



Fungalpedia, an illustrated compendium of the fungi and fungus-like taxa

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Abstract

Fungalpedia is an online illustrated compendium of the fungi and fungus-like taxa. In this database we provide notes on the genera and higher taxa of fungi and definitions and descriptions of terms generally used in mycology. Where possible the notes are enhanced with plates and drawings to make the terms easier to understand. In the case of genera, we provide 1) notes on habit, host and lifestyle, 2) higher level classification, 3) genes and other evidence to support the genus, 4) main characters, 5) a critical assessment of the genus and its placement, and 6) photographic plates and/or drawings of the main characters of the genus. For higher taxa we give similar information but a drawing will not be provided. For the various terms we provide definitions and explanations and diagrams to facilitate understanding. We also provide accounts of eminent mycologists both living and deceased. We also provide notes on methodology and biotechnology. Although many of the entries are by invited authors and published in scientific papers, other interested persons are welcome to contribute to entries and/or modify existing entries. Those interested should contact the lead author.

Keywords – *Achrochaeta* – *Agaricus* – *Alveariospora* – *Anastomitrabeculia* – *Aphelidiales* – Applied mycology – *Ascagilis* – *Asterosporium* – *Austropleospora* – Basal fungi – *Beltraniella* – *Blastocladiomyceta* – *Brunneofissura* – *Bryostigma* – Borderline fungi – *Castanedomyces* – *Chaetomella* – *Clitopaxillus* – Coelomycetes – *Colletotrichum* – *Coniella* – *Comoclathris* – *Conioscypha* – *Coprotaceae* – Databases – Definitions – Dematiaceous hyphomycetes – *Diaporthomycetidae* – *Dicephalospora* – Discomycetes – *Dothideomycetes* – Epifoliar fungi – *Eurotiomycetes* – Eminent mycologists – Forest pathology – Freshwater fungi – Fungicolous fungi – *Fusarium* – *Fusasporis* – Genera – Grass fungi – *Halodiatrype* – Higher taxa – *Hypocreomycetidae* – *Hypomyces* – Invertebrate fungi – Lichenicolous fungi – *Juxtiphoma* – Online database – Marine fungi – *Megacoelomyces* – *Moheitospora* – Mushrooms – Mycoprotein – *Nematocentator* – *Naevia* – *Neoamphisphaeria* – *Obruspora* – *Oxydothis* – Palm fungi – *Palmiascoma* – *Pandanaceomyces* – *Parameliola* – *Pararousoella* – pileus – *Pirozynskiomyces* – Plant pathology – *Pleopunctum* – *Polycephalomyces* – *Pseudoalternaria* – *Purpureocorticium* – *Quixadomyces* – *Salmacisia* – *Sanchytriomycota* – *Savitreea* – *Setoapiospora* – Soil fungi – *Sordariomycetidae* – *Synchaetomella* – *Towyspora* – Wetland fungi – *Willeya* – *Xylariomycetidae* – Yeasts

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Introduction

Data on the fungi are scattered in numerous journals, published articles and in online databases. There is however, no comprehensive database dealing with taxa, terms and other interesting information on the fungi and fungus-like taxa. Perhaps the most important databases are the online registries for fungal names (Index Fungorum 2023) and its sister platform (Species Fungorum 2023). MycoBank and the Chinese registry provide similar functions, but MycoBank provides more details than the others. GenBank provides details of sequence data and whole genome data. Other databases deal with specific areas of fungal information. Perhaps the most important and well-cited is the Outline of fungi and fungus-like taxa (Wijayawardene et al. 2020, 2022), which provides a continually updated account of the classification of taxa. Some other databases of importance are listed in Table 3. However, despite these databases there is no single comprehensive arena bringing all of the information together into one platform. The last dictionary of the fungi was published in 2008 (Kirk et al. 2009) and this very useful publication provided brief notes on all fungal names and various definitions of fungal terminology. It is however, 15 years since the dictionary was published. Since this time numerous higher taxa, genera and species have been published and there has been no attempt to compile data on these into a comprehensive book or database. Thus, it is timely to promote such a project which is initiated in this paper.

Arrangement of entries in Fungalpedia

Fungalpedia provides up to date entries on fungal genera, families, orders and higher taxa. For these taxa we provide 1) notes on habit, host and lifestyle, 2) higher level classification, 3) genes and other evidence for new genera, 4) the important characters, 5) a critical assessment of the taxon and its placement, and 6) photographic plates and/or drawings of the main characters in the case of the genera. We provide explanations with drawings and/or plates of terminology generally used in mycology. Information on various topics studied in mycology (e.g. mycotoxins, biocontrol, melanin) are also be detailed. We also provide accounts of eminent mycologists both living and deceased. In all cases, entries are hyperlinked to datasets and publications where further information can be obtained. For example, under genera, taxa are hyperlinked to Index Fungorum, Facesoffungi, MycoBank, GenBank and other useful databases. For terminology entries, links to other platforms with useful data are added.

Future Fungalpedia papers deal with the recent years in which the genera were published or specific groups of fungi. CS Bhunjun and collaborators will prepare papers on new genera published in 2017 and 2018. CS Bhunjun and collaborators will also prepare papers on new genera and higher taxa in *Eurotiomycetes*, *Hypocreomycetidae* and yeasts. C. Phukhamsakda and collaborators will prepare papers on new genera and higher taxa published from marine habitats, grasses, algae and salt marsh plants. I. Manawasinghe and collaborators will prepare a paper on new genera and higher taxa published in palm fungi. Furthermore, as new papers are published and new taxa are introduced, we will also write entries for Fungalpedia.

Below we provide examples of entries from a range of disciplines and years.

1). Applied Mycology

Fungi grow almost anywhere in nature irrespective of the environment. Fungi are essential to the earth as crust cleaners, and are extremely important in forest health (Niego et al. 2023a). They

can be consumed by lower and higher organisms including humans, which keeps biodiversity balanced on the earth. The value of fungi has been estimated as USD 54.57 trillion annually (Niego et al. 2023b). Fungi benefit nature and humanity by producing antimicrobial drugs, in archaeology research, beauty care products, beverages, biocontrol agents, bioenergy, bioindicators, biofilters, biorefining, biomaterials in medicine and textiles, enzymes, forensic mycology, mycoarchitecture, mycoforestry, mycoremediation, mycosystem, mycotechnology, paper and pulp industry, plastic degradation, pigments, traditional culture and waste management (Hyde et al. 2019, Niego et al. 2023b). Meakala and collaborators will provide a Fungalpedia entry on applied mycology.

1. Fungalpedia – Note 77 Mycoprotein

Mycoprotein

Citation when using this entry: Meakala et al., in prep – Fungalpedia, more than 300 beneficial uses of fungi.

Mycoprotein has been produced since the 1960s from *Fusarium venenatum* and has been marketed under the trade name Quorn in several countries (Finnigan et al. 2019, Derbyshire 2022). Mycoprotein is a whole-food protein with high fiber, rich in essential amino acids, vitamins, beta-glucan and micronutrients and these are listed in Table 1 (Finnigan et al. 2019). It is also low in calories, saturated fatty acids, sodium and cholesterol (Souza Filho et al. 2019). Mycoproteins differ from single cell proteins in that filamentous hyphae are used as proteins rather than single cells (Biocyclopedia, Fellows 2009). There are many fungi capable of producing single cell proteins (Amara & Ei-Baky 2023) and mycoproteins (Landeta-Salgado et al. 2021). Marine and terrestrial mycoprotein producing fungi are listed in Table 2. Mycoproteins are not only used for consumption by humans, but can also be an edible protein in animal feed produced from *Paecilomyces variotii* (Amara & Ei-Baky 2023). Industrially, mycoproteins are produced by airlift fermentation with the addition of glucose, other nutrient-rich substrates, and inocula (Derbyshire & Delange 2021). After fermentation is complete, the mycelia is collected and then ribonucleic acids are degraded by heating. Further, steaming, chilling and freezing and carried out to enhance the meat-like texture. Depending on the diet, the product is combined with spices, egg albumin or gluten (Derbyshire & Delange 2021).

Several companies such as MyForest Foods, Mycorena, Eternal and Better Meat Co. have been producing mycoproteins in different brand names such as Quorn, Mycolein, Myprotein, Promyc and fungal mediated proteins such as Lifeway Kefir, Shirakiku (miso) and tempeh (<https://www.myprotein.co.th/>, Amara & Ei-Baky 2023). Products are available in supermarkets in various forms, such as burgers, cutlets, ice creams, MyBacon, patties, protein cheese, sausages and strips (Souza Filho et al. 2019, <https://myforestfoods.com/mybacon>, www.perfectdayfoods.com, <https://www.realvegancheese.org/>).

Mycoprotein and its health benefits (Fig. 2) were reviewed by Derbyshire (2022), using data from controlled trials, clinical trials, interventions and observational studies. Mycoprotein showed health benefits in different age populations. It helps young people in good muscle growth and regulates LDL (low-density lipoprotein), insulin and blood glucose levels (Derbyshire 2022). In healthy adults, mycoprotein intake results in a high dietary quality score, and lower glycemic and body mass index (Derbyshire 2022). It is also a healthy dietary supplement for older people due to its high protein and fiber content and muscle maintenance (Derbyshire 2022). Mycoprotein reduces cholesterol, and controls short-term energy intake, protein response and satiety (Monteyne et al. 2020, Cherta-Murillo & Frost 2022). The nutritionally rich mycoproteins can replace cereals and meat. Compared with animal proteins, such as chicken breast and beef mince, mycoprotein has high fiber, vitamin B9, phosphorous, zinc, choline and less carbohydrates (Finnigan et al. 2019, Bartholomai et al. 2022, Fig. 1). Mycoprotein has high saturated fat, Vitamin B12 and magnesium as compared to the plant protein tofu (Williamson et al. 2006, Ruxton 2010, Dunlop et al. 2017, Derbyshire & Delange 2021).

Mycoprotein production has a positive effect on the environment by lowering the environmental footprint and reducing deforestation, carbon dioxide and methane emissions

(Derbyshire 2022). Compared to animal and plant proteins, the production of mycoproteins requires less water, time, space and energy (Amara & Ei-Baky 2023, Saeed et al. 2023). To meet food supply requirements, mycoproteins have been approved in 17 countries, and are classified by the European Commission, FDA and UK as a safe food category and are sold for public use (Finnigan et al. 2019, Saeed et al. 2023). Thailand recently developed mycoprotein “vegan ground meat and ready-to-eat food” products that are ready for the market (<https://www.biotec.or.th/home/en/mycoprotein/>). The current global market is 641.5 million USD (Mycoprotein - Global Strategic Business Report 2023) and is expected to reach 1100 million USD by 2030. With this in mind, future research focuses on reducing allergic reactions from new and existing mycoproteins in humans.

Table 1 List of micro and macronutrients in wet mycoprotein.

Macronutrients	In 100 g mycoprotein	Micronutrients	In 100 g mycoprotein
Energy	85 kcals	Phosphorous	290 mg
Protein	11 g	Zink	76 mg
Fiber	6 g	Potassium	71 mg
Carbohydrates	3 g	Magnesium	49 mg
Fat	2.9 mg	Calcium	48 mg
		Iron	0.39 mg
		Vitamin B6	0.1 mg
		Choline	180 µg
		Vitamin B9	114 µg
		Vitamin B12	0.72 µg

Collection source from Derbyshire & Delange (2021).

Table 2 List of fungi used for mycoprotein production.

List of species	References
1. <i>Agaricus bisporus</i>	Kim et al. (2011)
2. <i>Agaricus subrufescens</i> , <i>Auricularia fuscusuccinea</i> and <i>Pleurotus albidus</i>	Stoffel et al. (2019)
3. <i>Agrocybe aegerita</i> , <i>Pleurotus sapidus</i> , <i>Lentinula edodes</i> , <i>Stropharia rugosoannulata</i> , <i>Pleurotus sajor-caju</i> and <i>Pleurotus salmoneostramineus</i>	Ahlborn et al. (2019)
4. <i>Aspergillus oryzae</i>	Gamarra-Castillo (2022)
5. <i>Aspergillus oryzae</i> , <i>Fusarium venenatum</i> , <i>Neurospora intermedia</i> , <i>Monascus purpureus</i> and <i>Rhizopus oryzae</i>	Souza Filho et al. (2018)
6. <i>Aureobasidium pullulans</i>	Campbell et al. (2004)
7. <i>Auricularia</i> spp.	Amara & Ei-Baky (2023)
8. <i>Flammulina velutipes</i>	Zou et al. (2023)
9. <i>Fusarium graminearum</i>	Trinci (1992)
10. <i>Fusarium venenatum</i>	Amara & Ei-Baky (2023)
11. <i>Ganoderma lucidum</i>	
12. <i>Grifola frondosa</i>	Amara & Ei-Baky (2023)
13. <i>Lepista nuda</i>	Lee et al. (2006)
14. <i>Morchella</i> spp.	Amara & Ei-Baky (2023)
15. <i>Neurospora crassa</i> , <i>N. intermedia</i> and <i>N. sitophila</i>	Bartholomai et al. (2022)
16. <i>Paecilomyces variotii</i>	Amara & Ei-Baky (2023)
17. <i>Paradendryphiella salina</i>	Landeta-Salgado et al. (2021)
18. <i>Pleurotus eryngii</i>	Mandliya et al. (2022)
19. <i>Pleurotus flabellatus</i> , <i>Volvariella volvacea</i>	Hendartina (2014)
20. <i>Pleurotus ostreatus</i>	Papaspyridi et al. (2012)
21. <i>Rhizopus oligosporus</i>	Wikandari et al. (2023)
22. <i>Schizophyllum commune</i>	Saetang (2022)
23. <i>Tremella fuciformis</i>	Amara & Ei-Baky (2023)
24. <i>Trichoderma koningii</i> , <i>Aspergillus ochraceus</i> and <i>A. terreus</i>	Helal (2005)
25. <i>Trichoderma reesei</i>	Zaki & Said (2018)

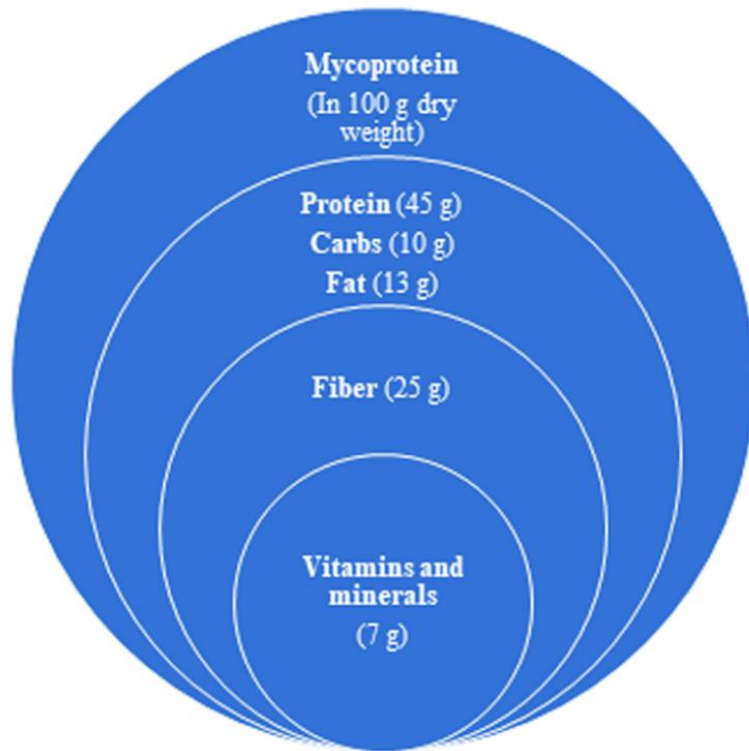


Figure 1 – Composition of mycoprotein.

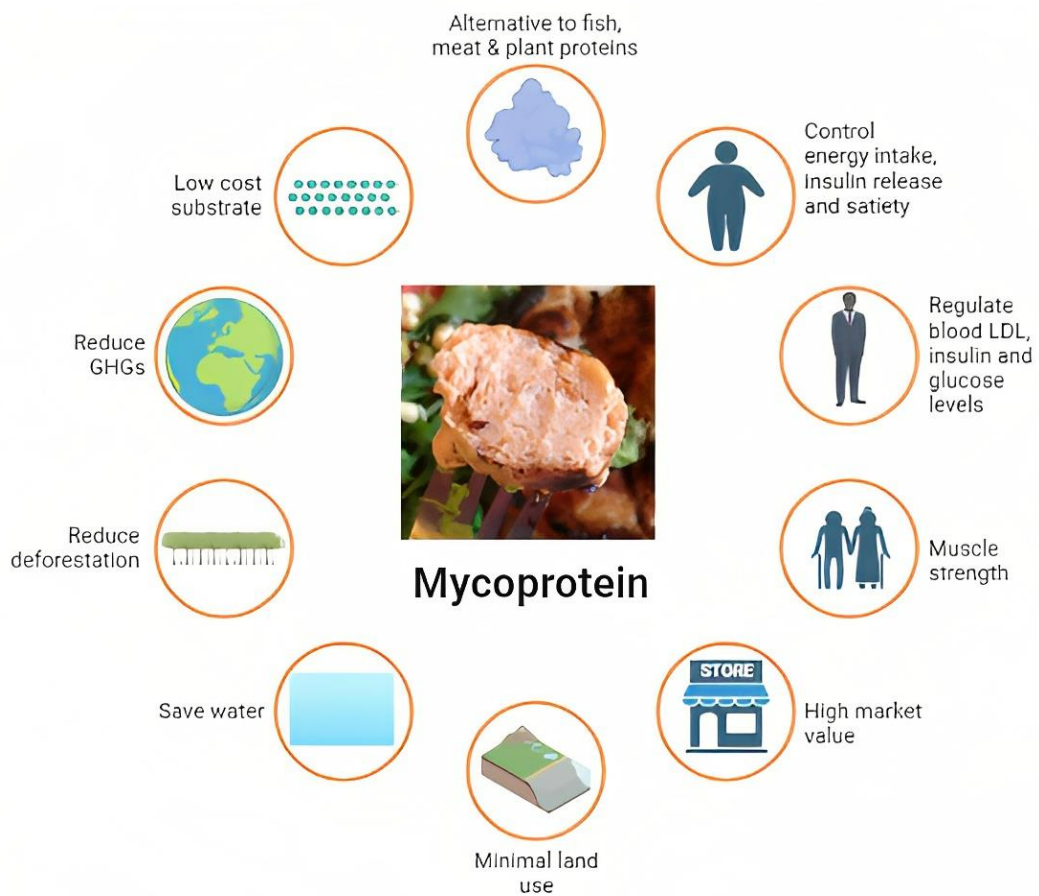


Figure 2 – Mycoprotein benefits.

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Entry by

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(Edited by **Kevin D Hyde** & **Chitrabhanu S. Bhunjun**)

2). Basal fungi and fungus-like organisms

The higher taxonomic ranks of the Kingdom *Fungi* have been subjected to frequent revision with the advent of novel sequence data including environmental sequences (James et al. 2006, Hibbett et al. 2007, Tedersoo et al. 2018). The latest classification of *Fungi* by Tedersoo et al. (2018) was based on both phylogenies and divergence time estimates and 18 phyla were accepted. Taxa in *Caulochytriomycota* lack DNA sequences. Galindo et al. (2021) introduced a new phylum, *Sanchytriomycota* in *Holomycota*. Among 20 phyla, 17 have been proposed to accommodate early divergent taxa (Wijayawardene et al. 2022). Voigt et al. (2021) agreed with the arrangement provided

by Tedersoo et al. (2018), but the placement of *Rozellomycota*, Microsporidia and Aphelida is debatable since they are sometimes regarded as *Fungi* (James et al. 2006, Tedersoo et al. 2018, Wijayawardene et al. 2018, 2022), while others accept them in a sister position to *Fungi* (Karpov et al. 2014, Letcher et al. 2013, 2017).

The fungus-like taxa are mainly included in the Kingdom *Nucleariæ* (Superkingdom *Holomycota*), sister to the Kingdom *Fungi*. Wijayawardene et al. (2020) followed the classification presented by Beakes & Thines (2017), Sheikh et al. (2018) and Leontyev et al. (2019) for the higher-level classification of *Oomycota*, Dictyosteliomycetes and Myxomycetes respectively. A Fungalpedia entry on the basal fungi and fungus-like taxa will be provided by Wijayawardene and collaborators and include genera and higher taxa as well as notes on terminology

2. Fungalpedia – Note 78 *Aphelidiales*

Aphelidiales Tedersoo, Sánchez-Ramírez, Kõljalg, Bahram, Döring, Schigel, T. May, M. Ryberg & Abarenkov

Citation when using this entry: Wijayawardene et al., in prep – Fungalpedia, taxa of the basal fungi and fungus-like organisms.

Index Fungorum, Facesoffungi, MycoBank, GenBank

Classification: *Aphelidiidae*, *Aphelidida*, *Incertae sedis*, *Aphelidea*, *Incertae sedis*, *Aphelida*, *Protozoa*

Aphelidiales (*Aphelidiomycetes*, *Aphelidiomycota*) was introduced within *Holomycota* in the Kingdom *Fungi* based on phylogenies and divergence time estimates (Tedersoo et al. 2018). *Aphelidiales* belongs to subkingdom *Aphelidiomycota*, phylum *Aphelidiomycota* (= *Aphelida*), subphylum *Aphelidiomycotina*, in class *Aphelidiomycetes* (= *Aphelidea*) (Gromov et al. 2000, Tedersoo et al. 2018). The order contains one family *Aphelidiaceae* (= *Aphelidiidae*), comprising four genera (*Aphelidium*, *Paraphelidium*, *Amoeboaphelidium*, *Pseudaphelidium*) Thirteen *Aphelidium* species are listed in Index Fungorum (2023). The morphology diagnosis of *Aphelidiales* was mentioned in Tedersoo et al. (2018), Gromov (2000) and Karpov et al. (2014).

Type genus: *Aphelidium* Zopf

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(Edited by **Kevin D. Hyde**)

3. Fungalpedia – Note 79 *Blastocladiomycota*

Blastocladiomycota Tedersoo, Sánchez-Ramírez, Kõljalg, Bahram, Döring, Schigel, T. May, M. Ryberg & Abarenkov

Citation when using this entry: Wijayawardene et al., in prep – Fungalpedia, taxa of the basal fungi and fungus-like organisms.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 3

Classification: *Blastocladiaceae*, *Blastocladiales*, *Incertae sedis*, *Blastocladiomycetes*, *Incertae sedis*, *Blastocladiomycota*, *Fungi*

The subkingdom *Blastocladiomycota* covers a single phylum (*Blastocladiomycota*), introduced based on phylogenies and divergence time estimates (Tedersoo et al. 2018). It was found and reported as saprotrophs or parasites on plants, animals, and fungi. Morphological descriptions were given by James et al. (2006) and Tedersoo et al. (2018). The phylum *Blastocladiomycota* contains one subphylum (*Blastocladiomycotina*) and two classes (*Blastocladiomycetes*, *Physodermatomycetes*) (Tedersoo et al. 2018). Thirty-five species are named in Index Fungorum (2023).

Type genus: *Blastocladia* Reinsch.

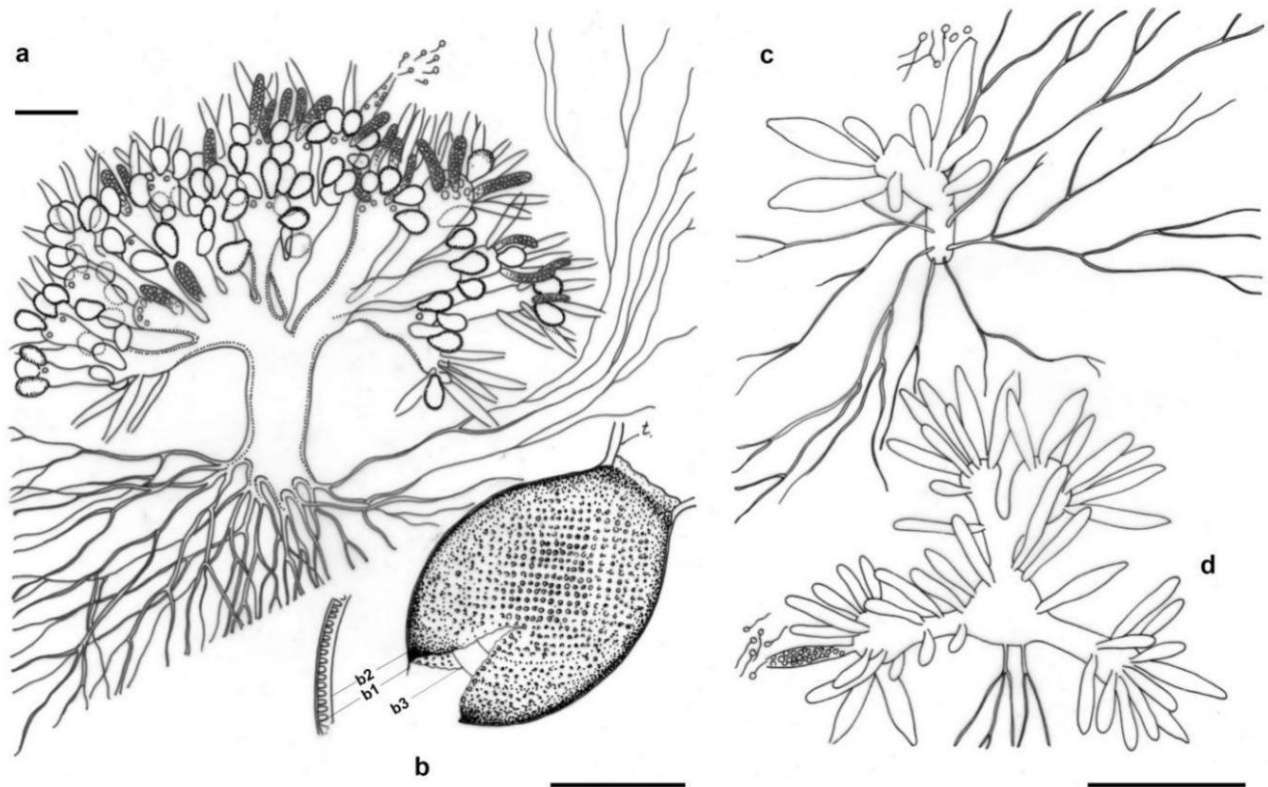


Figure 3 – *Blastocladia pringsheimii* (Redrawn from Blackwell 1940). a *Blastocladia pringsheimii* with far-reaching rhizoidal mycelium. b A dried resistant sporangium cracked open to show the three wall layers (b1, b2, b3). c, d Sporangia grown on sterile corn meal agar. c A two-day old thallus (seen from the side). d A seven-day old thallus (seen from above). e Basidiospores. Scale bars: a, c, d = 100 µm, b = 25 µm.

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4. Fungalpedia – Note 80 *Nematocenator*

Nematocenator A. Sapir, A.R. Dillman, S.A. Connon, B.M. Grupe, J. Ingels, M. Mundo-Ocampo, L.A. Levin, J.G. Baldwin, V.J. Orphan & P.W. Sternberg

Citation when using this entry: Wijayawardene et al., in prep – Fungalpedia, taxa of the basal fungi and fungus-like organisms.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 4

Classification: *Unclassified*, *Unclassified*, *Unclassified*, *Microsporea*, *Unclassified*, *Microsporidia*, *Protozoa*

The monotypic genus *Nematocenator* was discovered as a fungus-related parasitic microsporidium that infects benthic nematodes at methane seeps on the Pacific Ocean floor (Sapir et al. 2014). This genus is a microsporidian which is a group of single-cell parasites somewhat related to fungi. This genus was introduced based on morphology and SSU rDNA sequence data from selected microsporidia and close relatives (Sapir et al. 2014). An editorial comment is given in Index Fungorum; “the generic name in this combination is not currently considered to apply to an organism within the fungal clade”. Bojko (2022), introduced a new microsporidia genus (*Knowlespora*) from pheasant shell mussels, which is sister to *Nematocenator marisprofundi* in neopereziida clade.

Type species: *Nematocenator marisprofundi* A. Sapir, A.R. Dillman, S.A. Connon, B.M. Grupe, J. Ingels, M. Mundo-Ocampo, L.A. Levin, J.G. Baldwin, V.J. Orphan & P.W. Sternberg

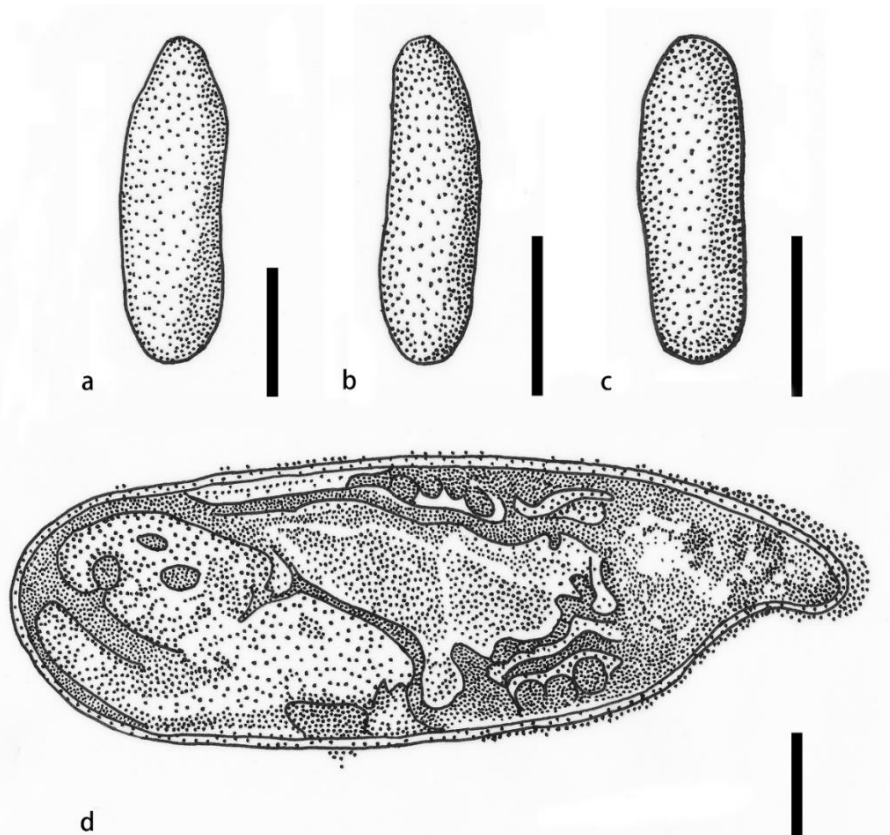


Figure 4 – Morphology of *Nematocenator marisprofundi* spores (Redrawn from Sapir et al. 2014). a–c Spores. d Longitudinal cross section of spore. Scale bars: a–c = 2.5 μ m, d = 1 μ m.

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5. Fungalpedia – Note 81 *Obruspora*

Obruspora A. Diamant, S.B.S. Rothman, M. Goren, B.S. Galil, M.B. Yokes, A. Szitenberg & D. Huchon

Citation when using this entry: Wijayawardene et al., in prep – Fungalpedia, taxa of the basal fungi and fungus-like organisms.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 5

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Microsporea*, *Incertae sedis*, *Microsporidia*, *Protozoa*

The monotypic genus *Obruspora* (*Microsporidia*, *Enterocytozoonidae*) was introduced by Diamant et al. (2014). This genus was described from *Callionymus filamentosus* in the Mediterranean Sea. It is a fish parasite and spores are developed within the host cell cytoplasm (Diamant et al. 2014). However, this genus is not currently considered a member of the fungal clade (Index Fungorum 2023).

Type species: ***Obruspora papernae*** A. Diamant, S.B.S. Rothman, M. Goren, B.S. Galil, M.B. Yokes, A. Szitenberg & D. Huchon

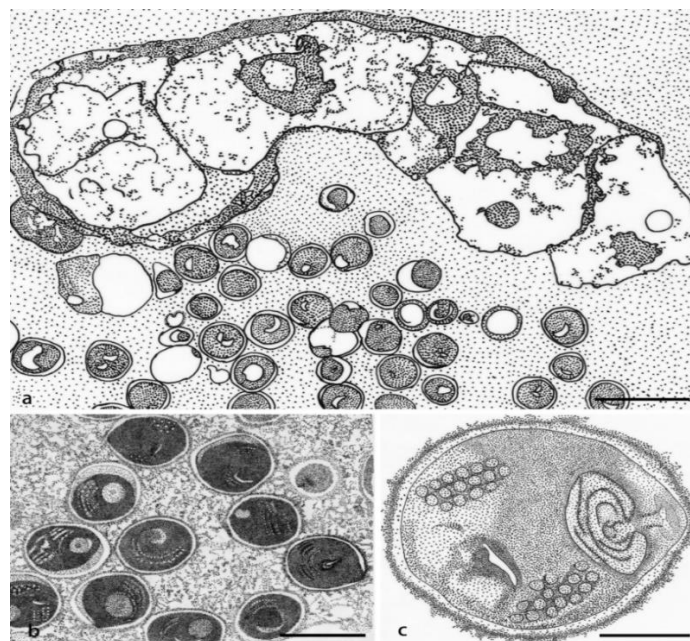


Figure 5 – Sporogonial plasmodia surrounded by mature spores of *Obruspora papernae* (Redrawn from Diamant et al. 2014). a Mature spores in the cytoplasm next to an unidentified electron lucent

body containing dark nucleus-like inclusion. b Mature spores in the paracrystalline array. c A single spore. Scale bars: a = 5 μm , b = 1 μm , c = 0.5 μm .

Reference

Diamant A, Rothman S, Goren M, Galil B et al. 2014 – Biology of a new xenoma-forming gonadotropic microsporidium in the invasive blotchfin dragonet *Callionymus filamentosus*. *Diseases of Aquatic Organisms* 109, 35–54.

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(Edited by **Kevin D. Hyde**)

6. Fungalpedia – Note 82 *Sanchytriomycota*

Sanchytriomycota Galindo, López-García, Torruella, Karpov & Moreira

Citation when using this entry: Wijayawardene et al., in prep – Fungalpedia, taxa of the basal fungi and fungus-like organisms.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 6

Classification: *Sanchytriaceae*, *Sanchytriales*, *Incertae sedis*, *Sanchytriomycetes*, *Incertae sedis*, *Sanchytriomycota*, *Fungi*

Sanchytrids are obligate parasitoids of freshwater algae and superficially resemble *Chytridiomycetes*. They have a rounded to elongated anatropeous sporangium and unusual amoeboid zoospores with filopodia and posterior pseudocilium (reduced immotile flagellum). Currently, the phylum *Sanchytriomycota* comprises a single class (*Sanchytriomycetes*), one order (*Sanchytriales*) and one family (*Sanchytriaceae*). Two monotypic genera have been placed in *Sanchytriomycota* viz., *Sanchytrium* Karpov et al 2017 (type: *Sanchytrium tribonematis* fide Karpov et al. 2017) and *Amoeboradix* Karpov et al. (2017) (type species: *Amoeboradix gromovii* fide Karpov et al. 2018). However, *Amoeboradix* and *Amoeboradix gromovii* were invalid (Art. F.5.1, Shenzhen) but validated in Index Fungorum (2020).

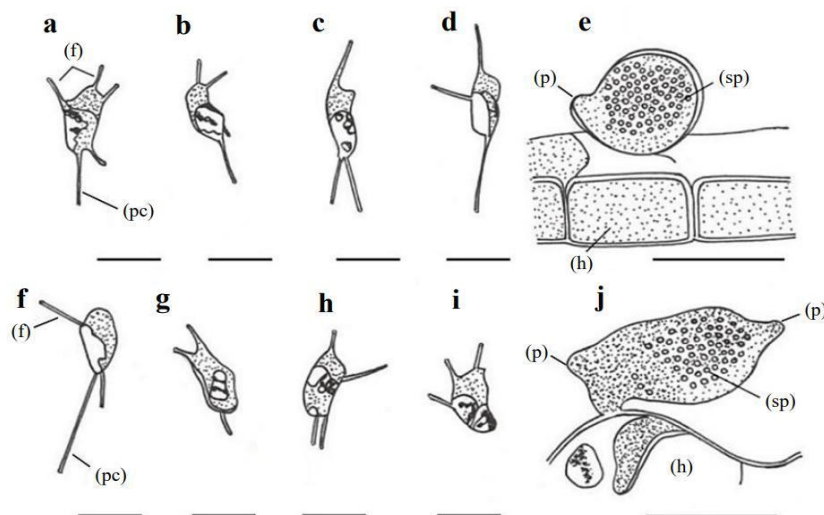


Figure 6 – Light microscopy observations of sanchytrid cells. a–e Life cycle stages of *Sanchytrium tribonematis*. f–j Life cycle stages of *Amoeboradix gromovi*. a–d, f–i Amoeboid crawling zoospores

with filopodia (f) and posterior pseudocilium (pc). g–i Zoospores with retracted pseudocilium. e, j Sporangium (sp) with one (e) or two (j) papillae (p) on the host (h) surface. Scale bars: a–d, f–I = 5 µm, e, j = 10 µm.

Both *Amoeboradix* and *Sanchytrium* are closely related and formed a long branch among higher fungi on the 18S phylogenetic tree, sister to *Glomeromycota* (Karpov et al. 2018). However, in multigene phylogenetic analyses, these two genera formed a separate lineage sister to *Blastocladiomycota* (Galindo et al. 2021). Ultrastructural studies of their zoospores and sporangia revealed extreme peculiarities in both species. They have a highly reduced flagellar apparatus with a very long kinetosome (up to 1.5 µm) composed of 9 singlets (*Sanchytrium*) and singlets/doublets (*Amoeboradix*) of microtubules and the axoneme of just four microtubules supporting a thin immobile pseudocilium. The centrioles in sporangia are also composed of nine singlets (Karpov et al. 2017, 2018, 2019). Based on phylogenetic position and morphological peculiarities *Amoeboradix* and *Sanchytrium* were placed in the new phylum *Sanchytriomycota* (Galindo et al. 2021).

Type species: *Sanchytrium tribonematis* Karpov & Aleoshin

References

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3). Borderline fungi and *Ostropales*

Borderline lichens are also known as facultatively lichenized, doubtfully lichenized, weakly lichenized, primitive lichens or loose symbionts (Coppins 2002, Motiejunaite 2005). They are poorly studied groups and the members form loose association between photobiont and mycobiont, and are often associated with lichenized groups (Hawksworth and Honegger 1994, Kohlmeyer et al. 2004, Grube and Hawksworth 2007). The taxa are morphologically different from true lichens in lacking a true thallus (upper and lower cortex, medulla and photobiont) and often form inconspicuous crustose thallus-like structures. The nutritional transitions of borderline lichens have not yet been clearly stated and they are assumed to have a saprotrophic mode despite chiefly being reported from young twigs and bark (Grube and Hawksworth 2007). *Ostropales* mainly comprised non-lichenized species which belong to the largest lichenized class *Lecanoromycetes* (Baloch et al. 2010, 2013, Thiyagaraja et al. 2021). Several members show optional lichenization, whereas individuals of the same fungus show both lichenized and saprobic lifestyles depending on the substrate (Wedin et al. 2004).

A *Fungalpedia* will be prepared for borderline lichen genera and *Ostropales* by Thiyagaraja and collaborators.

7. Fungalpedia – Note 49 *Naevia*

Naevia Fr.

