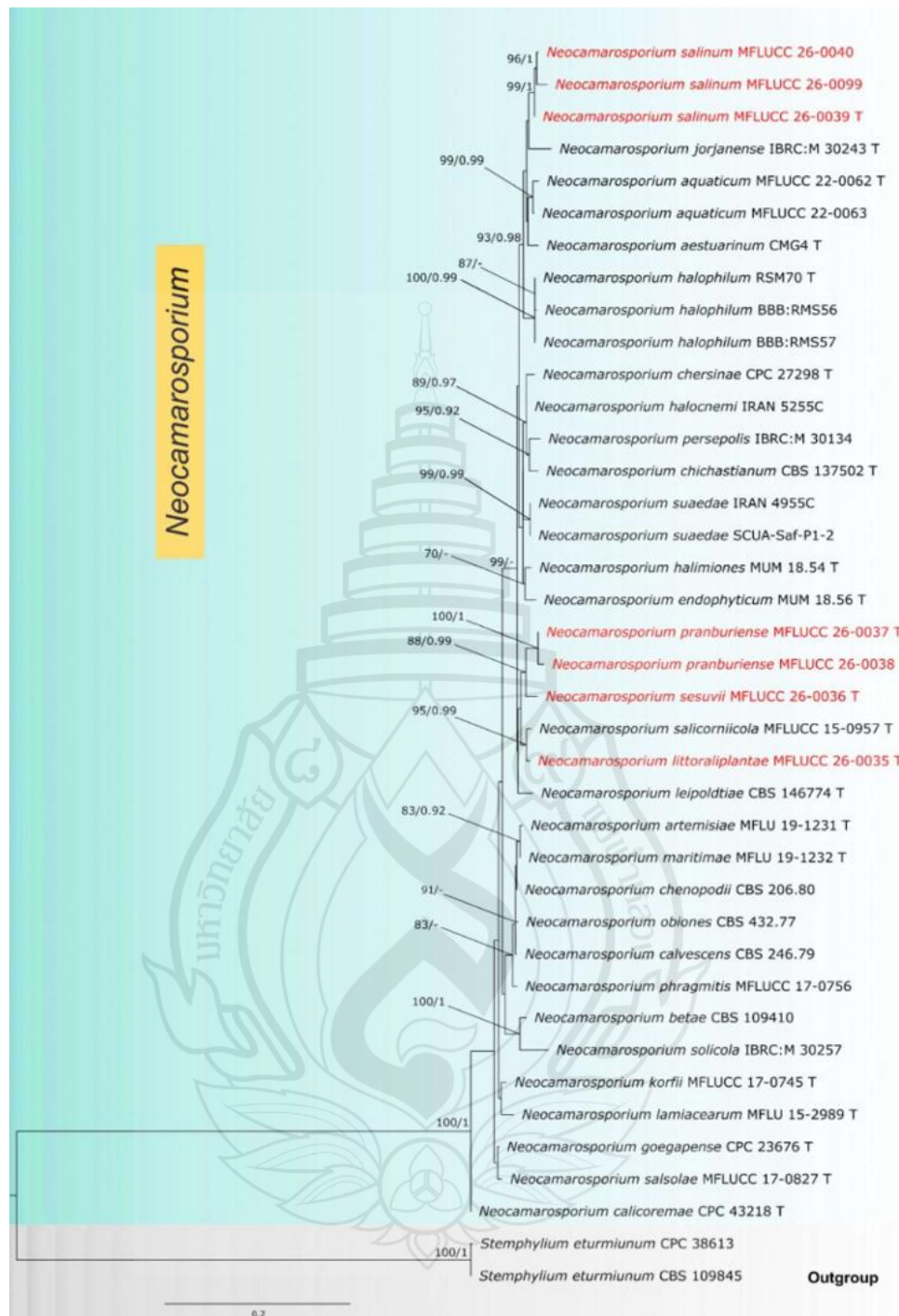
Figure 5.11 *Laburnicola suaedae* (MFLU 26-0018, holotype)

Neocamarosporiaceae Wanas., Wijayaw., Crous & K.D. Hyde

Neocamarosporiaceae was introduced by Wanasinghe et al. (2017) based on morphological characteristics and multi-gene phylogenetic analyses using LSU, SSU, *tefl*, and ITS sequences. The family forms a distinct clade within the *Pleosporales*, comprising many *Neocamarosporium* species, and is distinct from *Pleosporaceae*. Members of *Neocamarosporium* produce a coelomycetous asexual morph, whereas *Pleosporaceae* species typically produce hyphomycetous asexual morphs (Wanasinghe et al. 2017a). Therefore, *Neocamarosporiaceae* was established based on both morphological and phylogenetic distinctions. *Neocamarosporium* is the type genus of the family (Wanasinghe et al. 2017a).

Neocamarosporium Crous & M.J. Wingf.

Neocamarosporium was introduced by Crous et al. (2014) and typified by *N. goegapense*. The genus was described based on its coelomycetous asexual morph, characterized by immersed to erumpent, ostiolate conidiomata; ampulliform conidiogenous cells lining the inner layer of the conidioma; and solitary conidia that are initially hyaline and aseptate, becoming muriformly septate and brown (Crous et al. 2014). Currently, 26 epithets are listed for this genus in Index Fungorum (accessed November 2025), with species isolated from diverse substrates as endophytes, saprobes, or pathogens (Crous et al. 2014; Papizadeh et al. 2017; Wanasinghe et al. 2017a). Most species are associated with halophytic hosts from saline and marine habitats, including salt marshes and mangroves (Prematunga et al. 2023; Safi et al. 2025). Papizadeh et al. (2017) introduced three novel *Neocamarosporium* species from hypersaline lakes in Iran and examined their growth on saline media containing NaCl and MgCl₂, confirming their halotolerant characteristics. In the present study, we isolated seven *Neocamarosporium* strains from salt marsh plants along the Thai coast — five from *Sesuvium portulacastrum* and two from *Suaeda maritima*. An updated phylogenetic tree of the genus is provided.



Note The tree is rooted to *Stemphylium eturmiunum* (CPC 38613 and CBS_109845). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red, while type strains are indicated with T.

Figure 5.12 Phylogram generated from the ML analysis based on the combined ITS, LSU, and *tef1* sequence data of *Neocamarosporium*

Neocamarosporium littoraliplantae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.13

Etymology – referring to the isolation of the fungus from a coastal plant.

Saprobic on dead stems of *Sesuvium portulacastrum*. **Asexual morph:** *Conidiomata* pycnidial 130–250 × 180–300 µm ($\bar{x}$ = 200 × 230 µm, n = 10), solitary or gregarious, immersed to erumpent, oval to subglobose, with an inconspicuous ostiole, black. *Peridium* 12–25 µm ($\bar{x}$ = 20 µm, n = 15), thick walled, outer layer dark brown to black, inner layer lighter brown, *textura angularis*. *Paraphyses* 20–41 × 1–2.5 µm ($\bar{x}$ = 32 × 1.8 µm, n = 15), cylindrical, taller than conidiogenous cells, straight or curved, narrower at the tip, aseptate, smooth walled, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 4–8(25) × 3.5–5 µm ($\bar{x}$ = 6 × 4.5 µm, n = 15), enteroblastic, ampulliform, doliiform, annellidic, proliferating percurrently, smooth-walled, hyaline, originated from the inner layer of pycnidium wall. *Microconidiogenous cells* 1.5–4.5 × 1.8–4.5 µm ($\bar{x}$ = 3 × 3 µm, n = 10), enteroblastic, doliiform, smooth-walled, hyaline, shortly originated from the inner layer of pycnidium wall. *Conidia* 10–21 × 6–10.5 µm ($\bar{x}$ = 15.5 × 8.5 µm, n = 30), ellipsoidal, oblong with obtuse base or rounded ends, straight or curved, 1–5-transversely septate, 1–2 longitudinal septa, constricted at septa, muriform, guttulate, rough-walled, brown to dark brown, surrounded by a gelatinous sheath. *Microconidia* 4–5.8 µm diam. ($\bar{x}$ = 4.8 µm, n = 10), globose, guttulate, smooth-walled, hyaline. **Sexual morph:** Undetermined.

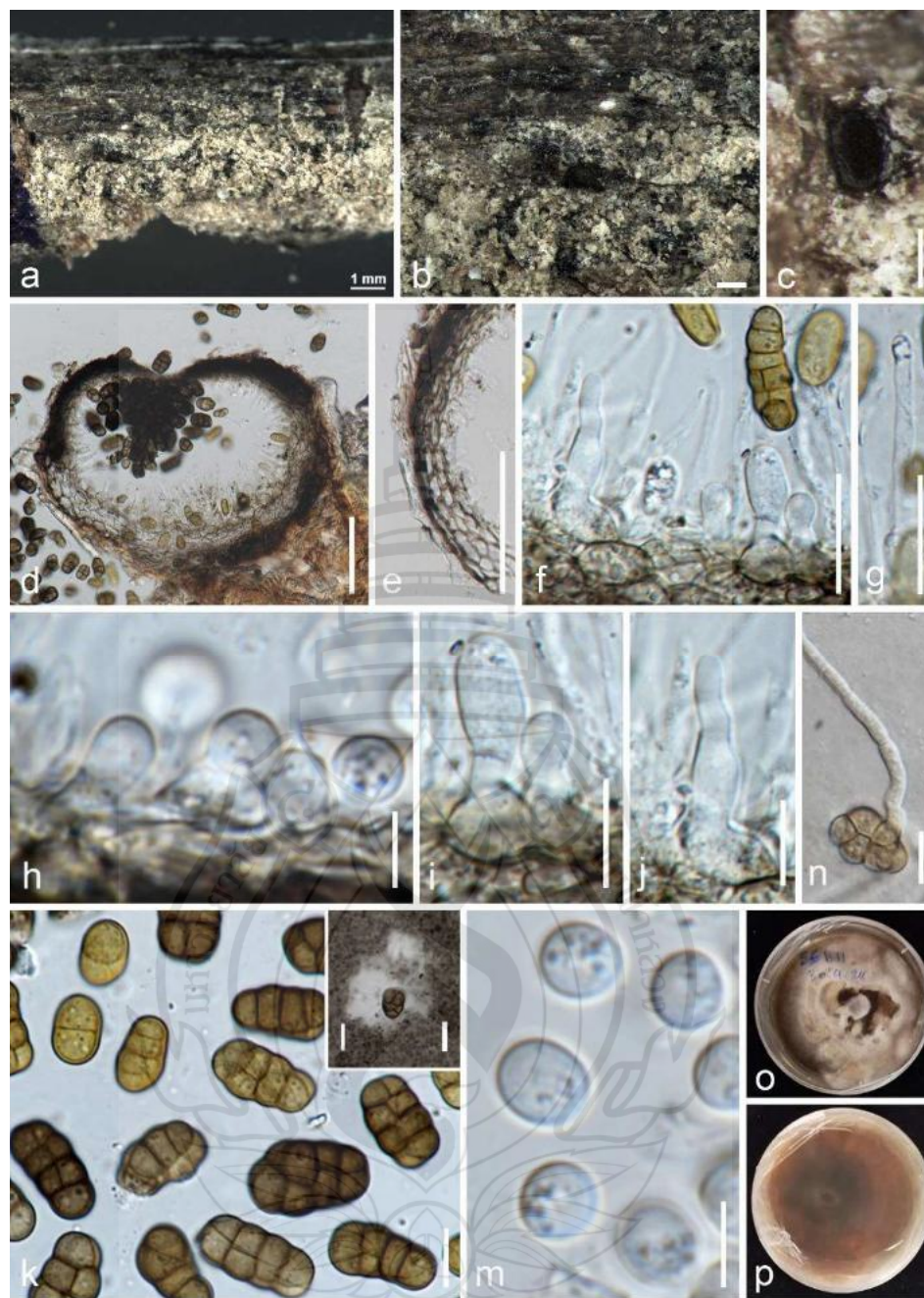
Culture characteristics – Colonies on PDA reaching 5 cm diam. after one months at 25±2°C, flat or low convex, felted, dull, medium dense, entire margin, slightly radiating; from surface, white with brownish gray to dark brown at the center; from reverse, dark brown at the center, reddish brown toward the margin.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on margin of a dry saltern, on dry dead stems of *Sesuvium portulacastrum*, 6 April 2024, R. Asghari, S6B11 (MFLU 26-0008, holotype); ex-type culture (MFLUCC 26-0035).

Notes – Multi-gene phylogenetic analyses from ITS, LSU, and *tef1* sequence data placed *Neocamarosporium littoraliplantae* sister to *N. salicorniicola* with 95% ML/0.99 BPP support. Morphologically, *N. littoraliplantae* is similar to *N. salicorniicola* in having thick walled black conidiomata, enteroblastic, doliiform,

annellidic conidiogenous cells and oblong, muriform brown conidia but differs in having larger rough-walled conidia, with more septa and presence of paraphyses, microconidiogenous cells, and globose hyaline microconidia (Wanasinghe et al. 2017a). *Neocamarosporium littoraliplantae* (MFLUCC 26-0035) showed 0.3% (2/848, without gaps) and 2.0% (11/543, with gaps) base pair differences with *N. salicorniicola* (MFLUCC 15-0957) in LSU and ITS respectively, without including gaps. Sequence data for *tef1* is not available for *N. salicorniicola* (MFLUCC 15-0957) for the base pair comparison. Based on the phylogeny and morphological evidence, *N. littoraliplantae* is introduced as a novel species from a halophyte.





Note a Decaying branch of host. b, c Colonies on natural substrate. d Section of conidioma. e Peridium. f Paraphyses and conidiogenous cells. g Paraphysis. h Microconidiogenous cells. i, j Conidiogenous cells and conidia. k Conidia. l Conidium in black ink. m Microconidia. n Germinated conidium. o, p Colony on PDA (front and below). Scale bars: a = 1 mm, b, c = 250 μm , d, e = 50 μm , f, g, n = 20 μm , k, l = 10 μm , h, m = 5 μm .

Figure 5.13 *Neocamarosporium littoraliplantae* (MFLU 26-0008, holotype)

Neocamarosporium pranburiense R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.14

Etymology – Referring to Pranburi, Thailand, the locality where the fungus was collected.

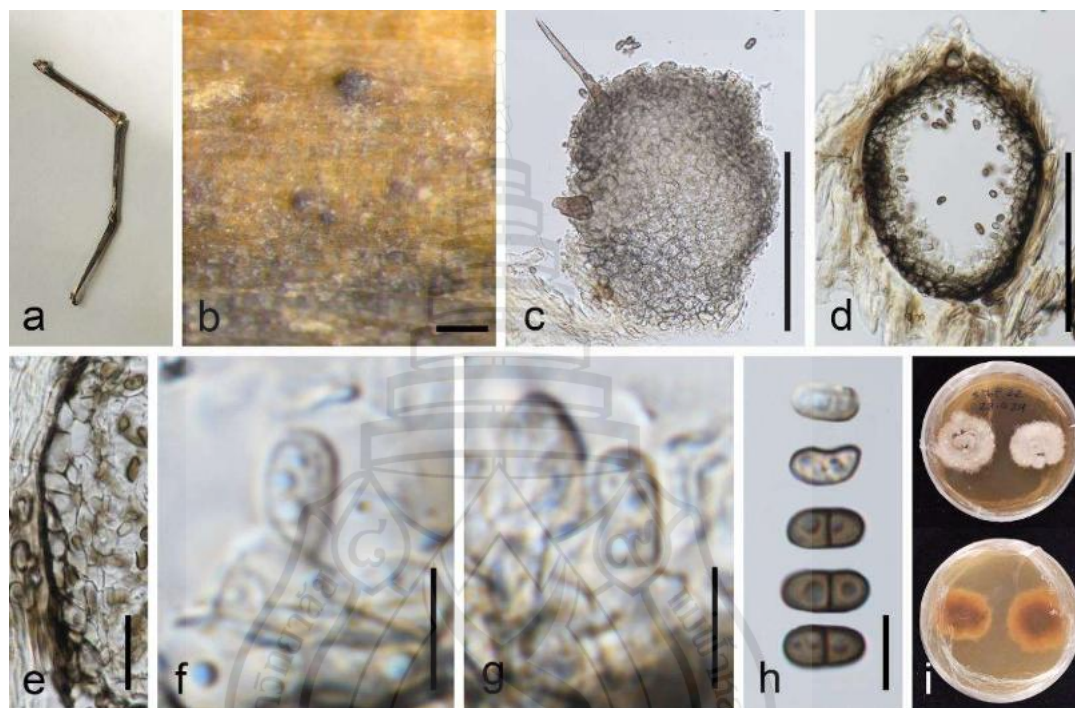
Saprobic on dead stems of *Sesuvium portulacastrum*. **Asexual morph:** *Conidiomata* pycnidial 110–135 × 80–110 µm ($\bar{x}$ = 120 × 95 µm, n = 10), solitary, immersed to erumpent, oval to subglobose, dark brown. *Peridium* 11–22 µm ($\bar{x}$ = 15 µm, n = 20), thick walled, outer layer dark brown, inner layer lighter brown, *textura angularis*. *Setae* up to 60 µm high and 7.5 µm diam. at the base, occasionally on the pycnidial wall, cylindrical, brown, septate. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 1.8–6.5 high × 4.5–6.5 wide at the base ($\bar{x}$ = 4.3 × 5.5 µm, n = 15), 1.5–2.5 µm wide at the apex ($\bar{x}$ = 2 µm, n = 15), enteroblastic, doliiform, smooth-walled, pale brown, originated from the inner layer of pycnidium wall. *Conidia* 5.5–7.5 × 2.5–4 µm ($\bar{x}$ = 6.5 × 3 µm, n = 30), ellipsoidal with obtuse base or rounded ends, straight or slightly curved, 1-septate, slightly constricted at septa, guttulate, smooth-walled, thick-walled, pale brown to dark brown, without a gelatinous sheath. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2.5 cm diam. after one month at 25±2°C, flat, powdery, fimbriate margin; from surface reddish gray; from reverse, reddish brown at the center, grayish orange at the margin.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pran Kiri Beach, on dead dry stems of *Sesuvium portulacastrum* on seashore rocks, 8 November 2024, R. Asghari, S7P22 (MFLU 26-0010, holotype); ex-type culture (MFLUCC 26-0037); *ibid.*, Forest Park (water salinity 15 ppt), on dead submerged stems of *Suaeda maritima*, 8 November 2024, R. Asghari S7S37 (MFLU 26-0011, isotype); ex-isotype living culture (MFLUCC 26-0038).

Notes – In Multi-gene phylogenetic analyses, *Neocamarosporium pranburiense*, formed a distinct lineage sister to *N. sesuvii* with 88% ML/0.99 BPP support. *Neocamarosporium pranburiense* shares similar morphology with *N. sesuvii* in having semi immersed to immersed thick-walled conidiomata but it differs by its doliiform, smooth-walled, pale brown conidiogenous cells, ellipsoidal, 1-septate, smooth-walled, pale brown to dark brown conidia and lacking paraphyses and budding

conidia. Based on base difference, *N. pranburiense* (MFLUCC 26-0037) and *N. sesuvii* (MFLUCC 26-0036) differed by 0.8% (7/900, with gaps), 4.3% (25/577, with gaps) and 2.5% (24/968, without gaps) in LSU, ITS and *tef1* respectively. *Neocamarosporium pranburiense* is introduced as a novel species based on morphological and molecular results.



Note a Decaying twig of host. b Colonies on natural substrate. c Microscopic view of conidioma. d Section of conidioma. e Peridium. f, g Conidiogenous cells and developing conidia. h Conidia. i Colonies on PDA (front and below). Scale bars: b–d = 100 µm, e = 15 µm, f–h = 5 µm.

Figure 5.14 *Neocamarosporium pranburiense* (MFLU 26-0010, holotype)

Neocamarosporium salinum R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.15

Etymology – Referring to the salty habitat, from which the fungus was collected.

Saprobic on dead stems of *Suaeda maritima* and *Sesuvium portulacastrum*.

Asexual morph: *Conidiomata* pycnidial 100–180 × 90–160 µm ($\bar{x}$ = 135 × 125 µm, n = 10), solitary or gregarious, immersed to erumpent, subglobose, black, ostiole central. *Peridium* 8.5–20 µm ($\bar{x}$ = 15 µm, n = 15), thick walled, outer layer brown, inner layer

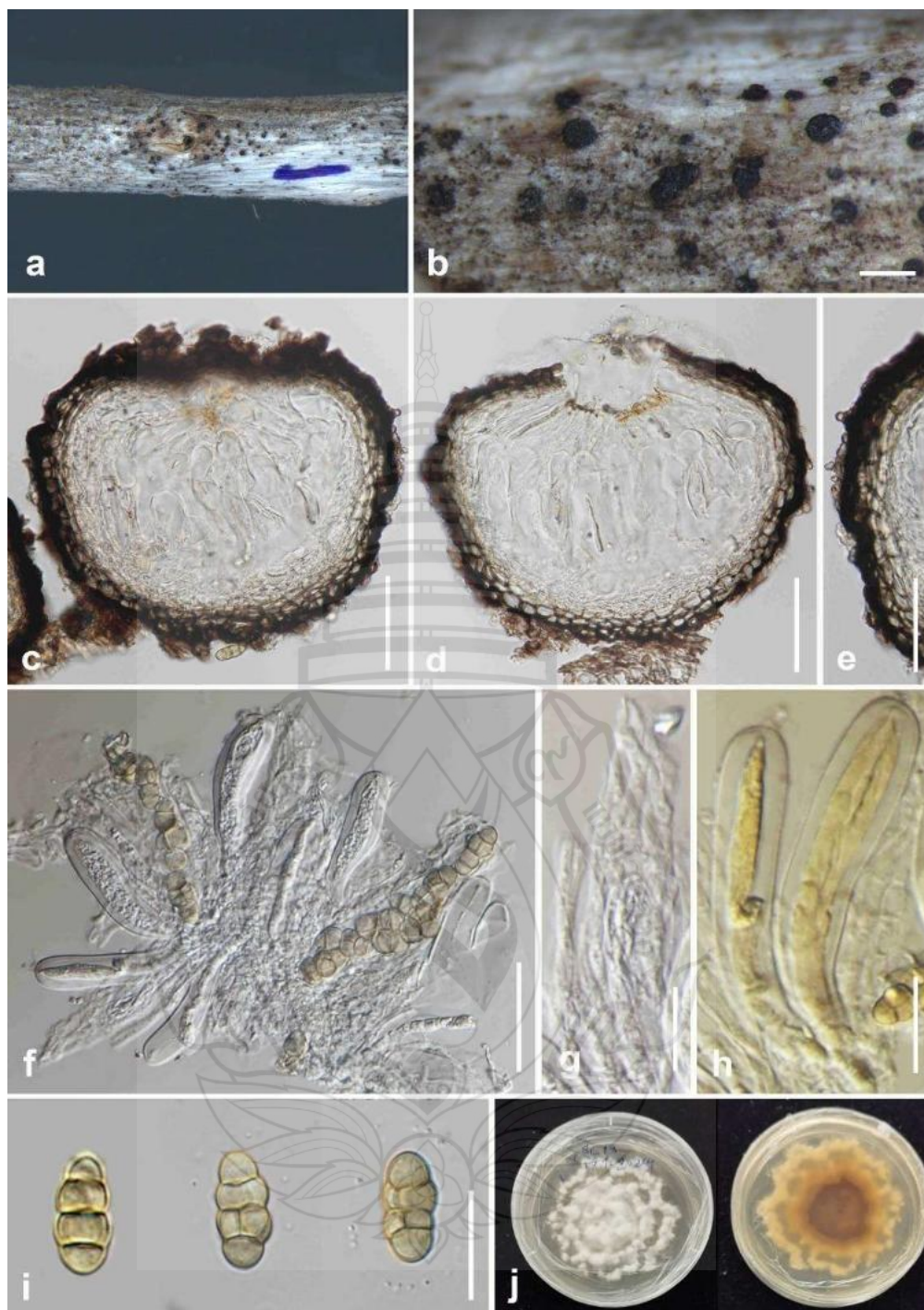
lighter brown to hyaline, *textura angularis*. *Paraphyses* $25\text{--}33 \times 1.2\text{--}2.7 \mu\text{m}$ ($\bar{x} = 29 \times 1.9 \mu\text{m}$, $n = 15$), cylindrical, taller than conidiogenous cells, straight or flexuous, narrower at the tip, aseptate, simple or branched, smooth walled, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* $2.5\text{--}7.5 \times 3.5\text{--}6.5 \mu\text{m}$ ($\bar{x} = 4.6 \times 4.8 \mu\text{m}$, $n = 15$), enteroblastic, conical or doliiform, rough-walled, pale brown to hyaline, originated from the inner layer of pycnidium wall. *Microconidiogenous* cells if present $4.5\text{--}10 \times 2.5\text{--}5.5 \mu\text{m}$ ($\bar{x} = 7 \times 4 \mu\text{m}$, $n = 10$), enteroblastic, conical or doliiform, rough-walled, pale brown to hyaline, originating from the inner layer of pycnidium wall. *Conidia* $10\text{--}16.5 \times 4.5\text{--}7 \mu\text{m}$ ($\bar{x} = 13.5 \times 6 \mu\text{m}$, $n = 30$), immature conidia obovoid, rough-walled, aseptate, hyaline to pale brown, mature conidia oblong with obtuse base or rounded ends, straight or curved, 1–3(4)-transversely septate, 0–1 longitudinal septum, constricted at septa, muriform, guttulate, rough-walled, brown, without a gelatinous sheath. *Microconidia* $3.5\text{--}5.5 \mu\text{m}$ ($\bar{x} = 4.5 \mu\text{m}$, $n = 15$), globose, subglobose, guttulate, rough-walled, hyaline. **Sexual morph:** *Ascomata* $120\text{--}170 \times 130\text{--}190 \mu\text{m}$ ($\bar{x} = 145 \times 160 \mu\text{m}$, $n = 10$), solitary or gregarious, superficial to semi-immersed, subglobose to obpyriform, black, ostiole central, papillate. *Peridium* $12\text{--}25 \mu\text{m}$ ($\bar{x} = 20 \mu\text{m}$, $n = 15$), outer layer dark brown to black, with 2–3(4) pigmented cell layers, inner layer absent or hyaline with 0–3 cell layers, *textura angularis*. *Hamathecium* $70\text{--}115 \times 1.8\text{--}4 \mu\text{m}$ ($\bar{x} = 95 \times 3 \mu\text{m}$, $n = 15$), composed of cylindrical, straight or flexuous, septate pseudoparaphyses, constricted at septa or not, hyaline, embedded in a gelatinous matrix, round and yellowish tip. *Asci* $60\text{--}110 \times 12\text{--}21 \mu\text{m}$ ($\bar{x} = 80 \times 16 \mu\text{m}$, $n = 15$), eight-spored, clavate, short pedunculate, bitunicate, fissitunicate, round apex. *Ascospores* $16\text{--}20 \times 6\text{--}8.8 \mu\text{m}$ ($\bar{x} = 17 \times 7 \mu\text{m}$, $n = 20$), overlapping uniseriate, oblong, rounded ends, 1–4-transversely septate, 1–2 longitudinal septa, constricted at septa, muriform, guttulate, smooth-walled, brown, surrounded by a gelatinous sheath.

Culture characteristics – Colonies of the sexual morph (MFLUCC 26-0039) on PDA reaching 4 cm diam. after one month at $25 \pm 2^\circ\text{C}$, flat or raised, cottony, concentric, undulate margin; from surface, white; from reverse, reddish brown at the center, paler toward the periphery, pale orange at the margin; Colonies of the asexual morph (MFLUCC 26-0040) on PDA reaching 3 cm diam. after one month at $25 \pm 2^\circ\text{C}$, flat or

effuse, medium sparse, entire margin, slightly fimbriate; from surface, white; from reverse, pale orange.

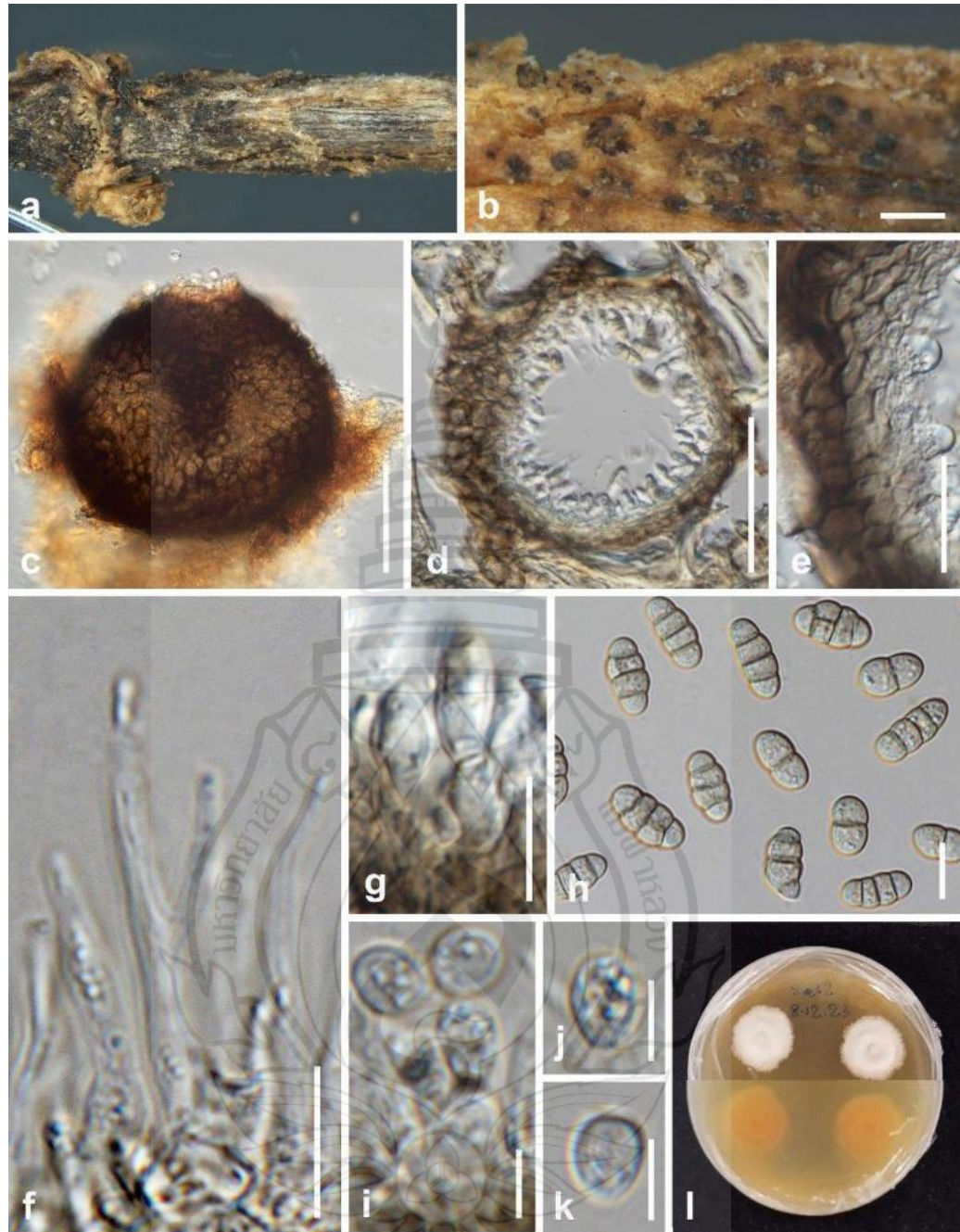
Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on margin of a saltern (water salinity 28 ppt), on dead dry stems of *Suaeda maritima*, 30 November 2023, R. Asghari, SC13 (MFLU 26-0012, holotype, sexual morph); ex-type culture (MFLUCC 26-0039); *ibid.*, on dead stems of *Sesuvium portulacastrum*, 30 November 2023, R. Asghari, Sa12 (MFLU 26-0013, asexual morph); living culture (MFLUCC 26-0040); Thailand, Phetchaburi Province, on margin of a saltern (water salinity 50 ppt), on dead dry stem of *Suaeda maritima*, 6 February 2023, R. Asghari, B1-1 (MFLU 26-0014, asexual morph); living culture (MFLUCC 26-0099).

Notes: In phylogenetic analyses, *Neocamarosporium salinum* shows a close phylogenetic affinity to *N. jorjanense*. Morphologically, *N. salinum* resembles *N. jorjanense* in having ostiolate conidiomata, cylindrical paraphyses, and conidia that are initially aseptate and hyaline, becoming muriform and brown at maturity. However, it differs in having narrower paraphyses and small, globose to subglobose, hyaline microconidia (Papizadeh et al. 2017). *Neocamarosporium salinum* (MFLUCC 26-0039) shows 3.2% (15/471 bp, including gaps) sequence divergence from *N. jorjanense* (IBRC-M 30243, type) in the ITS region. Based on morphological and molecular evidence, *N. salinum* is introduced as a novel species. Both sexual and asexual morphs of the species were collected in this study. Sequence comparison indicates that the asexual strain (MFLUCC 26-0040) has identical ITS (with one gap) and LSU (without gaps) sequence data to the sexual strain (MFLUCC 26-0039), supporting the identification of the asexual morph.



Note a Decaying branch of host. b Colonies on natural substrate. c, d Section of ascomata. e Peridium. f Paraphyses and asci. g Paraphyses. h Asci stained in Melzer's reagent. i Ascospores. j Colony on PDA (front and below). Scale bars: b = 250 μm , c–f = 50 μm , g–i = 20 μm .

Figure 5.15 *Neocamarosporium salinum* (MFLU 26-0012, holotype)



Note a Decaying branch of host. b Colonies on natural substrate. c Microscopic view of conidioma. d Section of conidioma. e Peridium. f Paraphyses. g Conidiogenous cells and developing conidia. h Conidia. i Microconidiogenous cells and developing conidia. j, k Microconidia. l Colonies on PDA (front and below). Scale bars: b = 500 μm , c, d = 50 μm , e = 20 μm , f–h = 10 μm , i–k = 5 μm .

Figure 5.16 *Neocamarosporium salinum* (MFLU 26-0013)

Neocamarosporium sesuvii R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.17

Etymology – Referring to the fungus isolated from the coastal plant *Sesuvium portulacastrum*.

Saprobic on dead stems of *Sesuvium portulacastrum*. **Asexual morph:** *Conidiomata* pycnidial 125–180 × 90–125 µm ($\bar{x}$ = 150 × 105 µm, n = 10), immersed to erumpent, subglobose to obpyriform, ostiolate, black. *Peridium* 14–31 µm ($\bar{x}$ = 21 µm, n = 15), thick walled, outer layer dark brown, lighter brown to hyaline toward the inner layer, *textura angularis*. *Paraphyses* 25–47 × 1–2.5 µm ($\bar{x}$ = 35.5 × 1.7 µm, n = 15), cylindrical, taller than conidiogenous cells, straight or flexuous, simple or branched, round apex, septate, rough-walled, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 5–11 × 3.5–9 at the base, 2–2.6 µm at the apex ($\bar{x}$ = 8.5 × 5.3 × 2.3 µm, n = 15), enteroblastic, cylindrical, ampulliform or conical, smooth-walled, hyaline, originated from the inner layer of pycnidium wall. *Conidia* 6–12.5 × 3.8–6.5 µm ($\bar{x}$ = 9.5 × 5 µm, n = 20), oblong with slightly obtuse base, aseptate, guttulate, rough-walled, hyaline, occasionally budding with age. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 1.5 cm diam. after two weeks at 25±2°C, umbonate, cottony, undulate margin; from surface, white, pale yellow at the center; from reverse orange white.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on margin of a dry saltern, on dead dry stems of *Sesuvium portulacastrum*, 6 April 2024, R. Asghari, S6B21 (MFLU 26-0009, holotype); ex-type culture (MFLUCC 26-0036).

Notes – See the note under *N. pranburiense*.



Note a Decaying branch of host. b Colonies on natural substrate. c, d Section of conidiomata. e Peridium. f Paraphyses and conidiogenous cells. g, h Conidiogenous cells and developing conidia. i Conidia. j Budding conidia. k Germinated conidium. l, m Colony on PDA (front and below). Scale bars: b = 250 μ m, c = 100 μ m, d = 50 μ m, e, k = 20 μ m, f, h, i = 10 μ m, g, j = 5 μ m.

Figure 5.17 *Neocamarosporium sesuvii* (MFLU 26-0009, holotype)

Periconiaceae Nann.

Periconiaceae was introduced by Nannizzi (1934); however, the family received limited taxonomic attention, and its type genus, *Periconia*, was previously placed in *Massarinaceae* (Hyde et al. 2013). Based on phylogenetic evidence, Tanaka et al. (2015) reinstated *Periconiaceae* as a distinct family, which was subsequently accepted by later studies (Phukhamsakda et al. 2016; Hongsanant et al. 2020a). The family currently comprises two genera, *Flavomyces* and *Periconia* (Hyde et al. 2024).

Periconia Tode

Periconia is the type genus of *Periconiaceae* and was introduced by Tode (1791) to accommodate *Periconia lichenoides*. The genus is commonly described based on its asexual morph, which produces macronematous, mononematous conidiophores, blastic conidiogenous cells, and verruculose to echinulate, unicellular, brown conidia (Ellis 1971; Tanaka et al. 2015). The sexual morph has been linked to *Didymosphaeria*, *Massarina*, or *Okeanomyces* (Booth 1968; Kohlmeyer 1969; Pang et al. 2004; Tanaka et al. 2015; Hyde et al. 2020a; Dayarathne et al. 2026). The genus has been collected as saprobes, endophytes, or pathogens from various habitats, with several species reported from marine or salt marsh environments (Jones et al. 2019; Calabon et al. 2021; Salimi et al. 2023; Pem et al. 2024; Zhang et al. 2024a). In this study, a strain of *Periconia atropurpurea* was isolated from submerged decaying wood in marine water in Thailand.

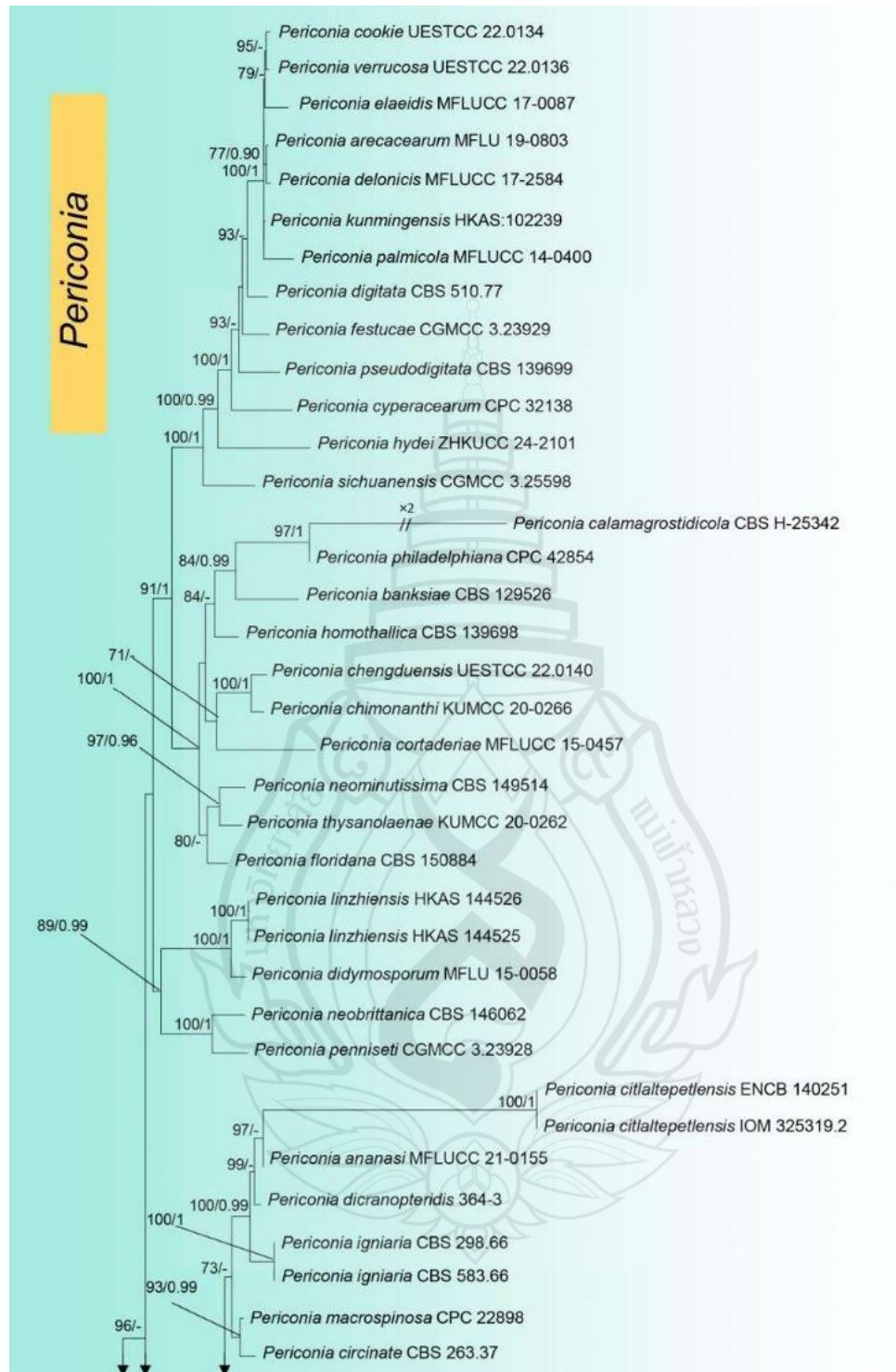
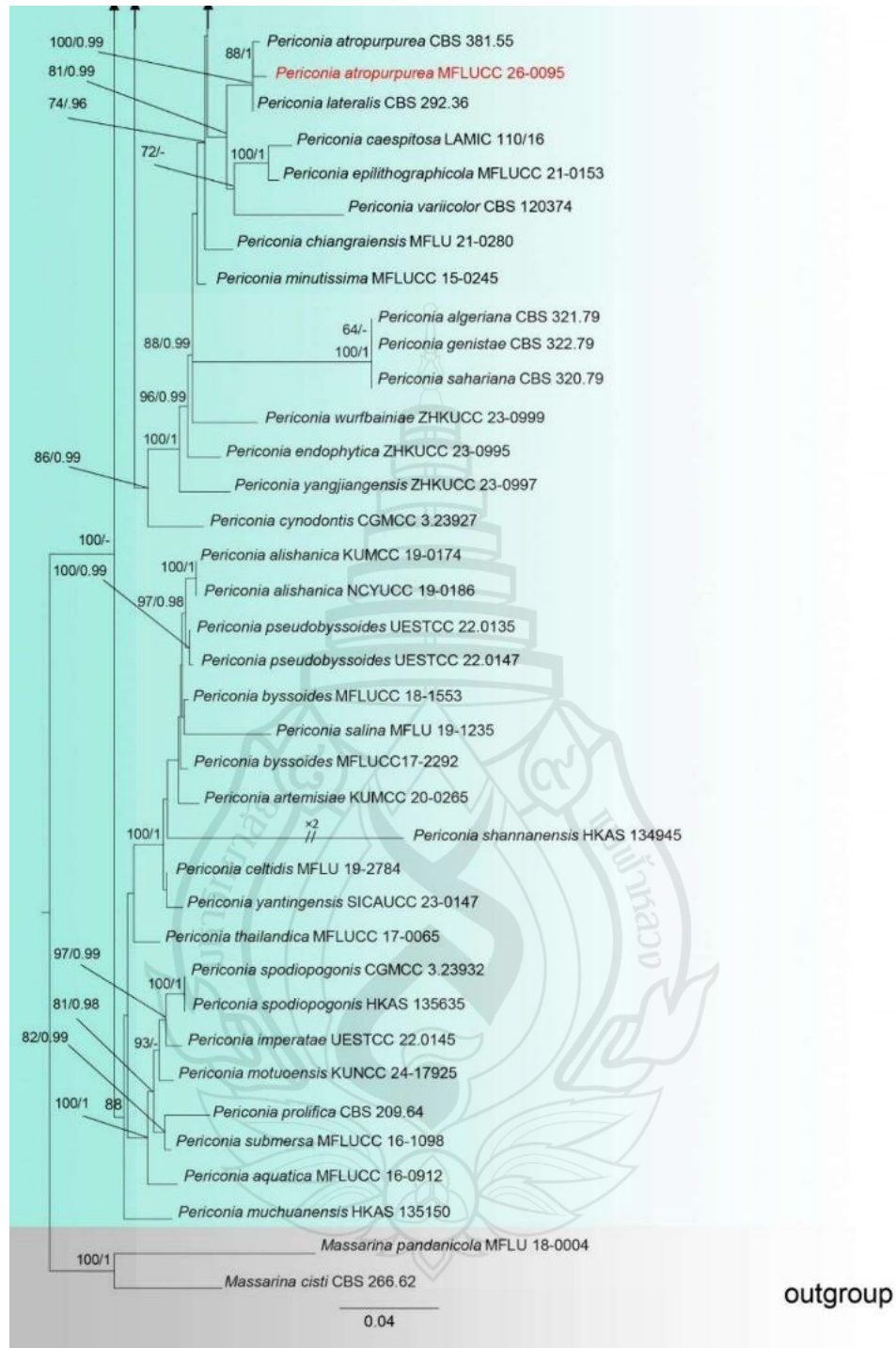


Figure 5.18 Phylogram generated from the ML analysis based on the combined ITS, SSU, LSU and *tef1* sequence alignments of *Periconia*



Note The scale bar indicates expected changes per site. The tree is rooted to *Massarina cisti* (CBS 266.62) and *M. pandanicola* (MFLU 18.0004). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.18 (continued)

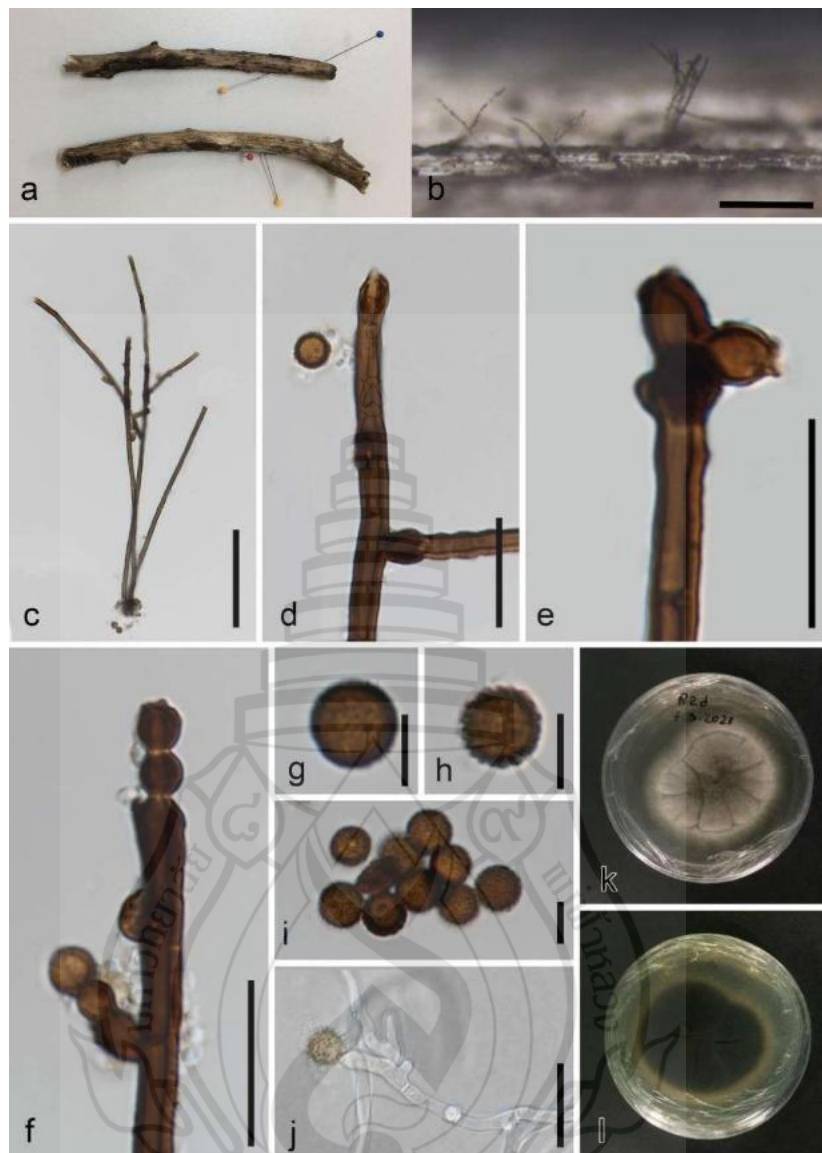
Periconia atropurpurea (Berk. & M.A. Curtis) M.A. Litv. Fig. 5.19

Saprobic on submerged decaying wood in seawater. **Asexual morph:** Colonies on the host surface, hairy, black. *Conidiophores* 135–355 × 3–6 µm ($\bar{x}$ = 234 × 4.5 µm, n = 15), macronematous, mononematous, erect, cylindrical, straight or curved, sparingly branched at the upper part, proliferating percurrently, thick-walled, brown. *Conidiogenous cells* 5–25 × 3.5–5.5 µm ($\bar{x}$ = 13 × 4 µm, n = 15), integrated, cylindrical, ellipsoidal, terminal and intercalary, sometimes proliferating percurrently, thick-walled, brown. *Conidia* 5–7 µm diam. ($\bar{x}$ = 6 µm, n = 20), globose, lenticular from the side, thick-walled, guttulate, echinulate, solitary or catenated, with isthmuses between the conidia. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 3 cm diam. after two weeks at 25±2°C, raised with flat edge, radiating at the middle, velvety, entire margin; from surface, olive gray, gray at the margin; from reverse, olive, grayish green at the margin.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on submerged decaying wood in rocky shore (water salinity 19 ppt), 25 October 2022, KD Hyde, R2d (MFLU 26-0037); living culture (MFLUCC 26-0095).

Notes – In the phylogenetic analyses from ITS, SSU, LSU, and *tef1* sequence data, our newly obtained strain (MFLUCC 26-0095) clustered as a sister clade to *Periconia atropurpurea* (CBS 381.55) with 88% ML/1.00 BPP support. Morphologically, it is similar to the holotype of *P. atropurpurea* in having sparsely branched conidiophores, catenated echinulate conidia with isthmuses (Saccardo 1886). Our strain (MFLUCC 26-0095) showed 1.2% (7/542 bp, with gaps) and 0.2% (2/883 bp, without gaps) sequence divergence from *P. atropurpurea* (CBS 381.55) in the ITS and LSU regions, respectively. Based on both morphological and molecular evidence, our collection is identified as *P. atropurpurea*, reported here as a new geographical and habitat record from marine habitats in Thailand.



Note a Decaying twig of host. b Colonies on natural substrate. c Conidiophores. d–f Conidiogenous cell and developing conidia. g–i Conidia. j Germinated conidium. k, l Colonies on PDA (front and below). Scale bars: b = 200 μm , c = 50 μm , d–f, k = 20 μm , g–i = 5 μm .

Figure 5.19 *Periconia atropurpurea* (MFLU 26-0037, new geographical record)

Phaeosphaeriaceae M.E. Barr

Phaeosphaeriaceae was established by Barr (1979) and typified by *Phaeosphaeria* as the type genus. The family currently comprises 87 genera, mostly collected from terrestrial habitats, and exhibits diverse morphological characteristics

(Phookamsak et al. 2017; Hyde et al. 2024). Studies on this family have increased in recent years (2019–2025), with the introduction of several new genera and over 100 new species (Zhang et al. 2019; Mapook et al. 2020; Wanasinghe and Maharachchikumbura 2023; Absalan et al. 2024; Sun et al. 2025). In this study, we provide a multigene phylogenetic analysis of the family and, based on both morphological and molecular data, introduce one new genus and eight new species from coastal plants.

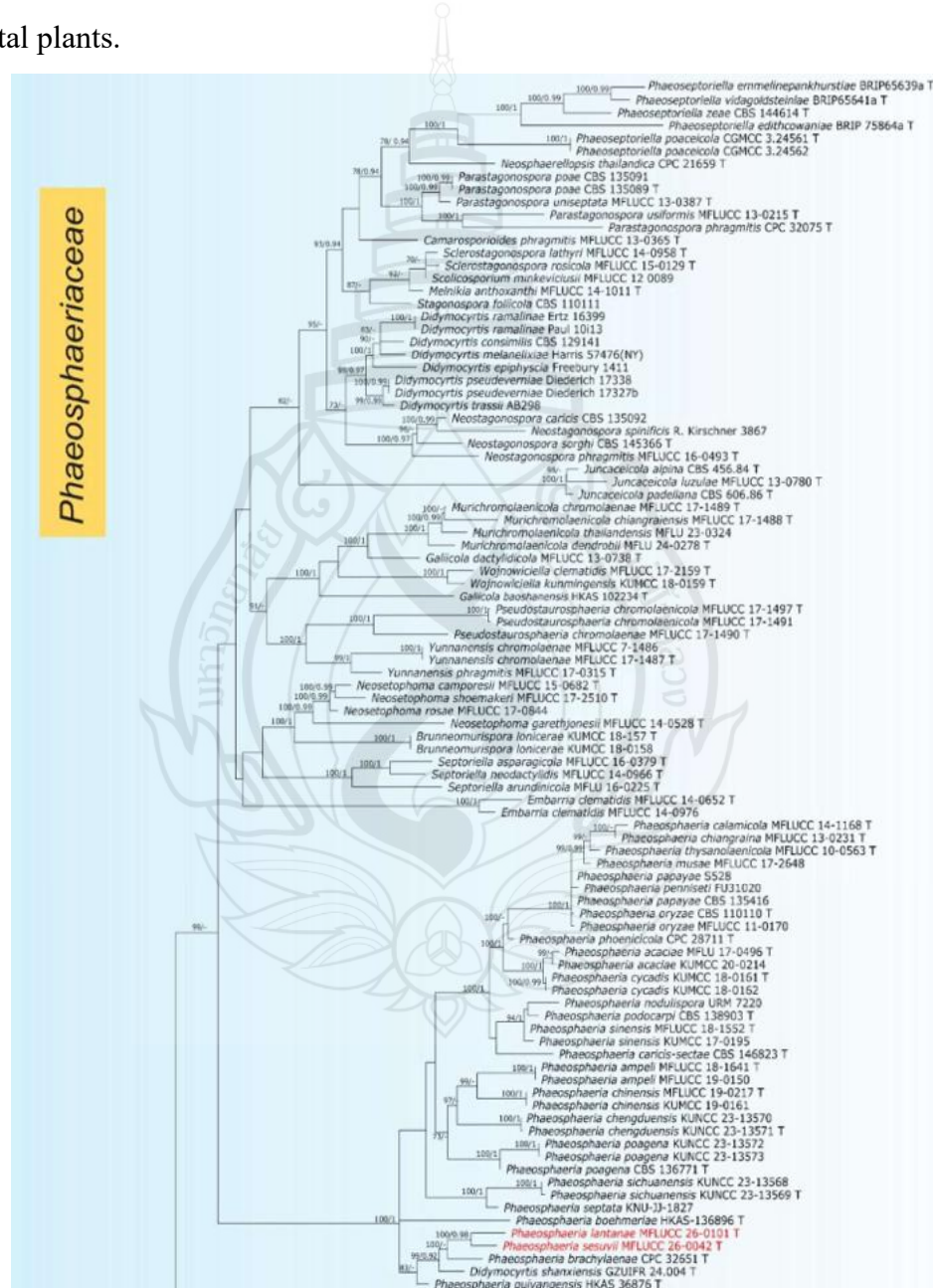


Figure 5.20 Phylogram generated from the ML analysis based on the combined ITS, LSU, SSU, *tef1* and *rpb2* sequence data of *Phaeosphaeriaceae*

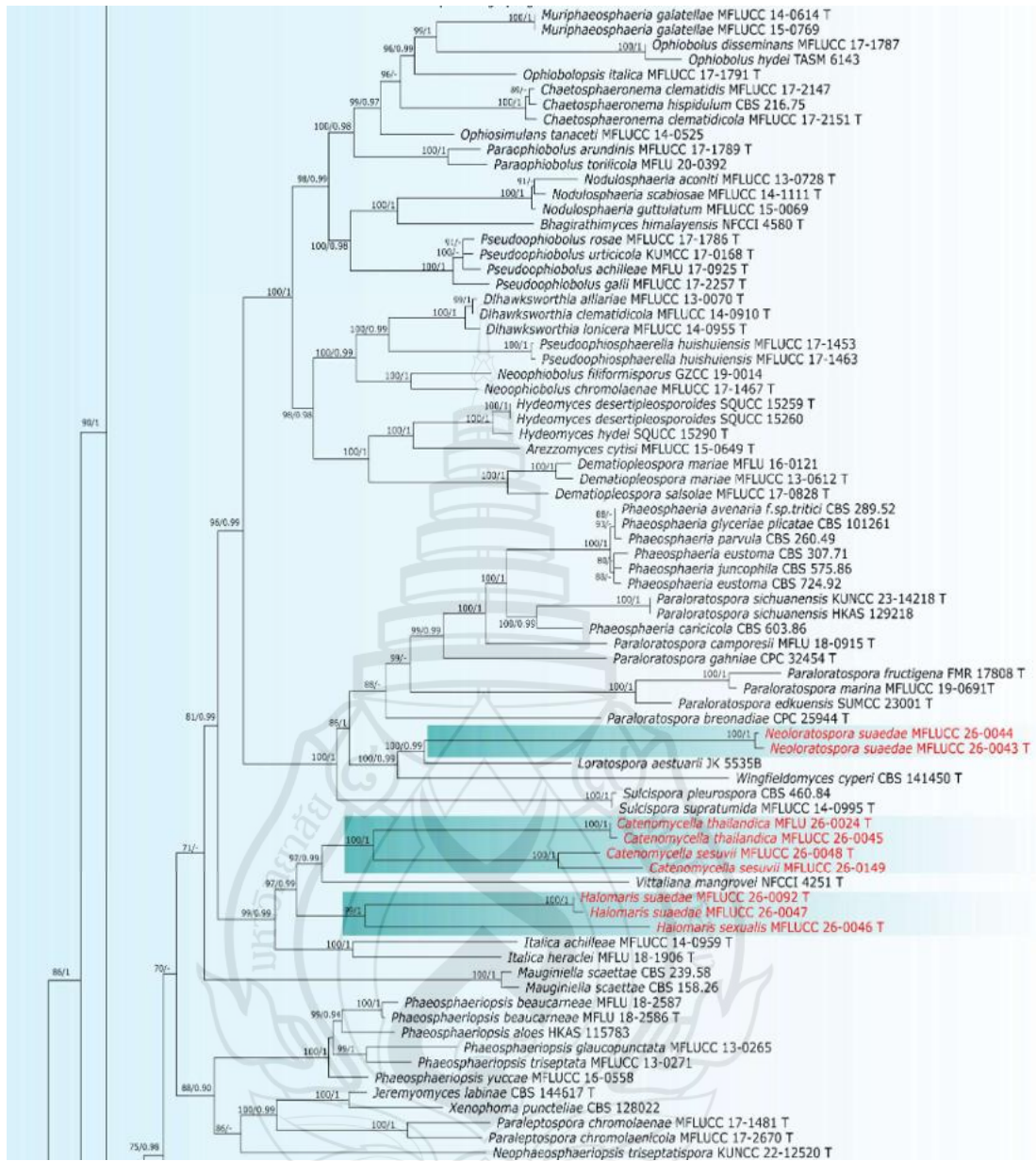
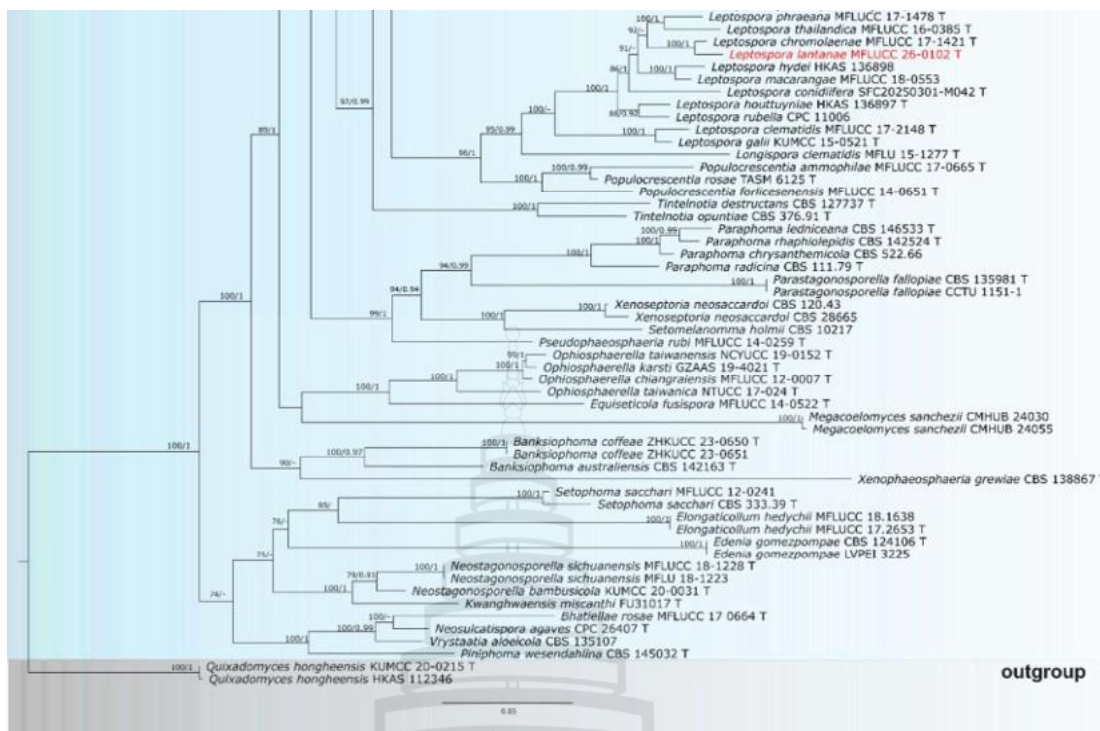


Figure 5.20 (continued)



Note The tree is rooted to *Quixadomyces hongheensis* (KUMCC 20 0215, HKAS 112346). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red, while type strains are indicated with T.

