TAXONOMY AND PHYLOGENY OF SOIL ASCOMYCETES IN THAILAND

ERANDI YASANTHIKA WEERAGALLE ARACHCHILLAGE

DOCTOR OF PHILOSOPHY

IN

BIOLOGICAL SCIENCE

SCHOOL OF SCIENCE

MAE FAH LUANG UNIVERSITY

2024

©COPYRIGHT BY MAE FAH LUANG UNIVERSITY

TAXONOMY AND PHYLOGENY OF SOIL ASCOMYCETES IN THAILAND

ERANDI YASANTHIKA WEERAGALLE ARACHCHILLAGE

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

SCHOOL OF SCIENCE
MAE FAH LUANG UNIVERSITY
2024
©COPYRIGHT BY MAE FAH LUANG UNIVERSITY

DISSERTATION APPROVAL

MAE FAH LUANG UNIVERSITY

FOR

DOCTOR OF PHILOSOPHY IN BIOLOGICAL SCIENCE

Dissertation Title: Taxonomy and Phylogeny of Soil Ascomycetes in Thailand

Author: Erandi Yasanthika Weeragalle Arachchillage

Examination Committee:

Dhanushka Wanasinghe, Ph. D.	Chairperson
Thilini Chethana Kandawatte Wedaralalage, Ph. D.	Member
Adjunct Professor Kevin David Hyde, Ph. D.	Member
Mahamarakkalage Mary Ruvishika Shehali Jayawardena, Ph. D.	Member
Professor Rasoul Zare, Ph. D.	Member
Dan-Feng Bao, Ph. D.	Member

Advisors:

.....Advisor

(Thilini Chethana Kandawatte Wedaralalage, Ph. D.)

.....Co-Advisor

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

Dean:

.....

(Professor Surat Laphookhieo, Ph. D.)

ACKNOWLEDGEMENTS

Firstly, I would like to express my sincere gratitude to my advisor Prof. Kevin David Hyde, for giving me the opportunity to pursue my PhD in the Center of Excellence in Fungal Research, and for his invaluable guidance, motivation, financial support and encouragement throughout my PhD study. His immense knowledge and insightful feedback always helped me in developing my research and writing of this thesis. I am truly grateful for his patience and continuous support throughout my PhD study. I extend my sincere gratitude towards Dr. Thilini Chethana for her enormous guidance, unwavering support and encouragement throughout my PhD study. She has been a great teacher to me and is always dedicated to sharing knowledge with us. I am thanking her for giving me valuable ideas and suggestions that truly inspired me and enhanced my research and paper-writing skills. Also, I am grateful to Dr. Dhanushka Wanasinghe for his encouragement, invaluable guidance and motivation that enriched my academic knowledge throughout my PhD study and for helping me from the beginning of my PhD study. I would like to thank Prof. Rasoul Zare for his valuable ideas, suggestions and support to improve my research study. Besides them, I am grateful for the rest of my thesis committee: Dr. Ruvishika Jayawardena and Dr. Dan Feng Bao for their insightful comments and encouragement to widen my research from various perspectives. I would also like to thank the Thesis or Dissertation Writing Grant, reference no 7702(6)/580 and Mushroom Research Foundation (MRF), Chiang Rai Province, Thailand, for providing financial support during this study.

I am grateful to Dr. Samantha Karunarathna, Prof. D. Jayarama Bhat, Prof. Peter E. Mortimer, Dr. Eric H. McKenzie, Dr. Shaun Pennycook, Dr. Sajeewa Mahaarchchikumbura for their guidance, knowledge enormous support to enhance my research work over six years.

I am thankful to Dr. Roberto Farias for his guidance and support in developing my research. I would like to thank Dr. Danushka Tennakoon, Dr. Ishara Manawasinghe, Dr. Milan Samarakoon, Dr. Nimali De Silva, Dr. Thatsanee Luangharn Dr. Saranyaphat Boonmee, Dr. Jutmart Monkai, Dr. Hansika Perera, Dr. Binu Samarkoon, Dr. Diana Marasinghe, Dr. Nuwanthika Wijesinghe, Dr. Achala Rathnayaka, Dr. Anusha H.

Ekanayaka, Dr. Lakmali Dissanayaka, Dr. Vinodini Thyagaraja, Dr. Janith Vishwakirithi, Dr. Eleni Gentekaki, Dr. Ren Guang Cong, Dr. Gui Heng and Dr. Elina for their invaluable guidance, suggestions and the great help during my studies. I thank my fellow colleagues in the Center of Excellence in Fungal Research for the stimulating discussions, for the sleepless nights we spent working together. In particular, I am grateful to Achala Jeevani, Dilini Thakshila and Vidyamali for helping me and always being there for me.

My sincere thanks also go to Mr. Kasiphat Limsakul, Ms. Wilawan Punyaboon, Ms. Witchuda Taliam, Mr. Sornram Sukpisit, Ms. Areerat Manowong, Ms. Naruemon Huanraluek and Ms. Pattaranan Sornkaew for their invaluable assistance. Without their precious support, it would not be possible to conduct this research.

Last but not least, I would like to thank my parents, my brother and my friends for supporting me spiritually and being the strength throughout my Ph.D. and my life in general.

Erandi Yasanthika Weeragalle Arachchillage

Dissertation Title	Taxonomy and Phylogeny of Soil Ascomycetes in Thailand
Author	Erandi Yasanthika Weeragalle Arachchillage
Degree	Doctoral of Philosophy (Biological Science)
Advisor	Thilini Chethana Kandawatte Wedaralalage, Ph. D.
Co-Advisor	Adjunct Professor Kevin David Hyde, Ph. D.

ABSTRACT

Soil covers a large area of the earth's crust and supports a high biodiversity. Fungi are a highly abundant group of organisms found in soils worldwide. Soil fungi use extensive hyphal networks to break down complex organic materials, transport nutrients, and improve the soil structure. In soil ecosystems, fungi maintain interactions with plant roots and other micro and macro soil organisms while providing ecosystem services. They have saprobic, pathogenic or mutualistic nutritional modes. Understanding fungi is essential as they are key drivers of below-ground ecosystem functions. Taxonomy of soil-associated fungal species is important as it paves the way to biodiversity, ecology, and biotechnological studies. Ascomycota is one of the largest and most abundant fungal phyla in edaphic habitats. Currently, there are two methods available for soil fungal detection; High-throughput sequencing (HTS) and culture-dependent methods, but most of the modern studies focus on HTS methods. Culture-dependent methods are less focused yet essential in identifying the species and genera in the soil. Although HTS provides an intangible estimate of fungal number, only culturing methods can yield living specimens necessary to understand the true number of Ascomycota species recovered from soil. However, soil-associated Ascomycota species and genera identified through culturing methods have not been compiled in recent studies, which poses a challenge to determine the exact number of Ascomycota species and genera worldwide. Ascomycota species have a wide distribution in different types of soil ecosystems in the world. Some of the Ascomycota species are commonly found in soil and can easily be detected, however, there are some uncommon species that can rarely be detected from the isolation methods. Thus, isolating the uncommon soil fungal groups is a challenge. As reported by the Global Fungi

website, fungal diversity in Asia is well studied, but most of the soil habitats in Thailand are poorly explored; thus, there is a need to focus the taxonomic studies on soil fungi in Thailand.

This study provides a comprehensive review on the value of culturing soil fungi in the modern molecular era, providing a compilation of soil-inhabiting Ascomycota genera worldwide, with a web-based platform to record soil Ascomycota, and offers a taxonomic account of uncommon soil ascomycetes found in both disturbed and undisturbed habitats in Thailand.

For the taxonomy and detection of soil fungi, several approaches have been used over the years, including both culture-dependent and culture-independent methods. The culture-dependent methods are based on morpho-molecular identification techniques. However, this approach has been largely been overtaken by culture-independent high-throughput sequencing (HTS) methods, which are now widely used in global soil fungal studies. Both culture-dependent and culture-independent methods are significantly important in understanding fungal taxonomy and estimating the total fungal number of fungal species in soil. This study provides a comprehensive discussion on the contributions of both approaches, emphasizing the continued relevance of culture-dependent methods in modern taxonomy and advocating for a complementary approach to enhance the recovery of fungal taxa and the fungal numbers in global soils. While each method has its own advantages and disadvantages, HTS has revealed numerous unculturable soil taxa and provided valuable insights into global fungal numbers. However, HTS also have several limitations, particularly in identifying species due to short read lengths and the inability to link physical specimens with species identifications. Therefore, morpho-molecular identifications are important to study fungal species. There are several culture-dependent methods available, namely the soil dilution series method, baiting method, soil plate method, heat treatment method, and soil steaming method. Among these, the dilution series method is widely used in many taxonomic studies. This study compiled a detailed account of twelve soil-fungal isolation methods, each described with the steps, advantages, disadvantages, uses and importance. This compilation will be helpful for taxonomists, researchers, and students engaged in soil-related research. Combining both culture-

dependent and -independent methods could represent a significant step towards the fungal taxonomic investigations within soil ecosystems.

Soil-based ecosystems in the world can be categorized as disturbed (e.g., agricultural and urbanized environments) or undisturbed (e.g., forests), each with distinct biological, chemical, and physical factors that influence fungal distribution. Ascomycota is the most abundant fungal phylum in global soils, with Sordariomycetes and Dothideomycetes being the dominant classes found. They play vital roles in ecosystem functioning in various edaphic habitats. In general, the ascomycete taxa present in soil can be categorized as common or uncommon genera/species. There are several genera commonly found in the soil, such as Acremonium, Alternaria, Aspergillus, Cladosporium, Curvularia, Fusarium, Penicillium and Trichoderma. These common groups have high adaptability and fast-growing nature, and can be easily detected and isolated from culturing and HTS methods. There are also rare species in the soil that have received little attention in scientific studies. However, these uncommon fungi have a greater share of the biodiversity in edaphic habitats. Most of the uncommon species are slow-growing and highly adapted to the soil micro-climatic conditions, which make it difficult to isolate them in the artificial environments. Although some uncommon fungal groups can possibly be detected from the HTS methods, identifying smaller or low-abundance communities is a challenge. Therefore, isolating and detecting these uncommon soil fungi are important to uncover new taxa and the hidden fungal diversity in soil ecosystems.