Citation when using this entry: Thiyagaraja et al., in prep – Fungalpedia, borderline fungi and *Ostropales*.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 7

Classification: *Discinellaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Naevia was established by Fries (1824) to accommodate *N. orbicularis*. Massalongo (1855) added five species including *N. punctiformis* and compared the genus with *Arthopyrenia* rather than *Arthonia*. de Casati (1858) placed *Naevia* close to *Arthonia*. Almquist (1880) considered *Naevia* as a synonym of *Arthonia*. Rehm (1896) described *Naevia sensu* Fries (1849) as having hemiangiocarpous ascomata with pale discs and producing aseptate ascospores, and most other species subsequently included in the genus were based on this character combination (Kirschstein 1935, Hein 1976). Thiyagaraja et al. (2020) resurrected this genus within *Arthoniaceae* based on mtSSU, LSU and *rpb2* sequence data. Consequently, *A. dispersa* (barely lichenized or non-lichenized), *A. punctiformis* (non-lichenized) and *A. pinastri* (non-lichenized) were synonymized under *Naevia* and recovered between *Arthonia sensu stricto* and the mycoporoid clade in the phylogenetic analyses. The members are non-lichenized but often form thallus-like, whitish to greyish patches on the substrate. Apothecial ascomata are black, circular to irregular to almost stellate in outline, with a hyaline hymenium, and olive-brown epithecium with K + reaction. Asci are ovoid to clavate, bitunicate, fissitunicate with 4–8 ascospores. The asexual morph produces black pycnidia which are semi immersed to immersed. The genus shares similar morphological characteristics to *Arthonia* but mainly differs in the non-lichenized lifestyle and the presence of amyloid (I + blue, KI + blue) in the ascospores (Thiyagaraja et al. 2020).

Type species: *Naevia orbicularis* Fr.

Other accepted species: Species Fungorum, search *Naevia* for names

References

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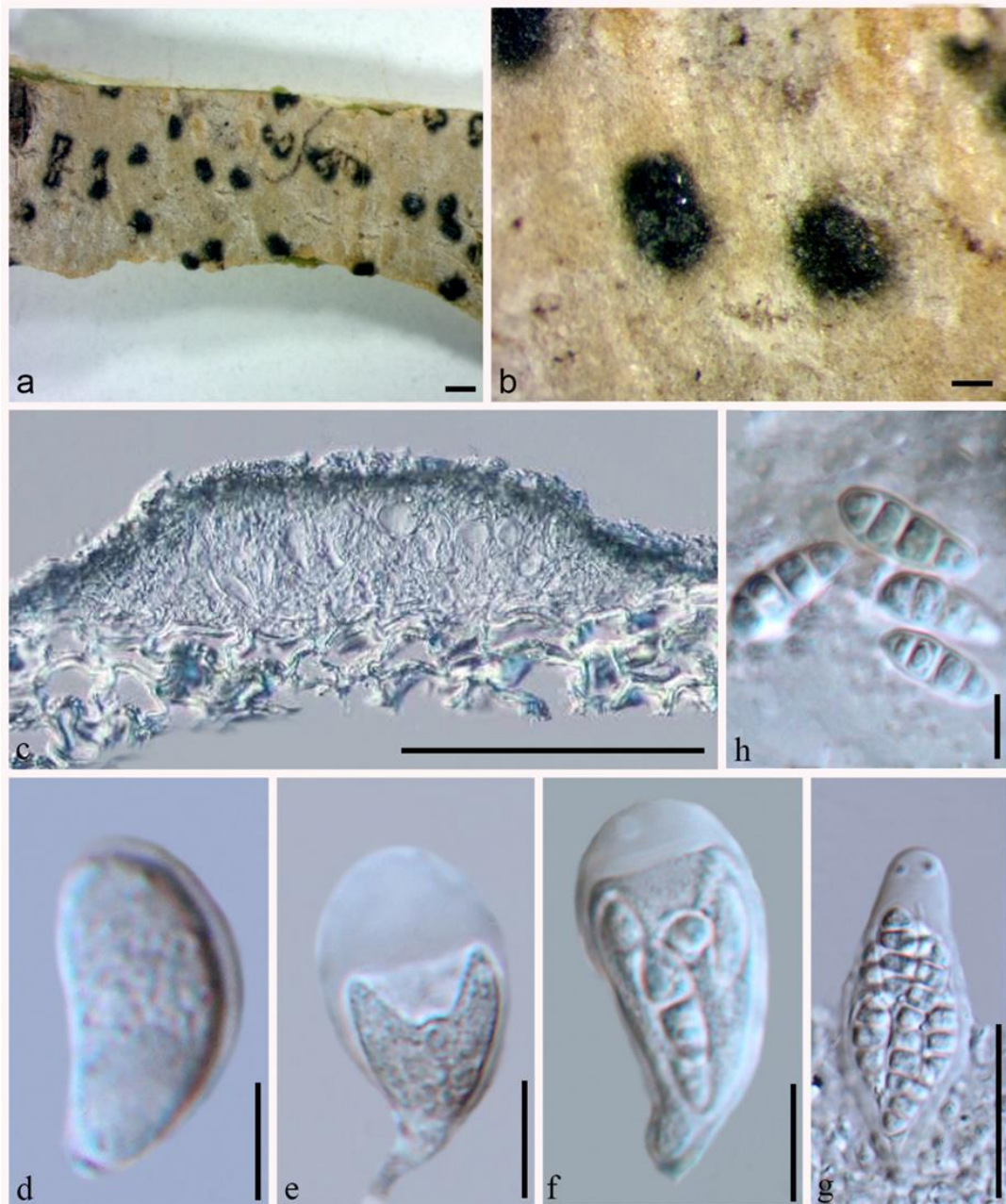


Figure 7 – *Naevia pinastri* (MFLU 17-1696). a, b Ascomata on host substrate. c Vertical section of ascoma. d–g Asci. h Ascospores. Scale bars: a = 200 μm , b, c = 100 μm , d–f = 10 μm , g = 30 μm , h = 5 μm .

4. Coelomycetes

Coelomycetes are important plant pathogens but also endophytes, epiphytes, saprobes and even lichenicolous (Wijayawardene et al. 2016, Li et al. 2020). The coelomycete entries will be published in a paper on coelomycetes.

8. Fungalpedia – Note 21 *Chaetomella*

Chaetomella Fuckel

Citation when using this entry: Huanraluek et al., in prep – Fungalpedia, coelomycetes.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 8

Classification: *Chaetomellaceae*, *Chaetomellales*, *Leotiomyetidae*, *Leotiomyetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Based on phylogenies of SSU and LSU sequence data, *Chaetomella* was transferred to *Leotiomyetes* (*Chaetomellaceae* *Chaetomellales*, *Leotiomyetes*) (Li et al. 2020). The type species, *Chaetomella oblonga*, is a coelomycete. *Chaetomella* species are characterized by pycnidial or sporodochial conidiomata with brown, unbranched setae, long acropleurogenous conidiophores, and hyaline, ellipsoid to fusiform or falcate, unicellular conidia (Sutton 1980, Rossman et al. 2004). *Chaetomella* is saprobic or parasitic on the host plant in terrestrial habitats or has been isolated from soil (Li et al. 2020). This genus is distributed in Australia, Canada, India, Zambia and the USA (Rossman et al. 2004, Crous et al. 2014, 2019).

Chaetomella comprises 60 species in Species Fungorum and the sexual morph of this genus is not yet recorded.

Type species: *Chaetomella oblonga* Fuckel

Other accepted species: See Species Fungorum – search *Chaetomella* for species names

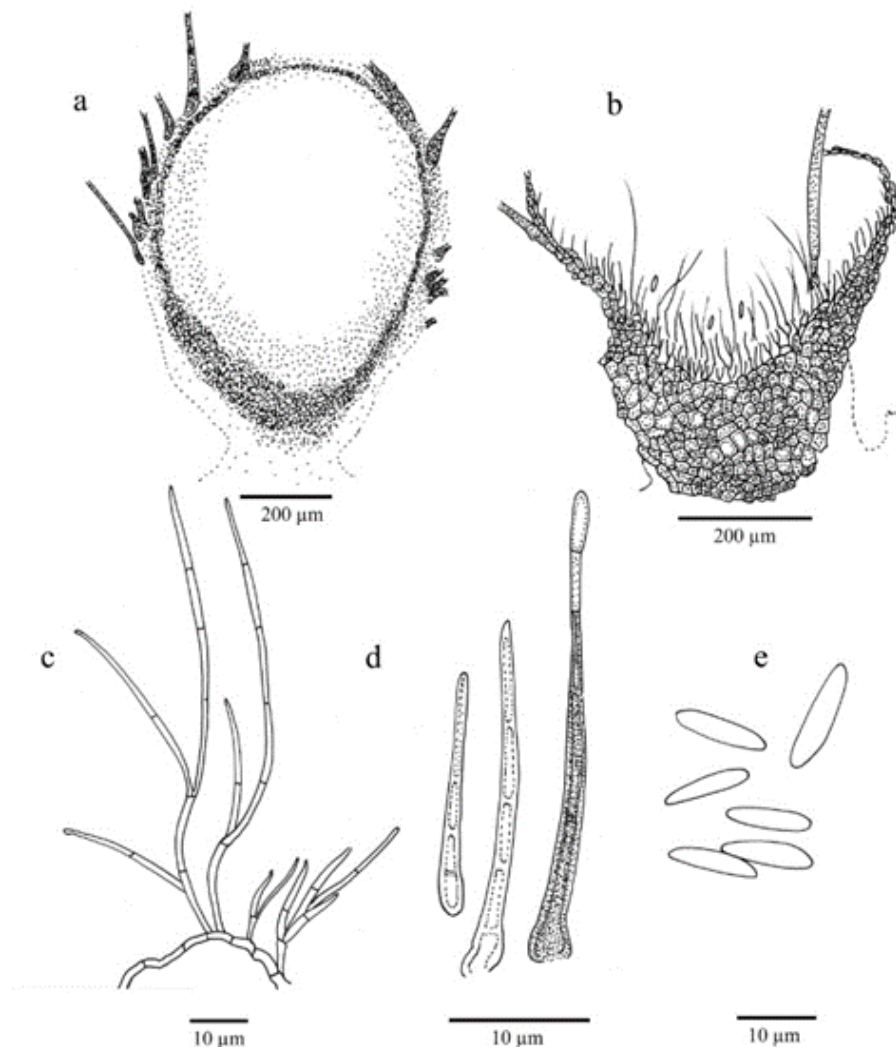


Figure 8 – *Chaetomella oblonga* (Redrawn from Rossman et al. 2004). a Vertical section of pycnidium. b Vertical section of sporodochium. c Conidiophores and conidiogenous cells. d Conidiomatal setae. e Conidia. Scale bars: a, b = 200 µm, c–e = 10 µm.

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5). Databases

We provide a list of some important web pages (Table 3). Databases are becoming increasingly important and many are being developed, however, it is important that they are continually maintained and updated.

9. Fungalpedia – Note 9 basidio.org

basidio.org: an online platform on Basidiomycota

Index Fungorum, Facesoffungi, MycoBank, GenBank

Basidiomycota constitute a major phylum of the kingdom Fungi, and includes four subphyla, 18 classes, 68 orders, 241 families, 1948 genera, and approximately 41,000 species (He et al. 2019). Information regarding species of *Basidiomycota* are published in scattered publications, and lacks a single platform. Basidio.org, accessible at <https://basidio.org>, was established to compile scattered data in a single platform. This webpage conveys a coherent and complete up-to-date outline of *Basidiomycota*, notes on orders, families, and genera of *Basidiomycota*, and updated accounts of each genus, including illustrations and photoplates of genera. The information uploaded to the website is based upon morphology, phylogeny, and recent classification of the accepted species. Raghoonundon et al. (2021) described all components of the website for easy access by the scientific community. Renowned national and international mycologists and curators periodically update the website based on newly emerged information with the aim of providing a one-stop-shop for users. The interfaces of the platform are user-friendly.

Table 3 Useful databases in Mycology.

Webpages	Content	Reference
Basidiomycetes (basidio.org)	This online platform establishes and compiles data on a single platform of basidiomycetes by providing an up-to-date outline of families, genera, species levels, phylogenetic trees, and annotations.	Raghoonundon et al. (2021)
Botryosphaerales (botryosphaerales.org)	Botryosphaerales webpage was established to compile different online journal archives and gather all published data with updates on the present taxonomy of Botryosphaerales.	Wu et al. (2021)

Table 3 Continued.

Webpages	Content	Reference
Coelomycetes (coelomycetes.org)	This online platform updates the current taxonomy in the Coelomycetes class, which updated the descriptions of an extensive collection of photo plates, illustrations, phylogenetic trees, and notes.	Huanraluek et al. (2021)
Discomycetes (discomycetes.org)	This platform updated the current taxonomy in the discomycetes, which provides up-to-date details of the extensive notes on orders, families, genera, and species.	Discomycetes (2023)
Dothideomycetes (dothideomycetes.org)	This comprehensive online platform dedicates several species, genera, families, orders, and other useful information related to fungi that belong to Dothideomycetes.	Pem et al. (2019)
Global Fungi (GlobalFungibio.tools)	It includes sequencing data, sample locations, and sample metadata. It contains 600 million observations of fungal sequences across more than 17,000 samples with geographic areas.	Větrovský et al. (2020)
Faces of Fungi (facesoffungi.org)	This portal webpage provides the fungal nomenclatural deposition of taxonomic data, phenotypic features, and other valuable data into the existing fungal classification system.	Jayasiri et al. (2015)
Forest pathogens (forestpathogens.org)	This webpage gathers forest pathogens information, which provides up-to-date details of forest pathogens and notes on orders, families, genera, and species levels.	Forestpathogens (2023)
Fungi of Brazil (http://www.cybertruffle.org.uk/brazilfung/eng/index.htm)	The website offers digital resources about the mycology of Brazil, encompassing information such as records, dates, locations, associated organisms,	Minter (2011)
Fusarium-ID database (https://www.fusarium.org/)	This database includes all agricultural, environmental, and clinically important fusarioid genera and species based curated sequences of DNA including ITS, LSU, act, cmdA, his3, <i>rpb1</i> , <i>rpb2</i> , <i>tefl</i> , and <i>tub2</i> .	Torres-Cruz et al. (2022)
Genera of Fungi (fungalgenera.org)	This platform provides basic data on all genera of fungi such ascomata, basidiomata, and lower fungi, with appropriate codes and links to important references.	Monkai et al. (2019)
GMS microfungi (gmsmicrofungi.org)	The GMS microfungi webpage is an online platform regularly updated on the taxonomic diversity, molecular phylogeny, and host-specificity of microfungi from the Greater Mekong Subregion (GMS).	Chaiwan et al. (2021)
GMS mushrooms (gmsmushrooms.org)	This developed webpage serves as a portal for updating the taxonomy, illustrations, descriptions, and other useful information for mushroom species online platform from the Greater Mekong Subregion (GMS).	Phonemany et al. (2022)
Index Fungorum (https://www.indexfungorum.org/)	The database contains names of fungi (including yeasts, lichens, chromistan fungal analogues, protozoan fungal analogues, and fossil forms) at all ranks, linked to digitized images of the protologues, in the publication where the name was first published.	Index Fungorum (2023)
Invertebrate fungi (invertebratefungi.org)	This webpage gathers and updates entomopathogenic fungi information. Species associated with invertebrate hosts, information on other invertebrates and rotifers are included.	Wei et al. (2022)

Table 3 Continued.

Webpages	Content	Reference
Italian microfungi (italianmicrofungi.org)	This comprehensive online platform is dedicated to microfungi such as Ascomycetes, Dothideomycetes, and Sordariomycetes collected from over 300 host species in terrestrial habitats in different places in Italy.	Wijesinghe et al. (2021)
Mycobank (https://www.mycobank.org/)	The database is aimed to document mycological nomenclatural novelties (new names and combinations), their associated descriptions, and illustrations. Nomenclatural experts are available to check the validity, legitimacy, and linguistic correctness of all proposed names for novel species. Also, it provides links to other databases.	Crous et al. (2004), Robert et al. (2005), Robert et al. (2013)
Mycology Collections Portal (https://www.mycportal.org/portal/index.php)	The website provides taxonomic, environmental, and specimen-based fungal diversity information. Also, it provides geo-referenced species checklists, distribution maps, and interactive identification keys along with digital imagery of fungal diversity of North America.	Miller & Bates (2017)
Onestopshop fungi (onestopshopfungi.org)	This platform focused on providing a stable platform for the taxonomy of phytopathogenic fungi and fungus-like species.	Onestopshopfungi (2023)
Outlineoffungi (outlineoffungi.org)	The comprehensive online platform is dedicated to the taxonomy and classification of fungi and fungus-like taxa and represents 500 international curators. The website provides an up-to-date outline of the fungi, which notes the phyla, classes, orders, families, and genera of fungi.	Wijayawardene et al. (2022)
Soilfungi (soilfun.org)	This webpage compiles data on all taxonomic aspects of soil fungi. Details of up-to-date classification of soil-inhabiting fungi, notes on genera and species, and current trends in soil fungal research were described.	SoilFungi (2023)
Sordariomycetes (sordariomycetes.org)	A gateway to convey coherent and up-to-date information on the ranking and classification of Sordariomycetes. Details of notes, descriptions, and photographic plates of the type or reference materials, phylogenetic trees, and their ecological and economic importance in each genus are provided.	Bundhun et al. (2020)
Species Fungorum (https://www.speciesfungorum.org/)	The website is an RBG Kew coordinated initiative to compile a global checklist of the fungi. With these systematically defined and taxonomically complete datasets, global species databases can be searched.	Species Fungorum (2023)
Trichoblast (https://trichokey.com/index.php/trichoblast)	This web portal is an accessory tool that allows comparison of a query <i>rpb2</i> sequence with reference sequences of <i>Trichoderma</i> species. It includes all 88 genetically characterized species of the genus and an almost complete set of phylogenetic markers: ITS1, ITS2, <i>tef1_int4</i> (large), <i>tef1_int5</i> (short), and <i>tef1_exon6</i> (large).	Kopchinskiy et al. (2005)

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6). Dematiaceous hyphomycetes

Dematiaceous hyphomycetes are a group of economically and ecologically important fungi. Some dematiaceous hyphomycetes are serious plant pathogens, causing devastating diseases on major crops (Klaubauf et al. 2014, Manamgoda et al. 2014, Ariyawansa et al. 2015, Kaur 2019). Some can also infect humans or directly affect human health (Hyde et al. 2018, Jayawardena et al. 2020). Dematiaceous hyphomycetes in aquatic habitats are crucial microbial decomposers (Cai et al. 2002, Hyde et al. 2016, Yang et al. 2023). Many dematiaceous hyphomycetes can produce secondary metabolites and are industrially useful (Hyde et al. 2019). Therefore, the study on dematiaceous hyphomycetes is very important. The genera of dematiaceous hyphomycetes will be treated in Liu et al. (under review).

10. Fungalpedia – Note 83 *Pleopunctum*

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

Citation when using this entry: Liu et al., in prep – Taxonomy and phylogeny of brown-spored hyphomycetes. *Fungal Diversity*, in review.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 9

Classification: *Phaeoseptaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Peizizomycotina*, *Ascomycota*, *Fungi*

Based on phylogenetic analyses of combined LSU, SSU, ITS and *tefl-α* sequence data, Liu et al. (2019) introduced *Pleopunctum* with the type species *P. ellipsoideum* and *P. pseudoellipsoideum* in the family *Phaeoseptaceae* (*Pleosporales*, *Dothideomycetes*). Subsequently, seven other *Pleopunctum* species were described in China and Thailand (Phukhamsakda et al. 2020, Boonmee et

al. 2021, Senwanna et al. 2021, Wanasinghe et al. 2022, Xu et al. 2023). *Pleopunctum* is a saprobic genus in terrestrial habitats. The sexual morph of *Pleopunctum* has not been reported. The asexual state is characterized by macronematous, mononematous, short conidiophores, monoblastic, integrated conidiogenous cells and oval to ellipsoidal, brown, muriform conidia often with a hyaline, globose to ellipsoidal basal cell (Liu et al. 2019, Phukhamsakda et al. 2020, Boonmee et al. 2021, Senwanna et al. 2021, Wanasinghe et al. 2022, Xu et al. 2023). Hyaline phragmosporous or dictyosporous conidia has been reported in this genus (Phukhamsakda et al. 2020, Senwanna et al. 2021, Wanasinghe et al. 2022).

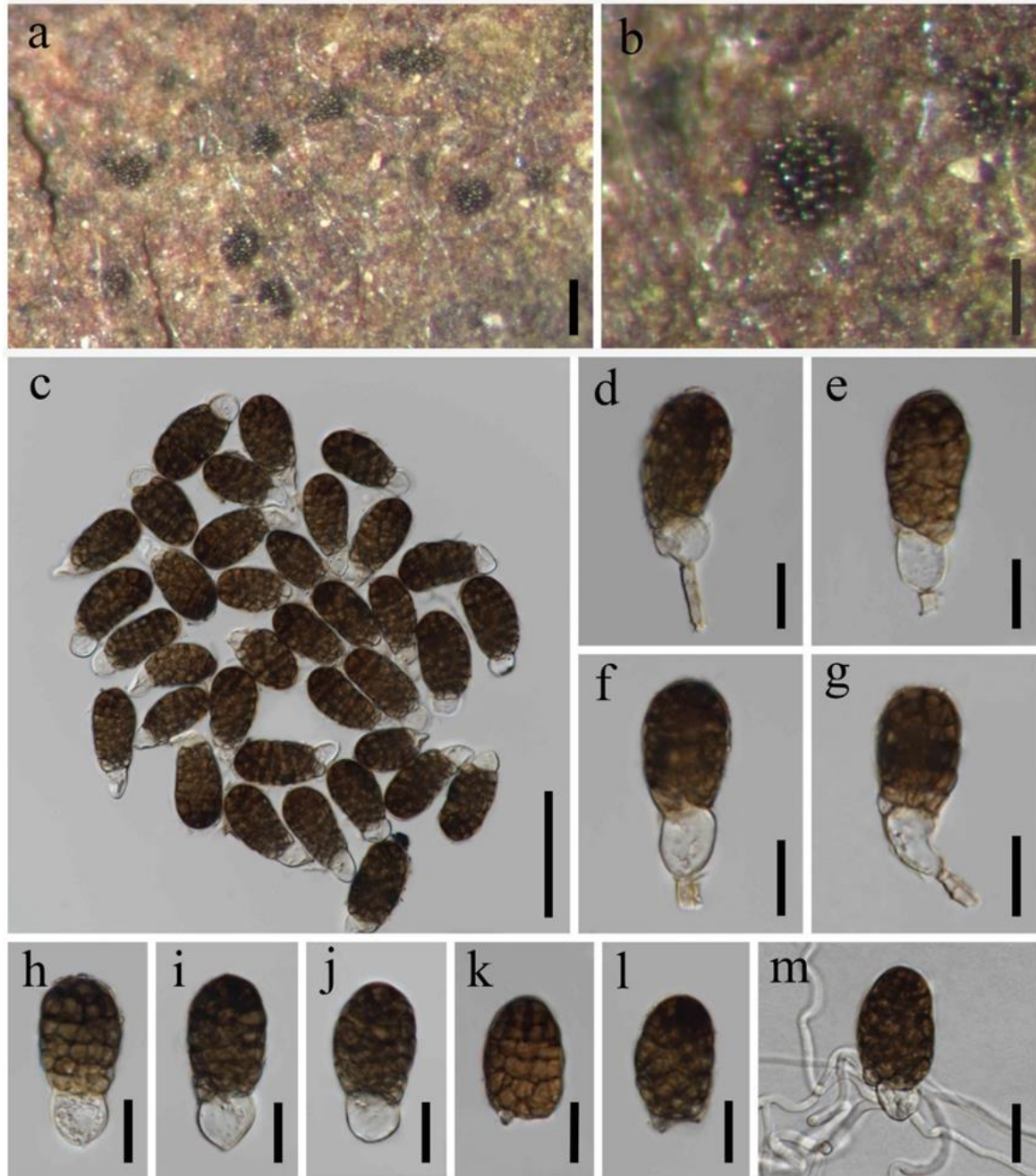


Figure 9 – *Pleopunctum ellipsoideum*. a, b Colonies on natural substrate. c Conidial mass. d–g Conidia with short conidiophores. h–l Conidia with or without hyaline basal cell. m Germinated conidium. Scale bars: a = 200 μ m, b = 100 μ m, c = 50 μ m, d–l = 15 μ m.

Type species: *Pleopunctum ellipsoideum* N.G. Liu, K.D. Hyde & J.K. Liu

Other accepted species:

Pleopunctum bauhiniae (Phukhams., D.J. Bhat & K.D. Hyde) Koukol & G. Delgado
Pleopunctum heveae Senwanna, Cheew. & K.D. Hyde
Pleopunctum megalosporum R.J. Xu, Q. Zhao & Boonmee
Pleopunctum menglaense Wanas.
Pleopunctum multicellularum R.J. Xu, Q. Zhao & Boonmee
Pleopunctum pseudoellipsoideum N.G. Liu, K.D. Hyde & J.K. Liu
Pleopunctum rotundatum R.J. Xu, Q. Zhao & Boonmee
Pleopunctum thailandicum J.Y. Zhang, Y.Z. Lu & K.D. Hyde

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7). *Diaporthomycetidae*

The subclass *Diaporthomycetidae* is important as it has many pathogenic genera (Senanayake et al. 2016, 2017a, b, 2018). Senanayake and collaborators will provide a Fungalpedia notes on all genera and some terminology of *Diaporthomycetidae*.

11. Fungalpedia – Note 84 *Asterosporium*

Asterosporium Kunze

Citation when using this entry: Senanayake et al., in prep – Fungalpedia, *Diaporthomycetidae*.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 10

Classification: *Asterosporiaceae*, *Diaporthales*, *Diaporthomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Asterosporium was introduced by Kunze (1819) based on *A. hoffmannii* Pers. Hughes (1958), regarded *Stilbospora asterosperma* Pers. as the older name for this taxon based on morphology. Thus, a new combination, *Asterosporium asterospermum* (Pers.) S. Hughes was proposed. Further, *A. asterospermum* and *A. hoffmannii* are phylogenetically identical according to molecular analysis (Hyde et al. 2020). *Asterosporium* species were previously assigned to *Sordariomycetes* genera *incertae sedis* based on molecular phylogeny (Tanaka et al. 2010). However, Wijayawardene et al. (2016) showed that *Asterosporium* species are related to *Diaporthales* based on a combined ITS and LSU sequence analyses and they placed the genus in *Diaporthales* genera *incertae sedis*

(Norphanphoun et al. 2016, Jayawardena et al. 2018). Senanayake et al. (2017a) introduced *Asterosporiaceae* (*Diaporthales*) to accommodate *Asterosporium* species. *Asterosporium* species are distinct from other genera of *Diaporthales* in having star-like, brown conidia and acervular, subepidermal, erumpent, solitary or occasionally confluent conidiomata (Senanayake et al. 2018). Four species are listed in Species Fungorum. Most species of *Asterosporium* are saprobes on decaying wood of *Betulaceae*, *Fagaceae*, *Juglandaceae* and *Sapindaceae* (Wijayawardene et al. 2016) and have been recorded from twigs of *Alnus* and *Betula* as endophytes (Tanaka et al. 2010). *Asterosporium asterospermum* has been reported to cause cankers on *Fagus crenata* and *F. sylvatica* as a mild pathogen (Sieber 2007, Senanayake et al. 2017b) and also branch dieback of peach (Pirone 1978).

Type species: *Asterosporium asterospermum* (Pers.) S. Hughes

Other accepted species:

Asterosporium acerinum Wijayaw., Camporesi, McKenzie, K. Tanaka & K.D. Hyde

Asterosporium attenuatum Murvan. & Dekan

Asterosporium strobilorum Roum. & Fautrey

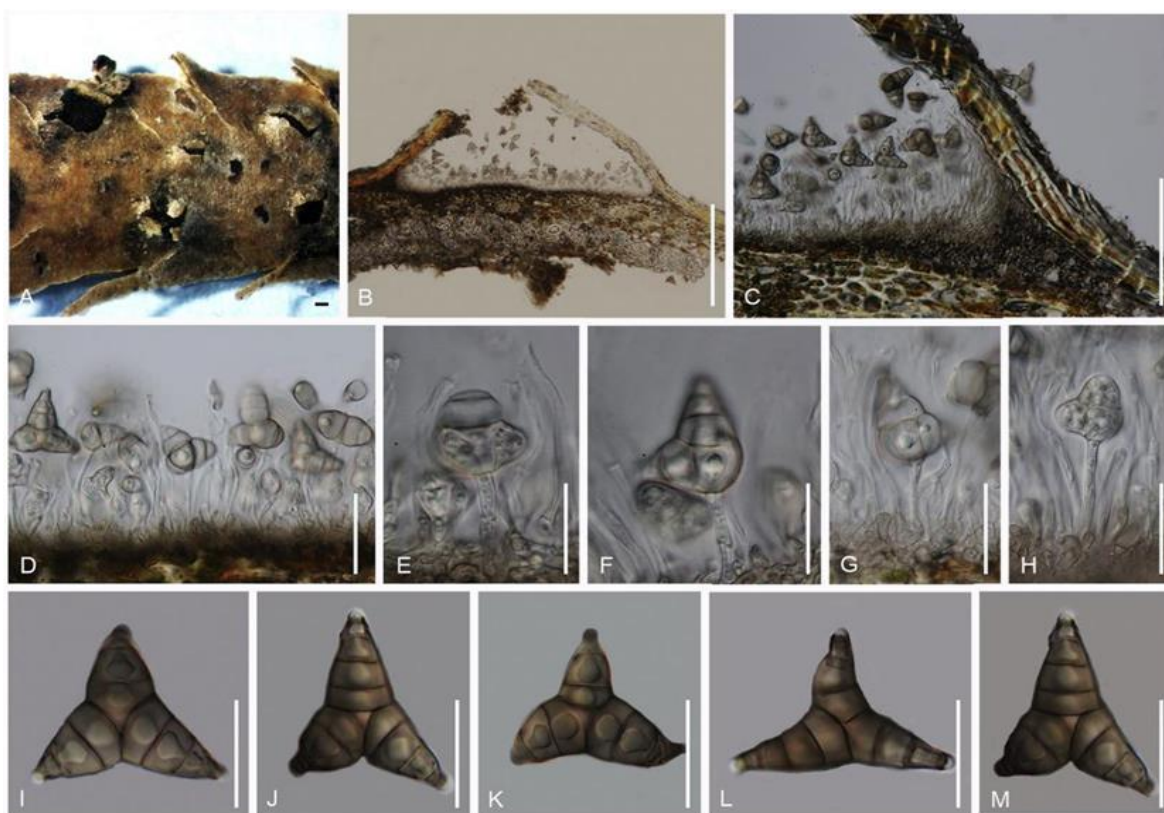


Figure 10 – *Asterosporium asterospermum* (Specimen examined – Italy, Forlì-Cesena Province, Santa Sofia, near Passo la Calla, on dead branch of *Fagus sylvatica* (*Fagaceae*), 29 September 2012, E. Camporesi, IT 805, MFLU 15-3555, HKAS 92536). a Conidiomata on host substrate. b, c Vertical sections of conidiomata. d-h Different stages of conidiogenesis. i–m Conidia. Scale bars: a = 1 mm, b = 400 μ m, c = 50 μ m, d–h = 20 μ m, i–m = 30 μ m.

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8). Discomycetes

Discomycetes represent a fascinating and diverse group of fungi with unique cup-shaped or disc-shaped fruiting bodies. They encompass a wide variety of forms and shapes and are classified across eleven classes within the *Ascomycota* (Ekanayaka et al. 2017). In addition to the discomycete entries published here, several manuscripts focusing entries on morphological characters, families, and genera of discomycetes in various classes, including *Arthoniomycetes*, *Coniocybomycetes*, *Dothideomycetes*, *Eurotiomycetes*, *Geoglossomycetes*, *Lecanoromycetes*, *Leotiomycetes*, *Lichinomycetes*, *Neolectomycetes*, *Orbiliomycetes*, and *Pezizomycetes*, are currently in preparation.

12. Fungalpedia – Note 85 *Coprotaceae*

Coprotaceae U. Lindem. & Van Vooren

Citation when using this entry: Li CJY et al., in prep – Fungalpedia, Discomycetes 1.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 11

Classification: *Incertae sedis*, *Pezizales*, *Pezizomycetidae*, *Pezizomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Based on multiple-gene analyses of LSU, *tef1* and *rpb2* sequence data by Hansen et al. (2013), *Boubovia* Svrček and *Coprotus* Korf & Kimbr. formed a sister lineage to *Ascodesmidaceae* J. Schröt. Despite previous results, Jaklitsch et al. (2016) and Ekanayaka et al. (2018) suggested integrating

them into *Ascodesmidaceae*. Following subsequent analyses by Lindemann et al. (2019), Van Vooren (2021) erected *Coprotaceae* to accommodate them. *Coprotaceae* species are usually found on dung of herbivores and omnivorous animals, rarely on soil, duff and rotten leaves (Kušan et al. 2018). They are found in eastern and southwestern Asia, Europe, and the USA (Kušan et al. 2018). There are 35 species in *Coprotaceae*, including 28 *Boubovia* species and seven *Coprotus* species (Index Fungorum 2023). Van Vooren (2021) established *Coprotaceae*, with *Coprotus* as the type genus and *Coprotus sexdecimsporus* as the type species. *Coprotaceae* is characterized by glabrous and sessile apothecia, mostly bent to uncinately paraphyses with numerous refractive bodies when live, operculate, 8–256-spored, inamyloid asci, and uni- or irregularly biserial, ellipsoid ascospores with De Bary bubbles when dry. The phylogenetic evidence of multiple-loci analyses show it as an independent lineage sister to *Ascodesmidaceae* (Lindemann et al. 2019, Van Vooren 2021). The taxonomic placement of *Coprotaceae* is in *Pezizales* (*Pezizomycetes*).

Type species: *Coprotus sexdecimsporus* (P. Crouan & H. Crouan) Kimbr. & Korf

Other accepted species: see Species Fungorum, search *Coprotus* for names.

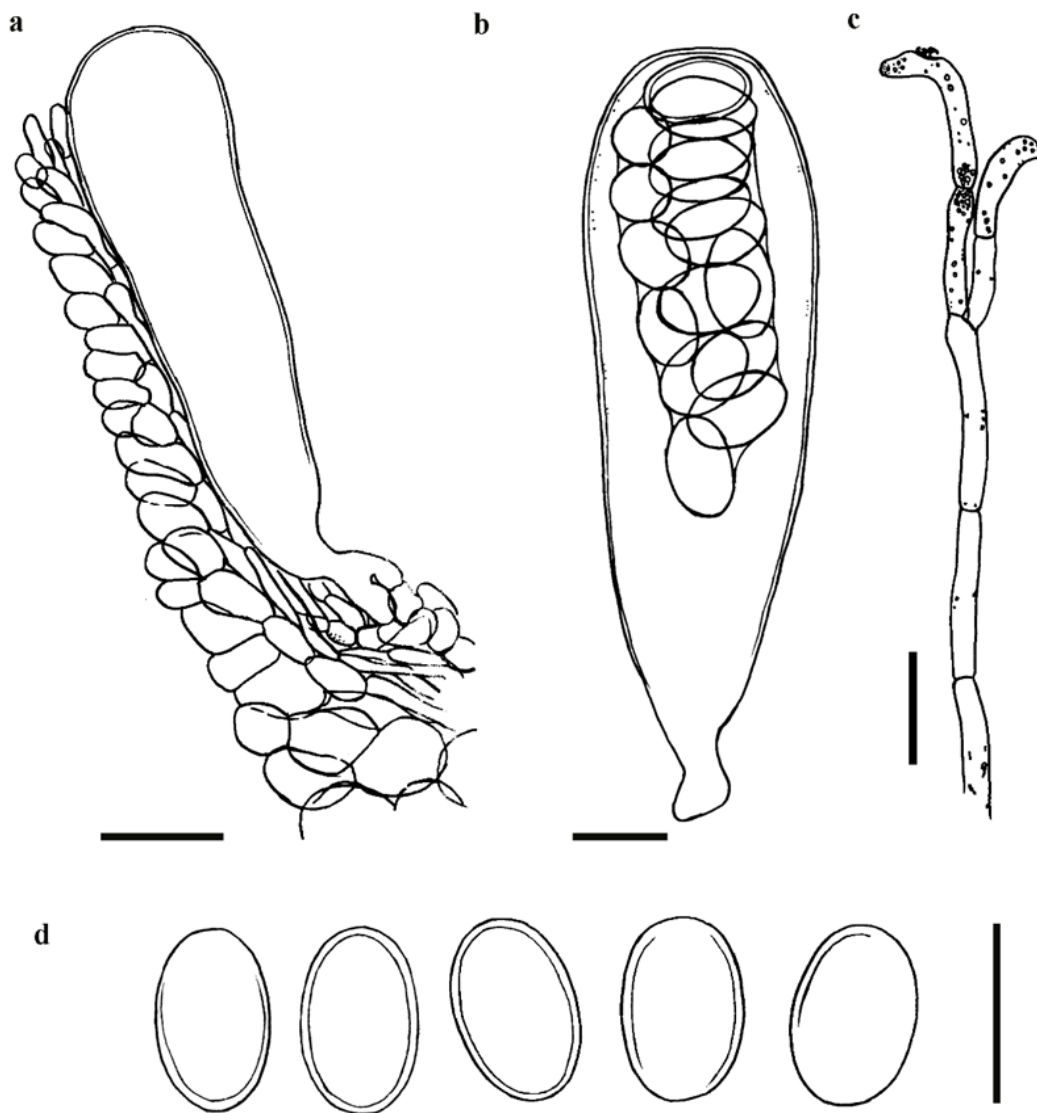


Figure 11 – *Coprotus sexdecimsporus* (CNF 2/8394 and CNF 2/894). a Excipular and marginal tissue. b Ascus. c Paraphyses. d Ascospores. Scale bars: a = 20 μm , b–d = 10 μm (Redrawn from Kušan et al. 2018).

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Entry by

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13. Fungalpedia – Note 86 *Dicephalospora*

Dicephalospora Spooner

Citation when using this entry: Luo et al., in prep – Fungalpedia, discomycetes III.

Index Fungorum, Facesoffungi; MycoBank, GenBank, Fig. 12

Classification: *Helotiaceae*, *Helotiales*, *Leotiomycetidae*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Dicephalospora is a genus of *Halotthiaceae* (*Helotiales*) reported by Spooner (1987) with *D. calochroa* as the type species. The genus comprises 18 species, of which 13 were reported from China and three from Thailand. The species occur on leaf petioles, rotten wood and twigs (Zhuang et al. 2016). *Dicephalospora* species are characterized by an erumpent or superficial, stipitate, yellow, orange, red to blackish apothecia. The ectal excipulum is composed of *textura prismatica* cells with refractive walls, and the medullary excipulum is composed of *textura intricata* cells. The species have filiform asci, J+ or J- in Melzer’s reagent, straight or slightly curved paraphyses at the apex, and hyaline, sub-ellipsoid to fusoid, guttulate ascospores, with a mucilaginous cap in the poles (Hosoya et al. 1999). There are 18 *Dicephalospora* species listed in Index Fungorum (2023). *Dicephalospora* species produce an interesting secondary metabolite named dicephalosterol, which can be used to develop drugs against prostatic hypertrophy (Hosoya et al. 1999). Due to the difficulty of obtaining pure cultures and their slow-growth on the medium, applications of *Dicephalospora* sp. are rarely published.

Type species: *Dicephalospora calochroa* (Syd. & P. Syd.) Spooner

Other accepted species: see Species Fungorum, search *Dicephalospora* for names.