Figure 5.20 (continued)

Catenomycella R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, gen. nov.

Etymology – Referring to the chain-like paraphyses composed of uneven cells.

Type species – *Catenomycella thailandica* R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde

Saprobic on salt marsh plants. **Asexual morph:** *Conidiomata* pycnidial, immersed, to semi-immersed, subglobose, obpyriform, ostiolate, with or without a short papilla. *Peridium* comprising pale brown to dark brown cells of *textura angularis* to *textura intricata*. *Paraphyses* septate, constricted at the septa, composed of short chains of uneven, subglobose to short cylindrical cells. *Conidiophores* if present, cylindrical, straight or flexuous, percurrently proliferating, septate, hyaline. *Conidiogenous cells* enteroblastic, phialidic or annellidic, extending percurrently, ampulliform, cylindrical to subcylindrical, hyaline, originated from the inner layer of pycnidium wall or

integrated at the apex of conidiophores. *Conidia* ellipsoidal to oblong, guttulate, hyaline, 0–2-septate, round apex, truncate base, with or without budding conidia.

Sexual morph: Undetermined.

Notes – Two novel species, *Catenomycella sesuvii* and *C. thailandica*, are introduced as coelomycetous asexual taxa characterized by percurrently proliferating conidiophores, chain-like paraphyses, and enteroblastic conidiogenous cells. Phylogenetic analyses placed these two taxa in a strongly supported lineage within *Phaeosphaeriaceae*, close to *Vittaliana mangrovei*. *Vittaliana mangrovei* was isolated from mangrove wood and described based on its sexual morph (Devadatha et al. 2019). Additional collections are needed to clarify the sexual–asexual relationship between *Catenomycella* and *Vittaliana*.

Catenomycella sesuvii R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.21

Index Fungorum number: IFxxx; Facesoffungi number: FoF19429

Etymology – Refers to the host plant *Sesuvium portulacastrum*, from which the fungus was collected.

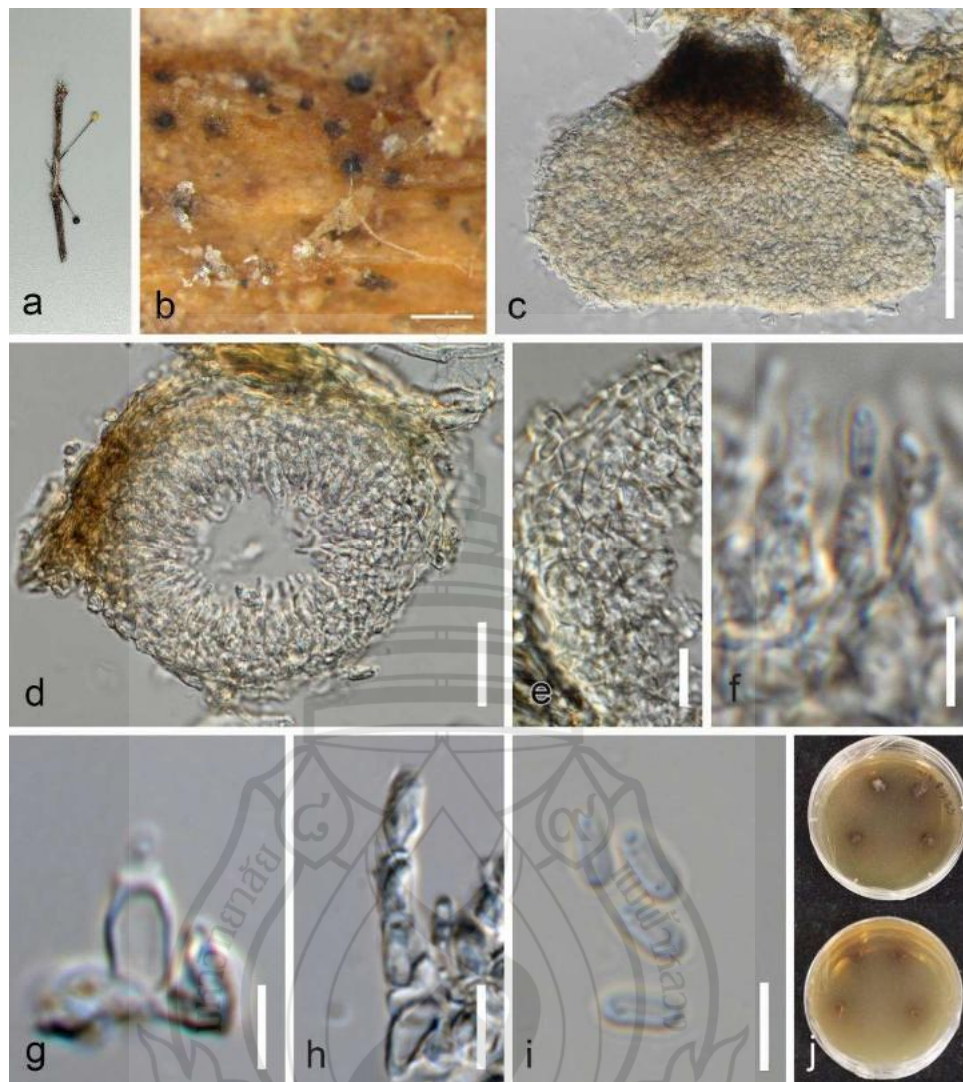
Holotype – MFLU 26-0029

Saprobic on dead stems of *Sesuvium portulacastrum*. **Asexual morph:** *Conidiomata* 90–120 × 95–180 µm ($\bar{x}$ = 100 × 140 µm, n = 10), pycnidial, solitary, immersed, to semi-immersed, subglobose, obpyriform, black, ostiolate, with a short papilla. *Peridium* 8–15 µm ($\bar{x}$ = 13 µm, n = 15), subhyaline to pale brown, dark brown at the apex, *textura angularis*, at the surface view *textura intricata*. *Paraphyses* septate, constricted at the septa, composed of short chains of uneven, subglobose to short cylindrical cells. *Conidiophores* up to 20 µm high, or reduced to conidiogenous cells, hyaline, cylindrical, straight or flexuous, percurrently proliferating, septate, constricted at the septa. *Conidiogenous cells* 4–14.5 × 2.5–6 µm ($\bar{x}$ = 7 × 3.5 µm, n = 20), enteroblastic, phialidic, extending percurrently, ampulliform, cylindrical to subcylindrical, hyaline, originated from the inner layer of pycnidium wall or integrated at the apex of conidiophores. *Conidia* 3.5–6.5 × 1–2 µm ($\bar{x}$ = 4.5 × 1.5 µm, n = 30), ellipsoidal to oblong, guttulate, aseptate, hyaline, round apex, truncate base. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 0.5 cm diam. after two months at $25\pm 2^{\circ}\text{C}$, dome-shaped, dense, folded, undulate, light brown pigment diffusing in agar; from surface, grayish brown; from reverse, brownish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on margin of a saltern (water salinity 28 ppt), on dead dry stems of *Sesuvium portulacastrum*, 30 November 2023, R. Asghari, SA14 (MFLU 26-0029, holotype); ex-type culture (MFLUCC 26-0048); *ibid.*, SA14b (MFLU 26-0030, isotype); ex-isotype living culture (MFLUCC 26-0149).

Notes –Multi-gene phylogenetic analyses of ITS, LSU, SSU, *tef1*, and *rpb2* sequence data, placed *Catenomycella sesuvii* sister to the strains of *C. thailandica* with 100% ML/1.00 BPP support. Morphologically, *C. sesuvii* resembles *C. thailandica* by its ostiolate conidiomata with a short papilla, chain-like paraphyses, percurrently proliferating conidiophores, and enteroblastic conidiogenous cells. However, *C. sesuvii* differs in having aseptate conidia, whereas *C. thailandica* has 1–2-septate conidia that are constricted at the septa and produce budding conidia. *Catenomycella sesuvii* (MFLUCC 26-0048) showed 15% (69/457, with gaps), 1.7% (15/906, with gaps), 0.6% (6/1037, without gaps), and 5.3% (50/929, with gaps) base pair differences with *C. thailandica* (MFLUCC 26-0164), in ITS, LSU, SSU, and *tef1* respectively. Based on morphological and molecular results, *Catenomycella sesuvii* is introduced as a novel species.



Note a Decaying twig of host. b Colonies on natural substrate. c Conidioma. d Section of a conidioma. e Peridium. f, g Conidiogenous cells and developing conidia. h Conidiophore. i Conidia. j Colony on PDA (front and below). Scale bars: b = 250 μm , c = 50 μm , d = 20 μm , e = 10 μm , f–i = 5 μm .

Figure 5.21 *Catenomycella sesuvii* (MFLU 26-0029, holotype)

Catenomycella thailandica R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.22

Index Fungorum number: IFxxx; Facesoffungi number: FoF19432

Etymology – Referring to Thailand, the country where the fungus was collected.

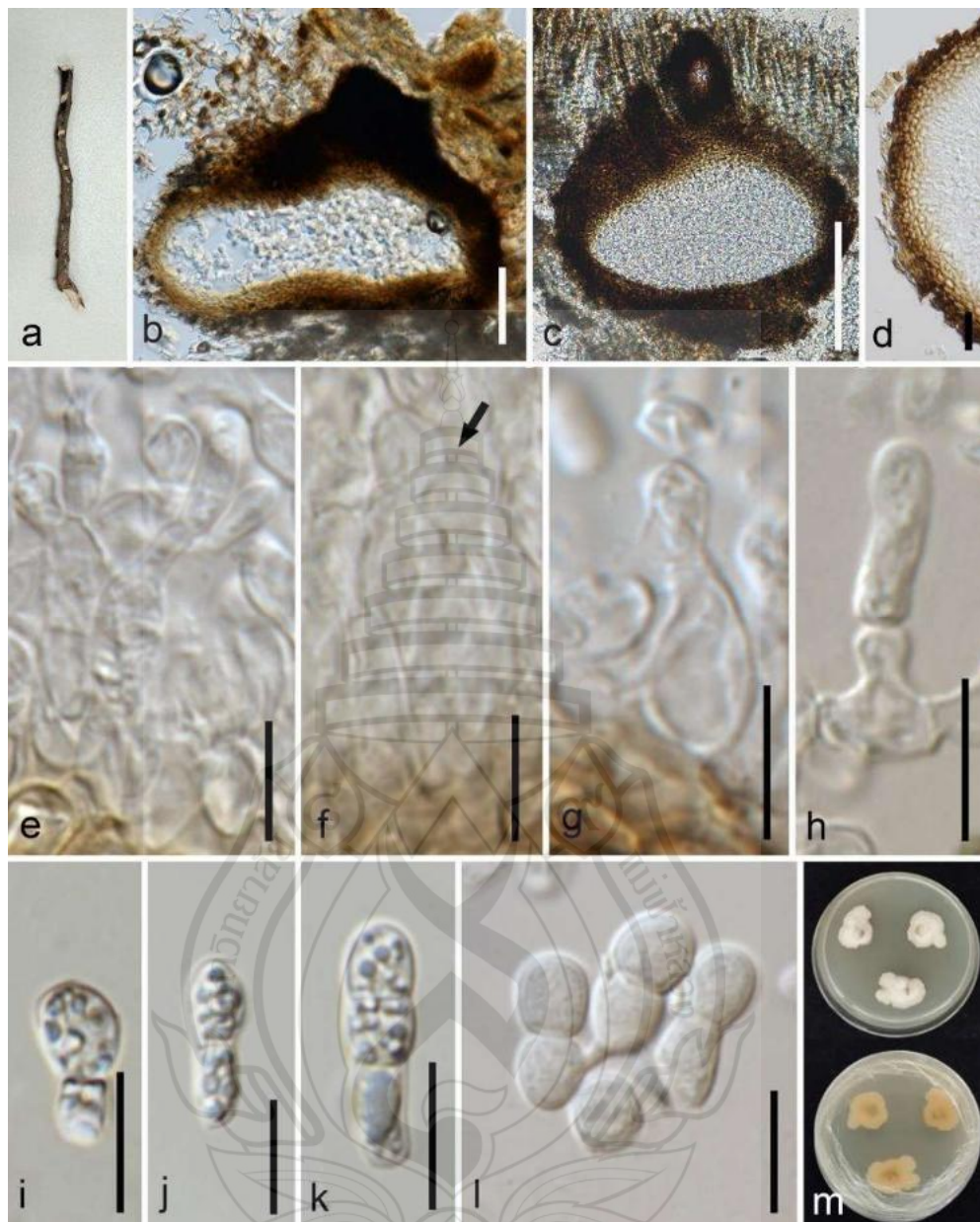
Holotype – MFLU 26-0024

Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** *Conidiomata* 160–230 × 230–250 µm ($\bar{x}$ = 200 × 240 µm, n = 10), pycnidial, solitary, immersed, subglobose, to obpyriform, black, ostiolate, with a short papilla. *Peridium* 19–50 µm ($\bar{x}$ = 35 µm, n = 15), thick-walled, brown to dark brown, *textura angularis*. *Paraphyses* septate, often constricted at the septa, composed of chains of uneven, subglobose to subcylindrical cells. *Conidiophores* 13–25 × 2–6 µm ($\bar{x}$ = 19 × 4 µm, n = 15), or reduced to conidiogenous cells, if present, cylindrical, straight or flexuous, occasionally anastomosing, hyaline, percurrently proliferating, septate. *Conidiogenous cells* 6–16 × 3.5–5 µm ($\bar{x}$ = 11 × 4 µm, n = 15), enteroblastic, rarely polyblastic, extending percurrently, or annellidic, ampulliform, cylindrical, subcylindrical, finely rough-walled, hyaline, originated from the inner layer of pycnidium wall or integrated at the apex of conidiophores. *Conidia* 8–18 × 3.5–6 µm ($\bar{x}$ = 12.5 × 4.5 µm, n = 20), broadly ellipsoidal, or oblong, lower cell narrower, finely rough-walled, thick-walled, guttulate, hyaline, 1–2-septate, deeply constricted at septa, often segments of ascospores separating completely in globose or subglobose partspores, with budding conidia. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 1.5 cm diam. after one month at 25±2°C, umbonate, fairly fluffy, medium dense, undulate; from surface, white, orange white at the margin; from reverse, pale orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park, on dead dry stems of *Suaeda maritima*, 6 April 2024, R. Asghari, S6d10 (MFLU 26-0024, holotype); ex-type culture (MFLUCC 26-0164); *ibid.*, S6d10b (MFLU 26-0025, isotype); ex-isotype living culture (MFLUCC 26-0045).

Notes – See the notes under *Catenomyces sesuvii*.



Note a Decaying twig of the host. b, c Section of conidiomata. d Peridium. e, f Conidiophores (arrow indicating anastomosing cells). g, h Conidiogenous cells and developing conidia. i–k Conidia. l Budding conidia. m Colonies on PDA (front and below). Scale bars: b = 50 μ m, c = 100 μ m, d = 20 μ m, e–l = 10 μ m.

Figure 5.22 *Catenomycella thailandica* (MFLU 26-0024, holotype)

Halomaris R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, gen. nov.

Etymology – Referring to the saline and marine habitat where the type species was collected.

Type species – *Halomaris sexualis* R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde

Saprobic on salt marsh plants. **Asexual morph:** *Conidiomata* pycnidial, immersed, to semi-immersed, obpyriform or oval, ostiolate, with or without a short papilla. *Peridium* comprising golden brown to brown cells of *textura angularis* to *textura globulosa*, darker at the apex. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, annellidic, ampulliform, cylindrical, rough-walled, hyaline, originated from the inner layer of pycnidium wall. *Conidia* ellipsoidal, narrower at the base, rough-walled, thick-walled, guttulate, 0–1-septate, constricted at the septum, hyaline, round apex. **Sexual morph:** *Ascomata* immersed to erumpent, subglobose, black, with a central ostiole. *Peridium* brown to dark brown, darker at the apex, *textura angularis*. *Hamathecium* comprised with numerous, filamentous, cylindrical, branched, hyaline, septate pseudoparaphyses, anastomosing. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to clavate, straight or curved, round apex, short pedicellate, with or without an ocular chamber. *Ascospores* fusiform, ends narrowly rounded, guttulate, multi-septate, hyaline when immature and becoming pale to golden brown with maturity, surrounded with a sheath.

Notes – Two novel saprobic fungal species, *Halomaris sexualis* and *H. suaedae*, were isolated from salt marsh plants in Thailand. Among them, *Halomaris sexualis* (type) is the species for which a sexual morph is observed. Multi-locus phylogenetic analyses of ITS, LSU, SSU, *tef1*, and *rpb2* sequence data recovered these taxa as a distinct monophyletic lineage with 97% ML/0.99 BPP statistical support, within *Phaeosphaeriaceae*. Species share anastomosing branched pseudoparaphyses and 1–6-septate fusiform guttulate ascospores that are hyaline to pale brown, together with coelomycetous asexual morphs bearing enteroblastic annellidic conidiogenous cells. In our phylogeny, they are closely related to *Vittaliana* and *Italica*. However, the sexual morph of *Halomaris* differs from *Vittaliana* by having branched pseudoparaphyses and rough-walled ascospores (Devadatha et al. 2019). It can be distinguished from *Italica* by having anastomosing pseudoparaphyses, and phragmosporous fusiform ascospores with a narrow base (Wanasinghe et al. 2018). These data support the introduction of *Halomaris* as a new genus to accommodate these two species.

Halomaris sexualis R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov.

Fig. 5.23

Etymology – Referring to the first sexual morph of the genus.

Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** Undetermined.

Sexual morph: *Ascomata* 190–350 × 150–240 µm ($\bar{x}$ = 220 × 195 µm, n = 10), immersed to erumpent, solitary, subglobose, black, with a central ostiole, without a papilla. *Peridium* 15–30 ($\bar{x}$ = 20 µm, n = 15), brown to dark brown, darker at the apex, *textura angularis*. *Hamathecium* 1.5–3 µm wide ($\bar{x}$ = 2.5, n = 15), comprising numerous, filamentous, cylindrical, branched, hyaline, septate, anastomosing pseudoparaphyses. *Asci* 55–100 × 6.5–10.5 µm ($\bar{x}$ = 75 × 8.5 µm, n = 15), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, straight or curved, round apex, short pedicellate, with an ocular chamber. *Ascospores* 16–20 × 2.8–6 µm ($\bar{x}$ = 18 × 4.5 µm, n = 20), fusiform, narrowly rounded ends, narrower at the base, guttulate, 1–6-septate, constricted at septa, middle cells swollen with maturity, initially hyaline, pale brown to golden brown with maturity, surrounded with a large sheath.

Culture characteristics – Colonies on PDA reaching 1.5 cm diam. after one month at 25±2°C, umbonate, glabrous, dense, entire margin; from surface, orange gray, orange white at the center and margin; from reverse, grayish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park, on dead dry stems of *Suaeda maritima*, 6 April 2024, R. Asghari, S6D31 (MFLU 26-0026, holotype); ex-type culture (MFLUCC 26-0046).

Notes – In our multi-gene phylogenetic analyses *Halomaris sexualis* shares a close phylogenetic affinity sister to *H. suaedae* with a strong support. Morphologically, *H. sexualis* is not comparable with *H. suaedae*, based on the sexual morphic characteristics. *Halomaris sexualis* (MFLUCC 26-0046) showed 18% (71/391, with gaps), 0.6% (6/1051, with gaps), and 4.6% (42/905, without gaps) base pair differences with *H. suaedae* (MFLUCC 26-0092), in ITS, SSU and *tef1* respectively. *Halomaris sexualis* is introduced herein as a novel species.



Note a Decaying twig of host. b, c Colonies on natural substrate. d Section of an ascoma. e Peridium. f, g Paraphyses. h, i Asci. j Ascospores. k Ascospores mounted in black ink. l Colony on PDA (front and below). Scale bars: b = 500 μ m, c = 250 μ m, d = 100 μ m, e, k = 20 μ m, f = 5 μ m, g–j = 10 μ m.

Figure 5.23 *Halomaris sexualis* (MFLU 26-0026, holotype)

Halomaris suaedae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.24

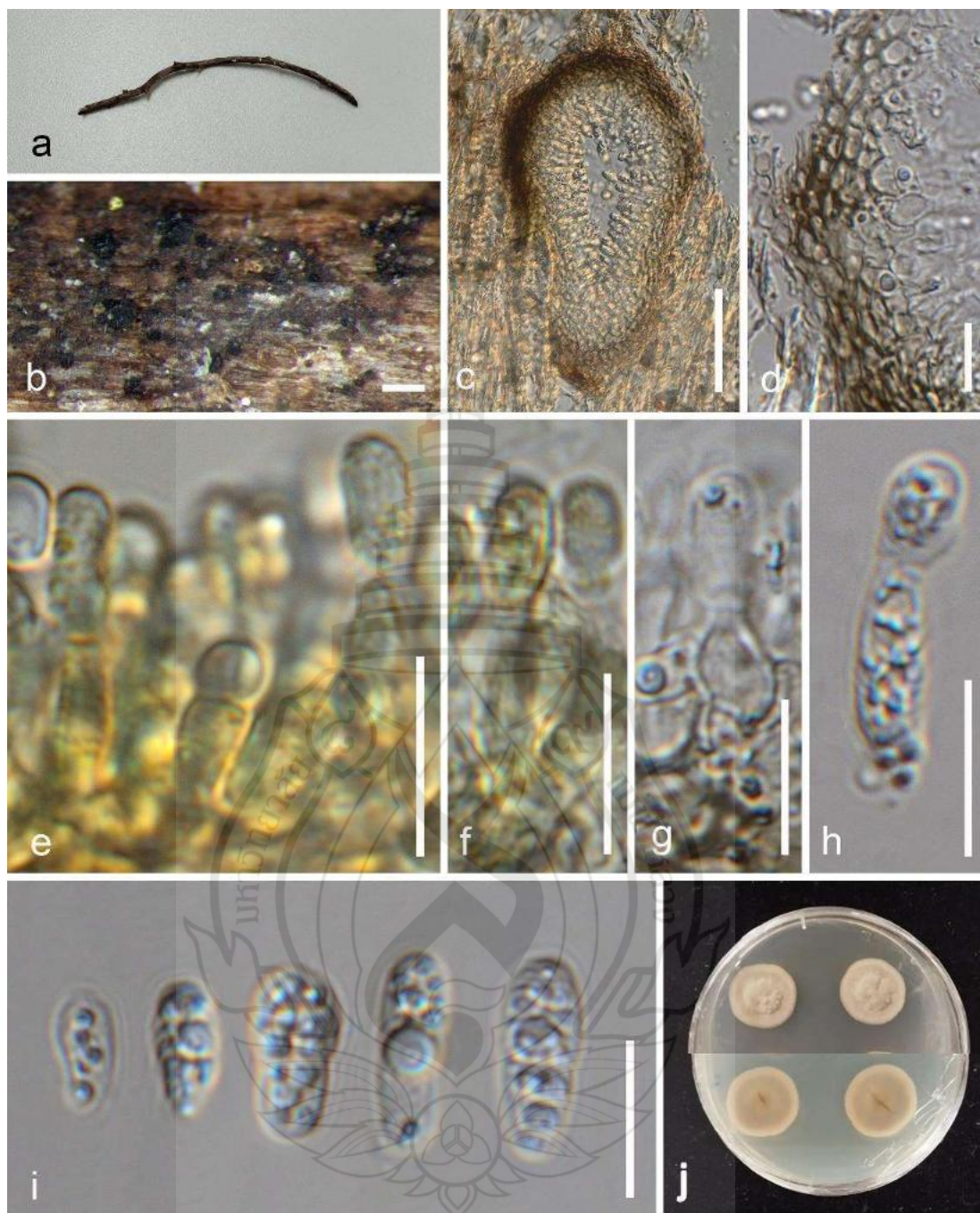
Etymology – Refers to the host plant *Suaeda*, from which the fungus was collected.

Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** *Conidiomata* 100–180 × 50–100 µm ($\bar{x}$ = 140 × 80 µm, n = 10), pycnidial, solitary, immersed, to semi-immersed, pyriform, obpyriform, oval, black, ostiolate, with or without a short papilla, black area visible at the host surface. *Peridium* 10–30 µm ($\bar{x}$ = 19 µm, n = 20), thick-walled, thicker at the apex, golden brown to brown, darker at the apex, *textura angularis* to *textura globulosa*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3.5–12 × 2–4 µm ($\bar{x}$ = 8 × 3 µm, n = 20), enteroblastic, annellidic, ampulliform, cylindrical, rough-walled, hyaline, originated from the inner layer of pycnidium wall. *Conidia* 6–11.5 × 2.5–4.5 µm ($\bar{x}$ = 8 × 3.8 µm, n = 20), ellipsoidal, narrower at the base, rough-walled, thick-walled, guttulate, aseptate to uniseptate, constricted at the septum, hyaline, round apex. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diam. after one month at 25±2°C, raised at the middle, flat at the periphery, wooly, medium dense, entire margin; from surface, orange gray; from reverse, gray, orange gray at the center and margin.

Material examined: Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park (water salinity 28 ppt), on dead stems of submerged *Suaeda maritima*, 30 November 2023, R. Asghari, SB34 (MFLU 26-0027, holotype); ex-type culture (MFLUCC 26-0092); *ibid.*, SB34b (MFLU 26-0028, isotype); ex-isotype living culture (MFLUCC 26-0047).

Notes – See the notes under *Halomaris sexualis*.



Note a Decaying twig of the host. b Colonies on natural substrate. c Section of a conidioma. d Peridium. e, f Conidiophores, Conidiogenous cells and developing conidia (stained in Melzer's reagent). g, h Conidiogenous cells and developing conidia. i Conidia. j Colonies on PDA (front and below). Scale bars: b = 100 μ m, c = 50 μ m, d–i = 10 μ m.

Figure 5.24 *Halomaris suaedae* (MFLU 26-0027, holotype)

Leptospora Rabenh.

Rabenhorst (1857) introduced *Leptospora*, typified by *L. rubella* based on *Sphaeria rubella*. A reference specimen of *L. rubella* was provided by Hyde et al. (2016). The genus produces scattered, solitary ascomata with a reddish-brown area on the host and pale brown to yellowish brown, filiform ascospores (Hyde et al. 2020a). *Leptospora* currently comprises about 20 species (Index Fungorum, November 2025), mostly reported as saprobes from terrestrial habitats (Mapook et al. 2020; Sun et al. 2025). In this study, we report a new species collected from a coastal area in Thailand.

Leptospora lantanae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.25

Etymology – Referring to the isolation of the fungus from a *Lantana camara*.

Saprobic on dead stems of *Lantana camara*. **Asexual morph:** Undetermined.

Sexual morph: *Ascomata* 140–200 × 120–190 µm ($\bar{x}$ = 170 × 155 µm, n = 10), immersed to semi-immersed, solitary, globose to obpyriform, black, ostiolar neck, with hyaline periphyses like cells. *Peridium* 11–20 ($\bar{x}$ = 16 µm, n = 15), 3–6 layers, inner layers pale brown to hyaline, outer layers reddish brown to dark brown, *textura angularis*. *Hamathecium* 1.5–2.5 µm wide ($\bar{x}$ = 2, n = 15), comprising cylindrical, septate, hyaline pseudoparaphyses. *Asci* 70–105 × 8.5–13 µm ($\bar{x}$ = 87 × 10.5 µm, n = 20), 8-spored, bitunicate, cylindric-clavate, straight or curved, round apex, short pedicellate, bulbous pedicel. *Ascospores* 35–87 × 2.5–5 µm ($\bar{x}$ = 60 × 3.5 µm, n = 20), filiform, fasciculate, yellowish brown, straight or curved, guttulate, granular, 7–15-septate, constricted at septa, each cell cylindrical to globose, pointed apex, with or without polar appendages.

Culture characteristics – Colonies on PDA reaching 4 cm diam. after one month at 25±2°C, raised, woolly, crenated; from surface, concentric zones, alternatively gray and brownish gray; from reverse, brownish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on dead dry stems of *Lantana camara*, 23 May 2023, R. Asghari, LC41 (MFLU 26-0021, holotype); ex-type culture (MFLUCC 26-0102).

Notes – In the combined phylogenetic analysis, *Leptospora lantanae* is sister to *L. chromolaenae* with strong bootstrap support (100% ML/1 BPP). *Leptospora*.

lantanae is similar to *L. chromolaenae* in having immersed to semi-immersed ascomata with an ostiolar neck, filled with hyaline periphyses-like cells; bitunicate, cylindric-clavate asci with a short bulbous pedicel; and filiform, fasciculate ascospores with polar appendages (Mapook et al. 2020). However, it differs by its ascospores with pointed ends (vs. rounded ends in *L. chromolaenae*) and a fewer number of septa (7–15 vs. 27–28) (Mapook et al. 2020). *Leptospora lantanae* (MFLUCC 26-0102) showed 1.9% (10/518, with gaps), 0.4% (3/818, without gaps), base pair differences with *L. chromolaenae* (MFLUCC 17-1421), in ITS and LSU respectively. Based on morphological and molecular evidence, *Leptospora lantanae* is introduced as a new species.





Note a Decaying twig of host. b Colonies on natural substrate. c Section of an ascoma. d Section of an ostiole and peridium. e Paraphyses. f–i Asci. j–m Ascospores. n, o Colony on PDA (front and below). Scale bars: b = 1 mm, c, d = 50 μ m, d = 50 μ m, f–m = 20 μ m.

Figure 5.25 *Leptospora lantanae* (MFLU LC41, holotype)

Neoloratospora R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, gen. nov.

Index Fungorum number: IFxxx; Facesoffungi number: FoFxxx

Etymology – The generic name refers to its phylogenetic relationship with *Loratospora*.

Type species – *Neoloratospora suaedae* R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde

Saprobic on salt marsh plants. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* immersed to erumpent, globose to subglobose, with a central ostiole. *Peridium* comprising brown to dark brown cells of *textura angularis*. *Hamathecium* comprised with numerous, filamentous, cylindrical, branched, hyaline, septate pseudoparaphyses. *Asci* 8-spored, bitunicate, fissitunicate, cylindrical to clavate, straight or curved, round apex, short pedicellate, with or without an ocular chamber. *Ascospores* broadly ellipsoidal, muriform, rounded ends, guttulate, multiseptate, pale brown to brown, surrounded with a sheath.

Notes – *Neoloratospora* is introduced as a monotypic genus to accommodate, *N. suaedae* collected from halophyte hosts in Thailand. In Multi-locus phylogenetic analyses, *N. suaedae* was clustered with *Loratospora* within *Phaeosphaeriaceae* with 100% ML/0.99 BPP. *Neoloratospora* is distinct with the presence of hamathecium, cylindrical, pedicellate asci, and broadly ellipsoidal, muriform ascospores. Phylogenetic placement and distinct morphology support the introduction of *Neoloratospora* as a novel genus.

Neoloratospora suaedae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.26

Index Fungorum number: IFxxx; Facesoffungi number: FoF19434

Etymology – Referring to the isolation of the fungus from *Suaeda maritima*.

Holotype – MFLU 26-0022

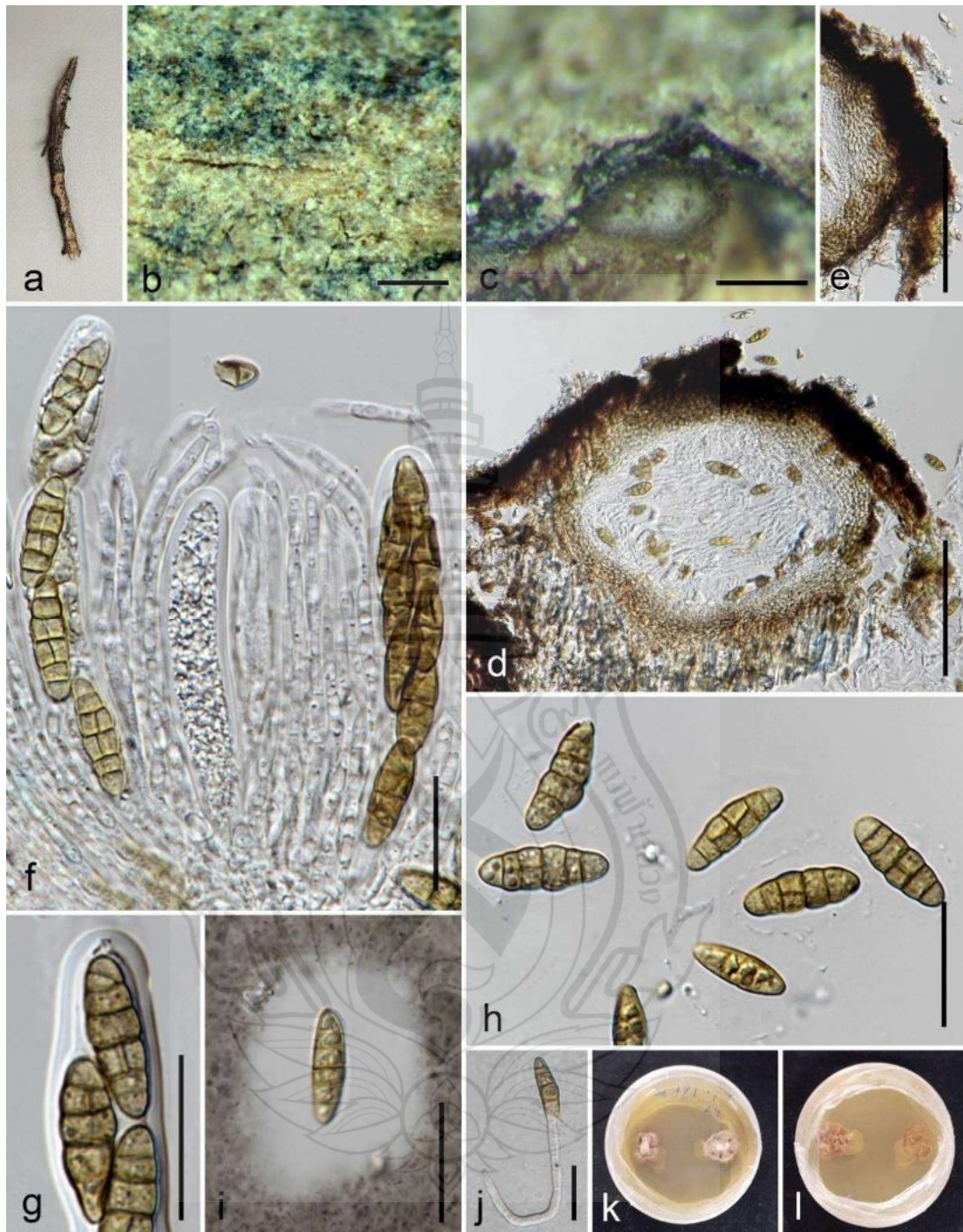
Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 230–350 µm diam. ($\bar{x}$ = 270 µm, n = 10), immersed to erumpent, solitary, globose to subglobose, black, visible with carbonaceous erumpent black spots on the surface, with a central ostiole. *Peridium* 20–45 ($\bar{x}$ = 30 µm, n = 15), brown to dark brown, *textura angularis*. *Hamathecium* 1.5–2.5 µm wide ($\bar{x}$ = 2, n =

15), comprising numerous, filamentous, cylindrical, branched, hyaline, septate, constricted at septa, anastomosing pseudoparaphyses. *Asci* $65\text{--}107 \times 11\text{--}14 \mu\text{m}$ ($\bar{x} = 88 \times 12.5 \mu\text{m}$, $n = 15$), 8-spored, bitunicate, fissitunicate, cylindrical to clavate, straight or curved, round apex, short pedicellate, with an ocular chamber. *Ascospores* $17\text{--}22 \times 5.5\text{--}7 \mu\text{m}$ ($\bar{x} = 20 \times 6.5 \mu\text{m}$, $n = 20$), overlapping uniseriate or biseriate, broadly ellipsoidal, muriform, rounded ends, guttulate, granular, 1–5-septate, constricted at septa, with or without one transversally septum in the middle cells, pale brown to brown, surrounded with a sheath.

Culture characteristics – Colonies on PDA reaching 2 cm diam. after one month at $25 \pm 2^\circ\text{C}$, dome-shaped, dense, folded, lobate, irregularly submerged at the margin; from surface, brownish gray, gray at the center; from reverse, brownish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park, on dead dry stems of *Suaeda maritima*, 6 April 2024, R. Asghari, S6d81 (MFLU 26-0022, holotype); ex-type culture (MFLUCC 26-0043); *ibid.*, S6d62 (MFLU 26-0023, isotype); ex-isotype living culture (MFLUCC 26-0044)

Notes – In our phylogeny of combined ITS, LSU, SSU, *tef1*, and *rpb2* sequence data, *Neoloratospora suaedae* (MFLUCC 26-0043 and MFLUCC 26-0044) formed a separate lineage sister to the marine species, *Loratospora aestuarii* with 100% ML/0.99 BPP support. Morphologically, *N. suaedae* is distinguishable in having hamathecium, cylindrical, pedicellate asci, and overlapping uniseriate to biseriate, broadly ellipsoidal, muriform ascospores. However, in *L. aestuarii*, hamathecium is absent, and asci are ovoid to ampulliform containing 4–5-seriate, phragmosporous ascospores (Kohlmeyer & Volkmann-Kohlmeyer 1993, Phookamsak et al. 2014). Based on these morphological differences and phylogenetic placement, *N. suaedae* is introduced as a novel species, saprobic on salt marsh hosts, from Thailand.



Note a Decaying twig of host. b, c Colonies on natural substrate. d Section of an ascoma. e Peridium. f Paraphyses and asci. g Apex of an ascus. h Ascospores. i Ascospore mounted in black ink. k, l Colonies on PDA (front and below). Scale bars: b = 500 μ m, c = 250 μ m, d, e = 100 μ m, f–i = 20 μ m.

Figure 5.26 *Neoloratospora suaedae* (MFLU 26-0022, holotype)

Phaeosphaeria I. Miyake

Phaeosphaeria is the type genus of *Phaeosphaeriaceae*, with *Phaeosphaeria oryzae* designated as the type species (Miyake 1909). Members of *Phaeosphaeria* produce scattered or clustered ascomata, cylindrical to cylindric-clavate asci, and phragmosporous ascospores (Hyde et al. 2013; Pem et al. 2024). The asexual morph of *Phaeosphaeria* is coelomycetous, producing cylindrical to subcylindrical conidia (Quaedvlieg et al. 2013). The genus comprises about 150 species, collected from various terrestrial and aquatic habitats, occurring as saprobes and plant pathogens (Wanasinghe and Maharachchikumbura 2023; Sun et al. 2025). Approximately 15 species are considered marine fungi (Jones et al. 2019), with several reports from salt marsh plants (Calabon et al. 2021). In this study, we introduce two novel species of *Phaeosphaeria* collected from coastal plants in Thailand.

Phaeosphaeria lantanae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.27

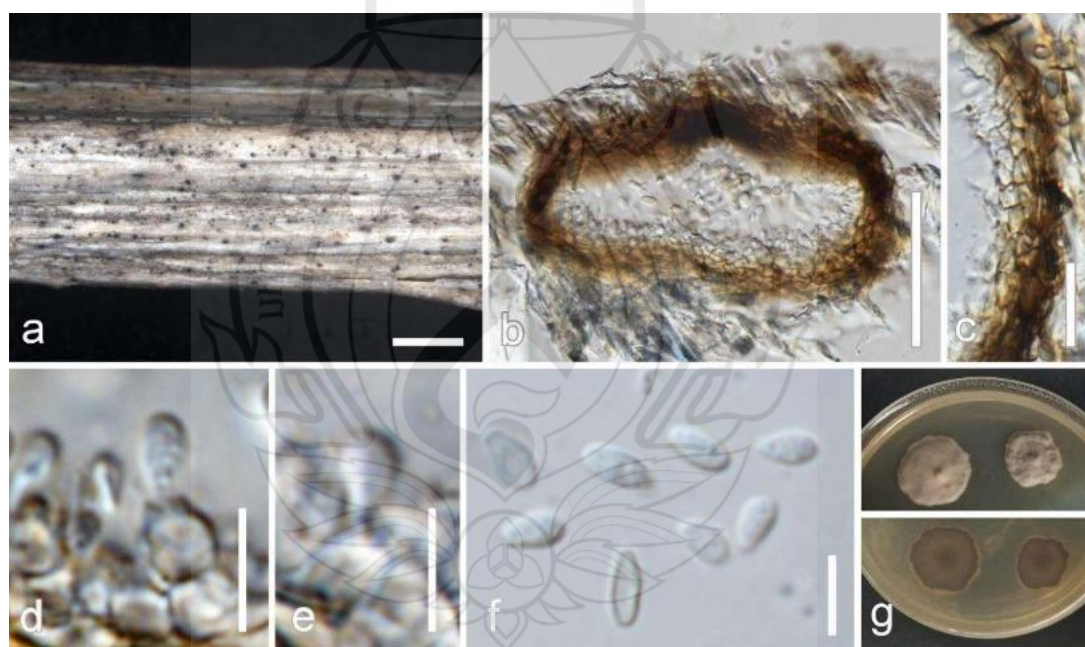
Etymology – Referring to the isolation of the fungus from a *Lantana camara*.

Saprobic on dead stems of *Lantana camara*. **Asexual morph:** *Conidiomata* 55–70 × 100–120 µm ($\bar{x}$ = 60 × 115 µm, n = 10), pycnidial, solitary, immersed, visible as black dots on the host surface, subglobose, oval, black, with central ostiole. *Peridium* 10–14 µm ($\bar{x}$ = 12 µm, n = 15), thick walled, brown to dark brown, *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 2.5–7 × 2.8–3.8 µm ($\bar{x}$ = 4 × 3.5 µm, n = 20), enteroblastic, phialidic, conical, dolliform or ampulliform, smooth-walled, hyaline, originated from the inner layer of pycnidium wall. *Conidia* 3.5–5.5 × 2.0–2.5 µm ($\bar{x}$ = 4.5 × 2 µm, n = 20), obovoid, truncate based or with a hilum, rough-walled, guttulate, aseptate, hyaline to pale brown. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2.5 cm diam. after one month at 25±2°C, flat, low convex, felted, entire margin, slightly undulate; from surface, brownish gray; from below, grayish brown, brownish gray at the margin.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on dead dry stems of *Lantana camara*, 23 May 2023, R. Asghari, LC51 (MFLU 26-0020, holotype); ex-type culture (MFLUCC 26-0101).

Notes – Based on the multi-gene phylogenetic analyses from ITS, LSU, SSU, *tef1*, and *rpb2* sequence data, *Phaeosphaeria lantanae* clustered with *Ph. sesuvii* with 100% ML/0.98 BPP support. *Phaeosphaeria lantanae* is similar to *Ph. sesuvii* by its solitary ostiolate black conidiomata, phialidic, hyaline conidiogenous cells, originating from the inner layer of pycnidium wall, and hyaline to pale brown conidia. It differs by its dolliform or ampulliform conidiogenous cells and obovoid, aseptate conidia without an appendage, whereas *Ph. sesuvii* has globose to subglobose conidiogenous cells, oblong, straight or curved, 0–1-septate conidia, sometimes with a funnel shape appendage (This study). *Phaeosphaeria lantanae* (MFLUCC 26-0101) showed 3.5% (19/538, with gaps), 0.2% (2/902, without gaps), 3.8% (42/1102, with gaps), and 5.4% (18/333, without gaps) base pair differences with *Ph. sesuvii* (MFLUCC 26-0042), in ITS, LSU, *rpb2* and *tub2* respectively. Based on morphological and molecular evidence, *Ph. lantanae* is introduced as a novel species.



Note a Colonies on natural substrate. b Section of a conidioma. c Peridium. d, e Conidiogenous cells and developing conidia. f Conidia. g Colonies on PDA (front and below). Scale bars: a = 1 mm, b = 50 μ m, c = 20 μ m, d–f = 5 μ m.

Figure 5.27 *Phaeosphaeria lantanae* (MFLU 26-0020, holotype)

Phaeosphaeria sesuvii R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.28

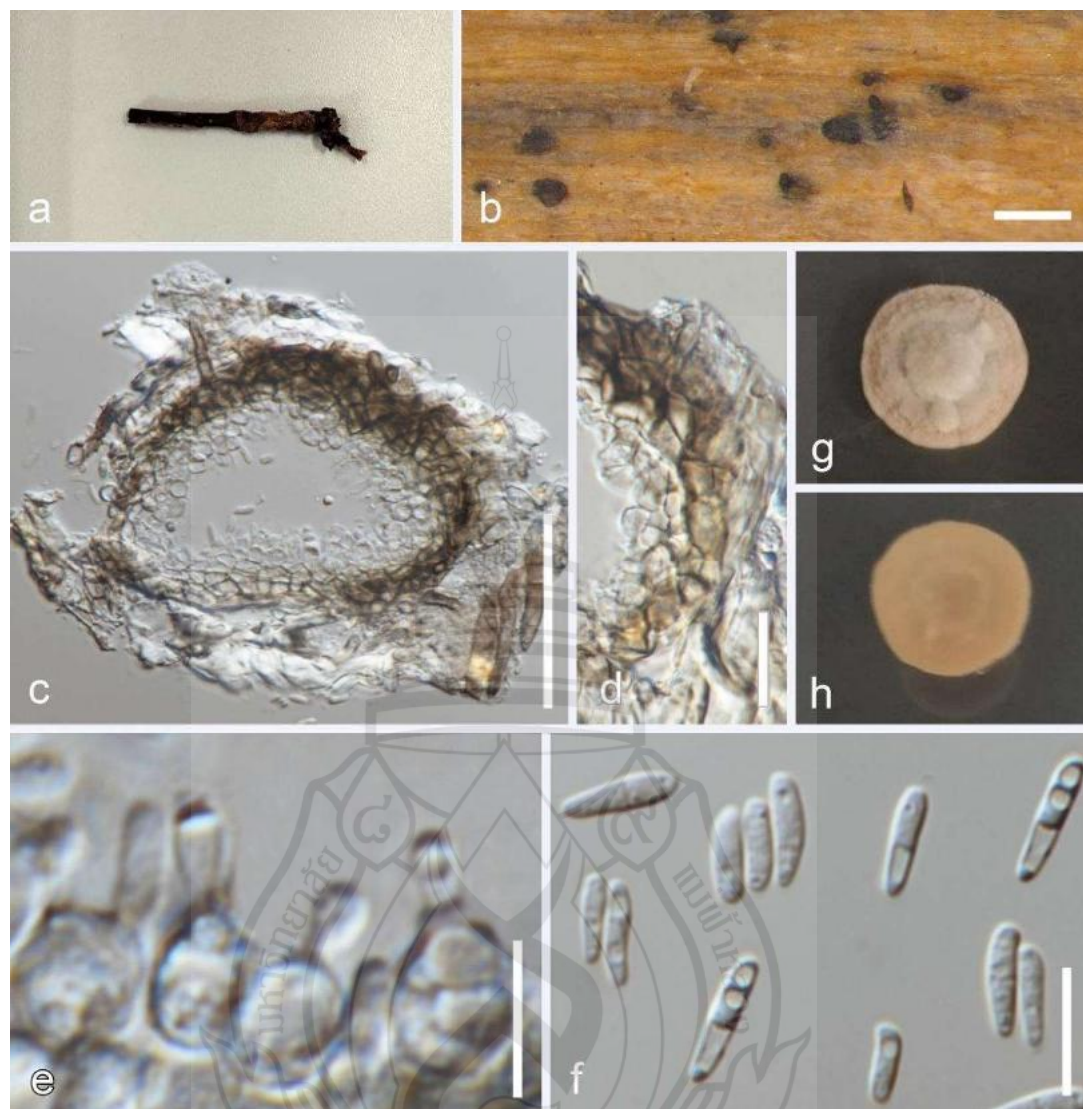
Etymology – Referring to the isolation of the fungus from *Sesuvium portulacastrum*.

Saprobic on dead stems of *Sesuvium portulacastrum*. **Asexual morph:** *Conidiomata* 65–135 × 60–70 µm ($\bar{x}$ = 90 × 65 µm, n = 10), pycnidial, solitary, immersed, semi-immersed, subglobose, oval, black, occasionally with cylindrical brown setae, with central ostiole, papillate. *Peridium* 6–12 µm ($\bar{x}$ = 9 µm, n = 15), 2–4 layers, brown to dark brown, darker at the apex, lighter at the base, *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 3–9 × 3.5–6 µm ($\bar{x}$ = 5.5 × 4.5 µm, n = 15), enteroblastic, phialidic, globose to subglobose, with a collarete, finely rough-walled, hyaline, originated from the inner layer of pycnidium wall. *Conidia* 5–10 × 1.5–2.5 µm ($\bar{x}$ = 7 × 2 µm, n = 30), oblong with obtuse base, straight or curved, with or without a funnel shape appendage at the base, 0–1-septate, guttulate, hyaline to pale brown. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 1 cm diam. after two weeks at 25±2°C, umbonate, felted, dense, entire margin; from surface, gray at the center, orange gray at the periphery; from reverse, brownish gray.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pran Kiri Beach, on dead dry stems of *Sesuvium portulacastrum* on seashore rocks, 8 November 2024, R. Asghari, S7P14 (MFLU 26-0104, holotype); ex-type culture (MFLUCC 26-0042).

Notes – For morphological and molecular comparison see the note of *Ph. lantanae* in this study.



Note a Decaying twig of host. b Colonies on natural substrate. c Section of a conidioma. d Peridium. e Conidiogenous cells and developing conidia. f Conidia. g, h Colony on PDA (front and below). Scale bars: b = 200 µm, c = 50 µm, d, f = 10 µm, e = 5 µm.

Figure 5.28 *Phaeosphaeria sesuvii* (MFLU 26-0104, holotype)

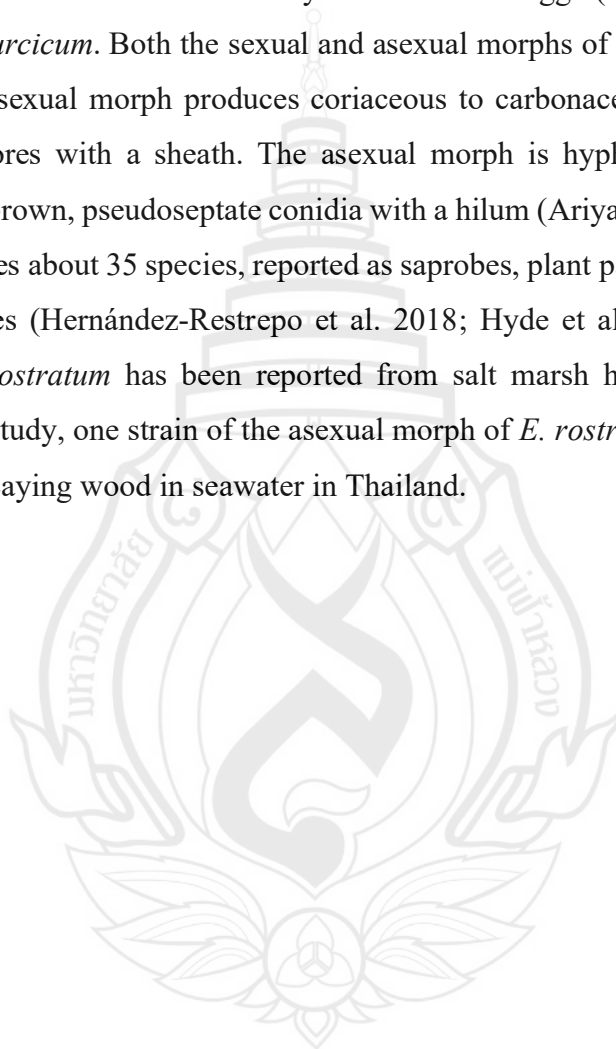
Pleosporaceae Nitschke

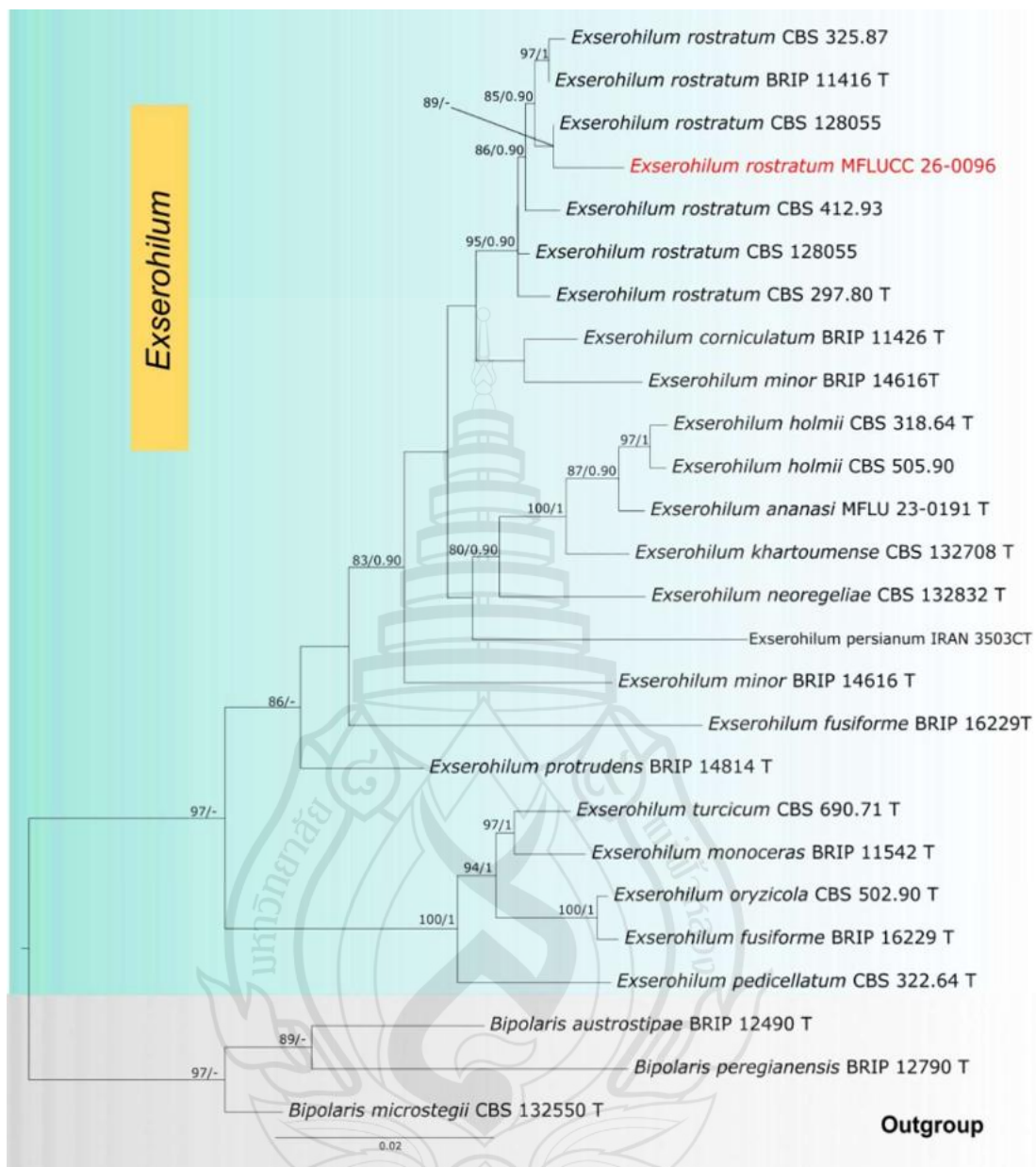
Pleosporaceae was established by Nitschke (1869), with *Pleospora* as the type genus, and was later placed in the order *Pleosporales* by Luttrell (1955). Ariyawansa et al. (2015) re-evaluated the family using morphological characters and multigene phylogenetic analyses and accepted 18 genera within *Pleosporaceae*. The family

currently comprises 28 genera, of which *Alternaria* and *Curvularia* are the most species-rich and include the highest number of species reported from marine habitats (Jones et al. 2019, Hyde et al. 2024).

Exserohilum K.J. Leonard & Suggs

Exserohilum was introduced by Leonard and Suggs (1974) and typified with *Exserohilum turcicum*. Both the sexual and asexual morphs of *Exserohilum* have been reported. The sexual morph produces coriaceous to carbonaceous ascomata and 1–8 fusoid ascospores with a sheath. The asexual morph is hyphomycetous, producing olivaceous to brown, pseudoseptate conidia with a hilum (Ariyawansa et al. 2015). The genus comprises about 35 species, reported as saprobes, plant pathogens, and clinically relevant species (Hernández-Restrepo et al. 2018; Hyde et al. 2025). Among them, *Exserohilum rostratum* has been reported from salt marsh habitats (Calabon et al. 2021). In this study, one strain of the asexual morph of *E. rostratum* was isolated from submerged decaying wood in seawater in Thailand.





Note The tree is rooted to *Bipolaris austrostipae* (BRIP 12490), *B. peregianensis* (BRIP12790) and *B. microstegii* (CBS 132550). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red, while type strains are indicated with T.

Figure 5.29 Phylogram generated from the ML analysis based on the combined ITS, LSU, *tef1* and *gapdh* sequence data of *Exserohilum*

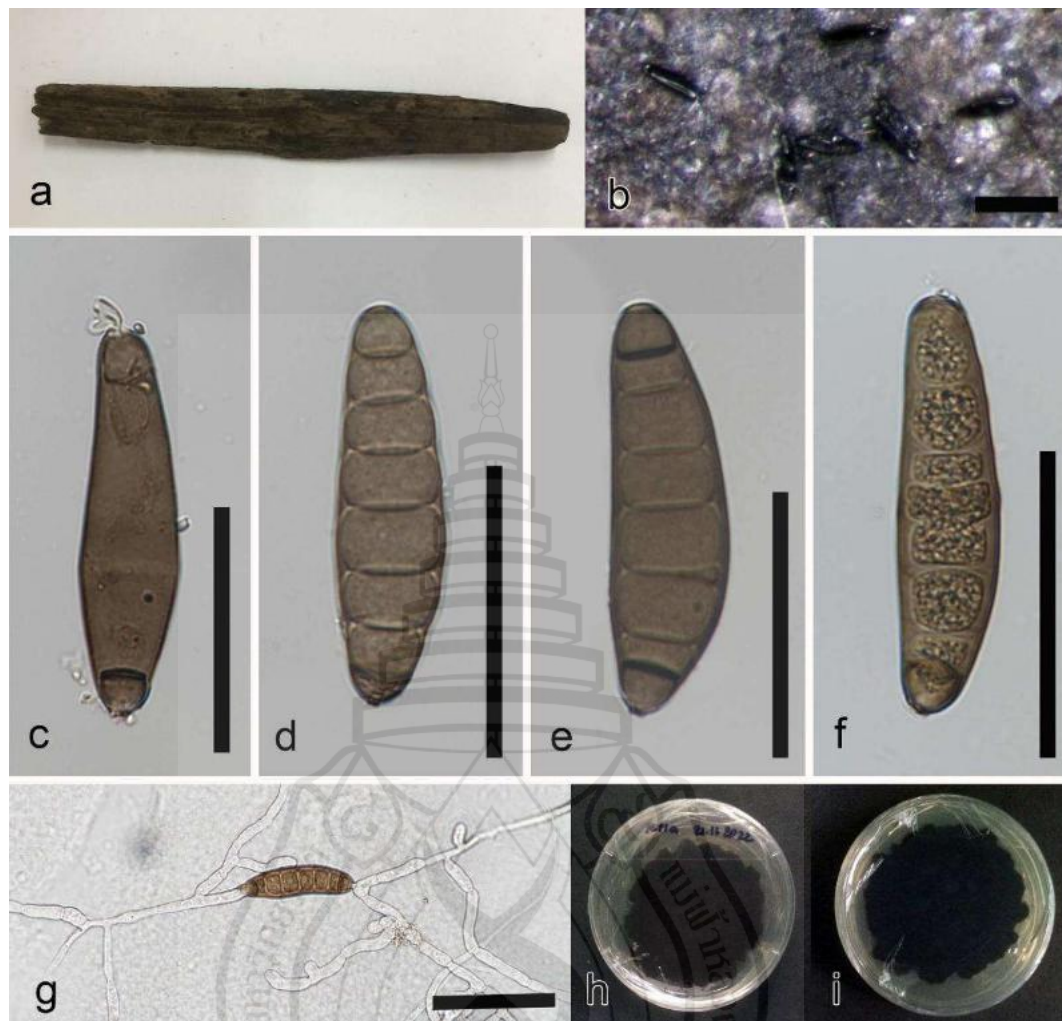
Exserohilum rostratum (Drechsler) K.J. Leonard & Suggs. Fig. 5.30

Saprobic on submerged decaying wood. **Asexual morph:** *Colonies* on the host surface, shiny, black, with a black spot on the host surface. *Vegetative hyphae* septate, branched, dark brown. *Conidiophores* not found on the host surface. *Conidiogenous cells* not found on the host surface. *Conidia* 70–80 × 17.5–22 µm ($\bar{x}$ = 76 × 20 µm, n = 15), clavate, obclavate or subcylindrical, thick-walled, guttulate, smooth to verruculose, distoseptate, with a dark septum at the basal and apical cells, with a hilum, pale brown to dark brown. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 4.5 cm diam. after one month at 25±2°C, flat, lobate margin, dark brown to black, from surface and reverse.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on submerged decaying wood in rocky shore (water salinity 19 ppt), 25 October 2022, KD Hyde, R11A (MFLU 26-0036); living culture (MFLUCC 26-0096).