Over the past two decades, numerous studies have investigated soil-dwelling Ascomycota species worldwide, generating a significant amount of taxonomic information. Further, the information derived from HTS methods is compiled, but much of the information from culture-dependent methods remains scattered across various publications. To address this, an updated taxonomic outline was compiled, with comprehensive notes and line drawings for 270 ascomycete genera reported in soils worldwide. The majority of these compiled genera belong to Sordariomycetes (45%), followed by Dothideomycetes (28%) and Eurotiomycetes. Based on this compilation, the distribution of each class varies across different soil habitats, which can primarily be influenced by their ecological adaptations and nutritional requirements. While some habitats have been well studied globally, many ecological niches remain unexplored. Most of the studies have conducted in the forests,

cultivated lands, and urban soils. Based on the available data, forest soils are considered to harbor high Ascomycota diversity. However, a thorough investigation of unexplored or poorly studied habitats is essential to fully understand the true diversity of soil Ascomycota. Thereby, this study serves as a key resource for taxonomists and researchers studying soil fungi, offering a comprehensive compilation of Ascomycota genera and species. It provides valuable insights into their diversity and ecological roles, while also emphasizing the importance of studying Ascomycota on understudied environments in global soils.

This study further focuses on investigating the uncommon Ascomycota species from the different soil ecosystems in Thailand. Being a tropical country with high biodiversity, Thailand has limited studies on soil fungi. Previous research has mainly focused on agricultural and forest soils, with around 185 species, belonging to 79 genera, reported over the past two decades. Most of the species are commonly found. To expand this knowledge, the current study investigated Ascomycota species from three distinct soil ecosystems in Thailand. Samples were collected from caves, forests and urban areas to capture a variety of genera present. In the current research, soil dilution series and the baiting methods have been employed to isolate a diverse range of Ascomycota, including the uncommon taxa, followed by a polyphasic approach for species identification, which included morphological characterization and phylogenetic analyses using maximum likelihood and Bayesian methods. The study reveals 39 species, including 11 new species and 28 host and geographical records from Thai soils. Among these, *Beltraniella fertilis*, *Chloridium gonytrichii*, *Cordana terrestris, Curvularia dactylocteniicola*, *Kionochaeta microspora*, *Neopestalotiopsis terricola*, *Neoroussoella entadae*, *Paraconiothyrium cyclothyrioides*, *Paraleptospora thailandica*, *Pararoussoella lincangensis*, *Pseudopithomyces chartarum, Pochonia chlamydosporia*, *Pyrenochaetopsis tropicalis* and *Roussoella terrestris, Neptunomyces soli*, and and, *Verruconis soli* and *V. thailandica* were reported from forests soils. Species such as *Anteaglonium soli, Acrocalymma medicaginis*, *Currahmyces indicus*, *Diaporthosporella soli*, *Hansfordia pruni*, *H. pulvinata*, *Microascus croci*, *Neoceratosperma soli*, *Neopyrenochaeta telephoni*, *Remotididymella ageratinae*, *Wardomycopsis fusca* and *Yunnania penicillata* were isolated from disturbed caves. Five species were found in undisturbed caves, including *Amorocoelophoma soli*, *Cumuliphoma indica*, *Nigrograna speluncae*, *Microascus croci*, and *Wardomycopsis fusca*, totaling 15

species isolated from cave habitats across 14 genera. We have isolated *Microascus croci* and *Wardomycopsis fusca* from both disturbed and undisturbed cave soils. *Curvularia suttoniae*, *Ectophoma multirostrata*, *Epicoccum catenisporum*, *Paraconiothyrium zingiberacearum*, *Pyrenochaetopsis orizicolz*, *Remotididymella ageratinae*, *Setophoma thailandica* and *Stachybotrys phaeophialis* were recorded from urban soils. This study also explored cellulophilic and keratinophilic taxa in tropical forest soils, leading to the identification of a new species, *Neptunomyces soli* (Didymosphaeriaceae), and a new habitat record for *Curvularia dactylocteniicola* (Pleosporaceae). The potential lingo-cellulophilic and keratinophilic characteristics of these taxa are discussed in detail.

The GlobalFungi website reports Asia as the second most studied region in the world. However, compared to neighboring countries, soil fungal studies in Thailand remain limited, particularly in caves, urban areas, and hot springs. Thai caves, which hold unexploited fungal diversity, and urban soils, which require further exploration due to their ecological roles and potential health risks, represent underexplored habitats for fungal research. Expanding investigations across these diverse habitats will significantly enhance our understanding of soil Ascomycota and their ecological significance. By focusing on these less-explored habitats, we can uncover new species, gain a better understanding of the fungal ecology, and contribute to the global knowledge of soil fungi.

The study expanded the data availability on soil Ascomycota by digitizing a database that includes genera and species isolated from the culture-based methods. While most recent studies and databases on soil Ascomycota rely on high-throughput techniques, typically focusing on higher taxonomic ranks, detailed information at the genus and species levels remains scattered and inaccessible. To address this gap, we developed the Soil Fungi website (https://soilfun.org/), an online platform designed to compile soil-associated fungal species with comprehensive taxonomic descriptions. This platform is designed to be continuously updated to reflect the latest classifications. The Soil Fungi website aggregates scattered information from publications into a centralized, user-friendly database. It provides detailed descriptions of soil-associated fungal species, their taxonomic classifications, and other relevant information. The platform allows users to easily access and retrieve data, making it an essential resource for researchers, students, and anyone interested in soil mycology. The website also includes a guide outlining its objectives,

functions, and instructions for data access and retrieval. By serving as a central repository for soil fungal taxonomy, the Soil Fungi website aims to support and advance research, education, and global collaboration in this field.

Keywords: *Ascomycota*, Culture-dependent Methods, *Dothideomycetes,* Soil Fungi, *Sordariomycetes*

TABLE OF CONTENTS

CHAPTER	Page
1 INTRODUCTION	**1**
1.1 Soil and Soil Fungi	1
1.2 Characteristics and Functions of Fungi in Soil	2
1.3 Detection of Soil Fungi for Taxonomy and Diversity Studies	3
1.4 Current Taxonomy of Soil *Ascomycota* in the World	4
1.5 Common and Uncommon Soil *Ascomycota*	4
1.6 Taxonomy of Soil *Ascomycota* in Thailand	6
1.7 *Ascomycota* Distribution Various Ecosystems and Current Taxonomic Trends in Thailand Soils	6
1.8 Research Objectives	8
1.9 Research Contents	8
2 MATERIAL AND METHODS	**10**
2.1 Sample Collections	10
2.2 Isolations and Morphological Studies	14
2.3 Morphological Studies	15
2.4 DNA Extraction, PCR Amplification, Sequencing, and Phylogenetic Analyses	16
2.5 Writing the Outline and the Generic Notes of Soil Ascomycota and Providing the Drawings for Genera	18
3 VALUE OF CULTURING SOIL ASCOMYCOTA IN MODERN MOLECULAR ERA AND EMPHASIS ON TWELVE ISOLATION METHODS	**19**
3.1 History and the Development of Soil *Ascomycota* Investigations	19
3.2 Isolation and Culturing Methods for Fungi	21
3.3 Baiting Method	24
3.4 Dilution Plate Method	30
3.5 Soil Plate Method	32

TABLE OF CONTENTS

CHAPTER	Page
3.6 Alcohol Treatment Method (Chemical Pasteurization)	33
3.7 Acid Treatment (Chemical Pasteurization)	34
3.8 Heat Treatment Method	35
3.9 Soil Immersion Tube	36
3.10 Soil Steaming Method	37
3.11 Isolation of Fungal Hyphae Attached to Soil Particles	38
3.12 Isolation of Rhizosphere and Mycorrhizal Fungi	38
3.13 The Method to Isolate Nematophagous Soil Fungi	39
3.14 Novel Techniques Introduced to Isolate Soil Fungi	39
3.15 A Brief Comparison of Different Isolation Methods	41
3.16 Sample Collection, Media Selection, Growth Conditions, and Preservation of Cultures from Soil Studies	41
3.17 The Value and Potential of Culturing Soil Fungi	44
3.18 New Trends in Soil Ascomycota Taxonomy: The Use of HTS in Soil Fungal Studies	45
4 THE GENERA OF SOIL ASCOMYCOTA WORLDWIDE AND ACCOUNT ON TAXONOMY AND PHYLOGENY OF SOIL-INHABITING SPECIES ISOLATED FROM THAILAND WITH THE EMPHASIS ON UNCOMMON SPECIES	49
4.1 Introduction	49
4.2 Outline of *Ascomycota* from Soil	53
4.3 Genera Notes and the Taxonomy of Soil *Ascomycota*	69
4.4 Discussion	466

TABLE OF CONTENTS

CHAPTER	Page
5 WEBSITE TO SERVE AS THE ONLINE DATABASE FOR SOIL *ASCOMYCOTA*	**483**
5.1 Introduction	483
5.2 Why is it Important to have a Database for Soil Fungi Recovered from Culturing Methods	486
5.3 Soil Fungi Website	488
5.4 Construction	489
5.5 Interface and Visualization of the Database	489
6 CONCLUSION	496
6.1 Overall Conclusion	496
6.2 Research Advantages	498
6.3 Future Directions	500
6.4 Publications	502
REFERENCES	**505**
APPENDICES	**652**
APPENDIX A CHEMICAL REAGENTS AND MEDIA	652
APPENDIX B PUBLICATIONS	653
CURRICULUM VITAE	**661**