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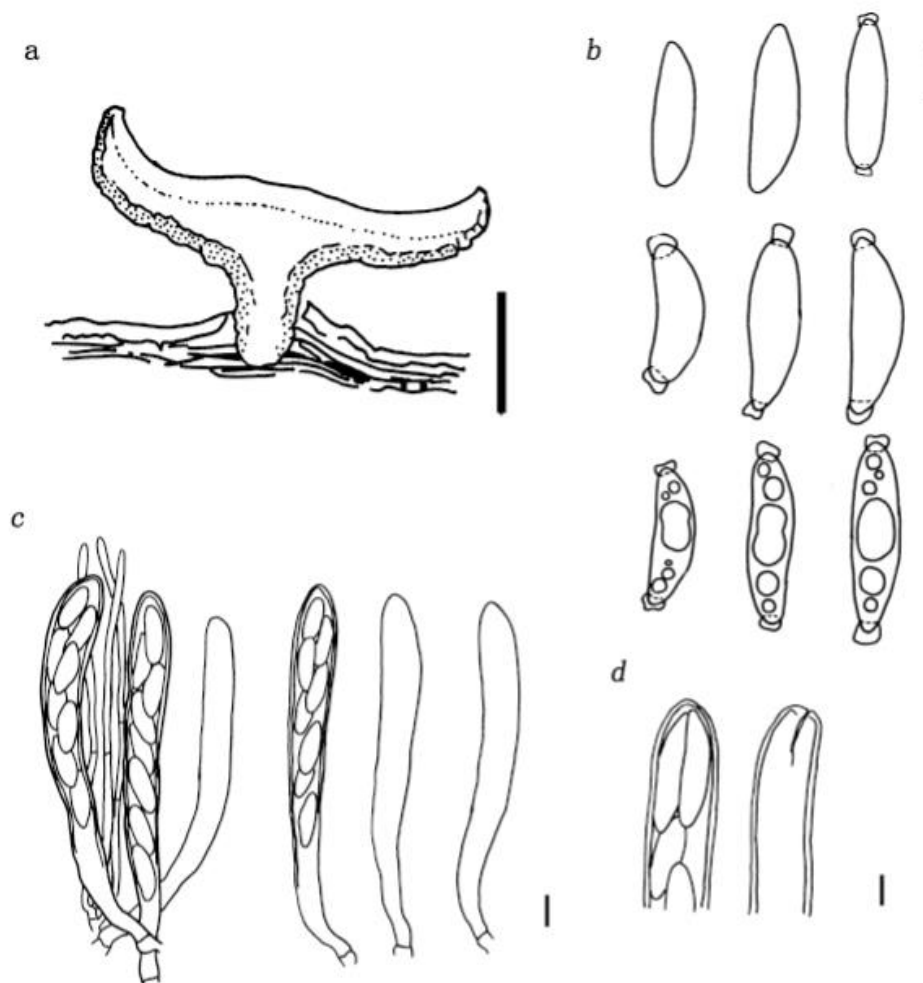


Figure 12 – *Dicephalospora chrysotricha* (PDD 78708, PDD 78710). a Section through apothecium. b Ascospores. c Asci and paraphyses. d Ascus tips before and after dehiscence. Scale bars: a = 0.5 mm, b, d = 5 μ m, c = 10 μ m (Redrawn from Verkley 2004).

14. Fungalpedia – Note 87 *Synchaetomella*

Synchaetomella Decock & Seifert

Citation when using this entry: Su et al., in prep – Fungalpedia, Discomycetes II.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 13

Classification: *Chaetomellaceae*, *Chaetomellales*, *Leotiomyces*, *Leotiomyces*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Following morphological studies and the phylogenetic analyses of SSU, Decock et al. (2005) established *Synchaetomella* and designated *Synchaetomella lunatospora* as the type species, without precise order and family affinities. Baral (2015) relied on the phylogeny of Johnston et al. (2014) to introduce *Chaetomellaceae* within *Helotiales* and transferred *Synchaetomella* into *Chaetomellaceae* (*Helotiales*) as the genus was morphologically and phylogenetically closely related to *Zoellneria* and *Discohainesia*. *Synchaetomella* was reported as a saprobic genus (Wijayawardene et al. 2017). *Synchaetomella* is a hyphomycete genus characterized by macronematous conidiophores, synnematos conidiomata with a capitulum, phialidic conidiogenesis, terminal or lateral, acropleurogenous conidiogenous cells, and falcate, allantoid or ellipsoidal, hyaline conidia accumulating in a mucilaginous mass (Decock et al. 2005, Crous et al. 2012, Fiuza et al. 2016). The genus includes three species (Decock et al. 2005, Crous et al. 2012, Fiuza et al. 2016). *Synchaetomella acerina* was found on leaves of *Acer rubrum* in the USA (Crous et al. 2012), while *S. aquatica* was found on decaying submerged leaves of *Calophyllum brasiliense* in Brazil (Fiuza et al. 2016). *Synchaetomella lunatospora* was isolated from decaying leaves of angiosperms in a tropical forest of Singapore (Decock et al. 2005).

Type species: *Synchaetomella lunatospora* Decock, G. Delgado & Seifert

Other accepted species:

Synchaetomella acerina Seifert

Synchaetomella aquatica Fiúza, Gusmão & R.F. Castañeda

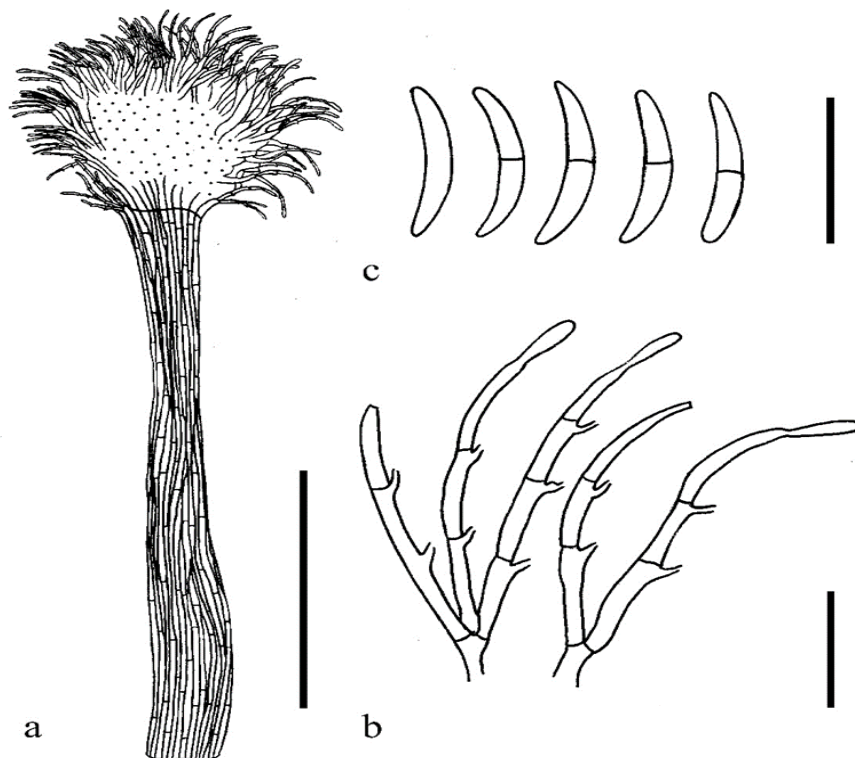


Figure 13 – *Synchaetomella lunatospora* (MUCL 43804). a Synnema. b Acropleurogenous chains of phialides. c Conidia. Scale bars: a = 150 μ m, c, d = 10 μ m. (Redrawn from Figs 1, 2 of Decock et al. 2005).

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(Edited by: **K. W. Thilini Chethana & Kevin D. Hyde**)

9). *Dothideomycetes*

Dothideomycetes is the largest and most diverse fungal class of *Ascomycota*. The class comprises the subclasses *Dothideomycetidae* and *Pleosporomycetidae*, 50 orders, 223 families, 2154 genera and over 20,000 species (Pem et al. in prep). Members of *Dothideomycetidae* appear to have adapted to (hemi-)biotrophy, while those of *Pleosporomycetidae* tend to be more necrotrophic (Haridas et al. 2020). The best-known members of this class comprise important plant pathogens such as *Alternaria*, *Phoma*, *Pseudocercospora* infecting mainly food crops and feedstocks (Crous et al. 2013). Most *Dothideomycetes* are saprobic occurring on organic material such as woody debris, dung, leaf litter and branches in terrestrial and aquatic environments (Cai et al. 2003, Tsui et al. 2000, Hyde et al. 2020, Hongsanan et al. 2020a). Others are endophytes and may have bioactive properties (Bodade 2023). Some are mutualistic as mycorrhizae, for example *Cenococcum* (LoBuglio 1999), or parasitic on bryophytes or vascular plants such as the genus *Bryosphaeria* (Döbbeler 1997). A few exist as lichens such as *Acrocordia* and *Anisomeridium* (Hongsanan et al. 2020b). The genera of *Dothideomycetes* will be annotated in the publication of Pem et al. (in prep).

15. Fungalia – Note 88 *Megacoelomyces*

Megacoelomyces Dianese, Guterres, M.D.M. Santos & G.F. Sepúlveda

Citation when using this entry: Pem et al., in prep – Genera of *Dothideomycetes*

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 14

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

Dos Santos et al. (2020) introduced *Megacoelomyces* to accommodate *M. sanchezi* based on morphology and analysis of combined ITS and LSU sequence data. *Megacoelomyces sanchezi* was collected on trichomes of living leaves of *Myrcia feniziana* (*Myrtaceae*) in Brazil (Dos Santos et al. 2020). *Megacoelomyces* is known only from its asexual state, and is characterized by large, superficial, barely setose pycnidial conidiomata situated on a loose, trichome-associated subiculum.

Megacoelomyces resembles *Callistospora* (*Ascomycota incertae sedis*), *Orphanocoela* (*Pezizomycotina incertae sedis*) and *Urohendersoniella* (*Pezizomycotina incertae sedis*) in having pycnidial, dematiaceous coelomyceteous morph with appendiculate, phragmosporous, or distoseptate conidia, but phylogenetic evidence obtained from analysis of ITS and LSU sequence data show it as a distinct lineage (Dos Santos et al. 2020). *Megacoelomyces* is a well-supported epiphytic genus in *Phaeosphaeriaceae* based on morphology and phylogenetic evidence.

Type species: *Megacoelomyces sancheziae* Dianese, Guterres, M.D.M. Santos & G.F. Sepúlveda

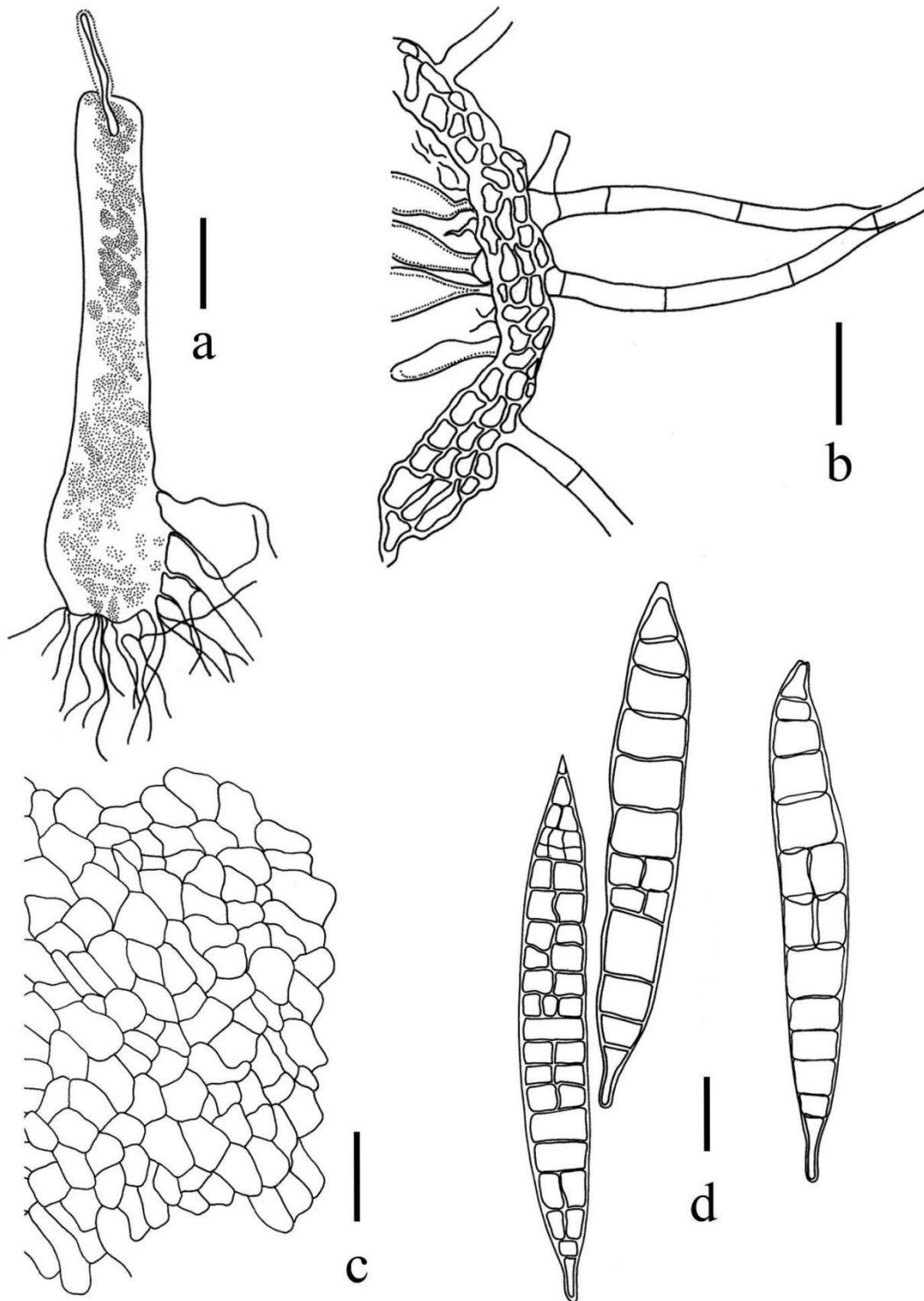


Figure 14 – *Megacoelomyces sancheziae* (UB Mycol. Col. 24030, holotype; re-drawn from Figs 2, 3 in Dos Santos et al. 2020). a Conidioma with a conidium at the ostiole and mycelial projections

forming a loose subiculum at the base. b Section through the base of a conidioma. c Conidiomatal wall cells of *textura angularis*. d Conidia. Scale bars: a = 100 µm, b, d = 20 µm, c = 30 µm.

Reference

Dos Santos MDDM, Guterres DC, Sepúlveda-Chavera GF, Souza ESDC et al. 2020 – New genus of trichomatous coelomycete on *Myrcia fenziiana* from the Brazilian Cerrado. *Mycologia* 113, 231–244.

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16. Fungaldia – Note 89 *Palmiascoma*

Palmiascoma Phook. & K.D. Hyde

Citation when using this entry: Pem et al., in prep – Genera of *Dothideomycetes*

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 15

Classification: *Bambusicolaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Palmiascoma is a monotypic genus described by Phookamsak & K.D. Hyde (Liu et al. 2015) with *P. gregariascomum* as the type species. *Palmiascoma* are basically saprobic and grow on bamboo culms. The genus has corticolous, coriaceous, gregarious uni- or multi-loculate perithecia, which are scattered, immersed to erumpent, ostiolar necks are papillate, and the peridium is composed of *textura subglobosa* and *textura angularis* cell layers. Asci are bitunicate with long pedicels. Ascospores are brown, didymosporous, apical cells are wider and more acute than basal cells. The anamorphs of *Palmiascoma* produce pycnidial conidiomata that contain one-celled conidia on artificial agar media. The present collection has small differences with type species (Liu et al. 2015) in having slightly larger ascomata (140–203 × 148–213 µm vs. 130–180 × 130–250 µm), asci ((46) 48 – 62 (67) × 7 – 9.5 vs (45–)50–60(–67) × 7–10 µm) and ascospores (10.5–14 × 5.5 vs. 11–13 × 3–4 µm). Although the genus *Palmiascoma* was introduced based on its occurrence on palm hosts, its host range is extended from palm fronds (*Areaceae*) to decaying twigs of *Morinda citrifolia* (*Rubiaceae*). *Palmiascoma* belongs to the family *Bambusicolaceae* as a single complex formed in multigene phylogeny, but is distinct morphologically having brown spores rather than hyaline, fusiform spores that are found in *Bambusicola* (Liu et al. 2015, Dai et al. 2017). Currently *Palmiascoma* has sequence data for ITS, LSU and SSU regions. *Palmiascoma* also shares similarities in morphological characters with genera such as *Didymosphaeria* and *Verruculina* in having brown didymosporous ascospores (Zhang et al. 2012) but is distinct in phylogeny. In the present study, the specimen has been collected from India, thus expanding its geographical range in Asia (India and Thailand).

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Zhang Y, Crous PW, Schoch CL, Hyde KD. 2012 – Pleosporales. *Fungal diversity* 53, 1–221.

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Figure 15 – *Palmiascoma gregariascomum* (India, Andaman and Nicobar Islands, South Andaman, Dollygunj NIOT campus (11°64'51.4" N 92°70'37.4" E PUFNI 17630). a, b Ascomata. c Vertical section of ascoma. d, e Ascospores. f Pseudoparaphyses. g–i Asci. Scale bars: c = 50 μ m, g–i = 20 μ m, d–f = 10 μ m.

10. Eminent mycologists

The human impact on the natural world significantly outweighs the reciprocated contributions. Nonetheless, the fungal kingdom presents an avenue for reevaluating our association with the natural world, imparting glimpses of optimism amidst the escalating pace of climate change. Fungi display ubiquitous presence across nearly all terrestrial and aquatic ecosystems, exerting substantial influence and instigating modifications within their respective environments (Hyde et al. 2018). Mycologists are scientists who study the diversity and evolution of these amazing organisms. Mycology, like other branches of science, is thought to have transitioned from amateur to professional in natural history during the nineteenth century (Allen 2009). Thus, the paper by Gunarathne and collaborators will include entries for eminent mycologists, as well as their contributions to the advancement of the field.

17. Fungalpedia – Note Mary Elizabeth Banning

Citation when using this entry: Gunarathne et al., in prep – Fungalpedia, Eminent mycologists.

Mary Elizabeth Banning

Mary Elizabeth Banning, the first mycologist of Maryland, USA was born to a noble family in Talbot County Maryland in 1822, as the youngest of nine children (Matta 2008). Her father – Robert Banning, a member of the Maryland House of Delegates was the influence of her appreciation of “Toadstools” (Maroske & May 2017). After her father died in 1845, she moved to Baltimore with her ailing mother and her half-sister Catherine (Matta 2008). In the face of everything, she was able to pursue her interest in fungal studies thoroughly, in the 1860s. In Banning’s “The Fungi of Maryland”, she has written, “The study of Natural Science in any of its departments has a refining influence that when used in its truest highest sense it is the Divinely appointed means of teaching faith as well as cultivating the minds and morals” (Maroske & May 2017).

According to Matta (2008) she was provided with the best schooling in Talbot County by her parents. Her interest toward mycology made her collect and observe mushrooms throughout Maryland, maintain watercolor illustrated records, a private herbarium, and a scientific library (Mary Elizabeth Banning. 2022). Charles Horton Peck, a curator of the cryptogam collections at the New York State Museum of Natural History (NYS) was a mentor and friend for Banning through her fungal taxonomic journey. Even though they never met, Peck responded to her scientific inquiries and also to her personal stories for about three decades (Haines 1995).

Banning was able to describe five fungal species in her own right and 16 more taxa with Peck based on her specimens. According to Maroske & May (2017) she has eight scientific publications to her credit, including the “The fungi of Maryland”, a water color illustrated manuscript.

Even without any assistance from a major institution, as an amateur, self-taught scientist, her writings, observations of the life cycle of fungi and morphology, and taxonomic discussion has emphasized her outstanding skills. When Banning was moved out of her mother’s house her specimens and most of her drawings seem to have been lost, but the specimens and letters she sent to Peck are kept at NYS. A fungus species *Hypomyces banningiae* based on one of her specimens was named in her honor (Peck 1879). Mary Bannings presented the remaining paintings to the New York State Museum in 1890, where they remained obscured for almost a century. The exhibit “Each a Glory Bright” has featured them as its focus since 1981, and they have been exhibited at museums across the United States (Women's history in the collections: Mary Banning)

Banning died in 1903 in a boarding house in Virginia, restrained with poverty and poor health (Maroske & May 2017). She is recognized as a prominent female figure in the field of mycology, noted for her adeptness in taxonomic nomenclature despite encountering educational limitations.

She was not recognized for her work in her lifetime. But after she was chosen to the Maryland Women’s Hall of Fame, she was awarded posthumous recognition for her contribution in mycology in 1994 (Creese 2004).



Figure 16 – Mary Elizabeth Banning (Image credits: Women’s history in the collections: Mary Banning).

Main publications

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(Edited by **Kevin D. Hyde**)

11). Epifoliar fungi

Epifoliar fungi are a group that typically inhabit leaves or occasionally other plant parts (Marasinghe et al. 2022a). They are often referred to as nutrition guilds and are commonly found in tropical and subtropical regions. In addition to being epiphytes, they typically exist as saprobes, obligate parasites, or commensals with their host plants, without causing any infection. This fungal group has garnered attention for its diverse taxonomy and ecological characteristics, but the lack of molecular data has hindered understanding of numerous genera of this group (Marasinghe et al. 2022a). Epifoliar fungi will be annotated in a Fungalpedia paper by Hyde and collaborators,

18. Fungalpedia – Note 90 *Brunneofissura*

Brunneofissura Marasinghe, Hongsanan & K.D. Hyde.

Citation when using this entry: Marasinghe et al., 2023 – Taxonomic monograph of epifoliar fungi. *Fungal Diversity* 121, 139–334

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 17

Classification: *Brunneofissuraceae*, *Asterinales*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Brunneofissura was introduced by Marasinghe et al. (2022b) with the type species of *B. thailandica*. This genus morphologically resembles *Morenoina* in its brown to black X- or Y-shaped or elongated thyriothecia, opening by a linear fissure, hyaline, oblong to cylindrical, 8-spored asci and ovoid to clavate, 1-septate, hyaline ascospores (Marasinghe et al. 2022b). However, it differs by its pale brown linear fissures, with free dark brown hyphae, appressoria at the margin of thyriothecia, and filiform pseudoparaphyses, all features that *Morenoina* lacks (Hongsanan et al. 2014, Marasinghe et al. 2022b). Phylogenetically (LSU and ITS), *B. thailandica* is close to *Cylindrohyalospora fici* to which it is morphologically comparable due to their different morphs. *Cylindrohyalospora* has superficial, rounded to oval, flattened pycnothyria with unicellular, cylindrical hyaline conidia (Tennakoon et al. 2021). The hyphae with appressoria like structures at the margins of thyriothecia reflects its biotrophic nature. This a monotypic genus and no further species have been recorded yet.

Type species: ***Brunneofissura thailandica*** Marasinghe, Hongsanan & K.D. Hyde

Other accepted species: this genus in monotypic

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Entry by

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(Edited by **Kevin D. Hyde**)

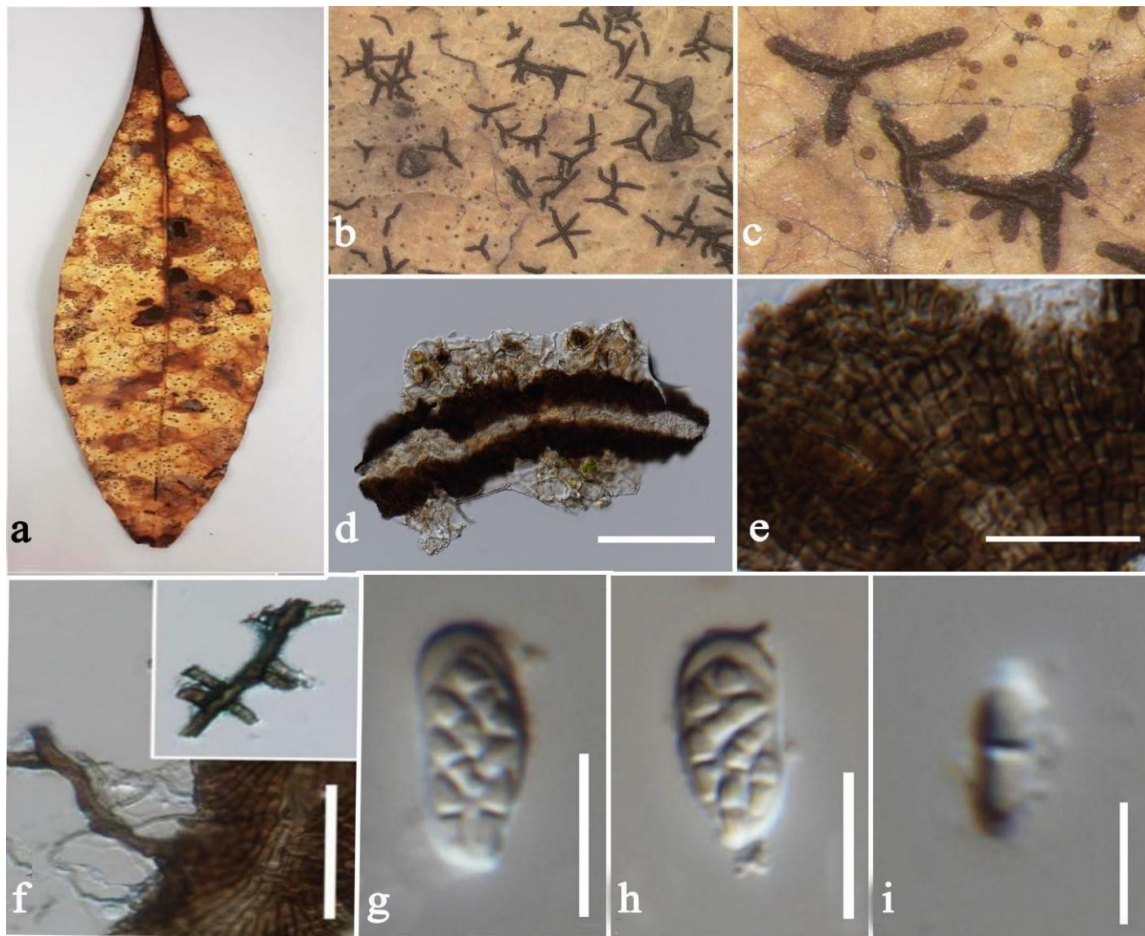


Figure 17 – *Brunneofissura thailandica* (Specimen examined – Thailand, Chiang Mai Province, Mushroom Research Center, on unidentified leaves, 11 September 2020, Diana Sandamali, MFLU 21–0040). a Leaf specimen. b, c Colonies on the leaf surface. d Thyriothecium. e Upper wall of thyriothecium. f Appressoriate hyphae at the margin. g, h Asci. i Ascospore. Scale bars: d = 100 µm, e, f = 20 µm, g, h = 10 µm, i = 5 µm.

12). Eurotiomycetes

Eurotiomycetes comprise some important human pathogens, medicinal compound producers, food spoilage organisms, lichenized taxa, rock inhabiting taxa, foliar epiphytes, endophytes, plant pathogens and saprobes (Hibbett et al. 2007, Chomnunti et al. 2012, 2014, Isola et al. 2016, Réblová et al. 2016, 2017, Wood et al. 2016, Teixeira et al. 2017, Quan et al. 2020, Sun et al. 2020, Muggia et al. 2021, Tian et al. 2021, Kandemir et al. 2022). Thakshila and collaborators will provide Fungalpedia notes on genera of order *Onygenales*, *Eurotiales* and *Verrucariales* in *Eurotiomycetes*. Tian and collaborators will provide notes on other genera and higher taxa of *Eurotiomycetes*.

19 Fungalpedia – Note 91 *Castanedomyces*

Castanedomyces Cano, L.B. Pitarch & Guarro

Citation when using this entry: Thakshila et al., in prep – Fungalpedia, *Onygenales*, *Eurotiales* and *Verrucariales*.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 18

Classification: *Onygenaceae*, *Onygenales*, *Eurotiomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

The monotypic genus *Castanedomyces* was introduced by Cano et al. (2002) in the family *Onygenaceae* (*Onygenales*, *Eurotiomycetidae*, *Eurotiomycetes*). The genus is typified by *C. australiensis* which was isolated from soil samples from Mount Lofty in South Australia (Cano et al. 2002). Only the sexual state has been reported. Based on 18S rDNA sequences, *C. australiensis* clustered with *Aphanoascus fulvescens* (Cano et al. 2002). *Castanedomyces australiensis* is morphologically similar to *A. fulvescens* in having a membranous peridium (only found in a few onygenalean genera) and lenticular ascospores with an equatorial crest and polar thickenings (Cano & Guarro 1990). However, the pseudoparenchymatous peridium is distinct between these two genera. *Castanedomyces* is characterized by solitary, more or less globose, non-ostiolate, 2–3-layered ascomata and a peridium of *textura angularis*. Asci are hyaline, globose to subglobose, and evanescent while ascospores are light brown, unicellular, and lenticular with a tuberculate wall. *Castanedomyces* has appendages which are single or in pairs, straight to flexuose, tapering to the apex, with a broad hemispherical base distributed on the surface of the ascomata.

Type species: *Castanedomyces australiensis* Cano, Pitarch & Guarro

Other accepted species: this genus is monotypic.

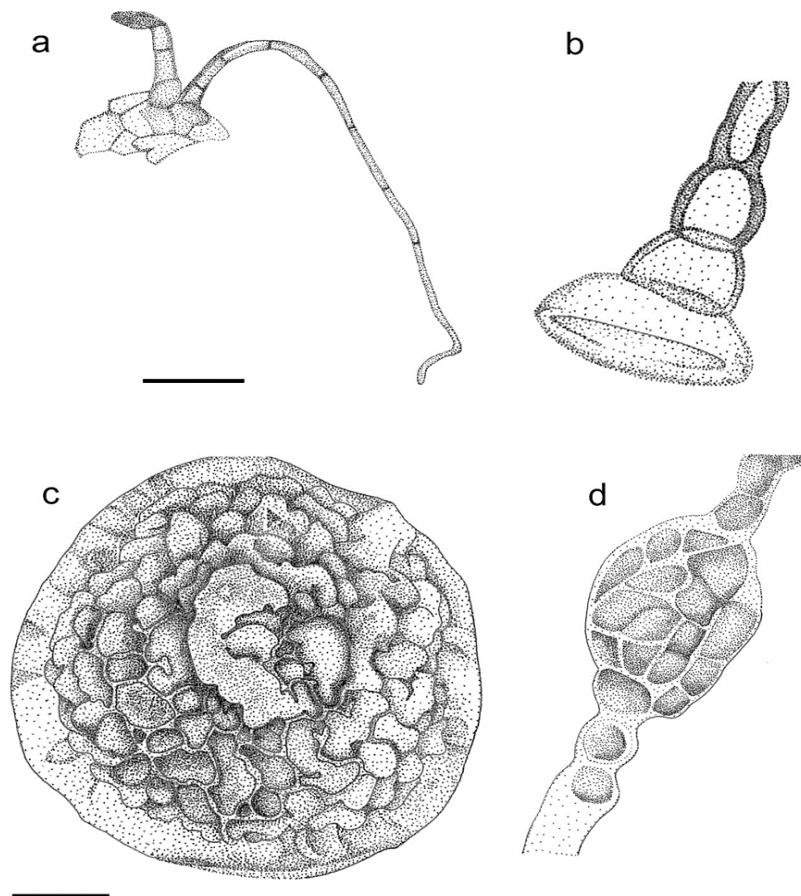


Figure 18 – *Castanedomyces australiensis* (Isotype: FMR 5484, redrawn from Cano et al. 2002). a Appendages b. Base of the appendages. c Ascospore (SEM). d Initial forms of ascospore. Scale bars: a = 25 μm , b, d = 10 μm and c = 1 μm .

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20. Fungalpedia – Note 92 *Willeya*

Willeya Müll. Arg.

Citation when using the entry: Tian et al., in prep – Fungalpedia, *Eurotiomycetes*.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 19

Classification: *Verrucariaceae*, *Verrucariales*, *Chaetothyriomycetidae*, *Eurotiomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

The genus *Willeya* was established by Müller (1883) to accommodate a saxicolous species *Willeya diffractella* which was segregated from the lichenized genus *Staurothele* initially because of its ascospores remaining pale at maturity, while species in *Staurothele* become dark brown. However, Clements (1909) described the genus *Phalostauris* for *Staurothele* with pale ascospores, so until 2014, most mycologists considered *Willeya* as a synonym of *Staurothele* (Thomson 1991, Brodo et al. 2001). Gueidan et al. (2014) resurrected the genus *Willeya* with 11 saxicolous species occurring mostly in tropical and subtropical Asia, Australia, and North America based on morphological characters and phylogenetic analysis (Tuckerman 1872, Thomson 1991, Gueidan et al. 2014). *Willeya* has only a sexual morph with a crustose, thick, cracked, pale brown, epilithic thallus with a pseudocortex, globose, hymenial algae, largely immersed perithecia with a large pale ostiole, and muriform ascospores that remain hyaline to pale brownish at maturity (Gueidan et al. 2014, Aptroot 2016, Orange & Chhetri 2022). Phylogenetically, species in *Willeya* formed a distinct clade in *Verrucariaceae*, *Verrucariales*, *Eurotiomycetes* based on phylogenies of ITS and LSU sequences (Gueidan et al. 2014). Orange and Chhetri (2022) introduced four species to this genus from Nepal which remains a monophyletic group in *Verrucariaceae*. Several further *Staurothele* species may belong in *Willeya*, but they cannot be reasonably transferred because no type material has been examined and there is no molecular data (Gueidan et al. 2014, Aptroot 2016, Orange & Chhetri 2022). Currently, the genus includes 16 saxicolous species listed by Index Fungorum (2023). Five have been included based on morpho-molecular approaches.

Type species: *Willeya diffractella* (Nyl.) Müll. Arg.

Other accepted species:

Willeya australis (Groenh.) Gueidan

Willeya eminens Orange

Willeya fusca Gueidan

Willeya honghensis (H. Harada & Li S. Wang) Orange

Willeya irrigata Orange

Willeya iwatsukii (H. Harada) Gueidan

Willeya japonica (B. de Lesd.) Gueidan

Willeya laevigata Gueidan

Willeya malayensis (Zahlbr.) Gueidan

Willeya microlepis (Zahlbr.) Gueidan

Willeya nepalensis Orange

Willeya pallidipora (P.M. McCarthy) Gueidan

Willeya protrudens Gueidan

Willeya ramosa Müll. Arg.

Willeya tetraspora Aptroot

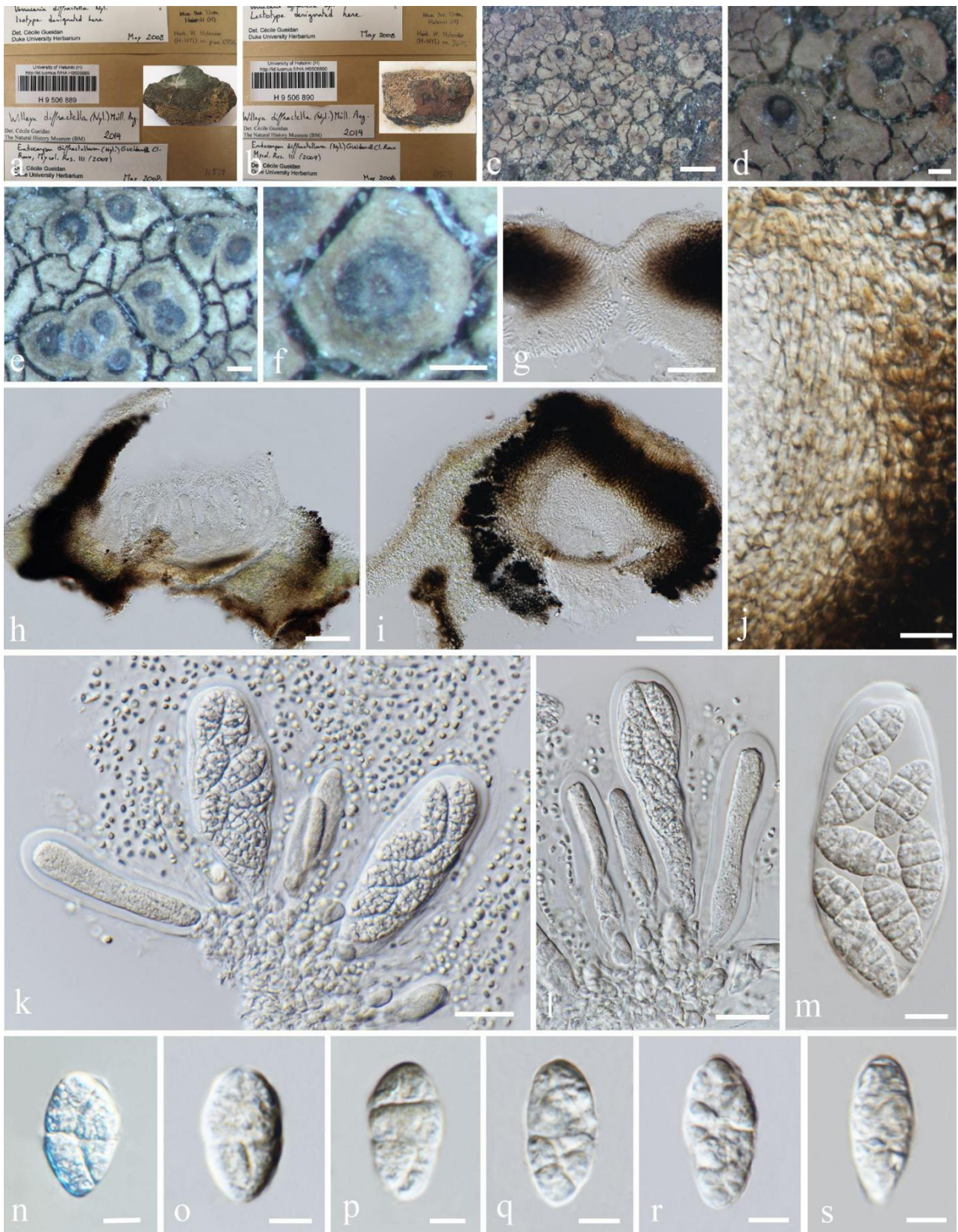


Figure 19 – *Willeya diffractella* (H, H9506889, isolectotype of *Verrucaria diffractella*; H, H9506890, lectotype of *Verrucaria diffractella*). a, b Herbarium specimen. c Habitat of *Willeya diffractella*. d-f Ascomata immersed in thallus on the host surface. g Vertical section through ostiole. h, i Vertical section of ascomata. j Vertical section through peridium. k–m Asci with hyemial algal cells. n–s Ascospores. Scale bars: c = 1000 μ m, d–f = 200 μ m, g = 50 μ m, h, i = 100 μ m, j–l = 20 μ m, m = 10 μ m, n–s = 5 μ m.

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13). Forest pathology

Forest pathogens play a critical role in the dynamics and health of forest ecosystems. A healthy ecosystem comprises fungal pathogens, but they cause diseases including root rots, cankers and wilts that can lead to tree mortality, reduced growth rates and altered natural forest composition (Fisher et al. 2020). Many forest diseases are attributed to multiple fungal genera that cause a range of diseases. For example, *Cryphonectria parasitica* causes chestnut blight in American and European chestnut trees (Rigling et al. 2018). *Dothistroma septosporum* causes needle blight of *Pinus* spp. in Australasia and South America (Barnes et al. 2014). *Hymenoscyphus fraxineus* causes dieback of *Fraxinus excelsior* in Europe (Baral et al. 2014). Diseases caused by forest pathogenic fungi lead to significant ecological and economic implications and disease impacts are pernicious when the pathogens emerge (Avila-Quezada et al. 2018, Gomdola et al. 2022). A thorough understanding of the role of fungal pathogens in forest health is imperative for maintaining the resilience and diversity of forest ecosystems. Notes on forest pathogens and terminology will be provided by Gomdola and collaborators.

21. Fungalpedia – Note 93 *Fusarium*

Fusarium Link

Citation when using this entry: Gomdola et al., in prep – Fungalpedia, forest pathogenic fungi.

Index Fungorum, MycoBank, Facesoffungi, GenBank, Fig. 20

Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Fusarium (*Gibberella*) was established and described by Link (1809) based on morphological characters, depicted by its conspicuous banana or canoe-shaped conidia. *Fusarium roseum* was designated as the type species. In 1821, the nomenclature of *Fusarium* was sanctioned by Fries, followed by the first monograph (Appel & Wollenweber 1910). Subsequently, many studies employing multiple approaches to revise the genus and delineate its species were carried out (Wollenweber 1935, Booth 1971, Crous et al. 2021, Yilmaz et al. 2021, Wang et al. 2022). *Fusarium* belongs to *Nectriaceae* (*Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*) (Maharachchikumbura

et al. 2016, Hyde et al. 2020, Wijayawardene et al. 2020, 2022, Index Fungorum 2023). To date, 1742 and 433 species epithets are listed in Index Fungorum and Species Fungorum, respectively.