Notes – A new isolate of *Exserohilum* (MFLUCC 26-0096) was collected from submerged decaying wood in Thailand. In the multi-gene phylogeny, the new isolate formed a close relationship with the strains of *Exserohilum rostratum*. The new collection is similar to *E. rostratum* in having clavate, obclavate, or subcylindrical conidia that are smooth to verrucose, distoseptate, with dark septa at the basal and apical cells, and having a hilum (Hernández-Restrepo et al. 2018). However, in our collection, the conidia were found detached on the host surface, and therefore, the morphology of the conidiophores and conidiogenous cells could not be described. Based on both morphological and molecular evidence, our isolate is reported here as a new collection of *E. rostratum* from a marine habitat in Thailand.



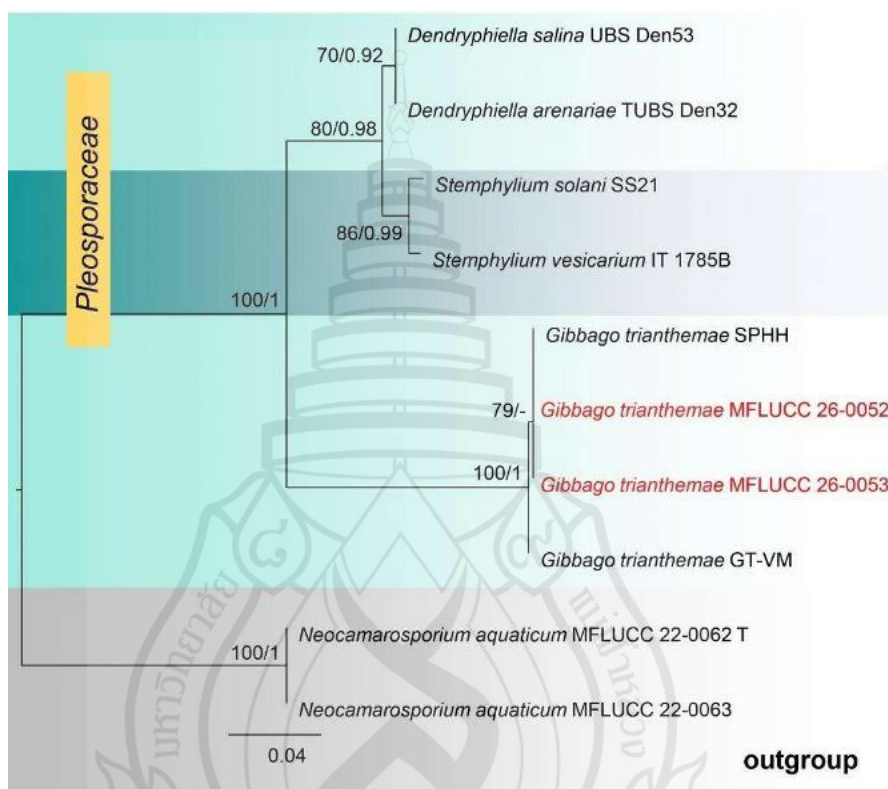
Note a Decaying wood of the host. b Close up of Colonies. c–f Conidia with hilum. g Germinated conidium. h, i Colony on PDA (front and below). Scale bars: b = 100 μ m, c–f = 50 μ m.

Figure 5.30 *Exserohilum rostratum* (MFLU 26-0036, new collection)

Gibbago E.G. Simmons

Gibbago is a monotypic genus in *Pleosporaceae*, introduced by Simmons (1986) to accommodate *Gibbago trianthemae*, collected from foliar lesions of *Trianthema portulacastrum* (Horse purslane). *Gibbago* is known by its hyphomycetous asexual morph producing phaeodictyoconidia, which distinguish it from similar genera such as *Alternaria* and *Stemphylium* by the production of secondary conidia (Simmons 1986). The species has been reported on *T. portulacastrum*, from different countries including Texas, the USA, India, Pakistan, Cuba, and Venezuela (Simmons 1986;

Aneja and Kaushal 1998; Akhtar et al. 2013; Kumara et al. 2016). Kumar and Gaddeyya (2014), mentioned about the host specificity of this species on *T. portulacastrum*, however, Chen et al. (2022b) reported it as a pathogen on *Sesuvium portulacastrum* in coastal area of China. In this study, two strains of *G. trianthemae* were isolated from halophyte *S. portulacastrum*, representing the first geographical record in Thailand.



Note The tree is rooted to *Neocamarosporium aquaticum* (MFLUCC 22.0062, MFLUCC 22.0063). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.31 Phylogram generated from the ML analysis based on the combined ITS sequence data of *Pleosporaceae*

Gibbago trianthemae E.G. Simmons. Fig. 5.32

Index Fungorum number: IF130298; Facesoffungi number: FoF 00523

Saprobic on dead stems of *Sesuvium portulacastrum*. **Asexual morph:** Colonies on the host surface, hairy, aggregated, brown, with a black area on the host surface. *Conidiophores* 80–180 × 5–7.5 μm ($\bar{x}$ = 110 × 6 μm, n = 20), cylindrical, straight or

flexuous, simple or proliferated percurrently, slightly swollen at apex, 1–8-septate, guttulate, brown. *Conidiogenous cells* $8\text{--}24 \times 4\text{--}6.5 \mu\text{m}$ ($\bar{x} = 15 \times 5.5 \mu\text{m}$, $n = 20$), cylindrical, integrated, brown, with a distinct depression at the conidiogenous cells' locus. *Conidia* $13\text{--}35 \times 5\text{--}20 \mu\text{m}$ ($\bar{x} = 24 \times 12 \mu\text{m}$, $n = 20$), ellipsoid; becoming broadly ellipsoid, thick-walled, guttulate, 1–4 transverse septa, 1–2 complete longitudinal septa, constricted at septa, with a minute basal pore-scar, brown. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diam. after one month at $25 \pm 2^\circ\text{C}$, flat, powdery, entire margin, circular; from surface, white with grayish white margin; from reverse, brown and orange brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pran Kiri Beach, on dead dry (aerial) stems of *Sesuvium portulacastrum* on seashore rocks, 8 November 2024, R. Asghari, S7P16 (MFLU 26-0034); living culture (MFLUCC 26-0052); *ibid.*, S7P12 (MFLU 26-0035); living culture (MFLUCC 26-0053).

Notes – Based on the phylogenetic analyses from ITS sequence data, our strains (MFLUCC 26-0052 and MFLUCC 26-0053) grouped with *Gibbago trianthemae* (SPHH) with 79% ML support. Morphologically, our collections are similar to the holotype of *G. trianthemae* in having simple or proliferated, septate conidiophores, with very slightly swollen at apex, with a distinct depression at the conidiogenous locus, ellipsoid to broadly ellipsoid conidia, with transverse and longitudinal septa (Simmons 1986). Based on morphological and molecular similarities, our collections are introduced as new geographical records of *G. trianthemae* on *Sesuvium portulacastrum* in Thailand.



Note a Decaying twig of host. b, c Colonies on natural substrate. d–g Conidiophores. h Conidiogenous cell and developing conidium. i–l Conidia. m Germinated conidium. n Colonies on PDA (front and below). Scale bars: b = 250 μm , c = 100 μm , d = 40 μm , e–l = 20 μm .

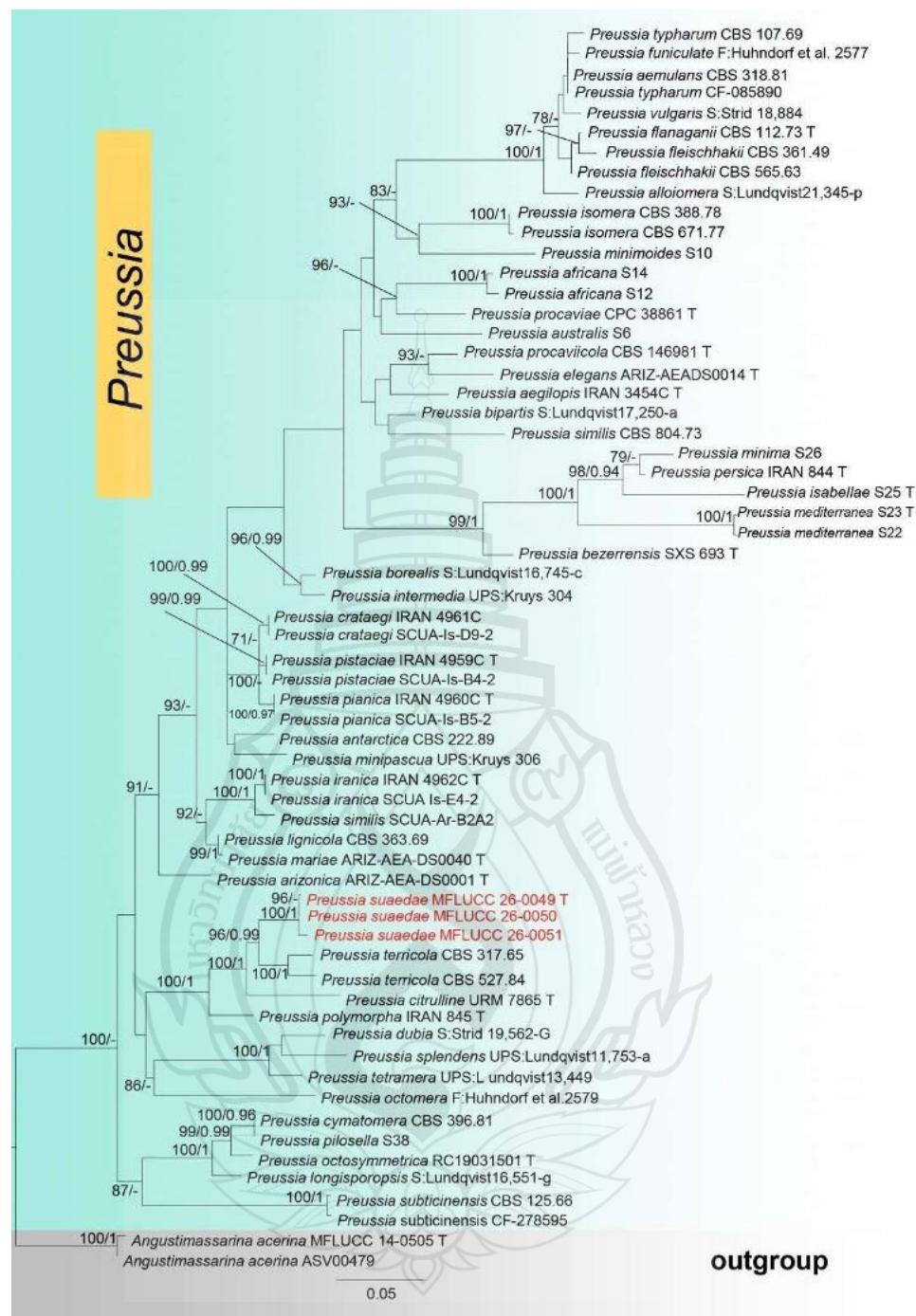
Figure 5.32 *Gibbago trianthemae* (MFLU 26-0034, new geographical record)

Sporormiaceae Munk 1957

Munk (1957) introduced the family *Sporormiaceae* based on its type genus, *Sporormia*. Members of *Sporormiaceae* are widely distributed across various substrates, reported as saprobes on dung, soil, and wood, and plant endophytes (Mapperson et al. 2014; González-Menéndez et al. 2017; Lytvynenko et al. 2022). The family comprises eleven genera, of which *Preussia* is the most species-rich genus (Hyde et al. 2024).

Preussia Fuckel 1867

Preussia, with about 60 species, is one of the largest genera in the family *Sporormiaceae* (Hyde et al. 2024). The genus was introduced by Fuckel (1866) to accommodate its type species, *Preussia funiculata*. The sexual morph of *Preussia* produces long pedicellate asci and brown, cylindrical ascospores that split into separate cells, each with a germ slit (Fuckel 1866). *Preussia* species have been reported from various substrates, including plants, salt marshes, soil, and dung, in both terrestrial and aquatic habitats, living as saprobes, endophytes, or associates of symptomatic forest trees (Calabon et al. 2021; Sandberg et al. 2022; Tan et al. 2022; Mehrabi et al. 2022; Phurbu et al. 2024; Eisvand and Mehrabi Koushki 2025). In this study, three strains of *Preussia* were isolated from *Suaeda maritima* in salt marsh habitats in Thailand. We provide an updated phylogenetic tree for the genus and introduce one new species.



Note The tree is rooted to *Neocamarosporium aquaticum* (MFLUCC 22.0062, MFLUCC 22.0063). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.33 Phylogram generated from the ML analysis based on the combined ITS, LSU, TUB and *tef1* sequence data of *Preussia*

Preussia suaedae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov.

Fig. 5.34

Etymology – Referring to the isolation of the fungus from *Suaeda maritima*.

Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** Undetermined.

Sexual morph: *Ascomata* 450–600 × 420–520 µm ($\bar{x}$ = 550 × 460 µm, n = 10), immersed to erumpent, reddish pigments are visible in the host tissue, solitary, subglobose, obpyriform, black, papillate, with a central ostiole. *Peridium* 48–70 ($\bar{x}$ = 61 µm, n = 15), outer layer, reddish black to black, *textura angularis*, inner layer, hyaline, *textura globosa*. *Pseudoparaphyses* 1.5–3.5 µm wide ($\bar{x}$ = 2.5, n = 15), numerous, filiform, cylindrical, branched, hyaline, septate. *Asci* 160–415 × 17–30 µm ($\bar{x}$ = 260 × 23.5 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, elongate-clavate, elongating with the maturity, straight or curved, broadly rounded apex, short pedicellate, with an ocular chamber. *Ascospores* 45–58 × 8.5–13 µm ($\bar{x}$ = 52 × 11 µm, n = 20), fusiform, rounded ends, guttulate, granular, 3-septate, initially hyaline, becoming brown and deeply constricted at septa with maturity, segments of ascospores separating completely in four partspores, each partspore with a longitude germ slit.

Culture characteristics – Colonies on PDA reaching 3.5 cm diam. after one month at 25±2°C, umbonate, medium dense, radiating, slightly lobate margin; from surface, reddish gray, dull red at the margin; from reverse, dark magenta, dull red at the periphery.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park (water salinity 15 ppt), on dead submerged stems of *Suaeda maritima*, 8 November 2024, R. Asghari, S7S33 (MFLU 26-0031, holotype), ex-type culture (MFLUCC 26-0049); *ibid.*, (water salinity 28 ppt), on dead submerged stems of *Suaeda maritima*, 30 November 2023, R. Asghari, SB51 (MFLU 26-0032), living culture (MFLUCC 26-0050); *ibid.*, SB52 (MFLU 26-0033); living culture (MFLUCC 26-0051).

Notes: Our strains of *Preussia suaedae* formed a sister clade to *P. terricola* (CBS 317.65 and CBS 527.84) with 96% ML/0.99 BPP support. Ecologically, *P. terricola* (CBS 317.65) and (CBS 527.84) were isolated from *Musa sapientum* and elephant dung, respectively (Kruys and Wedin 2009); however, this species was also

reported from a salt marsh plant (*Elymus pungens*) (Apinis and Chesters 1969; Calabon et al. 2021). Morphologically, *P. suaedae* is similar to the holotype of *P. terricola* in having branching filiform paraphyses, elongate-clavate asci, and ascospores with three septa that separate into four segments. However, *P. suaedae* differs in having papillate ascomata, a reddish coloration in host tissue, a thick peridium despite being membranous, and distinctly larger ascomata, asci, and ascospores. Pairwise comparison between *Preussia suaedae* (MFLUCC 26-0049) and *P. terricola* (CBS 317.65), showed 7.7% (39/502, with gaps) and 0.8% (7/881, with gaps) differences in ITS and LSU respectively. Morphological characteristics together with molecular data support the introduction of *P. suaedae* as a novel species.



Note a Colonies on natural substrate. b Section of an ascoma. c Peridium. d Paraphyses and ascus. e–i Asci. j–l Ascospores. m, n Colony on PDA (front and below). Scale bars: a = 1 mm, b = 200 μ m, c = 100 μ m, d–f, j–l = 20 μ m, g, h = 40 μ m.

Figure 5.34 *Preussia suaedae* (MFLU 26-0031, holotype)

Dothideomycetes orders incertae sedis

Botryosphaeriales C.L. Schoch, Crous & Shoemaker

Botryosphaeriaceae Theiss. & Syd.

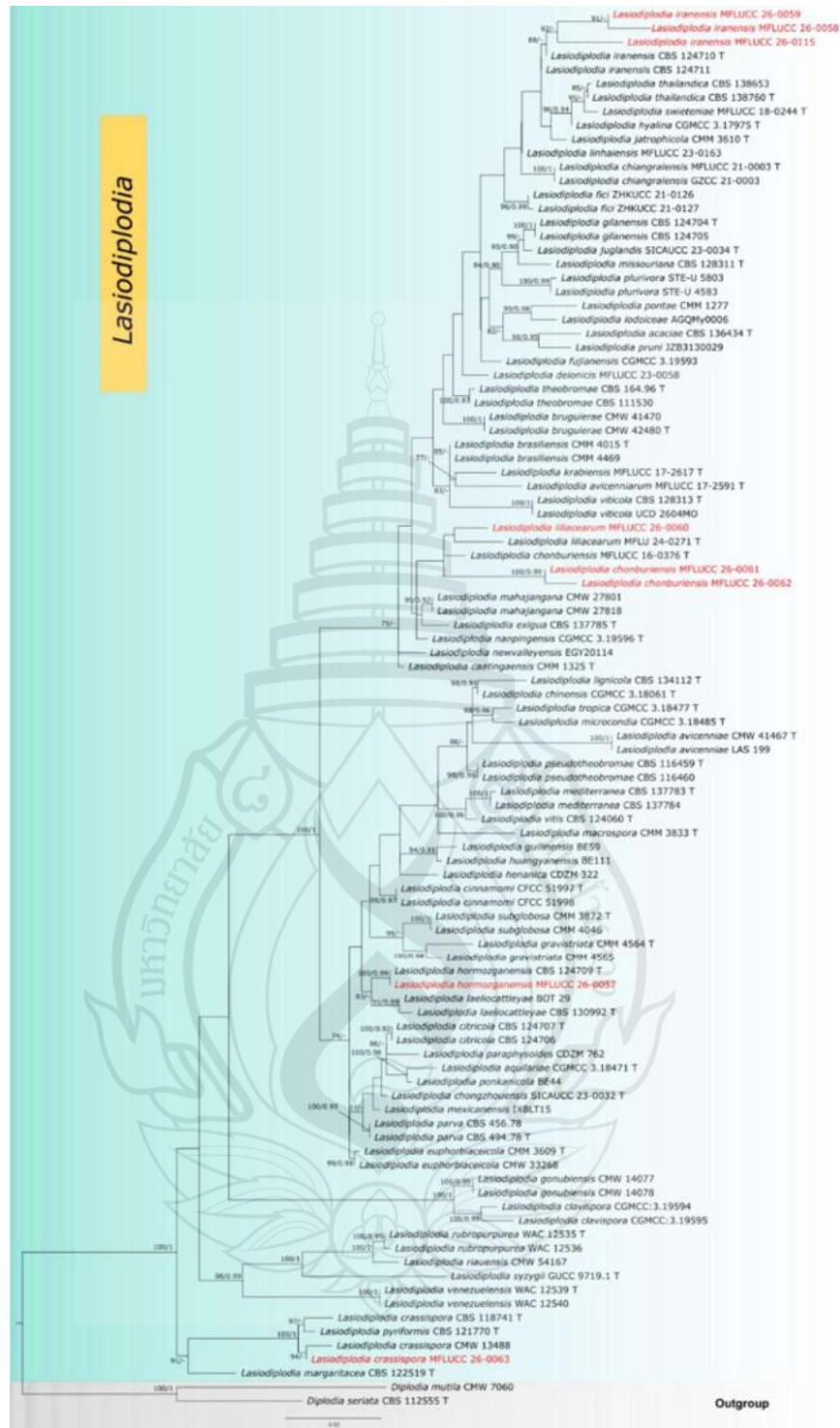
Lasiodiplodia Ellis & Everh.

Botryosphaeriaceae Theiss. & Syd.

Botryosphaeriaceae was introduced to accommodate three genera, *Botryosphaeria*, *Phaeobotryon*, and *Dibotryon* (Theissen and Sydow 1918), and has since expanded to 23 accepted genera based on morphological and molecular studies (Crous et al. 2006a; Phillips et al. 2013, 2019; Hyde et al. 2024). The sexual morph is characterized by uniloculate, solitary or clustered ascomata, 8-spored bitunicate asci with an ocular chamber, and hyaline or pigmented ascospores, mostly lacking a mucoid sheath. The asexual morph is coelomycetous (Phillips et al. 2013, 2019). Members of *Botryosphaeriaceae* are reported as endophytes, pathogens, and saprobes on a wide range of hosts (Dissanayake et al. 2016; Wang et al. 2024c; Armand et al. 2025a; Jayawardena et al. 2025). a few marine species have been reported in genera such as *Amarenomyces*, *Diplodia*, and *Lasiodiplodia* (Jones et al. 2019), and representative species of *Botryosphaeria*, *Macrophomina*, and *Tiarosporella* have been recorded from salt marsh plants (Calabon et al. 2021).

Lasiodiplodia Ellis & Everh.

Lasiodiplodia was established by Ellis (1896) and typified with *L. tubericola*. However, Ellis did not describe the genus and species and this was done by Clendenin (1896). Subsequently, *Botryodiplodia theobromae* was introduced by Patouillard (Patouillard and Lagerheim 1892) and recognized as an earlier taxon to *Lasiodiplodia* and given priority by Griffon and Maublanc (1909) who designated it the type species—*L. theobromae*. *Lasiodiplodia* is related to *Diplodia*, but differs in having conidia with striations and is phylogenetically distinct (Denman et al. 2000; Zhou and Stanosz 2001). *Lasiodiplodia* species have been found on a broad range of hosts in various geographical locations, including marine and freshwater habitats (Manawasinghe et al. 2016; Jayawardena et al. 2019; Jones et al. 2019; Afshari et al. 2025; Karimi et al. 2025).



Note The tree is rooted to *Diplodia mutila* (CMW 7060) and *D. seriata* (CBS 112555). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.35 Phylogram generated from the ML analysis based on the combined ITS, *tef1* and TUB sequence data of *Lasiodiplodia*

Lasiodiplodia chonburiensis Tibpromma & K.D. Hyde. Fig. 5.36

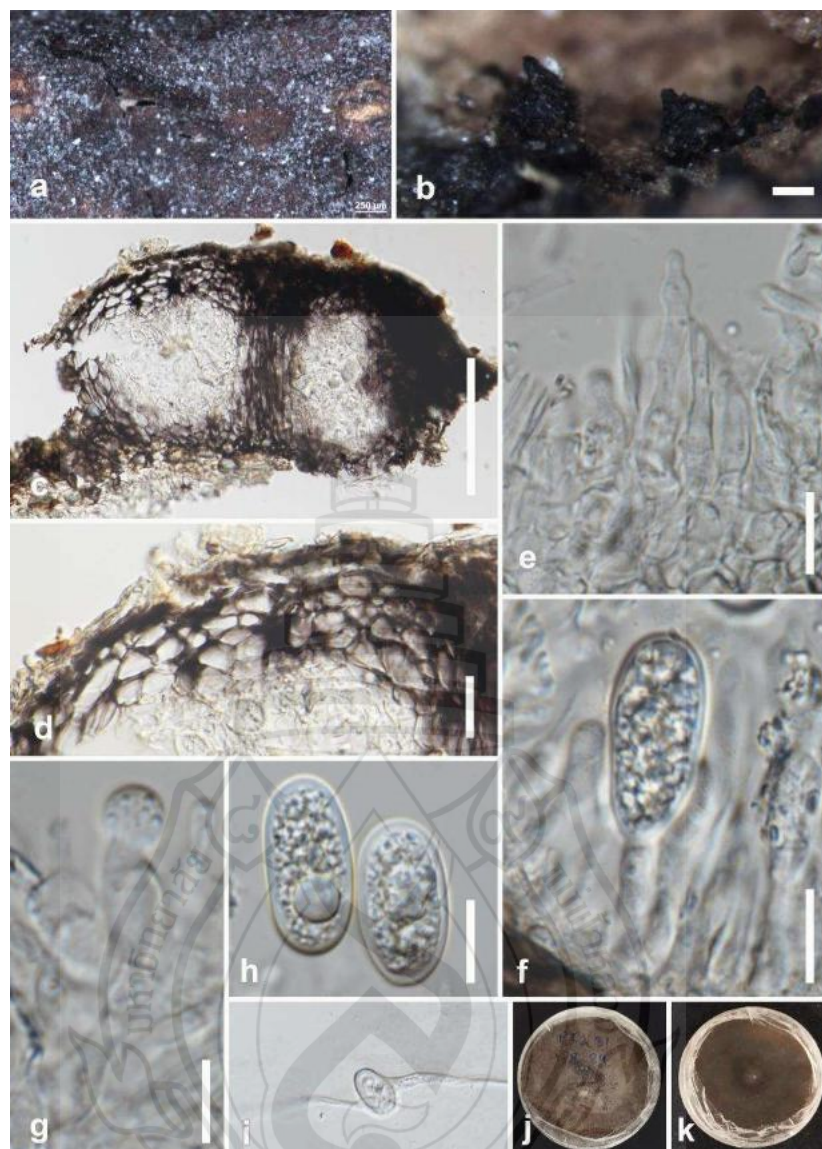
Index Fungorum number: IF554472; Facesoffungi number: FoF04564

Saprobic on dead branch of *Ficus microcarpa*. **Asexual morph:** *Conidiomata* 150–250 µm diam. ($\bar{x}$ = 175 µm diam., n = 10), pycnidial, immersed, erumpent to superficial, aggregated, globose to subglobose, with or without a short neck, dark brown to black. *Peridium* 20–53 µm ($\bar{x}$ = 33 µm diam., n = 10), thick, dark brown to black, *textura angularis*. *Paraphyses* 29–50 × 1.5–4 µm ($\bar{x}$ = 40 × 2 µm, n = 15), cylindrical, straight or curved, unbranched or branched, base, middle and apical cells swollen, aseptate to 3-septate, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 13–17.5 × 2–4 µm ($\bar{x}$ = 15 × 3 µm, n = 15), holoblastic, cylindrical, hyaline, determinate. *Conidia* 18–26 µm × 9.5–12.5 µm ($\bar{x}$ = 22 × 11 µm, n = 20), ellipsoidal to oval, granular, rounded at both ends, hyaline, aseptate, guttulate, thick-walled.. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 5 cm diam. after one week at 25±2°C, circular, raised, fluffy, dull, from surface, smoke-gray to grayish brown; from reverse grayish brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on dead attached dry stem of *Ficus microcarpa*, 1 December 2023, R. Asghari, PFA31 (MFLU 26-0051); living culture (MFLUCC 26-0061); *ibid.*, on an attached dead dry twig of *Chromolaena odorata*, 23 May 2023, R. Asghari, BM11 (MFLU 26-0052); living culture (MFLUCC 26-0062).

Notes – Based on the multi-gene phylogenetic analyses from ITS, *tef1*, and *tub2* sequence data, our strains (MFLUCC 26-0061 and 26-0062) grouped with *L. chonburiensis* (MFLUCC 16-0375) (ex-type). Morphologically, our collections are similar to the holotype of *L. chonburiensis* in having oval aseptate hyaline conidia (Tibpromma et al. 2018). Although the bootstrap support is low, ITS sequence comparison of our strain (MFLUCC 26-0061) revealed only minor differences (3/469 bp, including gaps) from *L. chonburiensis*. Based on morphological similarities, phylogenetic placement, and base pair comparison, our collections are reported as new host records of *L. chonburiensis* on *Ficus microcarpa* and *Chromolaena odorata* in Thailand.



Note a, b Appearance of conidiomata on host tissue. c Vertical section of conidiomata. d Section through peridium. e Paraphyses. f Developing conidia attached to conidiogenous cells. g, h Conidia. i, j Culture on PDA (above and below). Scale bars: b = 250 μm , c = 100 μm , d–f = 20 μm , g, h = 5 μm .

Figure 5.36 *Lasiodiplodia chonburiensis* (MFLU 26-0051, new host record)

Lasiodiplodia crassispora T.I. Burgess & P.A. Barber. Fig. 5.37

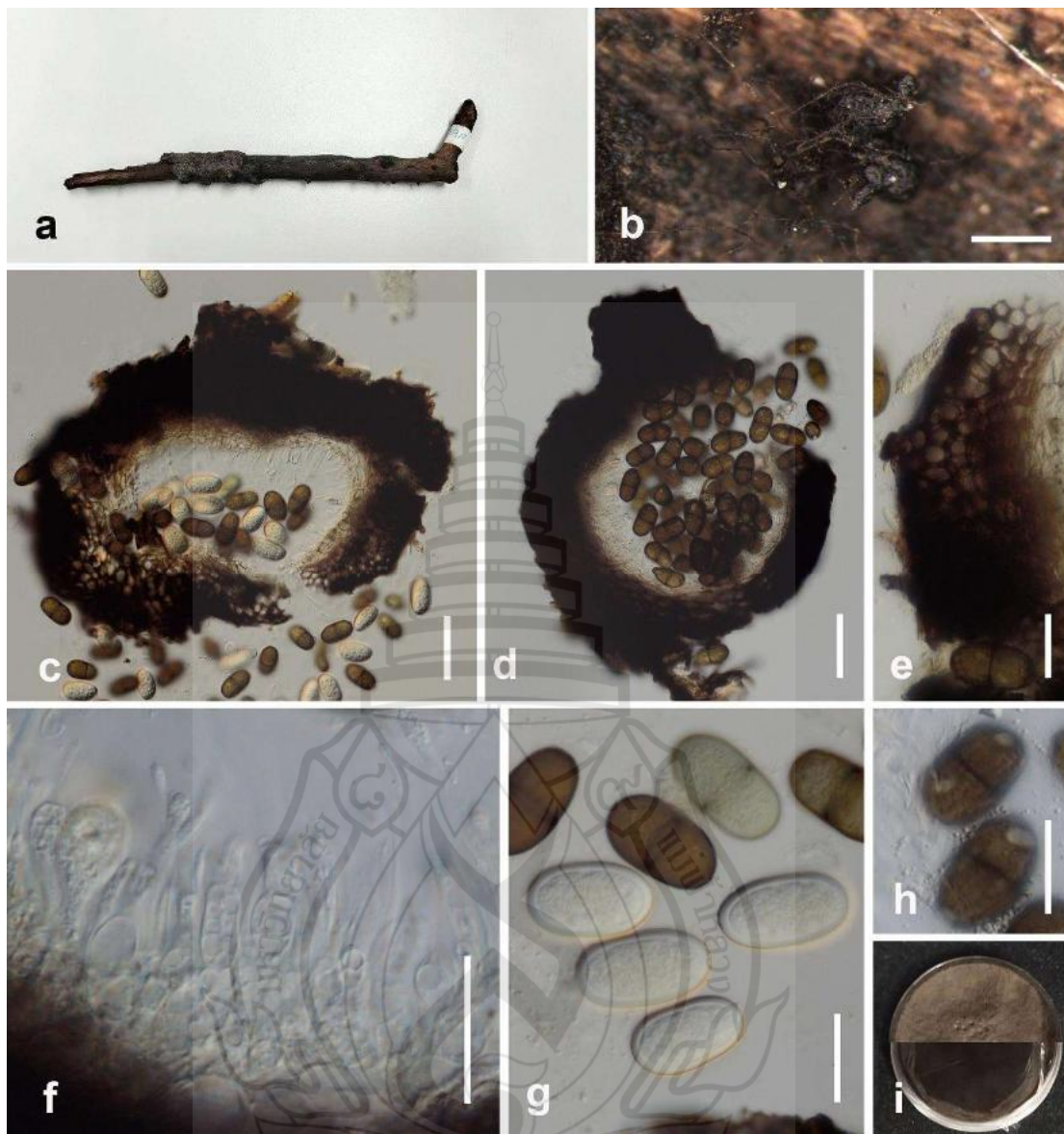
Saprobic on decaying wood submerged in seawater. **Asexual morph:** *Conidiomata* 190–330 μm diam. ($\bar{x}$ = 260 μm diam., n = 10), pycnidial, superficial, solitary, or in small groups, globose to subglobose, with or without a short neck, dark brown to black. *Peridium* 35–65 μm ($\bar{x}$ = 47 μm diam., n = 10), thick, dark brown to

black, *textura globosa* to *angularis*. *Paraphyses* cylindrical, straight or curved, unbranched, apical somewhat cells swollen, aseptate to septate, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 8–16.5(–20) × 2–6 µm ($\bar{x}$ = 13 × 3.8 µm, n = 15), holoblastic, cylindrical to ampulliform, hyaline, determinate. *Conidia* (14–)22–35 µm × 11–16.5 µm ($\bar{x}$ = 25 × 14 µm, n = 20), ellipsoid to obovoid, rounded at apex, occasionally truncate base, guttulate, thick-walled, initially hyaline, aseptate, becoming brown, 1-septate with age, with vertical striations. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 4 cm diam. after one week at 25±2°C, circular, raised aerial fluffy mycelia, dull, from surface, brownish gray; from reverse, violate gray.

Material examined: Thailand, Narathiwat Province, on decaying wood submerged in seawater, 5 August 2023, O. Karimi, NB21 (MFLU 26-0053); living culture (MFLUCC 26-0063).

Notes – In multi-gene phylogenetic analyses, our strain (MFLUCC 26-0063) grouped with *L. crassispota* (CMW 13488) with 94% ML support. Morphologically, our collection is similar to the holotype of *L. crassispota* in having cylindrical to ampulliform conidiogenous cells, ellipsoid to obovoid, thick-walled conidia, with pigmentation, septation and surface striations in mature conidia (Burgess et al. 2006). Base pair comparisons between our strain and the ex-type of *L. crassispota* (CBS 118741) revealed minor differences of 3/482 bp (0.6%, with gaps) in ITS₁ region. Based on morphological similarity, phylogenetic placement, and base pair comparisons, our collection is reported as a new geographical and habitat record of *L. crassispota* from marine environments in Thailand.



Note a Host. b Appearance of conidiomata on host tissue. c, d Vertical section of conidiomata. e Section through peridium. f Paraphyses and developing conidia attached to conidiogenous cells. g, h Conidia. i Culture on PDA (above and below). Scale bars: b = 500 μm , c–e = 50 μm , f–h = 20 μm .

Figure 5.37 *Lasiodiplodia crassispora* (MFLU 26-0053, new geographical record)

Lasiodiplodia hormozganensis Abdollahz., Zare & A.J.L. Phillips. Fig. 5.38

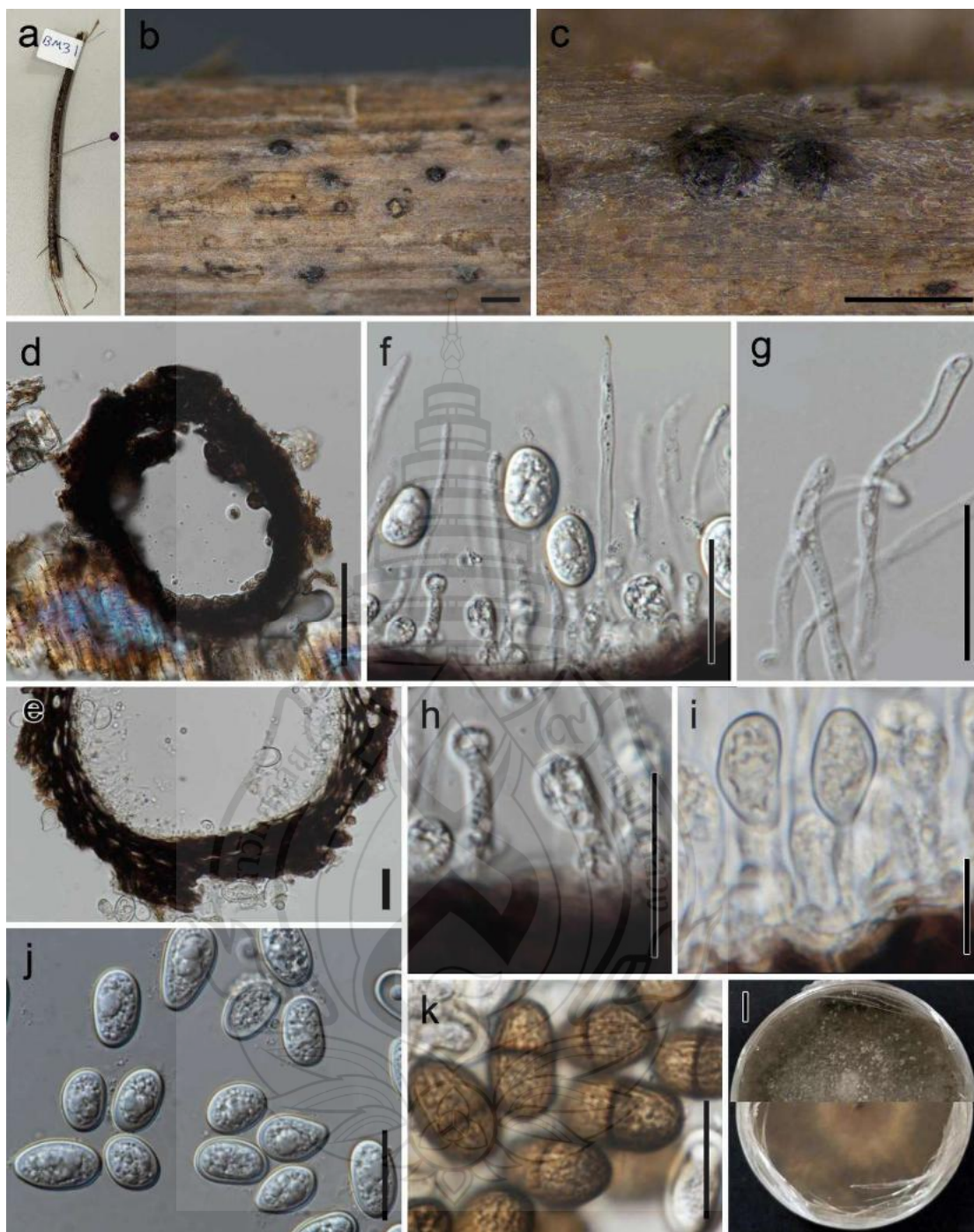
Saprobic on dead twig of *Chromolaena odorata*. **Asexual morph:** *Conidiomata* 145–600 $\mu\text{m} \times 155$ –480 μm . ($\bar{x}$ = 340 $\times$ 245 μm , n = 10), stromatic, pycnidial, semi-immersed, solitary, globose to subglobose, papillate or non-papillate, uniloculate,

black. *Peridium* thick, black to dark brown, *textura angularis* with narrow cells. *Paraphyses* (19–)32–65 $\times$ 1.5–2.5 μm ($\bar{x}$ = 48 $\times$ 1.8 μm , n = 15), cylindrical, straight or curved, rarely branched, apical cells swollen, round apex, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* (4.5–)6–15(–20) $\times$ 2–4 μm ($\bar{x}$ = 12 $\times$ 3 μm , n = 15), holoblastic, cylindrical, hyaline, discrete, determinate. *Conidia* 15–21.5 μm $\times$ 9–12 μm . ($\bar{x}$ = 17.5 $\times$ 10.5 μm , n = 25), subcylindrical, rarely obovoid, granular, rounded at both ends, wall 0.5 – 1.2 μm ($\bar{x}$ = 1, n = 20), initially hyaline, aseptate, becoming brown, with one dark brown to black septum, verrucose, ellipsoid to obovoid, with longitudinal striations. **Sexual morph**: Undetermined.

Culture characteristics – Colonies on PDA reaching 5 cm diam. after one week at 25 $\pm$ 2°C, with medium density, circular, raised aerial fluffy mycelia, from above, smoke-gray to olivaceous-gray to dull green above; from reverse olivaceous-gray to vinaceous-buff in reverse.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on an attached dead dry twig of *Chromolaena odorata*, 23 May 2023, R. Asghari, BM32 (MFLU 26-0046); living culture (MFLUCC 26-0057).

Notes – In the present phylogenetic analyses data, our new collection of *Lasiodiplodia hormozganensis* (MFLUCC 26-0057) formed a sister clade to *L. hormozganensis* (CBS 124709, holotype) with strong support (100% ML/0.99 BPP). Morphologically, our collection resembles *L. hormozganensis* in having similar dimension of conidiogenous cells and conidia (Abdollahzadeh et al. 2010). The ITS sequence of our strain is identical to that of *L. hormozganensis* (CBS 124709). Based on morphological and molecular evidence, our collection is reported as a new host record of *L. hormozganensis* on *Chromolaena odorata*, from a coastal region in Thailand.



Note a Host. b, c Appearance of conidiomata on host tissue. d Vertical section of conidiomata. e Section through peridium. f–g Paraphyses. h–i Developing conidia attached to conidiogenous cells. j, k Conidia. l culture after one month on PDA (above and below). Scale bars: b, c = 500 μ m, d = 100 μ m, f–k = 20 μ m.

Figure 5.38 *Lasiodiplodia hormozganensis* (MFLU 26-0046, new host record)

Lasiodiplodia iranensis Abdollahz., Zare & A.J.L. Phillips. Fig. 5.39

Index Fungorum number: IF516780

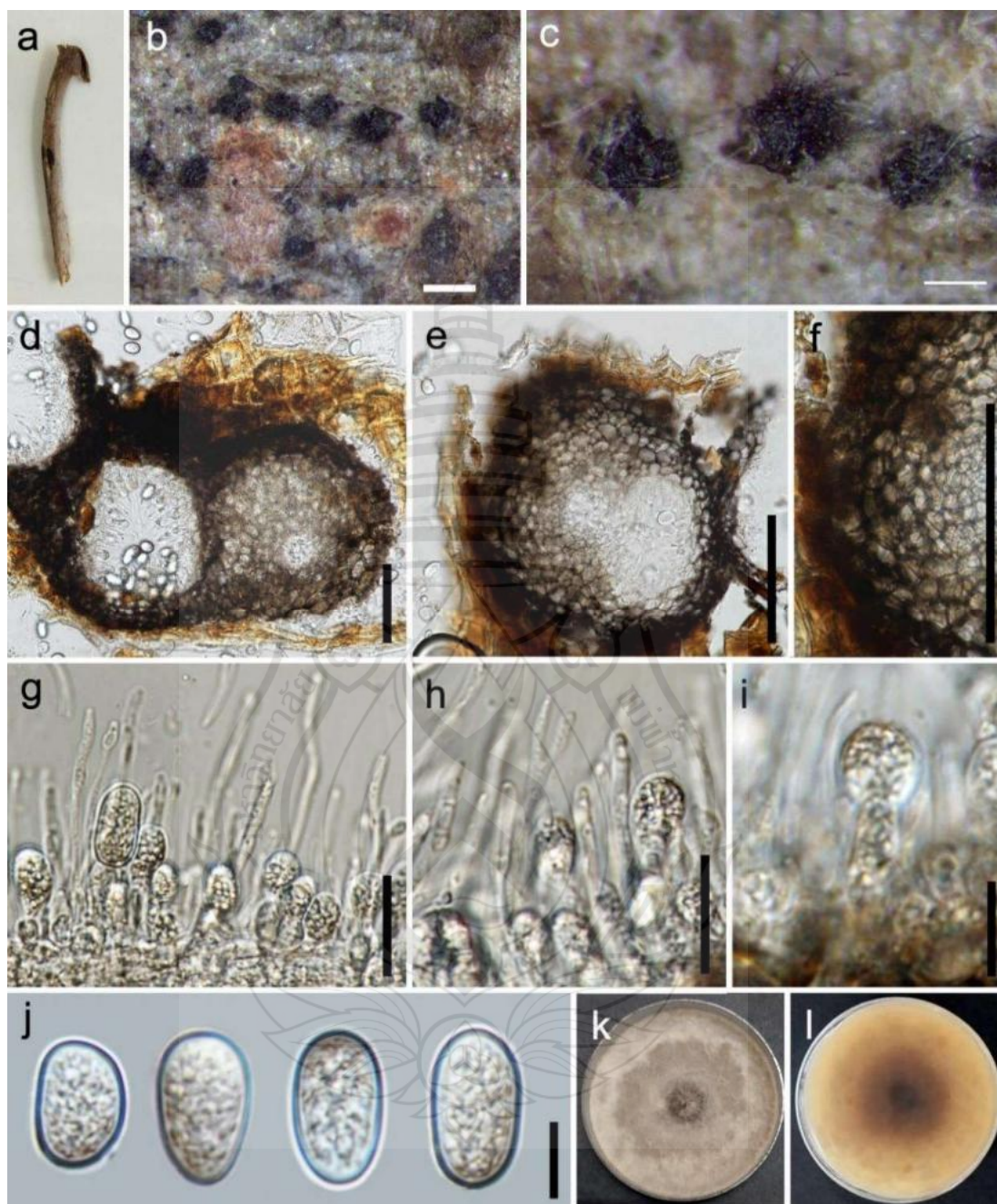
Saprobic on dead wood, submerged in seawater. **Asexual morph:** *Conidiomata* 180–370 μm $\times$ 130–340 μm . ($\bar{x}$ = 240 $\times$ 200 μm , n = 10), stromatic, pycnidial, aggregated, rarely solitary, globose to subglobose, non-papillate, uniloculate, black, peridial hair dark brown to black. *Peridium* thick, outer layer thick-walled, dark brown to black, *textura angularis*, inner layer thin-walled, pale brown to hyaline, *textura angularis*. *Paraphyses* (20–)30–86 $\times$ 1–2 μm ($\bar{x}$ = 62 $\times$ 1.5 μm , n = 15), cylindrical, straight or curved, rarely branched, basal, middle or apical cells swollen occasionally, up to 6 septa, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6–10.5 $\times$ 2–5.5 μm ($\bar{x}$ = 8 $\times$ 3.5 μm , n = 15), holoblastic, cylindrical, hyaline, discrete, determinate. *Conidia* 16–23 μm $\times$ 9.5–13.5 μm . ($\bar{x}$ = 19.5 $\times$ 12 μm , n = 20), subcylindrical, rarely obovoid, granular, rounded at both ends, wall 0.5 – 1.7 μm ($\bar{x}$ = 1, n = 20), initially hyaline, aseptate, becoming brown, with one dark brown to black septa, verrucose, ellipsoid to obovoid, with longitudinal striations. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 5 cm diam. after one week at 25 $\pm$ 2°C, with medium density, circular, raised aerial fluffy mycelia, dull surface, from surface, smoke-gray to olivaceous-gray above; from reverse, olivaceous-gray to hazel.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on submerged decaying wood (water salinity 19 ppt), trapped between rocks, 25 October 2022, KD Hyde, R22A (MFLU 26-0047); living culture (MFLUCC 26-0058); *ibid.*, R19A (MFLU 26-0048); living culture (MFLUCC 26-0059); *ibid.*, R5D (MFLU 26-0049); living culture (MFLUCC 26-0115).

Notes – Phylogeny revealed that the new collections of *Lasiodiplodia* (MFLUCC 26-0058, MFLUCC 26-0059 and MFLUCC 26-0115) grouped with the strains of *L. iranensis*. They share common characters with *L. iranensis* in the dimension of conidia (Abdollahzadeh et al. 2010). ITS sequence comparisons between our collections and the ex-type strain (IRAN 1520C = CBS 124710) showed complete identity for MFLUCC 26-0059 (477/477 bp, 100%), while minor differences were observed in MFLUCC 26-0058 (470/471 bp, 99.8%) and MFLUCC 26-0115 (475/476

bp, 99.8%). Based on morphological and molecular evidence, our collections represent new habitat records of *L. iranensis* from marine habitats in Thailand.



Note a Host. b, c Appearance of conidiomata on host tissue. d, e Vertical section of conidiomata. f Section through peridium. g–i Paraphyses and developing conidia from the conidiogenous cells. j Conidia. k, l Culture after one month on PDA (above, below). Scale bars: b = 200 μ m, c–f = 100 μ m, g, h = 20 μ m, l, j = 10 μ m.

Figure 5.39 *Lasiodiplodia iranensis* (MFLU 26-0047, new habitat record)

Lasiodiplodia liliacearum Y.R. Sun, Yong Wang bis & K.D. Hyde. Fig. 5.40

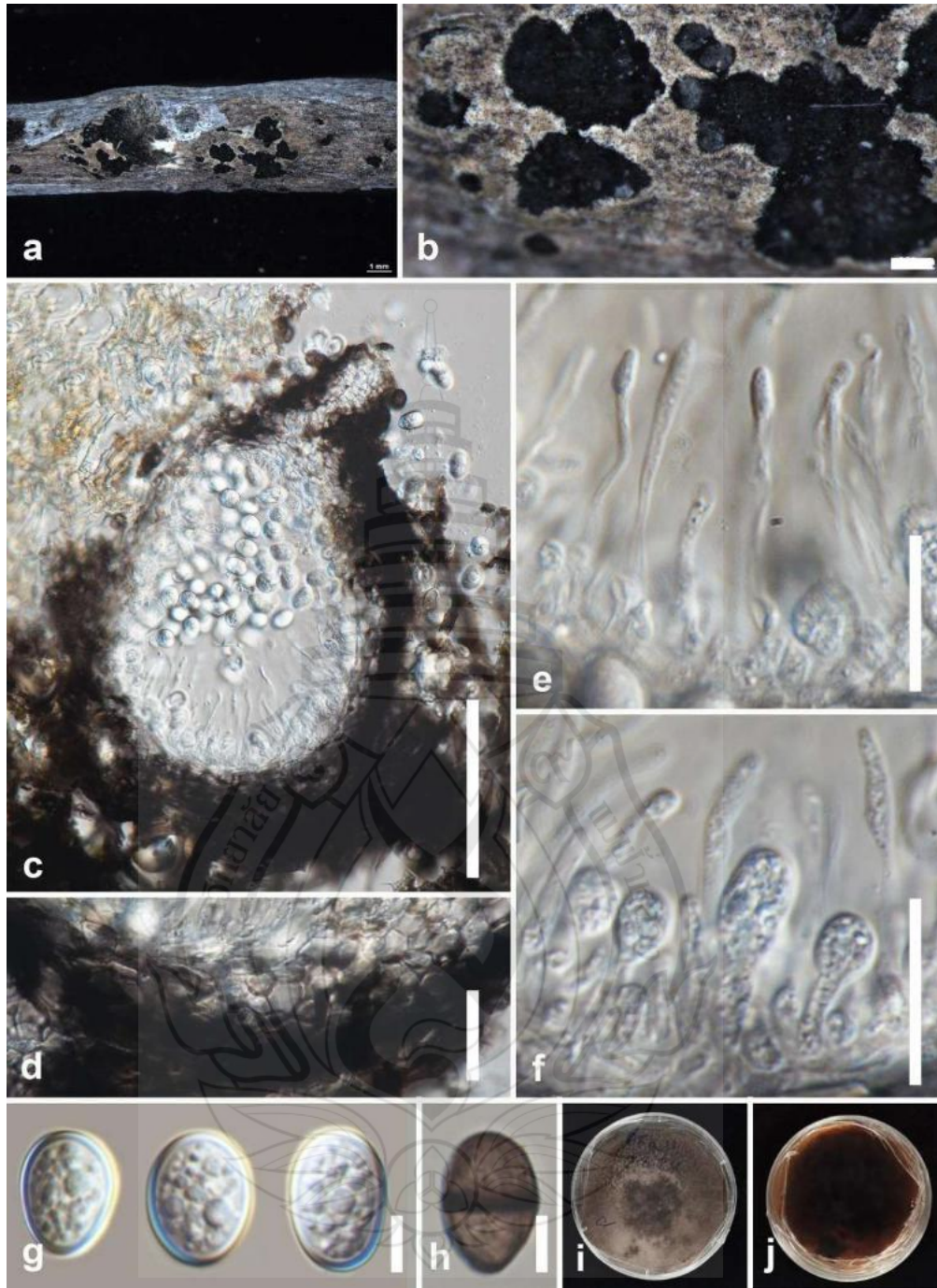
Index Fungorum number: IF903084

Saprobic on dead attached branch of *Ficus microcarpa*. **Asexual morph:** *Conidiomata* 170–220 µm diam. ($\bar{x}$ = 200 µm diam., n = 10), pycnidial, aggregated, globose to subglobose, with a short neck, uniloculate, dark brown to black. *Peridium* 17–40 µm ($\bar{x}$ = 30 µm diam., n = 10), thick, dark brown to black, *textura angularis*. *Paraphyses* 23–42 × 1–2.5 µm ($\bar{x}$ = 32 × 1.5 µm, n = 15), cylindrical, straight or curved, unbranched, apical cells swollen, aseptate, hyaline. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* 6.5–18.5 × 2–3.5 µm ($\bar{x}$ = 11 × 2.5 µm, n = 15), holoblastic, cylindrical, hyaline, determinate. *Conidia* 11.5–16.5 µm × 8.5–11 µm. ($\bar{x}$ = 14.5 × 10 µm, n = 20), subglobose to oval, granular, rounded at both ends, initially hyaline, aseptate, becoming brown, with one dark brown to black septa, guttulate, thick-walled. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 5 cm diam. after one week at 25±2°C, circular, raised aerial fluffy mycelia, from surface, grayish brown; from reverse reddish brown.

Material examined: Thailand, Prachuap Khiri Khan Province, Pranburi, on dead dry attached stem of *Ficus microcarpa*, 1 December 2023, R. Asghari, PFA11 (MFLU 26-0050); living culture (MFLUCC 26-0060).

Notes – Based on the multi-gene phylogenetic analyses from ITS, *tef1*, and *tub2* sequence data, our strain (MFLUCC 26-0060) grouped with *L. liliacearum* (MFLUCC 24-0283). Morphologically our collection is similar to *L. liliacearum* by its aseptate unbranched paraphyses, 1-septate brown mature conidia and the dimension of conidiomata (Sun et al. 2025). Although the bootstrap support is low, ITS sequence comparison revealed only minor differences (3/459 bp, including gaps; 0.65%) from *L. liliacearum*. Based on morphological similarities and phylogenetic placement, our collection is reported as a new host record of *L. liliacearum* on *Ficus microcarpa* in Thailand.



Note a, b Appearance of conidiomata on host tissue. c Vertical section of conidioma. d Section through peridium. e Paraphyses. f Developing conidia attached to conidiogenous cells. g, h Conidia. i, j Culture on PDA (above and below). Scale bars: b = 250 μm , c = 100 μm , d–f = 20 μm , g, h = 5 μm .

Figure 5.40 *Lasiodiplodia liliacearum* (MFLU PFA11, new host record)

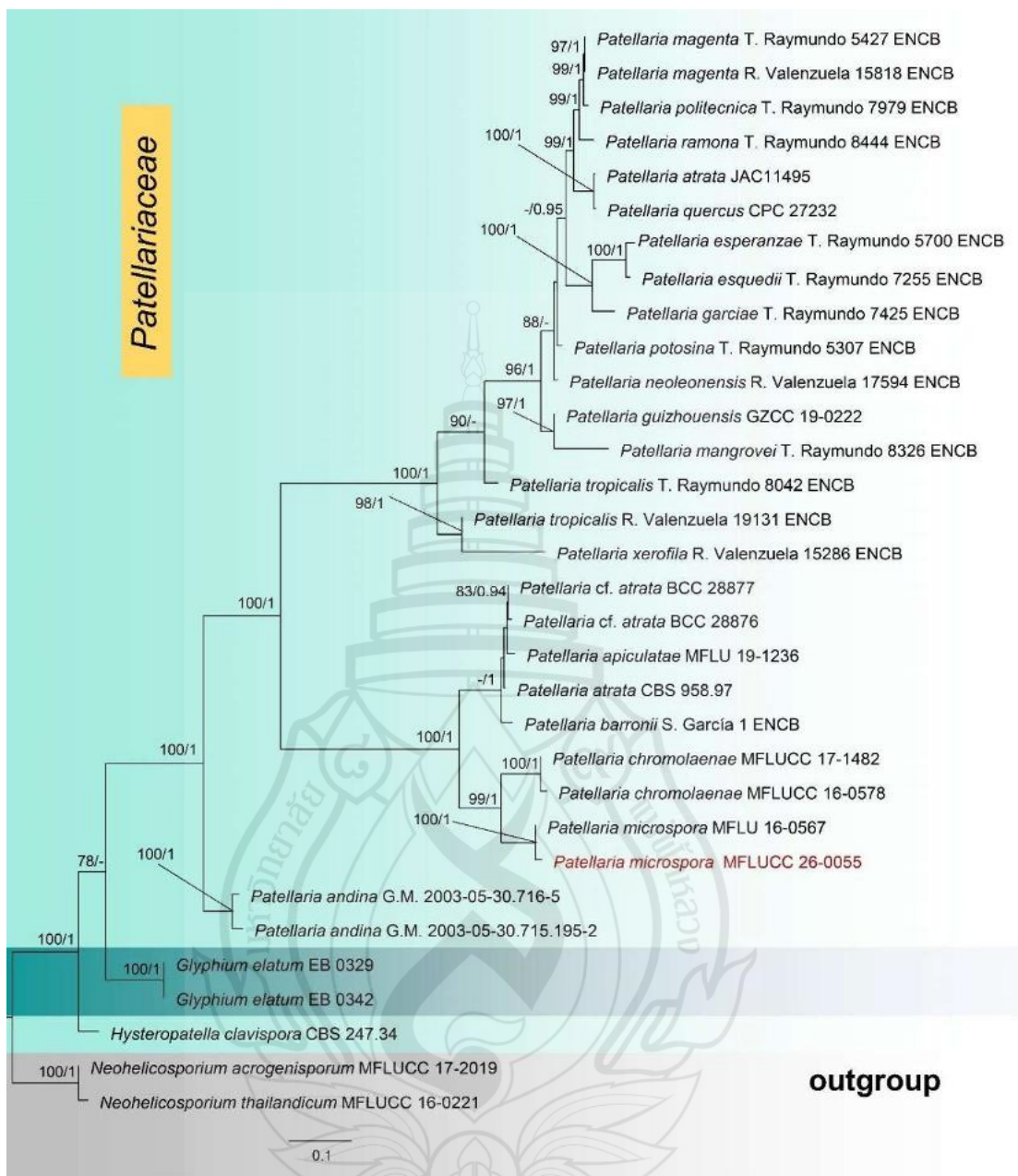
Patellariales D. Hawksw. & O.E. Erikss.

Patellariaceae Corda 1838

Patellariaceae is a family in *Dothideomycetes* comprising 19 genera, with *Patellaria* as the type genus (Hyde et al. 2024). The family was introduced by Corda (1838). Members of the family are widespread and mainly saprobic on woody plants, with a few reports of weakly parasitic, endophytic, or fungicolous species (Kutorga and Hawksworth 1997). Two genera, *Banhegyia* and *Patellaria*, include representative species from marine habitats (Jones et al. 2019).

Patellaria Fr. 1822

Patellaria, with about 50 species, is the largest genus in *Patellariaceae* (Hyde et al. 2024). The genus was introduced by Fries (1822) and is characterized by its sexual morph. Most species lack molecular data and morphology is important for species identification. It produces apothecial, black ascomata; filiform, branched paraphyses with pigmented apices; fissitunicate asci; and hyaline, greenish, or brown septate ascospores (Kutorga and Hawksworth 1997; Hongsanan et al. 2020b). *Patellaria atrata* and *P. apiculatae* have been reported from marine habitats (Jones et al. 2019; Dayarathne et al. 2020a). Here, a new species on *Sesuvium portulacastrum* in Thailand is introduced.



Note The tree is rooted to *Neohelicosporium acrogenisporum* (MFLUCC 17.2019) and *N. thailandicum* (MFLUCC 16.0221). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.41 Phylogram generated from the ML analysis based on the combined LSU, ITS and SSU sequence data of *Patellariaceae*

Patellaria sesuvii R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov.

Fig. 5.42

Etymology – Referring to the isolation of the fungus from *Sesuvium portulacastrum*.