LIST OF TABLES

Table	Page
2.1 The details of the 20 collection sites	13
2.2 Partial gene regions and primers that will be used in the study	18
3.1 Available methods to isolate different fungal taxa from soil	23
3.2 The different types of baits used for fungal isolations from soil	27
4.1 *Cladosporium* species isolated from soil	70
4.2 *Ramichloridium* species isolated from soil	72
4.3 *Pseudoramichloridium* species isolated from soil	73
4.4 *Piedraia* species isolated from soil	78
4.5 *Aureobasidium* species isolated from soil	80
4.6 *Acidiella* species isolated from soil	81
4.7 *Devriesia* species isolated from soil	82
4.8 *Acrocalymma* species isolated from soil	83
4.9 *Amorocoelophoma* species isolated from soil	89
4.10 *Pithomyces* species isolated from soil	97
4.11 *Coniothyrium* species isolated from soil	98
4.12 *Corynespora* species isolated from soil	98
4.13 *Neocucurbitaria* species isolated from soil	99
4.14 *Neodendryphiella* species isolated from soil	100
4.15 *Ascochyta* species isolated from soil	101
4.16 *Cumuliphoma* species isolated from soil	104
4.17 *Didymella* species isolated from soil	107
4.18 *Ectophoma* species isolated from soil	108
4.19 *Epicoccum* species isolated from soil	112
4.20 *Juxtiphoma* species isolated from soil	115
4.21 *Neoascochyta* species isolated from soil	116
4.22 *Neodidymelliopsis* species isolated from soil	118
4.23 *Nothophoma* species isolated from soil	119

LIST OF TABLES

Table	Page
4.24 *Paraboeremia* species isolated from soil	119
4.25 *Pseudoascochyta* species isolated from soil	120
4.26 *Remotididymella* species isolated from soil	122
4.27 *Stagonosporopsis* species isolated from soil	125
4.28 *Vandijckomycella* species isolated from soil	126
4.29 *Xenodidymella* species isolated from soil	127
4.30 *Alloconiothyrium* species isolated from soil	128
4.31 *Bimuria* species isolated from soil	129
4.32 *Didymocrea* species isolated from soil	131
4.33 *Neptunomyces* species isolated from soil	131
4.34 *Paraconiothyrium* species isolated from soil	136
4.35 *Phaeodothis* species isolated from soil	143
4.36 *Pseudopithomyces* species isolated from soil	144
4.37 *Spegazzinia* species isolated from soil	149
4.38 *Latorua* species isolated from soil	150
4.39 *Matsushimamyces* species isolated from soil	151
4.40 *Multiverruca* species isolated from soil	152
4.41 *Polyschema* species isolated from soil	153
4.42 *Bahusandhik*a species isolated from soil	154
4.43 *Leptosphaeria* species isolated from soil	155
4.44 *Neocamarosporium* species isolated from soil	156
4.45 *Nigrograna* species isolated from soil	157
4.46 *Setophoma* species isolated from soil	165
4.47 *Alternaria* species isolated from soil	168
4.48 *Alternaria* species isolated from soil	170
4.49 *Curvularia* species isolated from soil	171
4.50 *Pyrenophora* species isolated from soil	183

LIST OF TABLES

Table	Page
4.51 *Pseudopyrenochaeta* species isolated from soil	184
4.52 *Neopyrenochaeta* species isolated from soil	185
4.53 *Pyrenochaetopsis* species isolated from soil	189
4.54 *Neoroussoella* species isolated from soil	194
4.55 *Roussoella* species isolated from soil	201
4.56 *Preussia* species isolated from soil	203
4.57 *Westerdykella* species isolated from soil	205
4.58 *Tetraploa* species isolated from soil	206
4.59 *Torula* species isolated from soil	207
4.60 *Setophaeosphaeria* species isolated from soil	209
4.61 *Lasiodiplodia* species isolated from soil	210
4.62 *Arthrographis* species isolated from soil	211
4.63 *Rhexothecium* species isolated from soil	212
4.64 *Arxiella* species isolated from soil	213
4.65 *Leptodiscella* species isolated from soil	214
4.66 *Phaeotrichum* species isolated from soil	215
4.67 *Aptrootia* species isolated from soil	216
4.68 *Guizhoumyces* species isolated from soil	217
4.69 *Matsushimaea* species isolated from soil	218
4.70 *Scolecobasidium* species isolated from soil	219
4.71 *Verruconis* species isolated from soil	221
4.72 *Pseudorobillarda* species isolated from soil	228
4.73 *Bahusakala* species isolated from soil	229
4.74 *Monodictys* species isolated from soil	230
4.75 *Cladophialophora* species isolated from soil	231
4.76 *Exophiala* species isolated from soil	232
4.77 *Phialophora* species isolated from soil	232

LIST OF TABLES

Table	Page
4.78 *Rhinocladiella* species isolated from soil	234
4.79 *Veronaea* species isolated from soil	235
4.80 *Aspergillus* species isolated from soil	237
4.81 *Hamigera* species isolated from soil	238
4.82 *Penicillium* species isolated from soil	239
4.83 *Paecilomyces* species isolated from soil	241
4.84 *Thermoascus* species isolated from soil	243
4.85 *Sagenomella* species isolated from soil	244
4.86 *Talaromyces* species isolated from soil	245
4.87 *Blastomyces* species isolated from soil	246
4.88 *Emergomyces* species isolated from soil	247
4.89 *Emmonsiellopsis* species isolated from soil	248
4.90 *Arthroderma* species isolated from soil	249
4.91 *Ctenomyces* species isolated from soil	250
4.92 *Microsporum* species isolated from soil	252
4.93 *Nannizzia* species isolated from soil	252
4.94 *Trichophyton* species isolated from soil	253
4.95 *Arachniotus* species isolated from soil	254
4.96 *Gymnascella* species isolated from soil	255
4.97 *Gymnoascoideus* species isolated from soil	256
4.98 *Gymnoascus* species isolated from soil	257
4.99 *Kraurogymnocarpa* species isolated from soil	258
4.100 *Narasimhella* species isolated from soil	259
4.101 *Pseudoarachniotus* species isolated from soil	260
4.102 *Sporendonema* species isolated from soil	260
4.103 *Malbranchea* species isolated from soil	261
4.104 *Auxarthronopsis* species isolated from soil	262

LIST OF TABLES

Table	Page
4.105 *Canomyces* species isolated from soil	263
4.106 *Currahomyces* species isolated from soil	264
4.107 *Renispora* species isolated from soil	267
4.108 *Amauroascus* species isolated from soil	268
4.109 *Aphanoascus* species isolated from soil	270
4.110 *Brunneospora* species isolated from soil	271
4.111 *Coccidioides* species isolated from soil	272
4.112 *Keratinophyton* species isolated from soil	273
4.113 *Keratinophyton* species isolated from soil	273
4.114 *Pseudoamauroascus* species isolated from soil	275
4.115 *Pseudospiromastix* species isolated from soil	276
4.116 *Spiromastigoides* species isolated from soil	277
4.117 *Diploschistes* species isolated from soil	277
4.118 *Amorphotheca* species isolated from soil	278
4.119 *Acidea* species isolated from soil	278
4.120 *Soosiella* species isolated from soil	279
4.121 *Byssoascus* species isolated from soil	279
4.122 *Myxotrichum* species isolated from soil	280
4.123 *Oidiodendron* species isolated from soil	282
4.124 *Botrytis* species isolated from soil	282
4.125 *Sclerotinia* species isolated from soil	284
4.126 *Cadophora* species isolated from soil	284
4.127 *Scytalidium* species isolated from soil	285
4.128 *Hemileucoglossum* species isolated from soil	286
4.129 *Arthrobotrys* species isolated from soil	287
4.130 *Cephaliophora* species isolated from soil	287
4.131 *Peziza* species isolated from soil	288

LIST OF TABLES

Table	Page
4.132 *Lotinia* species isolated from soil	289
4.133 *Jattaea* species isolated from soil	291
4.134 *Pleurostoma* species isolated from soil	292
4.135 *Falciphoriella* species isolated from soil	298
4.136 *Myrmecridium* species isolated from soil	300
4.137 *Leptographium* species isolated from soil	302
4.138 *Sporothrix* species isolated from soil	303
4.139 *Brunneochlamydosporium* species isolated from soil	304
4.140 *Chordomyces* species isolated from soil	306
4.141 *Furcasterigmium* species isolated from soil	307
4.142 *Fuscohypha* species isolated from soil	308
4.143 *Gibellulopsis* species isolated from soil	309
4.144 *Lectera* species isolated from soil	311
4.145 *Paramusicillium* species isolated from soil	312
4.146 *Phialoparvum* species isolated from soil	313
4.147 *Plectosphaerella* species isolated from soil	314
4.148 *Sayamraella* species isolated from soil	315
4.149 *Sodiomyces* species isolated from soil	317
4.150 *Stachylidium* species isolated from soil	318
4.151 *Summerbellia* species isolated from soil	319
4.152 *Verticillium* species isolated from soi	320
4.153 *Acrostalagmus* species isolated from soil	322
4.154 *Dactylidispora* species isolated from soil	323
4.155 *Echinusitheca* species isolated from soil	323
4.156 *Vittatispora* species isolated from soil	324
4.157 *Colletotrichum* species isolated from soil	326
4.158 *Acremoniopsis* species isolated from soil	326