The genus has a cosmopolitan distribution, manifesting mostly as notorious phytopathogens that cause devastating diseases on a wide range of crops, ornamentals and forest trees (Summerell 2019). Different *Fusarium* species have varying host preferences and cause specific plant diseases, while others are generalists (Gomdola et al. 2022). These taxa are capable of infecting different parts of a plant including the leaves, stems, twigs, branches, roots and seeds. Diseases caused by *Fusarium* inflict significant economic losses worldwide. For example, fusarium wilt (Panama disease) of banana resulted in billion dollars losses to farmers (Ploetz 2015). *Fusarium* species also cause leaf and flower spots and root rots of ornamentals such as orchids (Srivastava et al. 2018). Furthermore, *F. circinatum*, an invasive necrotroph, causes pine pitch canker disease (McCain et al. 1987), and it is one of the major pathogens affecting pine worldwide (Wingfield et al. 2008). This pathogen has also been listed in the European and Mediterranean Plant Protection Organization (EPPO) A2 quarantine list (EPPO 2023).

Other diseases caused by *Fusarium* spp. include pitch canker (Bragança et al. 2009), crown rot (also known as foot rot and root rot) (Kazan & Gardiner 2018), ear rot (Mesterházy et al. 2012), fusarium wilt (Koike et al. 2009), and leaf spots and blights (Ichikawa and Aoki 2000, Li et al. 2013). While most *Fusarium* spp. are well-known plant pathogens, some species exhibit saprobic life modes and others colonize plants as endophytes (Summerell et al. 2011).

Fusarium species are traditionally delimited based on three species concepts namely, the biological, morphological and phylogenetic species concepts (Leslie et al. 2001). Crous et al. (2021) re-examined the fusarioid taxa in *Nectriaceae* and performed a phylogenetic analysis of the combined ITS, LSU, *rpb1*, *rpb2* and *tef1* sequences to classify *Fusarium* and allied genera. Yilmaz et al. (2021) categorized 196 *Fusarium* species into nine species complexes based on the combined ITS, LSU, *Btub*, *CAM*, *IGS*, *rpb1*, *rpb2* and *tef1* sequence data, whereby *rpb2* region was the most effective in the species delineation of many *Fusarium* species complexes. Some studies proposed to maintain *Fusarium* and allied genera as a single genus while others segregated *Fusarium sensu lato* into multiple genera including *Albonectria*, *Bisifusarium*, *Fusarium*, *Neocosmospora*, and *Rectifusarium* (Lombard et al. 2015, Crous et al. 2021, Yilmaz et al. 2021).

For morphological comparisons, it is ideal to incorporate data related to both sexual and asexual morphs (Crous et al. 2021). Regarding conidia, *Fusarium* species are delimited based on the presence of macro- and micro-conidia. They are characterized primarily by thick-walled macroconidia that have different apical and basal cell shapes. Microconidia are sometimes present (Samiksha & Kumar 2021). *Fusarium* species are depicted mostly by hyaline, guttulate, 0- to multi-septate, fusiform or falcate, oval to clavate, or straight to slightly curved conidia, with a curved or conical apical and basal cell (Wang et al. 2022). Colonies display a range of colours when grown in artificial media such as MEA, PDA or WA, mostly seen as yellowish- to orange-white or pink to reddish or lilac mycelium. Many pathogenic *Fusarium* species produce appressoria prior to infecting their hosts (Chethana et al. 2021a, b).

Type species: *Fusarium roseum* Link

Other accepted species: Species Fungorum – search *Fusarium* for names.

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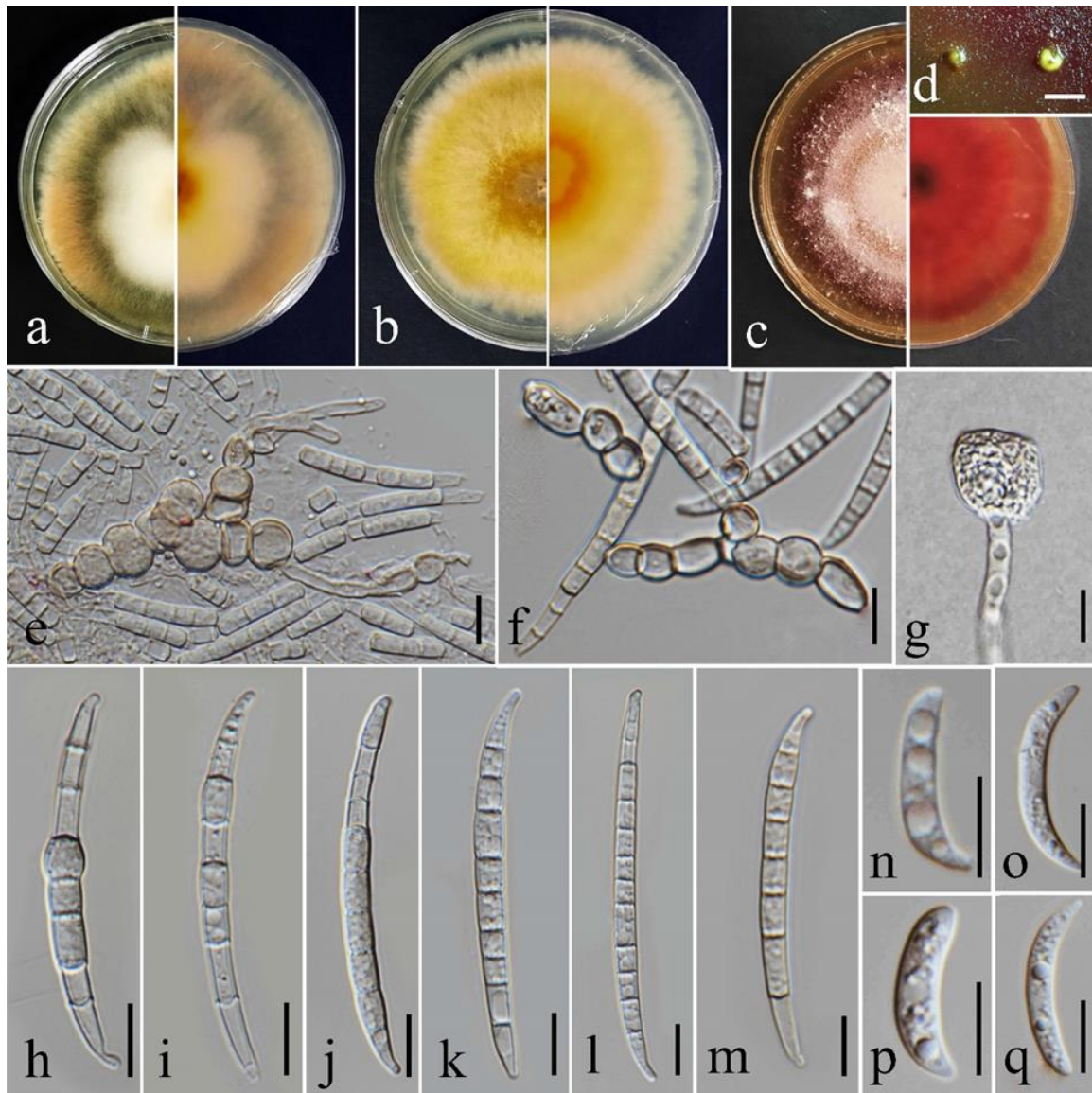


Figure 20 – *Fusarium* spp. a–c Top and reverse colony of *Fusarium* species. d Appearance of pycnidia in MEA. e, f Chlamydospores g Appressorium h–q Conidia. Scale bars: d = 2.5 mm, e–q = 10 μ m.

14). Freshwater fungi

Freshwater fungi constitute a distinct group that is dependent on freshwater environments for survival, resulting in a remarkable morphological diversity (Calabon et al. 2022, 2023). They have been studied over a long period (Shearer et al. 1993, Luo et al. 2004, Yang et al. 2023) and play an essential role in the decomposition of wood materials and carbon cycling (Wong et al. 1998, Bucher et al. 2004). The identification and revision of their taxonomy and classification have been well-documented, with recent comprehensive taxonomic monographs and freshwater fungal numbers published by Shearer et al. 2009, Luo et al. (2019), Dong et al. (2020), Calabon et al. (2022, 2023).

Fungalpedia notes will be provided on all genera and higher taxa of freshwater fungi by Calabon and collaborators.

22. Fungalpedia – Note 94 *Ascagilis*

Ascagilis K.D. Hyde

Citation when using this entry: Calabon et al., in prep – Fungalpedia, freshwater fungi.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 21

Classification: *Aliquandostipitaceae*, *Jahnulales*, *Incertae sedis*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Ascagilis has sessile or stalked ascomata, cellular pseudoparaphyses, and 1-septate, brown ascospores mostly with a refractive mucilaginous pad at each end. *Ascagilis* was established by Hyde (1992) to accommodate *A. bipolaris*, which was isolated from submerged wood at the base of a waterfall in Australia. However, subsequent study led to the suppression of *Ascagilis* as its type species *A. bipolaris* was considered to belong in *Jahnula* (Hyde & Wong 1999). According to Dong et al. (2020), the presence of fusiform to ellipsoidal ascospores with bipolar pads is sufficient for distinguishing *Ascagilis* as a distinct genus based on their new collections, which is also supported by phylogenetic analysis. *Ascagilis* species can be distinguished by their ascomata appendage and ascospores, which exhibit characteristic features such as septa, mucilaginous pads, dimension and dimorphic/monomorphic form. However, insufficient sequence data for certain species (e.g., *A. submersa*, *A. sunyatsenii* and *A. thailandensis*) may obscure their delimitation in phylogenetic analyses (Dong et al. 2020). The genetic markers recommended for current classification include LSU, SSU and ITS. All species in *Ascagilis* have been exclusively discovered in freshwater habitats. *Ascagilis* species are observed and isolated from submerged decaying wood, making them important decomposers that play a crucial role in nutrient cycling within freshwater habitats (Hyde & Wong 1999, Hyde 1992, Inderbitzin et al. 2001, Hyde et al. 2017, Hyde et al. 2019, Dong et al. 2020).

Type species: *Ascagilis bipolaris* K.D. Hyde

Other accepted species:

Ascagilis bipolaris K.D. Hyde – freshwater species

Ascagilis guttulaspora (Qing Tian, Y.Z. Lu & K.D. Hyde) W. Dong, Doilom & K.D. Hyde – freshwater species

Jahnula guttulaspora Qing Tian, Y.Z. Lu & K.D. Hyde

Ascagilis queenslandica (Dayar., Fryar & K.D. Hyde) W. Dong, Doilom & K.D. Hyde – freshwater species

Jahnula queenslandica Dayar., Fryar & K.D. Hyde

Ascagilis seychellensis (K.D. Hyde & S.W. Wong) W. Dong, Doilom & K.D. Hyde – freshwater species

Jahnula seychellensis K.D. Hyde & S.W. Wong

Ascagilis submersa W. Dong, H. Zhang & K.D. Hyde – freshwater species

Ascagilis sunyatsenii (Inderb.) W. Dong, Doilom & K.D. Hyde – freshwater species

Aliquandostipite sunyatsenii Inderb.

Ascagilis thailandensis W. Dong, H. Zhang & K.D. Hyde – freshwater species

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Entry by

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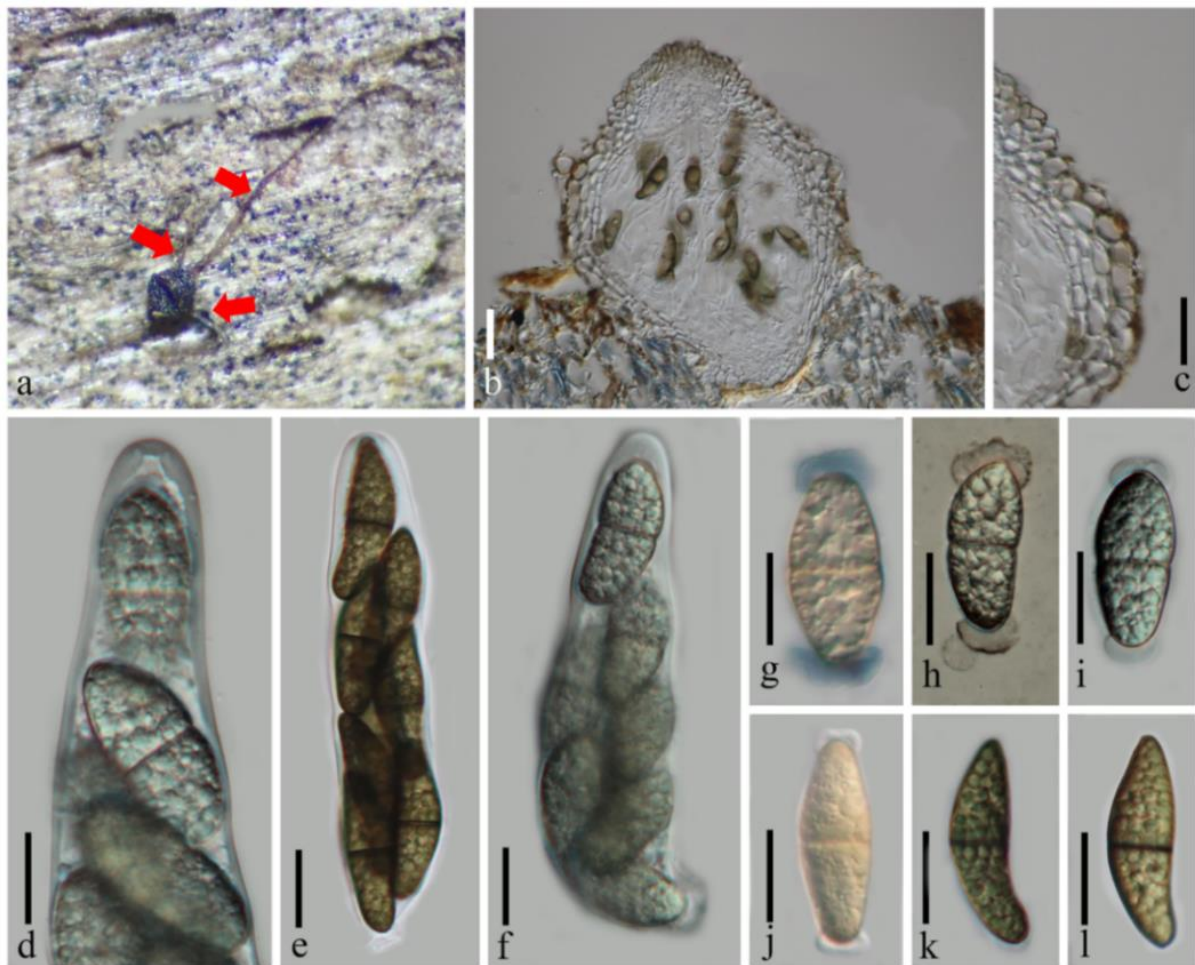


Figure 21 – *Ascagilis* species. a, d, f, h, i *A. submersa*. b, c, e, k, l *A. thailandensis*. g, j *A. bipolaris*. a Ascoma attached to the wood with broad hyphae (arrowed). b Section of an ascoma. c Structure of peridium. d–f Bitunicate asci. g–l Ascospores (h Ascospore in Indian Ink). Scale bars: b, c = 50 μ m, d–l = 20 μ m.

23. Fungalpedia – Note 95 *Conioscypha*

Conioscypha Höhn.

Citation when using this entry: Mukhopadhyay et al., in prep – Fungalpedia, *Savoryellomycetidae* and ascomycete terminology.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 22

Classification: *Conioscyphaceae*, *Conioscyphales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Höhnel (1908) established the dematiaceous hyphomycete genus *Conioscypha* (Shearer 1973), with *C. lignicola* as the type species from submerged *Carpinus* wood in Austria. *Conioscypha* has compact and erumpent colonies with immersed, hyaline to sub-hyaline branched and septate hyphae. Conidiogenous cells arise laterally or terminally on the hyphae, are enteroblastic, hyaline, and short-stalked. Conidia are one-celled, dark-brown, variable in shape, smooth-walled, and have a scar at the point of secession (Shearer 1973). Shearer (1973) also introduced another species *C. varia* Shearer, from balsa wood, which morphologically differs from *C. lignicola* by having smaller, more elongated, thinner-walled conidia which are more variable in shape as compared to *C. lignicola*. Réblová & Seifert (2004) introduced the sexual morph *C. varia* and named it *Conioscyphascus* Réblová & Seifert. *Conioscyphascus* produces small, several layered and pale orange perithecia with long ostioles, unitunicate, 8-spored asci with an inamyloid refractive apical ring, and septate, fusiform ascospores (Réblová & Seifert 2004). Réblová & Seifert (2004) observed the anamorph of *Conioscypha* from the isolated ascospores which were identical to *C. varia* (Shearer 1973). Based on molecular phylogeny using LSU, *Conioscypha* and *Conioscyphascus* formed a clade with strong statistical support, which proved that they are congeneric. Because of the “one fungus / one name” concept, *Conioscyphascus* was considered a synonym of *Conioscypha* (Zelski et al. 2015, Réblová et al. 2016). Based on the multigene phylogeny of LSU-SSU-*rpb2*, Réblová et al. (2016) established the monotypic order *Conioscyphales* (*Conioscyphaceae*, *Hypocreomycetidae*). Hongsanan et al. (2017), transferred *Conioscyphales* into *Savoryellomycetidae* with *Conioscypha* as the only genus, based on phylogeny. Out of 17 accepted species, six species grow on submerged wood in freshwater habitats and one was isolated from twigs in a freshwater habitat, eight are saprobes, and two were isolated from soil (Chuaseharonnachai et al. 2017, Liu et al. 2019b, Hyde et al. 2020).

Type species: *Conioscypha lignicola* Höhn.

Other accepted species:

- C. aquatica* Z.L. Luo, K.D. Hyde & H.Y. Su (2019)
- C. bambusicola* Matsush. (1975)
- C. boutwelliae* Hern.-Restr. (2018)
- C. dimorpha* Matsush. (1996)
- C. fabiformis* Matsush. (1993)
- C. gracilis* (Munk) Zelski, Raja, A.N. Mill. & Shearer (2014)
- C. hoehnellii* P.M. Kirk (1984)
- C. japonica* Udagawa & Toyaz. (1983)
- C. minutispora* Hern.-Restr., Gene & Guarro (2014)
- C. nakagirii* Chuas., Somrith., Suetrong, Boonyuen (2017)
- C. peruviana* Zelski, Raja, A.N. Mill. & Shearer (2015)
- C. pleiomorpha* Hern.-Restr., R.F. Castaneda & Gene (2017)
- C. submersa* Z.L. Luo, K.D. Hyde & H.Y. Su (2019)
- C. taiwania* J.L. Chen & Tzean (2000)
- C. tenebrosa* N.G. Liu, K.D. Hyde & J.K. Liu (2019)
- C. varia* Shearer (1973)
- C. verrucosa* J. Yang & K.D. Hyde (2020)

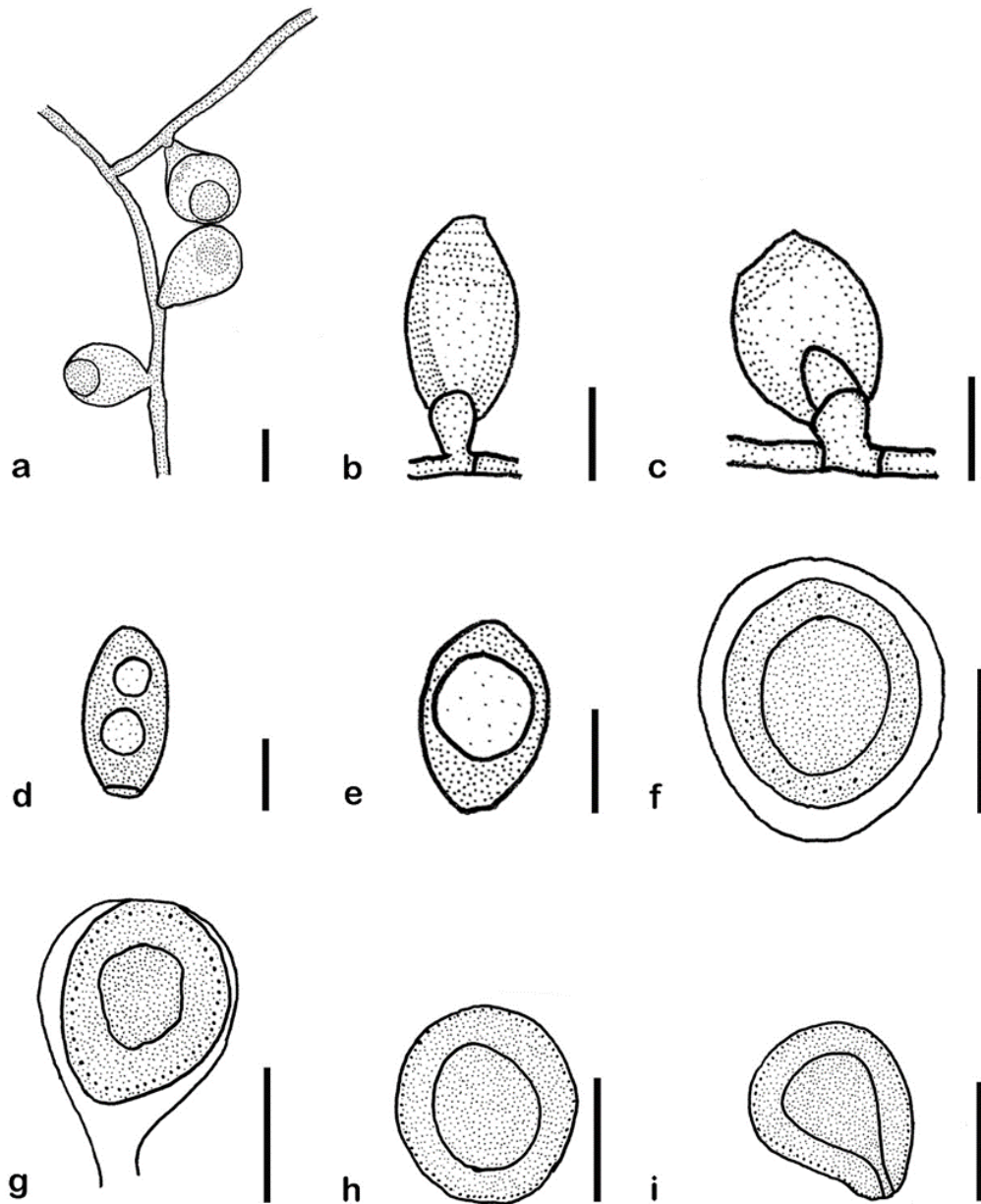


Figure 22 – *Conioscypha* spp. a *Conioscypha hoehnelii* conidiogenous cell. b-e *Conioscypha taiwaniana* conidiogenous cells and conidia with 1–2 oil droplets (Redrawn from Chen & Tzean 2000). f–i *Conioscypha lignicola* (CS-175, holotype, redrawn from Shearer 1973). f, g Mature conidia surrounded by collarettes. h, i Mature conidia with pigment deposited irregularly along the periphery of the thickened walls. Scale bars: a–i = 10 μ m.

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15). Fungicolous fungi

Fungicolous fungi are an ecologically and economically important, widespread group of organisms observed in both aquatic and terrestrial habitats (Jeffries 1995, Gams et al. 2004, Sun et al. 2019). These fungi typically have associations between various lineages across the fungal kingdom (Gams et al. 2004, Pöldmaa 2011, Lin et al. 2016, Sun et al. 2019). Gajanayake and collaborators will provide Fungalpedia notes on genera of fungicolous fungi.

24. Fungalpedia – Note 96 *Hypomyces*

Hypomyces (Fr.) Tul. & C. Tul.

Citation when using this entry: Gajanayake et al., in prep – Fungalpedia, fungicolous fungi. Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 23

Classification: *Hypocreaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Hypomyces (*Hypocreaceae*, *Hypocreales*) was originally considered as a subgenus of *Hypocrea* Fr. by Fries (1825), but later it was raised to genus rank by Tulasne & Tulasne (1860). *Hypomyces lactifluorum* (Schwein.) Tul. & C. Tul. which was originally discovered on *Agaricus lactifluus*, collected from the USA, was designated as the type species of *Hypomyces*. Arnold (1971) conducted the first comprehensive taxonomic study for *Hypomyces* and differentiated it from the closely related *Arachnocrea*, *Apiocrea*, and *Peckiella*. Thereafter, several studies on *Hypomyces* were conducted (Rogerson & Samuels 1985, 1989, 1993, 1994, Pöldmaa 1996, 2003, 2011, Pöldmaa et al. 1997, 2000). Accordingly, a link between asexual morphs of *Hypomyces* and *Cladobotryum* was revealed based on morphology and phylogeny (Rogerson & Samuels 1993, 1994, Pöldmaa 2003, 2011). The use of *Hypomyces* over *Cladobotryum* was recommended (Rossman et al. 2013, Hyde et al. 2020).

Hypomyces are fungicolous taxa associated with *Ascomycota* and *Basidiomycota*, but some taxa (*H. mycophilus*, *H. perniciosus*) are pathogenic on commercially cultivated mushrooms (Rogerson & Samuels 1993, 1994, Pöldmaa et al. 2000, Pöldmaa 2003, Gea et al. 2021, Zhang et al. 2023). Occasionally, *Hypomyces* taxa have been reported in association with plant and other substrates such as bark, wood, leaves, mosses, humus, rocks, insect galls and lichens (Rogerson & Samuels 1993, 1994, Lechat et al. 2017, Farr et al. 2021, Karimi et al. 2022, Perera et al. 2023). *Hypomyces* has a cosmopolitan distribution with most taxa reported as pathogens or saprobes

(Rogerson & Samuels 1993, 1994, Rossman et al. 1999, Pöldmaa 1996, 2003, 2011). Bioactive metabolites of *Hypomyces chrysospermus* are an important resource for the pharmaceutical and drug industries. *Hypomyces chrysospermus* has anticancer, antimicrobial, and antioxidant properties including anti-metastatic and anti-proliferative activity (Chakraborty et al. 2016, Dikmen et al. 2020).

The sexual morph of *Hypomyces* is characterized by peritheical ascomata which are superficial on or semi immersed to immersed in a concolorous subiculum. Asci are cylindrical and 8-spored. Ascospores are partially overlapping, uniseriate, fusiform with blunt or acute ends, spinulose to tuberculate or verrucose and hyaline (Rossman et al. 1999, Poldmaa 2011, Perera et al. 2023). The asexual morph of *Hypomyces* is hyphomycetous and it is characterized by conidiophores that are usually micronematous, occasionally semi-macronematous to macronematous, aseptate or septate and form verticils on the conidiogenous cells. Conidiogenous cells produce one to several conidiogenous loci. Conidia are solitary, usually ellipsoidal to fusiform, cylindrical, ovoid, obovoid or clavate and hyaline to green (Rossman et al. 1999, Poldmaa 2011, Perera et al. 2023).

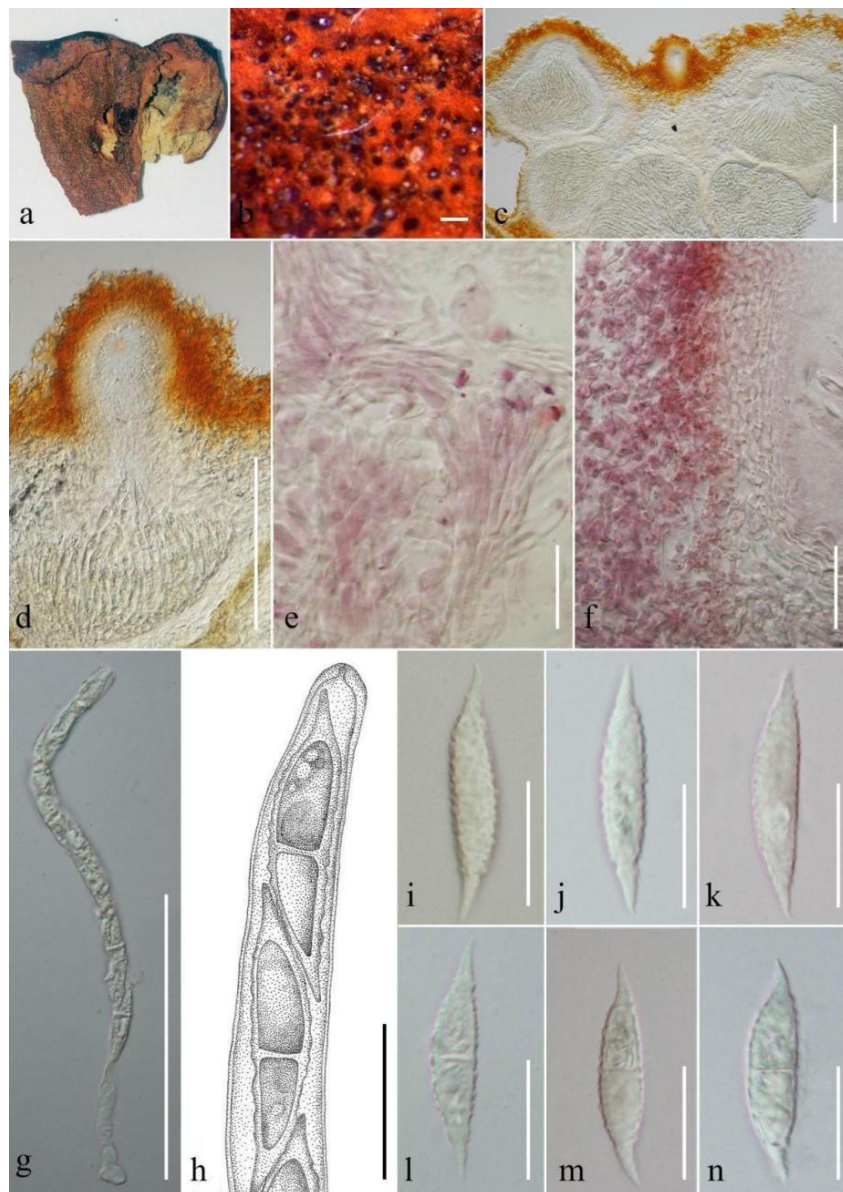


Figure 23 – *Hypomyces lactifluorum* (PH00076754). a Host (*Lactarius* sp.). b Ascomata on host. c, d Vertical section of ascomata. e Hyphae of the subiculum in 3% KOH. f Section of peridium in 3% KOH. g Ascus. h Illustration of ascus apex (Redrawn from Rogerson & Samuels 1994). i–n Ascospores. Scale bars: b, c, d = 200 μ m, g = 80 μ m, e = 50 μ m, f, h–n = 20 μ m. Photo Credits: R.H. Perera.

The current identification of *Hypomyces* taxa is based on morphological characteristics combined with multigene phylogenetic analyses. The recommended molecular markers for *Hypomyces* species are ITS, LSU, *rpb1*, *rpb2* and *tef 1-α* (Rehner & Samuels 1995, Põldmaa 2000, Põldmaa et al. 2000, Põldmaa 2011, Zare & Gams 2016). To date, 118 *Hypomyces* taxa are listed in Species Fungorum (2023) and around 60 taxa have molecular data.

Type species: *Hypomyces lactifluorum* (Schwein.) Tul. & C. Tul.

Other accepted species: See Species Fungorum – search *Hypomyces* for names.

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16). Grass and wetland fungi

Studies on the mycota associated with various plant families have been published, but those related to grasses (*Poaceae*) are few. Grasses are the most ecologically dominant monocotyledonous plant family. The family *Poaceae* consists of about 10,000 species many of which have agricultural importance (Thambugala et al. 2017). The effect of anthropological and climatic changes on ecosystems, facilitates grasses to be the dominant producers (Poon & Hyde 1998). They replace other species and expand their distribution. The study of fungi associated with grasses will therefore expand our understanding of ecological functions. That will have a positive impact on ecological conservation and economic development (Poon & Hyde 1998). Notes for fungalpedia on grasses will be provided by Bhagya and collaborators.

25. Fungalpedia – Note 97 *Comoclathris*

Comoclathris Clem.

Citation when using this entry: Bhagya et al., in prep – Fungalpedia, grass and wetland fungi. Index Fungorum, Faceoffungi, MycoBank, GenBank, Fig. 24

Classification: *Diademaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Comoclathris belongs to the family *Diademaceae*, order *Pleosporales*. *Comoclathris* was introduced by Clements in 1909 (Lumbsch & Huhndorf 2007). *Comoclathris* is a common genus associated with grasses. Ariyawansa et al. (2014) classified this genus under the order *Pleosporales* using morphology and a phylogenetic approach based on LSU and SSU sequence data. Members of

Comoclathris are mainly saprobic on the wood and stems of plants (Ariyawansa et al. 2014). *Comoclathris arrhenatheri* was recorded on dead aerial tissues of *Arrhenatherum elatius* from Italy (Thambugala et al. 2017). The ascomata of *Comoclathris* are scattered or loosely aggregated on host plants. The ascomata are leathery, black and usually immersed with a circular aperture on the globose ascomata. The hamathecium is very dense and hyaline. Asci are bitunicate, eight spored, cylindrical or clavate with ocular chambers (Ariyawansa et al. 2014). Ascospores are brown or reddish brown and oblong, tapering to the tips forming a fusiform shape. They are surrounded by a transparent gelatinous sheath. The type species *Comoclathris lanata* shares some morphological characteristics with *Pleospora herbarum*, but *C. lanata* differs by having a circular ascomata openings, superficial ascomata and gelatinous sheaths on the ascospores (Ariyawansa et al. 2014).

Type species *Comoclathris lanata* Clem.

Other accepted species: see Species Fungorum, search *Comoclathris* for names.

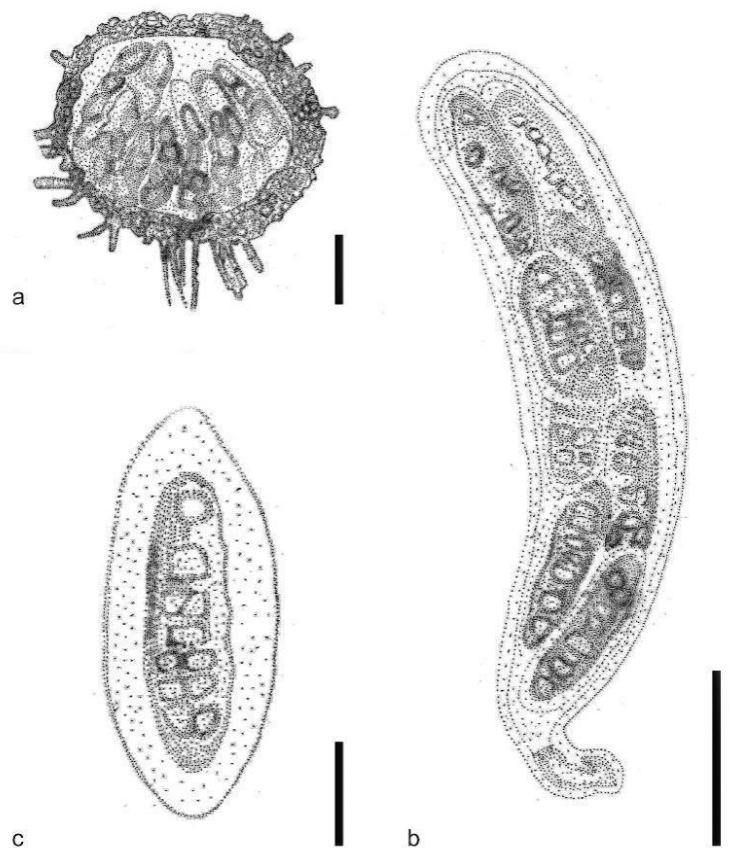


Figure 24 – *Comoclathris lanata* (COLO 62872, holotype). a Cross section of ascoma. b Ascus. c Ascospore with mucilaginous sheath. Scale bars: a = 40 μ m, b = 20 μ m, c = 10 μ m. (Redrawn from Ariyawansa et al. 2014).

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17). Hyaline-spored hyphomycetes

Hyaline-spored hyphomycetes are a group of fungi that produce hyaline asexual spores on hyphae without developing a fruiting body. These taxa are significant due to their ecological and biotechnological importance. For instance, hyaline-spored hyphomycetes play a crucial role in the decomposition of organic matter and the recycling of nutrients in soil and aquatic ecosystems (Cole & Kendrick 1981a, b, Cai et al. 2006). Furthermore, hyaline-spored hyphomycetes serve as a source of valuable metabolites, enzymes, and proteins with diverse applications in medicine, industry, and agriculture (Cole & Kendrick 1981a, b, de Hoog et al. 2000, Kavanagh 2018). The hyaline-spored hyphomycetes will be dealt with in an upcoming paper on this topic (Lin et al. in prep).

26. Fungalpedia – Note 98 *Beltraniella*

Beltraniella Subram.

Citation when using this entry: Lin et al., in prep – Notes, outline and phylogeny of hyaline-spored hyphomycetes. Fungal Diversity, in prep.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 25

Classification: *Amphisphaeriaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Beltraniella was introduced by Subramanian (1952) with the type species *B. odinae* Subram. Thirty species are accepted (Lin et al. 2017b, Crous et al. 2020, Hyde et al. 2020a, b, Tan & Shivas 2022, Species Fungorum – search *Beltraniella*). When present, the setae of *Beltraniella* species are sterile extensions of conidiophores or occur among conidiophores. They are unbranched and arise from radially-lobed basal cells. Conidiophores are branched, often with setiform apex, arising from radially-lobed basal cells. Conidiogenous cells are polyblastic, sympodial, with or without swollen separating cells, and produce acropleurogenous, turbinate or biconic conidia with a distinct hyaline transverse band (Lin et al. 2017a, Hyde et al. 2020b). This genus was placed in the family *Beltraniaceae* (*Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*) (Wijayawardene et al. 2022). Some species of *Beltraniella* have been identified as pathogens, e.g., *B. vateriae* K. Swapna, Nagaveni, Kunwar & Manohar. (Priya et al. 2011). *Pseudomassaria carolinensis* M.E. Barr & Hodges, which was previously reported to have a *Beltraniella* asexual morph, was synonymized under the new combination *B. carolinensis* by Jaklitsch et al. (2016) based on a phylogenetic analysis.

Type species: *Beltraniella odinae* Subram.

Other accepted species: See Species Fungorum, search *Beltraniella* for names.