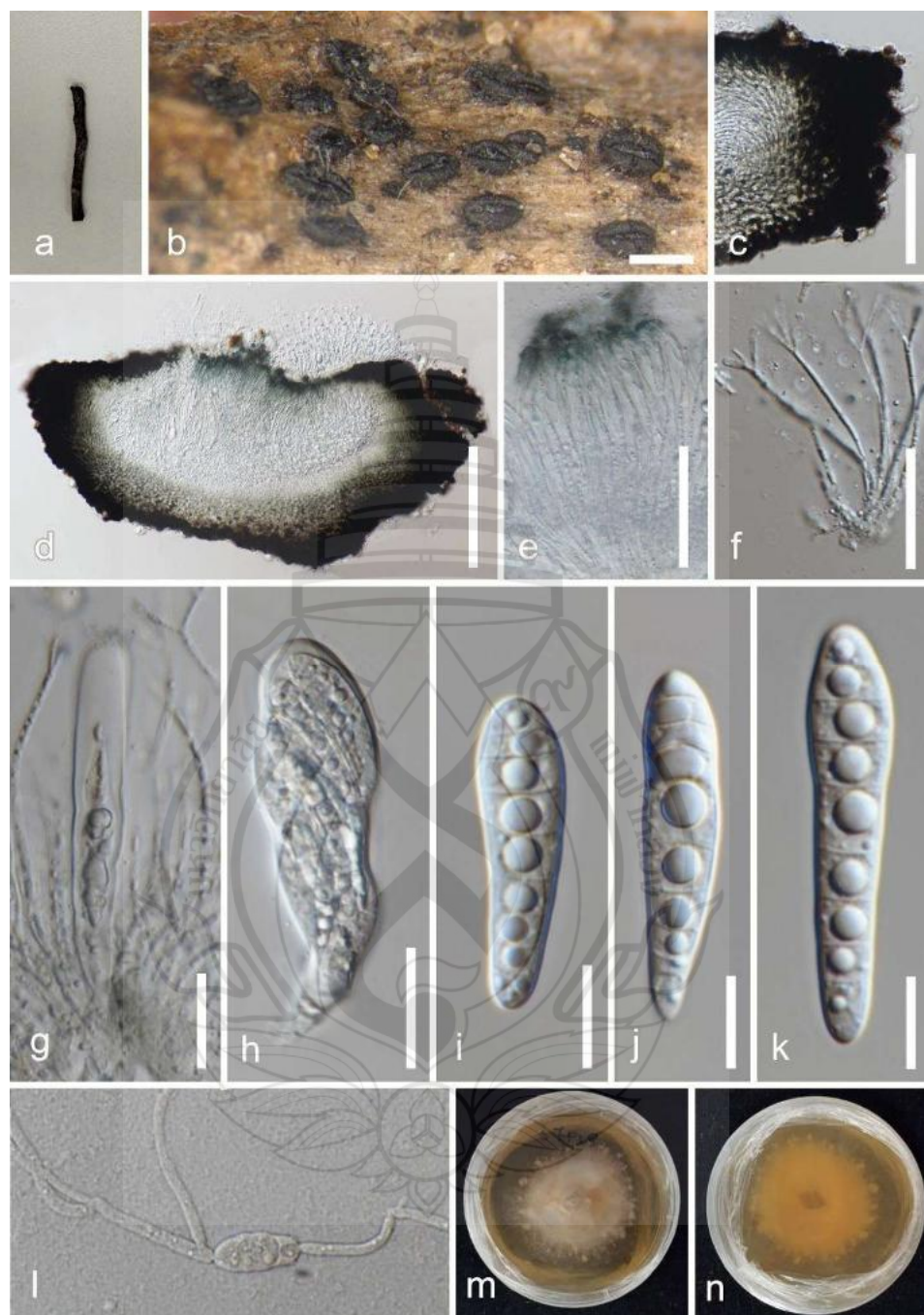
Saprobic on dead stems of *Sesuvium portulacastrum*. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata apothecial* 195–375 μm long $\times$ 120–340 μm wide ($\bar{x}$ = 260 $\times$ 232, n = 10), solitary or in small groups, sessile, black. *Receptacle* turbinate, disc slightly convex, black. *Ectal excipulum* 10–28 μm ($\bar{x}$ = 17.5 μm , n = 10), thick, black, compact subglobose to subangular cells. *Medullary excipulum* 13–37 μm ($\bar{x}$ = 23.5 μm , n = 10) composed of narrow, long cells, *textura porrecta*, hyaline to greenish. *Hymenium* hyaline. *Hamathecium* 1–2.5 μm wide ($\bar{x}$ = 1.5 μm , n = 20), numerous pseudoparaphyses, filiform, branched, septate, hyaline with greenish apex. *Asci* 32–83 $\times$ 9–16(–20) μm ($\bar{x}$ = 64 $\times$ 12 μm , n = 15), 8-spored, short pedicellate, cylindric to clavate, round apex. *Ascospores* 26–37 $\times$ 4.5–7.5 μm ($\bar{x}$ = 31 $\times$ 7 μm , n = 20), clavate, 5–9-septate, smooth-walled, hyaline, guttulate.

Culture characteristics – Colonies on PDA reaching 4 cm diam. after one month at 25 $\pm$ 2°C, flat, medium dense. fimbriate; from surface, orange white; from reverse, pale orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pran Kiri Beach, on dead dry (aerial) stems of *Sesuvium portulacastrum* on seashore rocks, 8 November 2024, R. Asghari, S7P18 (MFLU 26-0041, holotype); ex-type culture (MFLUCC 26-0055).

Notes – Concatenated phylogenetic analyses of ITS, LSU, and SSU sequence data resolved our strain of *Patellaria microspora* (MFLUCC 26-0055) as sister to *P. microspora* (MFLU 16-0567, holotype), with strong support (100% ML/1.00 BPP). Morphologically, it is similar to *P. microspora*, in having apothecia, turbinate receptacle, medullary excipulum with *textura porrecta*, numerus filiform branched paraphyses, cylindrical to clavate asci, hyaline, septate ascospores. However, it differs from the holotype of *P. microspora* in the dimensions of the ascospores (31 $\times$ 7 vs. 9.88 $\times$ 9.21 μm) (Hongsanant et al. 2020b). Similar dimensional variation has been reported in other collections of this species (Wanasinghe et al. 2025). Morphological and phylogenetic evidence, together with ITS sequence comparison (3/552 bp, 0.5%; with

gaps), supports the recognition of our collection as a new host record of *P. microspora* on *Sesuvium portulacastrum*.



Note a Decaying twig of host. b Colonies on natural substrate. c Exciple. d Section of an ascoma. e, f Paraphyses. g, h Asci. i–k Ascospores. l Germinated ascospore. m, n Colony on PDA (front and below). Scale bars: b = 250 μm , c = 40 μm , d = 100 μm , e = 50 μm , f, g, h = 20 μm , i–k = 20 μm .

Figure 5.42 *Patellaria microspora* (MFLU 26-0041, new host record)

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

Chaetothyriomycetidae Doweld

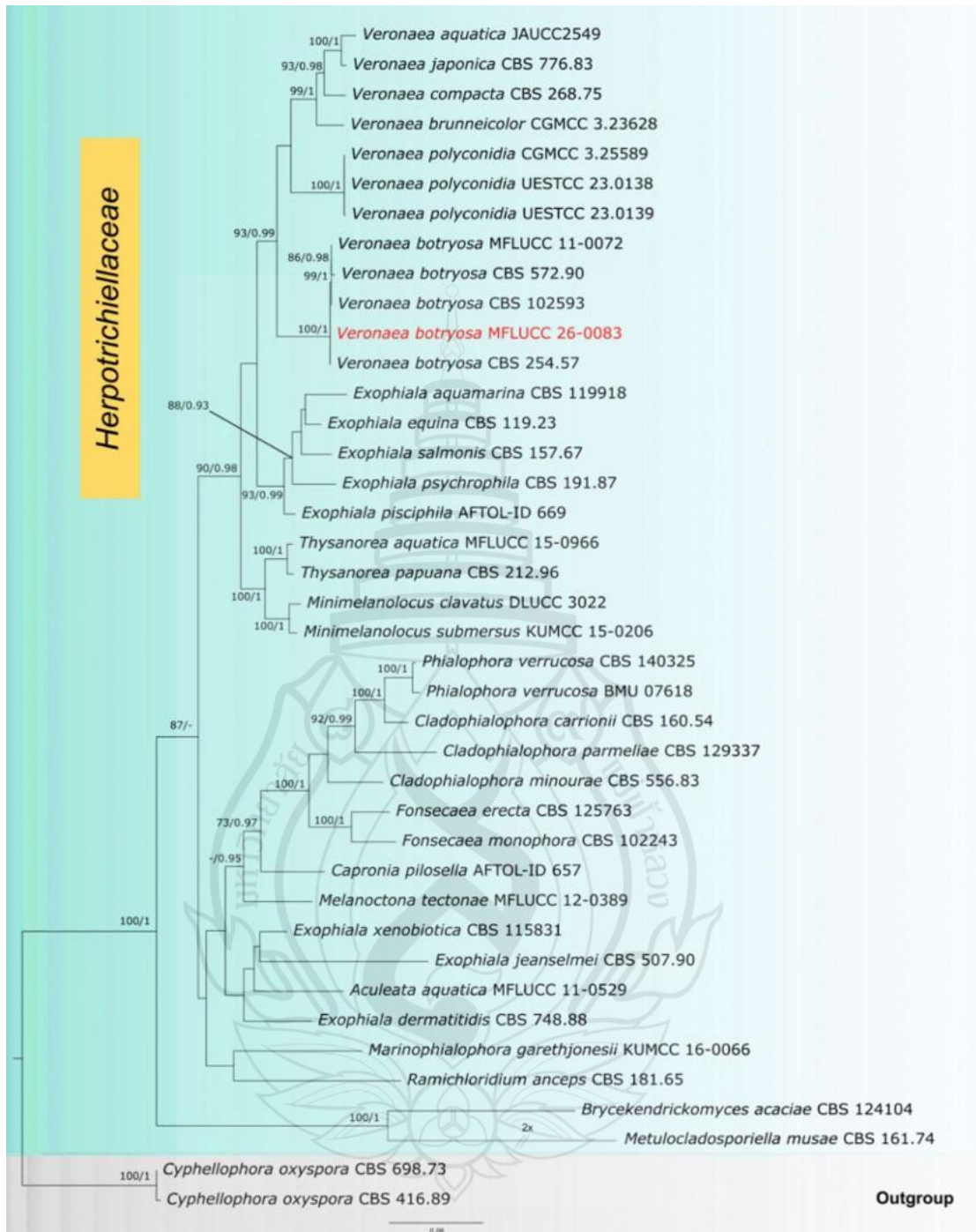
Chaetothyriales M.E. Barr

Herpotrichiellaceae Munk

Herpotrichiellaceae was introduced by Munk (1953) and is typified by *Herpotrichia moravica*. The type species was later synonymized with *Capronia moravica* based on the connection between the sexual and asexual morphs (Müller et al. 1987). The sexual morph of *Herpotrichiellaceae* is characterized by setose, ostiolate ascomata, bitunicate asci with a long endotunica, and didymosporous, phragmosporous, or dictyosporous ascospores (Müller et al. 1987; Tian et al. 2021). The asexual morph comprises dematiaceous hyphomycetes, commonly referred to as black yeasts (Müller et al. 1987; Tian et al. 2021). Species of *Herpotrichiellaceae* have been recorded from a wide range of substrates, including lichens, plants, rocks, soil, insects, and extreme environments such as high or low temperatures (Feng et al. 2014; Das et al. 2019; Libert et al. 2019; Lima et al. 2020; Sun et al. 2020; Thitla et al. 2023; Senwanna et al. 2025). Several species of *Herpotrichiellaceae* have also been reported from marine habitats (Jones et al. 2019). Here we provide a phylogenetic tree of family.

Veronaea Cif. & Montemart.

Veronaea was introduced by Ciferri and Montemartini (1957) and is typified by *V. botryosa*. The genus is known based on its hyphomycetous asexual morph, characterized by erect, brown conidiophores. The conidiogenous cells are polyblastic and sympodial, formed terminally or intercalarily, and produce cylindrical to pyriform, pale brown conidia (Arzanlou et al. 2007; Rambelli 2011; Su et al. 2023). The genus comprises approximately 20 species, mostly collected as saprobes from terrestrial and aquatic habitats (Arzanlou et al. 2007; Yang et al. 2023b; Hyde et al. 2024; Bao et al. 2025). Further collections and molecular sequence data are needed for accurate species delimitation and classification within this genus.



Note The tree is rooted to *Cyphellophora oxyspora* (CBS 698.73 and CBS 416.89) and *N. thailandicum* (MFLUCC 16.0221). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.43 Phylogram generated from the ML analysis based on the combined SSU, ITS, LSU and *tub2* sequence alignments of *Herpotrichiellaceae*

Veronaea botryosa Cif. & Montemart. Fig. 5.44

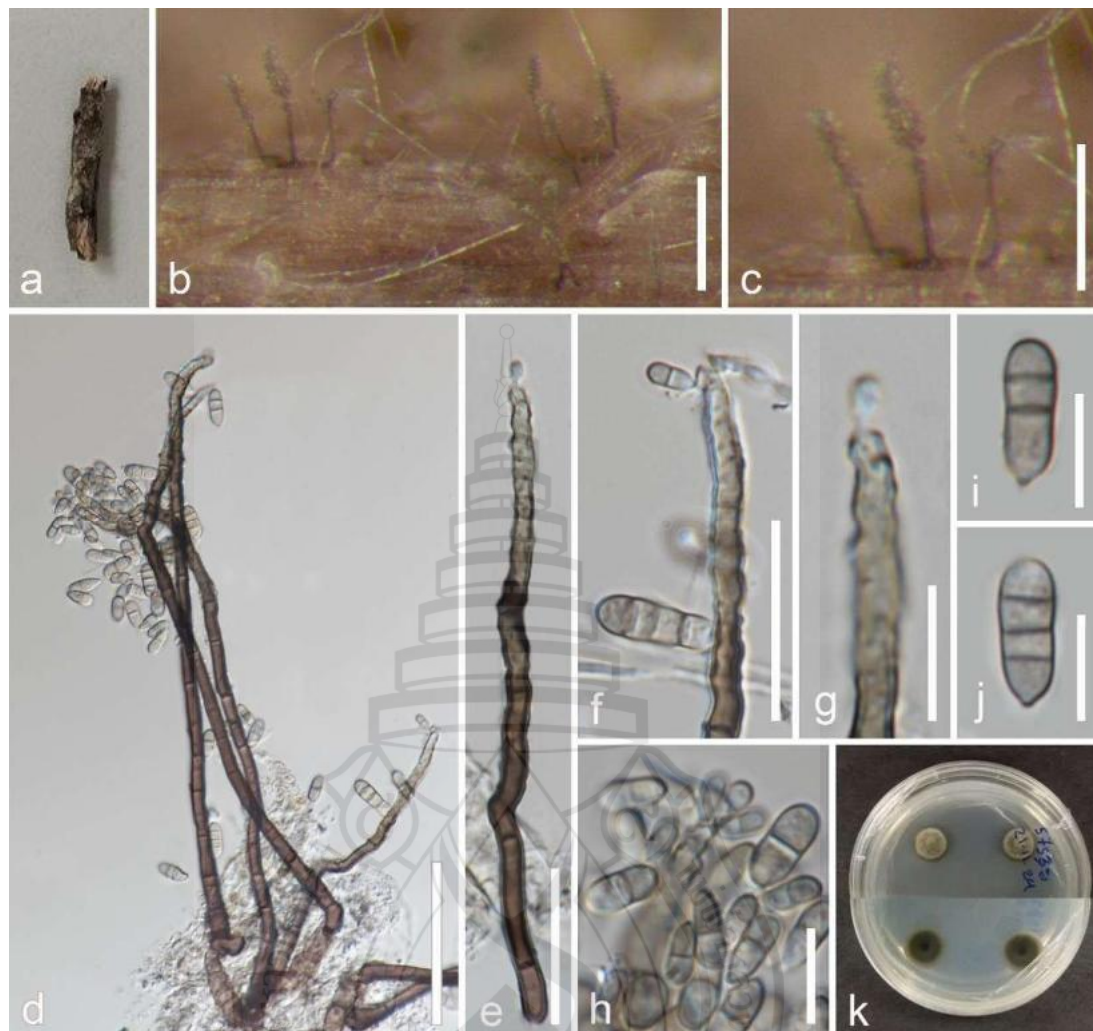
Index Fungorum number: IF307734; Facesoffungi number: FoF10445

Saprobic on dead stem of *Suaeda maritima*. **Asexual morph:** Colonies on natural substrate, effuse, in small groups, brown. *Mycelium* immersed, consisting of septate, brown hyphae. *Conidiophores* $100\text{--}185 \times 3.5\text{--}4.5 \mu\text{m}$ ($\bar{x} = 100 \times 3.7 \mu\text{m}$, $n = 20$), macronematous, mononematous, solitary, or in small groups, erect, straight or flexuous, dark brown, paler toward the apex, septate, thick-walled, unbranched. *Conidiogenous cells* $11\text{--}49 \times 2\text{--}3.5 \mu\text{m}$ ($\bar{x} = 30 \times 3 \mu\text{m}$, $n = 15$), polyblastic, cylindrical, sympodial, integrated, terminal, intercalary, pale brown, rachis with denticles. *Conidia* $5.5\text{--}9.5 \times 2\text{--}3.5 \mu\text{m}$ ($\bar{x} = 7.5 \times 3 \mu\text{m}$, $n = 30$), cylindrical, clavate to obovoid, round apex, with an obconical basal cell, with a darkened hilum, 0–3-aseptate, constricted at septa, subhyaline or pale brown, thick-walled. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 1 cm diam. after two weeks at $25\pm 2^\circ\text{C}$, convex, velvety, entire margin; from surface, olive gray, olive at the margin; from reverse, olive.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Forest Park (water salinity 15 ppt), on dead submerged stems of *Suaeda maritima*, 8 November 2024, R. Asghari S7S35 (MFLU 26-0079); living culture (MFLUCC 26-0083).

Notes – In the phylogenetic analyses, MFLUCC 26-0083 clustered with strains of *Veronaea botryose* with strong support. Our collection shares similar morphology with *V. botryose* by its erect, straight or flexuose conidiophores, terminal, intercalary, cylindrical pale brown conidiogenous cells and truncate base, pale brown septate conidia with hilum (Ellis 1971; Arzanlou et al. 2007; Dong et al. 2018; Yang et al. 2023b). Our collection is herein reported as a new host and habitat record of *V. botryose* from submerged *Suaeda maritima*, in salt marsh habitat in Thailand.



Note a Decaying twig of the host. b, c Appearance of colony on host. d, e Conidiophores. f, g Conidiogenous cells. h–j Conidia. k Culture on PDA (above and below). Scale bars: b, c = 100 µm, d–g = 50 µm, i–h = 20 µm, k, l = 5 µm.

Figure 5.44 *Veronaea botryose* (MFLU 26-0079, new host and habitat record)

Sordariomycetes O.E. Erikss. & Winka

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

Diaporthales Nannf

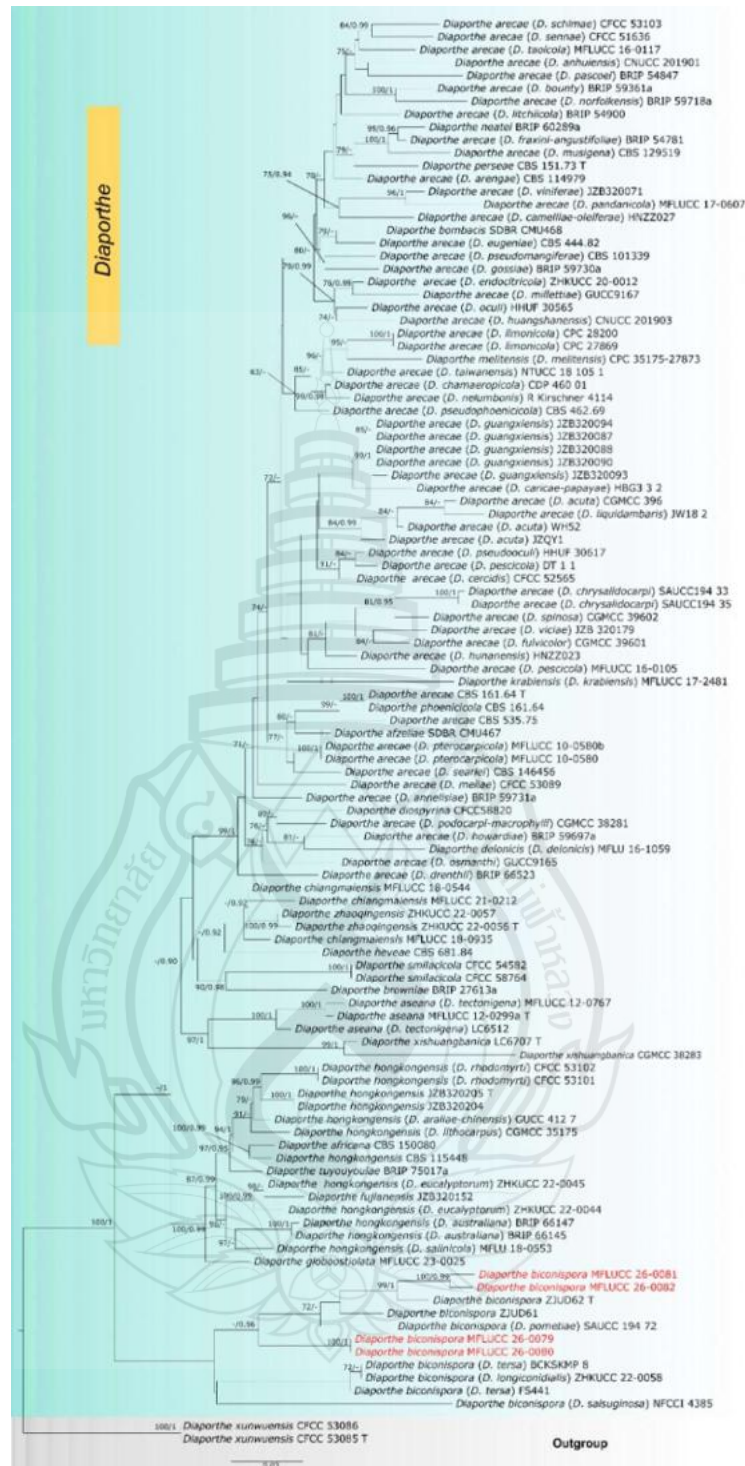
Diaporthaceae Höhn. ex Wehm.

Diaporthaceae was introduced by Höhnelt (1917) and is placed in the order *Diaporthales*. *Diaporthaceae* comprises 18 genera, which are mainly plant-associated saprobes, endophytes, or pathogens (Lamprecht et al. 2011; Hyde et al. 2020d, 2024). The sexual morph is characterized by ostiolate, papillate ascomata, unbranched, septate

paraphyses, and 8-spored asci with an apical ring. Ascospores are ellipsoid, oblong to fusiform, guttulate, and with or without appendages (Hyde et al. 2020d). The asexual morph is coelomycetous, producing acervular or pycnidial conidiomata with dimorphic alpha and beta conidia formed from phialidic alpha and beta conidiogenous cells. Alpha conidia are fusiform to ovate, subcylindrical to narrowly ellipsoid, guttulate, and 0–2-septate, and beta conidia are subcylindrical, fusiform to hooked, and aseptate (Hyde et al. 2020d).

Diaporthe Nitschke

Diaporthe was introduced by Nitschke (1867) and is typified by *Diaporthe eres*. The genus comprises approximately 300 species that occur as saprobes, endophytes, or pathogens (Hyde et al. 2024; Phukhamsakda et al. 2025). *Diaporthe* species represent an economically important group, causing diseases such as cankers, fruit rot, stem rot, dieback, leaf spots, and blights on agriculturally important crops and forest trees (Dissanayake et al. 2017; Bhunjun et al. 2024; Armand et al. 2025b; Fallahi et al. 2025). *Diaporthe salsuginosa* (currently treated as *D. biconispora*) has been listed as a marine fungus (Jones et al. 2019), and Aumentado et al. (2025) investigated the diversity of pathogenic *Diaporthe* species associated with mangrove hosts in Thailand. The asexual morph of *Diaporthe* was referred to as *Phomopsis*; however, under the “one fungus, one name” principle, *Diaporthe* has nomenclatural priority over *Phomopsis* (Rossman et al. 2015). Earlier classifications relied mainly on morphology and host association, but molecular phylogenetic studies have demonstrated that *Diaporthe* species are not strictly host-specific, and accurate identification requires DNA sequence data ((Dissanayake et al. 2017; Aumentado et al. 2025). In this study, we present a phylogenetic tree for *Diaporthe*, including four strains isolated from terrestrial coastal plants in Thailand.



Note The tree is rooted to *Diaporthe xunwuensis* (CFCC 53085 and CFCC 53086). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.45 Phylogram generated from the ML analysis based on the combined ITS, *tef1* and *tub2* sequence alignments of *Diaporthe*

Diaporthe biconispora F. Huang, K.D. Hyde & Hong Y. Li. Fig. 5.46

Index Fungorum number: IF810578; Facesoffungi number: FoF08406

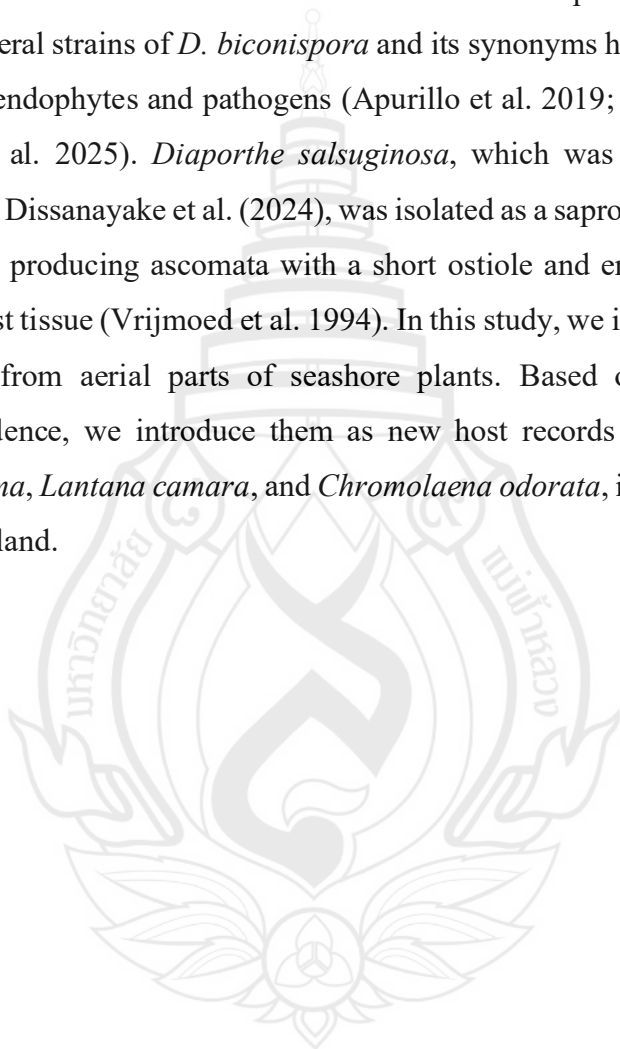
Saprobic on decaying twig of *Chromolaena odorata*, *Lantana camara* and *Suaeda maritima*. **Asexual morph:** *Conidiomata* 150–400 µm diam. ($\bar{x}$ = 280 µm, n = 20), pycnidial, immersed, aggregate subglobose, obpyriform, to obtuse, brown, to black, with a central neck, with or without aerial mycelia, enclosed within a wide blackened zone on the host surface or not. *Peridium* 8–33 µm ($\bar{x}$ = 17 µm, n = 30), greenish brown, brown to dark brown, *textura angularis*, outer cells fused with the host cells. *Conidiophores* (6)10–28 × 1–2 µm ($\bar{x}$ = 15 × 1.5 µm, n = 30), cylindrical to subcylindrical, straight or slightly curved, tapering toward the apex, unbranched, rarely branched, hyaline. *Alpha conidia* 6.5–10 × 1.8–3.5 µm ($\bar{x}$ = 8 × 2.5 µm, n = 50), ellipsoidal to fusoid, aseptate, multiguttulate, hyaline. *Beta conidia* 11.5–21.5 × 1–2 µm ($\bar{x}$ = 16.5 × 1.5 µm, n = 30), filiform, straight to curved, tapering toward the apex, aseptate, guttulate, hyaline. **Sexual morph:** Undetermined.

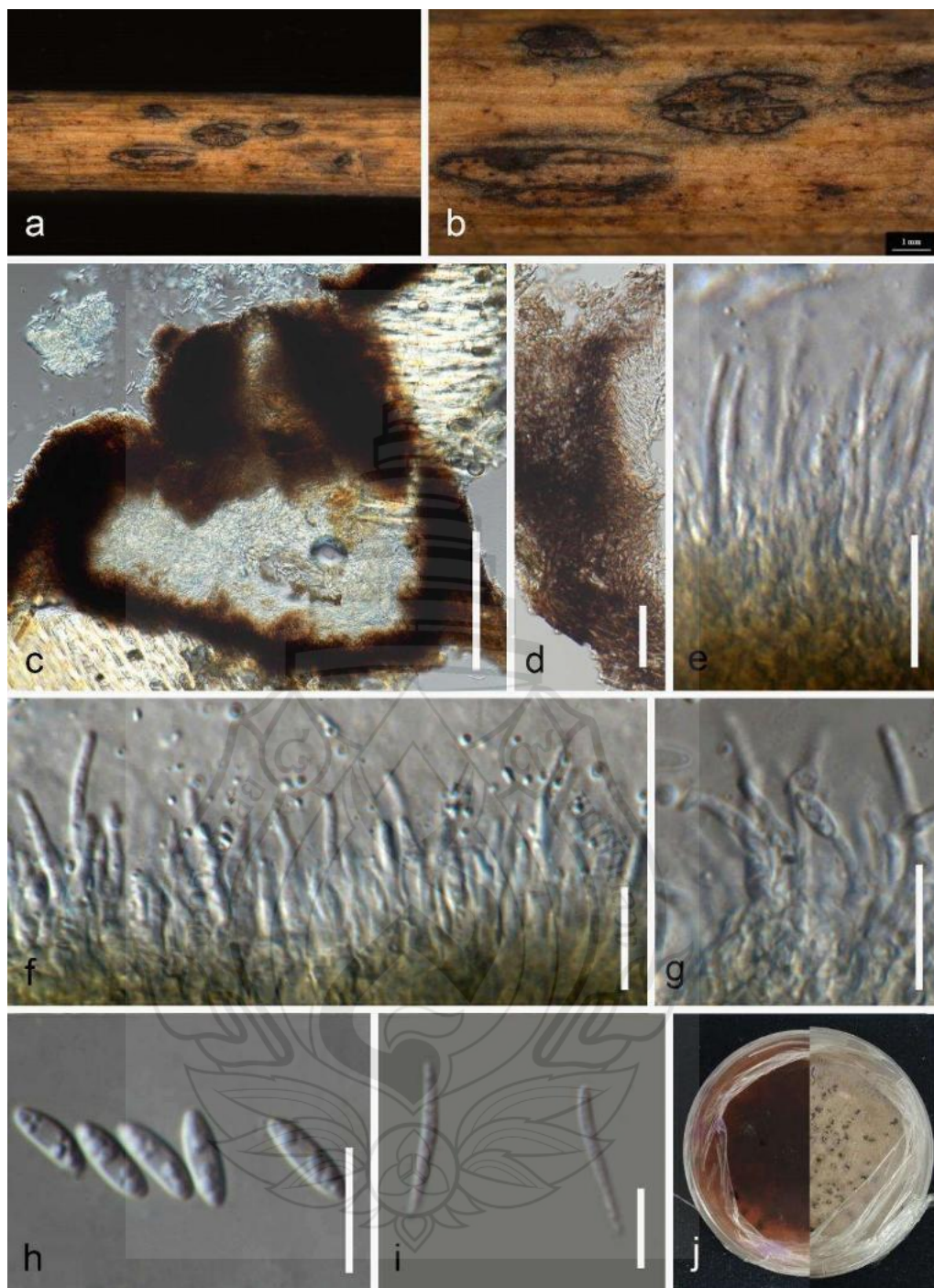
Culture characteristics – Colonies (BM21 and LC72) on PDA reaching 5 cm diam. after one week at 25±2°C, flat, with sparse aerial mycelia, entire margin, pycnidia scattered; from surface, light gray; from reverse, dark brown, or reddish brown. Colonies (S6D101 and S6D102) on PDA reaching 4.5 cm diam. after one week at 25±2°C, flat, with sparse aerial mycelia, concentric circles, entire margin or undulate, pycnidia scattered; from surface, orange white; from reverse, dark pale orange, or reddish brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on an attached dead dry twig of *Chromolaena odorata*, 23 May 2023, R. Asghari, BM21 (MFLU 26-0075); living culture (MFLUCC 26-0079); *ibid.*, Sam Roi Yot, on attached dead dry stems of *Lantana camara*, 23 May 2023, R. Asghari, LC72 (MFLU 26-0076); living culture (MFLUCC 26-0080); *ibid.*, Pranburi Forest Park, on dead aerial stems of *Suaeda maritima*, 6 April 2024, R. Asghari, S6D101 (MFLU 26-0077); living culture (MFLUCC 26-0081); *ibid.*, S6D102 (MFLU 26-0078); living culture (MFLUCC 26-0082).

Notes – Based on the multi-gene phylogenetic analyses from ITS, *tef1*, *tub2*, CAL, and HIS sequence data, our strains (MFLUCC 26-0079, MFLUCC 26-0080, MFLUCC 26-0081, and MFLUCC 26-0082) grouped with *Diaporthe biconispora*

strains. Two strains of MFLU 26-0075 and MFLU 26-0076, produced both alpha and beta conidia, while MFLU 26-0077 and MFLU 26-0078 produced only beta conidia. Our collections are similar to the ex-type strain of *D. biconispora* (ZJUD62) in morphology of conidiophores and conidia (Huang et al. 2015). However, there are differences in having obpyriform to obtuse conidiomata with a short neck, which could be due to the fact that our strains were described as saprobes from their natural substrates. Several strains of *D. biconispora* and its synonyms have been reported from mangroves as endophytes and pathogens (Apurillo et al. 2019; Chethana et al. 2021b; Aumentado et al. 2025). *Diaporthe salsuginosa*, which was synonymized with *D. biconispora* by Dissanayake et al. (2024), was isolated as a saprobe with a sexual morph on mangroves, producing ascomata with a short ostiole and enclosed in a blackened zone on the host tissue (Vrijmoed et al. 1994). In this study, we isolated four collections of *Diaporthe* from aerial parts of seashore plants. Based on morphological and molecular evidence, we introduce them as new host records of *D. biconispora* on *Suaeda maritima*, *Lantana camara*, and *Chromolaena odorata*, in Prachuap Khiri Khan Province, Thailand.





Note a, b Appearance of colony on the host. c Section through conidioma. d Section through peridium. e–g Conidiophores. h Alpha conidia. i Beta conidia. j Culture on PDA (above and below). Scale bars: b = 1 mm, c = 100 μ m, d = 20 μ m, e–i = 10 μ m.

Figure 5.46 *Diaporthe biconispora* (MFLU 26-0075, new host record)

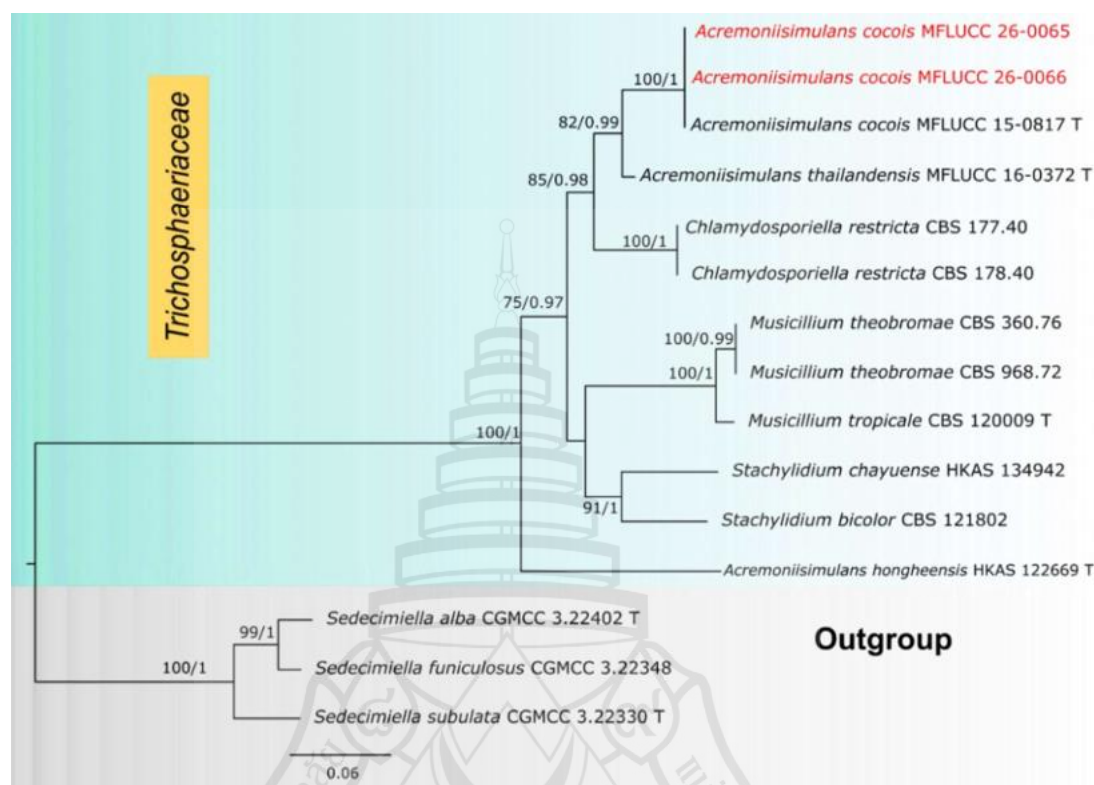
*Diaporthomycetidae families incertae sedis**Trichosphaeriaceae* G. Winter*Acremoniisimulans* Tibpromma & K.D. Hyde

Members of *Trichosphaeriaceae* are saprobic or pathogenic on plants and are commonly isolated from herbivore dung in terrestrial habitats, with some species occurring in aquatic environments (Jones et al. 2019; Hyde et al. 2020d; Maharachchikumbura et al. 2016). The sexual morph is characterized by ostiolate, globose to pyriform ascomata, with or without setae, 4–8-spored asci, and ellipsoidal to fusiform or ovoid, hyaline or brown ascospores. The asexual morph is either coelomycetous or hyphomycetous (Maharachchikumbura et al. 2016, Hyde et al. 2020d). *Trichosphaeriaceae* was introduced with *Trichosphaeria* as the type genus and has undergone extensive taxonomic revision (Winter 1884). Molecular phylogenetic studies have indicated an unstable familial placement, and the family is currently treated as *incertae sedis* within *Diaporthomycetidae* due to limited molecular data for the type species; *Trichosphaeria pilosa* (Hongsanant et al. 2017; Wijayawardene et al. 2018; Hyde et al. 2024).

Acremoniisimulans Tibpromma & K.D. Hyde

Acremoniisimulans was introduced by Tibpromma et al. (2018) to accommodate its type species, *A. thailandensis*, isolated from *Pandanus* sp. in Prachuap Khiri Khan Province, Thailand. *Acremoniisimulans thailandensis* was described based on its hyphomycetous asexual morph, characterized by unbranched, 3–4-septate, brown conidiophores; monophialidic, subhyaline conidiogenous cells; and solitary, oval, unicellular, pale brown to brown conidia. Subsequently, *Acremoniisimulans cocois* and *A. hongheensis* were introduced based on their sexual morphs, which are characterized by oval to globose or irregular ascomata, 4–8-spored asci, and oblong to broadly oblong or ellipsoidal, aseptate, hyaline ascospores (Konta et al. 2023; Yang et al. 2023a). *Acremoniisimulans cocois* was isolated from coconut in Prachuap Khiri Khan Province, Thailand and *A. hongheensis* was isolated from mango in Yunnan Province, China. In this study, we report a new host and habitat record of *Acremoniisimulans cocois* collected from submerged *Suaeda maritima* in a marine habitat. This collection

represents the first record of the genus in marine habitats and the first report of the asexual morph of *A. cocois*, supported by phylogenetic analyses.



Note Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.47 Phylogram generated from the ML analysis based on the combined ITS, LSU, *rpb2* and *tef1* sequence alignments of *Trichosphaeriaceae*

Acremoniisimulans cocois S. Konta & K.D. Hyde, Fig. 5.48

Index Fungorum number: IF559681

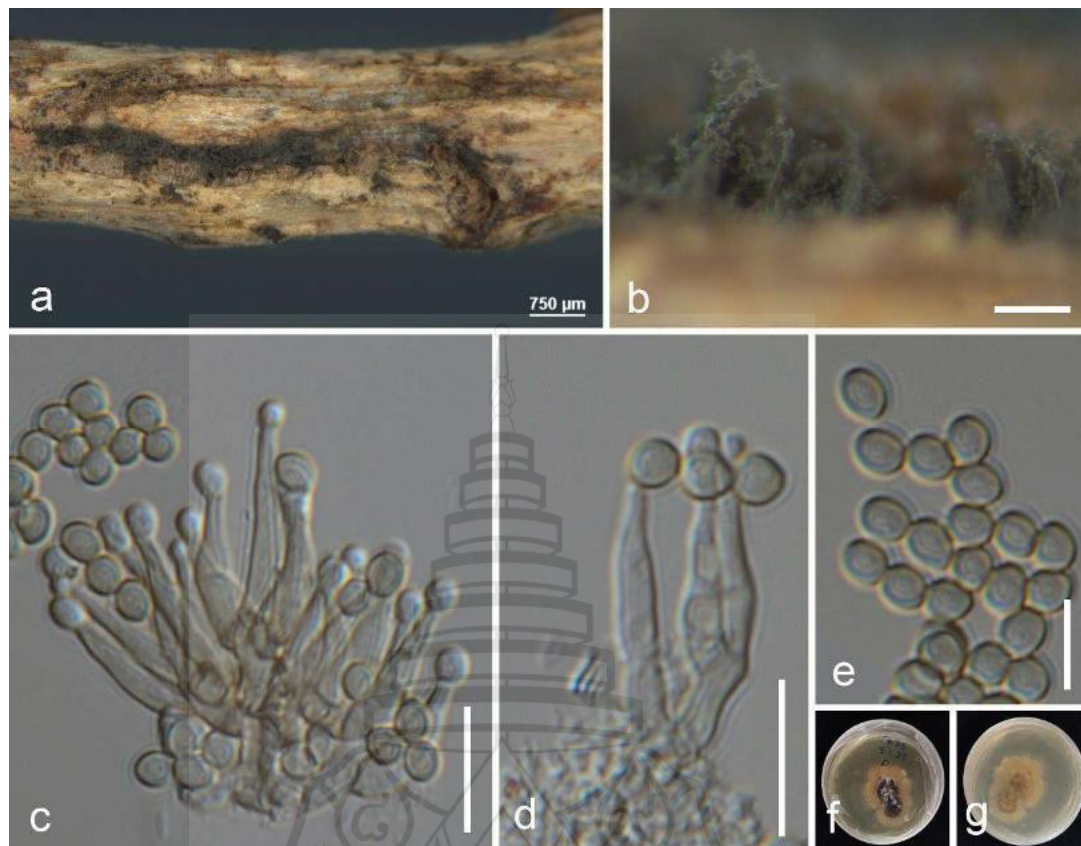
Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** Colonies on natural substrate fluffy, aerial, greenish. *Hyphae* 1.2–2.2 μm wide ($\bar{x}$ = 1.7, n = 20), superficial, branched, septate, subhyaline to pale brown, finely rough-walled. *Conidiophores* 18–36 $\times$ 2.5–3 μm ($\bar{x}$ = 25 $\times$ 2.8 μm , n = 20), aggregated, straight bent, branched, septate, or reduced to single phialides. *Conidiogenous cells* 6–15 $\times$ 1–3 μm ($\bar{x}$ = 9.5 $\times$ 2 μm , n = 20), phialidic, cylindrical, tapering toward the apex, terminal, pale brown. *Conidia* 2–3.5 μm diam., ($\bar{x}$ = 2.8 μm , n = 40), globose or subglobose, aseptate,

pale brown, solitary or catenated, flattened at the attaching points. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 3.5 cm diam. after one month at 25±2°C, flat or umbonate, dense, undulate; from surface, dark brown, gray at the center, pale orange at the periphery; from reverse, grayish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot National Park (water salinity 28 ppt), on dead submerged stems of *Suaeda maritima*, 1 December 2023, R. Asghari, SB35 (MFLU 26-0056); living culture (MFLUCC 26-0065); *ibid.*, SB42 (MFLU 26-0057); living culture (MFLUCC 26-0066).

Notes – In multi-gene phylogenetic analyses, our strains (MFLUCC 26-0065 and 26-0066) clustered together with *Acremoniisimulans cocois* (MFLUCC 15-0817). Morphologically, our collections are not directly comparable with *A. cocois*, as it was described based on its sexual morph (Konta et al. 2023). The holotype was collected from dead petioles of *Cocos nucifera* in Prachuap Khiri Khan Province, Thailand (Konta et al. 2023). ITS sequence comparisons revealed differences between our strains and *A. cocois*, with 1.3% (8/588 bp, including gaps) in MFLUCC 26-0065 and 1.2% (7/585 bp, including gaps) in MFLUCC 26-0066, while LSU sequences were identical (with one gap). Based on molecular data, our collections are introduced here as new host records of *A. cocois* from *Suaeda maritima* in Prachuap Khiri Khan Province, Thailand, representing the first report of the asexual morph of this species and the first record of the genus from marine habitats.



Note a, b Colony on the host surface. c, d Conidiogenous cells and conidia. e Conidia. f, g Colony on PDA (above and below). Scale bars: a = 750 µm, b = 750 µm, c, d = 10 µm, e = 5 µm.

Figure 5.48 *Acremoniisimulans cocois* (MFLU 26-0056, new host record)

Hypocreomycetidae O.E. Erikss. & Winka

Hypocreales Lindau

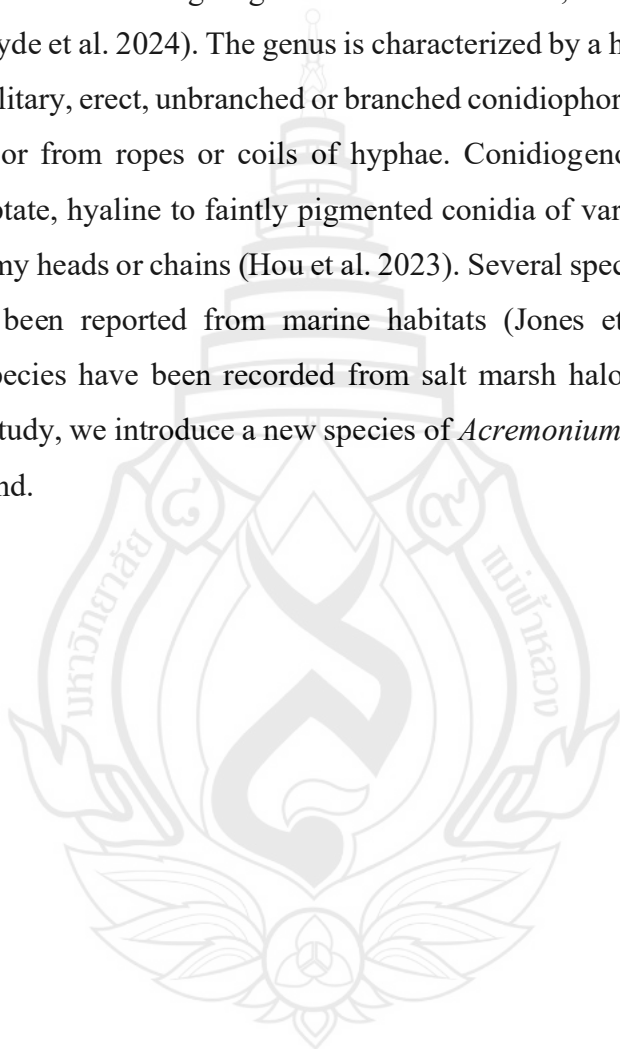
Bionectriaceae Samuels & Rossman

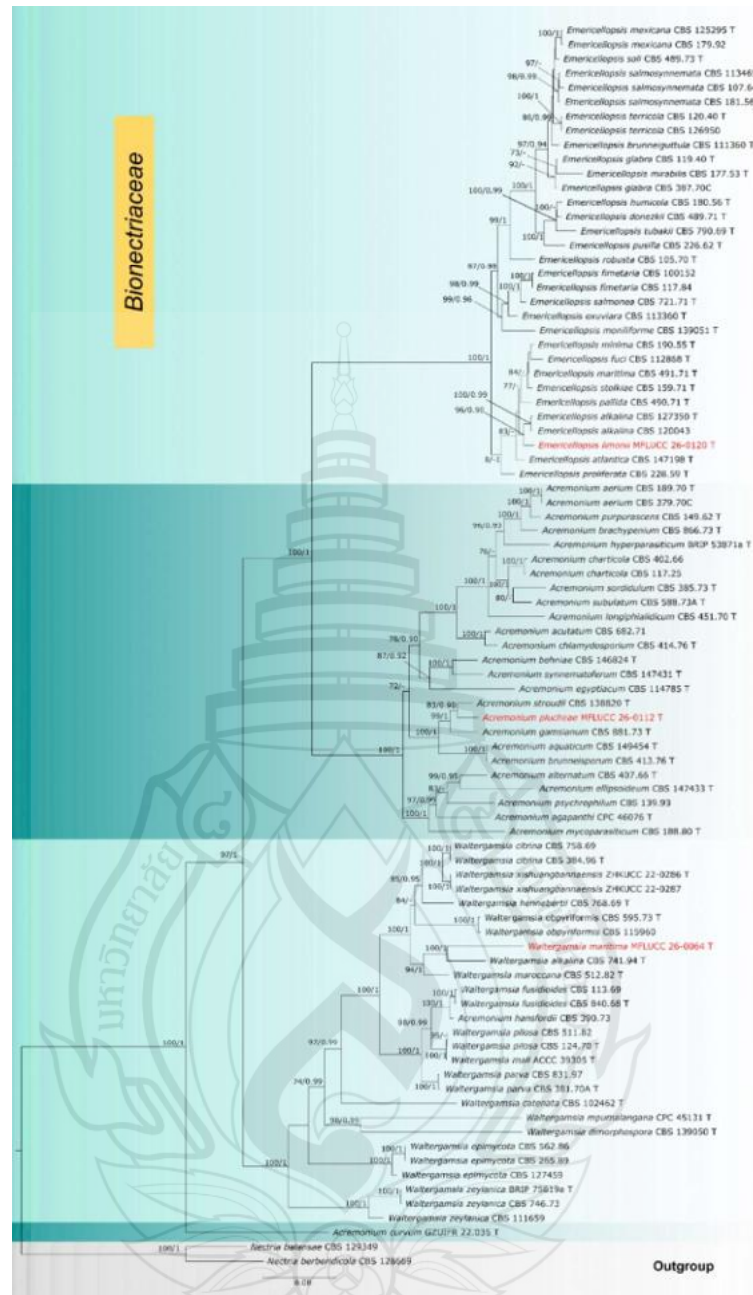
Bionectriaceae was established to accommodate 26 genera (Rossman et al. 1999), and subsequent molecular phylogenetic studies confirmed its monophyly within *Hypocreales* (Rossman et al. 2001). Later studies expanded the number of genera in *Bionectriaceae* (Maharachchikumbura et al. 2015; Wijayawardene et al. 2018), and the family currently includes 58 accepted genera (Hyde et al. 2024). *Bionectriaceae* is a diverse family, occurring mostly in terrestrial and freshwater habitats (Hyde et al. 2020d). Several species in genera such as *Acremonium* and *Clonostachys* are economically significant, reported as plant pathogens or as biological control agents

against fungal pathogens and environmental stresses (Sutton and Mason 2017; Mirtalebi et al. 2017; Bobeck and Pearce 2017). A phylogenetic tree of the family is provided.

Acremonium Link

Acremonium is the largest genus in *Bionectriaceae*, comprising approximately 100 species (Hyde et al. 2024). The genus is characterized by a hyphomycetous asexual morph, with solitary, erect, unbranched or branched conidiophores arising directly from the mycelium or from ropes or coils of hyphae. Conidiogenous cells are phialidic, producing aseptate, hyaline to faintly pigmented conidia of various shapes, which are arranged in slimy heads or chains (Hou et al. 2023). Several species of *Acremonium* (16 species) have been reported from marine habitats (Jones et al. 2019), and three undescribed species have been recorded from salt marsh halophytes (Calabon et al. 2021). In this study, we introduce a new species of *Acremonium* isolated from a coastal plant in Thailand.





Note The tree is rooted to *Nectria balansae* (CBS 129349) and *N. berberidicola* (CBS 128669). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.49 Phylogram generated from the ML analysis based on the combined combined ITS, LSU, *rpb2* and *tef1* sequence alignments of *Bionectriaceae*

Acremonium plucheae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.50

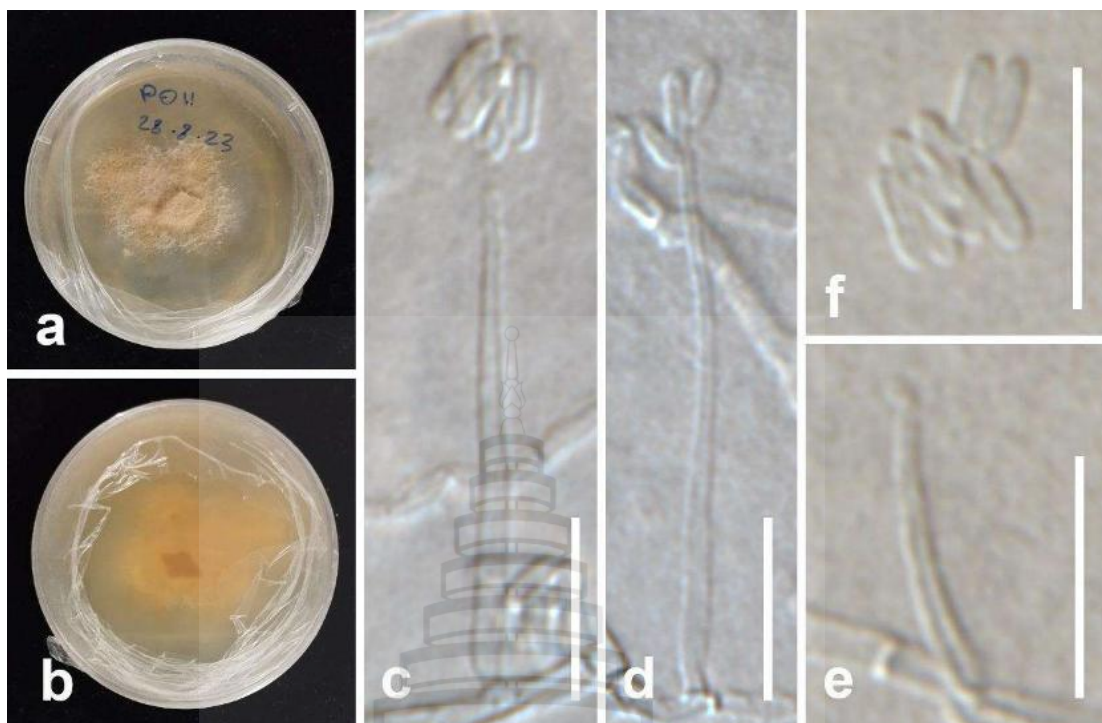
Etymology: Referring to the isolation of the fungus from *Pluchea indica*.

Saprobic on dead twig of *Pluchea indica*. **Asexual morph:** *Hyphae* 1–1.5(2) μm wide ($\bar{x}$ = 1.2, n = 20), branched, septate, hyaline, smooth-walled. *Conidiophores* solitary, straight, unbranched, reduced to a single phialide. *Conidiogenous cells* 12–31 $\times$ 1–1.5 μm ($\bar{x}$ = 22.5 $\times$ 1.2 μm , n = 20), cylindrical, tapering toward the apex, polyphialidic, terminal, hyaline, with an inconspicuous collarette. *Conidia* 3–5.2 $\times$ 1–1.5 μm ($\bar{x}$ = 4 $\times$ 1.2 μm , n = 30), oblong, round apex, slightly narrower at the base, aseptate, hyaline, smooth-walled, solitary or catenated. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 3 cm diam. after two weeks at 25 $\pm$ 2°C, initially convex, fluffy, entire margin, white from the surface, becoming pale orange; from the surface and reverse.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on dead dry attached stems of *Pluchea indica*, 23 May 2023, R. Asghari, PO11 (MFLU 26-0055, holotype); ex-type culture (MFLUCC 26-0112).

Notes – *Acremonium plucheae* forms a sister clade to *A. stroudii* (CBS 138.820, holotype), supported by 83% ML and 0.90 BPP values. Morphologically, *A. plucheae* resembles *A. stroudii* in having hyaline hyphae and conidia. However, in the protologue of *A. stroudii*, the morphology of the conidiogenous cells was not described, and the conidia are reported as spherical to oblong, up to 3 μm , which differs from *A. plucheae*, which has distinct phialides and larger oblong conidia (3–5.2 μm in length) (Hou et al. 2023). Ecologically, *A. stroudii* was isolated from an environmental sample taken from a seawater blowhole, whereas *A. plucheae* was isolated from a dry coastal plant in Thailand (Fletcher et al. 2017; Hou et al. 2023). *Acremonium plucheae* (MFLUCC 26-0112) showed 4.5% (23/514 bp) and 4.2% (32/755 bp) sequence divergence from *A. stroudii* (CBS 138.820) in the ITS and *rpb2* regions, respectively (including gaps). The combined morphological and molecular evidence supports the introduction of *A. plucheae* as a new species from *Pluchea indica* in Thailand.



Note a, b Colony on PDA (above and below). c–e Conidiophores, conidiogenous cells and conidia. f Conidia. Scale bars: 10 μ m.

Figure 5.50 *Acremonium plucheae* (MFLUCC 26-0112, ex-type)

Waltergamsia L.W. Hou, L. Cai & Crous

Waltergamsia was introduced by Hou et al. (2023) and typified with *Waltergamsia fusidioides*. The genus was first established to accommodate eight acremonium-like species and now comprises 17 species (Hou et al. 2023; Index Fungorum, November 2025). The genus produces hyphomycetous asexual morph with conidia arranged in slimy heads or in chains. In this study, a new species is described, based on a collection from a dead twig of *Suaeda maritima* in a marine habitat in Thailand.

Waltergamsia maritima R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.51

Etymology – Referring to the isolation of the fungus from *Suaeda maritima*.

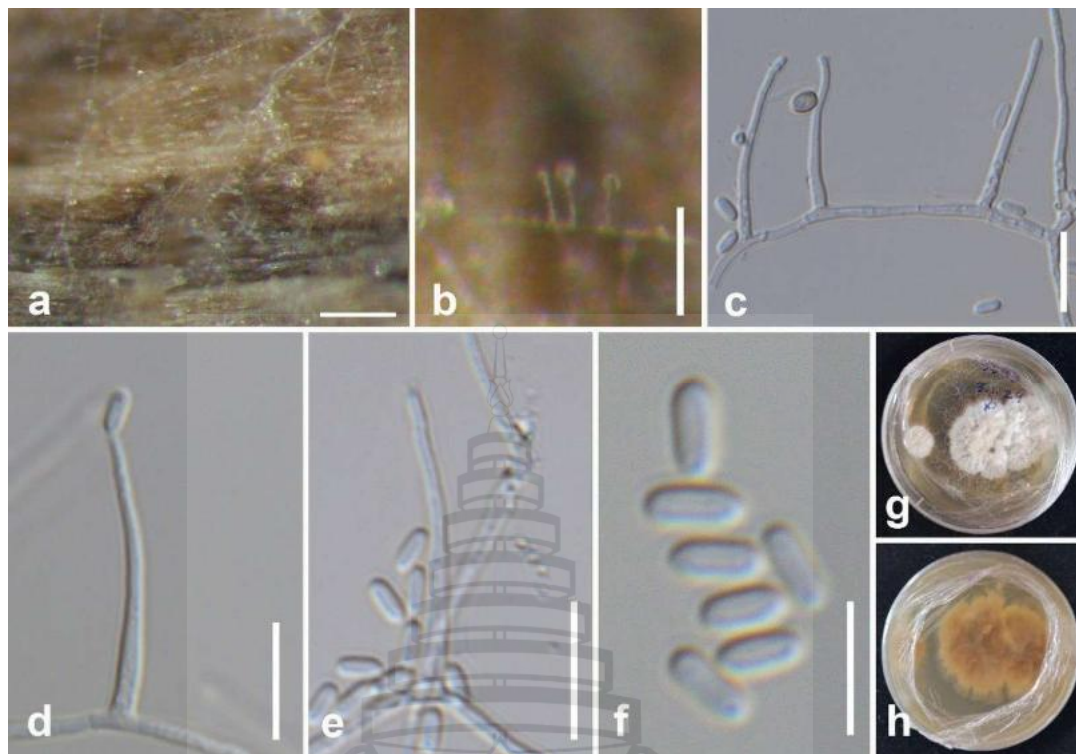
Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** *Hyphae* 0.9–1.5 μ m wide ($\bar{x}$ = 1.3, n = 20), superficial, branched, septate, hyaline, rough-walled.