LIST OF TABLES

Table	Page
4.159 *Acremonium* species isolated from soil	328
4.160 *Amphichorda* species isolated from soil	329
4.161 *Clonostachys* species isolated from soil	330
4.162 *Emericellopsis* species isolated from soil	331
4.163 *Keithomyces* species isolated from soil	332
4.164 *Marquandomyces* species isolated from soil	333
4.165 *Metapochonia* species isolated from soil	334
4.166 *Metarhizium* species isolated from soil	335
4.167 *Pochonia* species isolated from soil	336
4.168 *Romanoa* species isolated from soil	340
4.169 *Beauveria* species isolated from soil	341
4.170 *Cordyceps* species isolated from soil	342
4.171 *Gamszarea* species isolated from soil	343
4.172 *Lecanicillium* species isolated from soil	343
4.173 *Simplicillium* species isolated from soil	345
4.174 *Kiflimonium* species isolated from soil	345
4.175 *Trichoderma* species isolated from soil	346
4.176 *Trichothecium* species isolated from soil	347
4.177 *Calonectria* species isolated from soil	348
4.178 *Cylindrocladiella* species isolated from soil	349
4.179 *Fusarium* species isolated from soil	350
4.180 *Mariannaea* species isolated from soil	351
4.181 *Nectria* species isolated from soil	352
4.182 *Neocosmospora* species isolated from soil	353
4.183 *Paracremonium* species isolated from soil	354
4.184 *Purpureocillium* species isolated from soil	356
4.185 *Ophiocordyceps* species isolated from soil	356

LIST OF TABLES

Table	Page
4.186 *Tolypocladium* species isolated from soil	357
4.187 *Polycephalomyces* species isolated from soil	359
4.188 *Brevistachys* species isolated from soil	359
4.189 *Didymostilbe* species isolated from soil	360
4.190 *Memnoniella* species isolated from soil	361
4.191 *Myrothecium* species isolated from soil	362
4.192 *Stachybotrys* species isolated from soil	365
4.193 *Ceratocystis* species isolated from soil	368
4.194 *Graphium* species isolated from soil	370
4.195 *Acaulium* species isolated from soil	371
4.196 *Cephalotrichum* species isolated from soil	372
4.197 *Gamsia* species isolated from soil	373
4.198 *Lomentospora* species isolated from soil	374
4.199 *Microascus* species isolated from soil	377
4.200 *Petriella* species isolated from soil	380
4.201 *Pseudallescheria* species isolated from soil	381
4.202 *Scopulariopsis* species isolated from soil	381
4.203 *Scedosporium* species isolated from soil	383
4.204 *Wardomyces* species isolated from soil	384
4.205 *Wardomycopsis* species isolated from soil	358
4.206 *Yunnania* species isolated from soil	388
4.207 *Triadelphia* species isolated from soil	391
4.208 *Victoriomyces* species isolated from soil	392
4.209 *Caligospora* species isolated from soil	394
4.210 *Chaetosphaeria* species isolated from soil	395
4.211 *Chloridium* species isolated from soil	396
4.212 *Dinemasporium* species isolated from soil	402

LIST OF TABLES

Table	Page
4.213 *Kionochaeta* species isolated from soil	403
4.214 *Menispora* species isolated from soil	406
4.215 *Thozetella* species isolated from soil	406
4.216 *Verhulstia* species isolated from soil	407
4.217 *Coniochaeta* species isolated from soil	408
4.218 *Cordana* species isolated from soil	409
4.219 *Achaetomium* species isolated from soil	413
4.220 *Arxotrichum* species isolated from soil	415
4.221 *Chaetomium* species isolated from soil	416
4.222 *Humicola* species isolated from soil	417
4.223 *Staphylotrichum* species isolated from soil	418
4.224 *Stellatospora* species isolated from soil	419
4.225 *Thielavia* species isolated from soil	421
4.226 *Trichocladium* species isolated from soil	422
4.227 *Diplogelasinospora* species isolated from soil	423
4.228 *Naviculispora* species isolated from soil	424
4.229 *Cladorrhinum* species isolated from soil	425
4.230 *Podospora* species isolated from soil	427
4.231 *Triangularia* species isolated from soil	428
4.232 *Jugulospora* species isolated from soil	429
4.233 *Lundqvistomyces* species isolated from soil	430
4.234 *Boothiella* species isolated from soil	431
4.235 *Neurospora* species isolated from soil	432
4.236 *Pseudoneurospora* species isolated from soil	433
4.237 *Sordaria* species isolated from soil	434
4.238 *Eosphaeria* species isolated from soil	435
4.239 *Arthrinium* species isolated from soil	436

LIST OF TABLES

Table	Page
4.240 *Nigrospora* species isolated from soil	436
4.241 *Beltraniella* species isolated from soil	437
4.242 *Bartalinia* species isolated from soil	441
4.243 *Broomella* species isolated from soil	442
2.244 *Neopestalotiopsis* species isolated from soil	444
4.245 *Robillarda* species isolated from soil	447
4.246 *Coniocessia* species isolated from soil	448
4.247 *Hansfordia* species isolated from soil	449
4.248 *Idriella* species isolated from soil	454
4.249 *Microdochium* species isolated from soil	455
4.250 *Ascotricha* species isolated from soil	456
4.251 *Coniolariella* species isolated from soil	457
4.252 *Xylaria* species isolated from soil	457
4.253 *Acidothrix* species isolated from soil	458
4.254 *Trichomonascus* species isolated from soil	459
4.255 *Zygoascus* species isolated from soil	460
4.256 *Ogataea* species isolated from soil	460
4.257 *Pichia* species isolated from soil	461
4.258 *Saccharomycopsis* species isolated from soil	462
4.259 *Hanseniaspora* species isolated from soil	462
4.260 *Effetia* species isolated from soil	463
4.261 *Heterocephalum* species isolated from soil	464
4.262 *Gilmaniella* species isolated from soil	465
4.263 *Phaeotrichoconis* species isolated from soil	466
4.264 *Solosympodiella* species isolated from soil	466

LIST OF TABLES

Table	Page
4.265 The genera isolated from different soil habitats in Thailand from 2000 to 2024	472
5.1 List of curators for the https://soilfun.org/ website	489

LIST OF FIGURES

Figure	Page
2.1 Three types of soil-based localities selected for soil sample collection	12
3.1 Baiting technique for the isolation of soil fungi	26
3.2 Dilution method for the isolation of soil fungi	31
3.3 Soil plating method for the isolation of soil fungi	33
3.4 Alcohol treatment method for the isolation of soil fungi	34
3.5 The acid treatment method for the isolation of soil fungi	35
3.6 The heat treatment method for the isolation of soil fungi	36
3.7 Chester's soil immersion tube method for the isolation of soil fungi	37
3.8 Design and parts of the fungal highway column	40
4.1 *Cladosporium cladosporioides* a. Conidiophores and conidia	71
4.2 *Ramichloridium apiculatum* (CBS 156.59)	72
4.3 *Pseudoramichloridium henryi* (CBS 124775)	74
4.4 The best-scoring maximum likelihood tree generated of the combined LSU and ITS sequence data for selected species in *Mycosphaerellaceae*	74
4.5 *Neoceratosperma soli* (MFLUCC 24-0467, Holotype)	77
4.6 *Piedraia hortae*	79
4.7 *Acidiella bohemica.* (CBS 132721)	81
4.8 *Devriesia staurophora* (DAOM 230744)	82
4.9 The best-scoring maximum likelihood tree generated of the combined SSU, LSU and ITS sequence data for selected genera in *Acrocalymmacea*	84
4.10 *Acrocalymma medicaginis* (MFLU25-0116, new habitat and geographical record)	87
4.11 The best-scoring maximum likelihood tree generated of the combined SSU, ITS and LSU sequence data for selected genera in *Amorosiaceae*	88
4.12 *Amorocoelophoma soli* (MFLU25-0121)	91

LIST OF FIGURES

Figure	Page
4.13 The best-scoring maximum likelihood tree generated of the combined ITS, SSU, LSU, tef1-α and rpb2 sequence data for *Anteagloniaceae* and selected genera in adjacent families	93
4.14 *Anteaglonium soli* (MFLU25-0165, Holotype)	96
4.15 *Neodendryphiella tarraconensi* (FMR 16234)	100
4.16 The best-scoring maximum likelihood tree generated using the combined, ITS, LSU, *rpb2 and tub2* sequence data of *Didymellaceae* taxa	102
4.17 *Cumuliphoma indica* (MFLU25-0118)	106
4.18 *Ectophoma multirostrata* (MFLU25-0178)	110
4.19 The best-scoring maximum likelihood tree generated of the combined LSU and ITS, *rpb2* and *tub2* sequence data for *Epicoccum*	111
4.20 *Epicoccum catenisporum* (MFLU25-0128)	114
4.21 *Juxtiphoma eupyrena.*	116
4.22 *Neoascochyta exitialis* (CBS 389.86)	117
4.23 *Neodidymelliopsis cannabis*	118
4.24 *Paraboeremia selaginellae* (CBS 122.93)	120
4.25 *Pseudoascochyta pratensis* (CBS H-22735)	121
4.26 *Remotididymella ageratinae* (MFLUCC 24-0473)	124
4.27 *Vandijckomycella joseae* (CBS 143011)	126
4.28 *Xenodidymella applanata* (M0275818)	127
4.29 *Alloconiothyrium aptrootii* (CBS 980.95)	128
4.30 *Bimuria novae-zelandiae* (CBS 107.79)	130
4.31 Maximum likelihood phylogenetic tree generated based on the combined ITS-LSU sequence data for *Didymosphaeriaceae* taxa	132
4.32 *Neptunomyces soli* (MFLU24-0379, holotype)	135
4.33 The best-scoring maximum likelihood tree generated of the combined ITS and LSU sequence data for *Paraconiothyrium*	137