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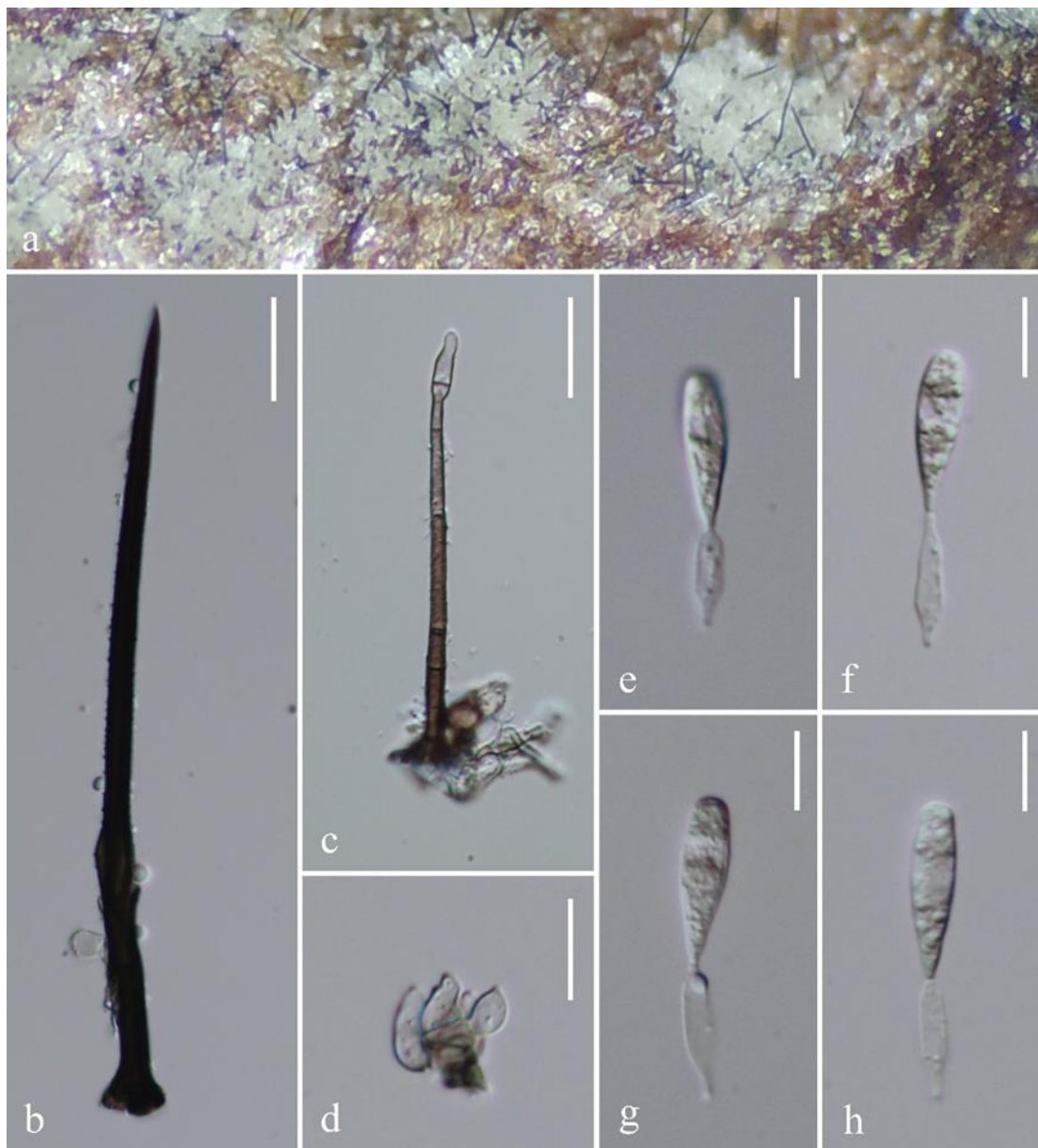


Figure 25 – *Beltraniella brevis* (From Hyde et al. 2020a) (a, b, d–h from holotype MFLU 19–2254, c from paratype MFLU 19–2253). a Conidiophores on leaf surface. b, c Setae. d Conidiogenous cells. e–h Conidia with separating cells. Scale bars: b, c = 20 μ m, d–h = 10 μ m.

18). *Hypocreomycetidae*

Hypocreomycetidae was introduced by Eriksson & Winka (1997) based on morphology and phylogenetic analysis of SSU sequence data. *Hypocreomycetidae* is diverse in terms of ecology and morphology. It can be found as endophytic, parasitic, saprobic, fungicolous, lichenicolous, algicolous, coprophilous, and on insects from diverse environments, including freshwater, marine and terrestrial habitats (Maharachchikumbura et al. 2015, Hyde et al. 2017, 2020a). *Hypocreomycetidae* members are characterized by light-colored perithecia, inamyloid or amyloid ascial rings, or no apical rings, and most taxa lack genuine paraphyses (Zhang et al. 2006).

27. Fungalpedia – Note 99 *Pandanaceomyces*

Pandanaceomyces Tibpromma & K.D. Hyde

Citation when using this entry: Bhunjun et al., in prep – Fungalpedia, genera and higher taxa in 2018.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 26

Classification: *Nectriaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Tibpromma & Hyde (2018) introduced the monotypic genus *Pandanaceomyces* with the type species *Pandanaceomyces krabiensis* within *Nectriaceae*, *Hypocreales* in *Hypocreomycetidae* based on phylogenies of ITS, LSU, SSU and *tef* sequences using maximum parsimony and maximum likelihood analysis. *Pandanaceomyces krabiensis* was collected from dead leaves of *Pandanus* sp. from Thailand. *Pandanaceomyces* has bright-colored, soft-textured, superficial, uniloculate ascomata, and unitunicate asci with an apical ring. The ascospores are fusiform, curved towards both ends, 1-septate and hyaline to subhyaline. *Pandanaceomyces krabiensis* is the only species listed under the genus in Index Fungorum (2023).

Type species: *Pandanaceomyces krabiensis* Tibpromma & K.D. Hyde

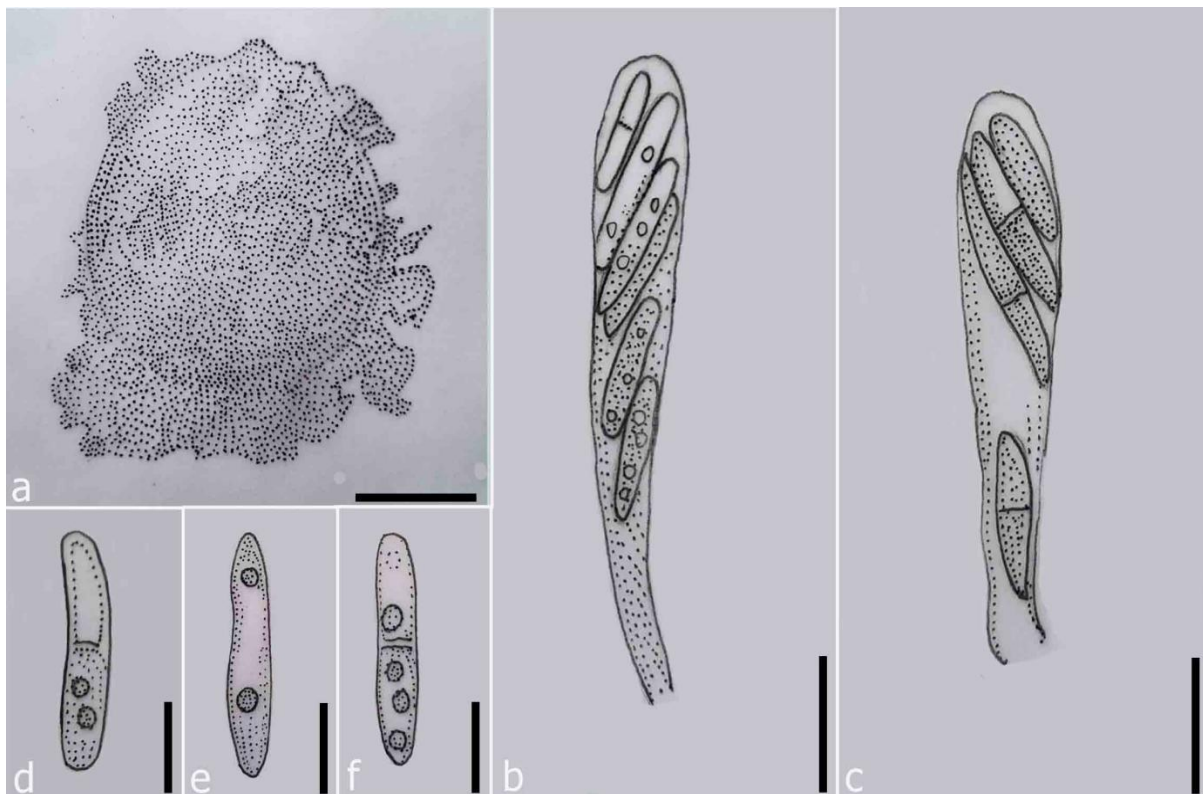


Figure 26 – *Pandanaceomyces pandanicola* (MFLU 16-1909, holotype). a Ascoma. b, c Asci. d–f Ascospores. Scale bars: a = 50 µm, b, c = 10 µm, d–f = 5 µm. (Redrawn from Tibpromma et al. 2018).

Reference

Tibpromma S, Hyde KD, McKenzie EH, Bhat DJ et al. 2018 – Fungal diversity notes 840–928: micro-fungi associated with Pandanaceae. *Fungal Diversity* 93, 1–60.

Entry by

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(Edited by **Chitrabhanu S. Bhunjun** & **Kevin D. Hyde**)

19). Invertebrate fungi

Invertebrate fungi range from cordyceps-like taxa parasitizing insects (Xiao et al. 2023), to Laboulbeniales living on insect exoskeletons (Calabon et al. 2023) or Trichomycetes in the gut of insects (Calabon et al. 2023) to nematode-trapping fungi (Li et al. 2005). The fungi occurring on invertebrates will be published by Xiao and collaborators.

28. Fungalpedia – Note 100 *Polycephalomyces*

Polycephalomyces Kobayasi

Citation when using this entry: Xiao et al., in prep – Fungalpedia, invertebrate fungi.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 27

Classification: *Ophiocordycipitaceae*, *Hypocreales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Polycephalomyces was introduced as an entomopathogenic genus with one species obtained from Japan, characterized by polycephalous synnemata (Kobayashi 1941). Several additional species were described and later, *Perennicordyceps* was segregated from *Polycephalomyces* with four species (Matočec et al. 2014). *Pleurocordyceps* was segregated from *Polycephalomyces* with ten species (Wang et al. 2021). Xiao et al. (2023) established a new family, *Polycephalomycetaceae*, to accommodate these three genera based on morphology and phylogenetic analyses of a combined ITS, LSU, SSU, *rpb1*, *rpb2* and *tef 1-α* sequence data. *Polycephalomyces* is the type genus in *Polycephalomycetaceae* (Xiao et al. 2023). *Polycephalomyces* is an asexual morph with phialidic conidiogenous cells and oblong to cylindrical conidia (Kobayashi 1941, Xiao et al. 2023). Nine *Polycephalomyces* taxa are listed in Species Fungorum (2023). These species are distributed in America, China, France, Ghana, Japan, Russia and Sri Lanka.

Type species: *Polycephalomyces formosus* Kobayasi

Other accepted species:

Polycephalomyces albiramus Y.P. Xiao, T.C. Wen, J.Z. Sun & K.D. Hyde

Polycephalomyces baltica Poinar & Vega

Polycephalomyces cylindrosporus Samson & H.C. Evans

Polycephalomyces ditmarii Van Vooren & Audibert

Polycephalomyces paludosus Mains

Polycephalomyces ponerae Z.Q. Liang, W.H. Chen, J.D. Liang, Y.F. Han & X. Zou

Polycephalomyces ramosus (Peck) Mains

Polycephalomyces tomentosus (Schrad.) Seifert

References

Kobayasi Y. 1941 – The genus *Cordyceps* and its allies. *Sci Rep Tokyo Bun Daig Ser B.* 84, 53–260.
Matočec N, Kušan I, Ozimec R. 2014 – The genus *Polycephalomyces* (*Hypocreales*) in the frame of monitoring Veternica cave (Croatia) with a new segregate genus *Perennicordyceps*. *Ascomycete org* 6, 125–133.

Wang YH, Sayaka B, Wang WJ, Li Y et al. 2021 – *Pleurocordyceps* gen. nov. for a clade of fungi previously included in *Polycephalomyces* based on molecular phylogeny and morphology. *Journal of Systematic Evolution* 59, 1065–1080.

Xiao YP, Wang YB, Hyde KD et al. 2023 – *Polycephalomycetaceae*, a new family of clavicipitoid fungi segregates from *Ophiocordycipitaceae*. *Fungal Diversity*, 1–76.

Entry by

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(Edited by **Kevin D. Hyde**)

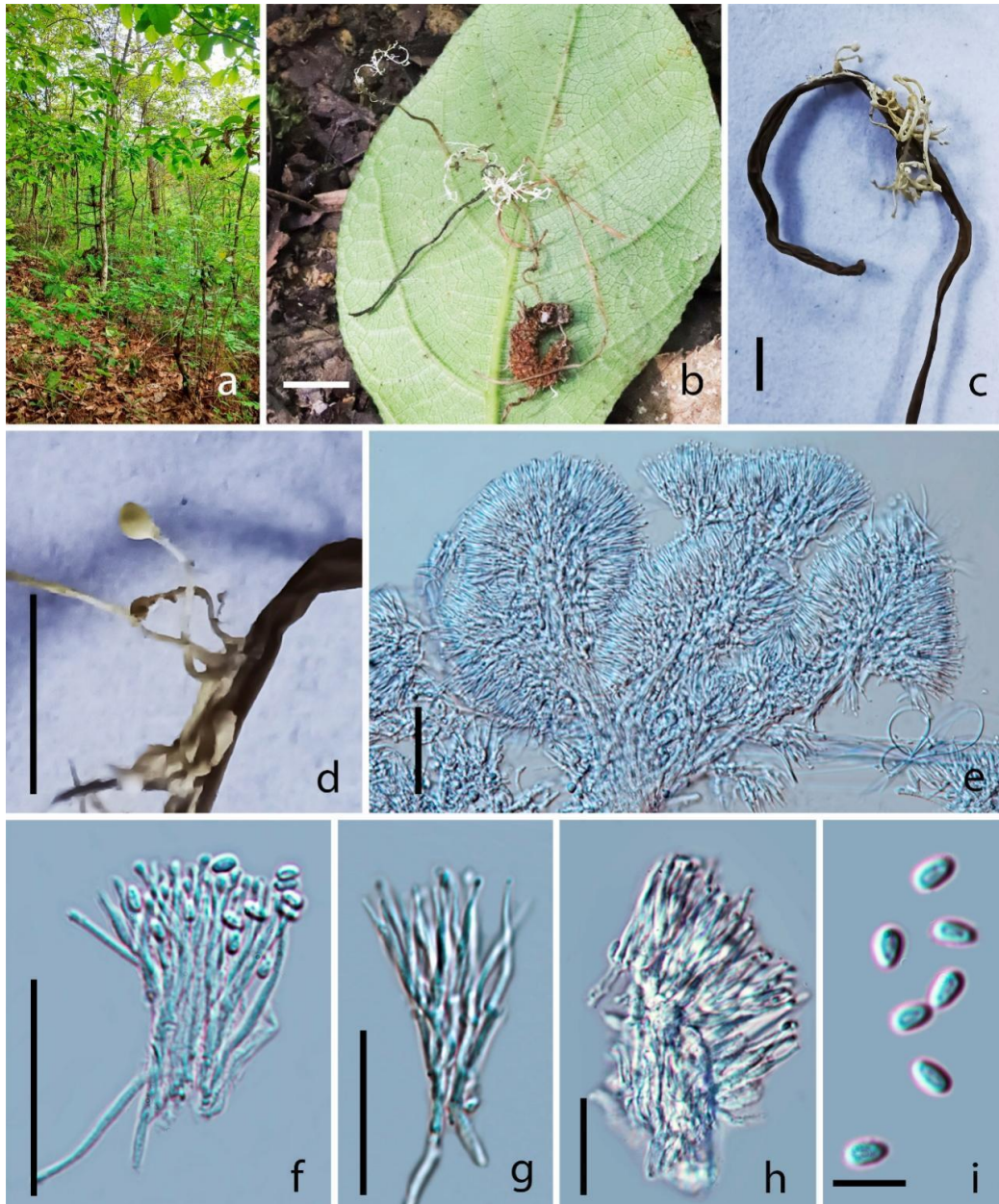


Figure 27 – *Polycephalomyces formosus* (Specimen examined – China, Guizhou Province, Zunyi City, parasitic on *Ophiocordyceps multibrachiata* on *Lepidoptera* in soil, 22 October 2020, Qingfeng Meng, GACP 21-WFKQ03, GACP 21-WFKQ04) a Habitat of *Polycephalomyces formosus*. b Synnemata emerging from infected *Ophiocordyceps multibrachiata*. c, d Synnemata. e Vertical section of synnemata. f–h Conidiophores. i Conidia. Scale bars: b, c = 1 cm, d = 5 mm, e = 50 μm , f–h = 20 μm , i = 5 μm .

20). Lichenicolous fungi

Lichenicolous fungi represent a group that grows specifically or facultatively on the surface of lichens, including the thallus, apothecia, or branches of fruticose lichens. Most species belong to *Ascomycota* and form various types of ascocarps. The exact nature of the relationship between lichenicolous fungi and their host lichens is not fully understood. However, based on the impact on the lichen, it can be broadly categorized as parasitic, commensal, or saprobic relationships. Entries for lichenicolous fungi will be published by Meng and collaborators.

29. Fungalpedia – Note 101 *Bryostigma*

Bryostigma Poelt & Döbbeler

Citation when using this entry: Meng et al., in prep – Fungalpedia, lichenicolous genera.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 28

Classification: *Incertae sedis*, *Arthoniales*, *Arthoniomycetidae*, *Arthoniomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Bryostigma was established by Poelt & Döbbeler (1979) to accommodate the lichen *B. leucodontis* which is characterized by the red or blue iodine staining of its hyphae, an undifferentiated excipulum, the type of asci, the small size of the fruiting bodies and its growth on moss (Poelt & Döbbeler 1979). Kondratyuk et al. (2019, 2020) published a phylogenetic tree of *Arthoniaceae* based on concatenated SSU and *rpb2* sequences. This showed that eight species of *Arthonia* clustered with *Bryostigma muscicola*. Kondratyuk et al. (2019, 2020) therefore transferred these species to *Bryostigma* based on the phylogenetic analysis. These species are all lichenicolous except for *B. lapidicola*, which is a lichen. *Bryostigma dokdoensis* is similar to *B. parietinaria*, but causes much smaller infection spots (from very indistinct to more or less recognizable to 0.5–1 mm across), and have smaller ascomata (0.08–) 0.1–0.13 (–0.14) mm wide, single, round and more or less regular. *Bryostigma dokdoensis* also has a lower mean number of ascomata per infection spot (5–10 apothecia together in spots to 0.4–0.6 mm diam.), more common conidiomata (conidiomata below ascomata and numerous at the first stages of infection development; conidia 3–4 × 0.8 mm) (Kondratyuk et al. 2019). Etayo et al. (2023) identified that *Arthonia excentrica*, previously classified as a lichen by Fries (1867), formed a grouping with *Bryostigma molendoi* and *B. dokdoense*. Notably, this species is more aligned with its host, encompassing certain members of *Lepraria* and *Leprocaulon*. Etayo therefore transferred *Arthonia excentrica* to *Bryostigma excentricum*. This species is characterized by I+ red spore walls, a brown hypothecium and 11–13 × 5–6 μm (Etayo et al. 2023). There are 13 lichenicolous species in this genus and 43 sequences belonging to LSU, ITS, *rpb2* and SSU in GenBank.

Type species: *Bryostigma leucodontis* Poelt & Döbbeler, Crustose lichen on moss

Other accepted species (lichenicolous):

Bryostigma apotheciorum (A. Massal.) S.Y. Kondr. & Hur, on *Myriolecis albescens*

Bryostigma biatoricola (Ihlen & Owe-Larss.) S.Y. Kondr. & Hur, on *Biatora efflorescens*

Bryostigma dokdoense (S.Y. Kondr., Lökös, B.G. Lee, J.J. Woo & Hur) S.Y. Kondr. & Hur, on *Orientophila*

Bryostigma epiphyscium (Nyl.) S.Y. Kondr. & Hur, on *Physcia*

Bryostigma excentricum (Th. Fr.) Etayo & Pino-Bodas, on *Lepraria* and *Leprocaulon*

Bryostigma huriellae S.Y. Kondr. & Hur, on *Huriella pohangensis*

Bryostigma lobariellae (Etayo) S.Y. Kondr. & Hur, on *lobariellae*

Bryostigma molendoi (Heufl. ex Arnold) S.Y. Kondr. & Hur, on *Caloplaca* and *Xanthoria*

Bryostigma neglectulum (Nyl.) S.Y. Kondr. & Hur, on *Lepraria neglecta?*

Bryostigma parietinarium (Hafellner & Fleischhacker) S.Y. Kondr. & Hur, on *Xanthoria parietina*

Bryostigma peltigerinum (Almq.) S.Y. Kondr. & Hur, on *Peltigera* and *Solorina*

Bryostigma phaeophysciae (Grube & Matzer) S.Y. Kondr. & Hur, on *Phaeophyscia orbicularis*

Bryostigma stereocaulinum (Ohlert) S.Y. Kondr. & Hur, on *Stereocaulon*

Other accepted species (lichens):

Bryostigma curvata Serusiaux, Foliicolous lichen

Bryostigma lapalmae van den Boom & Ertz, Foliicolous lichen

Bryostigma lapidicola (Taylor) S.Y. Kondr. & Hur, Crustose lichen on stone

Bryostigma muscigenum (Th. Fr.) Frisch & G. Thor, Crustose lichen on moss

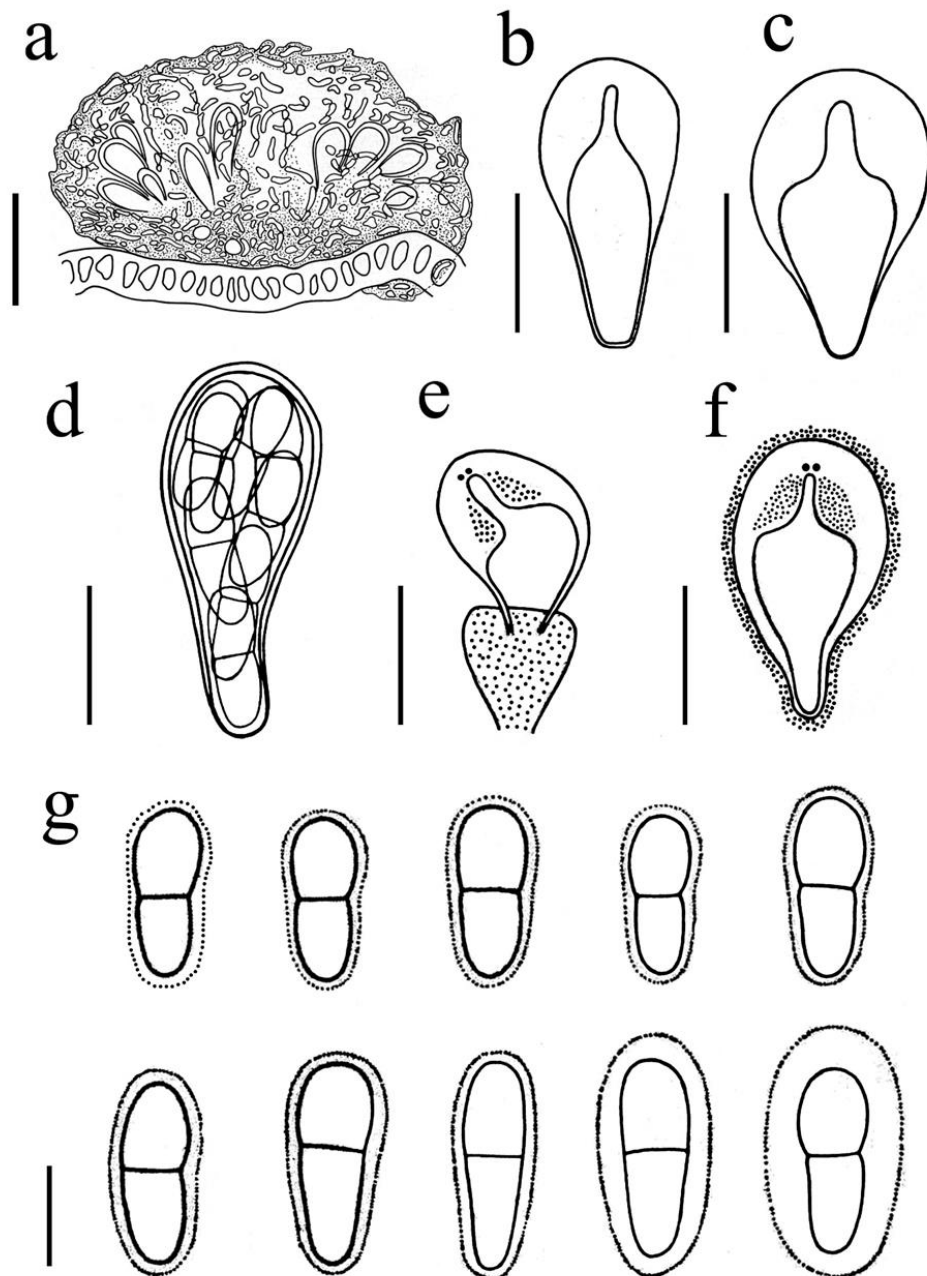


Figure 28 – *Bryostigma leucodontis* (Redrawn from Poelt & Döbbeler 1979). a Apothecium. b–f Asci. g Ascospores. Scale bars: a = 40 μ m, b–f = 10 μ m, g = 5 μ m.

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Entry by

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21). Marine fungi

Marine fungi play a crucial role in marine ecosystems including nutrient cycling as they live on or inside other organisms such as algae, corals, mangroves, sponges, as well as on decomposing materials (Hyde & Jones 1988, Hyde & Lee 1998, Richards et al. 2012). Jones (2011) estimated that there are 7000–10,000 marine taxa. A webpage on marine fungi has been prepared by Jones et al. (2019). The Fungalpedia on marine fungi will provide phenotypic information, integrated with available molecular data for a comprehensive database.

30. Fungalpedia – Note 102 *Halodiatrype*

Halodiatrype Dayar. & K.D. Hyde

Citation when using this entry: Apurillo et al., in prep – Fungalpedia, mangrove-associated fungi.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 29

Classification: *Diatrypaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Halodiatrype was introduced based on the analysis of combined ITS and β -*tub* sequence data. *Halodiatrype* species formed a distinct clade within the family *Diatrypaceae*, with good support (Dayarathne et al. 2016). This genus has ascomata that are dark brown to black, globose to subglobose with ostioles and papillae (Dayarathne et al. 2016). The peridium is thick and composed of multiple layers of brown cells fused with the host cells. The asci are cylindrical to clavate, 8-spored, and without an apical ring (Dayarathne et al. 2016). Ascospores are oblong to allantoid, light brown, slightly curved and smooth-walled (Dayarathne et al. 2016). *Halodiatrype* species share morphological similarities with the type species of *Cryptosphaeria*, however, they formed distinct clades in a phylogenetic tree (Dayarathne et al. 2016). The type species of *Halodiatrype*, *H. salinicola*, was isolated as a saprobe on decaying wood in a mangrove stand (Dayarathne et al. 2016). *Halodiatrype mangrovei* and *H. avicenniae* were also isolated as saprobes on mangroves (Hyde 1993, Dayarathne et al. 2016). *Halodiatrype mangrovei* was introduced by Hyde (1993) as *Cryptosphaeria mangrovei*, but was transferred to *Halodiatrype* based on morphology as it closely resembles the type species of *Halodiatrype*. However, there was no molecular data to support this placement and further studies are needed to confirm its classification. There are no reports of *Halodiatrype* species other than from mangrove ecosystems.

Type species: *Halodiatrype salinicola* Dayar. & K.D. Hyde

Other accepted species:

Halodiatrype avicenniae Dayar. & K.D. Hyde

Halodiatrype mangrovei (K.D. Hyde) Dayar. & K.D. Hyde

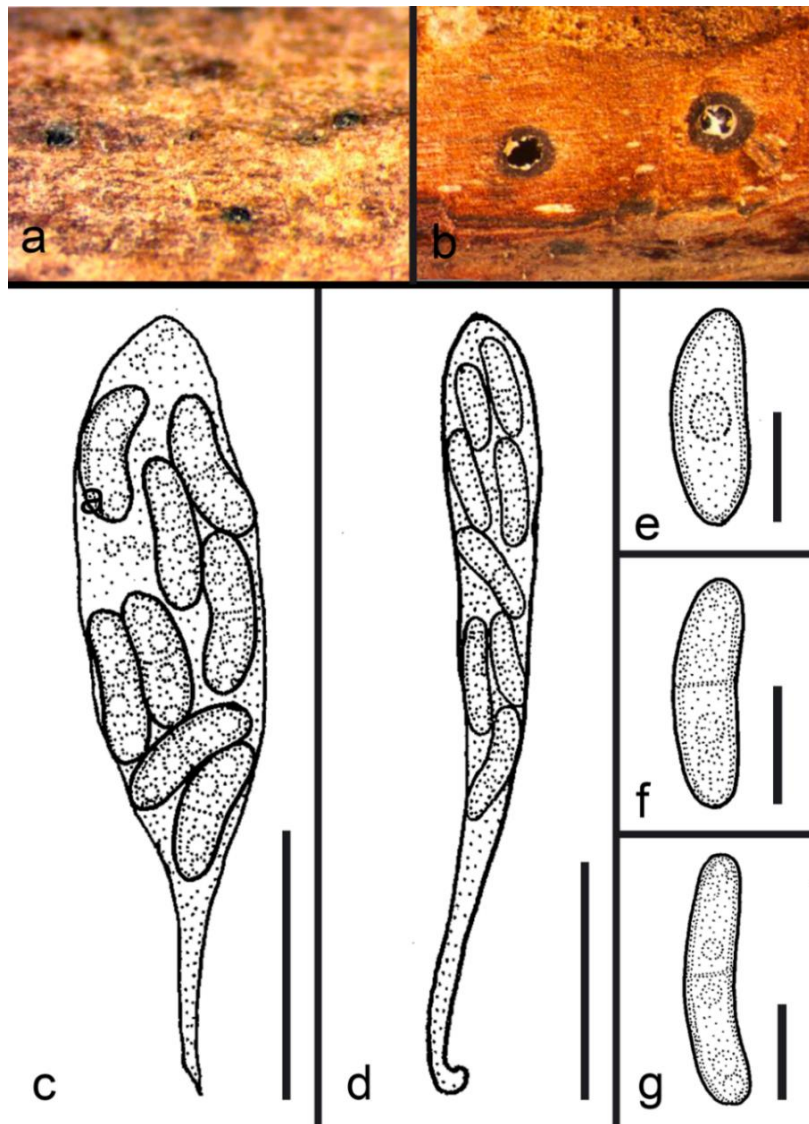


Figure 29 – *Halodiatrype salinicola* (MFLU 15-0179, holotype, redrawn from Dayarathne et al. 2016). a Ascomata on host. b Transverse section of ascoma on host. c–d Asci. e–g Ascospores. Scale bars: c–d = 10 µm, e–g = 5 µm. (Photo credits: MC Dayarathne & KD Hyde).

References

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- Hyde KD. 1993 – *Cryptosphaeria mangrovei* sp. nov. (Diatrypaceae) from intertidal mangrove wood. *Transactions of the Mycological Society of Japan* 34, 311–314.

Entry by

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(Edited by **Chayanard Phukhamsakda & Kevin D. Hyde**)

31. Fungalpedia – Note 103 *Juncigena*

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

Citation when using this entry: Asghari et al., in prep – Fungalpedia, genera of salt marsh fungi.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 30

Classification: *Incertae sedis*, *Incertae sedis*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Kohlmeyer et al. (1997) described *Juncigena* as a novel genus with *J. adarca* as a type species in the family *Magnaporthaceae* based on morphological data. Later the genus was transferred to the family *Juncigenaceae* (*Torpedosporales*) (Jones et al. 2014) and 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*. Later, 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. (2016) reclassified *Moheitospora* under *Juncigena*, in accordance with the one fungus one name protocol (Taylor 2011). The sexual morph is characterized by subglobose to pyriform, papillate ascomata, fusiform to cylindrical, short pedicellate with a J- apical ring asci. 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 muriform, irregularly helicoid, with densely attached yellow-brown to brown cells (Kohlmeyer et al. 1997, Abdel-Wahab et al. 2010). *Juncigena fruticosae* differs from the asexual morph of *J. adarca* in that it has small conidial cells that are comparable in size and colour. *Juncigena* comprises two species, *J. adarca* was first reported on *Juncus roemerianus* from the USA (Kohlmeyer et al. 1997), and *Juncigena fruticosae* was also reported on *Suaeda fruticosa* from Egypt (Abdel-Wahab et al. 2010).

Type species: *Juncigena adarca* Kohlm., Volkm.-Kohlm. & O.E. Erikss.

Other accepted species:

Juncigena fruticosae (Abdel-Wahab, Abdel-Aziz & Nagah.) A.N. Mill. & Shearer

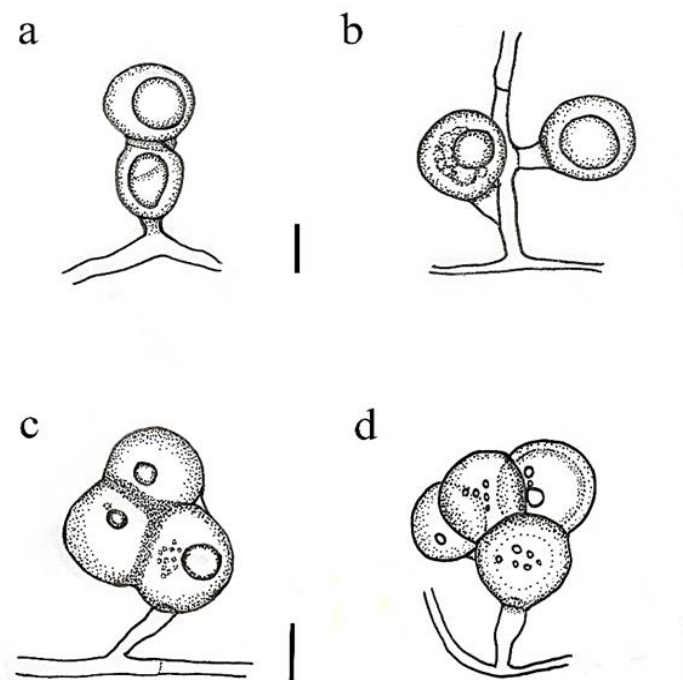


Figure 30 – *Juncigena fruticosae* (EF14, holotype, redrawn from Abdel-Wahab et al. 2010). a–d Various shapes of mature conidia, with a sheath surrounding the conidia and conidial cells attached to each other by connective bands. Scale bars: 5 μ m.

References

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Entry by

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(Edited by **Chayanard Phukhamsakda & Kevin D. Hyde**)

32. Fungalpedia – Note 104 *Pararousoella*

Pararousoella Wanas., E.B.G. Jones & K.D. Hyde

Citation when using this entry: Phukhamsakda et al., in prep – Fungalpedia, marine fungi. Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 31

Classification: *Thyridariaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Pararousoella was introduced as a monotypic genus, typified by *Pararousoella rosarum* Wanas., E.B.G. Jones & K.D. Hyde (Wanasinghe et al. 2018). The genus is distinct from other roussoella-like taxa in having a minute, visible ostiole on the host surface, solitary, immersed, subglobose to ampulliform ascomata, papillate, cellular pseudoparaphyses, uniseriate, broad cylindrical asci, and dark brown, ellipsoidal, 1-septate ascospores, with longitudinal striations. The asexual morph was reported based on *P. juglandicola* as a coelomycete, characterized by globose, brown, pycnidial conidiomata, phialidic conidiogenous cells and hyaline to brown, subcylindrical, aseptate, guttulate conidia (Crous et al. 2019). *Pararousoella* was classified within *Thyridariaceae* (*Dothideomycetes*, *Pleosporales*) and with extensive taxon sampling, Phookamsak et al. (2019) transferred this genus to *Rousoellaceae* based on a polyphasic approach. Molecular markers for a robust insight into the species identification requires LSU, SSU, ITS, *tefl-a* and *rpb2* gene (Wanasinghe et al. 2018). *Pararousoella* is highly diverse in terms of host associations. The type species was introduced from *Rosa* species from the UK (Wanasinghe et al. 2018), *Juglans regia* from Germany (Crous et al. 2019), *Quercus robur* from Ukraine (Crous et al. 2020), bamboo and submerged *Rhizophora* from Thailand (Dai et al. 2017, Hyde et al. 2018). *Pararousoella mukdahanensis* and *P. mangrovei* were classified as *Rousoella* members, however, they are classified as *Pararousoella* based on multigene phylogenetic analysis.

Type species: *Pararousoella rosarum* Wanas., E.B.G. Jones & K.D. Hyde

Other accepted species:

Pararoussoella juglandicola Crous & R.K. Schumach.
Pararoussoella mangrovei (Phukhams. & K.D. Hyde) Phukhams. & K.D. Hyde
Pararoussoella mukdahanensis (Phook., D.Q. Dai & K.D. Hyde) Crous
Pararoussoella quercina Crous & Akulov
Pararoussoella rosarum Wanas., E.B.G. Jones & K.D. Hyde

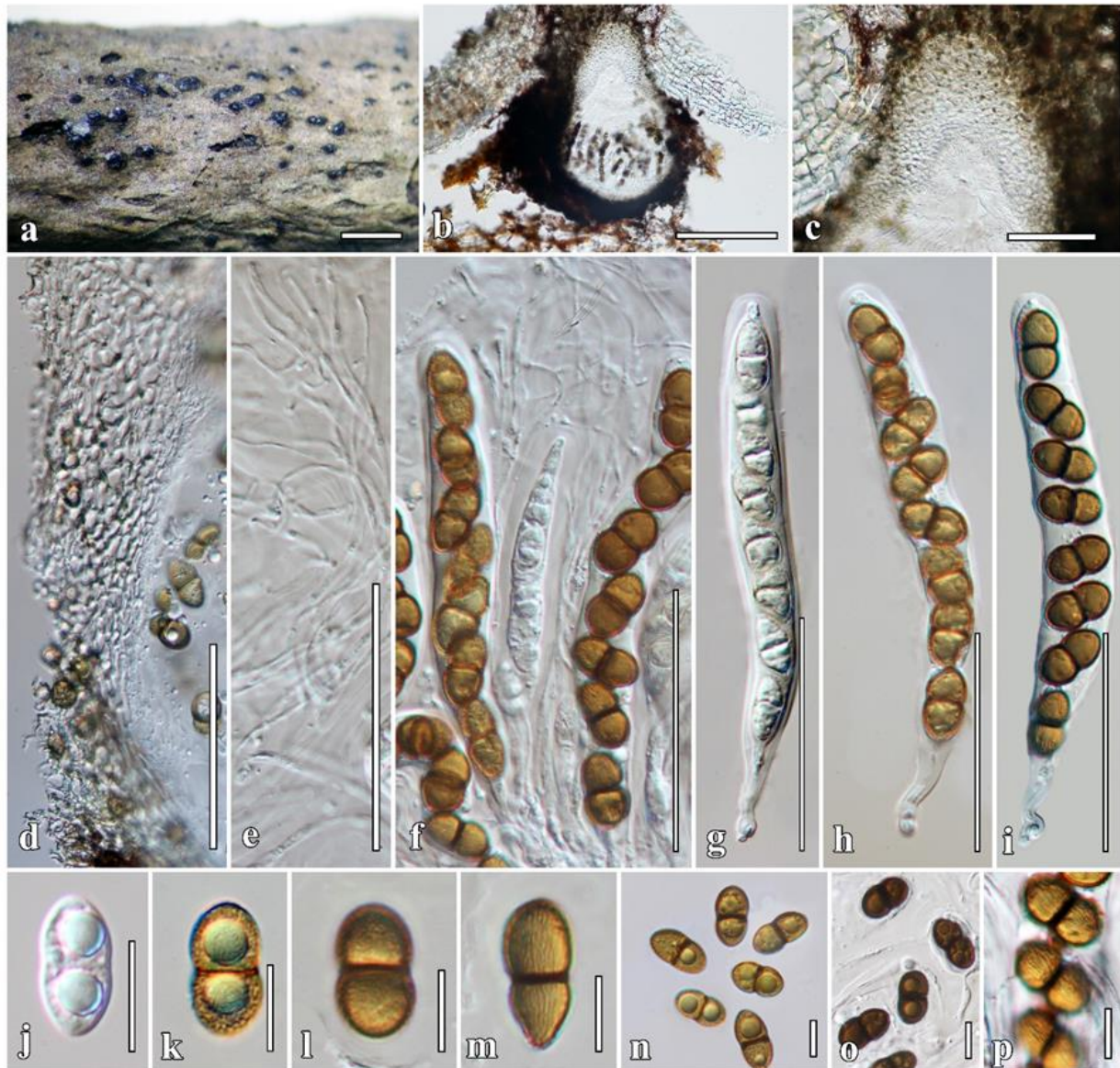


Figure 31 – *Pararoussoella mangrovei* (MFLU 17–1542, holotype). a Appearance of ascomata on *Rhizophora* species. b Vertical section through ascoma. c Ostiolar canal. d Vertical section through peridium. e Pseudoparaphyses. f–i Asci. j–p Ascospores. Scale bars: a, b = 500 μm , c = 200 μm , d–i = 50 μm , j–p = 10 μm .