Conidiophores 23–37(61) $\times$ 1.5–2.5 μm at the base ($\bar{x}$ = 29 $\times$ 2 μm , n = 20), solitary, straight or flexuous, unbranched, thick-walled, aseptate or 1-septate at the base, or reduced to conidiogenous cells. *Conidiogenous cells* 11–29 $\times$ 1.5–2.5 μm ($\bar{x}$ = 25 $\times$ 2 μm , n = 20), phialidic, terminal, hyaline, thick-walled, with periclinal thickening and cylindrical collarette. *Conidia* 3.5–5.5 $\times$ 1.2–1.7 μm ($\bar{x}$ = 4.5 $\times$ 1.4 μm , n = 30), cylindrical, round apex, aseptate, hyaline, arranged in slimy heads. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 3 cm diam. after one month at 25 $\pm$ 2°C, flat, low convex, undulate, medium dense, slightly radiating, woolly; from surface, white or bluish white; from reverse, light orange and brownish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot National Park (water salinity 28 ppt), on dead submerged stems of *Suaeda maritima*, 1 December 2023, R. Asghari, Sb43 (MFLU 26-0054, holotype); ex-type culture (MFLUCC 26-0064).

Notes – Phylogenetic analyses placed *Waltergamsia maritima* sister to *W. alkalina* (CBS 741.94, ex-type) with strong support (100% ML/1.00 BPP). The morphology of *W. maritima* is similar to *W. alkalina* in its phialidic conidiogenous cells with periclinal thickening and cylindrical collarettes, and cylindrical conidia in slimy heads; however, it differs in having narrower, rough-walled hyphae, predominantly aseptate conidiophores, and lacking sterile hyphal coils and percurrent proliferation (Hou et al. 2023). The holotype of *W. alkalina* was collected from alkaline soil in Indonesia and our strain was collected from submerged halophytic plant in a salt marsh habitat (Hou et al. 2023). *Waltergamsia maritima* (MFLUCC 26-0064) showed base pair differences of 7.5% (33/434 bp, with gaps) and 5.7% (43/755 bp, without gaps) from *A. stroudii* (CBS 138820) in ITS and *rpb2* regions, respectively. Combined morphological and molecular data support the introduction of *W. maritima* as a new species from *Suaeda maritima* in a marine habitat in Thailand.



Note a, b Appearance of colony on host tissue. c–e Conidiophores, conidiogenous cells and conidia. f Conidia. g, h Colony on PDA (above and below). Scale bars: a = 100 μ m, b = 50 μ m, c–e = 10 μ m, f = 5 μ m.

Figure 5.51 *Waltergamsia maritima* (MFLU 26-0054, holotype)

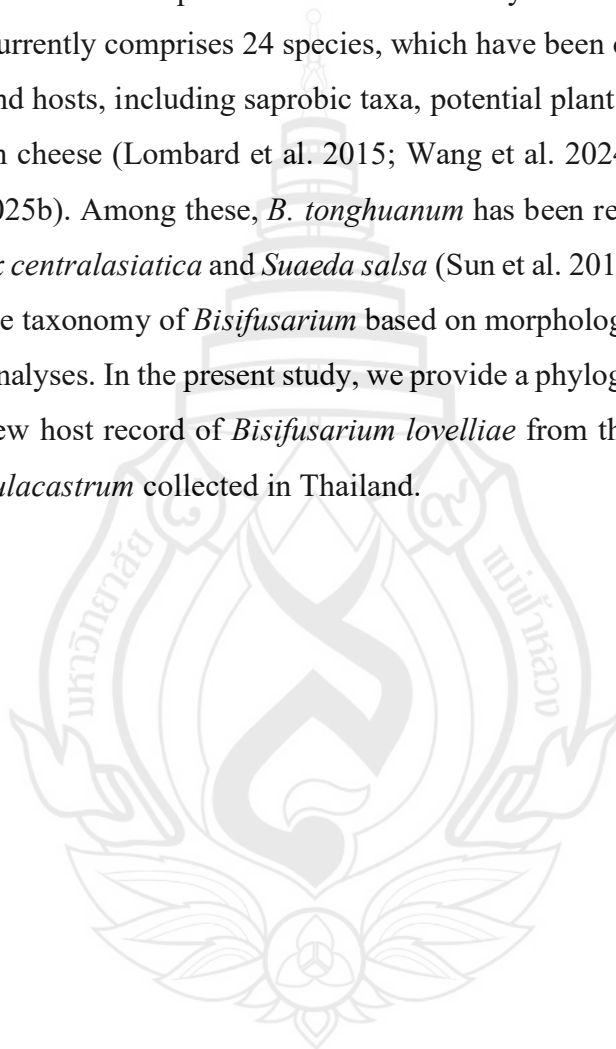
Nectriaceae Tul. & C. Tul.

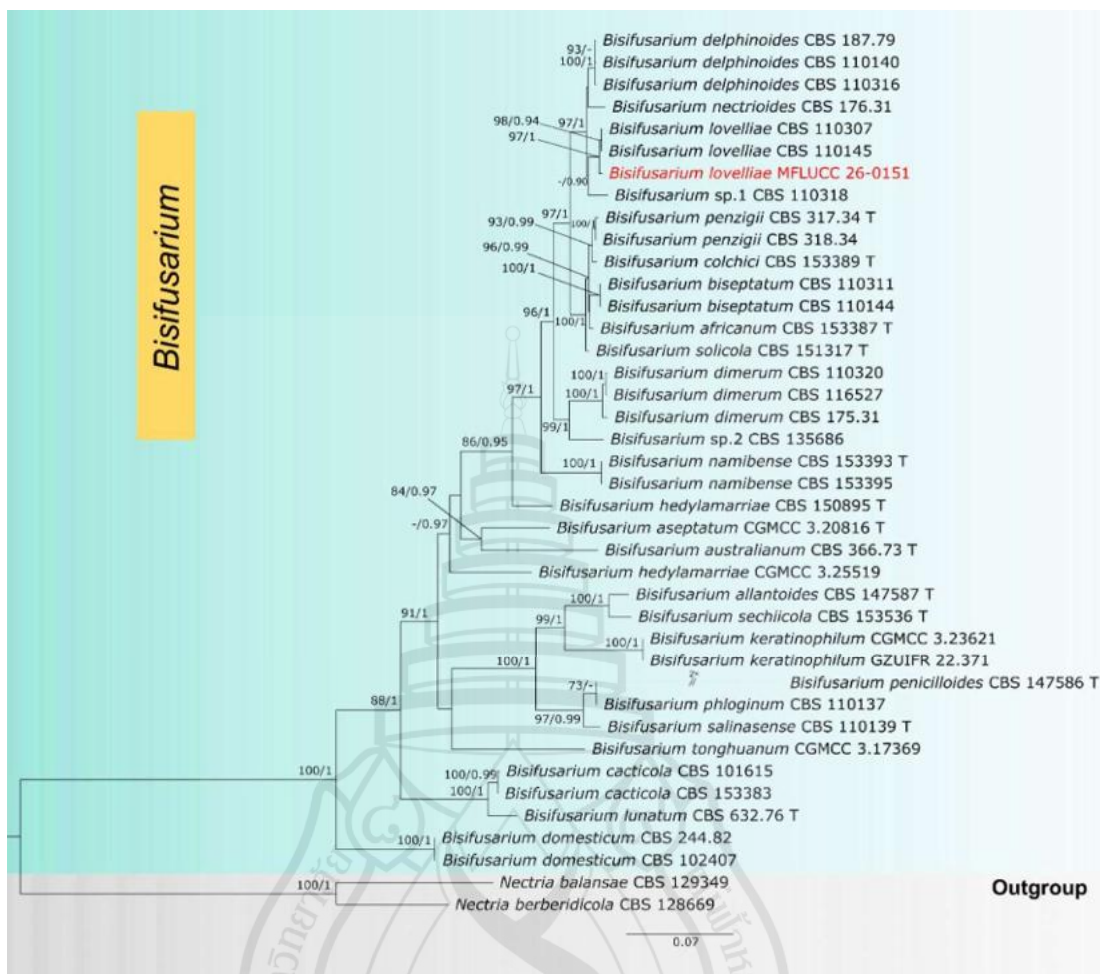
Nectriaceae comprises approximately 80 genera and is distributed worldwide, including endophytic, foliicolous, saprobic, entomogenous, and pathogenic taxa occurring in both terrestrial and aquatic habitats (Lombard et al. 2015; Hyde et al. 2020d; Perera et al. 2023). The sexual morph is characterized by stromatic or astromatic, perithecial ascomata that are solitary or aggregated and globose to pyriform in shape. Ascomata exhibit a wide range of colours, including white, red, orange, yellow, brown, and bluish to black, and are KOH positive or negative. Asci are unitunicate, 4–8-spored, and clavate to cylindrical. Ascospores are hyaline to pigmented, variable in shape, aseptate to muriform, and smooth- to ornamented-walled. The asexual morph is predominantly hyphomycetous, with fewer taxa forming coelomycetous morphs (Lombard et al. 2015; Maharachchikumbura et al. 2016).

Several species of *Nectriaceae*, particularly *Fusarium* spp., have been reported from marine habitats and salt-marsh hosts (Jones et al. 2019; Calabon et al. 2021).

Bisifusarium L. Lombard, Crous & W. Gams

The genus *Bisifusarium* was introduced by Lombard et al. (2015) to accommodate fusarioid species characterized by 1–2-septate macroconidia. *Bisifusarium* currently comprises 24 species, which have been collected from a variety of substrates and hosts, including saprobic taxa, potential plant pathogens, and species associated with cheese (Lombard et al. 2015; Wang et al. 2024a; Visagie et al. 2024; Zhang et al. 2025b). Among these, *B. tonghuanum* has been reported from halophytic plants, *Atriplex centralasiatica* and *Suaeda salsa* (Sun et al. 2017). Zhang et al. (2025b) re-evaluated the taxonomy of *Bisifusarium* based on morphological characteristics and phylogenetic analyses. In the present study, we provide a phylogenetic tree of the genus and report a new host record of *Bisifusarium lovelliae* from the salt-marsh halophyte *Sesuvium portulacastrum* collected in Thailand.





Note The tree is rooted to *Nectria balansae* (CBS 129349) and *N. berberidicola* (CBS 128669). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.52 Phylogram generated from the ML analysis based on the combined combined ITS, *tef1*, *rpb2* and *TUB* sequence alignments of *Bisifusarium*

Bisifusarium lovelliae Y.P. Tan, Bishop-Hurley & R.G. Shivas, Fig. 5.53

Index Fungorum number: IF900359

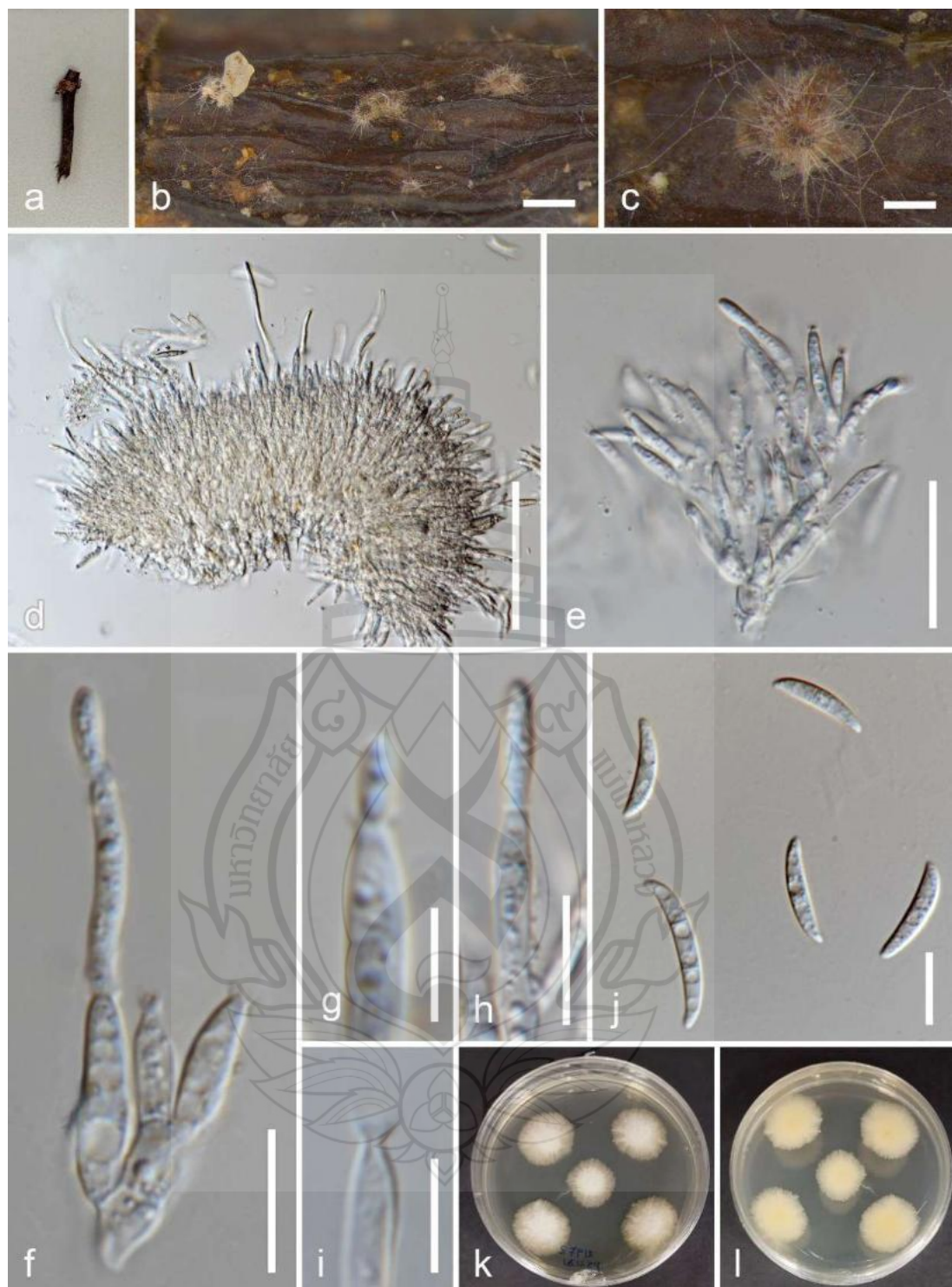
Saprobic on dead twig of *Sesuvium portulacastrum*. **Asexual morph:** *Conidiomata* sporodochial, solitary or in small group, superficial, convex, with aerial mycelia, pale orangish brown. *Conidiophores* densely packed, straight or flexuous, branched, septate, with terminal and lateral phialides. *Phialides* $8.5\text{--}12.5 \times 1.5\text{--}3 \mu\text{m}$ ($\bar{x} = 9 \times 2.2 \mu\text{m}$, $n = 20$), cylindrical, subulate to subcylindrical, tapering toward the

apex, terminal and lateral, monophialidic or polyphialidic, with a wide collarete, elongation above the collate, hyaline, subhyaline or pale yellow. *Conidia* $13\text{--}21.5 \times 2.5\text{--}3.8 \mu\text{m}$ ($\bar{x} = 17.5 \times 3.2 \mu\text{m}$, $n = 30$), fusiform, slightly curved to lunate, with tapering ends, the proximal end slightly more pointed than distal end, 0–2-septate, pale brown, solitary or catenated, flattened at the attaching points. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diam. after one week at $25 \pm 2^\circ\text{C}$, raised, hairy, medium sparse, circular, fimbriate; from surface, white or yellowish white; from reverse, yellowish white.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pran Kiri Beach, on dead dry stems of *Sesuvium portulacastrum* on seashore rocks, 8 November 2024, R. Asghari, S7P13 (MFLU 26-0058); living culture (MFLUCC 26-0151).

Notes – Our collection (MFLUCC 26-0151) clustered with *Bisifusarium lovelliae* (CBS 110145 and CBS 110307) with 90% ML/1.00 BPP support. *Bisifusarium lovelliae* was originally isolated from leaf spots of *Epipremnum pinnatum* (*Araceae*) in Australia and was introduced based on molecular data without a morphological description (Tan et al. 2023). A detailed morphological description was later provided by Zhang et al. (2025b) based on the ex-type strain (CBS 150777). Our collection showed minor base pair differences from *B. lovelliae* (CBS 110307), with 0.3% (2/533 bp, including gaps) in ITS and 0.1% (1/754 bp, without gaps) in *rpb2*. Morphologically, our collection is similar to the ex-type in having curved macroconidia; however, it differs in possessing a wide collarete on phialides (Zhang et al. 2025b). Based on morphological and molecular evidence, we report our collection as a new host record of *B. lovelliae* from *Sesuvium portulacastrum* in Thailand. Notably, *B. lovelliae* has also been reported from banana groves and associated soils in Thailand (Zhang et al. 2025b).



Note a Decaying twig of the host. b, c Colony on the host surface. d Sporodochium. e, f Conidiogenous cells and conidia. g–i Conidiogenous cells. j Conidia. k, l Colonies on PDA (above and below). Scale bars: b = 250 μm , c = 100 μm , d = 50 μm , e = 25 μm , f, h, j = 20 μm , g, i = 5 μm .

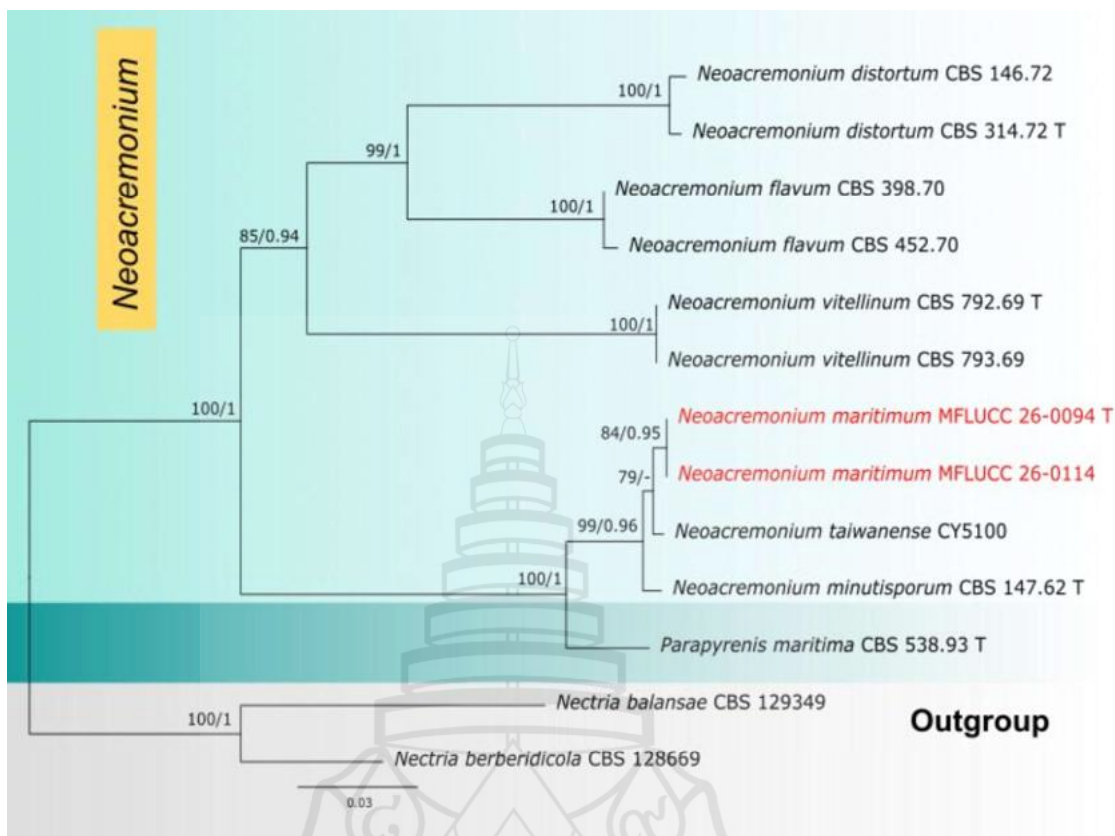
Figure 5.53 *Bisifusarium lovelliae* (MFLU 26-0058, new host record)

Neoacremoniaceae L.W. Hou, L. Cai & Crous

Neoacremoniaceae was introduced by Hou et al. (2023) to accommodate the single genus *Neoacremonium*. The family forms a well-supported clade within *Hypocreales* based on phylogenetic analyses of LSU, ITS, and *rpb2* sequence data. *Neoacremoniaceae* mostly is characterized by a hyphomycetous asexual morph, with one species described based on the sexual (Hou et al. 2023).

Neoacremonium L.W. Hou, L. Cai & Crous

Neoacremonium is the type genus of *Neoacremoniaceae* and currently comprises five species (Hou et al. 2023). The asexual morph is hyphomycetous, with unbranched or branched conidiophores arising directly from hyphae or ropes of mycelium. Conidiogenous cells are monophialidic or polyphialidic, developing terminally or laterally, with periclinal thickening and a cylindrical collarette, and producing unicellular, hyaline conidia arranged in slimy heads or chains. *Neoacremonium distortum*, *Ne. flavum*, *Ne. minutisporum*, and *Ne. vitellinum* are known from hyphomycetous asexual morphs (Hou et al. 2023). *Neoacremonium taiwanense* is the only species described based on a sexual morph, characterized by globose to subglobose, orange to dark brown ascomata with a periphysate neck. Asci are cylindrical, 16-spored, without an apical pore, and ascospores are globose, aseptate, and hyaline (Pang et al. 2010; Hou et al. 2023). In this study, we introduce a new species, *Neoacremonium maritimum*, which grouped with marine-associated taxa, including *Ne. taiwanense*, *Ne. minutisporum*, and *Parapyrenis maritima*. *Neoacremonium maritimum* was collected from submerged, decaying wood in seawater. *Neoacremonium taiwanense* was originally described as *Sedecimiella taiwanensis* by Pang et al. (2010) and was subsequently transferred to *Neoacremonium* by Hou et al. (2023) based on its close phylogenetic affinity with *Ne. minutisporum*. This species was collected from mangrove wood (Pang et al. 2010; Suetrong et al. 2017). *Neoacremonium minutisporum* was initially isolated from highly saline coastal salt-marsh soil (Sukapure and Thirumalachar 1963) and was later reported from mangrove sediments in China (Li et al. 2023). *Parapyrenis maritima* was collected from wood in a coastal forest on a coral island and from seashore sand (Aptroot 1995).



Note The tree is rooted to *Nectria balansae* (CBS 129349) and *N. berberidicola* (CBS 128669). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.54 Phylogram generated from the ML analysis based on the combined combined ITS, LSU, *rpb2* and *tef1* sequence alignments of *Neoacremonium*

Neoacremonium maritimum R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.55

Etymology – Referring to the isolation of the fungus from marine habitats.

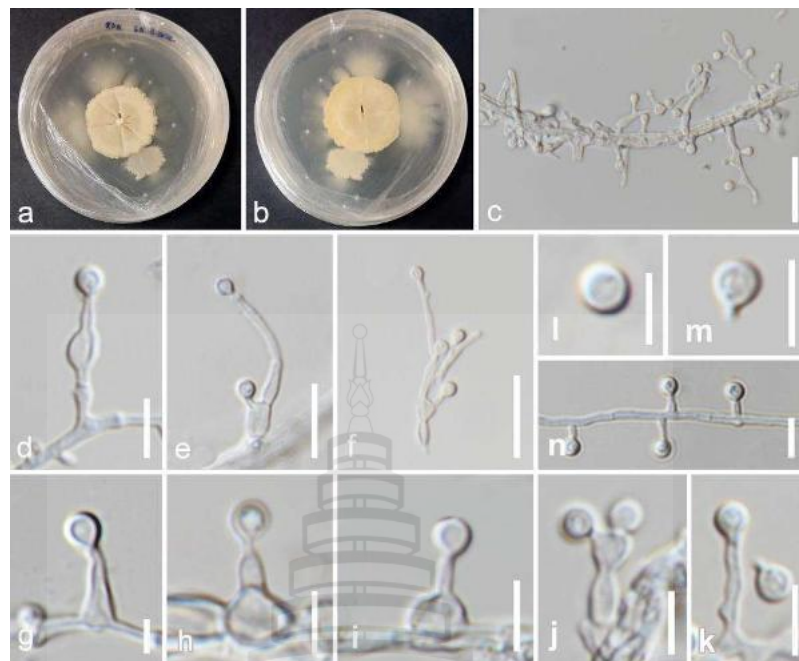
Saprobic on decaying wood, submerged in seawater. **Asexual morph:** *Hyphae* branched, septate, hyaline, thick walled. *Conidiophores* 20–35 × 1–3 μm ($\bar{x}$ = 26 × 1.5 μm, n = 20), solitary, straight or flexuous, subcylindrical, narrower toward the apex, unbranched or branched, 1-2-septate, hyaline, thick-walled, with terminal and lateral phialides, or reduced to phialidic conidiogenous cells. *Phialides* 2.5–20 × 1–4.5 μm ($\bar{x}$

= $7.5 \times 2.6 \mu\text{m}$, $n = 20$), subcylindrical or lageniform or subulate, tapering toward the apex, terminal and lateral, monophialidic or polyphialidic, with up to two conidiogenous loci, with a minute collarette, hyaline, smooth-walled. *Conidia* $1.8\text{--}2.5 \mu\text{m}$ diam. ($\bar{x} = 2 \mu\text{m}$, $n = 30$), globose, subglobose, aseptate, hyaline, smooth-walled, solitary, slimy heads not observed. *Chlamydospores* solitary, laterally on short stalks, globose to subglobose, hyaline. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2.5 cm diam. after one month at $25 \pm 2^\circ\text{C}$, flat, low convex, medium dense, slightly radiating, crenated, undulate, becoming punctiform or irregular at the periphery; from surface, yellowish white; from reverse, yellowish white or pale yellow.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on submerged decaying wood in seawater (water salinity 19 ppt), 25 October 2022, KD Hyde, R3A (MFLU 26-0059, holotype); ex-type culture (MFLUCC 26-0094); *ibid.*, R3Ab (MFLU 26-0060, isotype); ex-isotype culture (MFLUCC 26-0114).

Note – In our phylogenetic analyses from four loci, strains of *Neoacremonium maritimum* formed a sister clade to *Ne. taiwanense* (CY5100, ex-isotype), and were closely related to *Ne. minutisporum*. Morphologically, our collections are described based on their asexual morphs and are not comparable with *Ne. taiwanense* (Pang et al. 2010). *Neoacremonium maritimum* is similar to *Ne. minutisporum* in having unbranched or branched, 1-2-septate, hyaline conidiophores, subcylindrical or lageniform, hyaline, smooth-walled, terminal and lateral phialides, with a minute collarette, but differs in shorter and wider phialides ($2.5\text{--}20 \times 1\text{--}4.5$ vs. $9.3\text{--}35.5 \times 1\text{--}3 \mu\text{m}$), solitary globose conidia unlike short cylindrical, ovoid conidia arranged in slimy head in *Ne. minutisporum* (Hou et al. 2023). Sequence comparison of the ITS region showed that *Ne. maritimum* (MFLUCC 26-0094) differs from *Ne. minutisporum* (CBS 147.62) by 2.5% (14/486 bp, including gaps). ITS data are unavailable for *Ne. taiwanense* (CY5100) for direct comparison. *Neoacremonium maritimum* is introduced here as a new species from submerged decaying wood in seawater from Thailand. Further collections and sequence data are needed to clarify sexual and asexual relationships within *Neoacremonium*.

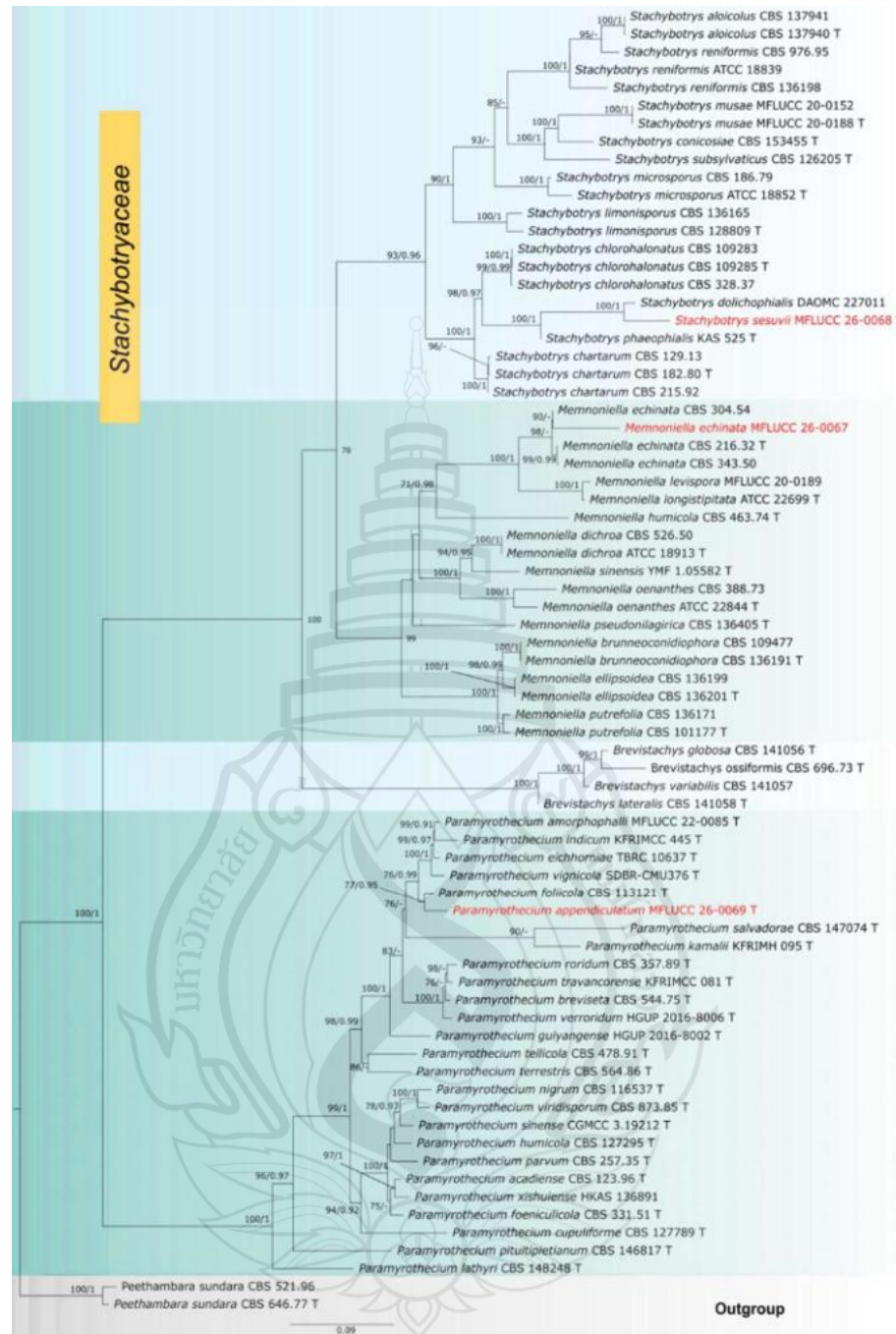


Note a Colony on PDA (above and reverse). c–f Colony on the host surface. g–k Phialides and conidia. l, m Conidia. n Chlamydospores. Scale bars: c, f = 20 μ m, d, e = 10 μ m, g–n = 5 μ m.

Figure 5.55 *Neoacremonium maritimum* (MFLUCC 26-0094, ex-type)

Stachybotryaceae L. Lombard & Crous 2014

Stachybotryaceae was established by Crous et al. (2014) to accommodate three genera, *Stachybotrys*, *Myrothecium*, and *Peethambara*. Phylogenetic studies based on multigene sequence data (LSU, ITS, *rpb2*, *cmdA*, *tef1*, *tub2*) have supported the monophyly of *Stachybotryaceae* (Lombard et al. 2016; Wijayawardene et al. 2018), and currently more than 41 genera are accepted within the family (Hyde et al. 2024). Members of *Stachybotryaceae* are saprobic or pathogenic on plants and are commonly isolated from soil (Hyde et al. 2020d; Samarakoon et al. 2021). Ecologically, several species are important plant pathogens, while a few *Stachybotrys* species produce mycotoxins that can result in economic losses in agriculture and cause building-related illnesses (Page and Trout 2001; Seifert et al. 2011; Zhang et al. 2011; Fujinawa et al. 2016; Hyde et al. 2020d). In this study, we provide a phylogenetic tree of the family and introduce two new saprobic species and one new record from a coastal area in Thailand.



Note The tree is rooted to *Peethambara sundara* (CBS 521.96) and *P. sundara* (CBS 646.77). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.56 Phylogram generated from the ML analysis based on the combined combined ITS, CMDA, *rpb2*, TUB and *tef1* sequence alignments of *Stachybotryaceae*

Memnoniella Höhn.

Memnoniella was initially introduced by Höhnelt (1923) and was later considered congeneric with *Stachybotrys* by Smith (1962) and Wang et al. (2015). However, Lombard et al. (2016) designated an epitype for the type species *M. echinata* and confirmed that *Memnoniella* and *Stachybotrys* are distinct genera based on phylogenetic analyses. This taxonomic concept has been followed by subsequent studies (Hyde et al. 2024d). *Memnoniella* differs from *Stachybotrys* mainly by its smooth, thick-walled conidiophores, which are typically unbranched, and by conidia that are sometimes arranged in dry chains (Lombard et al. 2016). Currently, 26 species are listed in *Memnoniella* (Index Fungorum, accessed January 2026), most of which are reported as saprobic on plants (Sun et al. 2025; Habib et al. 2025; Tian et al. 2024a; Zhang et al. 2025a). In this study, we report *Memnoniella echinata* from marine habitats in Thailand, representing the first report of the genus in marine water.

Memnoniella echinata (Rivolta) Galloway, Fig. 5.57

Index Fungorum number: IF263706

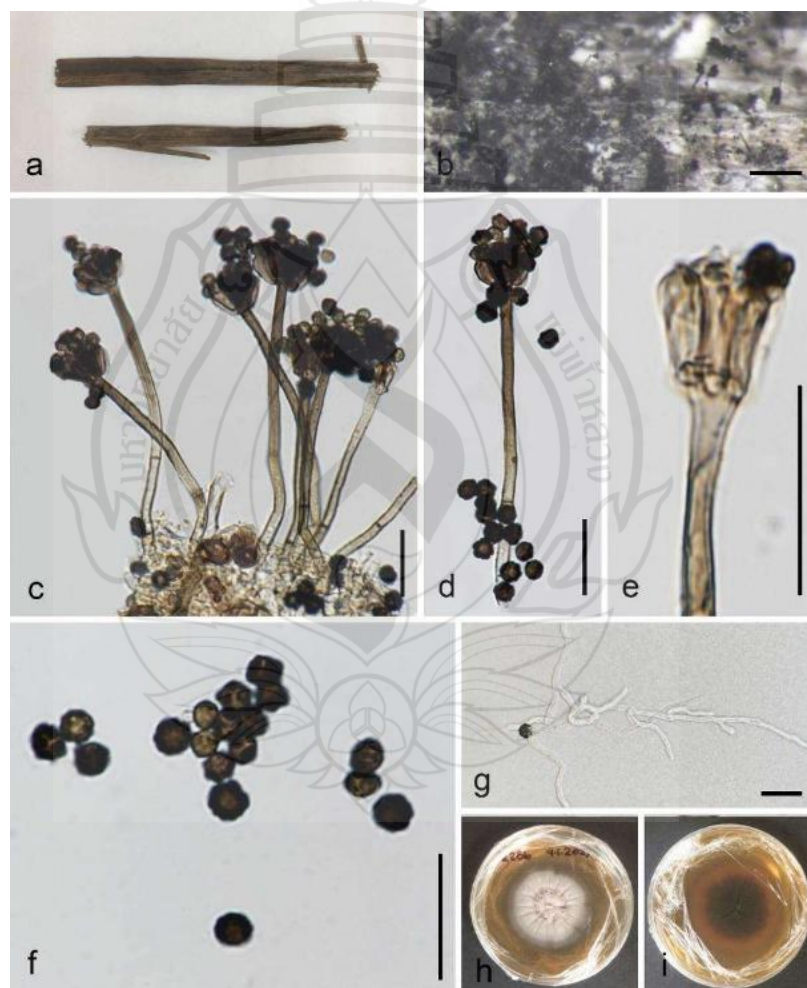
Saprobic on decaying wood submerged in seawater. **Asexual morph:** Colonies on natural substrate flat, aggregated, black. *Conidiophores* 56–101 × 2–4.5 µm ($\bar{x}$ = 80 × 3.3 µm, n = 20), solitary or in group, macronematous, mononematous, straight or slightly curved, unbranched, septate, pale brown to brown, darker toward the apex, smooth-walled to slightly verrucose, with 6–10 conidiogenous cells. *Conidiogenous cells* 9–12.5 × 2.5–4 µm ($\bar{x}$ = 10.5 × 3.5 µm, n = 20), phialidic, subcylindrical to clavate, brown, with conspicuous collarettes. *Conidia* 3.5–6.5 µm diam., ($\bar{x}$ = 5.2 µm, n = 40), arranging in chains, globose, aseptate, brown to dark brown, thick-walled, verrucose. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 4 cm diam. after one month at 25±2°C, flat, low convex, circular, felted, entire margin, radiating; from surface, white, pinkish white at the center; from reverse, dark brown, light brown at the periphery.

Material examined: Thailand, Prachuap Khiri Khan Province, Pranburi, on decaying wood submerged in seawater, trapped between rocks (water salinity 19 ppt),

25 October 2022, KD Hyde, R25b (MFLU 26-0061); living culture (MFLUCC 26-0067).

Notes – Our new collection of *Memnoniella* (MFLUCC 26-0067) clustered with strains of *Memnoniella echinata*. It has consistent morphology with *M. echinata* in having macronematous, mononematous, straight or curved, unbranched, brown, conidiophores with 6–10 conidiogenous cells; phialidic, subcylindrical to clavate conidiogenous cells, with conspicuous collarettes and globose, aseptate, verrucose conidia forming in chains (Lombard et al. 2016). Our collection is reported here as a new habitat record of *M. echinata* from decaying wood submerged in marine water in Prachuap Khiri Khan Province, Thailand.



Note a Decaying twig of the host. b Colony on the host surface. c, d Conidiophores, conidiogenous cells and conidia. e Phialides. f Conidia. g Germinated conidium. h, i Colonies on PDA (above and reverse). Scale bars: b = 100 μ m, c–f = 20 μ m.

Figure 5.57 *Memnoniella echinata* (MFLU 26-0061, new habitat record)

Paramyrothecium L. Lombard & Crous

Paramyrothecium was established by Lombard et al. (2016) based on taxa forming a well-supported clade distinct from *Myrothecium sensu stricto* and is typified by *Paramyrothecium roridum*. The genus is characterized by an asexual morph with sporodochial conidiomata, with or without a white, setose fringe; thin-walled, 1–3-septate setae; hyaline conidiophores; and phialidic or percurrently proliferating conidiogenous cells with collarettes and periclinal thickenings. Conidia are hyaline to pale green, 0–1-septate, and cylindrical to ellipsoidal or obovoid (Lombard et al. 2016). Currently, 24 species are accepted in the genus, most of which are reported as plant pathogens or saprobes associated with plants or soil (Lombard et al. 2016; Armand et al. 2023; Sun et al. 2025). *Paramyrothecium roridum* has also been listed as a marine fungus by Jones et al. (2019), reported as *Myrothecium roridum*. Here, we introduce a new species collected from a terrestrial coastal plant in Thailand.

Paramyrothecium appendiculatum R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.58

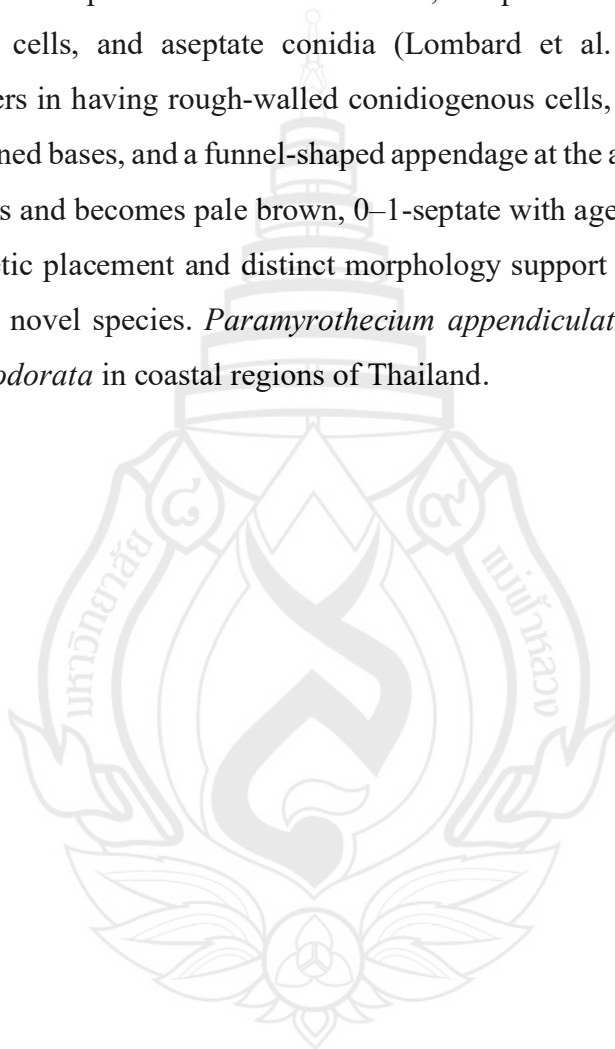
Etymology – Referring to having appendaged conidia in the fungus.

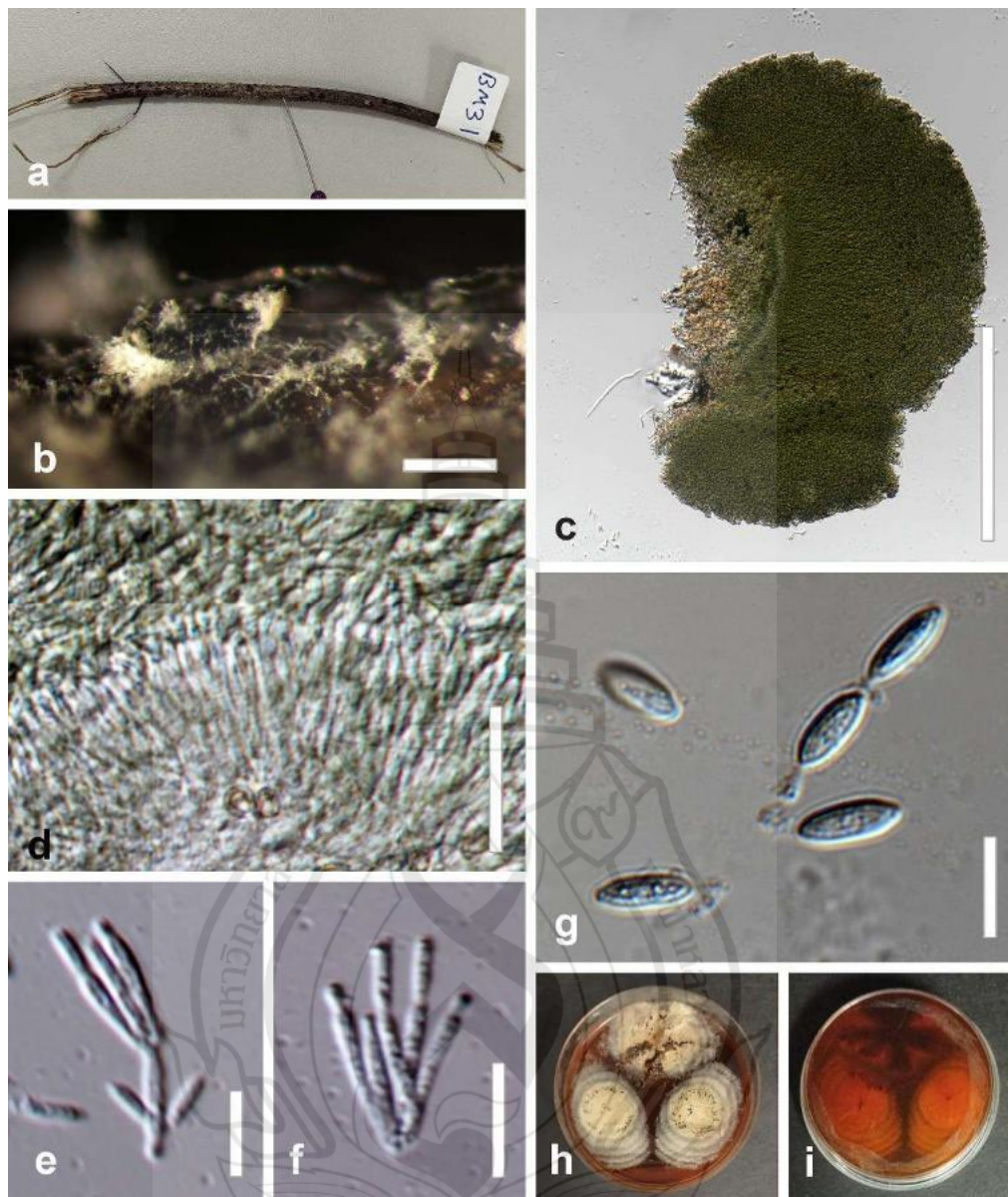
Saprobic on decaying twig of *Chromolaena odorata*. **Asexual morph:** Colonies on natural substrate, superficial, cupulate, black, surrounded with a white setose fringe. *Conidiomata* 250–550 × 250–410 µm ($\bar{x}$ = 400 × 350 µm, n = 10), sporodochial, stromatic, superficial, cupulate, oval. *Stroma* poorly developed, hyaline, to green, *textura angularis*. *Conidiophores* arising from the basal stroma, with unbranched stipe, bearing 3–several conidiogenous cells, aseptate, rough-walled, hyaline, covered by a green mucoid layer. *Conidiogenous cells* 7.5–14.5 × 1.2–2.4 µm ($\bar{x}$ = 10.5 × 1.7 µm, n = 20), phialidic, cylindrical to subcylindrical, hyaline, straight, rough-walled, with collarettes. *Conidia* 7–9.5 × 1.2–3.6 µm ($\bar{x}$ = 8.5 × 2.5 µm, n = 40), cylindrical to ellipsoidal, to fusiform, pointed and thickened at the base, aseptate, hyaline, to pale green, verrucose, with a funnel shape appendage at the apex, catenated in long chains, becoming pale brown 0–1-septate with age. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 3.5 cm diam. after one month at 25±2°C, flat, medium sparse, concentric circles, entire margin; from surface, yellowish white, becoming pale orange; from reverse, pale orange to brownish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on an attached dead dry twig of *Chromolaena odorata*, 23 May 2023, R. Asghari, BM31 (MFLU 26-0063, holotype); ex-type culture (MFLUCC 26-0069).

Notes – Phylogenetically, *Paramyrothecium appendiculatum* (MFLUCC 26-0069) formed a sister lineage to *P. foliicola* (CBS 113121, ex-type). It resembles *P. foliicola* by its sporodochial conidiomata, stiped conidiophores, phialidic conidiogenous cells, and aseptate conidia (Lombard et al. 2016). However, our collection differs in having rough-walled conidiogenous cells, verrucose conidia with pointed, thickened bases, and a funnel-shaped appendage at the apex, which is catenated into long chains and becomes pale brown, 0–1-septate with age (Lombard et al. 2016). The phylogenetic placement and distinct morphology support the introduction of this collection as a novel species. *Paramyrothecium appendiculatum* was collected from *Chromolaena odorata* in coastal regions of Thailand.





Note a Decaying twig of the host. b Colony on the host surface. c Sporodochium. d, e Conidiogenous cells and conidia. f Phialides. g Conidia. h, i Colonies on PDA (above and reverse). Scale bars: b, c = 250 μm , d–g = 10 μm .

Figure 5.58 *Paramyrothecium appendiculatum* (MFLU 26-0063, holotype)

Stachybotrys Corda

Stachybotrys, comprising approximately 100 species, is the largest genus in the family *Stachybotryaceae* (Hyde et al. 2024). Lombard et al. (2016) re-evaluated the family based on multigene phylogenetic analyses and demonstrated that *Stachybotrys* is a polyphyletic genus. Consequently, the genus was segregated into ten distinct

genera, and an epitype was designated for the type species, *Stachybotrys chartarum* (Lombard et al. 2016). The sexual morph of *Stachybotrys* develops stromatic, papillate ascomata with smooth to verrucose setae over the surface. The asci are clavate, 8-spored, with a refractive apical ring, and the ascospores are cylindrical, verrucose, and surrounded by a thick mucoid sheath (Hyde et al. 1999; Whitton et al. 2012). The asexual morph is hyphomycetous, with erect, unbranched or branched conidiophores bearing 3–12 hyaline to olivaceous, phialidic conidiogenous cells with collarettes. The conidia are aseptate, initially hyaline, and become pigmented at maturity (Lombard et al. 2016). Species of *Stachybotrys* are widely distributed in both terrestrial and aquatic ecosystems, on a broad range of substrates, including air, soil, plant litter, and damp indoor materials (Pinruan et al. 2004; Lombard et al. 2016; Hyde et al. 2020d; Samarakoon et al. 2021; Liu et al. 2024a). Several species have also been reported from marine habitats and salt marsh plants (Jones et al. 2019; Calabon et al. 2021). Here, we introduce a new species collected from the salt marsh plant *Sesuvium portulacastrum* in Thailand.

Stachybotrys sesuvii R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.59

Etymology – Referring to the isolation of the fungus from *Sesuvium portulacastrum*.

Saprobic on decaying twig of *Sesuvium portulacastrum*. **Asexual morph:** Colonies on natural substrate aerial, solitary or aggregated, white aerial hyphae with black heads. *Conidiophores* 30–52 × 2–3.2 µm ($\bar{x}$ = 43 × 2.5 µm, n = 15), solitary or in group, macronematous, mononematous, straight or slightly curved, unbranched, 1–2-septate, hyaline to subhyaline, slightly pigmented at the apex, smooth-walled to spinose-walled, with 3–11 conidiogenous cells. *Conidiogenous cells* 7.5–11 × 3.5–5 µm ($\bar{x}$ = 9 × 4.5 µm, n = 20), phialidic, clavate, subhyaline, olivaceous brown to olivaceous brown green, with conspicuous collarettes, occasionally one conidiogenous cell extending to form a new conidiogenous cells. *Conidia* 6.5–9.5 × 2.5–4.3 µm ($\bar{x}$ = 7.5 × 3.5 µm, n = 30), ellipsoidal to oblong, round apex, with thickened darkened truncate bases, aseptate, olivaceous brown to olivaceous brown green, thick-walled, verrucose, guttulate, catenated in slimy mass. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 1 cm diam. after one week at $25\pm 2^{\circ}\text{C}$, raised, umbonate, entire margin, dense; from surface, white, pinkish white; from reverse, grayish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pran Kiri Beach, on dead dry aerial stems of *Sesuvium portulacastrum* on seashore rocks, 8 November 2024, R. Asghari, S7P11 (MFLU 26-0062, holotype); ex-type culture (MFLUCC 26-0068).

Notes – Multi-gene phylogenetic analyses from ITS, CMDA, *rpb2*, *tub2*, and *tef1* sequence data, recovered *Stachybotrys sesuvii* sister to *St. dolichophialis* with strong support (100% ML/1.00 BPP). *Stachybotrys sesuvii* is similar to the type of *St. dolichophialis* in having macronematous, mononematous, straight or curved, unbranched, conidiophores; phialidic, clavate, elongating conidiogenous cells, with conspicuous collarettes and ellipsoidal, aseptate, verrucose conidia (Lombard et al. 2016). However, it differs in having rough wall conidiophore, subhyaline, olivaceous brown to olivaceous green conidiogenous cells, and larger olivaceous green conidia ($6.5\text{--}9.5 \times 2.5\text{--}4.3$ vs. $5.5\text{--}6.5(-7) \times 2\text{--}3$ μm , unlike smooth-walled conidiophore, hyaline conidiogenous cells, and olivaceous brown to dark brown conidia in *St. dolichophialis* (Lombard et al. 2016). Our collection (MFLUCC 26-0068) differed from *St. dolichophialis* (DOAMC 227011) by 2.6% (15/575 bp, including gaps) in the ITS region and 5.2% (18/343 bp, including gaps) in the *tub2* region. *Stachybotrys sesuvii* is introduced here as a new species isolated from *Sesuvium portulacastrum* in a salt marsh habitat in Thailand.



Note a Decaying twig of the host. b, c Colony on the host surface. d–f Conidiophores, conidiogenous cells and conidia. g Phialides. h Conidia. i Colonies on PDA (above and reverse). Scale bars: b = 250 μm , c = 100 μm , d, e = 20 μm , f–h = 10 μm .

Figure 5.59 *Stachybotrys sesuvii* (MFLU 26-0062, holotype)

Microascales Luttr. ex Benny & Kimbr.

Halosphaeriaceae E. Müll & Arx ex Kohlm

Halosphaeriaceae is the most species-rich family of marine ascomycetes and represents a major evolutionary lineage adapted to aquatic environments (Jones et al. 2009, 2015, 2017, 2019; Hyde et al. 2024). The family was formally validated by Kohlmeyer (1972), with *Halosphaeria* as the type genus, and is currently placed within *Microascales* based on molecular phylogenetic evidence (Jones et al. 2015; Maharachchikumbura et al. 2015, 2016). Early classifications were largely morphology-based and emphasized didymosporous taxa, although subsequent ultrastructural and molecular studies led to significant revisions in generic concepts and familial boundaries (Jones et al. 1983, 1984; Jones 1995; Abdel-Wahab and Nagahama 2011; Sakayaroj et al. 2011; Jones et al. 2015; Dayarathne et al. 2026). Several genera originally included in *Halosphaeriaceae*, such as *Lulworthia* and *Lindra*, were later segregated into *Lulworthiales* following DNA sequence analyses (Kohlmeyer et al. 2000; Campbell et al. 2003; Pang et al. 2003; Koch et al. 2007).

Members of *Halosphaeriaceae* are predominantly marine saprobes, colonizing submerged wood, mangrove debris, seagrasses, algae, and other plant-derived substrates in oceans, estuaries, and mangrove ecosystems, with a smaller number occurring in freshwater habitats (Jones 2011; Jones and Pang 2012a). They are characterized by perithecial ascomata, often with elongated necks and periphyses, deliquescent catenophyses, thin-walled unitunicate early deliquescent asci, and ascospores frequently with appendages or gelatinous sheaths that facilitate dispersal and attachment in aquatic environments. Asexual morphs are hyphomycetous with variable morphology of solitary, septate, muriform, coiled or helicoid conidia (Hyde et al. 2020d).

More than 30 genera in *Halosphaeriaceae* are monophyletic reflecting rapid diversification and ecological specialization in marine ecosystems (Jones et al. 2019). Ecologically, halosphaeriaceous fungi play a crucial role in coastal nutrient cycling through the degradation of lignocellulosic substrates, contributing to organic matter turnover in marine ecosystems (Jones and Hyde 1988; Jones and Pang 2012a). Here, we provide a phylogenetic tree of *Halosphaeriaceae*.

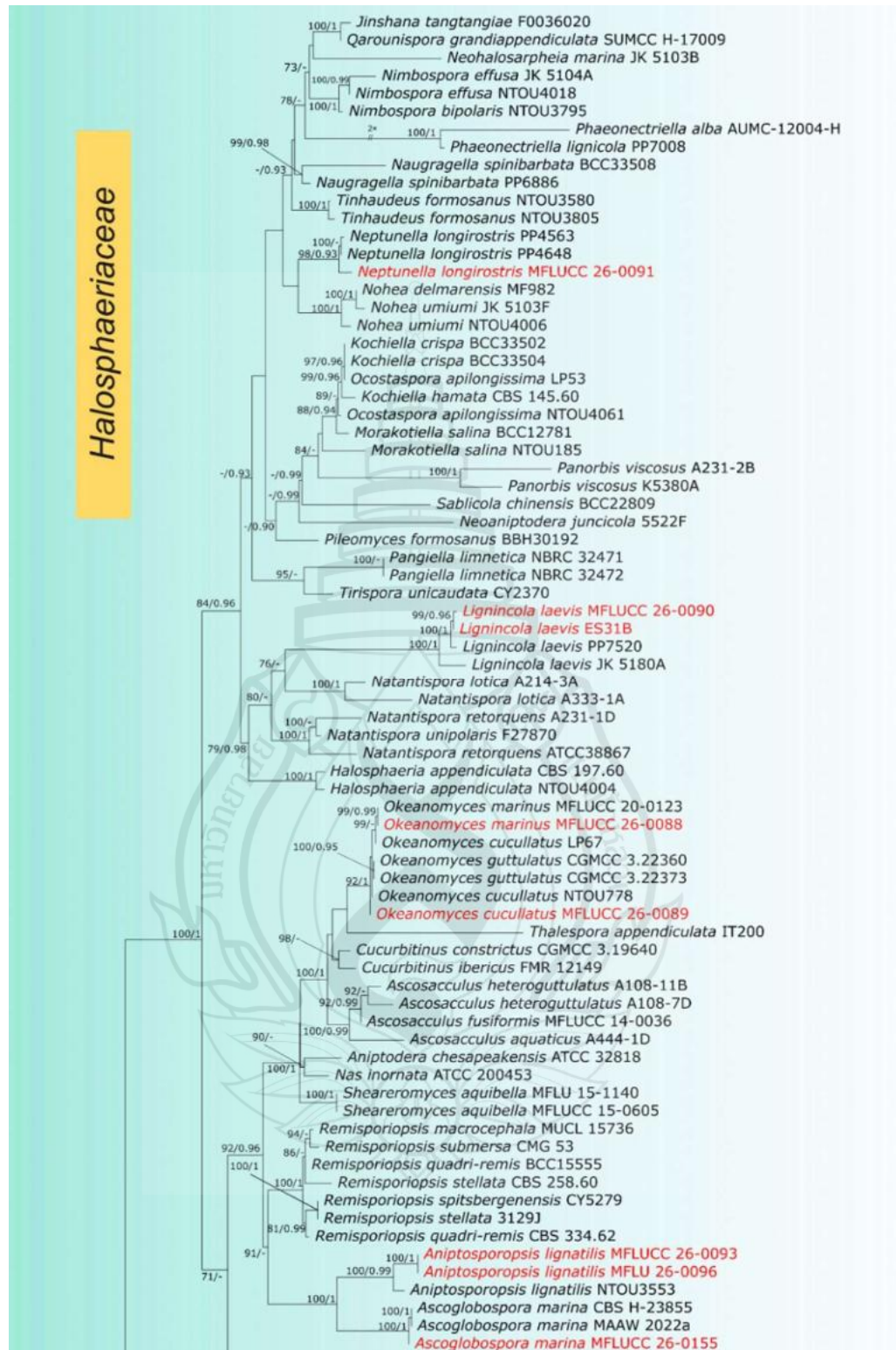


Figure 5.60 Phylogram generated from the ML analysis based on the combined combined LSU and SSU, sequence alignments of *Halosphaeriaceae*

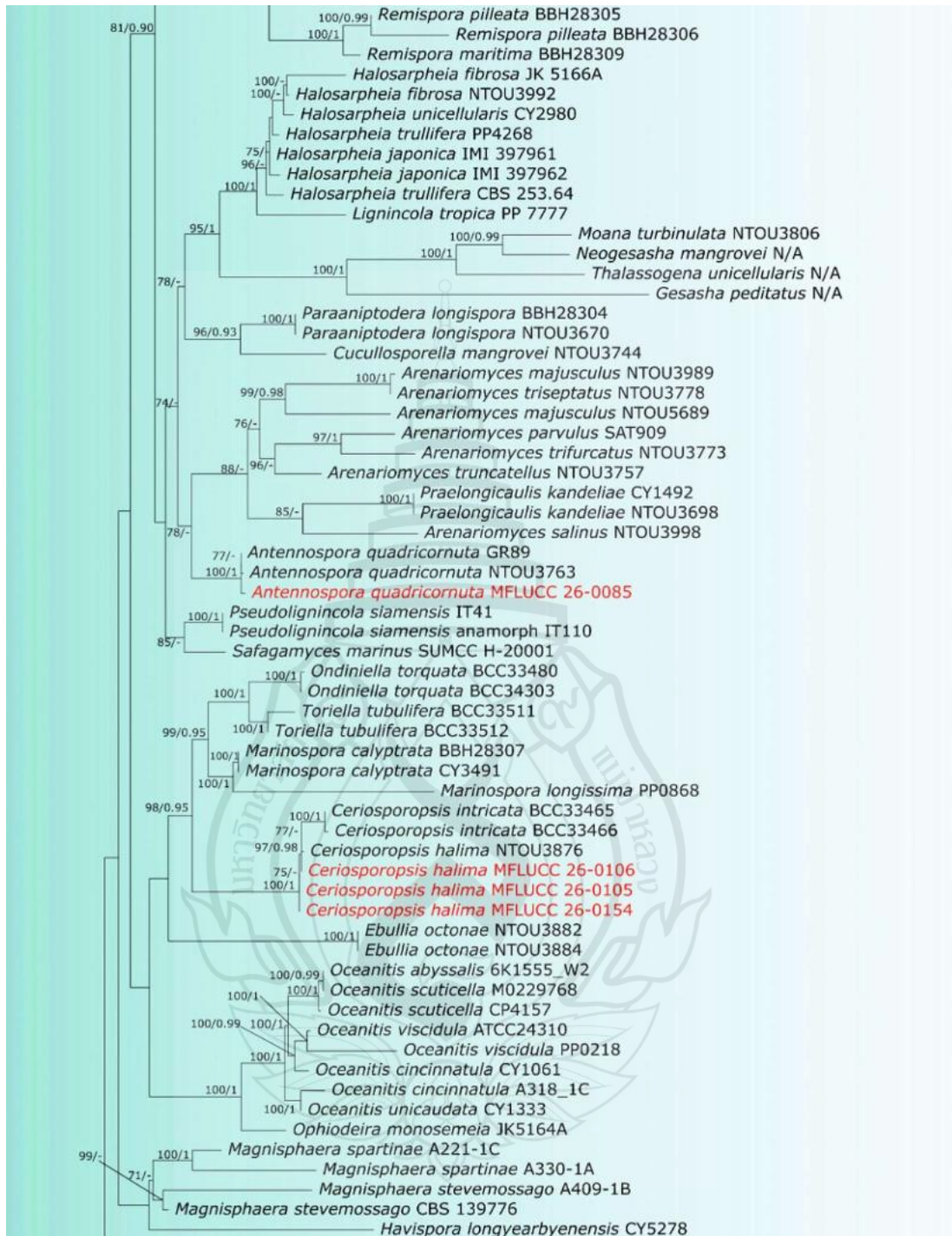
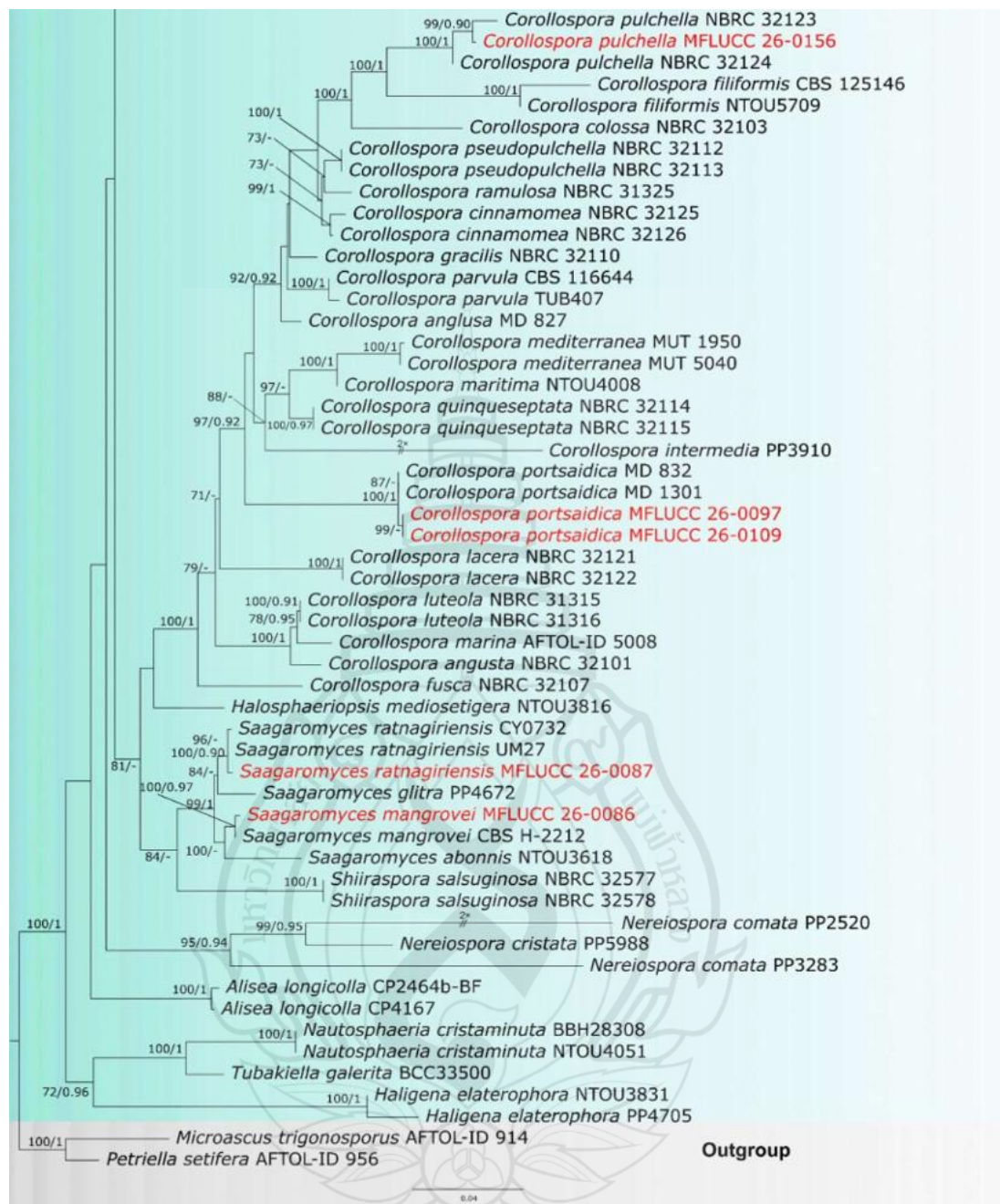


Figure 5.60 (continued)



Note The tree is rooted to *Microascus trigonosporus* (AFTOL ID 914) and *Petriella setifera* (AFTOL ID 956). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.60 (continued)

Antennospora Meyers 1957

Antennospora was introduced by Meyers (1957) based on *Antennospora caribbea*, which was collected from submerged wood in seawater. Subsequently, Johnson (1958) transferred *Halosphaeria quadricornuta* to *Antennospora* as *A. quadricornuta* and synonymized *A. caribbea* with this species. *Antennospora* is therefore a monotypic genus, represented by the type species *A. quadricornuta*. The sexual morph is characterized by subglobose to ellipsoidal, ostiolate ascomata with a large, deliquescing pseudoparenchymatous centrum, early deliquescing asci, and ellipsoidal, 1-septate ascospores bearing two subterminal appendages (Pang et al. 2011). Morphologically, *Antennospora* resembles *Halosphaeria* but differs in having subterminal ascospore appendages and lacking an episporium at the point of appendage attachment (Jones et al. 1984). Phylogenetic analyses have supported the separation of *Antennospora* as a distinct genus (Pang et al. 2008). The genus is widely distributed as a marine saprobe on submerged substrates, particularly dead mangrove wood (Pang et al. 2008, 2011). Here, we recollect *Antennospora quadricornuta* from submerged wood trapped between rocks in Thailand.