LIST OF FIGURES

Figure	Page
4.34 *Paraconiothyrium cyclothyrioides* (MFLU25-0160)	140
4.35 *Paraconiothyrium zingiberacearum* (MFLU25-0161)	142
4.36 The best-scoring maximum likelihood tree generated based on the combined LSU, ITS and *tef1-α* sequence data for *Didymosphiraceae*	145
4.37 *Pseudopithomyces chartarum* (MFLU25-0129)	148
4.38 *Latorua caligans* (CBS 576.65)	150
4.39 *Matsushimamyces bohaniensis* (CBEC 001)	151
4.40 *Multiverruca sinensis* (HMAS 351940)	152
4.42 *Polyschema terricola*	153
4.43 *Bahusandhik*a *indica* (HCIO 51509)	154
4.44 *Leptosphaeria doliolum* (MFLU 15-1875)	155
4.45 *Neocamarosporium goegapense* (CBS 138008)	157
4.46 The best-scoring maximum likelihood tree generated of the combined LSU, ITS and *tef1-α* sequence data for *Nigrograna*	158
4.47 *Nigrograna speluncam* (MFLU25-0130, Holotype)	161
4.48 The best-scoring maximum likelihood tree generated of the combined LSU and ITS sequence data for *Phaeosphaeriaceae*	162
4.49 *Paraleptospora thailandica* (MFLU25-0169, Holotype)	165
4.50 *Setophoma thailandica* (MFLU25-0135)	167
4.51 *Alternaria alternata* (CBS 326.65)	168
4.52 Maximum likelihood phylogenetic tree generated based on the combined ITS-*GAPDH- tef1-α* sequence data for *Curvularia* taxa	172
4.53 *Curvularia dactylocteniicola* (MFLU24-0381)	177
4.54 The best-scoring maximum likelihood tree generated based on the combined ITS, *gapdh*, and *tef1-α* sequence data for *Pleosporaceae*	178
4.55 *Curvularia suttoniae* (MFLU25-0134MFLU)	182
4.55 *Curvularia suttoniae* (MFLU25-0134MFLU)	187

LIST OF FIGURES

Figure	**Page**
4.56 *Pseudopyrenochaeta lycopersici*	184
4.57 The best-scoring maximum likelihood tree generated based on the combined ITS, LSU, and *rpb2* sequence data for *Pyrenochaetopsidaceae*	186
4.58 *Neopyrenochaeta telephoni* (MFLU25-0171)	188
4.59 *Pyrenochaetopsis oryzicola* (MFLU25-0119)	191
4.60 *Pyrenochaetopsis tropicalis* (MFLU25-0162, Holotype)	193
4.61 The best-scoring maximum likelihood tree generated based on the combined ITS, LSU, *tef1-α,* and *rpb2* sequence data for *Roussoellaceae*	195
4.62 *Neoroussoella entadae* (MFLU25-0139)	198
4.63 *Pararoussoella thailandensis.* (MFLU25-0140)	200
4.64 *Roussoella terrestris* (MFLU25-0168, Holotype)	203
4.65 *Preussia* sp.	204
4.66 *Westerdykella* sp.	205
4.67 *Tetraploa aristata*	207
4.68 *Torula herbarum* (CBS 220.59)	208
4.69 *Setophaeosphaeria hemerocallidis* (CBS 138006)	209
4.70 *Arthrographis kalrae* (UTHSC 05-17)	211
4.71 *Rhexothecium globosum*	212
4.72 *Arxiella terrestris*	213
4.73 *Leptodiscella Africana* (URM 86557)	214
4.74 *Phaeotrichum hystricinum*	215
4.75 *Aptrootia terricola* (*Lücking* 17211)	217
4.76 *Guizhoumyces aciculaea* (GUCC 18195)	218
4.77 *Scolecobasidium terreum*	220
4.78 *Verruconis gallopava* (CBS 437.64)	221

LIST OF FIGURES

Figure	Page
4.79 Phylogenetic tree generated from the maximum likelihood analysis based on combined SSU-ITS-LSU gene sequences data for the selected genera in the family *Sympoventuriaceae*	222
4.80 *Verruconis soli* (MFLU22-0257, holotype)	225
4.81 *Verruconis thailandica* (MFLU22-0258, new record)	227
4.82 *Pseudorobillarda phragmitis*	228
4.83 *Phialophora verrucosa* (CDC B1757)	233
4.84 *Rhinocladiella atrovirens*	234
4.85 *Veronaea botryose* (CBS 254.57)	235
4.86 *Aspergillus flavus*	237
4.87 *Penicillium expansum* (CBS 146.45)	240
4.88 *Paecilomyces variotii*	242
4.89 *Thermoascus* sp.	243
4.90 *Sagenomella diversispora* (CBS 354.36)	244
4.91 *Emmonsiellopsis terrestris* (CBS 273.77)	248
4.92 *Arthroderma curreyi*	249
4.93 *Ctenomyces serratus*	251
4.94 *Nannizzia incurvata* (CBS 173.64)	253
4.95 *Arachniotus ruber* (CBS 12.69)	254
4.96 *Gymnascella aurantiaca*	255
4.97 *Gymnoascus* sp.	257
4.98 *Kraurogymnocarpa lenticulospora*	258
4.99 *Malbranchea* sp.	261
4.100 *Canomyces reticulatus* (MCC 1486)	263
4.101 The best scoring maximum likelihood tree of the combined ITS sequence data for *Neogymnomycetaceae*	263
4.102 *Currahomyces indicus* (MFLU25-0172)	266

LIST OF FIGURES

Figure	Page
4.103 *Renispora flavissima*.	267
4.104 *Amauroascus niger*	269
4.105 *Aphanoascus fulvescens*	270
4.106 *Brunneospora reticulata* (FMR 784)	271
4.107 *Coccidioides immitis*	272
4.108 *Pectinotrichum llanense*	274
4.109 *Pseudoamauroascus australiensis*	275
4.110 *Byssoascus striatosporus*	280
4.111 *Myxotrichum* sp.	281
4.112 *Botrytis cinera*	283
4.113 *Hemileucoglossum littorale*	286
4.114 *Cephaliophora tropica.*	288
4.115 *Lotinia verna*	290
4.116 *Jattaea algeriensis*	291
4.117 *Pleurostoma candollei* (PC 0167640)	292
4.118 The best scoring IQ-tree generated of the combined ITS and LSU sequence data for selected families in *Diapothales*	294
4.119 *Diaporthosporella soli.* (MFLU25-0137,Holotype)	297
4.120 *Falciphoriella solaniterrestris* (CBS H-22572)	299
4.121 *Myrmecridium schulzeri* (CBS 325.74)	301
4.122 *Leptographium lundbergii*	302
4.123 *Brunneochlamydosporium nepalense* (CBS 971.72)	305
4.124 *Chordomyces antarcticus* (CBS 120045)	306
4.125 *Furcasterigmium furcatum* (CBS 122.42)	307
4.126 *Fuscohypha expansa* (CBS 419.89)	308
4.127 *Gibellulopsis serrae* (CBS 101221)	310
4.128 *Lectera colletotrichoides* ((IMI 332702)	311

LIST OF FIGURES

Figure	Page
4.129 *Paramusicillium asperulatum*	312
4.130 *Phialoparvum bifurcatum* (CBS 299.70B)	313
4.131 *Plectosphaerella cucumerina*	315
4.132 *Sayamraella subulata* (BCC 78964)	316
4.133 *Sodiomyces alkalinus*	317
4.134 *Stachylidium bicolor* (CBS 121802)	318
4.135 *Summerbellia oligotrophica* (CBS 657.94)	319
4.136 *Verticillium dahliae* (CBS205.26)	321
4.137 *Acrostalagmus luteoalbus* (CBS 121214)	322
4.138 *Vittatispora coorgii* (BICC 7817)	325
4.139 *Acremoniopsis suttonii* (CBS 138708)	327
4.140 *Amphichorda felina*. (CBS 250.34)	329
4.141 *Emericellopsis terricola*	331
4.142 *Keithomyces carneus*	333
4.143 *Marquandomyces marquandii*	334
4.144 *Metarhizium anisopliae*	336
4.145 Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data of *Clavicipitaceae* taxa	338
4.146 *Pochonia chlamydosporia* (MFLUCC 23-0021, new habitat record)	341
4.147 *Lecanicillium lecanii* (IMI 327441)	345
4.148 *Trichothecium roseum*	348
4.149 *Mariannaea elegans*	352
4.150 *Neocosmospora vasinfecta* (CBS 237.55)	354
4.151 *Paracremonium inflatum* (CBS 485.77)	356
4.152 *Tolypocladium inflatum*	359
4.153 *Brevistachys variabilis* (CBS 141057)	360

LIST OF FIGURES

Figure	Page
4.154 The best scoring IQ tree generated of the combined ITS, *tub2*, *tef1-α* and *rpb2* sequence data for *Stachybotryacea*	363
4.155 *Stachybotrys phaeophialis* (MFLU25-0138)	367
4.156 *Ceratocystis* sp.	369
4.157 *Graphium penicillioides*	370
4.158 *Acaulium albonigrescens* (IHEM 18560)	371
4.159 *Cephalotrichum stemonitis*	373
4.160 The best scoring maximum likelihood tree generated of the combined ITS, LSU, *tef*1-α, *tub2* sequence data for selected genera in *Microascaceae*	375
4.161 *Microascus croci* (MFLU25-0175)	379
4.162 *Scopulariopsis brevicaulis* (CBS273.30)	382
4.163 *Scedosporium apiospermum*	383
4.164 *Wardomyces anomalus*	384
4.165 *Wardomycopsis fusca* (MFLU25-0123)	387
4.166 *Yunnania penicillata* (MFLU25-0164)	390
4.167 *Triadelphia heterospora*	391
4.168 *Victoriomyces antarcticus*	393
4.169 *Caligospora dilabens* (CBS 734.83)	394
4.170 Phylogenetic tree generated from the maximum likelihood analysis based on combined LSU and ITS gene sequences data for the selected genera in the family *Chaetosphaeriaceae*	397
4.171 *Chloridium gonytrichii* (MFLUCC 21-0110)	401
4.172 *Kionochaeta microspora* (MFLUCC 21-0109)	405
4.173 *Thozetella nivea*	407
4.174 *Coniochaeta ligniaria* (HAH2883)	409