References

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Entry by

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(Edited by **Kevin D. Hyde**)

22). Macrofungi

Mushrooms represent the visible fruiting bodies of basidiomycete fungi that are typically produced above the ground. They play an indispensable role in the ecosystem which in most cases is unacknowledged. With only 2% being documented, discovery and proper identification should be given high priority for the conservation of their biodiversity as they control the survival system of many other living forms. However, to identify wild mushrooms, morphological features remain imperative despite the advancement of molecular phylogeny. A thorough macro- and micromorphological characterization is an age-old and crucial technique to diagnose, verify and even establish species. The set of entries by Khyaju and collaborators will deal with various aspects and approximately 300 genera of *Basidiomycota*. A second set by Bera and collaborators will deal with approximately 300 genera and terminology of *Basidiomycota*. A third set of entries will be provided by Sysouphanthong and collaborators.

33. Fungalpedia – Note 105 *Agaricus*

Agaricus L.

Citation when using this entry: Bera et al., in prep – Fungalpedia, *Basidiomycota*, genera, and terminology.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Figs 32, 33

Classification: *Agaricaceae*, *Agaricales*, *Agaricomycetidae*, *Agaricomycetes*, *Agaricomycotina*, *Basidiomycota*, *Fungi*

Agaricus was introduced in 1753 and belongs to *Agaricaceae*, *Agaricales*, *Agaricomycetes* (He et al. 2019). The genus includes over 500 species worldwide, with *Agaricus campestris* L. as the type species. *Agaricus* is a saprobic genus found in forests and grasslands. The genus is characterized by white to pink free lamellae when young, brown to dark brown when mature, and with an annulated stipe. There are approximately 6,000 records of *Agaricus* in Index Fungorum (www.indexfungorum.org; accessed in May 2023). The genus is divided into sections based on molecular phylogenetic and morphological characteristics. The taxonomy system of *Agaricus* is complex. The schäffer reaction, alkali reaction, discoloration of sporocarp when bruised, and odor are used to divide the taxa into sections; however, environmental effects and intraspecific variability makes it difficult to distinguish between close species. Therefore, molecular analysis has been used as a tool to identify *Agaricus* to the species level. Mitchell (1999) established a molecular phylogeny of *Agaricus* based on the ITS region + 28S rRNA gene. To date, molecular multigenes have been used for classification. Zhao et al. (2016) used multigenes (ITS, LSU, and *tef1*) and divergence time to divide *Agaricus* into five subgenera and 20 sections. Later, the genus was reported to have six subgenera and 23 sections (Chen et al. 2017, Parra et al. 2018). He et al. (2018) introduced a new section. The genus now contains seven subgenera and 28 sections (Ortiz-Santana et al. 2021, Bashir et al. 2023)

Type species: *Agaricus campestris* L

Other accepted species: see Species Fungorum – search *Agaricus* for names.



Figure 32 – Macrocharacters of *Agaricus subtilipes* (MFLU 120847, holotype), Thailand (Thongklang et al. 2016). a Basidiomes. b Light brown dot-like to triangular scales on pileus. c Well-developed floccose-squamulose ornamentation of the annulus. Scale bars: a, b = 5 cm, c = 2 cm.

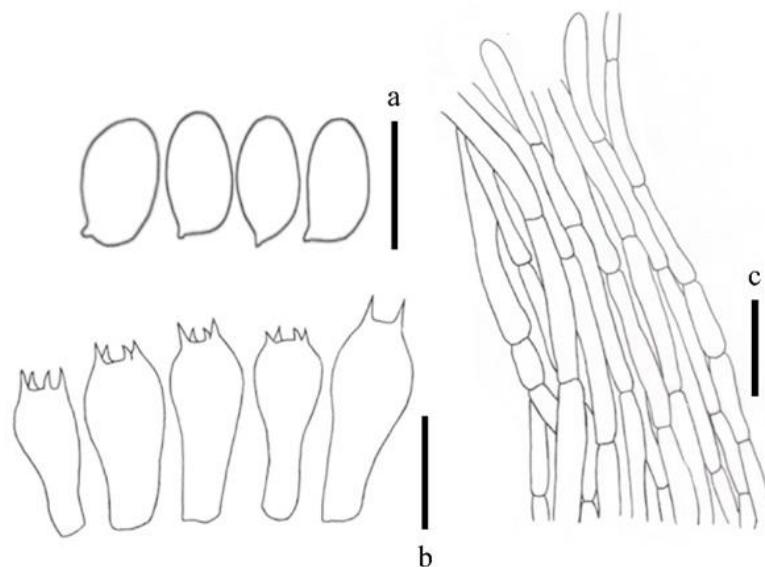


Figure 33 – Microcharacters of *Agaricus subtilipes* (MFLU 120847, holotype) from Thailand (Thongklang et al. 2016). a Basidiospores. b Basidia. c Pileipellis. Scale bars: a = 5 μ m, b, c = 10 μ m.

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Entry by

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34. Fungalpedia – Note 106 *Clitopaxillus*

Clitopaxillus G. Moreno, Vizzini, Consiglio & P. Alvarado

Citation when using this entry: Bera et al., in prep – Fungalpedia, *Basidiomycota* genera, and terminology.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 34

Classification: *Pseudoclitocybaceae*, *Agaricales*, *Agaricomycetidae*, *Agaricomycetes*, *Agaricomycotina*, *Basidiomycota*, *Fungi*

Alvarado et al. (2018) revised the systematics of the clitocyboid groups of mushrooms based on 18S, 28S, *tef1*, and *rpb2* sequence data and introduced the genus, *Clitopaxillus*, while establishing a new classification system for the family *Pseudoclitocybaceae*. Two species, *C. alexandri* (Gillet) G. Moreno, Vizzini, Consiglio & P. Alvarado (Basionym: *Paxillus alexandri* Gillet) and *C. fibulatus* P.A. Moreau, Dima, Consiglio & Vizzini, were accommodated under *Clitopaxillus* (Alvarado et al. 2018). The name “*Clitopaxillus*” is derived from the two genera, *Clitocybe* (Fr.) Staude and *Paxillus* Fr. under which the type species, *C. alexandri* was formerly placed (Alvarado et al. 2018). The genus is saprobic and usually found on leaf litter of trees such as *Pinus*, *Cedrus*, and *Quercus* (Alvarado et al. 2018). *Clitopaxillus* species usually have large convex to planoconvex basidiomata with a fleshy texture, and smooth pileus (Alvarado et al. 2018). The lamellae have a decurrent attachment to the stipe (Alvarado et al. 2018). The basidiospores of *Clitopaxillus* are amyloid and ovoid (Alvarado et al. 2018). The basidiomata of *C. alexandri* consists of a reddish-yellow to greyish-brown pileus with pale yellow stipe and has a characteristic cyanic odour (Alvarado et al. 2018). The hyphae of the

pileipellis have a trichocutis arrangement with intracellular pigments and some encrustations (Alvarado et al. 2018). No cystidia have been found and clamp connections are present generally in the hyphae of hymenophore and mycelia (Alvarado et al. 2018). Earlier, *C. alexandri* was placed under various genera such as *Clitocybe*, *Paxillus*, and *Lepista* (Fr.) W.G. Sm. (Gillet 1873, 1876, Alvarado et al. 2018). Since the original material of *C. alexandri* could not be traced, no typification has been proposed (Alvarado et al. 2018). However, the descriptions *C. alexandri* given are from specimens collected from an area in western France near to the type locality (Alvarado et al. 2018). Previously, specimens of *C. fibulatus* were misidentified as *C. alexandri* but on close examination, the presence of clamp connections in all the tissues, hymenial cystidia, and its occurrence in alpine habitats separated *C. fibulatus* as a distinct species (Alvarado et al. 2018). Most species of *Clitopaxillus* are found in Europe, North Africa, and Northern Hemisphere (Alvarado et al. 2018). An edible mushroom from Shanxi Province in North China, *C. dabazi* L. Fan & H. Liu has been described (Li et al. 2020). This species differs from *C. fibulatus* and *C. alexandri* in having a pileus in earthy brownish tones, a clavate and robust stipe, and a typical agaric odour (Li et al. 2020).

Type species: *Clitopaxillus alexandri* (Gillet) G. Moreno, Vizzini, Consiglio & P. Alvarado,
Basionym: *Paxillus alexandri* Gillet

Other accepted species: *Clitopaxillus fibulatus* P.A. Moreau, Dima, Consiglio & Vizzini
Clitopaxillus dabazi L. Fan & H. Liu

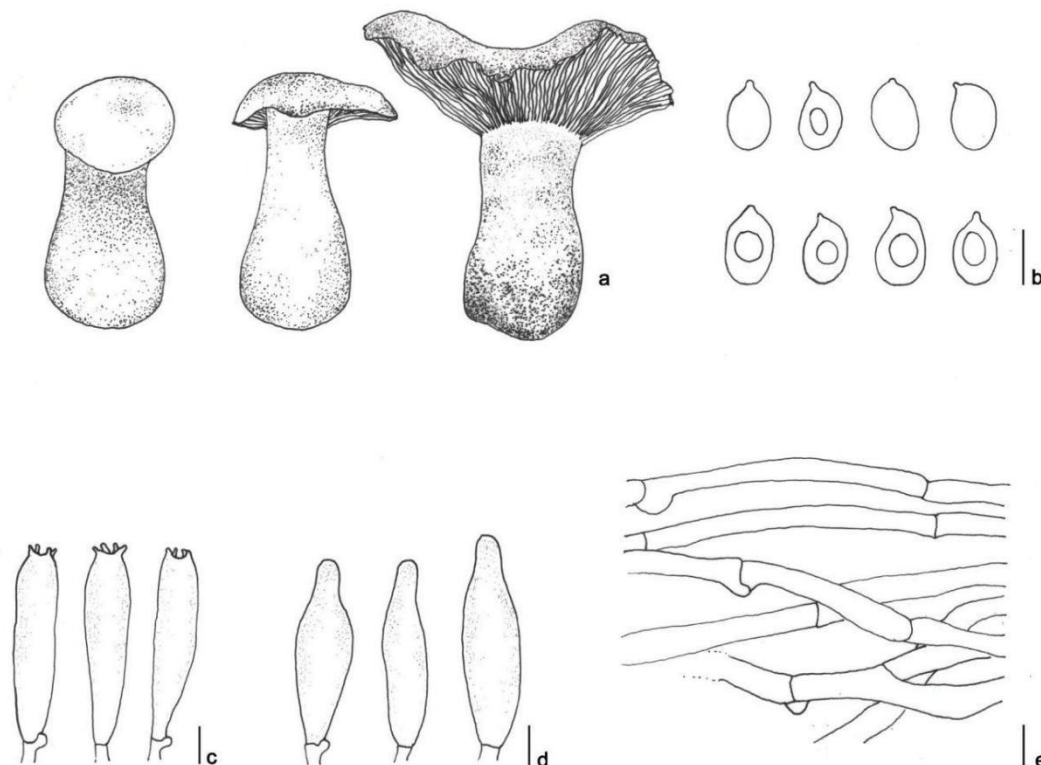


Figure 34 – a–d *Clitopaxillus dabazi* (BJTC FM085, holotype). a Basidiomata. b Basidiospores. c Basidia. d Cheilocystidia. e *Clitopaxillus fibulatus* (AMB 18222) clamped hyphae. Scale bars: b–d = 5 μ m, e = 10 μ m. (Redrawn from Li et al. 2020 and Alvarado et al. 2018).

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Alvarado P, Moreau PA, Dima B, Vizzini A et al. 2018 – *Pseudoclitocybaceae* fam. nov. (*Agaricales*, *Tricholomatineae*), a new arrangement at family, genus and species level. *Fungal Diversity* 90, 109–133.

Li SL, Liu H, Guo LJ, Fan L. 2020 – *Clitopaxillus dabazi* (*Pseudoclitocybaceae*): a new species from Shanxi Province of North China. *Mycosystema*, 39, 1719–1727.

Entry by

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(Edited by **Kevin D. Hyde**)

35. Fungalpedia – Note 107 Pileus

Pileus

Citation when using this entry: Bera et al., in prep – Fungalpedia – *Basidiomycota*, genera, and terminology.

The structure covering and supporting the spore-bearing layer in most mushrooms is the pileus, also simply known as the cap of the *Basidiomycota*. Size is one of the characteristics of the pileus but this is an inconsistent trait that can vary within a species, depending on its maturity and habitat. During development, the pileus expands laterally; thus, there is a continuum of the pileus shape from the young to the mature. The pileus has a wide variety of colors. Even within a single species, young basidiomata have dark-colored pileus, which usually fades with age. This is mainly affected by weather, such as moisture (continuous rain fades the water-soluble pigments), light (harsh sunlight can break down the complex pigment molecules), and other biochemical reactions. Other significant taxonomic attributes are change of color on bruising, exposure to air, or chemical reactions with specific reagents that help to separate species. The wide variety of the surface of the pileus reflects the various degrees of its developmental process. The surface may seem polished and lustrous, termed shiny, or on the contrary dull. The pileus context or flesh (often also known as trama) has a few valuable traits such as its colour and colour changes, odour, taste, thickness, and consistency. The characteristics are relatively constant for one particular species, but differ greatly among species making it quite valuable for identification.

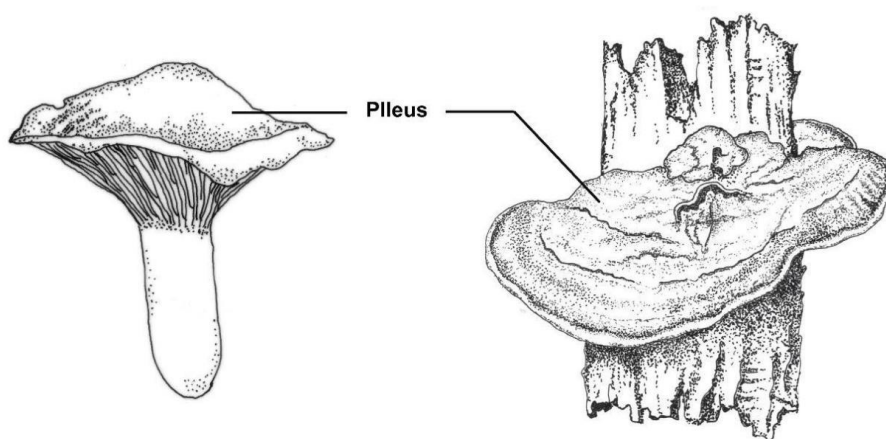


Figure 35 – Pileus.

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23). Palm fungi

Palm fungi are one of the most diverse groups of fungi restricted to the tropics and subtropics. Their association is commonly unique to the palm species as saprobes, pathogens, and endophytes. Studies on palm fungi go back to the late 1900s in which over 200 species belonging to more than 100 genera were introduced from palms. Most of these old records are based on morphology and lack molecular data. Moreover, these important taxa are recorded in books/theses which are rarely referred to in recent studies. There is a necessity for a revisited collection of genera of palm fungi. The fungalpedia on palm fungi will be dedicated to genera of palm fungi and some terminology which will be dealt with by Manawasinghe and collaborators.

36. Fungalpedia – Note 108 *Oxydothis*

Oxydothis Penz. & Sacc.

Citation when using this entry: Manawasinghe et al., in prep – Fungalpedia, palm fungi, genera, and terminology.

Index Fungorum: IF3661, Facesoffungi: FoF05091, MycoBank 3661, GenBank 63191, Fig. 36

Classification: *Oxydothidaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Oxydothis was introduced by Penzig & Saccardo (1897) from Cibodas, Java, Indonesia. *Oxydothis grisea* (= *O. nigricans*) is the type species (Penzig & Saccardo 1897). These species are characterized by ascomatal orientation, which is often horizontal, unitunicate asci which are fusiform or filiform with a J+ (rarely J-), wedge-shaped or discoid, subapical ring and ascospores which are 1-septate with spine-like or rounded ends (Hyde 1994). Following *Oxydothis* taxa develop two types of ascomata (Fröhlich & Hyde 2000), The first type develops on the host surface singly or in clusters. They are dark and ellipsoidal raised areas on the host surface and have eccentric ostioles. The second type develops below a raised sheet of host epidermis and is usually not darkened. The asci of *Oxydothis* are most similar to those of *Diatrypaceae* species (Wang & Hyde 1999). Therefore, the taxonomic position of this genus has gone through several changes. Penzig & Saccardo (1897) placed *Oxydothis* in *Amphisphaeriaceae*, *Xylariales*, *Sordariomycetes*. However, *Oxydothis* was transferred to *Hyponectriaceae* (Barr 1990, Hawksworth et al. 1995), then *Clypeosphaeriaceae* (Kang et al. 1998), and *Pseudomassariaceae* (Jeewon et al. 2003). Based on morphology and phylogeny, previous studies treated *Oxydothis* as genus *incertae sedis* in *Xylariales* (Maharachchikumbura et al. 2015). Konta et al. (2016) introduced *Oxydothidaceae* and placed *Oxydothis* in this new family. *Oxydothis* species are mostly reported on leaves or petioles of palms or leaves of *Pandanus* species (Hyde 1993). They are mostly reported as saprobic (Konta et al. 2016). However, *O. parasitica* and *O. oraniopsis* have been associated with palm leaf spots (Fröhlich & Hyde 2000), while Taylor (1988) and Konta et al. (2016) reported their potential role as endophytes. The current taxonomic placement of *Oxydothis* is *Oxydothidaceae*, *Sordariomycetidae* (Wijayawardene et al. 2022).

Type species: *Oxydothis grisea* Penz. & Sacc.,

Synonyms: = *Merrilliopeltis* Hennings, Hedwigia 47: 261. 1908.

= *Plagiothecium* Schrantz, Bull. Soc. Myc. France 76: 335. 1960.

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Other accepted species: see Species Fungorum – search *Oxydothis*

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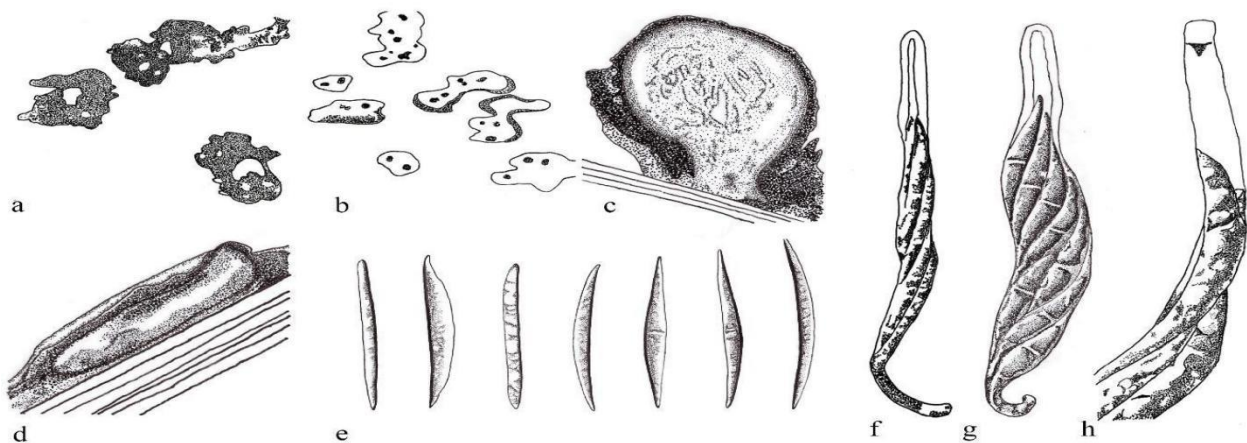


Figure 36 – *Oxydothis* spp. redrawn from Hyde (1993, 1994) and Konta et al. (2016). Appearance of ascomata of *O. froehlichii* on the host surface. b Ascomata of *O. metroxylonis* on the host substrate. c Section through ascoma of *O. poliothea*. d Section through ascoma of *O. grisea*. e Ascospores of *O. maquilingian*, *O. hoehnelii*, *O. licualae*, *O. nypicola*, *O. maculosa*, *O. aequalis* and *O. frondicola*. f Ascus of *O. metroxylonis*. g Ascus of *O. palmicola*. h J+ reaction of apical ring in Melzer's reagent of *O. metroxylonis*. Scale bars:

24). Plant pathology

Fungal plant pathogens are very important to human life and cause considerable losses, both in the field and after harvesting (post harvest). Plant pathology is therefore a very important component of Fungalpedia and has commonly been written about. Hyde et al. (2014) and Jayawardena et al. (2019a, b, 2020) have written a one stop shop series on fungal pathogens and these will be referred to. The genera and higher taxa of plant pathogenic fungi will be dealt with by Aumentado and collaborators. The terminology and other important areas of plant pathology will also be defined with these entries.

37. Fungalpedia – Note 109 *Colletotrichum*

Colletotrichum Corda

Citation when using this entry: Aumentado et al., in prep – Fungalpedia, plant pathology.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 37

Classification: *Glomerellaceae*, *Glomerellales*, *Hypocreomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Colletotrichum was introduced by Corda (1831) to accommodate *C. lineola*. Many species of this genus are known as pathogens causing symptoms commonly referred to as anthracnose on a wide range of hosts and with a worldwide distribution (Cannon et al. 2012, Lima et al. 2013, Jayawardena et al. 2020, 2021, Talhinhos & Baroncelli 2021). Symptoms of anthracnose appear as water-soaked or dark necrotic lesions that are oval or angular in shape, sometimes with visible conidial masses. These species are characterized by a distinctive hemibiotrophic lifestyle (Jayawardena et al. 2021). Some *Colletotrichum* species are endophytes, saprobes, entomopathogens, and animal/ human pathogens (Manamgoda et al. 2013, Jayawardena et al. 2016).

Colletotrichum is the sole member of *Glomerellaceae* (Hyde et al. 2020). Jayawardena et al. (2020) provided the most recent formal genus description for *Colletotrichum*. *Colletotrichum* species are mainly asexual, but some have a sexual morph (*Glomerella*) that can be either homothallic or heterothallic (Talhinhos & Baroncelli 2021).

About 750 epithets existed at the time of the first monograph on *Colletotrichum* (von Arx 1957). However, based solely on morphological characters von Arx (1957) accepted only 11 taxa. utton (1980) accepted 22 species and Sutton (1992) accepted 39 species based on morphological and cultural characteristics, respectively. Hyde et al. (2009) provided the first comprehensive overview of *Colletotrichum* and accepted 66 species and considered 19 as doubtful while highlighting the need for a molecular approach to revise the genus.

Cannon et al. (2012) based on molecular sequence data (ITS, TUB2, ACT, CHS-1, GAPDH, CAL, GS, and SOD2) revised the genus, accepting 113 species and nine species complexes. Weir et al. (2012) revised the gloeosporioides species complex based on (ITS, TUB2, ACT, CHS-1, GAPDH, CAL, GS, and SOD2) and accepted 22 species. Damm et al. (2012a, b, 2013, 2014, 2019) revised the acutatum, boninense, destructivum, and orbiculare complexes and introduced dracaenophilum, magnum, and orchidearum complexes based on morphology, host distribution and molecular sequence data. Liu et al. (2014) introduced the gigasporum species complex based on conidial size and ITS, ACT, TUB2, CHS-1, GAPDH sequence data. Crouch (2014) introduced caudatum species complex based on appendage-bearing conidia and ITS, SOD2, APN2, and Mat/ Apn2 gene regions. Hyde et al. (2014) noted that the same resolution of the species can be obtained when using the ITS, ACT, TUB2, CHS-1, and GAPDH sequence data, and suggested finding a single gene that can provide a better resolution for each species complex. Bhunjun et al. (2021a) accepted 248 species and emphasized using coalescent approaches and multi-locus phylogeny for species delimitation in *Colletotrichum*. Agaves species complex was introduced by Bhunjun et al. (2021a). Jayawardena et al. (2021) accepted 248 species, 14 species complexes, and 13 singleton species and provided an updated account of the accepted species while providing information on 450 morpho species. Talhinhos & Baroncelli (2021) reported that 88 species are common in nature, based on geographical distribution and host range, 128 are data deficient and 41 are threatened. Liu et al. (2022) introduced

the bambusicola species complex and accepted 280 species, 16 species complexes, and 15 singleton species. They also generated and assembled whole-genome sequences of the 30 new and a further 18 known species, providing a comprehensive genomic tree with 94 *Colletotrichum* species.

Type species: *Colletotrichum lineola* Corda

Other accepted species: (Species Fungorum – search *Colletotrichum* for names, see Jayawardena et al. (2021) for accepted species).



Figure 37 – *Colletotrichum*. Symptoms caused by *Colletotrichum* species (a pepper, b grapes, c papaya, d banana). e Conidiomata and setae. f–g Conidiomata on leaf surface. h–m Conidial attachment. n–r Appressoria. s–t, aa–ab Conidia. u Seta, v–w Tips of setae. x Basal part of setae. y–z Conidiophores. Scale bars: i–j, u, x = 20 µm, h, k–m, n–r, s–t, v–w, z–ab = 10 µm.

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Entry by

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(Edited by **Kevin D. Hyde & Eric H.C. McKenzie**)

38. Fungalpedia – Note 110 *Coniella*

Coniella Höhn.

Citation when using the entry: Senanayake et al., in prep – *Diaporthomycetidae*.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 38

Classification: *Schizoparmaceae*, *Diaporthales*, *Diaporthomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Coniella was introduced by Höhn (1918) with the type species *Coniella pulchella* Höhn. Petrak & Sydow (1927) divided the genus into two subgenera, *Euconiella* and *Pseudoconiella*, and introduced another asexual genus for *Schizoparme* Shear, and *Pilidiella* Petr. & Syd. Following the proposal of Castlebury et al. (2002), Rossman et al. (2007) transferred the genus from *Melanconidiaceae* to the newly introduced family *Schizoparmaceae* in *Diaporthales*. *Coniella* has been subjected to several comprehensive taxonomic refinements by several morpho-molecular studies (Castlebury et al. 2002, Van Niekerk et al. 2004, Rossman et al. 2007, Alvarez et al. 2016). Alvarez et al. (2016) synonymized both *Pilidiella* and *Schizoparme* under *Coniella*, and the latter was accepted as the only genus in *Schizoparmaceae*. Members of *Coniella* are commonly found in different habitats including soil, decaying plant material, and endophytes within living plant tissues (Castlebury et al. 2002, Van Niekerk et al. 2004, Alvarez et al. 2016, Chethana et al. 2017). This asexual genus exhibits a wide range of morphological characteristics, with their ostiolate conidiomata typically being pycnidial, immersed to semi-immersed, subepidermal, erumpent, unilocular, brown to dark brown or black, and globose or slightly depressed globose to subglobose. The conidiophores may be formed singly or in clusters, simple to branched at the base, and septate. Percurrently proliferating conidiogenous cells are hyaline, subcylindrical, obclavate to lageniform and of annellidic or phialidic origin. The conidia are often unicellular, ellipsoidal, globose, and smooth with a truncate base and obtuse to apiculate apex. The sexual morph of *Coniella* is characterized by solitary, scattered, subepidermal, erumpent to superficial, perithecial, globose, coriaceous, and papillate ascomata with a periphysate ostiole. Asci are 8-spored, unitunicate, sessile, clavate to subcylindrical, with an apical ring, with biseriate, ellipsoidal, aseptate ascospores that are initially hyaline, becoming pale brown at maturity, with or without mucoid caps (Van Niekerk et al. 2004, Alvarez et al. 2016). They are cosmopolitan in distribution and known for their ecological significance (Van Niekerk et al. 2004, Mirabolfathy et al. 2012, Alvarez et al. 2016, Chethana et al. 2017, Raudabaugh et al. 2018). Some species are saprobic, playing a crucial role in decomposing organic matter and nutrient recycling (Raudabaugh et al. 2018). Other *Coniella* species are often associated with foliar, fruit, stem and root diseases in a wide range of hosts, such as grape white rot caused by *Coniella diplodiella* (Speg.) Petr. & Syd. and *C. vitis* Chethana, JY. Yan, XH. Li & KD. Hyde (Chethana et al. 2017), strawberry fruit and leaf diseases caused by *C. castaneicola* (Ellis & Everh.) B. Sutton (Grantina-Ievina & Kalniņa 2016), and pomegranate cankers, crown rots, dieback, fruit rots, leaf spots, shoot blights, and twig blights caused by *C. granati* (Sacc.) Petr. & Syd. (Mirabolfathy et al. 2012, Chen et al. 2014). Alvarez et al. (2016) and Chethana et al. (2017) adapted a morphology combined with multi-gene phylogeny and Genealogical Concordance Phylogenetic Species Recognition (GCPSR) for defining species boundaries in *Coniella*. Recommended genetic markers for the genus include ITS, LSU, *tef1-α*, *rpb2* and histone (Alvarez et al. 2016, Chethana et al. 2017). Sixty-four species epithets are listed for *Coniella* in Index Fungorum (2023), of which 38 have been accepted based on morpho-molecular approaches.

Type species: *Coniella pulchella* Höhn.

Other accepted species: see Species Fungorum, search *Coniella* for names.

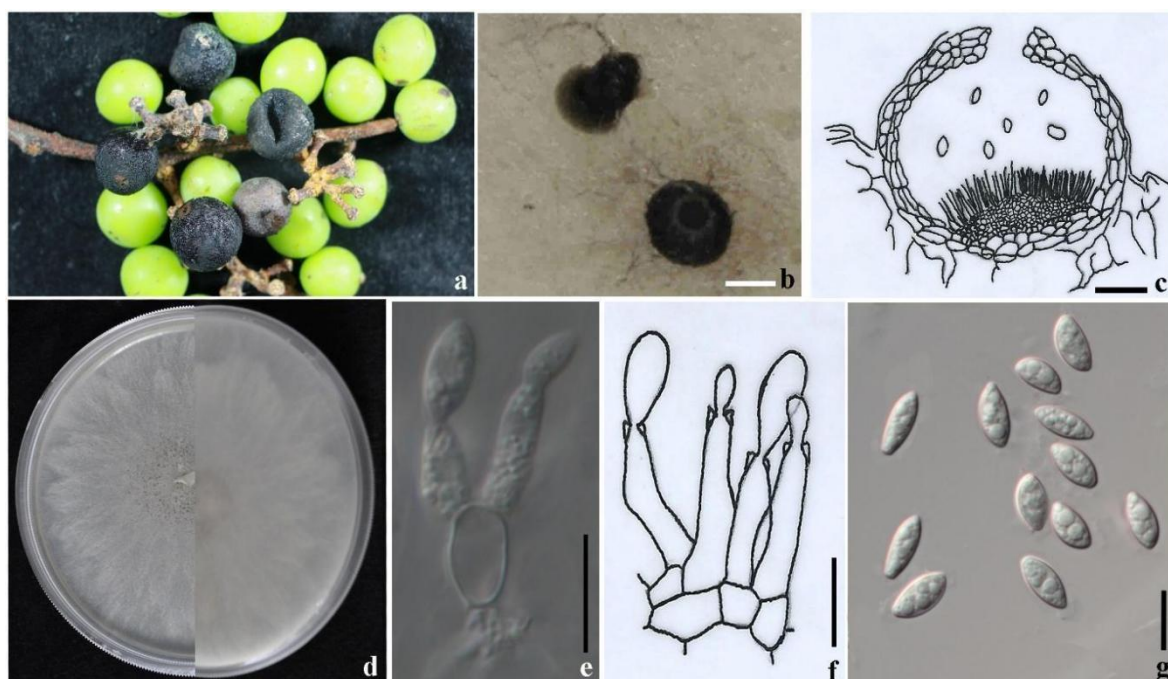


Figure 38 – *Coniella vitis* (MFLUCC 16-1404). a Conidiomata on diseased fruits. b Conidiomata on PDA. c Cross section of a conidioma (Re-illustrated from Van Niekerk et al. 2004). d Upper (left) and reverse (right) views of the colony on the PDA. e, f Conidiophores and conidiogenous cells. g Conidia. Scale bars: b = 100 μ m, c, e–g = 10 μ m.

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(Edited by **Kevin D. Hyde**)

25). Soil fungi

Fungi have an important role in edaphic ecosystems, contributing to decomposition, nutrient cycling and maintenance of mutual or pathogenic interactions with soil organisms (Peršoh et al. 2018, Averill et al. 2021, Bahram & Netherway 2022). Global soil fungi numbers have been predicted by high throughput sequencing studies (Tedersoo et al. 2020, 2021, 2022, Janowski & Leski 2023). The Global Soil Mycobiome consortium (GSMc) of Tedersoo et al. (2021) reported that fungi represent 62.4% OTUs (Operational Taxonomic Units) of microorganisms, with *Ascomycota* being the dominant group. They are significantly adapted to spatial and vertical variability of soil properties (physical, biological and chemical), thus isolating them is challenging (Bridge & Spooner 2001, Wu et al. 2019, Yasanthika et al. 2021, 2022). Hence, many soil taxa remain to be discovered at the generic and species level (Tedersoo et al. 2017, Wu et al. 2019, Yasanthika et al. 2022). Yasanthika et al. (in prep) will provide an updated account with notes on genera of soil fungi and taxonomy and phylogeny of soil-associated species discovered from Thailand. Yasanthika and collaborators (in prep) will also provide notes on terminology related to soil fungi.

39. Fungalpedia – Note 111 *Juxtiphoma*

Juxtiphoma Valenzuela-Lopez, Cano, Crous, Guarro & Stchigel

Citation when using this entry: Yasanthika et al., in prep – Genera of soil fungi.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Figs 39, 40

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

Juxtiphoma (*Didymellaceae*, *Pleosporales*) was introduced by Valenzuela-Lopez et al. (2018) with the type species *J. eupyrena* (\equiv *Phoma eupyrena*) based on multigene phylogeny (LSU, ITS, *tub2* and *rpb2*) and morphological support. Three species have been accepted in this genus (Index Fungorum 2023). The asexual morph is characterized by brown pycnidial conidiomata with a wall of cells of *textura angularis*. Conidiogenous cells are phialidic, hyaline and ampulliform forming aseptate, hyaline, smooth- and thin-walled, ovoid, ellipsoidal or cylindrical, biguttulate conidia. The sexual morph is undetermined (Domsch et al. 1993). *Juxtiphoma* is characterized by chlamydospores which are important for isolating species from soil particles. They are aseptate, ochraceous-brown, single or in chains, subglobose, barrel-shaped or ellipsoidal (Domsch et al. 1993, Valenzuela-Lopez et al. 2018). All species of this genus have been isolated from soil-based habitats (Yasanthika et al. 2021). *Juxtiphoma eupyrena* has been isolated from *Solanum tuberosum* and is commonly found in soils in the UK, India, Malaysia, Netherlands and the USA (Domsch et al. 1993). *Juxtiphoma kolkmaniorum* and *J. yunnanensis* have been described from garden soil in the Netherlands and industrial waste-contaminated soil in China (Hou et al. 2020, Yasanthika et al. 2021). *Juxtiphoma* is phylogenetically close to *Cumuliphoma* and morphologically similar in having pycnidia with hyaline conidia. However, *Cumuliphoma* lacks chlamydospores (Valenzuela-Lopez et al. 2018).

Type species: *Juxtiphoma eupyrena* (Sacc.) Valenz.-Lopez, Crous, Stchigel, Guarro & Cano

Other accepted species:

Juxtiphoma kolkmaniarum Hern.-Restr., L.W. Hou, L. Cai & Crous

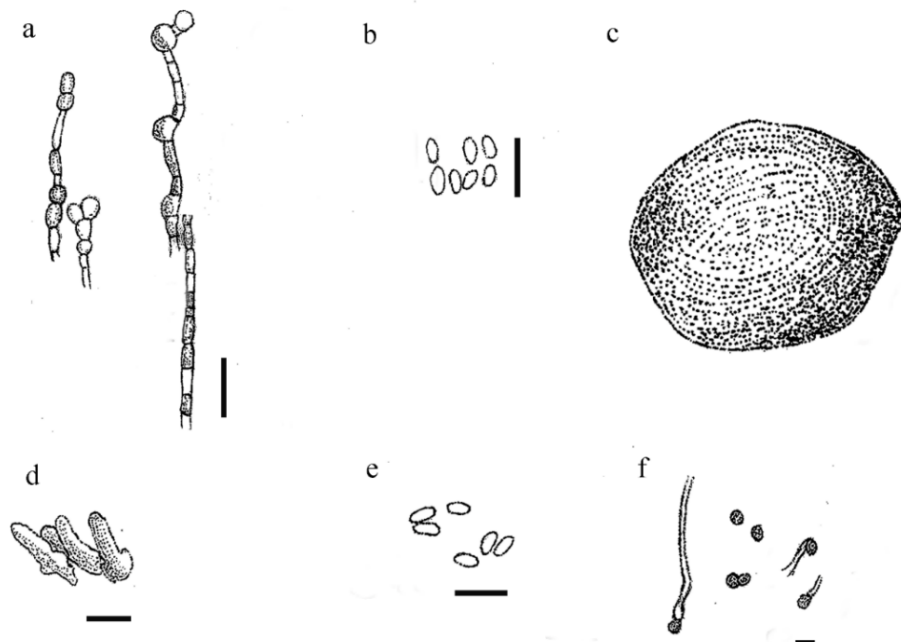


Figure 39 – *Juxtiphoma eupyrena* (Redrawn from Fig. 280 in Domsch et al. 1993). a Chlamydospores. b Pycnoconidia. *Juxtiphoma kolkmaniorum* (CBS 146005) (Redrawn from Hou et al. 2020). c Pycnidia forming on oatmeal agar. d Conidiogenous cells. e Conidia. f Chlamydospores. Scale bars: a, b = 500x, c = 100 μm , d–f = 10 μm .

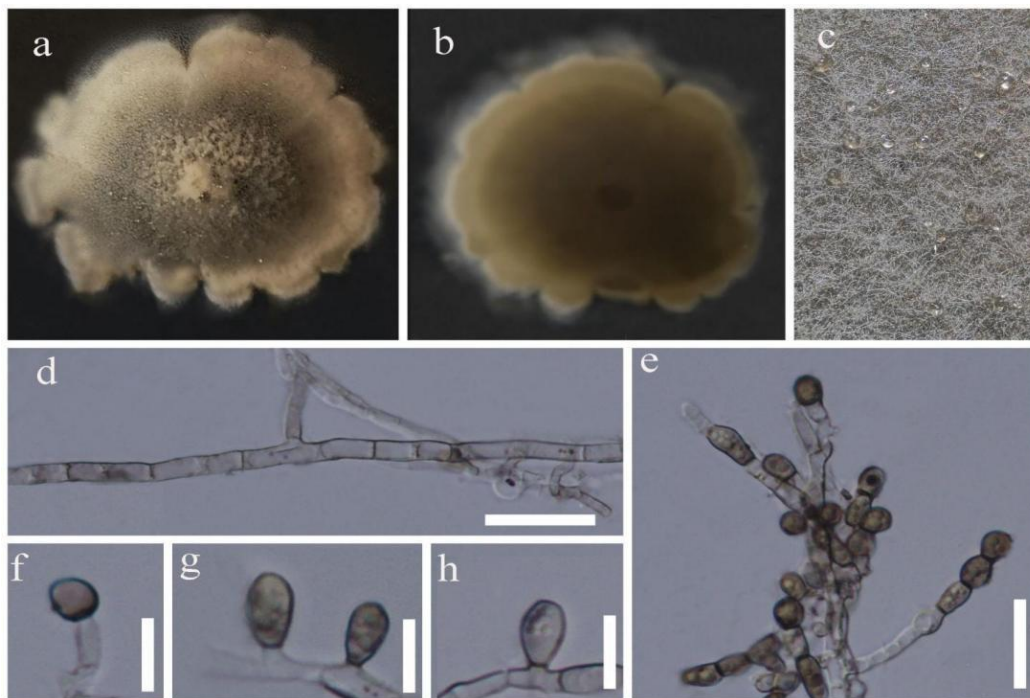


Figure 40 – *Juxtiphoma yunnanensis* (HKAS 107657). a Colony from above. b Colony from below. c Mycelia on the colony. d Mature septate hyphae. e Terminal, branched and chained chlamydospores. f–h Chlamydospores. Scale bars: d = 25 μm , e = 20 μm , f–h = 10 μm .