Antennospora quadricornuta (Cribb & J.W. Cribb) T.W. Johnson, Fig. 5.61

Index Fungorum number: IF292555

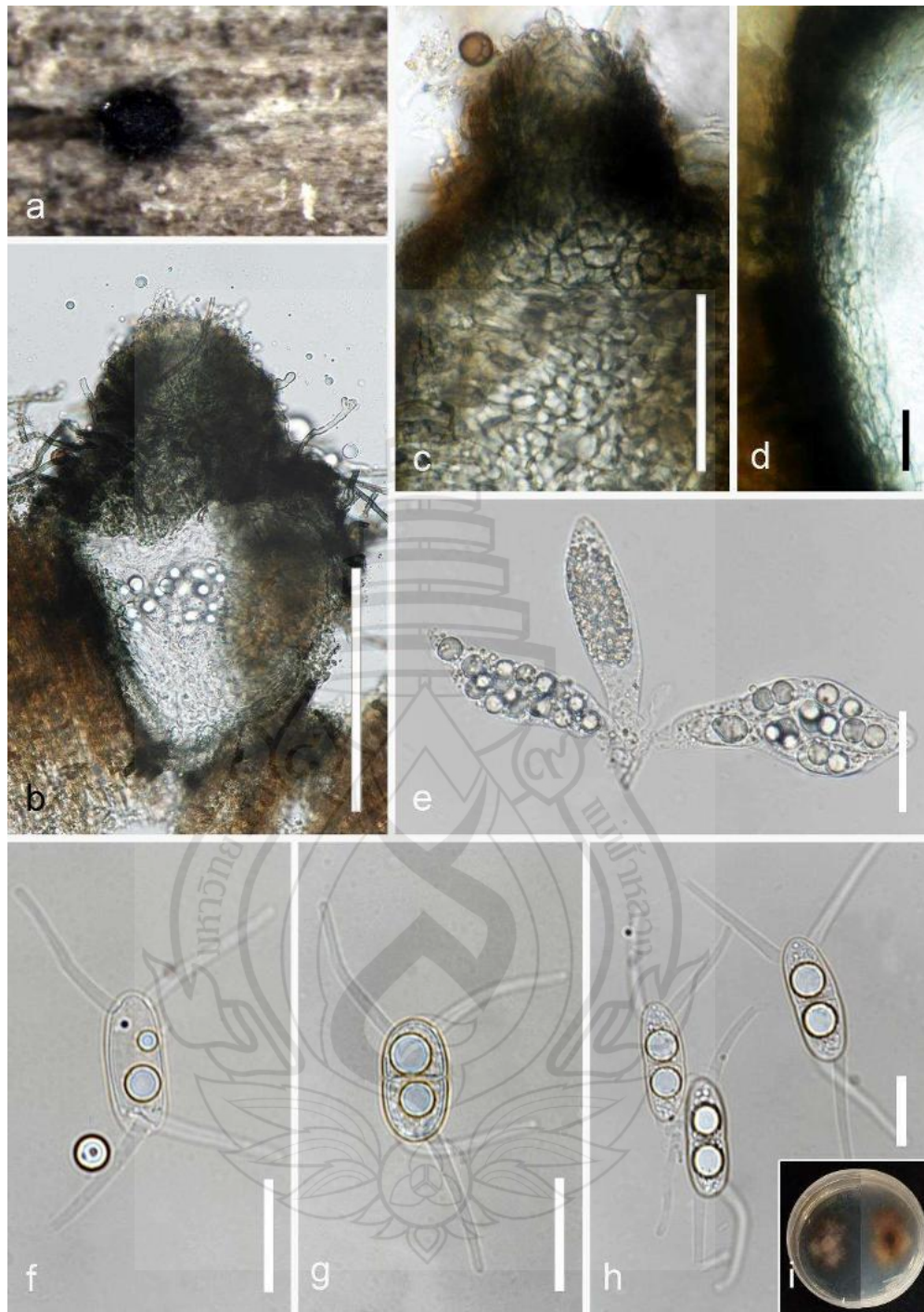
Saprobic on decaying wood submerged in seawater. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 200–250 × 130–170 µm ($\bar{x}$ = 235 × 150 µm, n = 10) (including neck), solitary, immersed to superficial, black, papillate, ostiolate, surrounded by dark brown hyphae. *Neck* 45–90 × 60–100 µm ($\bar{x}$ = 70 × 75 µm, n = 10), subconical to subcylindrical, centric, black. *Peridium* 13–20 µm ($\bar{x}$ = 16 µm, n = 20), outer layer dark brown to black, *textura angularis*, inner layer hyaline, composed of irregular elongated cells, merging into the large polygonal cells of pseudoparenchyma of the venter. *Asci* 46–85 × 16–28 µm ($\bar{x}$ = 65 × 21 µm, n = 10), 8-spored, clavate, short pedicilliate, unitunicate, deliquescing early, round apex. *Ascospores* 22–29 × 8.5–13 µm ($\bar{x}$ = 26 × 10 µm, n = 20) (excluding appendages), overlapping biseriate, triseriate or multiseriate, ellipsoidal, straight, 1-septate, slightly constricted at the septum, guttulate, hyaline, smooth-walled, appendaged. *Appendages* 19–39 µm long × 2–3 µm

diam., at the base ($\bar{x} = 27 \times 2.5 \mu\text{m}$, $n = 30$), cylindrical, two subterminal appendages at each end of the ascospore, attenuate and stiff.

Culture characteristics: Colonies on CMA Seawater reaching 1.5 cm diam. after two months at $25 \pm 2^\circ\text{C}$, umbonate, fluffy, submerged margin, irregular margin; from surface, brownish gray, grayish brown at the periphery; from reverse, dark brown, yellowish brown.

Material examined: Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on decaying wood submerged in seawater (water salinity 34 ppt), 3 February 2023, R. Asghari, A5-1 (MFLU 26-0084); living culture (MFLUCC 26-0085).

Notes – Multi-gene phylogenetic analyses of LSU and SSU sequences placed our collection (MFLUCC 26-0085) within *Antennospora quadricornuta* with strong support (100% ML/1.00 BPP). Morphologically, it matches *An. quadricornuta* in having papillate, ostiolate black ascomata with a neck, clavate asci, and hyaline 1-septate ascospores bearing two subterminal appendages at each end (Pang et al. 2011; Dayarathne et al. 2026). Combining molecular and morphological evidence, this strain is reported here as a new collection of *An. quadricornuta* from marine habitats in Thailand.



Note a Appearance of ascoma on the host. b Section through an ascoma. c Surface microscopic view of peridium. d Section through peridium. e Asci. f-i Ascospores. i Culture on CMA Seawater (above and below). Scale bars: b = 100 μm , c = 50 μm , c = 15 μm , e = 25 μm , f-h = 20 μm .

Figure 5.61 *Antennospora quadricornuta* (a5-1)

Ascoglobospora Abdel-Wahab

Ascoglobospora is a monotypic genus established by Abdel-Wahab (in Liu et al. 2024) to accommodate *Ascoglobospora marina*. The type species was originally collected from decaying driftwood on a rocky beach in Japan (Liu et al. 2024). The genus is characterized by erumpent to superficial, hyaline to light-brown ascomata with a periphysate neck, and the presence of catenophyses. Asci are 8-spored, subglobose, and early deliquescing, lacking an apical apparatus. Ascospores are ellipsoidal, uniseptate, and bear bipolar, hamate appendages that uncoil in water to form long filamentous structures (Liu et al. 2024). Here, we report a new geographical record of *Ascoglobospora marina* from trapped wood between rocks submerged in seawater in Thailand.

Ascoglobospora marina Abdel-Wahab, Fig. 5.62

Index Fungorum number: IF559818; Facesoffungi number: FoF12718

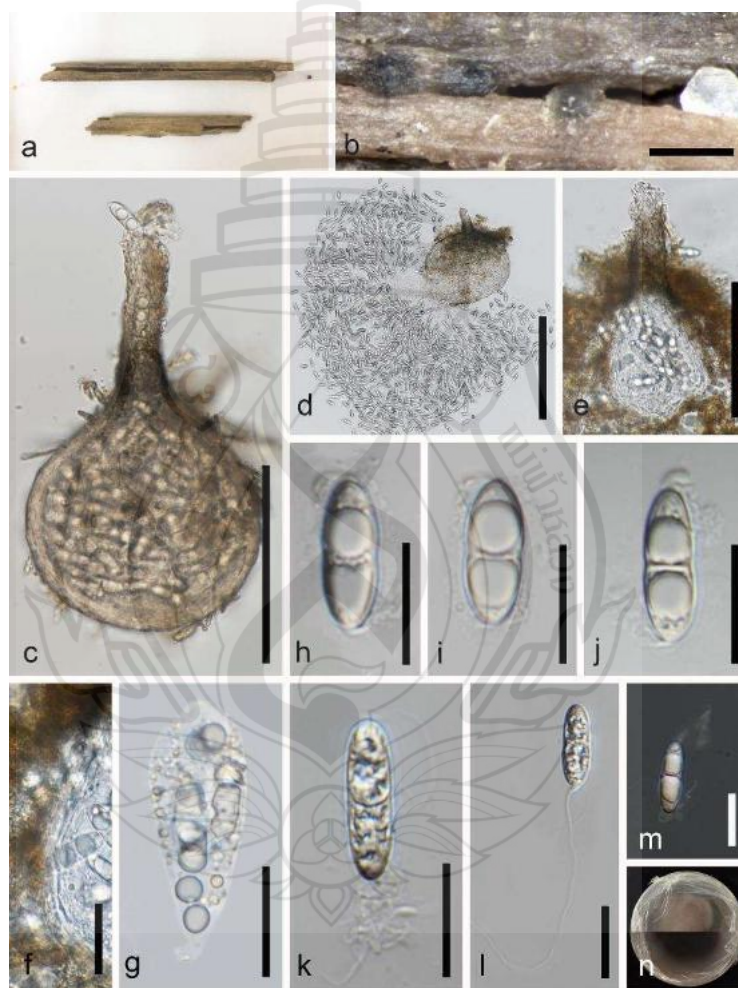
Saprobic on decaying wood submerged in seawater. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 90–175 × 86–186 µm ($\bar{x}$ = 127 × 130 µm, n = 5), globose to subglobose, solitary or gregarious, erumpent to superficial, ostiolate, papillate, membranous, grayish black on the host surface, in microscopic view hyaline to pale brown, pigmented around the base of the neck. *Necks* 32–136 × 10–31 µm ($\bar{x}$ = 88 × 23 µm, n = 5), cylindrical, central, grayish black at the base, paler to hyaline at the apex. *Peridium* 7–12 µm ($\bar{x}$ = 10 µm, n = 15), composed of *textura angularis* or elongated cells. *Asci* 30–35 × 9.5–11 µm ($\bar{x}$ = 32 × 10.5 µm, n = 5) (size for immature asci), 8-spored, clavate, short pedicillate, unitunicate, early deliquescing, without an apical apparatus. *Ascospores* 22–26 × 7.5–9 µm ($\bar{x}$ = 24 × 8.5 µm, n = 30) (excluding appendages), ellipsoidal, straight, round ends, 1-septate, slightly constricted at the septum, guttulate, appendaged. *Appendages* bipolar, becoming uncoiled and long and filamentous in water.

Culture characteristics – Colonies on CMA seawater reaching 1 cm diam. after one month at 25±2°C, convex, with aerial mycelia, flat margin, filamentous margin; from surface, gray, brownish gray; from reverse, dark brown, black.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on decaying wood submerged in seawater (water salinity 34 ppt), 3 February

2023, R. Asghari, A6-3 (MFLU 26-0093); living culture (MFLUCC 26-0155); *ibid.*, A3-3 (MFLU 26-0094); living culture (MFLUCC 26-0110).

Notes – Our collection of *Ascoglobospora marina* clustered with strains of *As. marina* (CBS H-23855 and MAAW 2022a), with strong support (100% ML/1.00 BPP). Morphologically, it resembles the holotype in having light-colored ascomata and ellipsoidal, 1-septate, hyaline ascospores with bipolar uncoiling appendages (Liu et al. 2024). Together, the molecular and morphological evidence support its recognition as a new geographical record of *As. marina* from marine habitats in Thailand.



Note a Appearance of the host. b Appearance of colony on the host. c, d Microscopic view of ascomata. e Section through an ascoma. f Section through peridium. g Immature ascus. h–l Ascospores. m Ascospore in black ink. n Culture on CMA seawater (above and below). Scale bars: b = 100 μ m, c–e = 100 μ m, f–m = 20 μ m.

Figure 5.62 *Ascoglobospora marina* (a6-3)

Ceriosporopsis Linder

Ceriosporopsis was established by Barghoorn and Linder (1944) based on the type species *Ceriosporopsis halima*, which was collected from a submerged test block. Subsequent studies expanded the genus to include seven species, all reported from submerged wood in marine environments (Kohlmeyer 1972; Sakayaroj et al. 2011; Abdel-Wahab et al. 2017). The sexual morph of *Ceriosporopsis* is characterized by subglobose to cylindrical, ostiolate, papillate ascomata, with immature ascomata filled with pseudoparenchyma. Asci are clavate, 8-spored, and early deliquescent. Ascospores are ellipsoidal, hyaline, and uniseptate, surrounded by a gelatinous exosporic sheath that ruptures to release a mucilaginous polar appendage (Kohlmeyer and Kohlmeyer 1979). Curved, coiled, and catenated chlamydospores have also been reported (Pang et al. 2011; www.marinefungi.org). Here, we report three strains of *Ceriosporopsis halima* isolated from trapped wood submerged in seawater in Thailand.

Ceriosporopsis halima Linder, Fig. 5.63

Index Fungorum number: IF285108

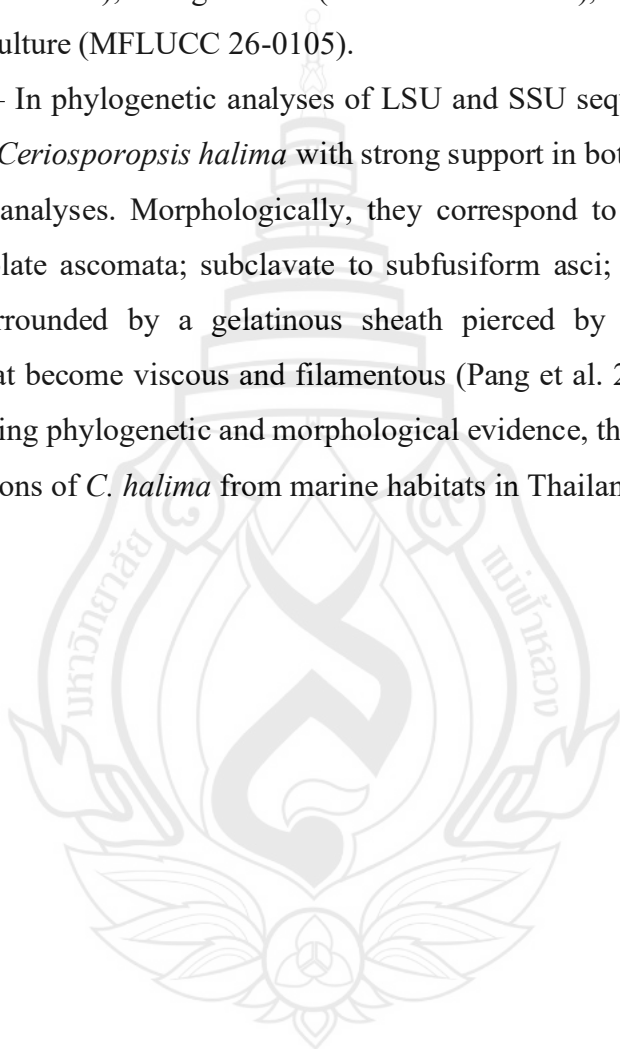
Saprobic on decaying wood submerged in seawater. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 250–350 µm diam. ($\bar{x}$ = 300 µm diam., n = 10) (excluding neck), globose to subglobose, solitary or gregarious, immersed, semiimmersed or to superficial, dark brown to black, papillate, ostiolate. *Neck* 100–350 × 20–26 µm ($\bar{x}$ = 225 × 23 µm, n = 10), cylindrical to subcylindrical, centric. *Peridium* reddish brown to brown on the surface, *textura angularis*. *Asci* 47–92 × 24–36 µm ($\bar{x}$ = 74 × 30 µm, n = 10), 8-spored, subclavate or subfusiform, short pedicillate, unitunicate, deliquescent early, round or obtuse apex, without apical apparatus. *Ascospores* 19–29 × 9–12 µm ($\bar{x}$ = 24.5 × 10.5 µm, n = 40) (excluding appendages), ellipsoidal, straight, 1-septate, constricted at the septum, guttulate, hyaline, smooth-walled, surrounded by a gelatinous sheath pierced by bipolar appendages. *Appendages* 4–7 µm diam. ($\bar{x}$ = 5.5 µm, n = 30), subcylindrical, tapering toward the apex, becoming viscous and filamentous, two appendages at each end of the ascospore.

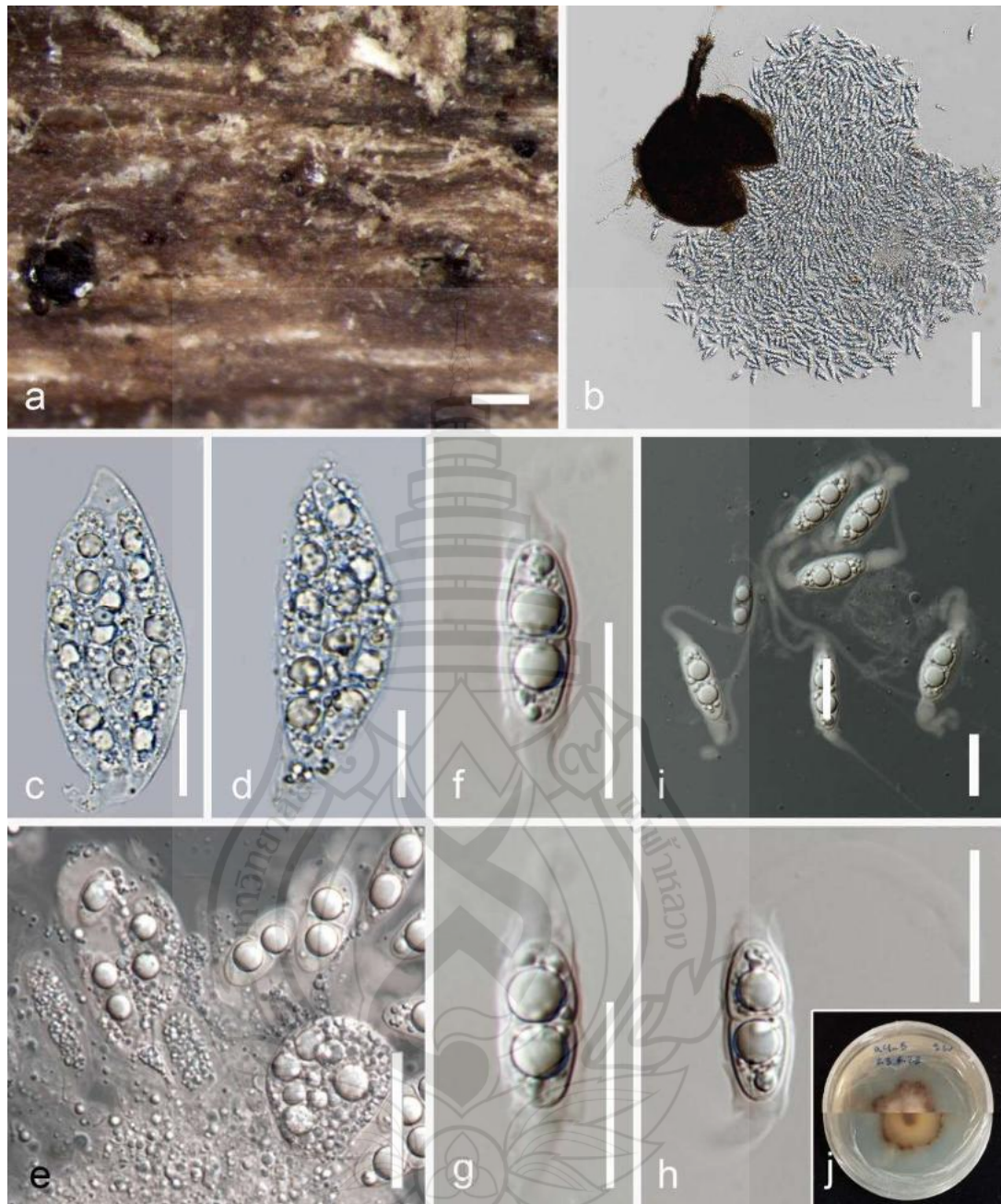
Culture characteristics – Colonies on CMA seawater reaching 0.5 cm diam. after one month at 25±2°C, umbonate, with aerial mycelia at the center, undulate, or irregular

margin; from surface, brownish gray, grayish brown at the periphery; from reverse, grayish orange, brown margin.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on decaying wood submerged in seawater (water salinity 34 ppt), 3 February 2023, R. Asghari, A4-2 (MFLU 26-0085); living culture (MFLUCC 26-0106); *ibid.*, A6-4 (MFLU 26-0086); living culture (MFLUCC 26-0154); *ibid.*, A4-5 (MFLU 26-0087); living culture (MFLUCC 26-0105).

Notes – In phylogenetic analyses of LSU and SSU sequences, our collections clustered with *Ceriosporopsis halima* with strong support in both maximum likelihood and Bayesian analyses. Morphologically, they correspond to *C. halima*, exhibiting papillate, ostiolate ascomata; subclavate to subfusiform asci; and hyaline, 1-septate ascospores surrounded by a gelatinous sheath pierced by bipolar subcylindrical appendages that become viscous and filamentous (Pang et al. 2011; Dayarathne et al. 2026). Integrating phylogenetic and morphological evidence, these strains are reported as new collections of *C. halima* from marine habitats in Thailand.





Note a Appearance of colony on the host. b Squash mount of ascoma. c, d Asci. e Asci in black ink. f–h Ascospores. i Ascospores in black ink. j Culture on CMA seawater (above and below). Scale bars: a = 100 μm , b = 150 μm , c–i = 25 μm .

Figure 5.63 *Ceriosporopsis halima* (a4-5)

Corollospora Werderm.

Corollospora was introduced by Werdermann (1922) with *C. maritima* as the type species, originally described from marine habitats in Germany. The genus was

later expanded by Kohlmeyer (1962), who synonymized *Peritrichospora* with *Corollospora* and transferred several species from related genera. *Corollospora* is now regarded as a diverse marine genus within *Halosphaeriaceae*, although a number of species transferred to other genera following morphological and molecular studies (Jones et al. 2009; Correia et al. 2023). Most species are known from their sexual morphs, characterized by superficial, carbonaceous ascomata, deliquescent asci lacking an apical apparatus, and ascospores with morphological variation in shape, septation, pigmentation, and the presence of distinctive appendages (Jones et al. 2009). Phylogenetic analyses support *Corollospora* as a distinct lineage within the *Halosphaeriaceae* (Jones et al. 2015). Correia et al. (2023) explored cryptic diversity within *C. maritima* using sequence data and proposed ten new genera to accommodate species previously placed in *Corollospora*. However, subsequent studies have retained *Corollospora* as a single genus (Nakagiri et al. 2025; Dayarathne et al. 2026). Species of *Corollospora* are saprobic in marine environments, predominantly arenicolous, and attached to hard substrates by a subiculum (Pang et al. 2011; Calabon et al. 2021).

Corollospora portsaidica Abdel-Wahab & Nagah. Fig. 5.64

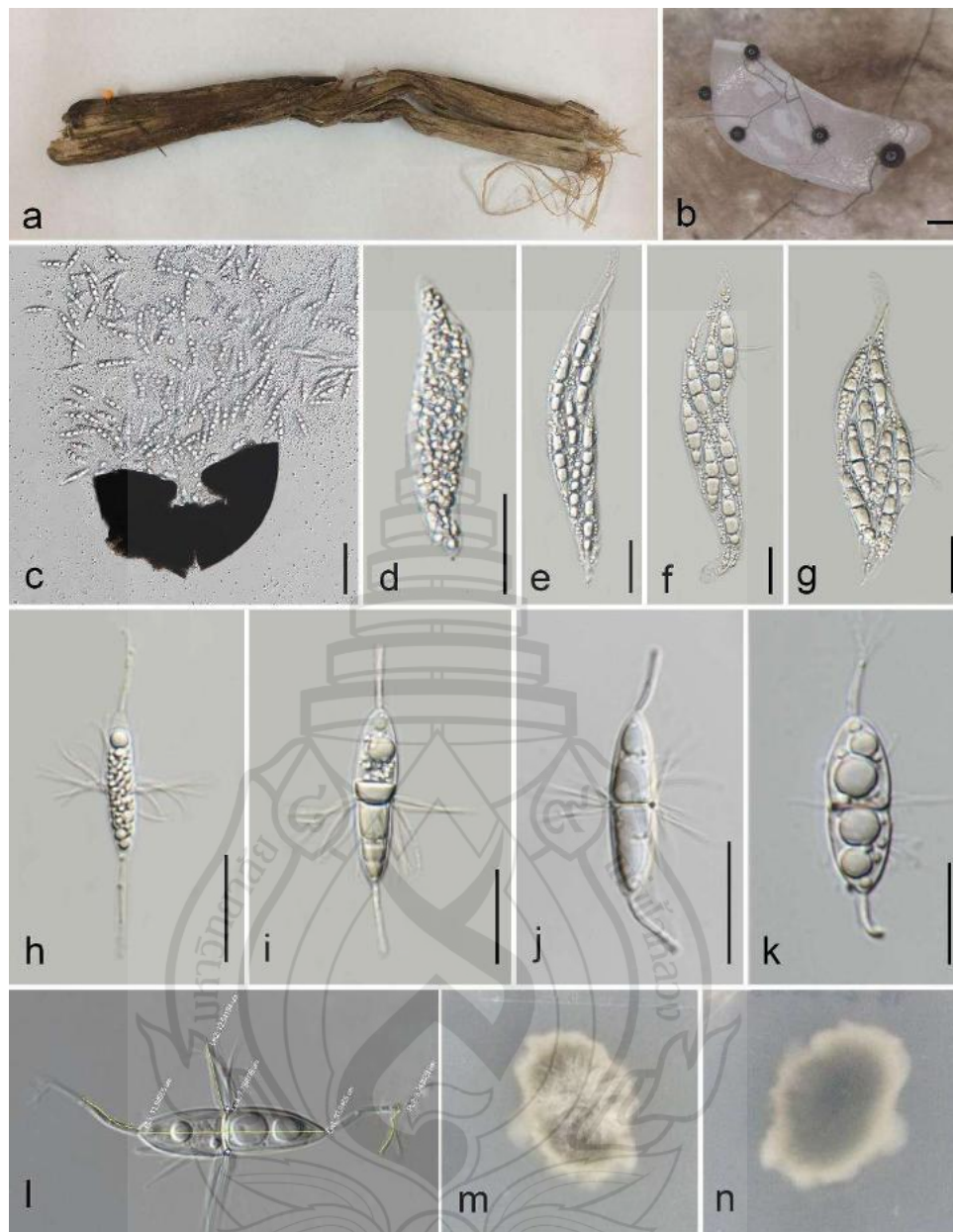
Index Fungorum number: IF535864

Saprobic on decaying stem of *Bambusa* sp. submerged in seawater. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 90–140 µm diam. ($\bar{x}$ = 110 µm diam. n = 5), globose, solitary or gregarious, superficial, attached to the shell or sand grain on decaying wood, black, shiny, carbonaceous, ostiolate, with a basal papilla. *Peridium* thin, composed of dark brown to black, thick-walled *textura angularis* cells on the surface. *Subiculum* dark brown *textura epidermoidea*. *Asci* 84–145 × 14–24 µm ($\bar{x}$ = 119 × 18.5 µm, n = 10), 8-spored, broadly fusiform, short pedicillate, unitunicate, deliquescing early. *Ascospores* 26–35 × 6.5–10 µm ($\bar{x}$ = 31 × 8 µm, n = 30) (excluding appendages), fusiform, straight, 1-septate, constricted at the septum, guttulate, hyaline to light brown, smooth-walled, appendaged. *Appendages* two kinds; (a) 8–14.5 × 1–1.5 µm long ($\bar{x}$ = 12 × 1 µm, n = 30), bipolar, simple, spine-like or thorn-like, attenuate, with apical fragments 5.5–11.5 µm long ($\bar{x}$ = 8.5; n = 30); (b) 10–16 × 1–1.5 µm ($\bar{x}$ = 13 × 1.2 µm, n = 30), equatorial ribbon-like appendages, around the septum, subcylindrical, tapering toward the apex.

Culture characteristics – Colonies on CMA seawater reaching 1 cm diam. after one month at $25\pm 2^{\circ}\text{C}$, raised, with aerial mycelia, fluffy, flat at the edge, entire margin; from surface and reverse, gray, olive gray.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on a submerged decaying wood in rocky shore (water salinity 19 ppt), 25 October 2022, KD Hyde, R7A (MFLU 26-0088); living culture (MFLUCC 26-0097); *ibid.*, Sam Roi Yot, on a decaying wood of *Bambusa* sp. submerged in seawater (water salinity 34 ppt), 5 February 2023, R. Asghari, D2-1 (MFLU 26-0089); living culture (MFLUCC 26-0109).

Notes – Based on the multi-gene phylogenetic analyses, our collections (MFLUCC 26-0097 and MFLUCC 26-0109) grouped with *Corollospora portsaidica* (MD 832 and MD1301) with 100% ML/1.00 BPP support. Morphologically, they are similar to the holotype of *C. portsaidica* in having globose shiny black ascomata, fusiform asci, and fusiform ascospores with two kinds of appendages; they differ in having longer asci (Abdel-Wahab et al. 2009). Our collections are reported as new hosts and geographical records of *C. portsaidica* from marine habitats in Thailand.



Note a Appearance of the host. b Appearance of colony on the host. c Squash mount of ascoma. e–g Asci. h–l Ascospores. m, n Culture on CMA seawater (above and below). Scale bars: b, c = 100 μ m, d–i = 20 μ m.

Figure 5.64 *Corollospora portsaidica* (R7a)

Corollospora pulchella Kohlm., I. Schmidt & N.B. Nair, Fig. 5.65

Index Fungorum number: IF328947

Saprobic on decaying wood submerged in seawater. **Asexual morph:** *in vitro*.

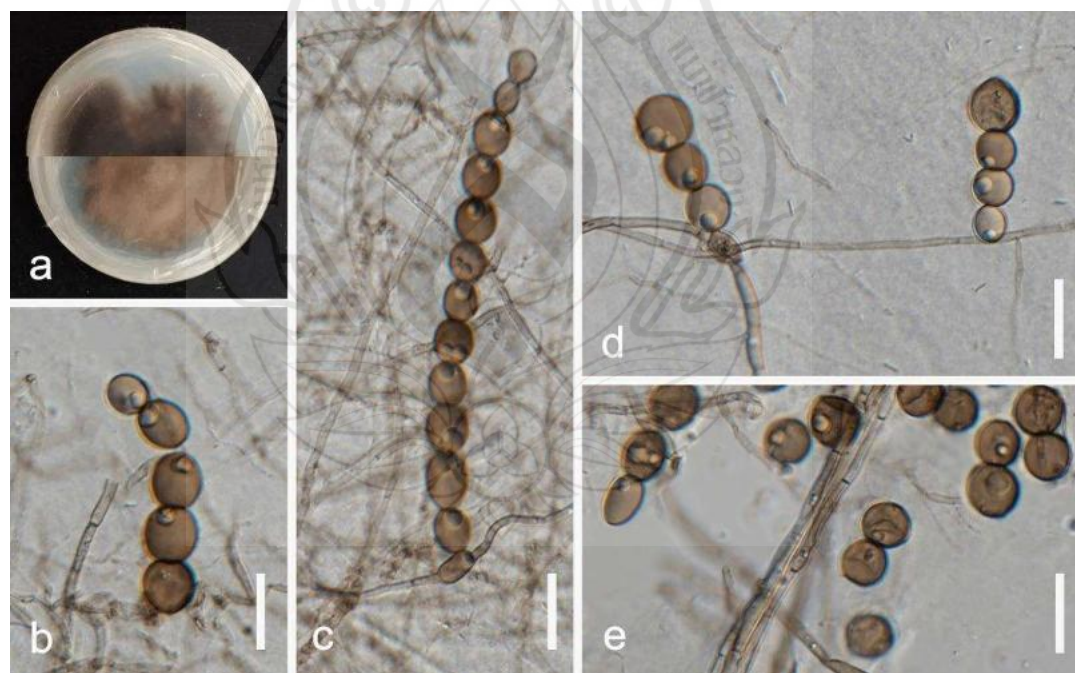
Conidiophores reduced to conidiogenous cells. *Conidiogenous cells* aggregated in

hyphae, hyaline to pale brown. *Chlamydospores* 9.5–13.5 μm ($\bar{x}$ = 11.5 μm , n = 30), globose to subglobose, brown, thick-walled, guttulate, catenated, cells becoming separate. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on CMA seawater reaching 1 cm diam. after one month at $25\pm 2^\circ\text{C}$, low convex, felty or fluffy, dull, undulate or irregular margin; from surface, brown; from reverse, dark brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on decaying wood submerged in seawater (water salinity 34 ppt), 3 February 2023, R. Asghari, A6-5 (MFLU 26-0090); living culture (MFLUCC 26-0156).

Notes – Phylogenetic analyses based on LSU and SSU sequences indicate that our collection is closely related to *Corollospora pulchella*, supported by 97% ML and 0.95 BPP. Morphologically, it matches *C. pulchella* in forming catenated chlamydospores in culture that develop basipetally (Anastasiou 1961). Combining molecular and morphological results, this strain is reported as a new collection of *C. pulchella* from marine habitats in Thailand.



Note a Culture on CMA seawater (above and below). b – e Chlamydospores. Scale bars: 20 μm .

Figure 5.65 *Corollospora pulchella* (A6-5)

Lignincola Höhnk

Lignincola is a cosmopolitan genus within *Halosphaeriaceae*, reported from a wide range of marine, freshwater, and brackish-water habitats (Jones and Pang 2012b; Pang et al. 2013; Jones et al. 2017). The genus was established by Höhnk (1955) and typified by *Lignincola laevis*. The sexual morph is characterized by ostiolate, papillate, light brown to black ascomata; deliquescent catenophyses; unitunicate, clavate to subfusiform, eight-spored, semi-persistent asci; and ellipsoidal, one-septate, hyaline ascospores lacking appendages (Pang et al. 2011). Although the size and position, of the ascomata may vary, ascospore morphology in *L. laevis* remains stable across different collections (Tan et al. 1995). Species of *Lignincola* have been recorded from various substrates, including submerged driftwood and coastal plants such as mangrove wood and reeds (Schmit and Shearer 2003; Pang et al. 2013b). In the present study, *Lignincola laevis* is recollected from submerged, decaying bamboo wood in Thailand.

Lignincola laevis Höhnk, Fig. 5.66

Index Fungorum number: IF299797

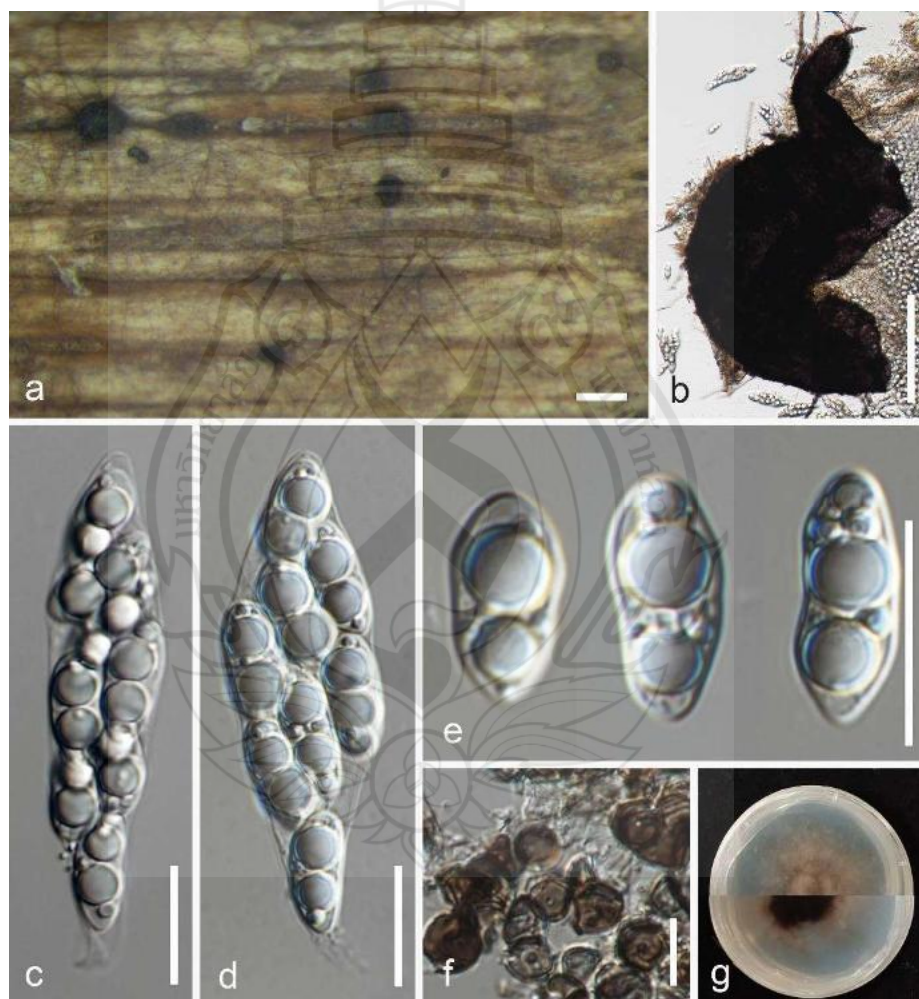
Saprobic on decaying stem of *Bambusa* sp. submerged in seawater. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 150–270 µm diam. ($\bar{x}$ = 225, n = 10), globose to subglobose, or ellipsoidal, solitary or gregarious, ostiolate, immersed or superficial, black. *Necks* up to 150 µm long × 30–50 µm ($\bar{x}$ = 130 × 40 µm, n = 10), cylindrical, central or lateral, black. *Peridium textura angularis*. *Asci* 54–72 × 34–44 µm ($\bar{x}$ = 105 × 39 µm, n = 15), 8-spored, subcylindrical, clavate or subfusiform, short pedicillate, unitunicate, persistent. *Ascospores* 15–20 × 6–7.5 µm ($\bar{x}$ = 17.5 × 7 µm, n = 20), ellipsoidal, straight, or slightly curved, 1-septate, slightly constricted at the septum, guttulate, without appendage, hyaline, becoming brown and cells separating from the septum with age.

Culture characteristics – Colonies on CMA seawater reaching 1.5 cm diam. after one month at 25±2°C, umbonate, with aerial mycelia, filamentous; from surface, grayish brown; from reverse, brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Khung Sai Beach, on decaying wood of *Bambusa* sp. submerged in seawater (water salinity 34

ppt), 24 May 2023, R. Asghari, ES31 (MFLU 26-0099); living culture (MFLUCC 26-0090).

Notes – Multi-gene phylogenetic analyses showed that our collections of *Lignincola laevis* clustered with *L. laevis* (JK 5180A) with full support (100% ML/1.00 BPP). Morphologically, they correspond to *L. laevis*, characterized by ostiolate, papillate ascomata; clavate to subfusiform persistent asci; and ellipsoidal, 1-septate, hyaline ascospores lacking appendages (Pang et al. 2011, 2013). Based on these molecular and morphological similarities, this strain is reported as a new recollection of *L. laevis* from marine habitats in Thailand.



Note a Appearance of colony on the host. b Squash mount of an ascoma. c, d Asci. e Ascospores f Ascospores in late stage. g Culture on CMA seawater. Scale bars: b = 250 μ m, b = 100 μ m, c–e = 15 μ m, f = 10 μ m.

Figure 5.66 *Lignincola laevis* (ES31)

Neptunella K.L. Pang & E.B.G. Jones

Neptunella was established by Pang et al. (2003) to accommodate its type species, *Neptunella longirostris*, which was originally described as *Gnomonia longirostris* from dead branches of *Avicennia marina* in Australia (Cribb and Cribb 1956). The genus is monotypic and is characterized by subglobose to bottle-shaped, membranous ascomata and lacking catenophyses. The asci are cylindrical-clavate to ellipsoidal-clavate or subfusiform and irregularly deliquescent, while the ascospores are ellipsoidal, uniseptate, and lack appendages (www.marinefungi.org). In the present study, *Neptunella longirostris* is recollected from Thailand, on submerged, decaying wood in a rocky shore.

Neptunella longirostris (Cribb & J.W. Cribb) K.L. Pang & E.B.G. Jones, Fig. 5.67

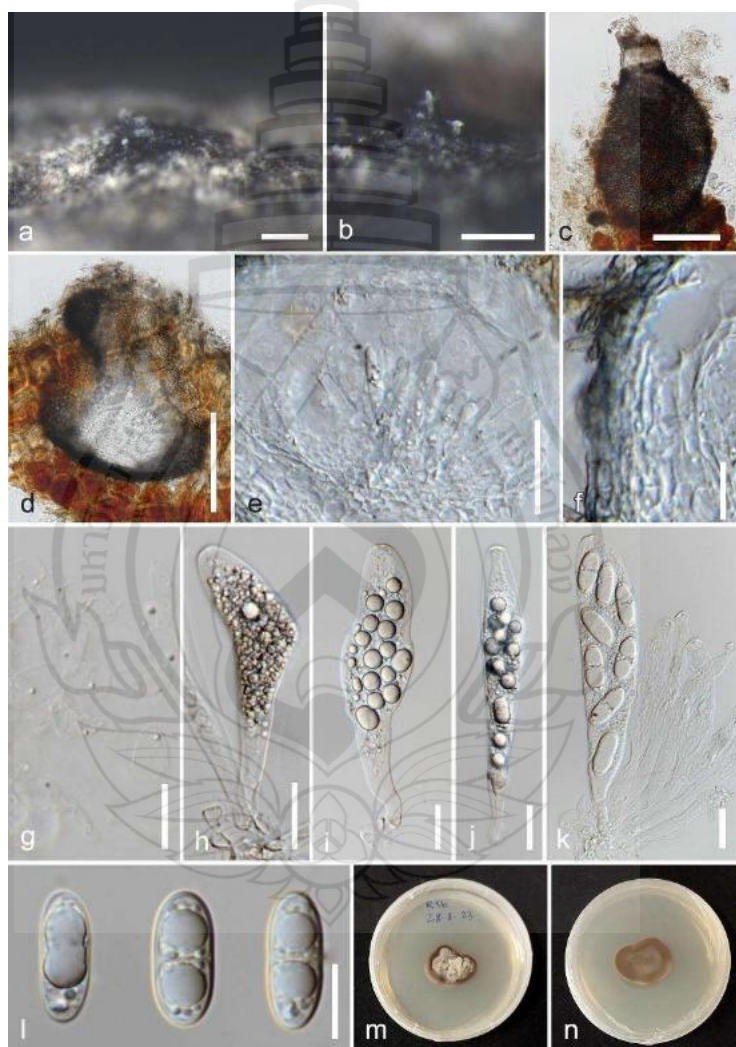
Index Fungorum number: IF299797

Saprobic on decaying wood submerged in seawater. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 115–330 × 160–195 µm ($\bar{x}$ = 205 × 180, n = 10), globose to subglobose, or ellipsoidal, solitary or gregarious, ostiolate, immersed erumpent, black. *Necks* 75–115 × 55–85 µm ($\bar{x}$ = 96 × 71, n = 10), subcylindrical or conical, grayish black, light brown or subhyaline. *Peridium* 10–18 µm ($\bar{x}$ = 13.5, n = 20), composed of elongated cells, *textura angularis*, outer layer grayish black, inner layer hyaline merging into the cells of pseudoparenchyma of the venter. *Catenophyses* present. *Asci* 73–111 × 14.5–28.5 µm ($\bar{x}$ = 95 × 20 µm, n = 20), 8-spored, subcylindrical or subcylindrical clavate, short pedicillate, unitunicate, persistent, with apical pore. *Ascospores* 20–23 × 7–8.5 µm ($\bar{x}$ = 20 × 7 µm, n = 20), ellipsoidal, straight, 0–1-septate, slightly constricted at the septum or not, guttulate, without appendage, hyaline.

Culture characteristics – Colonies on CMA seawater reaching 0.5 cm diam. after three months at 25±2°C, convex, velvety, dense, folded, irregular margin; from surface, gray, brown margin; from reverse, brown, grayish brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on submerged decaying wood in rocky shore (water salinity 19 ppt), 25 October 2022, KD Hyde, R1B (MFLU 26-0100); living culture (MFLUCC 26-0091).

Notes – Phylogenetic reconstruction placed our collection (MFLUCC 26-0091) clustered with strains of *Neptunella longirostris* (PP4648 and PP4563) with 98% ML/0.93 BPP. Morphologically, it resembles *N. longirostris*, showing subglobose ostiolate ascomata, a peridium composed of elongate cells, cylindrical-clavate asci, and hyaline, ellipsoidal, 1-septate ascospores lacking appendages, with asci and ascospore dimensions consistent with those reported for the species (Pang et al. 2003, 2011). Based on these molecular and morphological similarities, this strain is reported as a new collection of *N. longirostris* from marine habitats in Thailand.



Note a, b Appearance of ascomata on the host. c Microscopic view of an ascoma. d, e Section through ascomata. f Section through peridium. g Catenophyses. h–k Asci. l Ascospores. m, n Culture on CMA seawater. Scale bars: a–d = 100 μ m, e = 25 μ m, f, l = 10, h–k = 15 μ m.

Figure 5.67 *Neptunella longirostris* (R1B)

Okeanomyces K.L. Pang & E.B.G. Jones

Okeanomyces was introduced by Pang et al. (2004) to accommodate *Okeanomyces cucullatus*, a species previously classified in *Halosphaeria* and *Remispora*. Subsequent molecular phylogenetic analyses demonstrated that this taxon does not belong to either genus Pang et al. (2004). Consequently, *Okeanomyces* was established as a distinct genus, with *O. cucullatus* designated as the type species. The genus currently comprises three species, all reported as saprobes from marine habitats (Hyde et al. 2020c, 2024). The sexual morph is characterized by subglobose to ellipsoidal, brown to black ascomata, the presence of catenophyses, clavate, early-deliquescing asci, and cylindrical ascospores with or without appendages. The asexual morph is linked to *Periconia prolifica*, and is hyphomycetous, producing unicellular, subglobose to ovoid conidia that are light brown with a reddish tint to dark brown; conidia are catenated and become disarticulated at maturity (Pang et al. 2004; Pang et al. 2011; Hyde et al. 2020c).

Okeanomyces marinus Calabon, E.B.G. Jones, Boonmee & K.D. Hyde, Fig. 5.68

Index Fungorum number: IF557251

Saprobic on decaying wood submerged in seawater. **Asexual morph:** *in vitro* *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* aggregated in hyphae, hyaline to pale brown, smooth. *Conidia* 8.5–15.5 µm diam. ($\bar{x}$ = 10.5 µm, n = 30), globose to subglobose, or ovoid, subhyaline to brown, thick-walled, guttulate. **Sexual morph:** Undetermined.

Culture characteristics: Colonies on CMA seawater reaching 0.5 cm diam. after one month at 25±2°C, flat, low convex, undulate, fimbriate; from surface, grayish brown; from reverse, brown.

Material examined: Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on decaying wood submerged in seawater (water salinity 34 ppt), 5 February 2023, R. Asghari, D1-1 (MFLU 26-0097); living culture (MFLUCC 26-0088).

Notes: In the present phylogeny, our collection of *Okeanomyces* (MFLUCC 26-0088) grouped with *Okeanomyces marinus* (MFLUCC 20-0123). Its morphology matches *O. marinus*, characterized by reduced conidiophores to aggregated

conidiogenous cells and globose to subglobose, subhyaline to brown conidia (Hyde et al. 2020c). Therefore, it is identified as a new collection of *O. marinus* from marine habitats in Thailand, based on both morphology and phylogeny.



Note a, b Culture on PDA (above and below). c, d Conidiogenous cells and conidia. e Conidia. Scale bars: c = 20 μm , d, e = 5 μm .

Figure 5.68 *Okeanomyces marinus* (D1-1)

Okeanomyces cucullatus (Kohlm.) K.L. Pang & E.B.G. Jones, Fig. 5.69

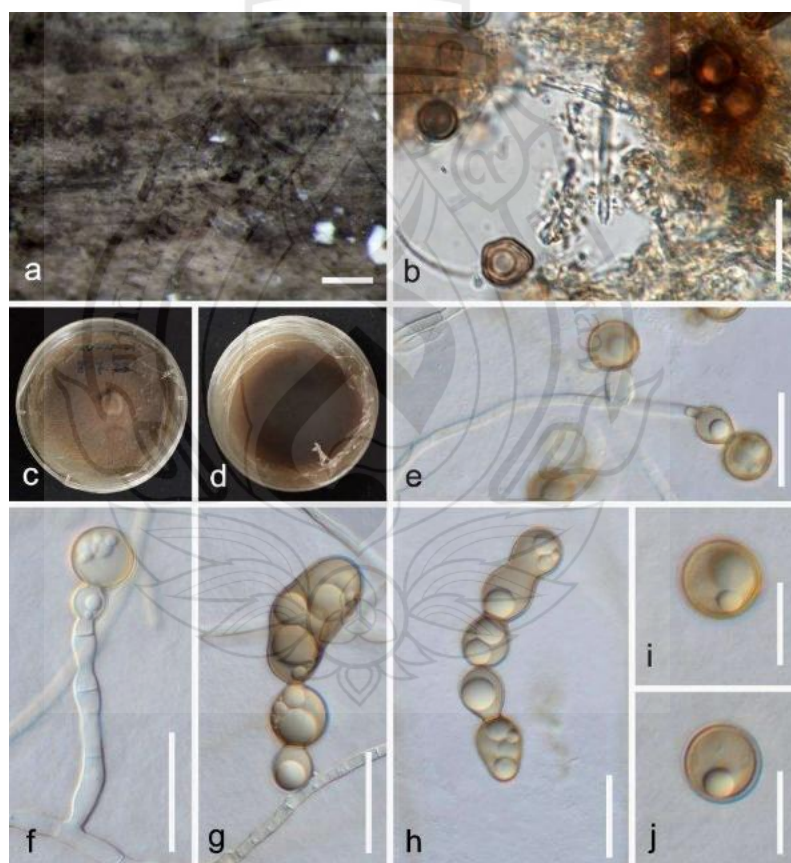
Index Fungorum number: IF369437

Saprobic on decaying wood submerged in seawater. **Asexual morph:** *in vitro* *Conidiophores* 21–27 $\times$ 2.5–8 μm ($\bar{x}$ = 29 $\times$ 5 μm , n = 15), cylindrical, simple, septate, hyaline; or reduced to conidiogenous cells. *Conidiogenous cells* 6–13 $\times$ 2.5–6.5 μm ($\bar{x}$ = 8.5 $\times$ 4.5 μm , n = 15), subcylindrical or ovoid, or aggregated in hyphae, hyaline, smooth. *Conidia* 7.5–14.5 $\times$ 8.5–11.5 μm ($\bar{x}$ = 11 $\times$ 9.5 μm , n = 30), globose, subglobose, or ovoid, light brown, thick-walled, smooth-walled, guttulate, developing basipetally, catenated in chain, becoming separate. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on CMA seawater reaching 1 cm diam. after one month at 25 $\pm$ 2°C, flat, circular, fimbriate; from surface and reverse, brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on decaying wood submerged in seawater (water salinity 34 ppt), 3 February 2023, Raheleh Asghari, A5-2 (MFLU 26-0098); living culture (MFLUCC 26-0089).

Notes – Based on the multi-gene phylogenetic analyses, MFLUCC 26-0089 formed a subclade to the species of *Okeanomyces* with 92% ML/1 BPP support value. This collection is similar to the asexual morph of *O. cucullatus* (*Periconia prolifica*) in having erect hyaline conidiophores, hyaline ovoid conidiogenous cells, subglobose or ovoid, light brown catenated conidia, developing basipetally (Pang et al. 2011). In the BLAST search, the closest matches for the LSU sequence of our collection were *O. cucullatus* (isolate NTOU778), showing 99.8% sequence similarity, differing by one base pair with no gaps. The closest matches for the SSU sequence were *O. marinus* (MFLUCC 20-0123) and *O. guttulatus* (CGMCC 3.22373), with 100% and 99.9% sequence similarity, respectively. Based on morphological and molecular similarities, our isolate is identified as a new collection of *O. cucullatus* from marine habitats in Thailand.



Note a Appearance of colony on the host. b Conidia on natural substrates. c, d Culture on CMA Seawater (above and below). e–g Conidiogenous cells and conidia. h–j Conidia. Scale bars: a = 100 μm , b–h = 20 μm , i, j = 10 μm .

Figure 5.69 *Okeanomyces cucullatus* (MFLUCC A5-2)

Saagaromyces K.L. Pang & E.B.G. Jones

Saagaromyces was established by Pang et al. (2023) based on phylogenetic analyses to accommodate three species, *Saagaromyces abonnis*, *S. glitra*, and *S. ratnagiriensis*, which were previously placed in *Halosarpheia* or *Nais*. The genus was typified by *S. ratnagiriensis*, originally collected from intertidal wood. A fourth species, *Saagaromyces mangrovei*, was later introduced by Abdel-Wahab, Bahkali and E.B.G. Jones (in Liu et al. 2015) collected from decayed wood of *Avicennia marina* in a mangrove habitat. The sexual morph of *Saagaromyces* is characterized by immersed, ostiolate, papillate ascomata that are hyaline to cream-coloured or brown to black, with a periphysate neck. Catenophyses are present, and asci are cylindrical to clavate and persistent. Ascospores are oval, multiguttulate, and may possess unfurling appendages (Pang et al. 2003). Here we report two *Saagaromyces* species from submerged halophyte in Thailand.