LIST OF FIGURES

Figure	Page
4.175 Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data of *Cordanales and Coniochaetales* tax	417
4.176 *Cordana terrestris* (MFLUCC 23-0022, new habitat record)	412
4.177 *Achaetomium* sp.	414
4.178 *Arxotrichum wyomingense*	415
4.179 *Chaetomium globosum*	416
4.180 *Humicola fuscoatra* (CBS 516.67)	417
4.181 *Staphylotrichum coccosporum*	419
4.182 *Stellatospora terricola*	420
4.183 *Trichocladium asperum*	422
4.184 *Diplogelasinospora* sp.	423
4.185 *Naviculispora terrestris*	424
4.186 *Cladorrhinum foecundissimum* (CBS180.66)	426
4.187 *Triangularia* sp.	428
4.188 *Jugulospora rotula* (FMR12428)	429
4.189 *Boothiella tetraspora*	431
4.190 *Pseudoneurospora amorphoporcata*	433
4.191 *Sordaria fimicola*	434
4.192 Maximum likelihood tree revealed by RAxML from an analysis of combined LSU-ITS matrix of *Beltraniella*	437
4.193 *Beltraniella fertilis* (MFLUCC 20-0119)	440
4.194 The best scoring maximum likelihood tree generated of the combined ITS, *tub2* and *tef1-α* sequence data for *Neopestalotiopsis*	442
4.195 *Neopestalotiopsis terricola* (MFLU25-0125)	446
4.196 *Coniocessia nodulosporoides*	448

LIST OF FIGURES

Figure	Page
4.197 The best scoring maximum likelihood tree generated of the combined ITS sequence data for *Xylariales*	449
4.198 *Hansfordia pruni* (MFLU25-0173)	451
4.199 *Hansfordia pulvinata* (MFLU25-0174)	453
4.200 *Idriella lunata*	454
4.201 *Acidothrix acidophila*	458
4.202 *Effetia craspedoconidica*	464
4.203 The percentage of *Dothideomycetes, Eurotiomycetes* and *Sordariomycetes* genera that are compiled in this study	467
4.204 The genera of *Dothideomycetes, Eurotiomycetes* and *Sordariomycetes* that have been compiled in this study are shown as a percentage	468
4.205 a The number of soil-inhabiting species collected in our research (total 39 species). b The species are distributed in 21 families in *Dothediomycetes, Eurotiomycetes* and *Sordariomycetes*	477
4.206 The number of species collected from each soil habitat (Forests, undisturbed caves, disturbed caves and urban areas) in our study	478
4.207 *Microascus croci* and *Wardomycopsis fusca* are collected from both disturbed and undisturbed caves and *Remotididymella ageratinae* was collected from disturbed caves and urban areas	481
5.1 Home page of the Soil Fungi webpage	492
5.2 Heading “Outline” contains soil-inhabiting *Ascomycota* taxa according to the latest classification	493
5.3 Heading “Archives” configured with a dropdown list of taxonomic hierarchy with links to order, family, genera, and species descriptions	493
5.4 Information provided for the soil-inhabiting species with taxonomic description	494

LIST OF FIGURES

Figure	Page
5.5 Heading “Curators” provides the list of curators with their contact details	495
5.6 Heading “History” provides the history and development of studies on soil fungal taxonomy	495

CHAPTER 1

INTRODUCTION

1.1 Soil and Soil Fungi

Fungi are eukaryotic organisms with a ubiquitous cosmopolitan distribution in terrestrial and aquatic habitats, including plant-based substrates, soil environments, air, and artificial materials (Wu et al., 2019). Because of their physiological, metabolic, structural, and genetic level adaptations to stressful conditions, they become one of the successful organisms in the ecological selection and evolutionary processes (Cowan et al., 2014). Fungi have diverse nutritional modes, and they are classified as saprobes, pathogens, and mutualists, with each group playing an essential role in ecosystem functioning, such as nutrient cycling, plant nutrition, and pathology (Tedersoo et al., 2014; Wu et al., 2019). Therefore, fungi have become the second most species-rich group of organisms on the planet (Wu et al., 2019), and the source of biotechnological, agricultural, engineering, and medical applications (Hyde et al., 2019) The value of fungi to the global economy has been estimated at 54.57 trillion USD based on the major individual products and services of fungi (Niego et al., 2023b)

Soil covers a large amount of the earth surface, and it is a dynamic living ecosystem. This is composed of biotic and abiotic properties derived from physical, biological, and chemical processes. Due to its highly diversified nature, it provides habitats to several microorganisms, including fungi (Bridge & Spooner, 2001; Wagg et al., 2019). Soil depth and spatial characteristics can affect the variations of soil fungal distributions in edaphic ecosystems. In forests, the surface soil layer (O-Horizon) consists of 20% leaf, wood litter, and humus. Beneath the O-Horizon, the A-horizon is found. These horizons are located within 20–30 cm depth from the surface in the vertical soil profile. They contain higher amounts of organic resources, moisture, and better aeration. Thus, the soil fungal population is generally higher on the surface than in the deeper soil layers (Mueller et al., 2004; Tedersoo et al., 2022). Soil also varies by geographical characters on the land, such as geo-biological factors, vegetation, and

other soil microorganisms (Mueller et al., 2004; Taylor & Sinsabaugh, 2015). Overall, the areas with high to mid precipitation have higher vegetation, water content, and organic substrates in the soil. Such soil composes more nutrients such as organic carbon, nitrogen, phosphorus, and potassium and thus has a greater fungal distribution (Bhattacharyya & Jha, 2011). In addition to the natural soil variability, human activities such as urbanization, industrialization, and agriculture have also influenced fungal diversity in soil (Tsai et al., 2007).

1.2 Characteristics and Functions of Fungi in Soil

Physically and functionally, fungi are exclusively adapted to the soil (Taylor & Sinsabaugh, 2015). They produce mycelia among soil particles, decaying wood, or litter. Hyphal growth is higher in nutrient-rich soils, while it is lower in nutrient-poor soils where fungi produce structures such as cords, strands, or rhizomorphs. Fungi also maintain interactions with other soil organisms, or sometimes fungal communities undergo succession phases in scarce nutrition conditions (Mueller et al., 2004; Fryar et al., 2005; Taylor & Sinsabaugh, 2015).

Fungi have functional guilds like saprobes, pathogens, and mutualists in edaphic ecosystems, which perform different ecosystem services. They translocate nutrients and carbon from inside their hyphae to less nutritious areas in the soil, contributing to the mineralization and cycling of nutrients such as Nitrogen (N) and Carbon (C), and also support hydraulic functioning, infiltration, and soil moisture storage. The surface soil layer has more biota compared to deeper layers due to nutritional availability, however, the presence and functions of fungi can be further varied based on the soil conditions. Therefore, fungi living in various disturbed and undisturbed soil ecosystems such as forests, agricultural fields, urban cities, caves and hot springs are functionally adapted to those ecosystems.

1.3 Detection of Soil Fungi for Taxonomy and Diversity Studies

Most of the fungal communities in edaphic habitats prefer specific locations or levels in the soil with favorable nutritional, physical, and chemical conditions. Thus, establishing a reliable method to recover all of these fungi is complicated (Kirk et al., 2004), and significant gaps remain in our present taxonomic knowledge of soil fungi because of methodological limitations (Wu et al., 2019; Tederso et al., 2014). There are two approaches currently being used in soil fungal detection: culture-dependent and culture-independent methods. High Throughput Sequencing (HTS) is one of the culture-independent methods that is extensively useful in global soil fungal studies, including estimating total fungal numbers, diversity studies, and detecting unculturable taxa in soil. However, the results in this approach are generated only up to higher taxonomic ranks. Therefore, culture-dependent methods are integral in identifying the species and genera in edaphic habitats. The culture-dependent methods provide live examples and morphological evidence of revealed fungal species. Hence, these methods are essential for soil fungal taxonomic identifications (Wu et al., 2019; Chethana et al., 2020).

The soil dilution series, direct plating method, and bating method are mostly used culture-dependent methods in recent studies (Senanayake et al., 2020). Soil dilution series is used for quantitative and qualitative studies and works well with saprophytic fungal isolations (Ramakrishnan, 1955). The baiting method is useful to isolate substrate-specific fungal strains from the soil (Giudice et al., 2012). Thereby, it provides living and dry cultures for further studies of identified fungal strains. Using suitable soil fungal isolation methods, along with appropriate growth conditions, is vital to obtaining various fungal strains. Nevertheless, most soil fungal research is currently focused on HTS methods without realizing the potential of culture-dependent methods in taxonomic studies (Mueller et al., 2004; Frac et al., 2018).

1.4 Current Taxonomy of Soil *Ascomycota* in the World

Worldwide fungal number is estimated to be up to 11.7–13.2 million species (Wu et al., 2019), and only 3–8% are described to the species level (Blackwell, 2011; Tedersoo et al., 2020). Out of the total, only around 100,000 species have been recognized, which are distributed among 156 orders, 46 classes, and 12 phyla (Tedersoo et al., 2017; Wu et al., 2019). In addition, most fungal taxonomic studies focus on countries such as Australia, Europe, North America, South Africa, and China, where the fungal species are well studied and documented. Conversely, many Asian countries lack information about fungi (Hyde et al., 2020). In addition, some substrates and habitats are well studied, including plants and freshwater, while fungi present in some substrates are poorly documented (Hyde et al., 2020; Tedersoo et al., 2022). Recent studies have shown the number of soil-inhabiting fungi around the world, such as the Global Soil Mycobiome consortium (Tedersoo et al., 2021) and GlobalFungi (Větrovský et al., 2020), and UNITE (Nilsson et al., 2019). The Global Soil Mycobiome consortium (GSMc) reported that fungi represent a total of 722,682 OTUs (Operational Taxonomic Units), which represent 62.4% of the total OTUs. *Ascomycota,* 28.3% *Basidiomycota,* 5.1% *Rozellomycota,* 3.1% *Glomeromycota,* and 2.7% *Chitridiomycota.* Most of these estimations and diversity studies are executed by culture-independent methods such as HTS. Culture-dependent methods are useful in identifying the species and genera in soil accurately. However, there is no recently updated compilation or database for *Ascomycota* genera isolated from soil habitats around the world.