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Entry by

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26). *Sordariomycetidae*

Sordariomycetidae was introduced by Eriksson & Winka (1997). It comprises eight orders (Bundhun et al. 2020, Hyde et al. 2020), representing microfungi with ascomata, periphysate ostioles and unitunicate asci (Huang et al. 2021). They are widely distributed in terrestrial, aquatic and

marine habitats, performing various ecological roles, such as plant and animal pathogens, endophytes, and saprobes. They are also found as coprophilous and lichenicolous (Maharachchikumbura et al. 2015, Bundhun et al. 2020, Zhang et al. 2006.) In addition, they contribute to ecosystem stability by facilitating mutualistic associations, decomposition and nutrient recycling and providing biotic diversity to the ecosystem. *Sordariomycetidae* species, in particular *Xylariales* also have high biotechnological potential (Hyde et al. 2019, Bundhun et al. 2020). These are the characteristics that make *Sordariomycetidae* one of the more interesting and important groups of fungi. Silva et al. (in prep) will provide Fungalpedia notes on all genera and some terminology for *Sordariomycetidae*

40. Fungalpedia – Note 112 *Achrochaeta*

Achrochaeta Réblová & Hern. -Restr.

Citation when using this entry: Silva et al., in prep – Fungalpedia, *Sordariomycetidae*.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 41

Classification: *Chaetosphaeriaceae*, *Chaetosphaeriales*, *Sordariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Achrochaeta was introduced by Réblová et al. (2021) as a monotypic genus to accommodate *Achrochaeta talbotii* (S. Hughes, W.B. Kendr. & Shoemaker). Réblová & Hern.-Restr., isolated from decaying wood collected from New Zealand (Réblová et al. 2021). The phylogenetic analysis using ITS and 28S sequences revealed that their isolate clustered with *Chaetosphaeria talbotii*, representing a novel lineage in the *Chaetosphaeriaceae* separating it from *Dictyochoeta*. Therefore, *C. talbotii* was synonymized under a new genus *Achrochaeta* (Réblová et al. 2021). Morphologically, it is characterized by its sexual and asexual morphs. The sexual morph is a perithecial, astromatic ascomata with a carbonaceous ascomatal wall and periphysate ostioles. Paraphyses are hyaline and septate, while asci are short-stipitate and unitunicate with 8-spores. The shape of the asci varies from cylindrical to cylindrical-fusiform and have a nonamyloid apical annulus. The ascospores are ellipsoidal to ellipsoidal-fusiform in shape (Réblová et al. 2021, Hughes et al. 1968). The asexual morph has macronematous and mononematous conidiophores that are unbranched or rarely simply branched. The conidiogenous cells are phialidic, terminal, and integrated with single or several lateral openings. The collarettes are narrowly funnel-shaped and do not become apically incurved. They are also hyaline. The conidia are smooth, cylindrical to clavate in shape, and gradually taper towards the basal end (Réblová et al. 2021). *Achrochaeta* can be distinguished from *Dictyochoeta* by its cylindrical-clavate conidia tapering more progressively towards the basal end and narrowly funnel-shaped collarettes (Réblová et al. 2021).

Type species: *Achrochaeta talbotii* (S. Hughes, W.B. Kendr. & Shoemaker) Réblová & Hern.-Restr.

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(Edited by **Roberto Farias & Kevin D. Hyde**)

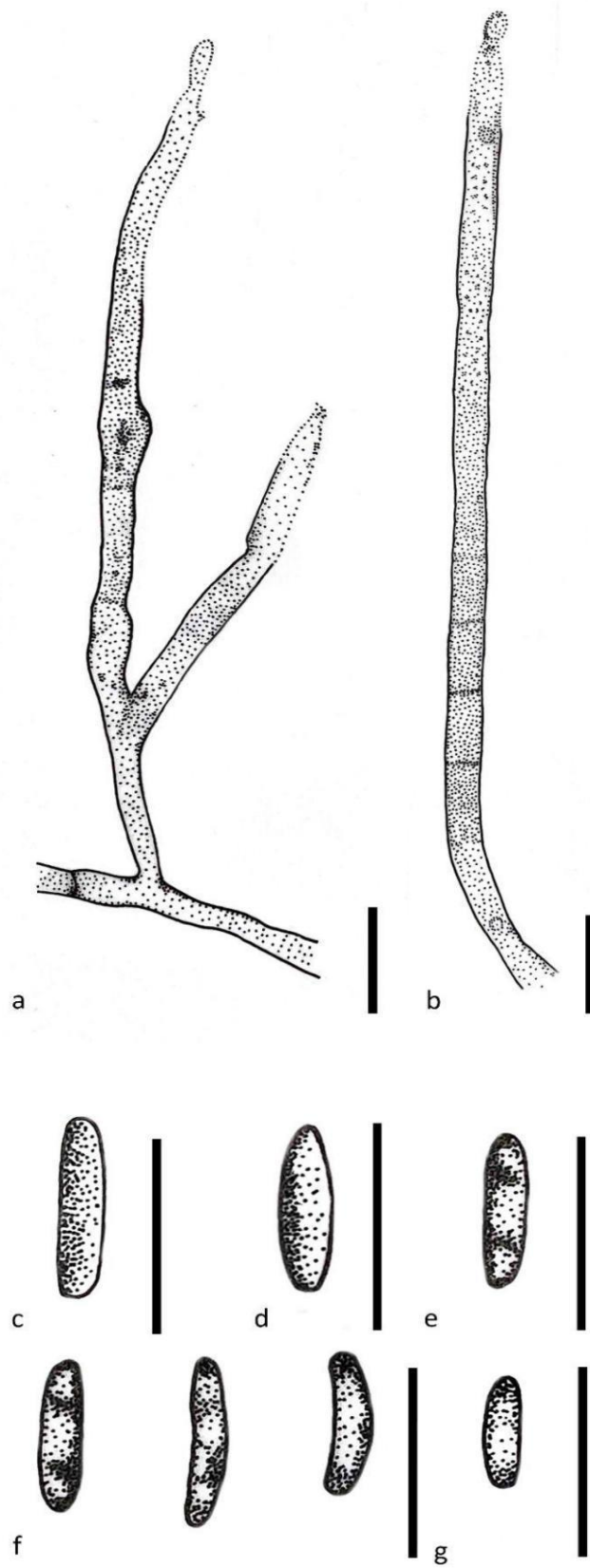


Figure 41 – *Achrochaeta talbotii*. a, b Conidiophores. c–g Conidia. Scale bars: a–g = 10 μ m.

27). Xylarariomycetidae

The large subclass Xylariomycetidae plays a significant role in the ecosystem, with many saprobic species, while others are pathogens or endophytes. The subclass is also important for

producing novel compounds and there have been many studies in this field (Intaraudom et al. 2017, Becker & Stadler 2021, Kuhnert et al. 2021, Mapook et al. 2022). Fungalpedia notes will be provided on all genera and higher taxa of *Xylariomycetidae* by Doilom and collaborators (in prep).

41. Fungalpedia – Note 113 *Neoamphisphaeria*

Neoamphisphaeria Samarak. & K.D. Hyde

Citation when using this entry: Doilom et al., in prep – Fungalpedia, Xylariomycetidae.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 42

Classification: *Appendicosporaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Neoamphisphaeria was introduced by Samarakoon et al. (2022) in *Appendicosporaceae*, *Amphisphaeriales*, *Xylariomycetidae*, *Sordariomycetes* with *Neoamphisphaeria hyalinospora* as the type species based on morphology and phylogenetic analysis of combined ITS-LSU-*rpb2-tub2-tef1* sequence data. The type species was reported as saprobic on dead twigs in Thailand. *Neoamphisphaeria* is characterized by solitary, immersed ascomata, conical with flattened or subglobose base and septate, branched paraphyses. Ostioles are filled with white amorphous tissue and asci are cylindrical, unitunicate, with a bi-lobed or dome-shaped, J-, apical ring, with a rounded apex. Ascospores are uniseriate, hyaline, broadly ellipsoidal, aseptate when immature, 1-septate when mature, and lacking a mucilaginous sheath (Samarakoon et al. 2022). The ostiolar canal is filled with amorphous hyaline cells and asci with a bi-lobed or dome-shaped apical ring and hyaline ascospores, distinguish it from *Amphisphaeria* (Samarakoon et al. 2022). The genus is monotypic.



Figure 42 – *Neoamphisphaeria hyalinospora* (MFLU 19-2131, holotype). a Substrate. b–d Ascomata on substrates. e Section through ascoma. f Peridium. g Section through ostiole. h Paraphyses. i–j Asci. k Apical ring. Scale bars: c, d = 1000 μ m, e–g = 20 μ m, h–p = 10 μ m.

Type species: *Neoamphisphaeria hyalinospora* Samarak. & K.D. Hyde.

Reference

Samarakoon MC, Hyde KD, Maharachchikumbura SSN, Stadler M et al. 2022 – Taxonomy, phylogeny, molecular dating and ancestral state reconstruction of *Xylariomycetidae* (*Sordariomycetes*). *Fungal Diversity* 112, 1–88.

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(Edited by **Kevin D. Hyde**)

28). Yeasts

Yeasts are unicellular microorganisms that belong to the Kingdom of Fungi (Dikarya) (Boekhout et al. 2022, Thapa et al. 2015). Yeast can be characterized asexually by budding or fission, and can sometimes be found in sexual states without a fruiting body (Thapa et al. 2015, Montes de Oca et al. 2016). Yeasts are ubiquitous and can be found in plants, insects, invertebrates, aquatic habitats, and soil (Boekhout et al. 2022, Thapa et al. 2015). Yeasts can also be found on the skin of warm-blooded animals and in their intestinal tracts, where they live symbiotically or parasitically (Maicas 2020, Thapa et al. 2015). Yeasts cause different kinds of infections, such as oral thrush, vaginitis, urinary tract infections, endocarditis, respiratory syndromes, and meningitis (Thapa et al. 2015). Yeasts are also used for commercial applications, for example in the production of alcoholic beverages and bread (Thapa et al. 2015). The yeasts will be dealt with by Linn and collaborators.

42. Fungalpedia – Note 114 *Savitreea*

Savitreea Sakpuntoon, Angchuan, Boonmak, Khunnamw., N. Jacques, Grondin, Casareg. & Srisuk

Citation when using this entry: Linn et al., in prep – Fungalpedia, genera described in the order *Saccharomycetales*

Index Fungorum, Facesoffungi, MycoBank, GenBank, TheYeasts, Fig. 43

Classification: *Saccharomycetaceae*, *Saccharomycetales*, *Saccharomycetidae*, *Saccharomycetes*, *Saccharomycotina*, *Ascomycota*, *Fungi*

Savitreea was introduced with *S. pentosicarens* as the type species using morphology, ecological evidence, and phylogenetic analysis of ITS, LSU, *tef*, and *rpb2* data (Sakpuntoonm et al. 2020). A polyphasic approach is recommended as using only morphological characters for yeast identification can lead to misidentification due to similar morphological characters (Lücking et al. 2020). *Savitreea pentosicarens* was isolated from a grease sample in Thailand and as an isolate from the ‘Montagne des Singes’ path in French Guiana (Jacques et al. 2019, Sakpuntoonm et al. 2020). *Savitreea* is classified in the family *Saccharomycetaceae* (*Saccharomycetales*, *Saccharomycetes*) (Sakpuntoonm et al. 2020). *Savitreea* has pseudohyphae, ellipsoid cells, and asexual reproduction by multilateral budding (Sakpuntoonm et al. 2020). Colonies are white to cream, convex and butyrous, with a dull surface and undulated margins (Sakpuntoonm et al. 2020). Ascospores and starch-like compounds are not formed. Acid production is positive but the Diazonium Blaue B (DBB) test and urease hydrolysis tests are negative (Sakpuntoonm et al. 2020). There is only one species listed under this genus in Index Fungorum (2023).

Type species: *Savitreea pentosicarens* Sakpuntoon, Angchuan, Boonmak, Khunnamw., N. Jacques, Grondin, Casareg. & Srisuk

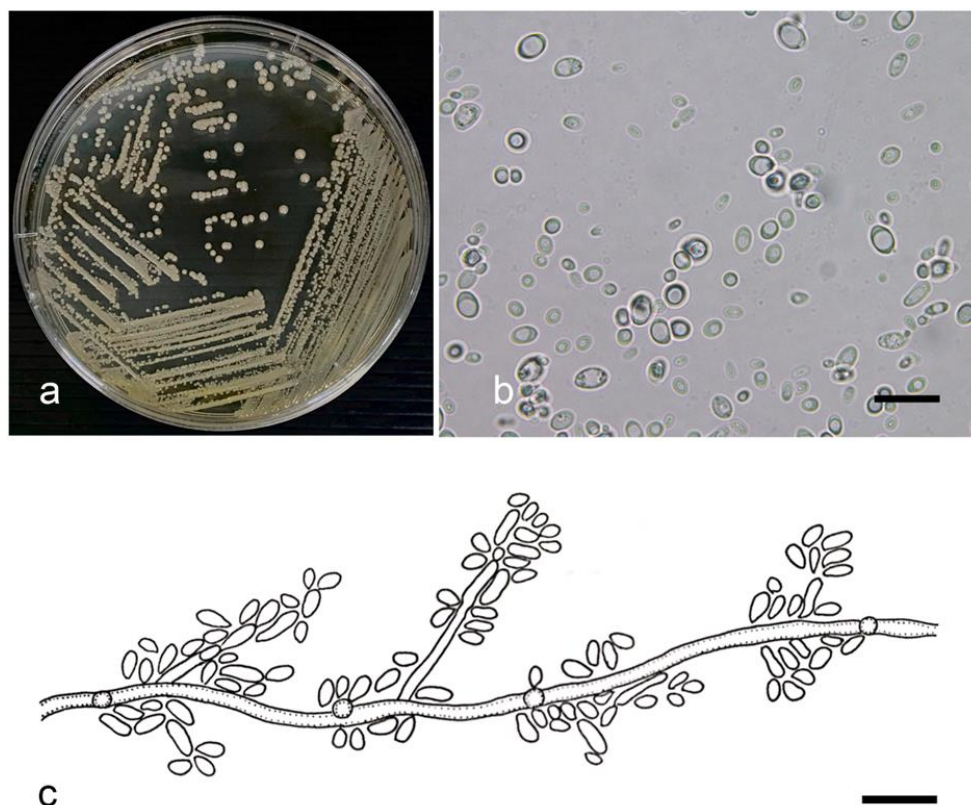


Figure 43 – Morphology of *Savitreea pentosicarens* (DMKU-GTCP10-8, holotype). a Colonies on YM for 3 days at 25 °C. b Budding cells in YM broth after incubation at 25 °C for 3 days. c Pseudohyphae formed on PDA at 25 °C for 3 days (Redrawn from Sakpuntoon et al. 2020). Scale bars: b, c = 10 µm.

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29). Taxa by individual years (2008-present)

The new genera and higher taxa from 2008 through to 2023 and onwards will be annotated in mostly fungalpedia dealing with single years.

43. Fungalpedia – Note 115 *Alveariospora*

Alveariospora Meir. Silva, R.F. Castañeda, O.L. Pereira & R.W. Barreto

Citation: Madagammana et al., in prep – Fungalpedia, genera described in 2012.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 44

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

Alveariospora was introduced by Silva et al. (2012) with *A. distoseptata* as the type species. *Alveariospora* is an asexual genus that is listed under *Ascomycota* genera *incertae sedis* (Wijayawardene et al. 2022). This genus was introduced using only morphology. Therefore, new isolates and sequence data are required to confirm the phylogenetic position of this genus. *Alveariospora* is characterized by single, unbranched, septate, brown, or olivaceous conidiophores, muriform, dictyosporous, distoseptate, verruculose conidia from large, thickened, dark washer-like conidiogenous loci (Silva et al. 2012). Morphologically, *Alveariospora* is similar to *Briansuttonia*, *Dictyospiropes*, and *Veracruzomyces* (Silva et al. 2012). However, *Briansuttonia* differs from *Alveariospora* by having monotretic, terminal, determinate, or indeterminate cells that are enteroblastic, percurrent conidiogenous cells (Silva et al. 2012). In contrast to *Alveariospora*, *Dictyospiropes* has polyblastic, sympodial conidiogenous cells with strongly cicatrized conidiogenous loci lacking percurrent extensions and euseptate-dictyoseptate conidia without strongly thickened and melanized basal hila (Silva et al. 2012). *Veracruzomyces* also differs from *Alveariospora* by having monoblastic, percurrently proliferating conidiogenous cells (Silva et al. 2012). Currently, there is only one species listed in Index Fungorum (2023), collected on the trichomes of leaflets of *Dimorphandra mollis* from Brazil (Silva et al. 2012).

Type species: *Alveariospora distoseptata* Meir. Silva, R.F. Castañeda, O.L. Pereira & R.W. Barreto.

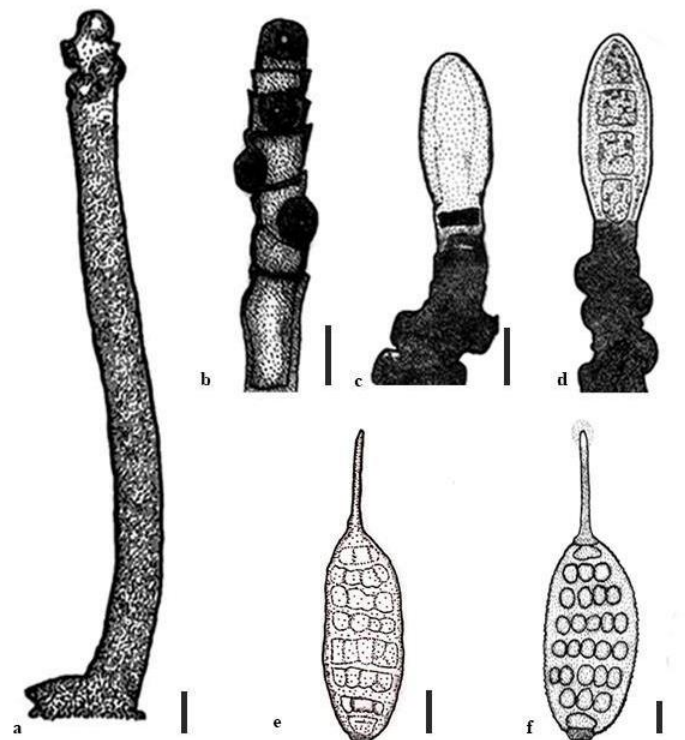


Figure 44 – *Alveariospora distoseptata* (VIC 31399, holotype). a Macronematous conidiophore with polyblastic conidiogenous cells. b Conidiogenous cells. c Initial conidial formation. d Initial conidial septation. e, f Conidia. Scale bars: a–d = 10 µm, e = 20 µm, f = 10 µm. (Redrawn from Silva et al. 2012).

References

- Silva MD, Castañeda-Ruiz RF, Pereira OL, Barreto RW. 2012 – *Alveariospora*, a new anamorphic genus from trichomes of *Dimorphandra mollis* in Brazil. Mycotaxon. 119, 109–16.
- Wijayawardene NN, Hyde KD, Dai DQ, Sánchez-García M et al. 2022 – Outline of Fungi and fungus-like taxa – 2021. Mycosphere 13, 53–453.

Entry by

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44. Fungalpedia – Note 116 *Anastomitrabeculia*

Anastomitrabeculia Bhunjun, Phukhams. & K.D. Hyde

Citation when using this entry: Norphanphoun et al., in prep – Fungalpedia, genera and higher taxa described in 2021.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 45

Classification: *Anastomitrabeculiaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Bhunjun et al. (2021) introduced *Anastomitrabeculia* as a monotypic genus within *Anastomitrabeculiaceae*, *Pleosporales* with the type species *Anastomitrabeculia didymospora*. *Anastomitrabeculia* fits the morphology of *Pleosporales* by having perithecioid ascomata, pseudoparaphyses, bitunicate asci and hyaline, septate ascospores (Hongsanan et al. 2020). The taxon was introduced as a saprobe based on morphology, phylogenetic analyses and divergence time estimates using a combined LSU, SSU and *tef-1α* dataset. *Anastomitrabeculiaceae* is closely related to *Halojulellaceae*, however, *Halojulellaceae* is morphologically different due to the presence of cellular pseudoparaphyses and golden brown ascospores (Ariyawansa et al. 2013). *Anastomitrabeculia* is known only from its sexual morph and it is characterised by having carbonaceous ascomata, with orange pigment near the ostiole and hyaline ascospores with longitudinally striate wall ornamentation (Bhunjun et al. 2021). *Anastomitrabeculia didymospora* was collected from dead bamboo culms from freshwater in Krabi Province, Thailand and it is the only species listed in Index Fungorum (2023).

Type species: *Anastomitrabeculia didymospora* Bhunjun, Phukhams. & K.D. Hyde

Other accepted species: This genus is monotypic.

References

- Ariyawansa HA, Jones EB, Suetrong S, Alias SA et al. 2013 – *Halojulellaceae* a new family of the order *Pleosporales*. Phytotaxa 130, 14–24.
- Bhunjun CS, Phukhamsakda C, Jeewon R, Promputtha I et al. 2021 – Integrating different lines of evidence to establish a novel ascomycete genus and family (*Anastomitrabeculia*, *Anastomitrabeculiaceae*) in *Pleosporales*. Journal of Fungi 7, 94.
- Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN et al 2020 – Refined families of dothideomycetes: *Dothideomycetidae* and *Pleosporomycetidae*. Mycosphere 11, 1553–2107.

Entry by

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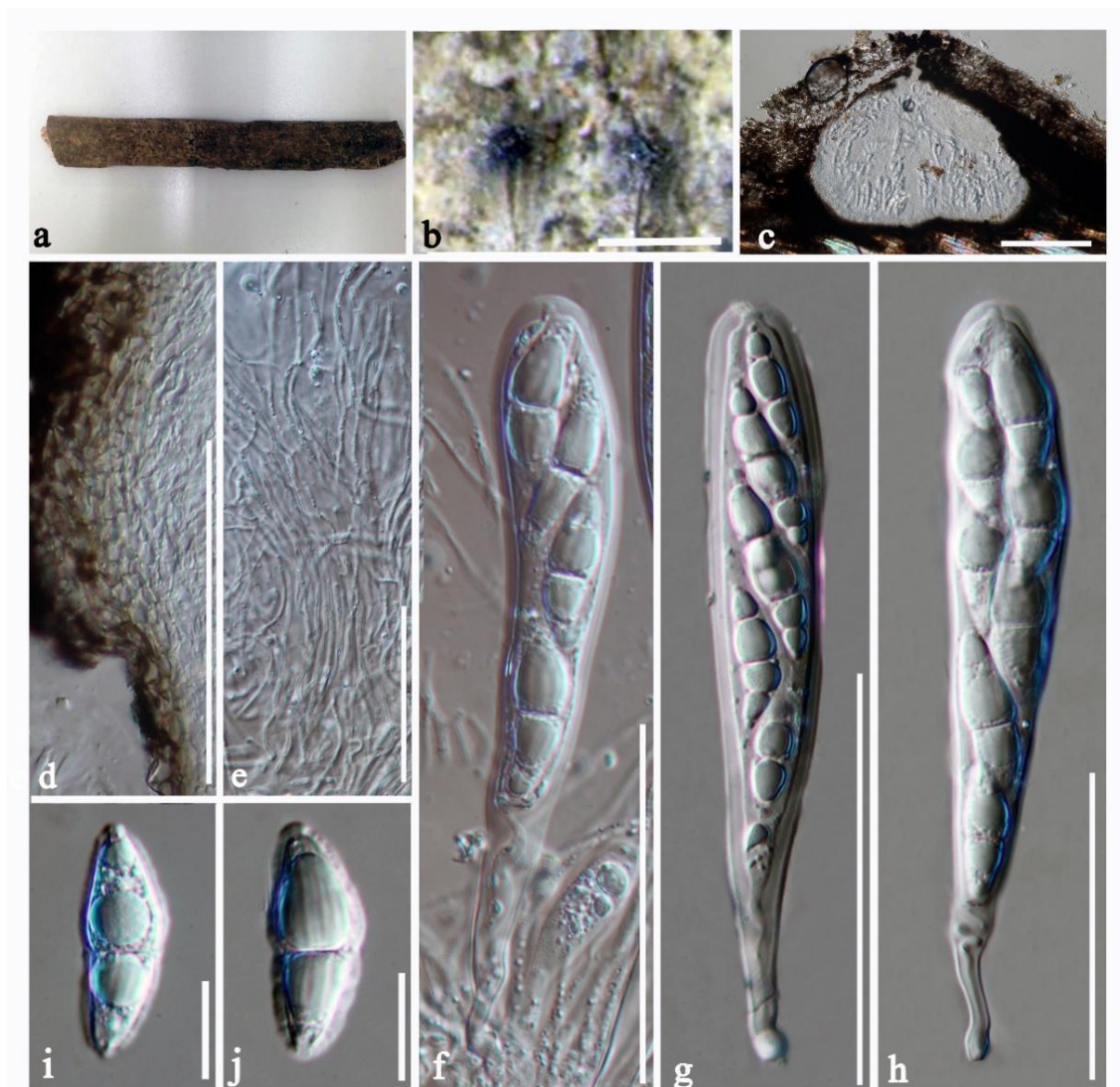


Figure 45 – *Anastomitrabeculia didymospora* (MFLU 20-0694, holotype). a Ascomata on host. b Close-up of ascomata. c Vertical section of ascoma. d Peridium layer. e Pseudoparaphyses. f–h Asci. i–j Ascospores. Scale bars: b = 500 µm, c = 200 µm, d–h = 50 µm, i–j = 10 µm.

45. Fungalpedia – Note 117 *Austropleospora*

Austropleospora R.G. Shivas & L. Morin

Citation when using this entry: Fallahi et al., in prep – Fungalpedia, new genera and higher taxa in 2010.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Figs 46, 47

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

Austropleospora was placed in *Pleosporales* without being assigned to any family by Morin et al. (2010) and was typified by *Austropleospora osteospermi* R.G. Shivas & L. Morin (synonym: *Hendersonia osteospermi* Wakef.). Thambugala et al. (2014) reexamined the holotype of *Austropleospora osteospermi* and based on morphological similarity, placed *Austropleospora* in *Pleosporaceae*. Ariyawansa et al. (2015) removed *Austropleospora* from *Pleosporaceae* and included it in *Didymosphaeriaceae*. *Austropleospora osteospermi* was introduced with both sexual and asexual morphs, and reported for the first time in coastal regions of New South Wales in

Australia, on leaf spots of *Chrysanthemoides monilifera* (an invasive plant), which caused severe necrosis (Morin et al. 2010). The genus also includes three other species; *Austropleospora archidendri* (Basionym = *Paraconiothyrium archidendri*) (Verkley, Göker & Stielow) Ariyaw. & K.D. Hyde, *Austropleospora keteleeriae* Jayasiri, E.B.G. Jones & K.D. Hyde. These two species were introduced with only their asexual morphs, and *Austropleospora ochracea* L.S. Dissan, J.C. Kang & K.D. Hyde was introduced with only its sexual morph.

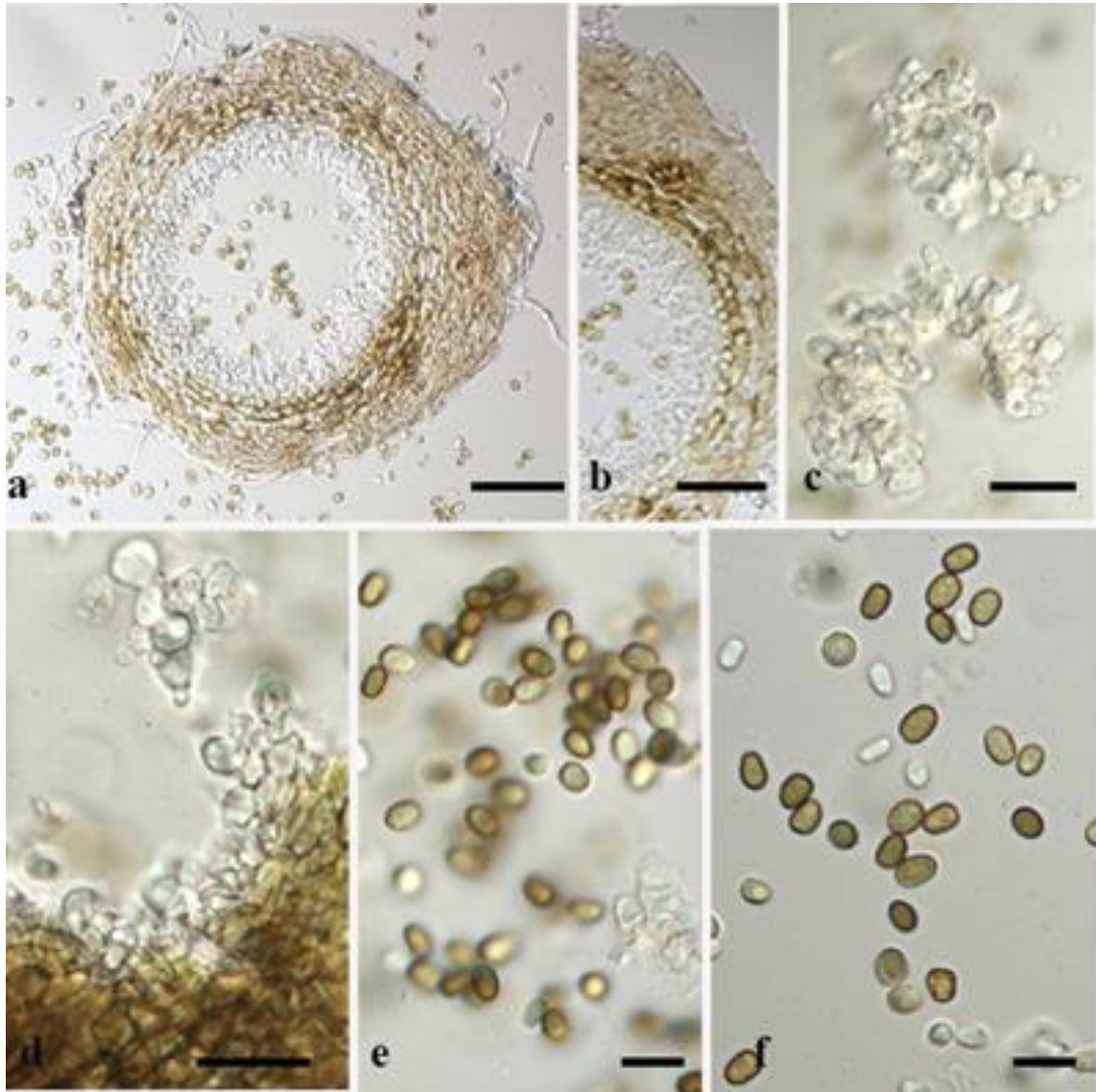


Figure 46 – *Austropleospora archidendri* (photo credits by Jayasiri et al. 2019). a Section through conidioma. b Conidioma wall. c, d Conidiogenous cells. e, f Conidia. Scale bars: a = 50 μm , b = 30 μm , c–f = 10 μm .

Studies based on morphology, host range tests and DNA sequence (ITS) analysis introduced *Austropleospora osteospermi* as the sexual morph of *Hendersonia osteospermi*. The genus name is inferred from the Latin word ‘auster’, which refers to its distribution in the Southern Hemisphere and its morphological similarity to *Pleospora*. *Austropleospora osteospermi* has perithecioid ascomata with protruding necks that are black, ostiolate, and dispersed throughout the leaves and stems of the host plant. Pseudoparaphyses are filiform, septate, branching, and hyaline. Asci are bitunicate and cylindrical and contain 6-8 ascospores. Ascospores are dictyosporous, ellipsoidal, smooth, and yellowish-brown. Conidiomata are pycnidial, globose, superficial on leaf and stem lesions, with a single ostiole. Conidiophores are absent and conidiogenous cells are inconspicuously annellidic,

discrete, and cylindrical. Conidia are cylindrical to narrowly ellipsoidal, initially hyaline and aseptate, becoming yellowish brown, and mostly transversely 3-septate (Morin et al. 2010).SSU, LSU, *tef1*, and ITS DNA sequence data are available for some species of the genus (Dissanayake et al. 2021, Ren et al. 2022).

Type species: *Austropleospora osteospermi* R.G. Shivas & L. Morin

Other accepted species:

Austropleospora archidendri (Verkley, Göker & Stielow) Ariyaw. & K.D. Hyde

Austropleospora keteleeriae Jayasiri, E.B.G. Jones & K.D. Hyde

Austropleospora ochracea L.S. Dissan, J.C. Kang & K.D. Hyde

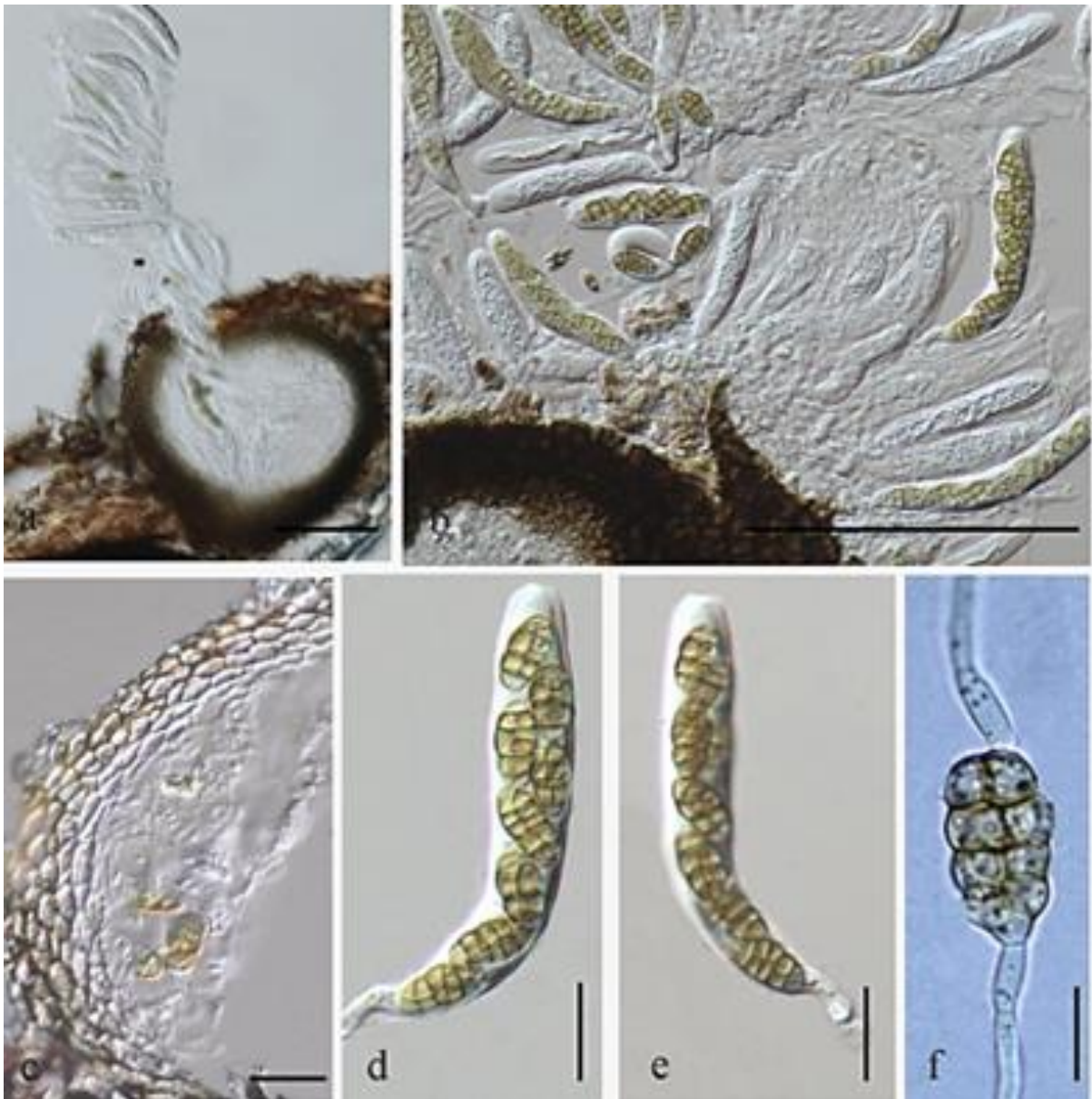


Figure 47 – *Austropleospora ochracea* (Photo credits by Dissanayake et al. 2021). a Vertical section of ascoma. b Pseudoparaphyses and asci. c Peridium. d, e Asci and ascospores. f Germinating ascospore. Scale bars: a, b = 100 μ m, c = 10 μ m, d, e = 20 μ m, f = 5 μ m.

References

Ariyawansa HA, Thambugala KM, Manamgoda DS, Jayawardena R et al. 2015 – Towards a natural classification and backbone tree for Pleosporaceae. *Fungal Diversity* 71, 85–139.

- Dissanayake LS, Wijayawardene NN, Samarakoon MC, Hyde KD, Kang JC. 2021 – The taxonomy and phylogeny of *Austropleospora ochracea* sp. nov. (*Didymosphaeriaceae*) from Guizhou, China. *Phytotaxa* 491, 217–229.
- Jayasiri SC, Hyde KD, Jones EB, McKenzie EH et al. 2019 – Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. *Mycosphere* 10, 1–86.
- Morin L, Shivas RG, Piper MC, Tan YP. 2010 – *Austropleospora osteospermi* gen. et sp. nov. and its host specificity and distribution on *Chrysanthemoides monilifera* ssp. *rotundata* in Australia. *Fungal Diversity* 40, 65–74.
- Thambugala KM, Singtripop C, Chunfang YU, Mckenzie EH et al. 2014 – Towards a natural classification of Dothideomycetes 7: the genera *Allosoma*, *Austropleospora*, *Dangeardiella*, *Griggsia* and *Karschia* (*Dothideomycetes incertae sedis*). *Phytotaxa* 181, 34–46.
- Ren G, Wanasinghe DN, de Farias ARG, Hyde KD et al. 2022 – Taxonomic novelties of woody litter fungi (*Didymosphaeriaceae*, *Pleosporales*) from the Greater Mekong Subregion. *Biology* 11, 1660.

Entry by

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(Edited by **Kevin D. Hyde**)

46. Fungalpedia – Note 118 *Fusasporis*

Fusasporis J. Lovy, R.P.E. Yanong, J.M. Stilwell, T.B. Waltzek, J.P. Shelley, D.B. Pouders, J.C. Wolf & A.C. Camus

Citation when using this entry: Selçuk et al., in prep – Genera and higher taxa introduced in 2023.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 48

Classification: *Pleistophoridae*, *Glugeida*, *Haplophasea*, *Microsporea*, *Incertae sedis*, *Microsporidia*, *Protozoa*

This genus is monotypic, which is the causative agent of tetra disseminated microsporidiosis, a new disease in ornamental fish of cardinal tetra and black tetra. The non-xenoma-forming microsporidium occurred diffusely in most internal organs and the gills, thus referring to the condition as tetra disseminated microsporidiosis. Based on combined phylogenetic and ultrastructural characteristics, the genus was proposed by Lovy et al. (2021), with *F. stethaprioni* as the type species. In microscopic preparations, spores were uniform measuring $3.9 \pm 0.33 \mu\text{m}$ (range = 3.2–3.7 μm) x $2 \pm 0.2 \mu\text{m}$ (range = 1.6–2.5) wide. It was identified from captive fish populations from the USA. The closest microsporidia to *F. stethaprioni* are *Glugea* spp., though its relationship to *Glugea* is not yet clear. The branching in the tree indicates that *F. stethaprioni* may form a basal group to *Glugea* spp. though this branching was poorly supported, due to inadequate taxa sampling of closely related species. Larger taxa sampling will reveal the relationship of *Fusasporis* to *Loma* and *Glugea*. The lower sequence similarity to species within *Glugea* also supports that it is separated from *Glugea* spp. The taxonomic placement of *Fusasporis* is in *Pleistophoridae* (*Marinosporidia*, *Microsporidia*).