Saagaromyces ratnagiriensis (S.D. Patil & Borse) K.L. Pang & E.B.G. Jones,
Fig. 5.70

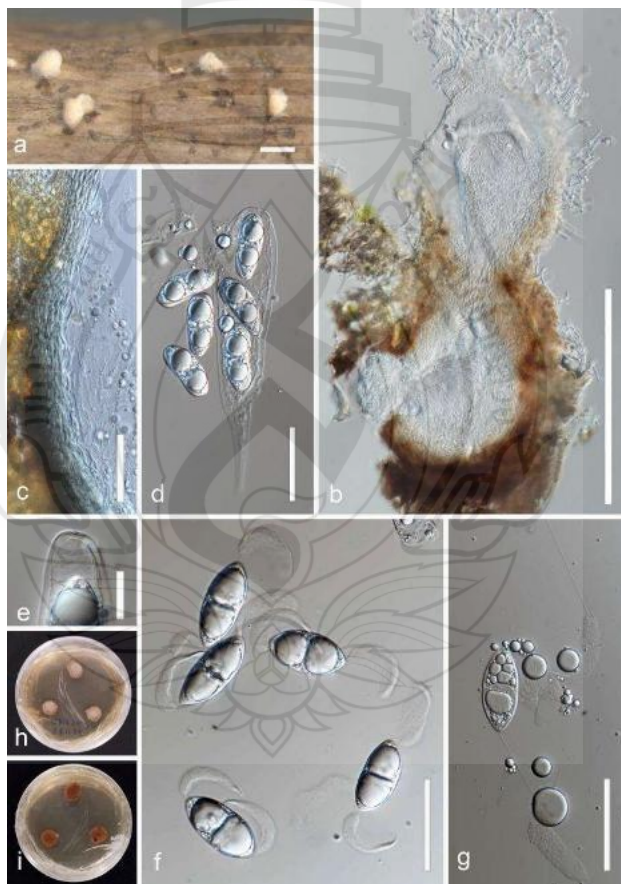
Index Fungorum number: IF373274

Saprobic on dead stems of *Suaeda maritima* submerged in seawater. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 150–350 × 100–170 µm ($\bar{x}$ = 250 × 130 µm, n = 5), subglobose to ellipsoidal, solitary or gregarious, ostiolate, immersed, with erumpent neck through the host surface, covered with whitish hyphae. *Necks* 120–600 × 70–125 µm ($\bar{x}$ = 370 × 85 µm, n = 5), cylindrical, central or lateral, periphysate ostiole. *Peridium* 23–30.5 µm ($\bar{x}$ = 26.5 µm, n = 15), outer layer dark brown to black, becoming paler to hyaline toward the inside, *textura angularis*. *Asci* 180–300 × 40–70 µm ($\bar{x}$ = 245 × 55 µm, n = 5), 8-spored, clavate, long pedicilliate, unitunicate. *Ascospores* 47–55 × 21–26.5 µm ($\bar{x}$ = 51 × 24 µm, n = 20) (excluding appendages), ellipsoidal to broadly fusiform, straight, 1-septate, guttulate, appendaged. *Appendages* bipolar, cap-like, becoming uncoil and filamentous in water.

Culture characteristics – Colonies on CMA seawater reaching 0.5 cm diam. after two months at 25±2°C, convex, dense, entire margin; from surface, gray, brownish gray; from reverse, light brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park (water salinity 15 ppt), on dead submerged stems of *Suaeda maritima*, 9 November 2024, R. Asghari, S7S30 (MFLU 26-0091); living culture (MFLUCC 26-0087).

Notes – In the phylogenetic analyses of LSU and SSU sequence data, *Saagaromyces ratnagiriensis* (MFLUCC 26-0087) clustered with the strains of *S. ratnagiriensis* (UM27 and CY0732), with 100% ML/0.90 BPP support. Morphologically, our collection resembles *S. ratnagiriensis* in having ascospores with uncoiling polar appendages (Kohlmeyer 1984, Baker et al. 2001, Dayarathne et al. 2026). Based on morphological and molecular evidence, it is reported as a new host record of *S. ratnagiriensis* from *Suaeda maritima* in saltmarsh habitats in Thailand.



Note a Appearance of perithecial necks on the host. b Section through an ascoma. c Section through peridium (stained in Melzer's reagent) d Ascus. e apex of an ascus. f, g Ascospores. h, i Culture on CMA seawater (above and below). Scale bars: a = 500 μ m, b = 100 μ m, b = 40 μ m, d, f, g = 50 μ m, e = 20 μ m.

Figure 5.70 *Saagaromyces ratnagiriensis* (s7s30, holotype)

Saagaromyces mangrovei Abdel-Wahab, Bahkali & E.B.G. Jones, Fig. 5.71

Index Fungorum number: IF551073; Facesoffungi number: FoF00488

Saprobic on decaying stem of *Suaeda maritima* submerged in seawater.

Asexual morph: Undetermined. **Sexual morph:** *Ascomata* 300–420 × 180–240 µm ($\bar{x}$ = 360 × 200 µm, n = 5), ellipsoidal, obpyriform, horizontal, solitary or gregarious, yellow brown to brown, immersed, ostiolate, with a neck. *Necks* 270–500 × 40–50 µm ($\bar{x}$ = 395 × 45 µm, n = 5), cylindrical, straight or curved, yellow brown, ostiolar canal periphysate. *Peridium* 14–21 µm ($\bar{x}$ = 17 µm, n = 15), outer layer yellow brown to dark brown, *textura angularis*, becoming paler to hyaline toward the inside, with elongated cells, inner cells merging with pseudoparenchyma of the venter. *Catenophyses* present. *Asci* 180–230 × 38–50 µm ($\bar{x}$ = 210 × 44 µm, n = 5), 8-spored, clavate, long pedicellate, round apex, persistent, unitunicate. *Ascospores* 26–33 × 11–15.5 µm ($\bar{x}$ = 29 × 13 µm, n = 30) (excluding appendages), ellipsoidal to broadly ellipsoidal, straight, 1-septate, slightly constricted at the septum or not, hyaline, guttulate, appendaged. *Appendages* 13–32 µm long × 4.5–10.5 µm wide at the middle ($\bar{x}$ = 20 × 7 µm, n = 20), bipolar, cap-like, stiff, becoming soft and forming a coil of filaments, uncoiling in water.

Culture characteristics – Colonies on CMA seawater reaching 0.7 cm diam. after two months at 25±2°C, convex, fluffy, entire margin; from surface, white; from reverse, brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park (water salinity 15 ppt), on dead submerged stems of *Suaeda maritima*, 9 November 2024, R. Asghari, S7S24 (MFLU 26-0092); living culture (MFLUCC 26-0086).

Notes – In the combined LSU and SSU phylogeny, strain MFLUCC 26-0086 clusters with *Saagaromyces mangrovei* (CBS H-22126) with strong support (100% ML/0.97 BPP). The morphology is consistent with the holotype, particularly in the ellipsoidal to obpyriform, horizontally oriented, yellow-brown ascomata with a neck and ascospores bearing uncoiling polar appendages, with overlapping dimensions. However, the holotype differs in possessing narrow, long-stalked asci (Liu et al. 2015). We therefore identify this collection as *S. mangrovei*, representing a new host and geographic record from *Suaeda maritima* in submerged saltmarsh habitats in Thailand.



Note a Appearance of colony on the host. b, c Section through an ascus. d Section through peridium. e Ascus. f Asci in black ink. g, h Ascospores. i Ascospores with uncoiling appendages (stained in Melzer's reagent). j Germinated ascospore. k, l Culture on CMA seawater (above and below). Scale bars: a, b = 250 μ m, c = 100 μ m, d = 15 μ m, e–j = 25 μ m.

Figure 5.71 *Saagaromyces mangrovei* (MFLU 26-0092, holotype)

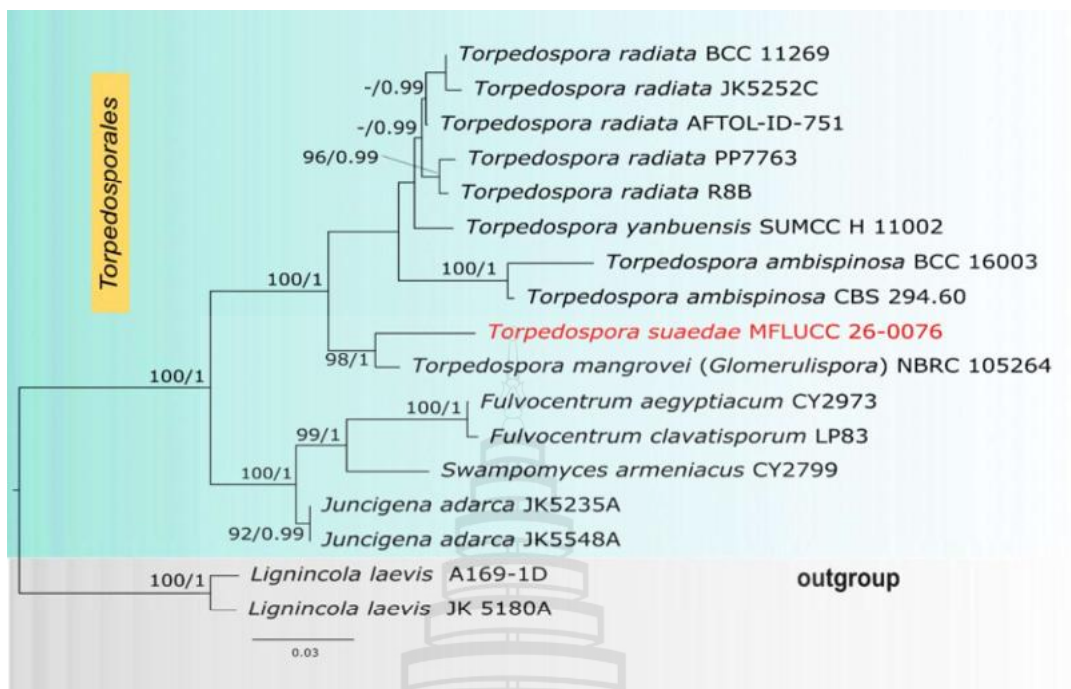
Torpedosporales E.B.G. Jones, Abdel-Wahab & K.L. Pang

Torpedosporaceae E.B.G. Jones & K.L. Pang

Torpedosporaceae was introduced by Jones et al. (2014) in the *Sordariomycetes*, and was later placed in the novel order *Torpedosporales* by Jones et al. (2015). The family was established based on phylogenetic analyses of SSU and LSU sequence data, to accommodate the genera *Torpedospora* and *Glomerulispora*. Subsequently, *Torpedospora* and *Glomerulispora* were considered congeneric (Abdel-Wahab et al. 2010; Jones et al. 2015), with a recommendation to use the name *Torpedospora* over *Glomerulispora* (Réblová et al. 2016).

Torpedospora Meyers

Torpedospora was introduced by Meyers (1957) to accommodate the marine fungus *T. radiata*. With the addition of *Torpedospora ambispinosa*, *T. mangrovei*, and *T. yanbuensis*, the genus currently comprises four species (Kohlmeyer 1960; Abdel-Wahab et al. 2010, 2022; Hyde et al. 2024). The sexual morph of *Torpedospora* is characterized by ostiolate, papillate ascomata and septate ascospores bearing radiating or irregular gelatinous appendages (Abdel-Wahab et al. 2022). *Torpedospora mangrovei* is the only known asexual morph in the genus, producing irregularly helicoid, muriform conidia; it was transferred from *Glomerulispora* to *Torpedospora* based on morphological and molecular evidence (Abdel-Wahab et al. 2010; Jones et al. 2015; Réblová et al. 2016). In this study, we report a new species isolated from dead stems of *Suaeda maritima*, supported by both morphological characteristics and phylogenetic analyses of combined SSU and LSU sequence data.



Note The tree is rooted to *Daldinia concentrica* (ATCC 36659) and *Hypoxylon fragiforme* (HKUCC 1022). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.2 Phylogram generated from the ML analysis based on the combined LSU and SSU sequence alignments of *Torpedosporales*

Torpedospora sp. Fig. 5.73

Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** Undetermined.

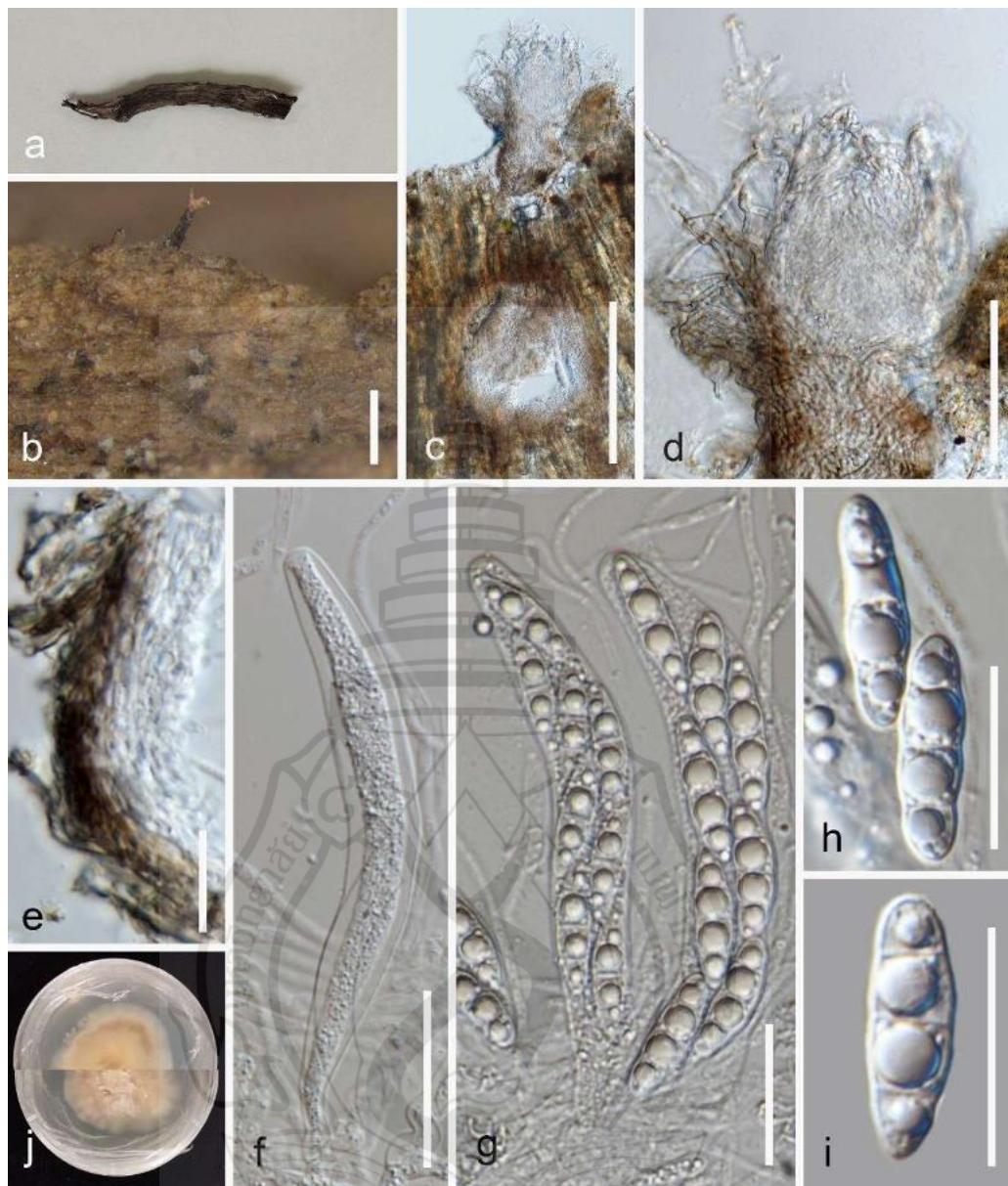
Sexual morph: *Ascomata* 150–200 × 120–160 μm ($\bar{x}$ = 180 × 140 μm, n = 15) (excluding neck), solitary, scattered, immersed, with an erumpent neck on the host surface, dark brown to black, ostiole central. *Neck* 100–240 μm ($\bar{x}$ = 168 μm, n = 15), unbranched, pale brown, periphyset, with apical branched subhyaline to pale brown hyphae. *Peridium* 16–26 μm ($\bar{x}$ = 20 μm, n = 20), outer layer brown to dark brown, *textura angularis*, inner layer hyaline, *textura angularis*. *Paraphyses* 1.6–3 μm wide ($\bar{x}$ = 2.3 μm, n = 20), filliform, straight or flexuous, branched, septate, hyaline. *Asci* 84–124 × 13–19.5 μm ($\bar{x}$ = 104 × 15 μm, n = 20), 8-spored, cylindrical-clavate, short pedicillate, unitunicate, persistent, round apex, with an apical apparatus. *Ascospores* 21–26 × 5.5–7.5 μm ($\bar{x}$ = 24 × 6.5 μm, n = 30), overlapping biserial, ellipsoidal to

oblong, straight to slightly curved, rounded apex, slightly obtuse base, 3-aseptate, constricted at septa, guttulate, hyaline, smooth-walled.

Culture characteristics – Colonies on PDA reaching 2.5 cm diam. after one month at 25±2°C, umbonate, thinly hairy at the center, flat or submerged at the periphery, entire margin; from surface, white, orange gray; from reverse, orange white or brownish orange.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park (water salinity 15 ppt), on dead submerged stems of *Suaeda maritima*, 8 November 2024, R. Asghari, S7S34 (MFLU 26-0072, holotype); ex-type culture (MFLUCC 26-0076).

Notes – The new species, *Torpedospora* sp. (MFLUCC 26-0076) is recovered as a sister taxon to *T. mangrovei* (NBRC 105264) in the LSU–SSU phylogeny, with high support (98% ML/1.00 BPP). Morphological comparison with *T. mangrovei* is not feasible, as it is known from its asexual morph (Abdel-Wahab et al. 2010). The new species is morphologically close to *T. yanbuensis*, sharing papillate immersed ascomata, persistent asci with apical thickening, and septate ellipsoidal ascospores, but differs in having an unbranched neck with apical hyphae, and lacking ascospore appendages (Abdel-Wahab et al. 2020). Sequence comparisons further support its novelty, with 7.3% (34/465, with gaps for ITS), and 1.9% (17/881, with gaps for LSU) divergence from *T. mangrovei* (NBRC 105264).



Note a Decaying twig of the host. b Appearance of colony on host. c Vertical section of ascoma. d Section through the neck. e Section through peridium. f, g Asci and paraphyses. g paraphyses. h, i Ascospores. j Culture on PDA (above and below). Scale bars: b = 250 μ m, c = 150 μ m, d = 50 μ m, e = 10 μ m f–i = 20 μ m.

Figure 5.73 *Torpedospora* sp. (S7S34)

Xylariomycetidae O.E. Erikss & Winka

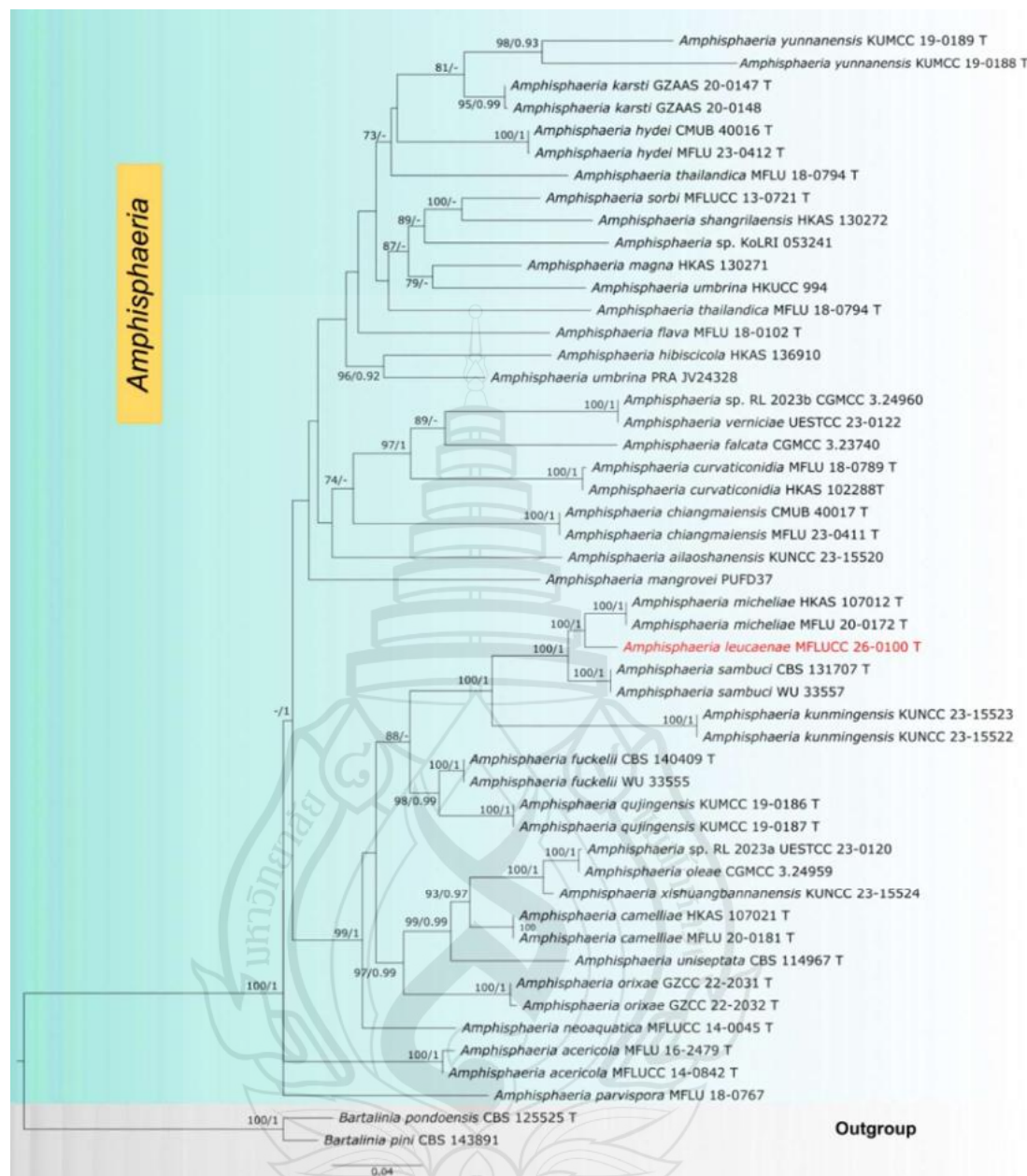
Amphisphaeriales D. Hawksw. & O.E. Erikss.

Amphisphaeriaceae G. Winter

Amphisphaeriaceae was established by Winter (1887) and is a family of ascomycetes within the order *Xylariales*. *Amphisphaeriaceae* comprises two genera, *Amphisphaeria* and *Labridella*, with around 10 species (Hyde et al. 2024). Species in this family are predominantly saprobic on plant leaves, twigs, and wood in terrestrial, freshwater, and marine habitats, and occasionally hemibiotrophic or necrotrophic (Senanayake et al. 2015; Hyde et al. 2020d; Samarakoon et al. 2020, 2024). The sexual morph produces perithecial, immersed ascomata that become raised at maturity, with a multilayered peridium, filamentous and septate paraphyses, cylindrical asci, and ellipsoidal to fusiform, 1-septate, light to dark brown ascospores. The asexual morph is coelomycetous, forming hyaline, unicellular conidia that are elongate to fusiform (Maharachchikumbura et al. 2016; Hyde et al. 2020d).

Amphisphaeria Ces. & De Not.

Amphisphaeria is the type genus of *Amphisphaeriaceae* and was established by Cesati and De Notaris (1863), typified with *Amphisphaeria umbrina* (based on *Sphaeria umbrina*). The sexual morph produces immersed, ostiolate ascomata, with or without a clypeus, filamentous and septate paraphyses, cylindrical unitunicate 8-spored asci with J⁺ or J⁻ apical rings, and ellipsoid to fusiform, 1–3-septate, light brown to dark brown ascospores. The asexual morph exhibits both hyphomycetous and coelomycetous structures (Samarakoon et al. 2020, 2022). *Amphisphaeria* species are mainly saprobic on plants (Samarakoon et al. 2020; Tun et al. 2025), with *A. culmicola* reported from marine habitats (Jones et al. 2019). Here, we provide the phylogenetic tree for the genus and introduce a novel *Amphisphaeria* species from coastal plants in Thailand.



Note The tree is rooted to *Bartalinia pondoensis* (CBS 125525) and *Bartalinia pini* (CBS 143891). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.74 Phylogram generated from the ML analysis based on the combined combined LSU, ITS, *rpb2* and TUB sequence alignments of *Amphisphaeria*

Amphisphaeria leucaenae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.75

Etymology – Referring to *Leucaena leucocephala*, the host from which the fungus was collected.

Saprobic on dead stems of *Leucaena leucocephala*. **Asexual morph:** Undetermined. **Sexual morph:** *Ascomata* 170–250 × 300–350 µm ($\bar{x}$ = 220 × 315 µm, n = 15), solitary, scattered, immersed, raising the host surface, with or without a longitude slit on the host tissue, oblate, black, ostiole central, papillate, 90–150 µm ($\bar{x}$ = 120 µm, n = 15), periphysate. *Peridium* 7.5–20 µm ($\bar{x}$ = 12 µm, n = 20), outer layer dense, dark reddish brown, *textura angularis*, thicker and more pigmented around the neck, inner layer hyaline, *textura angularis*. *Paraphyses* 2.5–4.5 µm wide ($\bar{x}$ = 3.2 µm, n = 20), cylindrical, tapering toward the apex, straight or flexuous, unbranched, septate, constricted at septa, guttulate. *Asci* 91–120 × 7–9.5 µm ($\bar{x}$ = 108 × 8 µm, n = 15), 8-spored, cylindrical, short pedicillate, unitunicate, round apex, with J+ triangular, apical apparatus. *Ascospores* 15–16.5 × 5.5–6.5 µm ($\bar{x}$ = 15.5 × 6 µm, n = 30), overlapping uniseriate, oblong or fusiform, straight to slightly curved, 1-septate, guttulate, hyaline, subhyaline to pale yellow, smooth-walled.

Culture characteristics – Colonies on PDA reaching 3.5 cm diam. after one month at 25±2°C, umbonate, powdery, cottony, undulate, fimbriate, reddish brown pigmentation in culture; from surface, yellowish gray; from reverse, violate brown.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Sam Roi Yot, on dead dry (aerial) stems of *Leucaena leucocephala*, 23 May 2023, R. Asghari, LL14 (MFLU 26-0071, holotype); ex-type culture (MFLUCC 26-0100).

Notes – Based on the multi-gene phylogenetic analyses from LSU, ITS, *rpb2*, and *tub2* sequence data, *Amphisphaeria leucaenae* (MFLUCC 26-0100) formed a sister lineage to *Am. micheliae* (HKAS 107012 and MFLU 20-0172) with 100% ML/1 BPP support. Morphologically, *Am. leucaenae* is similar to the holotype of *Am. micheliae* in having papillate immersed ascomata with periphysate ostiole, septate paraphyses, cylindrical asci, with round apex and 1-septate oblong or fusiform guttulate ascospores (Samarakoon et al. 2020). However, it differs in having raised surface of the host tissue with longitude slit, reddish brown pigmentation in culture media and triangular apical ring unlike discoid apical ring in *Am. micheliae* (Samarakoon et al. 2020).

Amphisphaeria leucaenae showed 2.4% (11/451, with gap), 0.5% (4/879, with gap), 3.5% (31/887, without gaps) base pair differences with *Am. micheliae* (HKAS 107012, holotype) in ITS, LSU and *rpb2*, respectively. Based on morphological and molecular evidence, *Am. leucaenae* is introduced as a novel species, collected on dead stems of *Leucaena leucocephala*, in Thailand.



Note a Decaying twig of the host. b Appearance of colony on host. c Vertical section of ascoma. d Section through ostiole. e Section through peridium. f Asci and paraphyses. g paraphyses. h Ascus. i Apical apparatus of an ascus in Melzer's reagent. j Ascospores. k Germinated ascospore. l, m Culture on PDA (above and below). Scale bars: b = 200 μ m, c = 100 μ m, d = 50 μ m, e = 10 μ m, f–i = 30 μ m, j, k = 15 μ m.

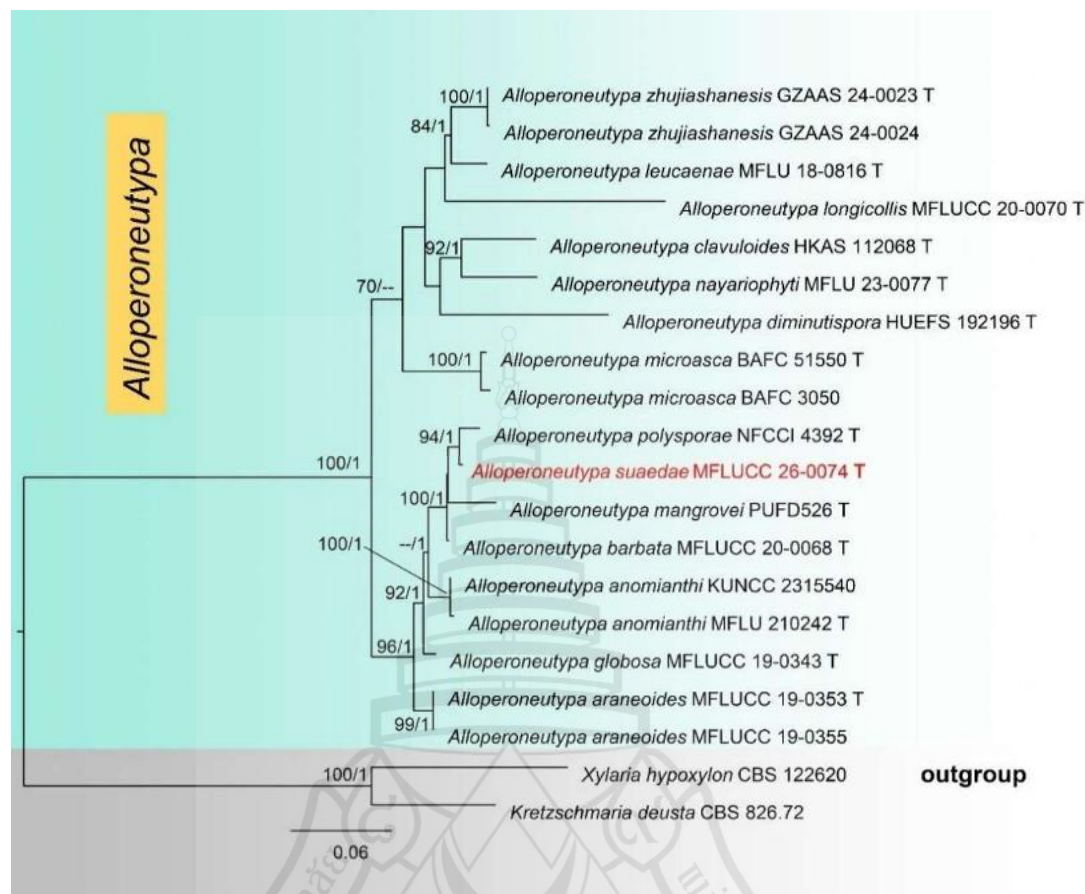
Figure 5.75 *Amphisphaeria leucaenae* (MFLU LL14, holotype)

Xylariales Nannf*Diatrypaceae* Nitschke

Diatrypaceae is a large family within *Xylariales*, comprising 31 genera (Hyde et al. 2024). Members of this family are ecologically diverse, occurring in terrestrial and aquatic habitats as saprobes, endophytes, or pathogens on a wide range of woody plants and crops (Acero et al. 2004; Afshari et al. 2023, 2025a). Their ability to produce extracellular ligninolytic enzymes facilitates wood decomposition (Mehrabi et al. 2015). Sexual morphs typically form dark stromata with perithecial ascomata, 8-spored or polysporous asci, and allantoid ascospores (Hyde et al. 2020d). Asexual morphs are coelomycetous or hyphomycetous, producing conidia in pycnidial, acervular, or synnematus structures (Seifert et al. 2011; Li et al. 2020; Hyde et al. 2020d). Overlapping morphological characters and limited type sequence data have rendered the classification of *Diatrypaceae* poorly resolved and problematic (Wijayawardene et al. 2022b; Hyde et al. 2024). Dissanayake et al. (2025) investigated the taxonomy of *Diatrypaceae* by combining morphology, herbarium specimens, and multi-gene phylogenetics to refine the generic boundaries within the family.

Alloperoneutypa Q.J. Shang, K.D. Hyde & Jian K. Liu

Alloperoneutypa was introduced by Dissanayake et al. (2025) and typified with *Alloperoneutypa longicollis*, with 13 accepted species. The genus is known from its sexual morph, producing ascomata immersed in stromatic or host tissues, with a thick-walled, multilayered peridium, branched septate paraphyses, 8-spored asci with a J–apical ring, and oblong to allantoid, unicellular, pale yellowish ascospores. Here, we introduce a novel species, *Alloperoneutypa suaedae*, collected from coastal halophytes in Thailand, based on the asexual morph.



Note The tree is rooted to *Xylaria hypoxylon* (CBS 122620) and *Kretzschmaria deusta* (CBS 826.72). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.76 Phylogram generated from the ML analysis based on the combined combined ITS and TUB sequence alignments of *Diatrypaceae*

Alloperoneutypa suaedae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.77

Etymology – referring collection of the fungus from *Suaeda maritima*.

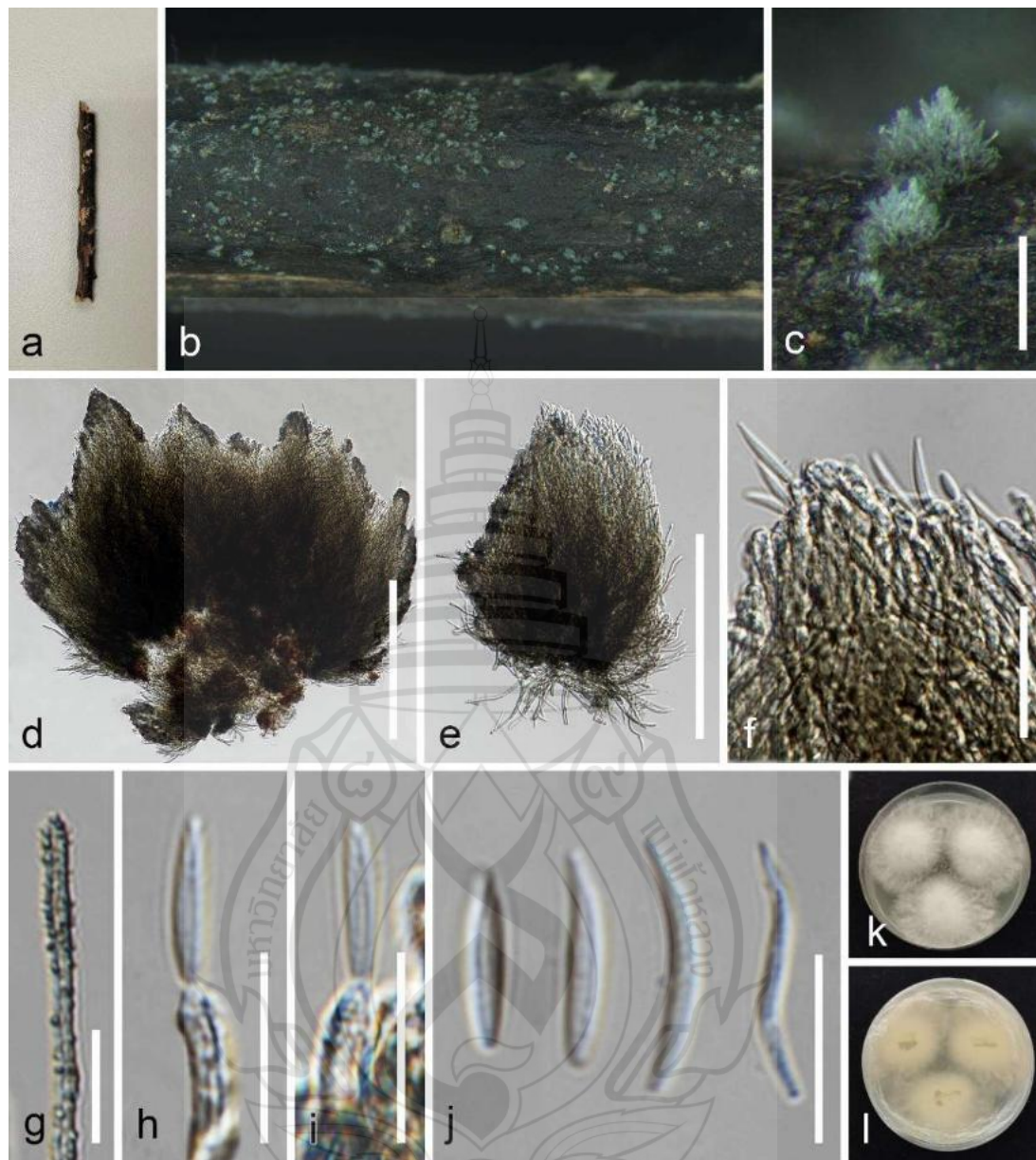
Saprobic on dead aerial stems of *Suaeda maritima*. **Asexual morph:** Colonies on natural substrate, superficial, effuse to compact, green. *Sporodochia* superficial, consisting of numerous interwoven cylindrical, flexuous, branched, septate, thick-walled, verrucose, dark green, or greenish brown hyphae. *Conidiophores* 1.5–3.5 µm diam ($\bar{x}$ = 2 µm, n = 30), flexuous, branched, septate, thick-walled, verrucose, greenish

brown, paler toward the apex. *Conidiogenous cells* $5\text{--}28 \times 1.5\text{--}3 \mu\text{m}$ ($\bar{x} = 17.5 \times 2 \mu\text{m}$, $n = 10$), blastic, cylindrical, thick-walled, verrucose, terminal, pale brown to subhyaline. *Conidia* $10.5\text{--}19.5 \times 1.5\text{--}2.5 \mu\text{m}$ ($\bar{x} = 15 \times 1.8 \mu\text{m}$, $n = 15$), solitary, fusiform, straight or curved, tapering toward the apex, aseptate, hyaline. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diam. after one week at $25\pm 2^\circ\text{C}$, convex, fluffy, with aerial mycelia, circular, filamentous margin; from above, white; from below, yellow white.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park, on dead aerial stems of *Suaeda maritima*, 6 April 2024, R. Asghari, S6D91 (MFLU 26-0069, holotype); ex-type culture (MFLUCC 26-0074).

Notes – Phylogenetic reconstruction based on ITS, *tub2*, and LSU sequences places strain MFLUCC 26-0074 (*Alloperoneutypa suaedae*) in a clade with *A. polysporae* (NFCCI-4392, ex-type), supported by 94% ML/1.00 BPP. Morphologically, *A. suaedae* is not comparable with *A. polysporae*, as the latter was described based on its sexual morph, characterized by deeply immersed ascomata and polysporous asci (Dayarathne et al. 2020a). Both taxa are associated with *Suaeda* hosts in mangrove ecosystems, but differ in host species and geographic origin (Dayarathne et al. 2020a). The asexual morph of *Alloperoneutypa* remains unknown. However, the present collection resembles species of the closely related genus *Peroneutypa*, which produce pycnidial conidiomata with branched conidiophores arising from interwoven hyphae or pseudoparenchymatous cells, and lunate to filiform, aseptate, hyaline conidia with a flattened base and blunt apex. Although pycnidia were not observed, our strain shows comparable features, including interwoven hyphae and curved, aseptate, hyaline conidia with a flattened base and blunt apex (Dissanayake et al. 2025). Sequence divergence from *A. polysporae* is 1.9% in ITS (10/525) and 1.2% in LSU (10/808), including gaps. Accordingly, *Alloperoneutypa suaedae* is proposed as a new species and represents the first documented asexual morph of the genus, from dead aerial stems of *Suaeda maritima* in Thailand. Additional data are needed to clarify sexual–asexual connections within the genus.



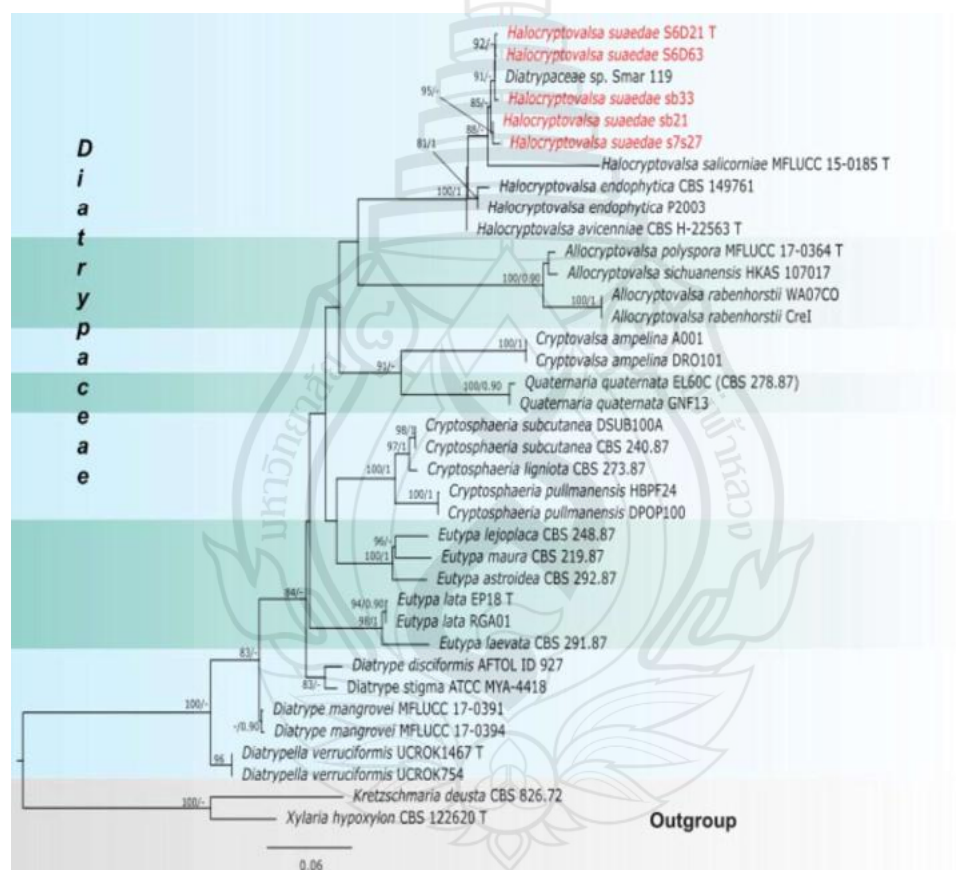
Note a Decaying twig of the host. b, c Colonies on the host surface. d, e Sporodochia. f Interwoven hyphae. g hyphae. h, i Conidiogenous cells and conidia. j Conidia. k, l Colony on PDA (above and reverse). Scale bars: c = 250 μ m, d, e = 200 μ m, f = 20 μ m, g = 50 μ m, h–j = 10 μ m.

Figure 5.77 *Alloperoneutypa suaedae* (S6D91, holotype)

Halocryptovalsa Dayar. & K.D. Hyde

Halocryptovalsa was introduced by Dayarathne et al. (2020b), to accommodate *Halocryptovalsa avicenniae* and *H. salicorniae*. The type species *H. avicenniae* was

isolated from a decaying mangrove tree, *Avicennia marina*, in Saudi Arabia, and the latter was collected from the salt marsh host *Salicornia* sp. in Thailand (Dayarathne et al. 2020b; Calabon et al. 2021). In addition to these two saprobic species, a third species, *H. endophytica*, was collected as an endophyte in the roots of the salt marsh plant *Salicornia patula* in Spain (Crous et al. 2023). Poorly developed stromata with long ascomatal necks and being deeply immersed in the host tissue are distinct characters of *Halocryptovalsa*. Asci are cylindrical and poly-spored, with hyaline or yellowish-brown to brown allantoid spores (Dayarathne et al. 2020b). In this study we introduced a new species, frequently observed on *Suaeda maritima* in Thailand.



Note The tree is rooted to *Xylaria hypoxylon* (CBS 122620) and *Kretzschmaria deusta* (CBS 826.72). Bootstrap values for ML equal to or greater than 70% and BPP values greater than 0.90 are labelled on the nodes. The newly described strains are in red.

Figure 5.78 Phylogram generated from the ML analysis based on the combined ITS, TUB and LSU sequence alignments of *Halocryptovalsa*

Halocryptovalsa suaedae R. Asghari, Phukhams., E.B.G. Jones & K.D. Hyde, sp. nov. Fig. 5.79

Etymology – referring to *Suaeda*, the host from which the fungus was collected.

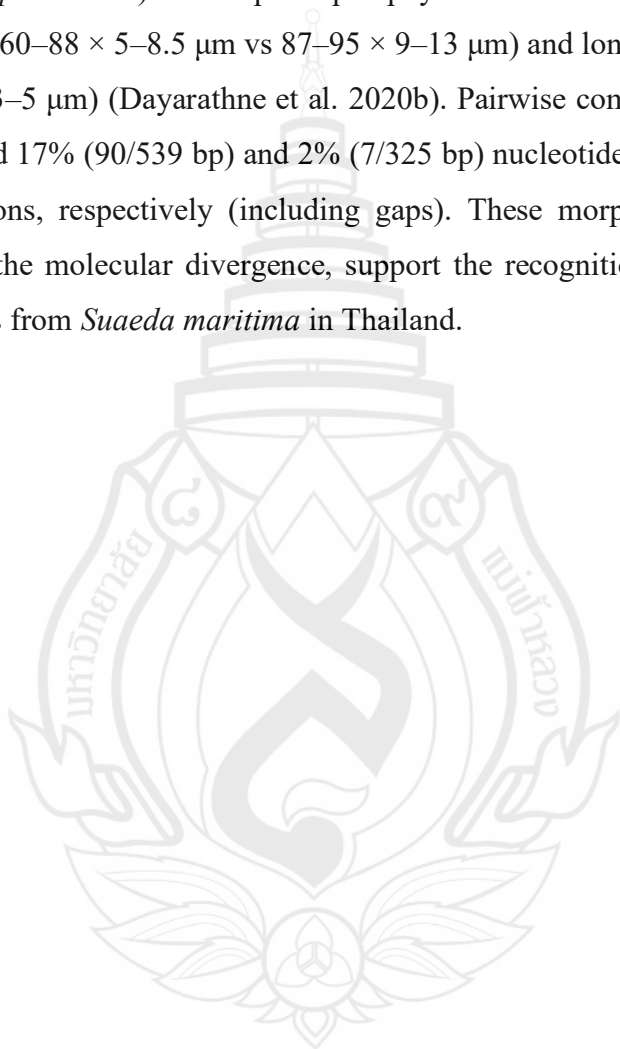
Saprobic on dead stems of *Suaeda maritima*. **Asexual morph:** Undetermined.

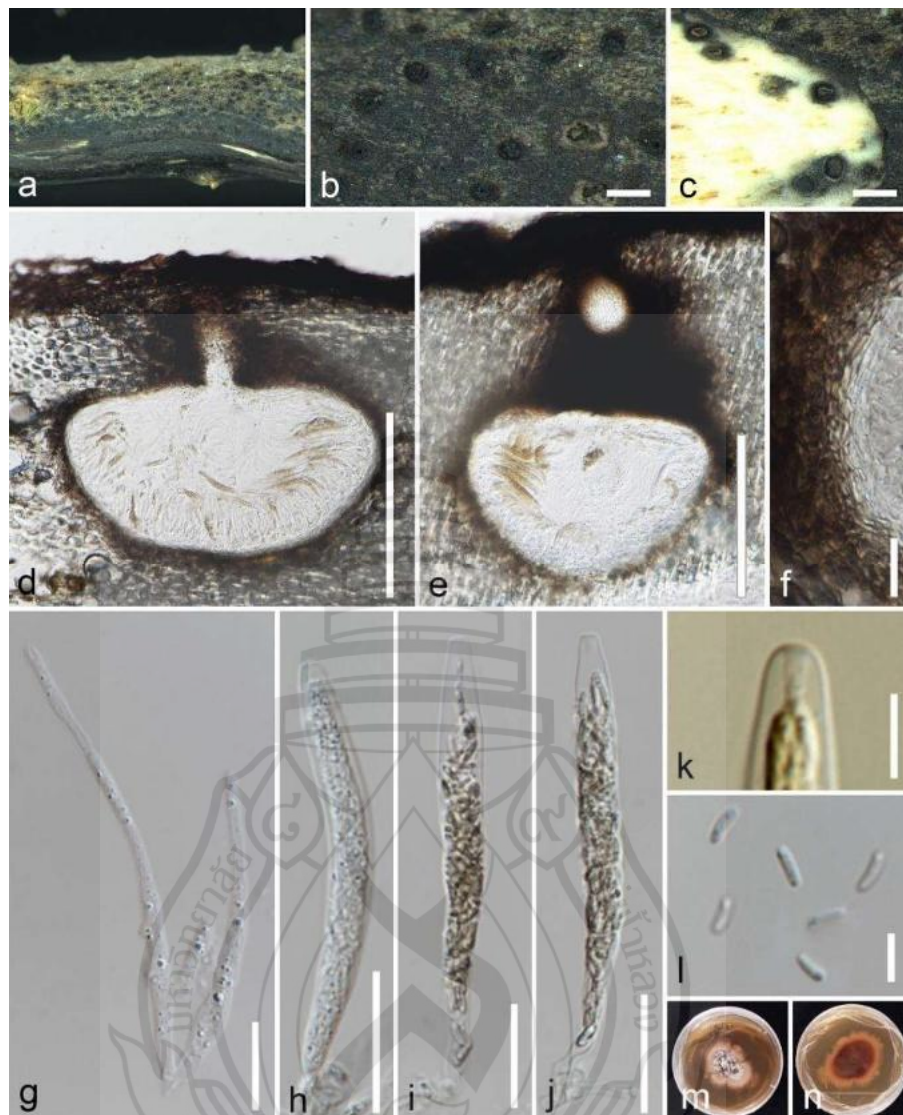
Sexual morph: *Stromata* poorly developed, black, immersed, erumpent, visible on the host surface with raised wrinkled black spots and protruding ostiolate necks, substrate around and between ascomata necrotic. *Ascomata* 250–350 × 200–250 µm ($\bar{x}$ = 300 × 230 µm, n = 15), solitary or in small group, immersed, globose, subglobose to oval, black, ostiole central, papillate, 90–150 µm ($\bar{x}$ = 120 µm, n = 15), periphysate. *Peridium* 7.5–22.5 µm ($\bar{x}$ = 15 µm, n = 20), outer layer thin, brown to dark brown, with polygonal cells, fusing to the host tissue, thicker and more pigmented around the neck, inner layer hyaline with 2–6 cell layers, *textura porrecta*. *Paraphyses* 1.8–4.5 µm wide ($\bar{x}$ = 2.7 µm, n = 20), longer than asci, cylindrical, wider at the base, tapering toward the apex, straight or flexuous, branched or unbranched, septate, constricted at the basal septa. *Asci* 60–88 × 5–8.5 µm ($\bar{x}$ = 71.5 × 6.5 µm, n = 15), multi-spored, cylindrical, short pedicillate, unitunicate, flat apex, with J-, cylindrical, conspicuous apical apparatus. *Ascospores* 3.8–8 × 1–1.7 µm ($\bar{x}$ = 5.2 × 1.5 µm, n = 30), oblong to allantoid, rounded ends, aseptate, guttulate, hyaline to subhyaline, with or without a longitudinal germ slit.

Culture characteristics – Colonies on PDA reaching 2.5 cm diam. after one month at 25±2°C, flat, umbonate, slightly folded, undulate; from surface, white, reddish gray, grayish brown at the margin; from reverse, brownish orange, pale orange at the margin.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, Pranburi Forest Park, on dead dry stems of *Suaeda maritima*, 6 April 2024, R. Asghari, S6d21 (MFLU 26-0064, holotype); ex-type culture (MFLUCC 26-0070); *ibid.*, S6d63 (MFLU 26-0065); living culture (MFLUCC 26-0071); *ibid.*, (water salinity 15 ppt), on dead submerged stems of *Suaeda maritima*, 8 November 2024, R. Asghari, S7S27 (MFLU 26-0066,); living culture (MFLUCC 26-0072); *ibid.*, Sam Roi Yot National Park (water salinity 28 ppt), on dead submerged stems of *Suaeda maritima*, 1 December 2023, R. Asghari, SB33 (MFLU 26-0067); living culture (MFLUCC 26-0073); *ibid.*, SB21 (MFLU 26-0068); living culture (MFLUCC 26-0152).

Notes – The five strains of *Halocryptovalsa suaedae* included in this study form a sister clade to *H. salicorniae*. The two species share similar morphological characteristics, including papillate, immersed ascomata, multi-spored asci with a flat apex and a J-, cylindrical apical ring, and unicellular, guttulate ascospores. However, *H. suaedae* can be distinguished by having a peridium with an inner layer of elongated cells (*textura prismatica*) and septate paraphyses. In addition, it has shorter and narrower asci ($60\text{--}88 \times 5\text{--}8.5 \mu\text{m}$ vs $87\text{--}95 \times 9\text{--}13 \mu\text{m}$) and longer, oblong ascospores ($3.8\text{--}8 \mu\text{m}$ vs $3\text{--}5 \mu\text{m}$) (Dayarathne et al. 2020b). Pairwise comparison of the ex-type strains revealed 17% (90/539 bp) and 2% (7/325 bp) nucleotide differences in the ITS and *tub2* regions, respectively (including gaps). These morphological distinctions, together with the molecular divergence, support the recognition of *H. suaedae* as a distinct species from *Suaeda maritima* in Thailand.





Note a–c Appearance of colony on host. d, e Vertical section of ascomata. f Section through peridium. g Paraphyses. h–j Asci. k Apical apparatus of an ascus. l Ascospores. m, n Culture on PDA (above and below). Scale bars: b = 500 μ m, c = 750 μ m, d, e = 150 μ m, f–j = 20 μ m, k, l = 5 μ m.

Figure 5.79 *Halocryptovalsa suaedae* (S6D21, holotype)

Zygosporiaceae J.F. Li, Phookamsak & K.D. Hyde

Zygosporiaceae was introduced by Li et al. (2017) to accommodate the type genus *Zygosporium*, based on *Z. oscheoides*, *Z. minus*, and *Z. gibbum*. It forms a well-supported monophyletic lineage within the *Xylariales* based on phylogenetic analyses of combined LSU and ITS sequence data. The family was later expanded with the

Zygosporium Mont.

Phylogenetic tree showing the relationships between various *Zygosporium* species and an outgroup. The tree is rooted with *Xylaria arbuscula* CBS 126416 and *Iodosphaeria tongrenensis* MFLU 15-0393 as the outgroup. The scale bar represents 0.03 substitutions per site.

Species and Strains (from top to bottom):

- Zygosporium masonii* CBS 138.71
- Zygosporium masonii* CBS 557.73
- Zygosporium masonii* MFLUCC 26-0075
- Zygosporium pseudomasonii* CPC 37503
- Zygosporium gibbum* CBS 137306
- Zygosporium pseudogibbum* CBS 143503
- Zygosporium mycophilum* CBS 894.69
- Zygosporium oscheoides* MFLUCC 14-0402
- Zygosporium minus* HKAS99625
- Zygosporium oscheoides* CBS 195.79
- Zygosporium cymodoceae* FMR 19851
- Zygosporium chartarum* CBS 384.53
- Xylaria arbuscula* CBS 126416
- Iodosphaeria tongrenensis* MFLU 15-0393

Bootstrap values (from top to bottom):

- 99/1
- 85/-
- 98/1
- 92/0.99
- 86/0.98
- 99/1
- /0.95
- 77/0.90
- 96/1
- 99/1
- 2*/

Scale bar: 0.03

Figure 5.80 Phylogram generated from the ML analysis based on the combined combined LSU sequence alignments of *Zygosporium*

Zygosporium masonii S. Hughes, Fig. 5.81

Index Fungorum number: IF308038; Facesoffungi number: FoF06496

Saprobic on decaying wood submerged in seawater. **Asexual morph:** *Colonies* on natural substrate, effuse to compact, black with flossy conidia. *Mycelium* mostly superficial, consisting of cylindrical, sinuous, branched, septate, thick-walled, hyaline to brown hyphae. *Conidiophores* $85\text{--}113 \times 3.5\text{--}5.5 \mu\text{m}$ ($\bar{x} = 100 \times 4.7 \mu\text{m}$, $n = 20$) (including hyaline apical hypha), macronematous, mononematous, erect, straight or slightly flexuous, unbranched, brown, 1–6-septate, with lateral rostrum vesicles in the middle cells, a long hyaline apical hypha with swollen apex at the apices of the setiform conidiophores $29\text{--}41 \mu\text{m}$ height ($\bar{x} = 34$, $n = 20$). *Conidiogenous cells* $7.5\text{--}12.5 \times 4.5\text{--}9.5 \mu\text{m}$ ($\bar{x} = 9.5 \times 6 \mu\text{m}$, $n = 20$), phialidic, arising from the vesicles, ovoid, upwardly curved, smooth, hyaline to pale brown. *Conidia* $10.5\text{--}18.5 \times 5.5\text{--}8.5 \mu\text{m}$ ($\bar{x} = 14 \times 7 \mu\text{m}$, $n = 20$), solitary, subglobose to oval, aseptate, hyaline, verruculose, granules, thick-walled. **Sexual morph:** Undetermined.

Culture characteristics – Colonies on PDA reaching 2 cm diam. after one month at $25 \pm 2^\circ\text{C}$, umbonate, submerged margin, medium dense, undulate; from surface, white, yellowish gray; from reverse, pale yellow.

Material examined – Thailand, Prachuap Khiri Khan Province, Pranburi, on decaying wood submerged in seawater (water salinity 19 ppt), 25 October 2022, KD. Hyde, R10C (MFLU 26-0070); living culture (MFLUCC 26-0075).

Notes – In the LSU phylogeny, the new isolate (MFLUCC 26-0075) clustered with *Zasmidium masonii* (CBS 557.73 and CBS 138.71) with strong support (99% ML/1.00 BPP). Its morphology is consistent with *Z. masonii*, characterized by erect, unbranched conidiophores with terminal vesicles and hyaline, oval conidia (Hughes 1951). This isolate is therefore identified as *Z. masonii*, representing a new collection from submerged marine wood in Thailand.



Note a Decaying twig of the host. b Colony on the host surface. d–f Conidiophores, conidiogenous cells and conidia. e–h Conidia. i Germinated conidium. j, k Colony on PDA (above and reverse). Scale bars: b = 200 μm , c, d = 20 μm , e, g = 10 μm , f = 5 μm , i = 50 μm .

Figure 5.81 *Zygosporium masonii* (R10C)

5.2.2 Taxonomic Classification and Distribution of Fungi from Marine Based Habitats in Thailand

In this study, we investigated saprobic fungal communities in marine-based habitats, based on fungi collected and isolated in Thailand. This study focused only on culturable isolates to enable the integration of both morphological observations and molecular data for accurate fungal identification, an approach widely used in modern fungal taxonomy and diversity studies (Yasanthika et al. 2022; Lu et al. 2025; Sun et al. 2025), including marine fungal diversity (Burgaud et al. 2009; Henríquez et al. 2014; Li et al. 2023; Abreu et al. 2026).

A total of 117 strains, including 53 strains from decaying wood submerged in seawater, and 64 strains from seashore plants, which includes both terrestrial and salt marsh plants were analyzed.

These 117 strains represent 80 species distributed across 61 genera, 38 families, and 19 orders in *Ascomycota*. A polyphasic taxonomic approach was employed for species delineation. Seventy species were identified to the species level using a combination of detailed morphological characterization and multi-gene phylogenetic analyses. For the remaining 10 taxa, identification was based on integrating morphological characteristics and ITS sequence similarity (BLAST) at the genus level, supported by the available morphological and molecular data.

With the exception of one species, *Nia singaporensis* (*Cyphellopsidaceae*, *Agaricales*) in *Basidiomycota* from decaying wood, the analysis showed that all strains belonged to *Ascomycota* and were distributed across three classes (Fig. 5.82): for decaying wood: 13 *Dothideomycetes*, 38 *Sordariomycetes*, and two *Eurotiomycetes*; and for seashore plants: 36 *Dothideomycetes*, 25 *Sordariomycetes*, and three *Eurotiomycetes*.

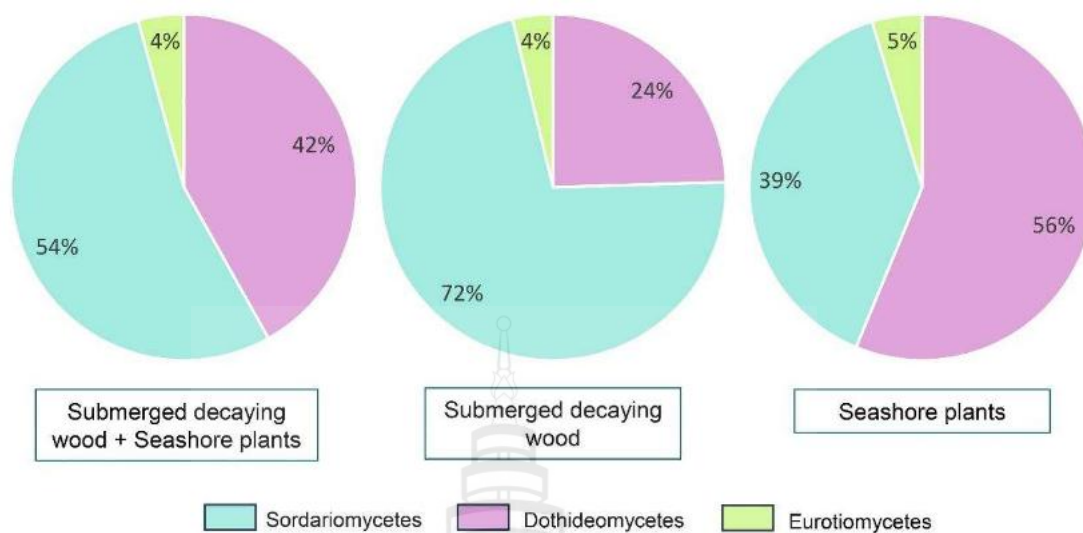


Figure 5.85 Distribution of saprobic fungi from submerged decaying wood and seashore plants in Thailand, in different classes

Fungi obtained from submerged decaying wood belonged to 12 orders, with *Microascales* being the dominant order (25 strains), followed by *Pleosporales* and *Hypocreales*, each represented by seven strains. Fungi isolated from seashore plants were distributed across 17 orders, among which *Pleosporales* was the most abundant (25 strains), followed by *Xylariales* (7 strains) and *Hypocreales* (5 strains) (Fig. 5.83).