1.5 Common and Uncommon Soil *Ascomycota*

As a result of high diversity, fungal taxa are variably distributed with some are commonly found while other species are uncommon in particular habitats (Egidi et al., 2019). Crop-associated fungal communities are dominated by a few abundant taxa belonging to *Sordariomycetes* and *Dothideomycetes* (Xiong et al., 2021). In edaphic habitats globally, studies have shown that *Ascomycota* are more abundant than *Basidiomycota* (Egidi et al., 2019). *Sordariomycetes, Dothideomycetes,* and

Eurotiomycetes classes have several genera, namely *Acremonium*, *Alternaria*, *Aspergillus*, *Aureobasidium*, *Cadophora*, *Cladosporium*, *Chaetomium*, *Curvularia*, *Fusarium*, *Penicillium*, *Podospora*, *Talaromyces* and *Trichoderma* that are very common in soil habitats across the world (Egidi et al., 2019; Tedersoo et al., 2020). These fungal species are common in soil because of their highly adaptive nature in stress tolerance. Because common fungal genera have flexible trophic capabilities and genera like *Acremonium, Chaetomium, Cladosporium, Curvularia, Fusarium,* and *Penicillium* are capable of long-distance dispersal, allowing them to be commonly found in soil habitats. Further, due to their high adaptability and fast-growing conditions, they can be easily detected and isolated from culturing and HTS methods and widely tested and identified the ecological, agricultural, and medical purposes (Bridge & Spooner, 2001; Mueller et al., 2004; Tederso et al., 2014; Taylor & Sinsabaugh, 2015; Egidi et al., 2019).

However, in most of mycobiomes worldwide, including soils, the diversity is majorly represented by rare taxa where the rare sub-community is more sensitive to host selection, and these taxa play an important role in fungal co-occurrence network and ecosystem functioning like crop yield and soil enzyme activities (Xiong et al., 2021). Some of these uncommon genera are detectable through HTS methods. However, isolating these species under in vitro conditions can be difficult; in contrast, some may also be challenging to detect through HTS methods when present in very small communities. This difficulty can be attributed to several factors, such as the slow growth rates of many of these fungi, lack of nutrients in standard growth media, the disruption of mutualistic relationships, and their high sensitivity to micro-climatic conditions in the soil (Bridge & Spooner, 2001; Tederso et al., 2014, 2017, 2018; Taylor & Sinsabaugh, 2015; Wu et al., 2019). Thus, it is important to obtain these uncommon portions of soil ascomycetes into cultures which can be useful in introducing new fungal taxa, biodiversity studies and biotechnological applications in the future.

1.6 Taxonomy of Soil *Ascomycota* in Thailand

According to the current knowledge, 55–96% of fungi from northern Thailand are new to science (Hyde et al., 2018). In 2020, the majority of new fungal species were recorded from Asia, accounting for 41% of the total. During the last decade, over 500 taxonomic novelties of fungi were investigated in northern Thailand. Hyde et al. (2018) suggested that it is necessary to use proper sampling strategies and explore the understudied host/ substrates and the regions to discover the missing fungal diversity in Thailand. Further, above-ground *Ascomycota* species are well studied compared with soil habitats in Thailand. Even though extensive studies have been carried out globally, the fungal distribution in Thai soil is poorly explored (Amma et al., 2018; Hyde et al., 2018; Tedersoo et al., 2014).

1.7 *Ascomycota* Distribution in Various Ecosystems and Current Taxonomic Trends in Thailand Soils

Various fungal taxa have been detected and introduced from different soil-based ecosystems, such as wild forests, cultivated lands, highest mountain peaks, deep permafrost, alkaline, acidic, saline, geothermal, humid, polar, volcanic horizons, caves, mines, and urban soils. These diverse environments provide high fungal diversity and distribution (Frac et al., 2004). However, studies estimated that higher soil fungal diversity is present in the forest soil ecosystems (deciduous forests, shrubs, and grasslands) (Taylor & Sinsabaugh, 2015; Satyanarayana et al., 2019). Conversely, cultivated and urban soil ecosystems have comparatively low species richness. The lowest species richness is reported in soils found in mud, riverbank, seashores, and polluted lands (Taylor & Sinsabaugh, 2015; Satyanarayana et al., 2019).

Forests are nutrition-rich environments; thus, studies have investigated the high taxonomic and ecological diversity of fungi in forest soils (Rusterholz & Baur, 2023). Globally, both culture-dependent and independent methods have been carried out for fungal taxonomic studies in forest soils. *Ascomycota* is highly distributed in tropical soils, specifically *Archaeorhizomycetes*, *Dothideomycetes*, *Eurotiomycetes*, *Orbiliomycetes*,

and *Sordariomycetes* (Tedersoo et al., 2014; Taylor & Sinsabaugh, 2014). *Pezizomycotina* are widely distributed in mid-latitude soils (Tedersoo et al., 2014; Taylor & Sinsabaugh, 2014). Soils in pole regions, including tundra and boreal forests, *Lecanoromycetes* and *Leotiomycetes* are abundant (Tedersoo et al., 2014; Taylor & Sinsabaugh, 2014). Based on HTS methods, forest soil fungi have been investigated by Amma et al. (2018). A study based on phyllosphere fungal communities in tropical forests in Thailand has been conducted, and *Ascomycota* is being recorded as the dominant group (Izuno et al., 2016). However, such studies for belowground fungal communities in Thai forests are yet to be discovered.

Alterations and disturbances of ecosystems can affect the persistence of fungal species. On the other hand, subtle changes in microbial communities can affect the ecosystem functioning. Currently, urbanization is one of the main anthropogenic activities that disturb natural ecosystems (Rusterholz & Baur, 2023; Zhang et al., 2019). Fungal communities that survive in urban ecosystems are beneficial to maintaining soil health (Zhang et al., 2019). However, the biodiversity in urban areas is still poorly documented. Simmons (2004) reported that urban soil in Thailand has a considerable level of soil contaminants as a result of various anthropogenic activities (agriculture, industrialization, and urbanization). These soils are disturbed and possibly contain extreme amounts of heavy metals and metalloids (Cyanides, Zinc, Lead, Cadmium, and Arsenic) as well as organic and chemical pollutants (Simmons, 2004; Newbound et al., 2010; Wu et al., 2014; Yang et al., 2016; Li et al., 2019; Zhen et al., 2019). Nonetheless, studies have revealed that some fungal communities have functionally adapted to survive in polluted soil. Some studies have conducted fungal taxonomic studies in urban cities in Thailand and found Scedosporium (Luplertlop et al., 2016, 2019). However, the fungal studies related to urban soils are poorly studied in Thailand.

Karst cave ecosystems are characterized by dark, relatively cool, humid, nutrient-limited conditions where fungi adapt to extreme conditions associated with oligotrophy (Preedanon et al., 2023). In karst caves, mostly the soils are thin layers, however, with an extensive spatial heterogeneity. The studies based on the biology and ecology of Karst cave soils are limited (Ren et al., 2021). Further, natural caves can be disturbed by farming, visitors, tourism infrastructure, and changes in water flow that can be unfavorable to the highly adapted cave organisms (Bai et al., 2020; Ren et al.,

2021). Species from genera such as *Aspergillus*, *Arthroderma*, *Penicillium*, *Fusarium*, *Trichoderma*, *Tritirachium*, *Allophoma* and *Pyrenochaetopsis* have been recovered from cave soils globally (Castrillón et al., 1976; Cunha et al., 2020; Preedanon et al., 2023; Taylor et al., 2013; Zhang et al., 2021). Caves are widespread across Thailand, many of which are disturbed by human interventions and constructions such as temples and tourist attractions. Despite these disturbances, Thai caves harbour high levels of biodiversity, including new taxa (Bolger & Ellis 2015; Preedanon et al., 2023; Deharveng et al., 2023). However, research on cave-associated fungal diversity in Thailand remains limited (Preedanon et al., 2023).

1.8 Research Objectives

1.8.1 To identify soil-inhabiting uncommon ascomycetes in selected disturbed and undisturbed environments in Thailand based on morphological and molecular characterization.

1.8.2 To update and digitalize the soil fungal genera recorded worldwide and update the phylogeny for selected Ascomycota taxa in soil.

1.8.3 To review the benefits of soil fungal cultures and the importance of culture-dependent methods in fungal taxonomy, diversity, and biotechnology studies in the current molecular era.

1.8.4 To investigate keratinophilic and cellulolphillic soil ascomycetes using the baiting method.

1.9 Research Contents

This thesis consists of six chapters.

Chapter 1 is the general introduction, which provides a general background about the soil and soil fungi, characteristics and functions of fungi in soil environment, detection methods to identify below ground fungal taxa, distribution of *Ascomycota* in the world and Thailand, common and uncommon ascomycetous taxa in edaphic habitats

and present studies about *Ascomycota* taxonomy in Thai soils in relation to different edaphic ecosystems, the objectives and the outline of the thesis.

Chapter 2 provides a list of material and methods usedthroughout the study.

Chapter 3 provides a comprehensive account of the history and development of the taxonomic approaches and detection methods of soil-inhabiting *Ascomycota*.

Chapter 4 provides outline of *Ascomycota* genera present in soil, the generic notes and drawings with a case study of uncommon *Ascomycota* isolated from Thai soils from three selected soil-based ecosystems (undisturbed soils: forests and natural caves) and (disturbed soils: urban places and disturbed caves).

Chapter 5 is an introductory illustration of the initiation and services of web web-based platform that is composed as an online database to collect and record soil *Ascomycota* species/genera around the world.

Chapter 6 provides the overall conclusion of above mentioned studies and suggestions for future work.

CHAPTER 2

MATERIAL AND METHODS

2.1 Sample Collections

During my study, I have focused on three distinct soil-based localities (forests, caves and urban areas) in Thailand. To obtain a more diverse fungal collection, we aimed to collect samples from both disturbed and undisturbed habitats within these ecosystems (Figure 2.1). Thereby, soil samples were collected from selected undisturbed (forests and caves) and disturbed environments (caves and city areas) in Chiang Rai, Chiang Mai and Krabi provinces, with a total of 20 collection sites in Thailand.