Type species: *Fusasporis stethaprioni* J. Lovy, R.P.E. Yanong, J.M. Stilwell, T.B. Waltzek, J.P. Shelley, D.B. Pouders, J.C. Wolf & A.C. Camus

Other accepted species: The genus is monotypic.

Reference

- Lovy J, Yanong RPE, Stilwell JM, Waltzek TB et al. 2021 – Tetra disseminated microsporidiosis: a novel disease in ornamental fish caused by *Fusasporis stethaprioni* n. gen. n. sp. *Parasitology Research* 120, 497–514.

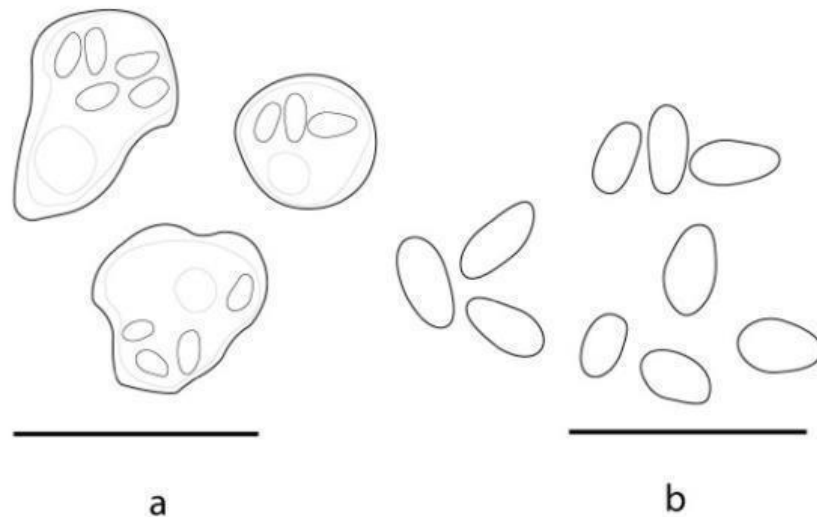


Figure 48 – *Fusasporis stethaprioni*. a Spores within host cells. b Spores. Scale bar: a = 20 µm, b = 10 µm. (Redrawn from Lovy et al. 2021).

Entry by

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(Edited by **Kevin D. Hyde**)

47. Fungalpedia – Note 119 *Parameliola*

Parameliola Hongsanan, Peršoh & K.D. Hyde

Citation when using this entry: Hongsanan et al., in prep – Fungalpedia, genera and higher taxa introduced in 2016.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 49.

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

Parameliola was introduced as an *incertae sedis* genus in *Pleosporales* by Li et al. (2016) to accommodate two species, *P. acaciae* and *P. dimocarpi*, with the latter the type species. *Parameliola* species have a hyperparasitic habitat. The asexual morph is characterised by superficial, solitary, globose to subglobose conidiomata, attached to the superficial hyphae of *M. thailandicum*. The hyphae are branched, septate, darker at the septa, brown to dark brown, with 2-celled, mostly alternate or sometimes opposite hyphopodia. Conidiogenous cells are holoblastic, cylindrical, and hyaline. Conidia are ellipsoid to cylindrical, both ends broadly rounded, aseptate, hyaline, borne singly at the apex of the conidiophore (Li et al. 2016). *Parameliola* shares similarities with *Coniothyrium*, but it is distinguished from *Coniothyrium* and other genera in *Pleosporales* by its unique hyperparasitic habitat on the thallus or hyphae of *Meliola* species. Li et al. (2016) successfully obtained sequence data of the two species of *Parameliola* directly from dry fruiting bodies which contained many conidia. Phylogenetic analyses based on LSU and SSU sequence data revealed that these two species clustered together, but formed a distinct clade separate from other known genera in *Pleosporales* (Li et al. 2016). Therefore, Li et al. (2016) introduced a new genus, *Parameliola* to accommodate the two species. Interestingly, these two species of *Parameliola* did not cluster in any family of *Pleosporales* in their phylogenetic tree. Li et al. (2016) noted that the *Parameliola* clade may represent a new family within *Pleosporales*. However, there is no other record except the original description for the genus. More collections are needed to confirm their placement.

Type species: *Parameliola dimocarpi* Hongsanan & K.D. Hyde

Other accepted species: *Parameliola acaciae* Hongsanan & K.D. Hyde

Reference

Li GJ, Hyde KD, Zhao RL, Hongsanan S et al. 2016 – Fungal diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity* 78, 1–237.

Entry by

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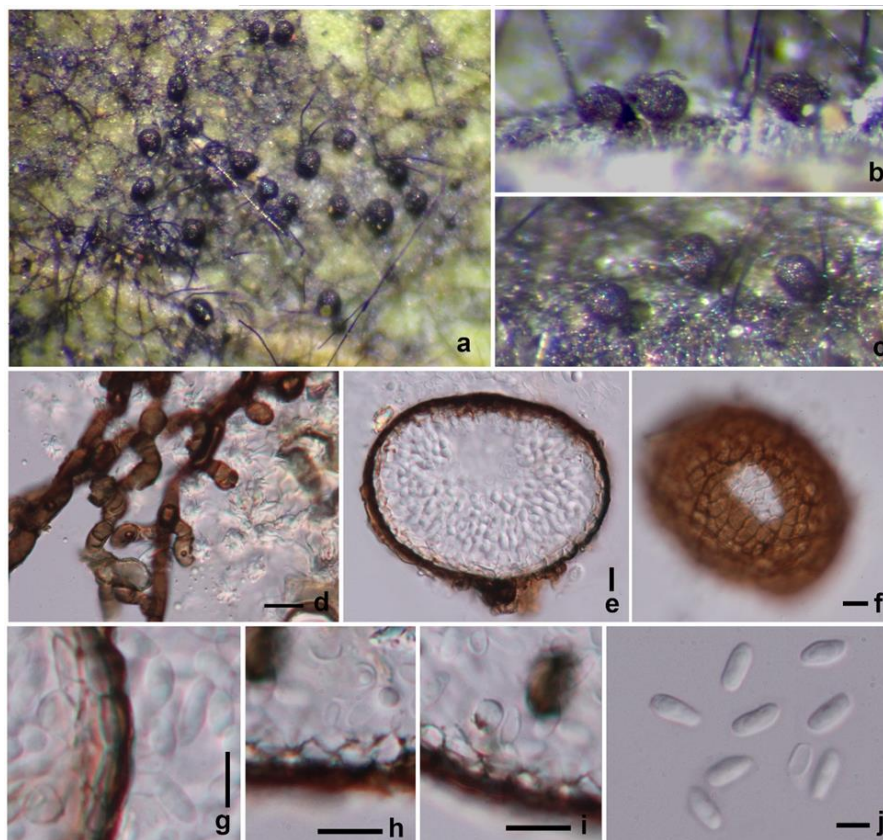


Figure 49 – *Parameliola dimocarpi* (MFLU15–0045, holotype). Hyperparasitic on the thallus or hyphae of *Meliola thailandicum*. a-c Conidiomata d Hyphae with hyphopodia. e Section through conidioma in 10% lactic acid. f Upper wall of conidioma. g Peridium of conidioma. h, i Conidiogenous cells. j Conidia in 10% lactic acid. Scale bars: d–i = 10 μ m, j = 5 μ m.

48. Fungalpedia – Note 120 *Pirozynskiomyces*

Pirozynskiomyces Hern.-Restr. & Crous

Citation when using this entry: Norphanphoun et al., in prep – Fungalpedia, genera and higher taxa of 2022.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 50

Classification: *Coniocessiaceae*, *Xylariales*, *Xylariomycetidae*, *Sordariomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Based on multi-locus analysis (ITS, LSU, *rpb2*) and morphological studies, Hernández-Restrepo et al. (2022) introduced *Pirozynskiomyces* (Coniocessiaceae) to accommodate *P. brasiliensis* and *P. sinensis* (\equiv *Circinotrichum sinense*). *Pirozynskiomyces* with *P. brasiliensis* as

the type was collected from a rotten leaf in Brazil, and *P. sinensis* was found on dead foliage of *Camellia cuspidata* in China (Hernández-Restrepo et al. 2022). *Pirozynskiomyces* is known only from its asexual morph and is characterized by simple or branched setae and conidiogenous cells that produce falcate, hyaline conidia with a cellular appendage at the apex (Li et al. 2017, Hernández-Restrepo et al. 2022). Phylogenetic evidence obtained from the analysis of ITS, LSU, and *rpb2* sequences of *Xylariales* show it as a distinct lineage and grouped within *Conioceciaceae* (Hernández-Restrepo et al. 2022). Therefore, based on phylogenetic inferences, *Circinotrichum sinense* was transferred to *Pirozynskiomyces* (Hernández-Restrepo et al. 2022). The taxonomic placement of *Pirozynskiomyces* is in *Conioceciaceae* (*Xylariales*, *Sordariomycetes*).

Type species: *Pirozynskiomyces brasiliensis* Hern.-Restr. & Crous

Other accepted species:

Pirozynskiomyces sinensis (D.W. Li, Neil P. Schultes, Jing Y. Chen, Yi X. Wang & R.F. Castañeda) Hern.-Restr. & Crous

References

Hernández-Restrepo M, Decock CA, Costa MM, Crous PW. 2022 – Phylogeny and taxonomy of *Circinotrichum*, *Gyrothrix*, *Vermiculariopsiella* and other setose hyphomycetes. *Persoonia* 49, 99–135.

Li DW, Schultes NP, Chen JY, Wang YX, Castañeda-Ruiz RF. 2017 – *Circinotrichum sinense*, a new asexual fungus from Hubei, China. *Botany* 95, 1099–1108.

Entry by

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(Edited by **Kevin D. Hyde**)

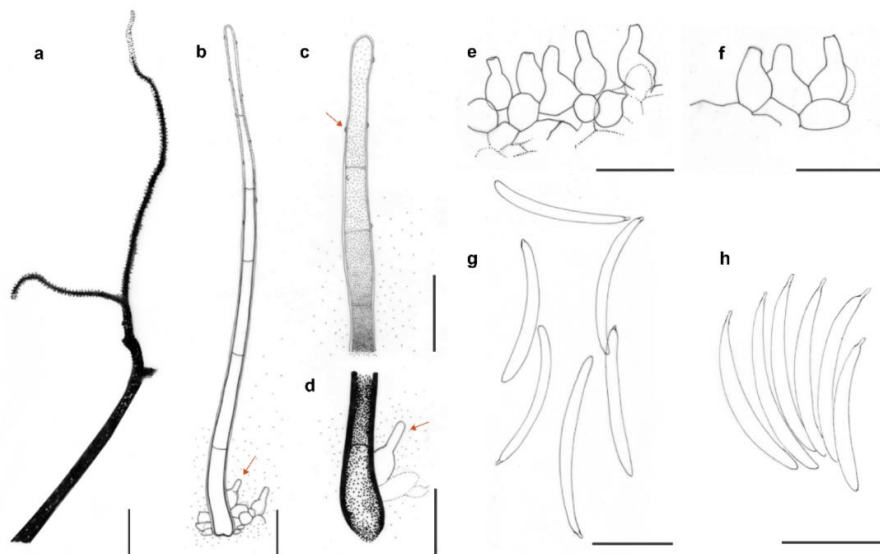


Figure 50 – *Pirozynskiomyces brasiliensis* (a, e–f, g) and *P. sinensis* (b–c, h), redrawn from Li et al. (2017), and Hernández-Restrepo et al. (2022). a, b Setae. c Apical portion of seta showing percurrent extension (arrow). d, e, f Conidiogenous cells (d at the arrow). g, h Conidia. Scale bars = 10 µm.

49. Fungaldia – Note 121 *Pseudoalternaria*

Pseudoalternaria D.P. Lawr., Gannibal, Dugan & B.M. Pryor

Citation when using this entry: Tibpromma et al., in prep – Fungalpedia, new genera and higher taxa in 2014.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 51

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

Pseudoalternaria was described with the type species *Pseudoalternaria arrhenatheria*, and *Alternaria rosae* was transferred to *Pseudoalternaria* based on morphological and molecular data (single and combined ITS/gpd/Plasma membrane ATPase) (Lawrence et al. 2014). The morphology of *Pseudoalternaria* is similar to *Alternaria*, but phylogenetic analysis, showed that *Pseudoalternaria* formed an independent lineage basal to *Alternaria*. Lawrence et al. (2016) transferred *Pseudoalternaria* to a new section of *Alternaria* (sect. *Pseudoalternaria*). However, *Pseudoalternaria* is invalid (Art. F.5.1, Shenzhen).

Type species: *Pseudoalternaria arrhenatheri* D.P. Lawr., Gannibal, F.M. Dugan & B.M. Pryor

Other described species:

Pseudoalternaria rosae (E.G. Simmons & C.F. Hill) D.P. Lawr., Gannibal, Dugan & B.M. Pryor

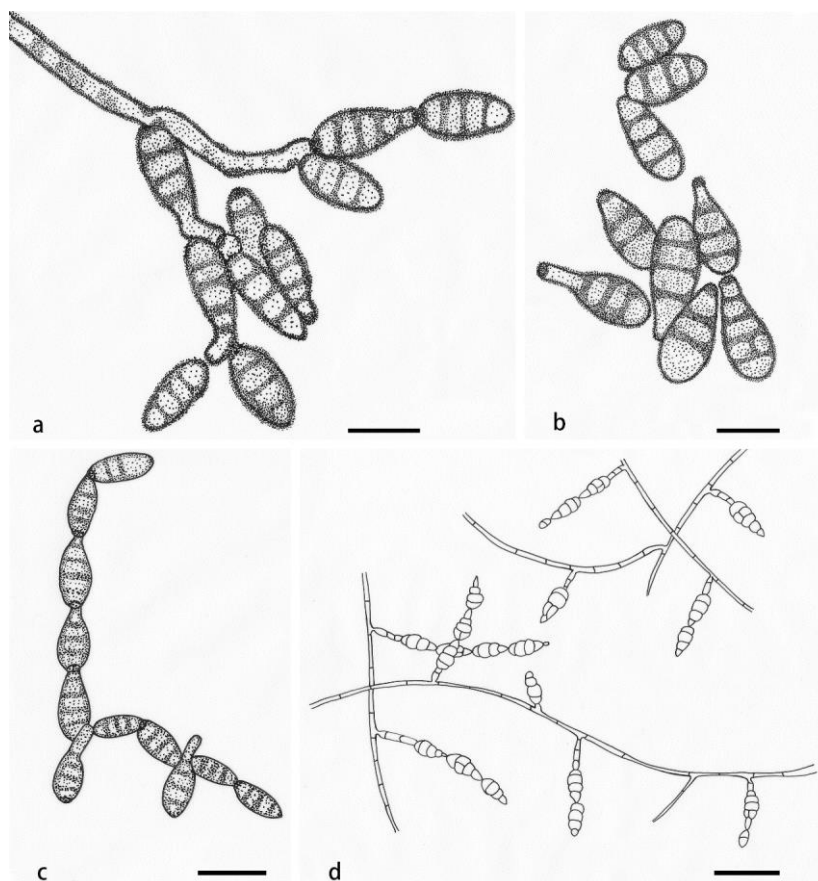


Figure 51 – *Pseudoalternaria arrhenatheria* (holotype, redrawn from Lawrence et al. 2014). a–d Conidiophores and conidia. Scale bars: a, b = 12.5 μm , c = 25 μm , d = 50 μm .

References

- Lawrence DP, Gannibal PB, Dugan FM, Pryor BM. 2014 – Characterization of *Alternaria* isolates from the infectoria species-group and a new taxon from *Arrhenatherum*, *Pseudoalternaria arrhenatheria* sp. nov. *Mycological Progress* 13, 257–276.
- Lawrence DP, Rotondo F, Gannibal PB. 2016 – Biodiversity and taxonomy of the pleomorphic genus *Alternaria*. *Mycological Progress* 15, 1–22.

Entry by

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(Edited by **Kevin D. Hyde**)

50. Fungalpedia – Note 122 *Purpureocorticium*

***Purpureocorticium* S.H. Wu**

Citation when using this entry: et al., in prep – Fungalpedia, genera and higher taxa of 2022. Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 52

Classification: *Incertae sedis*, *Incertae sedis*, *Incertae sedis*, *Agaricomycetes*, *Agaricomycotina*, *Basidiomycota*, *Fungi*

The corticioid genus *Purpureocorticium* was introduced by Wu et al. (2018) to accommodate *Purpureocorticium microsporum* (*Agaricomycetes*, *Basidiomycota*) based on morphological study and phylogenetic analyses of LSU and *efl-α*. It was found on an angiosperm branch in mountainous Taiwan. *Purpureocorticium* is characterized by having a resupinate basidiocarp with smooth hymenial surface, turning purple in KOH, and becomes purplish after storage. The subiculum has a compact texture, nodose-septate generative hyphae, without cystidia, basidia are subclavate with a median constriction, or utriform, and basidiospores are ovate-ellipsoid, smooth and thin-walled, inamyloid and nondextrinoid (Wu et al. 2018). A detailed description for this species was given in Wu et al. (2018).

Type species: *Purpureocorticium microsporum* S.H. Wu

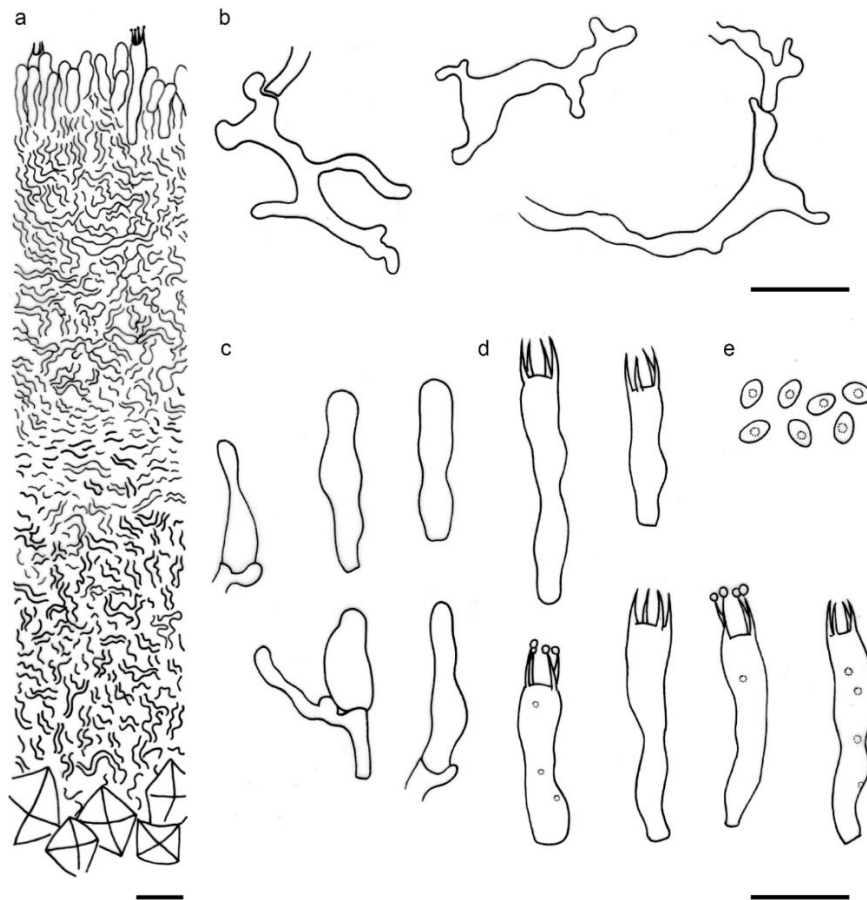


Figure 52 – *Purpureocorticium microsporum* (Redrawn from Wu et al. 2018). a Basidiocarp section. b Subicular hyphae. c Asidioles. d Basidia. e Basidiospores. Scale bars: a–e = 10 µm.

Reference

Wu SH, Wang DM, Chen YP. 2018 – *Purpureocorticium microsporium* (Basidiomycota) gen. et sp. nov. from East Asia. *Mycological Progress* 17, 357–364.

Entry by

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(Edited by **Kevin D. Hyde**)

51. Fungalpedia – Note 123 *Quixadomyces*

Quixadomyces Cantillo & Gusmão

Citation when using this entry: Norphanphoun et al., in prep – Fungalpedia, genera and higher taxa of 2022.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 53

Classification: *Parapyrenochaetaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

Based on analysis of combined ITS and LSU sequence data, Crous et al. (2018) introduced *Quixadomyces* to accommodate *Q. cearensis* Cantillo & Gusmão, a fungus that was collected from decaying bark in Brazil. However, they did not mention about development of internal structures. The taxonomic placement of *Quixadomyces* is in *Parapyrenochaetaceae* (*Pleosporales*, *Dothideomycetes*) (Crous et al. 2018). Wanasinghe et al. (2021) introduced *Q. hongheensis* Wanas. collected from dead twigs of *Dodonaea viscosa* in China. *Quixadomyces hongheensis* was introduced based on sequences of concatenated LSU, SSU, ITS, *rpb2*, *efl1a* and β -*tubulin* with strong statistical support (Wanasinghe et al. 2021).

Quixadomyces is characterized by brown to dark brown pycnidia and is known only from its asexual state produced in PDA (Crous et al. 2018, Wanasinghe et al. (2021)). The conidiomata are immersed to erumpent, solitary, globose, brown, with a central ostiole, and exuding a hyaline conidial mass. The conidiomata peridium wall has two to three layers of brown cells of *textura angularis*. Inside the conidiomata are paraphyses, conidiophores, conidiogenous cells, and conidia. Paraphyses are cylindrical, hyaline, and septate. Conidiophores are mostly reduced to conidiogenous cells. Conidiogenous cells are phialidic with periclinal thickening, ampulliform to subcylindrical lining the inner cavity, hyaline, and smooth. Conidia are allantoid with obtuse ends, solitary, hyaline, aseptate and smooth (Fig. 53, Wanasinghe et al. 2021).

Type species: *Quixadomyces cearensis* Cantillo & Gusmão

Other accepted species:

Quixadomyces hongheensis Wanas.

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Wanasinghe DN, Mortimer PE, Xu J. 2021 – Insight into the systematics of microfungi colonizing dead woody twigs of *Dodonaea viscosa* in Honghe (China). *Journal of Fungi* 7, 180.

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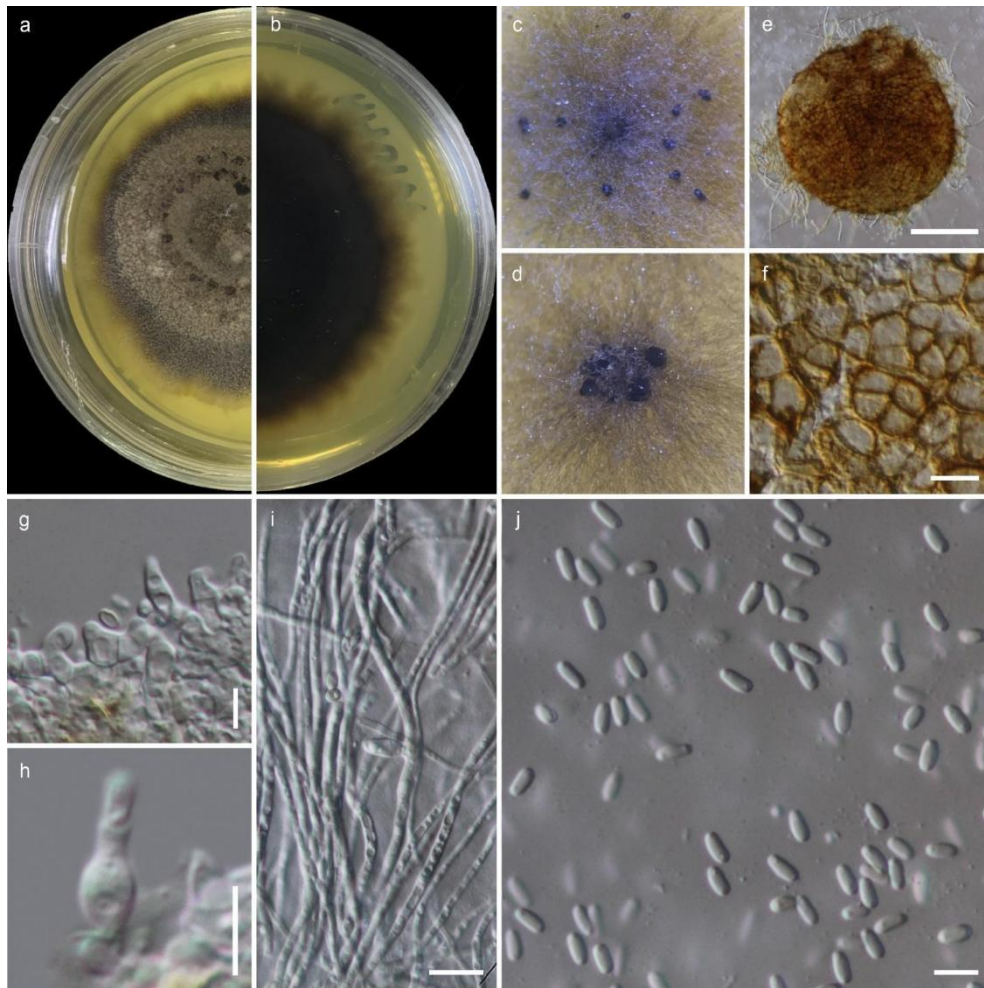


Figure 53 – *Quixadomyces hongheensis* (KUMCC 20-0215, ex-type culture). a, b Colony on PDA (a from top, b from bottom). c, d Pycnidia on PDA. e Squashed pycnidium. f Pycnidium wall. g, h Conidiogenous cells. i Mycelia. j Conidia. Scale bars: e = 200 μm , f, i = 10 μm , g, h, j = 5 μm .

52 Fungalpedia – Note 60 *Salmacisia*

Salmacisia D.R. Huff & Amb. Chandra

Citation if using this entry: Noorabadi MT et al., in prep – New genera in 2008-2009.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 54

Classification: *Tilletiaceae*, *Tilletiales*, *Exobasidiomycetidae*, *Exobasidiomycetes*, *Ustilaginomycotina*, *Basidiomycota*, *Fungi*

Based on phylogeny of LSU sequences using maximum parsimony and maximum likelihood analyses, Huff & Chandra (2008) introduced *Salmacisia* as a monotypic genus within *Tilletiaceae*, *Tilletiales* in *Exobasidiomycetes*, with the type species *Salmacisia buchloeana* (Kellerm & Swingle) D.R. Huff & Amb. Chandra. The species had initially been described as *Tilletia buchloëana* by Kellerman & Swingle (1889). This pathogenic species infects buffalograss (*Bouteloua dactyloides*) causing pistil smut and parasitic induced hermaphroditism (Huff & Chandra 2008). It is the only species in the order *Tilletiales* known to have hermaphroditic effects (Huff & Chandra 2008). *Salmacisia buchloeana* produces sori that originate from the ovaries of infected plants. These sori contain masses of dirty brown agglutinated spores (Huff & Chandra 2008). The teliospores are subglobose, globose, ovoid or elongated, pale yellow to light chocolate brown, 13–26 μm in diameter, usually with surface ornamentation. Teliospores germinate to produce a promycelium that gives rise to primary basidiospores that are either uninucleate and then fuse, or binucleate, giving rise to

secondary basidiospores. These infect the host producing a systemic infection (Huff & Chandra 2008). No further species have been introduced to this genus which remains monotypic.

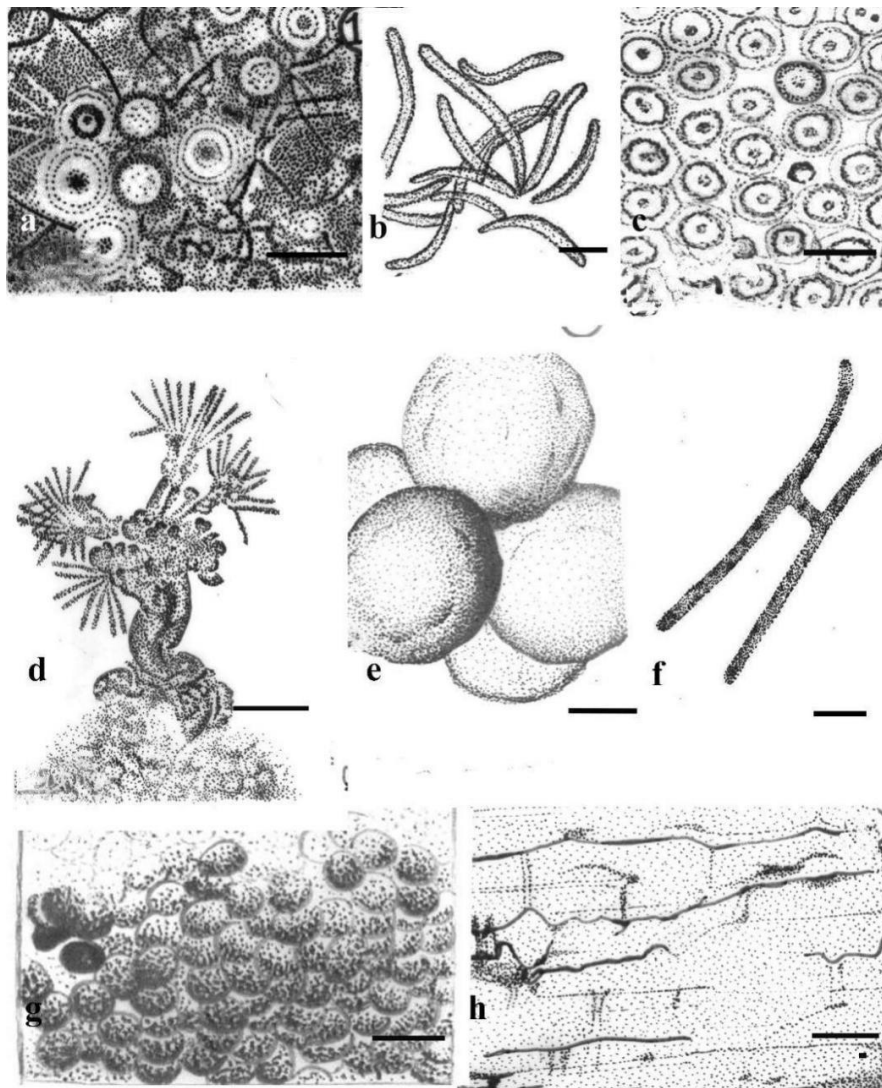


Figure 54 – Stages of *Salmacisia* pistil smut life-cycle *in vitro* and *in vivo* (redrawn from Chandra & Huff, 2008) a Teliospores produced from tips of mycelium growing in culture. b Blastospore-type secondary fusiform sporidia. c Teliospores. d Germinating teliospore with promycelium. e Teliospores of pistil smut exhibiting obscure tuberculate surface ornamentation. f Conjugating primary basidiospores forming a H-shaped bridge structure. g Cross-section of a teliospore filled ovary (smut ball). h Intercellular growth of pistil smut hyphae within buffalo grass vegetative meristem. Scale bars: a, c = 20 μm , b, f = 0.5 μm , c = 20 μm , d, e = 5 μm , g = 50 μm , h = 40 μm .

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53. Funglopedia – Note 124 *Setoapiospora*

Setoapiospora Mapook & K.D. Hyde

Citation when using this entry: Shah et al., in prep – The new genera and higher taxa described in 2020.

Index Fungorum, Facesoffungi, GenBank, Fig. 55

Classification: *Muyocoproneae*, *Muyocoproneales*, *Dothideomycetidae*, *Dothideomycetes*, *Pezizomycotina*, *Ascomycota*, *Fungi*

The monotypic genus *Setoapiospora* was introduced by Hyde et al. (2020), isolated as saprobe from dead wood found in a waterfall in Thailand. *Setoapiospora* is known only from its sexual morph. It has submersed, scattered, or sparsely distributed ascomata and appears as dark brown to black spots without uniform margins. The centrally located ostiole has dark-brown setae. The peridium is dark brown with cells of densely compact *textura epidermoidea*. The hamathecium may be thread-like or cylindrical and distinctly septate. Asci are bitunicate, slightly curved, containing eight spores with an ocular chamber. Ascospores are one seriate, hyaline, wide at the center, and tapered at the ends with numerous granules. It may have a slightly curved and constricted septum. The asexual morph remains unknown. Based on morphological and multigene (ITS, LSU, SSU, and *Tef1- α*) phylogeny, *Setoapiospora* is accepted in *Muyocoproneae*.

Type species: *Setoapiospora thailandica* Mapook & K.D. Hyde

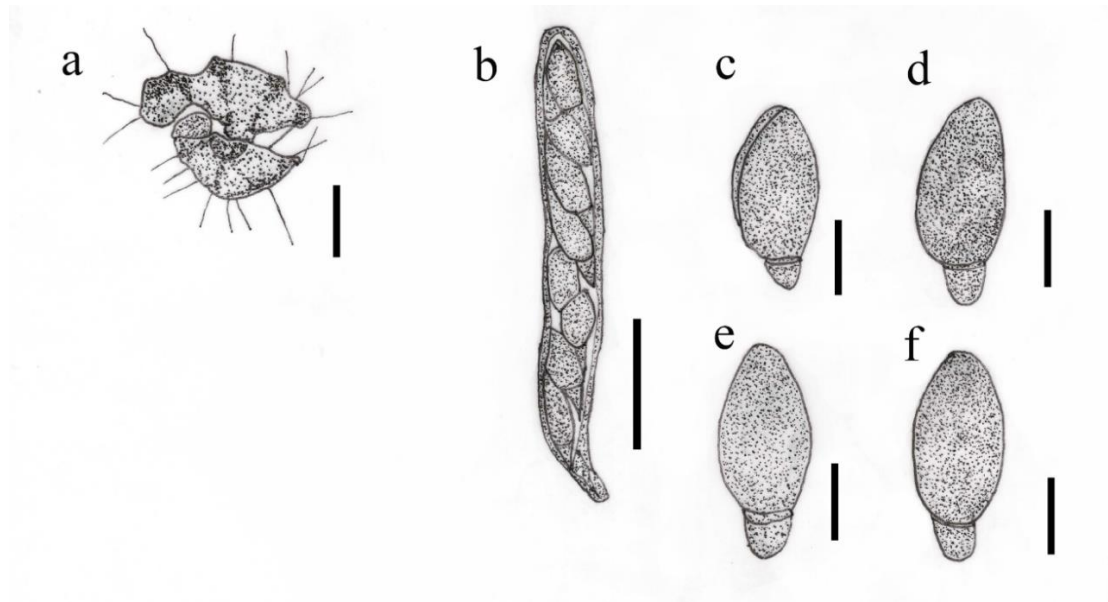


Figure 55 – Morphological characteristic of *Setoapiospora thailandica* (Redrawn from Hyde et al. 2020). a Ascomata structure. b Structure of asci. c–f Ascospores. Scale bars: a, b = 50 μ m, c–f = 10 μ m.

Reference

Hyde KD, Dong Y, Phookamsak R, Jeewon R et al. 2020 – Fungal diversity notes 1151–1276: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal diversity* 100, 5–277.

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54. Fungalpedia – Note 125 *Towyspora*

Towyspora Wanasinghe, E.B.G. Jones & K.D. Hyde

Citation when using this entry: Gunarathne et al., in prep – The new genera and higher taxa described in 2016.

Index Fungorum, Facesoffungi, MycoBank, GenBank, Fig. 56

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

The monotypic genus *Towyspora* was introduced by Li et al. (2016) to accommodate *Towyspora aestuari* based on phylogeny and morphology. The genus name is derived from the river Towy, Wales, in which the specimen was found. *Towyspora* is classified in *Lentitheciaceae*, *Pleosporales*, *Dothideomycetes*, *Ascomycota* (Li et al. 2016). *Towyspora aestuari* is saprobic on *Phragmites communis* (*Poaceae*); an aquatic shrub, and has semi-immersed to immersed, stromatic and pycnidial conidiomata. In the phylogenetic analysis based on ITS, SSU, LSU, and *Tef* sequence data, *T. aestuari* formed a separate clade from *Setoseptoria* with high bootstrap support. *Towyspora* is similar to *Setoseptoria* in having subcylindrical, hyaline conidiogenous cells and hyaline, smooth-walled, transversely euseptate, subcylindrical conidia with a single large central guttule per cell. However, *Towyspora aestuari* differs from *Setoseptoria phragmitis*, the type species of the genus *Setoseptoria*, which has smaller and aseptate conidia (Quaedvlieg et al. 2013). The sexual morph of the species is not determined.

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

Other accepted species: This genus in monotypic.

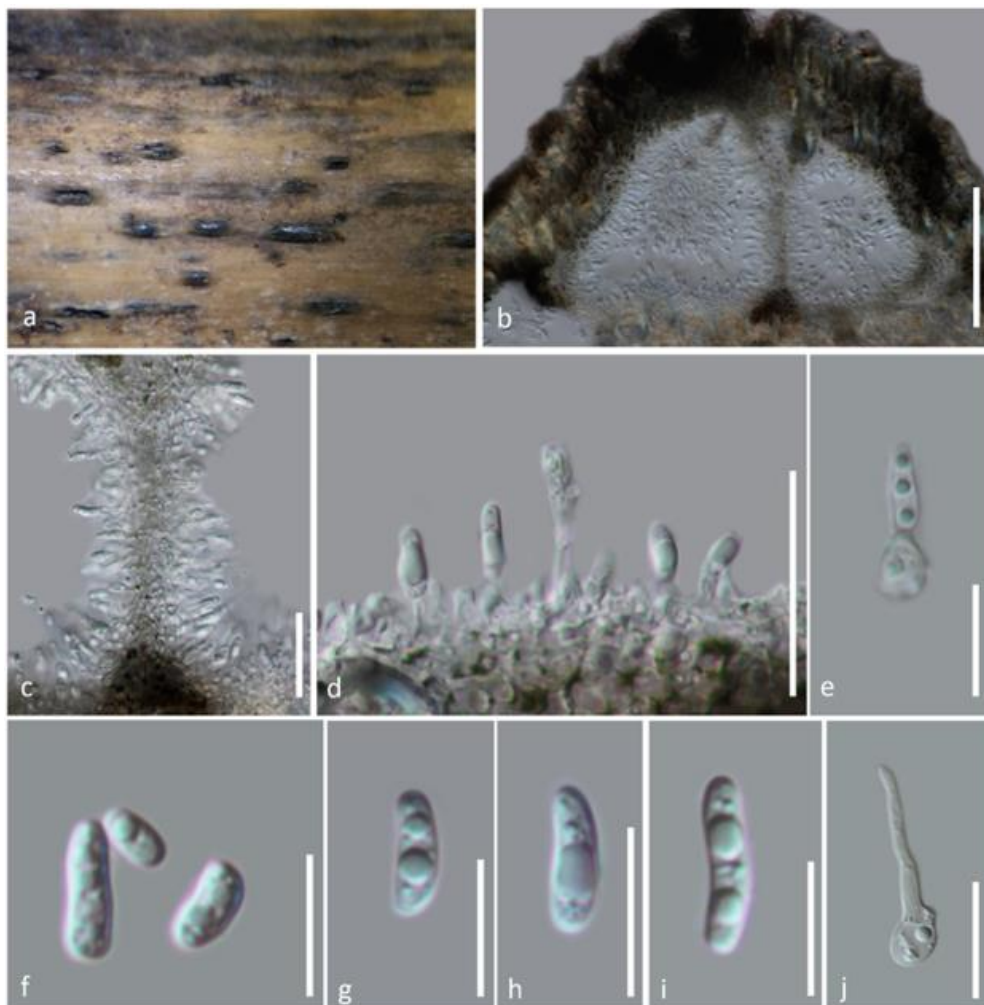


Figure 56 – *Towyspora aestuari* (MFLU 15–3543). a Conidiomata on host. b, c Vertical section

through conidioma. d, e Conidiogenous cells with conidia. f–i Conidia. j Germinated conidium. Scale bars: b–d = 100 µm, e–i = 10 µm, j = 20 µm. Photo Credits: Dhanushka N. Wanasinghe.

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(Edited by **Chitrabhanu S. Bhunjun & Kevin D. Hyde**)

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