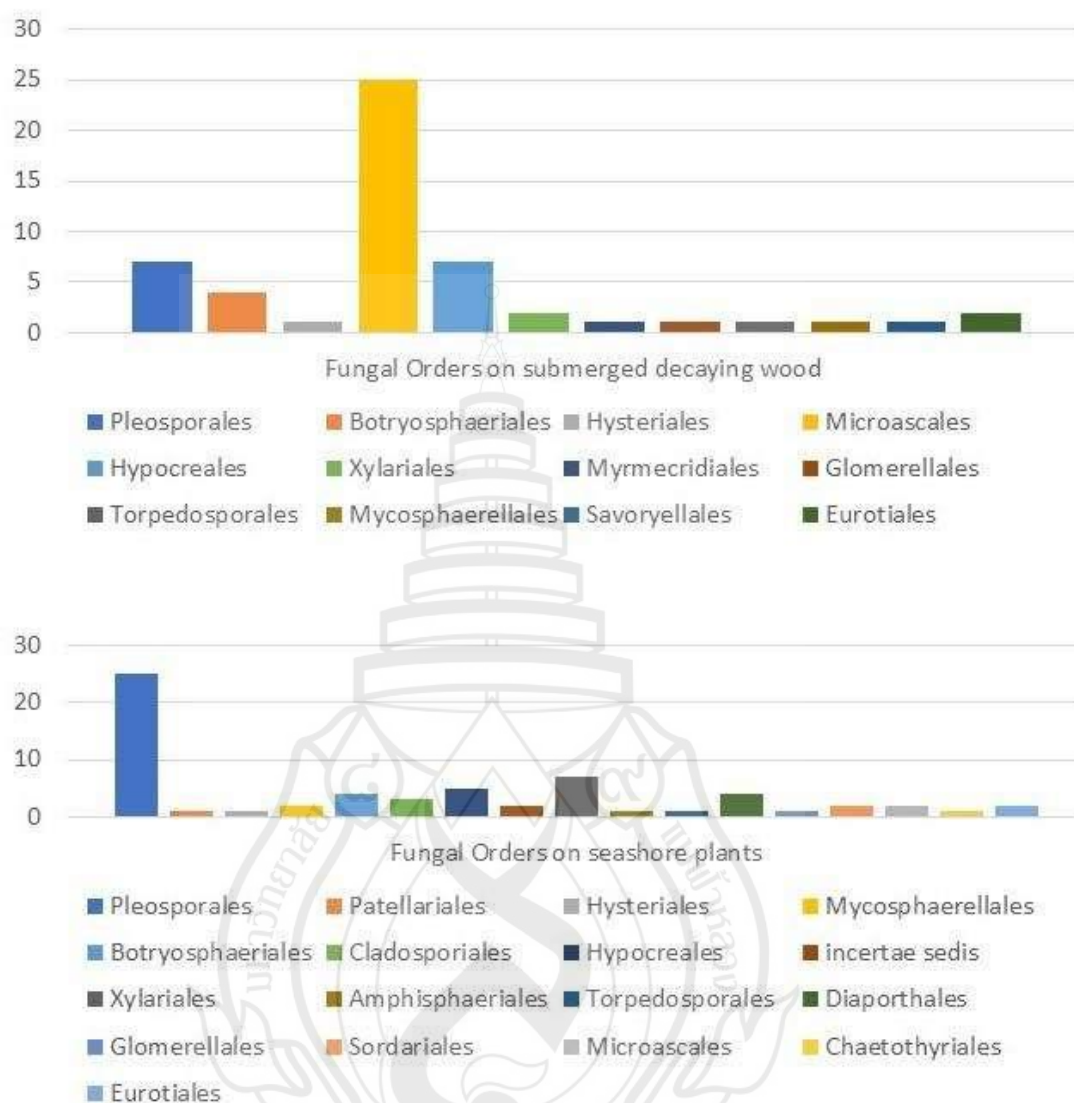


Figure 5.83 Distribution of saprobic fungi from submerged decaying wood and seashore plants in Thailand, in different orders (X-axis: fungal orders; Y-axis: number of strains)

From 53 strains obtained from decaying wood, the isolates were distributed across 21 families, with *Halosphaeriaceae* being the most abundant family (23 strains), followed by *Pleosporaceae* (5 strains) and *Botryosphaeriaceae* (4 strains). From 64 strains obtained from seashore plants, the isolates belonged to 26 families, with *Phaeosphaeriaceae* having the highest number of strains (8), followed by *Neocamarosporiaceae* and *Diatrypaceae* (7 strains each) (Fig. 5.84).

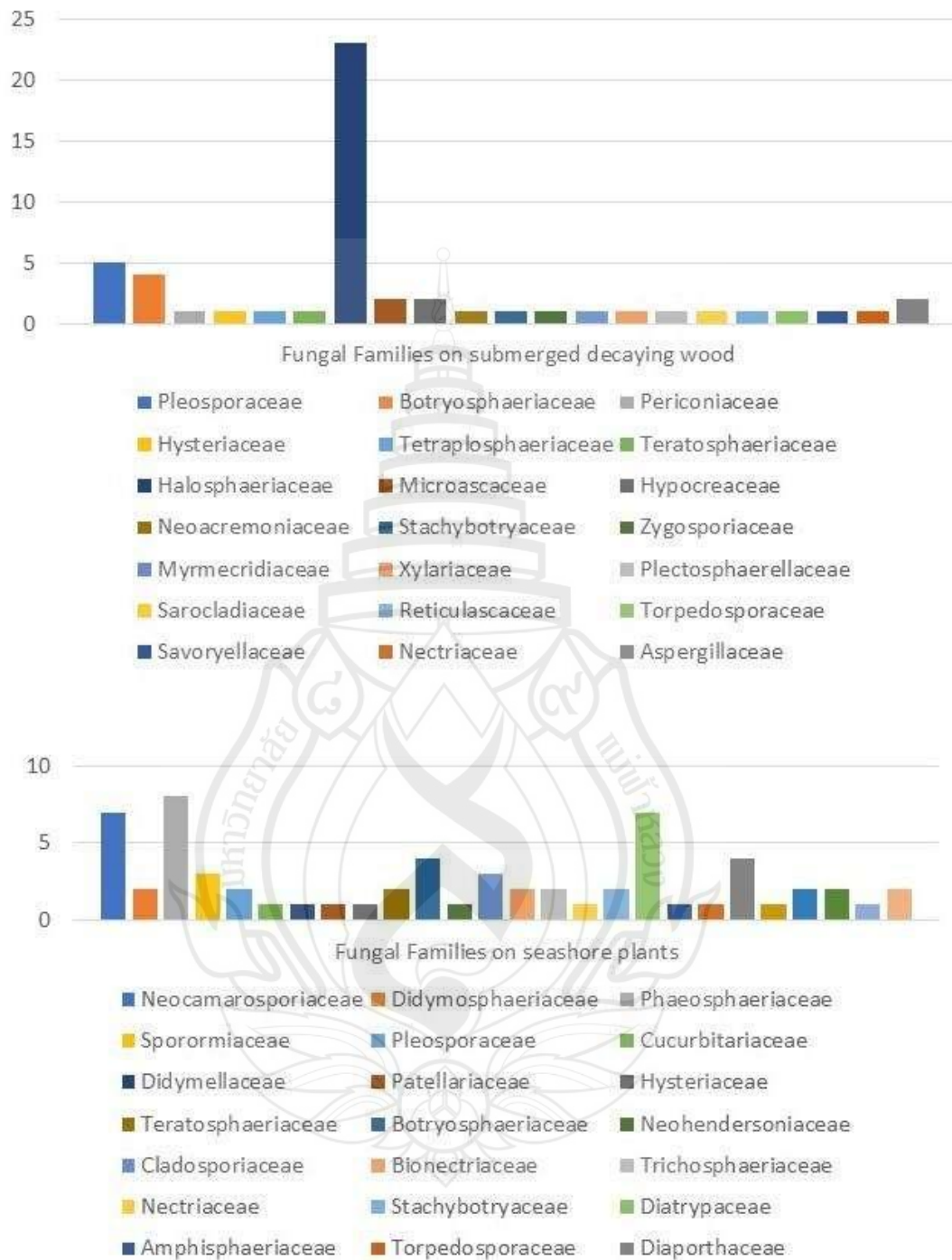


Figure 5.84 Distribution of saprobic fungi from submerged decaying wood and seashore plants in Thailand, in different families (X-axis: fungal families; Y-axis: number of strains)

Marine fungi from decaying wood belonged to 31 genera. *Corollospora* (*Halosphaeriaceae*) had the highest number of strains (8 strains), followed by *Lasiodiplodia* (*Botryosphaeriaceae*) and *Arenariomyces* (*Halosphaeriaceae*) with four strains, and *Ceriosporopsis* (*Halosphaeriaceae*) and *Alternaria* (*Pleosporaceae*), each represented by three strains. Fungi from seashore plants belonged to 35 genera, of which *Neocamarosporium* (*Neocamarosporiaceae*) was the most abundant genus (7 strains), followed by *Halocryptovalsa* (*Diatrypaceae*) (5 strains). *Lasiodiplodia* (*Botryosphaeriaceae*), and *Diaporthe* (*Diaporthaceae*) were each represented by four strains.

Overall, ten fungal orders were shared between seashore plant fungi and marine fungi isolated from submerged wood, including. *Botryosphaeriales*, *Eurotiales*, *Glomerellales*, *Hysteriales*, *Hypocreales*, *Microascales*, *Mycosphaerellales*, *Pleosporales*, *Torpedosporales*, and *Xylariales*. Within these orders, nine families occurred in both habitats, namely *Aspergillaceae*, *Botryosphaeriaceae*, *Halosphaeriaceae*, *Hysteriaceae*, *Nectriaceae*, *Pleosporaceae*, *Stachybotryaceae*, *Teratosphaeriaceae*, and *Torpedosporaceae*. At the genus level, five genera were common to both seashore plants and submerged wood, comprising *Aspergillus*, *Hortaea*, *Lasiodiplodia*, *Rhytidhysterion*, and *Torpedospora* (Fig. 5.85). Notable overlap at the species level was limited to *Hortaea werneckii* and *Rhytidhysterion bruguiera* being recovered from both submerged wood and seashore plant substrates.

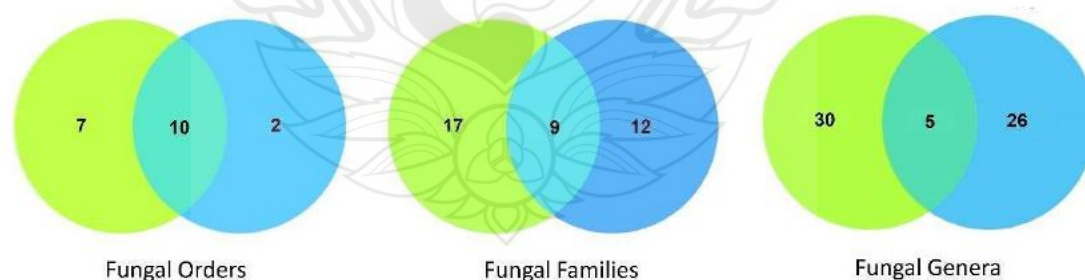


Figure 5.85 Overlapping fungal orders, families and genera between saprobic fungi from submerged decaying wood (green circles) and seashore plants (blue circles) in Thailand

Among fungi from submerged wood, 39% were sexual morphs and 61% were asexual morphs (88% hyphomycetous and 12% coelomycetous), with most asexual morphs collected at salinity levels below 20 ppt.

Of the fungi obtained from seashore plants, 18 isolates were recovered from substrates submerged in marine water, and 46 from terrestrial or aerial plant parts. Among submerged seashore plants isolates, 61% were sexual morphs, and 39% (71% hyphomycetes and 29% coelomycetes) asexual morphs. In contrast, fungi isolated from aerial seashore plants substrates were predominantly asexual (74%), 38% hyphomycetes and 62% coelomycetes, while sexual morphs comprised 26%. Considering all submerged strains from both decaying wood and seashore plants, 46% were sexual morphs and 54% were asexual morphs (Fig 5.88).

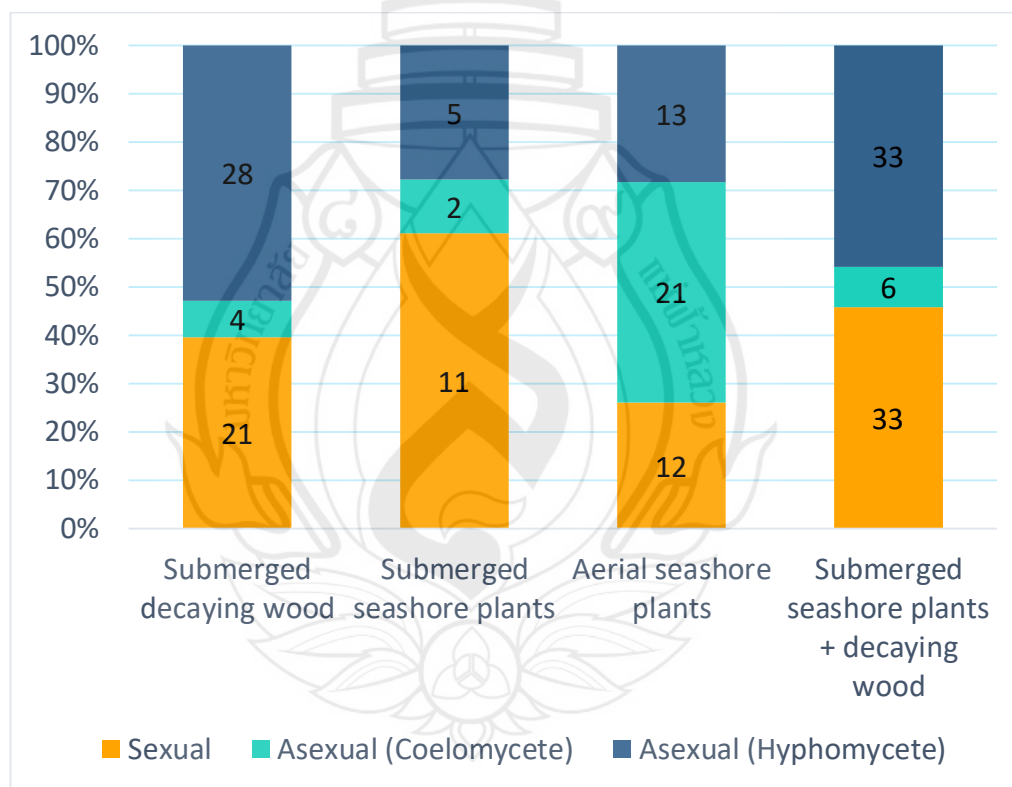


Figure 5.86 Distribution of sexual, asexual morphs of saprobic fungi from submerged decaying wood and submerged and aerial seashore plants in Thailand (X-axis: substrate types; Y-axis: percentage of strains)

Among fungi isolated from submerged decaying wood, 33 strains were obtained from salinity below 20 ppt. These strains were distributed across 10 orders, 16 families, and 23 genera (Fig. 5.87). The most abundant orders were *Microascales* (27%), *Pleosporales* (21%), and *Hypocreales* (21%). At the family level, *Halosphaeriaceae* (21%), *Pleosporaceae* (15%), and *Botryosphaeriaceae* (9%) were dominant. The most frequently recorded genera were *Lasiodiplodia* (9%), *Alternaria* (9%), and *Arenariomyces* (9%).

In contrast, 20 strains were obtained from higher salinities (>25 ppt; 30–34 ppt). These strains were distributed across five orders, five families, and 12 genera. *Microascales* was the dominant order (73%), and *Halosphaeriaceae* the most abundant family (80%). The most common genera were *Corollospora* (30%) and *Ceriosporopsis* (15%).

A total of 18 fungal strains were isolated from submerged seashore plants. Of these, seven strains were collected at salinities below 20 ppt and distributed across five orders, six families, and six genera. *Microascales* (represented by *Saagaromyces*) was the most abundant order at this salinity level, with two strains. The remaining 11 strains were obtained at higher salinities (>25 ppt) and distributed across four orders, seven families, and eight genera. *Pleosporales* was the most abundant order (four strains), while *Diatrypaceae* was the dominant family (three strains). The most common genera were *Preussia*, *Acremoniisimulans*, and *Halocryptovalsa*, each represented by two strains.

Additionally, *Hortaea werneckii* and *Neocamarosporium salinum* were collected from the margin of a saltern with high water salinity (50 ppt). Although these specimens were not submerged, they were isolated from the halophyte *Suaeda maritima*, near the water level. Their association with a halophytic host in a highly saline habitat suggests an ecological adaptation or tolerance to elevated salinity conditions.

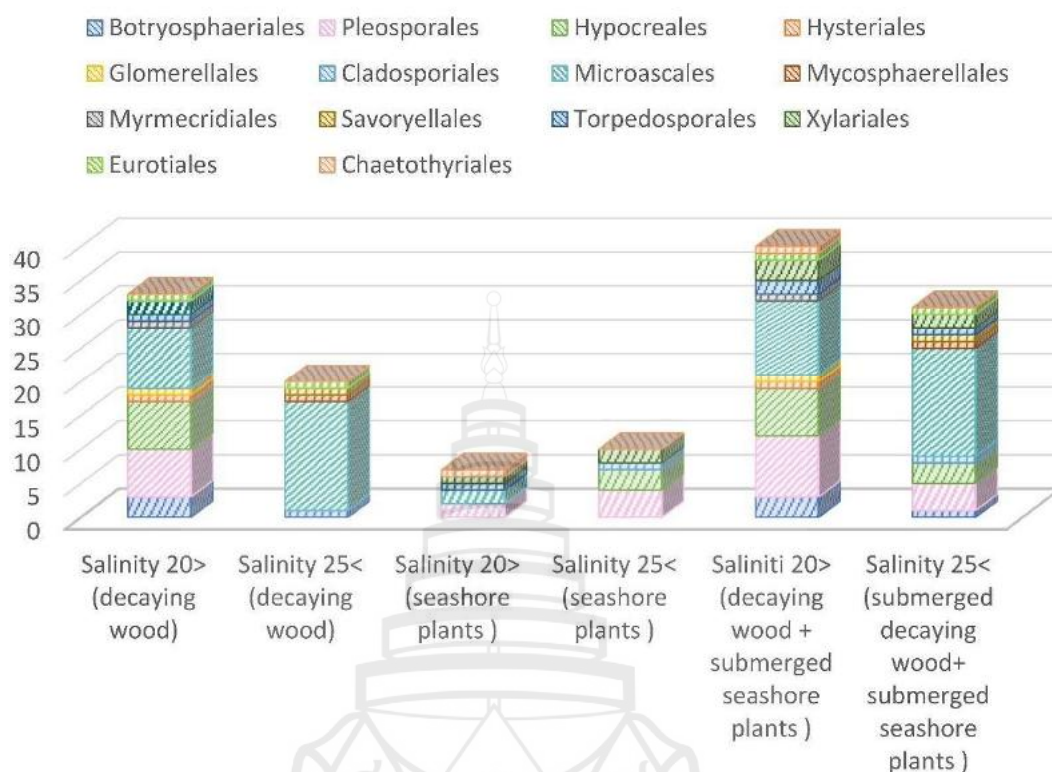


Figure 5.87 Distribution of saprobic fungal orders from submerged decaying wood and submerged seashore plants in Thailand, in different salinity levels (X-axis: substrate types across salinity levels; Y-axis: number of strains)

5.2.3 Distribution of Fungi from Seashore Plants in Thailand

Sixty-four fungal strains were isolated from seashore plants in Thailand, including six coastal terrestrial plant hosts—*Opuntia* sp., *Pluchea indica*, *Leucaena leucocephala*, *Lantana camara*, *Ficus macrocarpa* and *Chromolaena odorata*—and two semi-coastal marine (salt-marsh) hosts, *Sesuvium portulacastrum* and *Suaeda maritima*.

The distribution of these fungi is illustrated in a heatmap (Fig. 5.88), showing 35 genera across the host plants. Among them, *Diaporthe*, *Cladosporium* and *Phaeosphaeria* were recorded from both coastal terrestrial and semi-coastal marine hosts.

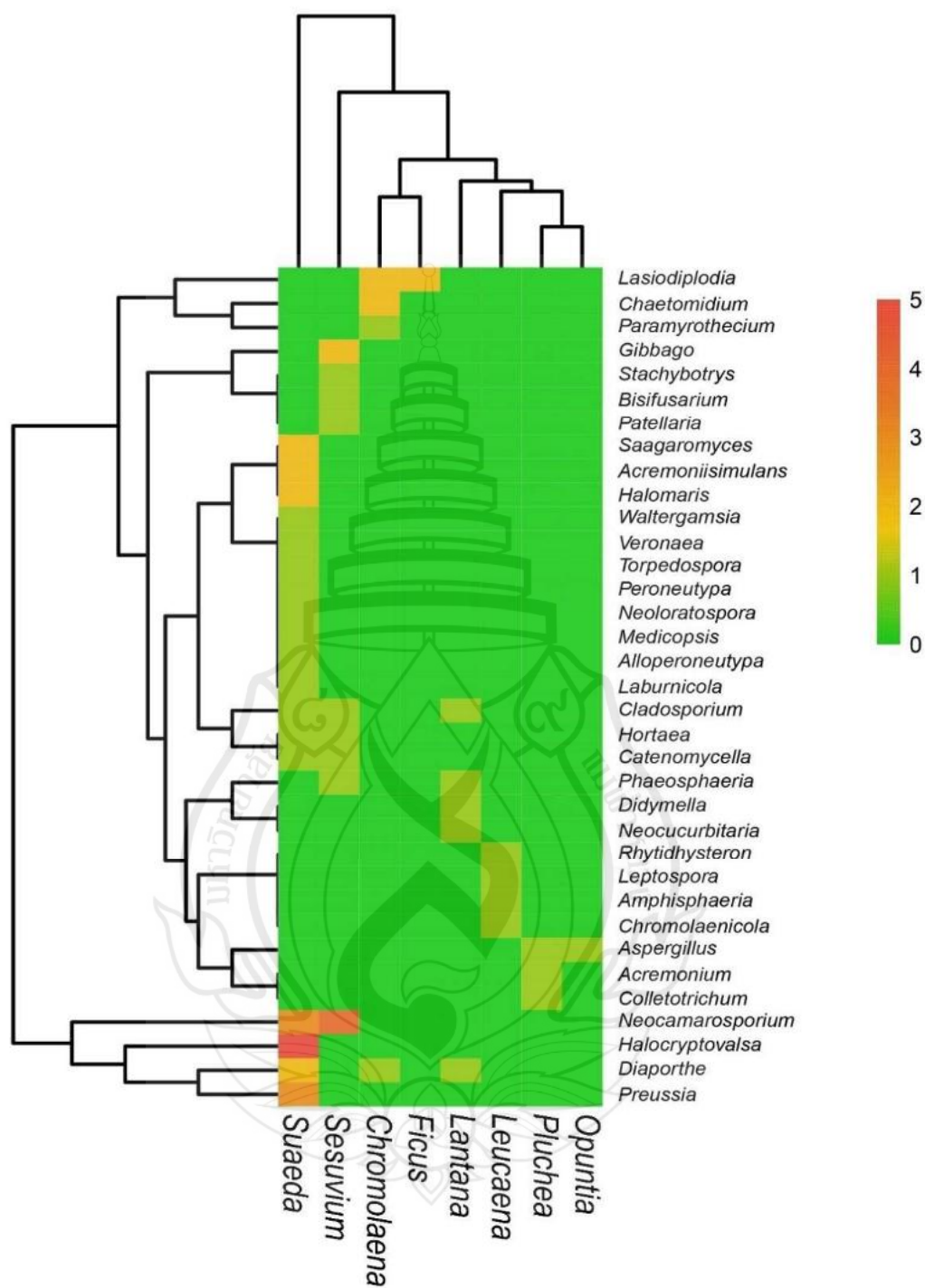


Figure 5.88 Distribution of saprobic fungal genera from seashore plants in Thailand

Collections of semi-coastal marine hosts were focused on the abundant salt marsh halophytes *Sesuvium portulacastrum* and *Suaeda maritima*, from which 42

fungal strains were isolated. The sunburst chart (Fig. 5.89) shows the taxonomic distribution of fungi associated with these two hosts.

At the class level, *Dothideomycetes* was dominant, comprising 25 strains (59.5%). At the order level, *Pleosporales* was the most represented, with 20 strains (48%).

Eighteen families were recovered, with *Neocamarosporiaceae* the most abundant (seven strains; 17%), followed by *Phaeosphaeriaceae* and *Diatrypaceae*, each with six strains (14%).

At the genus level, *Neocamarosporium* was the most frequently isolated genus (seven strains; 17%), followed by *Halocryptovalsa* (five strains; 12%).

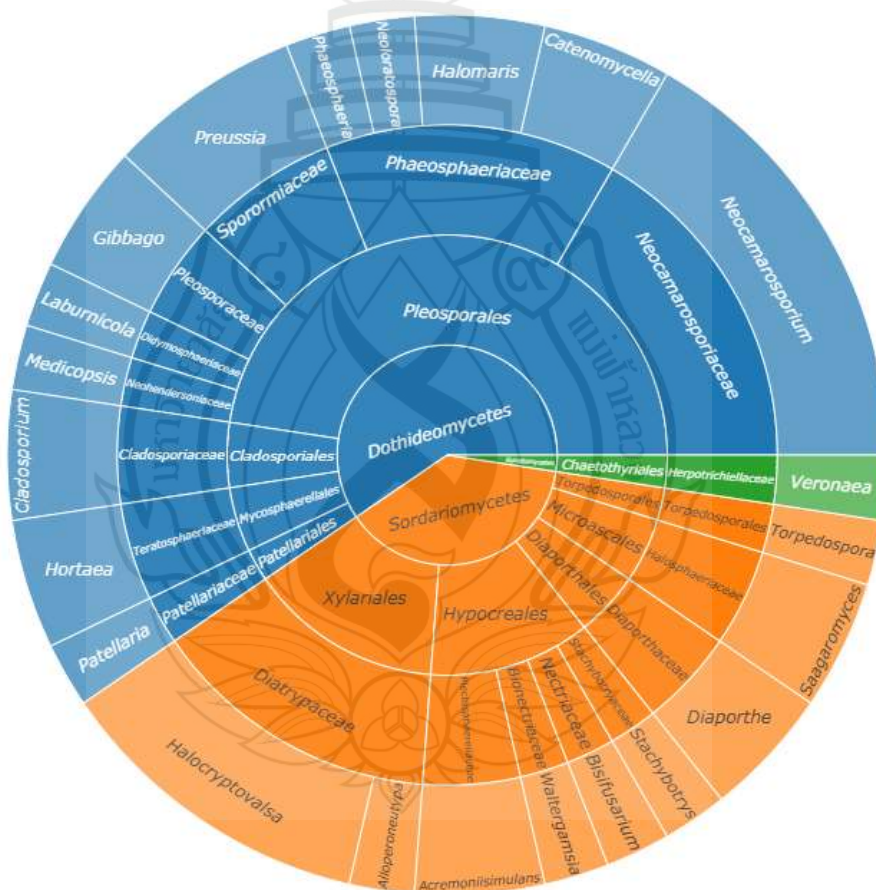


Figure 5.89 Distribution of saprobic fungi from *Sesuvium portulacastrum* and *Suaeda maritima*, in Thailand, in different classes, orders, families and genera

Among the fungi isolated from the two salt-marsh hosts, 13 strains were obtained from *Sesuvium portulacastrum*, all from aerial, dry specimens. In contrast, 29 strains were isolated from *Suaeda maritima*, including 17 from submerged material and 12 from aerial, dry specimens.

Fungi from *Se. portulacastrum* belonged to nine genera: *Bisifusarium*, *Catenomycella*, *Cladosporium*, *Gibbago*, *Hortaea*, *Neocamarosporium*, *Patellaria*, *Phaeosphaeria*, and *Stachybotrys*, with *Neocamarosporium* the most frequently isolated genus (four strains).

Fungi from *Su. maritima* belonged to 17 genera. *Halocryptovalsa* was the most frequently isolated genus (five strains), followed by *Neocamarosporium* represented by three strains.

The genera *Acremoniisimulans*, *Cladosporium*, *Halocryptovalsa*, *Halomaris*, *Laburnicola*, *Neocamarosporium*, *Preussia*, *Saagaromyces*, *Torpedospora*, *Veronaea*, and *Waltergamsia* were recovered from submerged *Su. maritima* specimens. The genera *Alloperoneutypa*, *Catenomycella*, *Diaporthe*, *Halocryptovalsa*, *Halomaris*, *Hortaea*, *Medicopsis*, *Neocamarosporium*, and *Neoloratospora* were isolated from aerial, dry specimens. *Halocryptovalsa*, *Neocamarosporium*, and *Halomaris* were the overlapping genera between submerged and aerial *Suaeda* specimens (Fig. 108). At the species level, *Halocryptovalsa suaedae* was the only species common to both submerged and aerial *Su. maritima* specimens.

At the genus level, *Catenomycella*, *Cladosporium*, *Hortaea*, and *Neocamarosporium* were collected from both *Suaeda maritima* and *Sesuvium portulacastrum*. At the species level, 21 fungal species were obtained from *Su. maritima*, with 12 species recovered from *Se. portulacastrum*. *Neocamarosporium pranburiense*, *Ne. salinum*, and *Hortaea werneckii* were isolated from both hosts (Fig. 5.90).

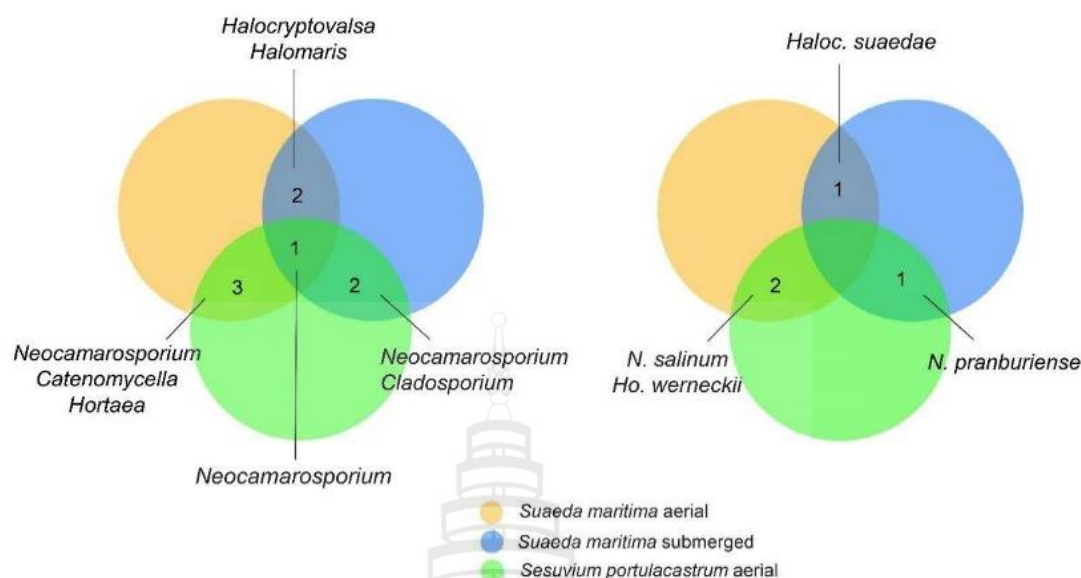


Figure 5.90 Overlapping saprobic fungi obtained from *Sesuvium portulacastrum* and *Suaeda maritima*, in genus level (left) and species level (right)

5.3 Discussion

This study investigated the fungal communities associated with marine submerged wood and seashore plants in Thailand. Our findings expand the documented diversity of marine-associated fungi within coastal habitats. Notably, the discovery of several new taxa underscores the immense taxonomic richness of these specialized environments. This integration allows for a broader assessment of fungal communities associated with marine and coastal plants in Thailand.

The integration of molecular data with detailed morphological observations is essential for accurate fungal identification and the delineation of novel taxa (Chethana et al. 2021a; Maharachchikumbura et al. 2021), and this approach was applied in the present study. For example, at the species level, our collection of *Bisifusarium lovelliae* is described here for the first time from a natural substrate and differs from its ex-type strain in having wide collarettes on the phialides (Zhang et al. 2025b), and its identification is supported by close phylogenetic affinity and molecular sequence data. Similarly, at the genus level, *Alloperoneutypa suaedae* is morphologically distinct from other species of *Alloperoneutypa*; however, its phylogenetic placement provides

sufficient evidence for its classification in the genus, and it is described here as the first asexual morph of *Alloperoneutypa*.

Consequently, further analyses were restricted to isolated fungi to ensure accurate identification using combined morphological and molecular data. In addition to providing DNA from pure cultures, viable cultures can yield additional morphological characters (Senanayake et al. 2020). For instance, *Neocremonium maritimum* provided higher-resolution morphological traits when examined in culture compared to those observed from woody specimens. Beyond improving identification accuracy, these cultured isolates provide a fundamental basis for future research on their potential biotechnological or biomaterial applications (Abreu et al. 2026).

Our results provided sufficient support to introduce several new taxa from trapped wood and seashore plants. While the checklist of salt marsh fungi documented 486 taxa from salt marsh hosts, our discovery of 23 novel taxa from salt marsh habitats alone represents a significant increase in known diversity. This may be attributed to the relatively limited attention previously given to fungal investigations in this ecosystem and to the limitations of methods used in earlier studies (Calabon et al. 2021).

However, while previous studies investigating fungal diversity in estuarine and coastal areas have reported a high number of taxa, identification was often based primarily on a single sequencing region (Arfi et al. 2012; Abreu et al. 2026). Jeffries et al. (2016), in their investigation of 65 sampling sites across different marine habitats in Australia, reported that more than 80% of fungal sequences could not be matched to known phylogenetic groups in the UNITE database using BLAST searches. This finding indicates either a lack of previous studies in these habitats or a shortage of reference sequences in databases, suggesting that these ecosystems harbor numerous undescribed taxa awaiting discovery. Consequently, multigene analyses combined with morphology are essential to improve species identification and enhance taxonomic understanding.

Following these taxonomic considerations, environmental factors such as pH, salinity and substrate types are known to influence fungal diversity in marine environments (Jones et al. 2019; Wijayawardene et al. 2022a). In the present study, we investigated saprobic fungi from submerged decaying wood and submerged and aerial (dry) seashore plants, collected across different salinity levels. Notably, pH was not

treated as a separate variable here, because measurements across sampling sites were similar (7.5 ± 0.5).

Our results reveal a distinct divergence between fungal communities inhabiting seashore plants and those found on decaying wood submerged in seawater. This pattern of distinct community partitioning across estuarine and marine habitats aligns with previous ecological surveys, which demonstrated that these environments host discrete fungal assemblages (Jeffries et al. 2016; Abreu et al. 2026), suggesting that different substrates provide distinct nutritional and physiological conditions that favor specific fungal taxa. Abreu et al. (2026), in a study investigating the diversity of culturable fungi in Portuguese coastal and estuarine habitats, also reported differences in fungal communities across substrates. They documented marine obligate taxa, including members of *Lulworthiaceae*, primarily associated with submerged wood and marine driftwood, whereas samples from brackish environments contained a higher diversity of marine-tolerant fungi distinct from those occurring in fully marine substrates.

Fungi associated with marine submerged wood belonged to 12 orders and were mainly dominated by members of *Halosphaeriaceae* (*Microascales*, *Sordariomycetes*), particularly at higher salinities (>25 ppt). This pattern is consistent with previous studies (Jones et al. 2019, Calabon et al. 2023). *Halosphaeriaceae* species have morphological adaptations, such as early deliquescing asci, passive release of ascospores frequently with appendages or gelatinous sheaths, which facilitate dispersal, attachment, and survival in aquatic habitats (Jones 1994).

Fungi associated with seashore plants showed greater taxonomic diversity, spanning 17 orders, with *Pleosporales* (*Dothideomycetes*) being the most abundant. This finding agrees with checklist studies of salt marsh fungi (Calabon et al. 2021), which identified *Dothideomycetes*, particularly *Pleosporales*, as dominant taxa on salt marsh plants. This reflects the ability of members of this group to explosively eject their ascospores securing wide dispersal of propagules (Calabon et al. 2021).

Of the 61 recovered genera from decaying wood and seashore plants, only five genera occurred in both substrates. These include *Aspergillus*, *Lasiodiplodia*, and *Rhytidhysterion*, which were recovered from decaying wood and coastal terrestrial seashore plants in our collection. These genera are mostly known from terrestrial habitats (Jones et al. 2019, Cobos-Villagrán et al. 2021, Visagie et al. 2024, Guerrero

et al. 2025), and their occurrence in marine environments may be attributed to their introduction from terrestrial sources followed by adaptation to saline seawater conditions (Li et al. 2016).

Another overlapping genus, *Torpedospora*, is primarily reported as a marine genus (Jones et al. 2019). In our collection, *Torpedospora* was found in both semi-coastal marine plants (salt marsh hosts) and decaying wood; notably, the salt marsh specimens were submerged in seawater, suggesting a preference of this genus for seawater conditions. This observation agrees with findings on the vertical distribution of salt marsh fungi, where marine species typically were associated with the lower part of the plant that are regularly submerged, whereas terrestrial fungi are more common on the upper parts that remain above water during high tides (Gessner 1977; Kohlmeyer and Kohlmeyer 1979).

The fifth overlapping genus, *Hortaea*, represented by *Hortaea werneckii*, has been reported from both terrestrial and marine habitats and is frequently recorded from hypersaline environments on various substrates, including seawater, rocks, soil, and saltern microbial mats (Cantrell et al. 2006; Marchetta et al. 2018). In the present study, this fungus was collected from submerged decaying wood and aerial salt marsh hosts located at the margins of salterns. Water currents and the movement of suspended particles facilitate spore dispersal in aquatic habitats (Calabon et al. 2023). The occurrence of *H. werneckii*, a species common in saline soils and saltern waters, on nearby plant hosts may therefore be attributed to dispersal via water movement and transport with dissolved and suspended particles from the salterns to the plant tissues.

At the species level, only *Hortaea werneckii* and *Rhytidhysterium bruguierae* were recovered from both substrates, indicating limited overlap in species composition.

In addition to differences between fungal communities on submerged decaying wood and seashore plants, fungi recovered from submerged and aerial salt marsh specimens showed limited overlap, with only three genera and one species shared between these conditions. This suggests that water immersion functions as an ecological filter shaping fungal distribution (Kohlmeyer and Kohlmeyer 1979; Boddy and Rayner 1983; Lyons et al. 2010; Al-Nasrawi and Hughes 2012). Submerged habitats were mainly colonized by fungi likely tolerant of marine conditions, including

fluctuating salinity, whereas aerial and terrestrial tissues were dominated by fungi that may be adapted to periodic drying and UV exposure.

We also compared the occurrence of fungal sexual and asexual morphs across different substrates based on our collection. The distribution of asexual morphs may reflect an adaptation to specific environmental conditions (Taylor et al. 1999; Descals and Moralejo 2001). Fungi from aerial SP were dominated by coelomycetous morphs, which likely reflects adaptation to drier conditions, increased UV exposure, and salt spray in exposed coastal environments.

Among fungi from decaying wood, hyphomycetous fungi dominated at lower salinity levels (<20 ppt) and belonged to diverse orders, families, and genera. In contrast, fungi recovered from higher salinity environments (>25 ppt) were mainly sexual morphs, particularly members of *Halosphaeriaceae*. This pattern suggests that lower salinity conditions permit colonization by hyphomycetous fungi, as hyphomycetes are generally sensitive to salt concentration (Descals and Moralejo 2001). Our results further support the influence of salinity on fungal composition, with greater taxonomic richness observed under lower salinity conditions.

These lower salinity conditions also enabled the recovery of some taxa from marine habitats for the first time, including species such as *Lasiodiplodia crassispora* and *L. iranensis*, and genera such as *Myrmecridium* and *Musicillium* (Asghari et al. 2023, 2025). This observation suggests that these taxa may have colonized woody substrates prior to immersion in marine water and were subsequently able to tolerate lower salinity conditions after submergence. Although the duration of substrate immersion in marine water could not be precisely estimated, the condition of the specimens such as the presence of barnacles and the trapping of woody tissues between rocks, indicates that they were likely submerged for extended periods rather than briefly. Therefore, the recovered fungi may represent taxa capable of adapting to saline environments rather than being recently introduced following substrate entry into marine water.

Further comparative studies including fungi from marine submerged wood, seashore plants, mangroves, mangrove associated plants, and other coastal vegetation from the same region would provide a more comprehensive understanding of habitat-

driven fungal community structure (Aumentado et al. 2024; Bhagya et al. 2024; Apurillo et al. 2025; Mukhopadhyay et al. 2025).

Since all fungal collections from Thai seashore plants in this study were obtained from host-attached tissues and standing plants, these fungi likely play an important role in the early stages of decomposition under high-salinity and regularly flooded conditions, and they may represent pioneer to intermediate colonizers (Gessner 1978; Chapela and Boddy 1988; Al-Nasrawi and Hughes 2012; Abreu et al. 2026). Through their enzymatic activities, these fungi can degrade lignocellulosic compounds, making nutrients more accessible for subsequent fungal succession and for invertebrate detritivores (Newell and Bárlocher 1993; Al-Nasrawi and Hughes 2012; Panno et al. 2013), thereby emphasizing their vital roles in coastal ecosystems, particularly in nutrient cycling and organic matter decomposition.

Among our collections, we specifically investigated two halophytes from Thai salt marshes: *Suaeda maritima* and *Sesuvium portulacastrum*. Our results indicate that *Suaeda maritima* harbored fungi belonging to more genera (17 genera) than *Se. portulacastrum* (9 genera). This suggests that, *Su. maritima* may represent a more favorable host, particularly under submerged conditions. The broader generic representation may be related to the more lignified, semi-woody stem structure of *Su. maritima*, providing a long-term carbon and nutrient source for fungi (Shearer 1992). Another possible reason is the presence of senescent plant material of *Su. maritima* in both aerial and submerged environments, which can provide increased nutritional resources for fungal colonization. Submerged conditions may enhance colonization by providing continuous water availability, promoting spore germination and dispersal, and maintaining stable moisture and nutrient availability (Goh and Hyde 1996; Gulis et al. 2019).

In contrast, *Se. portulacastrum* has succulent (fleshy) stems and leaves and remains largely green under submerged conditions throughout the year. During our field collections, senescent or dead plant material was primarily observed on exposed coastal rocks or soil during low tide and dry seasons. This lack of consistent decaying tissues may limit the available niches for saprobic fungal colonization, potentially explaining the lower generic diversity observed on this host compared to *Su. maritima*.

Neocamarosporiaceae and *Phaeosphaeriaceae* were the dominant families on these two halophytes collections. Members of these families have previously been reported as saprobes, endophytes, and pathogens (Crous et al. 2014; Papizadeh et al. 2018; Wanasinghe et al. 2017a; Wanasinghe and Maharachchikumbura 2023). This suggests that the species identified here may have transitioned to a saprobic lifestyle from an endophytic or pathogenic phase (Bhunjun et al. 2024b). Further research into the endophytic and pathogenic communities of these halophytes is required to clarify these lifestyle transitions.

Neocamarosporiaceae was represented by *Neocamarosporium*, a genus frequently documented in salt marsh and hypersaline habitats (Papizadeh et al. 2018; Prematunga et al. 2023). Previous studies have shown that *Neocamarosporium* species are commonly associated with halophytic genera within *Amaranthaceae* (Papizadeh et al. 2018), a pattern that was also observed in our collections where *Neocamarosporium* species were isolated from *Suaeda* (*Amaranthaceae*). However, we also isolated five strains from *Se. portulacastrum* (*Aizoaceae*). These findings support the view that halophytes and saline environments represent the preferred ecological niches for *Neocamarosporium* species, rather than being restricted to a single plant family.

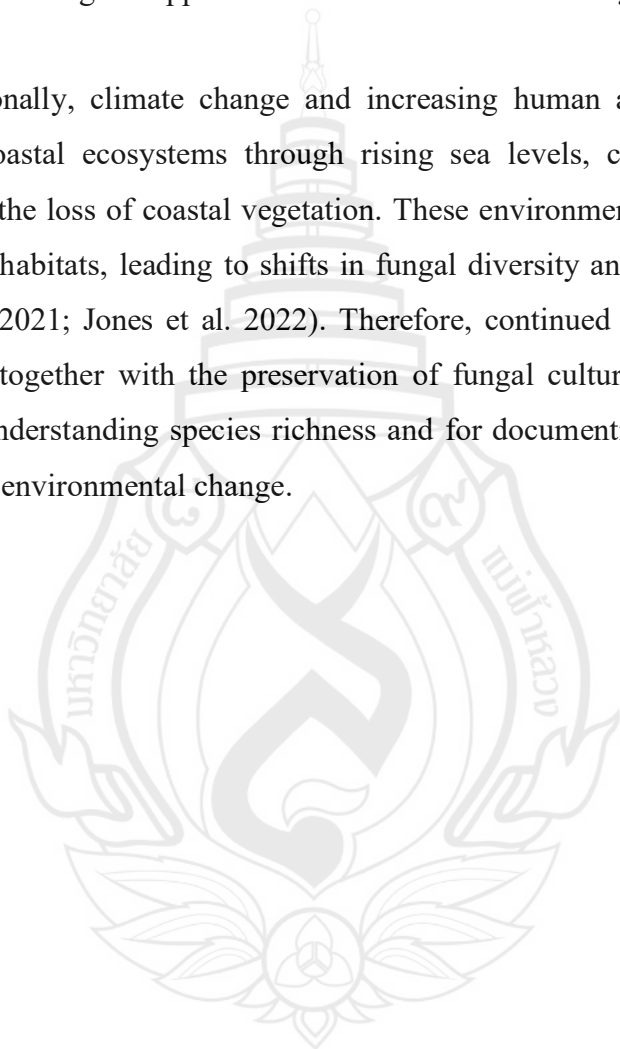
Due to the limited number of studies on *Su. maritima* and *Se. portulacastrum*, a definitive assessment of host specificity remains challenging. However, our findings provide important insights into the host ranges of certain taxa. For example, *Gibbago trianthemae* was previously considered host-specific to *Trianthema portulacastrum* (Kumar and Gaddeyya 2014), though it was later identified as a pathogen on *Se. portulacastrum* (Chen et al. 2022b). Our collection of *G. trianthemae* on *Se. portulacastrum* confirms that this fungus is not restricted to a single host species. Given that both hosts are halophytes within the family *Aizoaceae* (Joshi et al. 2013), this observation suggests that the fungus may instead exhibit a family-level preference toward salt-tolerant members of this group.

On *Su. maritima*, the species *Halocryptovalsa suaedae* was frequently observed on both submerged and aerial substrates. Its presence was sometimes visible to the naked eye on the host tissue. However, it is premature to conclude that this fungus specifically prefers *Su. maritima*, as other species within the genus *Halocryptovalsa* have been described from a different mangrove and salt marsh hosts (Dayarathne et al.

2020b; Calabon et al. 2021). Extensive further collections across a broader range of halophytes are necessary to confirm whether *H. suaedae* is a host-specialist or a generalist within saline ecosystems.

Overall, these findings highlight the importance of environmental conditions in shaping marine-associated fungal communities and emphasize the need for integrative taxonomic and ecological approaches to better understand fungal diversity in coastal ecosystems.

Additionally, climate change and increasing human activities are affecting marine and coastal ecosystems through rising sea levels, changing temperatures, pollution, and the loss of coastal vegetation. These environmental changes can affect marine fungal habitats, leading to shifts in fungal diversity and community structure (Kumar et al. 2021; Jones et al. 2022). Therefore, continued studies on marine and coastal fungi, together with the preservation of fungal cultures and specimens, are essential for understanding species richness and for documenting fungal biodiversity under ongoing environmental change.



CHAPTER 6

OVERALL CONCLUSIONS

6.1 Conclusion

Fungi in coastal habitats occur across a wide range of substrates and play an essential role in ecosystems functioning. As primary decomposers and stress-tolerant colonizers, they, regulate nutrient and energy flow, and support coastal food webs under challenging environmental conditions such as high salinity. In addition to their ecological importance, marine fungi are a valuable and still poorly explored source of bioactive compounds and enzymes with potential uses in medicine, industry, and agriculture. However, climate change, habitat loss, pollution, and coastal development are increasingly threatening fungal diversity and their ecosystems.

This thesis provides a literature review highlighting the diversity, importance, and challenges of marine-associated fungi. It also presents comprehensive notes on selected salt-marsh fungal genera through the Fungalpedia project, providing a reference for salt-marsh fungi by summarizing their taxonomy, ecological roles, distribution, and morphological characteristics, supported by illustrations.

This thesis provides a comprehensive taxonomic and ecological assessment of saprobic fungi associated with marine-based habitats in Thailand. A total of 117 fungal strains from Thailand were analysed, originating from submerged decaying wood and seashore plants, including salt-marsh halophytes. Through detailed morphological examination combined with multi-gene phylogenetic analyses, this study expands current knowledge of marine-associated fungal diversity and ecology.

The discovery of four new genera and 32 new species highlight the substantial, yet still underestimated, taxonomic richness of coastal and marine-influenced ecosystems. The application of integrative taxonomy was essential for accurate species identification, particularly in cases where morphological variation alone was insufficient to distinguish taxa. The recognition of novel morphological traits, new

substrate records, and previously undocumented morphs further emphasizes the importance of combining molecular data with morphology in marine mycology.

Distinct fungal assemblages were observed between submerged decaying wood and seashore plant substrates, with minimal overlap at the species level. This clear differentiation underscores the strong influence of substrate type on fungal community composition, reflecting differences in nutrient availability, tissue structure, and exposure to environmental stressors. Submerged decaying wood supported communities dominated by *Sordariomycetes*, particularly *Halosphaeriaceae*, especially at higher salinity levels, whereas seashore plants showed greater overall taxonomic diversity, with *Pleosporales* (*Dothideomycetes*) as the dominant order. These findings confirm that substrate specificity and habitat conditions act as ecological filters shaping marine fungal diversity.

Among the halophytic hosts examined, *Suaeda maritima* supported a more diverse fungal assemblage than *Sesuvium portulacastrum*, particularly under submerged conditions. This pattern likely reflects differences in host tissue structure, persistence of dead material, and availability of colonizable substrates. The dominance of families such as *Neocamarosporiaceae* and *Phaeosphaeriaceae* on salt-marsh plants indicates that these groups are well adapted to saline environments and play important roles in the early decomposition of coastal vegetation.

Overall, this study demonstrates that marine fungal diversity is structured by the combined effects of substrate type, salinity, and host characteristics. The results reinforce the ecological importance of saprobic fungi in coastal ecosystems, where they contribute to organic matter turnover and nutrient cycling under challenging environmental conditions. By documenting novel taxa and clarifying distributional and ecological patterns, this thesis provides a framework for future studies on marine fungal biodiversity. Continued exploration of understudied coastal habitats, along with culture-based approaches and molecular tools, will be essential for a more complete understanding of marine fungal diversity and its responses to environmental change.

6.2 Research Advantages

This research expands current knowledge of fungal diversity in tropical marine environments and addresses important gaps in marine mycology. The discovery of four new genera and 32 new species highlight the high and still underexplored taxonomic richness of coastal habitats. The use of a polyphasic approach, combining detailed morphological observations with multi-gene phylogenetic analyses, ensures accurate species delimitation and strengthens fungal systematics. All relevant sequence data and taxonomic information generated in this study provide valuable reference material for future biodiversity, ecological, and evolutionary research. In addition, this thesis provides an assessment of fungal community structure across different coastal substrates and environmental conditions, suggesting the strong influence of substrate type and salinity on fungal distribution. The analysis of sexual and asexual morphs across habitats provides new insights into fungal adaptation to marine based environments. Importantly, this study contributes detailed taxonomic notes on selected salt-marsh fungal genera through the Fungalpedia publication, presenting an illustrated reference that summarizes their taxonomy, ecological roles, and distribution. Together, these findings highlight the ecological importance of fungi in coastal ecosystems and provide baseline data for conservation, ecosystem management, and future research on marine fungal diversity and application.

6.3 Future Work

Following directions are recommended for future studies:

6.3.1 To investigate how environmental factors, such as seasonal variation, affect fungal diversity and distribution in marine and coastal habitats.

6.3.2 To explore underexplored host plants and substrates in marine and coastal ecosystems, including salt marsh vegetation, and other coastal plants, to improve understanding of host preference and fungal community structure.

6.3.3 Studying endophytic, and pathogenic fungi along with further studies on saprobes, to better understand their life strategies, and ecological roles.

6.3.4 To achieve a more comprehensive view of fungal diversity, future studies should integrate culture-dependent methods with culture-independent techniques, to detect both culturable and non-culturable fungal taxa.

6.3.5 Comparative studies across freshwater, brackish, and marine environments, as well as along salinity gradients, are recommended to explore fungal adaptation and biogeographic patterns.



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APPENDIX A

PUBLICATIONS



Article



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Myrmecridium hydei, a novel marine species from Thailand

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Abstract

Myrmecridium hydei was isolated from decaying branch of *Areca* species submerged in seawater from Prachuap Khiri Khan Province, Thailand. The new species is supported by phylogenetic analysis of combined ITS and LSU sequence data. *Myrmecridium hydei* formed a distinct clade from *M. phragmitigenum*, *M. phragmiticola* and *M. sambuci* with moderate statistical support. The species also differs from other *Myrmecridium* species by having a longer sympodial, straight or flexuous to geniculate-sinuous conidiophore and obovoid or fusoid to irregular, guttulate conidia without a wing-like sheath. *Myrmecridium hydei* is described as a novel species based on morphology and phylogeny.

Key words: 1 new species, asexual fungi, hyphomycetes, molecular phylogeny, taxonomy, *Myrmecridiaceae*

Introduction

Myrmecridium belongs to the family *Myrmecridiaceae* (*Myrmecridiales*, *Sordariomycetes*) and is typified by *M. schulzeri* (Hyde *et al.* 2020b, Wijayawardene *et al.* 2022). The genus has been found in various habitats such as submerged decaying wood in freshwater, leaf litter and the stems or leaves of herbaceous plants, dust, and soil (Crous *et al.* 2015, 2016, 2018, Peintner *et al.* 2016, Réblová *et al.* 2016, Tibpromma *et al.* 2017). There are 18 epithets for *Myrmecridium* in Species Fungorum (2023) and they are all known only from their asexual morph, with the exception of *M. montseguirum* (Réblová *et al.* 2016).

Myrmecridium was introduced by Arzanlou *et al.* (2007) to accommodate *M. schulzeri* and its varieties, which were formerly classified under *Ramichloridium*. *Myrmecridium* can be distinguished from other ramichloridium-like species by having hyaline vegetative hyphae and pimple-shaped denticles on the conidiophores (Arzanlou *et al.* 2007). Crous *et al.* (2015) established *Myrmecridiaceae* and *Myrmecridiales* to accommodate the *Myrmecridium* clade within *Sordariomycetes* based on the LSU sequence data. *Myrmecridium* is phylogenetically related to *Neomyrmecridium*, the other genus in *Myrmecridiaceae*, but *Neomyrmecridium* can be distinguished by its septate conidia (Crous *et al.* 2018). Based on phylogenetic analysis and conidial characters, *M. aquaticum* and *M. sorbicola* were transferred to *Neomyrmecridium* (Crous *et al.* 2018, 2021).

The sexual morph of *Myrmecridium* is characterized by having immersed ascomata with ostiolate papilla with a dark brown clypeus, two-layered peridium, cylindrical, septate paraphyses, and 8-spored, unitunicate asci with a slender long pedicel containing hyaline, ellipsoidal and 3-septate ascospores (Réblová *et al.* 2016). The asexual morph is characterized by hyaline, thin-walled mycelium, unbranched, subcylindrical, straight or flexuous, septate conidiophores that are brown at the base and become paler towards the apex and rise from creeping hyphae. The

Morphology and phylogeny reveal two new species and host records of hyphomycetous fungi on *Areca* species from marine habitats in Thailand

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Abstract

The marine ecosystem is the largest on Earth, supporting a wide variety of organisms. Fungi in this environment are diverse and play promising ecological roles. This study investigated fungi on submerged, decaying plant materials of *Areca* species trapped between rocks in seawater in Prachuap Khiri Khan Province, Thailand. Morphological and multi-gene phylogenetic analysis (LSU-ITS-*tub2*-SSU for *Tetraploa*, ITS-LSU-*tub2*-*rpb2* for *Rosellinia*, LSU-ITS-*tef1*-*α*-*rpb2* for *Musicillium* and LSU-ITS-*act* for *Sarocladium*) revealed two new species: *Tetraploa maritima*, characterized by the presence of a hilum and elongating appendages, and *Rosellinia maritima*, distinguished by a brown to black conidial-like structure composed of interwoven, irregular cells without distinct conidiophores produced in sterile conditions, unlike other *Rosellinia* asexual morphs. Additionally, two new host records (*Musicillium theobromae* and *Sarocladium gamsii*) are documented, with detailed descriptions of their *in vivo* and *in vitro* morphologies. Detailed morphological descriptions and illustrations are provided. This study contributes to the understanding of fungal diversity in marine environments.

Key words: 2 new species, marine fungi, molecular phylogeny, palm fungi, rocky shore, saprobe

Introduction

Fungi live in a variety of ecosystems, from terrestrial to aquatic habitats on various substrates such as plant materials (Hyde et al. 2019, 2020, 2024; Bhunjun et al. 2022). They have a high diversity in marine environments and are known for their important roles as well as for their potential use in medicine, bioremediation, biotechnology and industry (Hyde et al. 1998; Bonugli-Santos et al. 2015; Pang et al. 2016; Jones et al. 2019). Despite their importance, marine fungi have



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Role and Conservation of Fungi Associated with Marine Ecosystems

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Abstract

Marine fungi are found in a broad range of marine habitats and play crucial roles in nutrient cycling and ecosystem functioning. Despite their significance, marine fungi remain understudied as compared to terrestrial fungi. Moreover, there are many challenges that threaten marine fungi and their ecosystems through climate change and pollution. They are, however, a promising source of bioactive metabolites with applications in pharmacy and biotechnology. The biotechnological applications of marine fungal enzymes in bioremediation and industrial processes emphasize their importance. This mini-review summarizes the ecological roles, taxonomic diversity, and potential applications of marine fungi, with a focus on their contributions to bioremediation and natural product discovery. It provides an overview of the ecological adaptations of marine fungi to diverse ecosystem challenges, such as high salinity and low temperature, highlighting their responses to environmental changes. Additionally, it emphasizes the importance of conservation efforts and further research to discover and utilize marine fungi in the face of environmental changes.

Keywords – Aquatic Ecosystem – Aquatic Fungi – Climate Change – Enzymes – Secondary Metabolite

Introduction

Marine fungi are a diverse group thriving in marine environments across a range of substrates (Fig. 1), including algae, animals, corals, decaying driftwood, trapped plant materials, mangroves, sea grasses, saltmarsh plants, tunicates, muds, sands, sediments, detritus, soils, sea water, sea foam as well as oil spills (Jones & Moss 1978, Kohlmeyer & Kohlmeyer 1979, Hyde et al. 1990, Hyde & Lee 1998, Jones et al. 2006, 2015, 2019, Bovio et al. 2016, Grossart et al. 2019, Dayarathne et al. 2020, Li et al. 2023, Braconcini et al. 2024). They occupy various ecological niches spanning from the water surface to extreme deep-sea environments, hydrothermal vents, and methane cold seep locations (Nagahama et al. 2011, Vargas-Gastélum & Riquelme 2020, Pang & Jones 2023, Nagano et al. 2024). Marine fungi have the ability to colonize any submerged piece of wood in marine or estuarine environments over an extended period (Hyde & Jones 1988, Hyde & Lee 1998, Hyde et al. 2000).

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APPENDIX B

CHEMICAL REAGENTS AND MEDIA

Black ink used for mounting ascospores sheath and appendages.

Potassium hydroxide (KOH) used in the rehydration of dried specimens. 5% aqueous solution.

Lactoglycerol used for mounting semi-permanent slides: Lactic acid 10 ml, Glycerol 10 ml, Distilled water 10 ml. Mix 10 ml lactic acid, 10 ml glycerol, and add 10 ml distilled water.

Lactic acid for preserving fungal structures and for getting a true color image of the fungal spore and structures without staining. 85% Lactic acid 100 ml.

Lactophenol-Cotton Blue used to highlight fungal structures for viewing with the compound light microscope. Cotton blue is the most popular stain for observing pseudoparaphyses, septa or ascus walls. Phenol (crystals) 20 g, Lactic acid 16 ml, Glycerol 31 ml. Dissolve phenol in distilled water, add lactic acid, glycerol and 0.05 g of Poirrier's (cotton) blue or acid fuchsin.

Melzer's Reagent as the general mounting medium that clears the material somewhat and allows particularly a brilliant resolution under the microscope, and used for identification of ascomycete fungi. Amyloid reaction of asci changed to blue or heavily purple colors. Chloral hydrate 100 g, Potassium iodide 5 g, Iodine 1.5 g, Distilled water 100 ml.

Potato Dextrose Agar (PDA) used for fungal culturing. Potato starch (from infusion) 4 g, Dextrose 20 g, Agar 15 g. Suspend 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.

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