2.1.1 Tropical Forest Ecosystem (Undisturbed)

Samples were collected from the 8 tropical forests in Chiang Rai, Chiang Mai, and Krabi provinces in Thailand, which is shown in Table 2.1.

Initially, a 50 m^2 area was selected as the collecting site in the forest. The litter was removed around the tree. Random 20 trees were selected at least 8 m apart within each site. Below each tree, two soil subsamples were collected from the 5 cm diameter range and 5cm - 10cm depth, located 1-1.5 m apart from the trunk in opposite directions. Each sample was collected, including both the organic and upper mineral layers. Sample collection was done using the soil auger/shovel. The 40 samples were mixed into a composite sample and carried in sterilized, labelled Ziplock polyethylene bags.

2.1.2 Cave Soils (Undisturbed Caves and Disturbed Caves)

Samples were collected from seven caves in Chiang Rai and Chiang Mai provinces, Thailand, including six disturbed caves and one undisturbed cave (Table 2.1). Four soil samples were collected at each site. Prior to collecting each soil sample, the litter, other materials or gravel on the surface was removed from the collection site, and soil samples were collected using a soil auger/shovel up to 10 cm depth from the soil surface. The collected samples were carried in sterilized, labelled Ziplock polyethylene bags.

2.1.3 Urban Environments (Urban Parks, Construction Sites, Road-Sides) (Disturbed)

Samples were collected from urban parks, road-sides and market areas in Chiang Rai province, Thailand (Table 2.1). Four soil samples were collected using random sampling at each site. Prior to collecting each soil sample, the litter layer, gravel, and other non-soil material on the surface were removed from the place, and soil samples were collected using a soil auger/shovel up to 10 cm depth from the soil surface. Soil samples were collected and carried in sterilized, labelled Ziplock polyethylene bags.

The metadata, such as elevation, latitude, and longitude, were recorded from every collection site are shown in Table 2.1. Samples were stored at 4°C once they were taken to the laboratory. The samples were thawed to room temperature for further analyses.

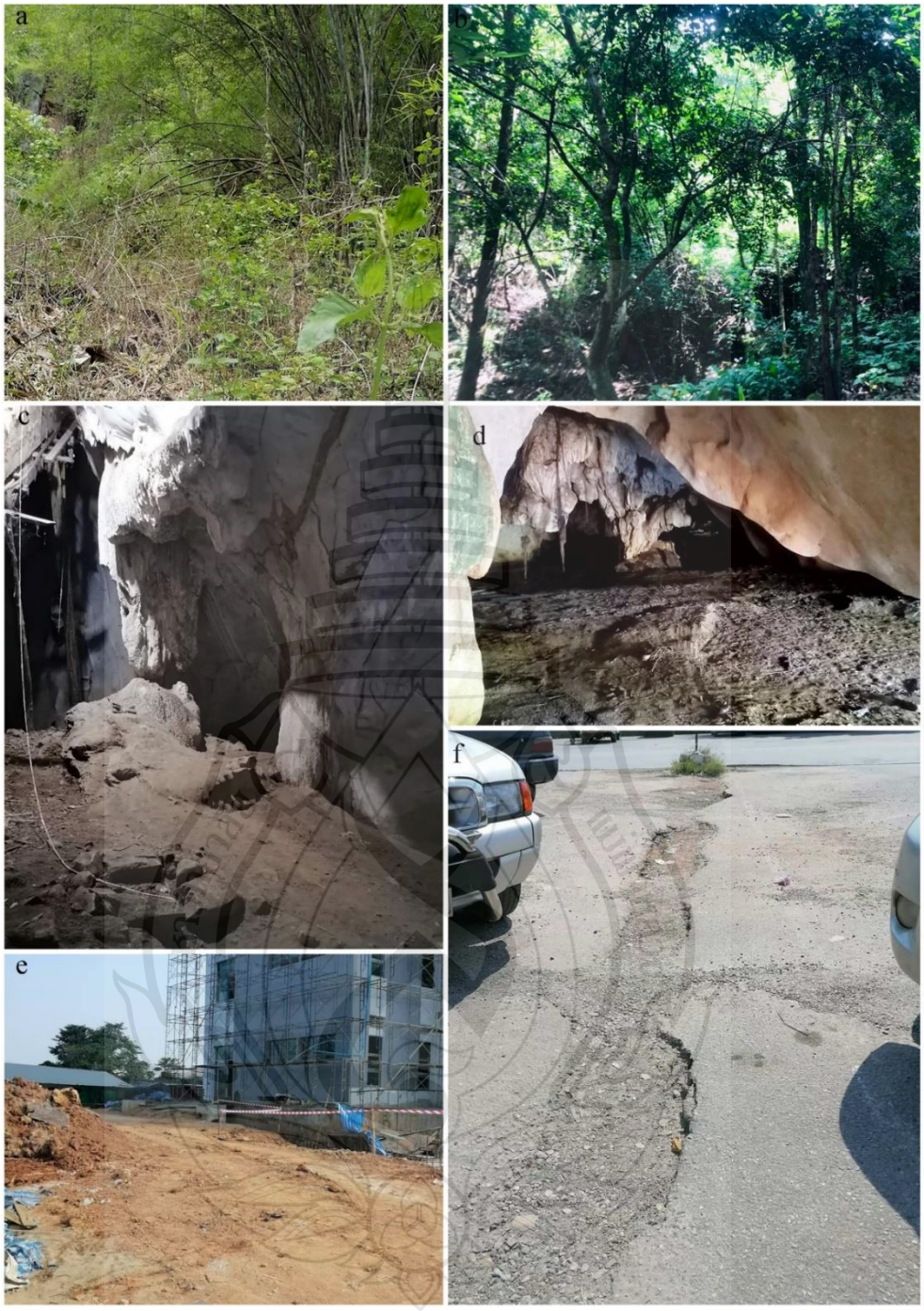


Figure 2.1 Three types of soil-based localities selected for soil sample collection

Figure 2.1 a, b Undisturbed forest habitats. c An undisturbed cave. d A disturbed cave. e, f Disturbed sites in urban areas.

Table 2.1 The details of the 20 collection sites

Sampling site	Disturbed or undisturbed	Location	Latitude	Longitude	Height	Collection date
Forests						
Forest 1	Undisturbed	Mushroom Research Centre, 1095, Pa Pae, Mae Taeng District, Chiang Mai	19.2145	98.5953	1440m	2/17/2019
Forest 2	Undisturbed	Thailand, Krabi Province, Khao Phanom District, Na Khao	8.3811N	98.9286 E		4/28/2019
Forest 3	Undisturbed	Thailand, Chiang Rai	20.0478N	99.7619E	863m	9/23/2019
Forest 4	Undisturbed	Yang Piang , Omkoi District Chiang Mai	17.7145	98.4286	935m	10/16/2019
Forest 5	Undisturbed	Sop Khong, Omkoi District Chiang Mai	17.7145	98.2619	1388m	10/16/2019
Forest 6	Undisturbed	Thailand, Krabi	8°4'11 "N	98°53'25" E	181m	10/28/2019
Forest 7	Undisturbed	Thailand, Chiang Rai	20°4'35"N	100°5'43"E	450m	1/7/2020
Forest 8	Undisturbed	Thailand, Chiang Rai Province	19°53'2" N	100°5'37" E	440m	1/7/2020
Caves						
Cave 1	Disturbed	Fish cave temple (Wat Tham Pla), Chiang Rai	99.863679 N	20.328605 E	440	2/8/2021
Cave 2	Disturbed	Tham Tu Pu Cave (Buddha image cave), Chiang Rai	99.802962	19.925411	424	6/21/2021
Cave 3	Disturbed	Buddha Cave (What Tham Phra), Chiang Rai	99.788928	19.9175247	425	6/21/2021
Cave 4	Disturbed	Tham Muang On cave, Mae On District, Chiang Mai	99.238054	18.7862964	496	5/9/2022
Cave 5	Disturbed	Chiang Dao cave, Chiang Dao District, Chiang Mai	98.929366	19.400409	451	5/9/2022
Cave 6	Disturbed	What Tham Tap Tao, Chai Prakan District, Chiang Mai	99.117570	19.662672	598	5/9/2022

Table 2.1 (continued)

Sampling site	Disturbed or undisturbed	Location	Latitude	Longitude	Height	Collection date
Cave 7	Undisturbed	What Tham Pha Tong cave, Chiang Rai	99.9038925	20.0918488	430	8/28/2022
Urban areas						
Site 1	Undisturbed	Construction site, Mae Fah Luang Hospital, Chiang Rai	20.031269	99.880183	398	10/17/2022
Site 2	Undisturbed	Car park and garden in a café, Chiang Rai	19.983438	99.892159	384	10/17/2022
Site 3	Undisturbed	Car park and road sides in Bandu market, Chiang Rai	19.967000	99.855912	393	10/17/2022
Site 4	Undisturbed	Public road sides, Chiang Rai	19.909030	99.835183	398	10/17/2022
Site 5	Undisturbed	Public road sides, Chiang Rai	19.82714926 5712865	99.7574546	407	10/28/2022

2.2 Isolations and Morphological Studies

As briefly described in the sequence, uncommon soil ascomycetes fungi were isolated using serial dilution (Aziz & Zainol, 2018) and baiting (Sundaram et al., 1976; Altayyar et al., 2016) methods, as follow: The Soil dilution series method was employed to isolate *Ascomycota* species from all of the three localities to obtain a more diverse fungal collection, while baiting method was applied only to forest soil samples in order to isolate keratinophilic and cellulophilic *Ascomycota* species.

2.2.1 Soil Dilution Series

From the bulk soil sample, ten grams of soil was measured and it was dissolved in 100 mL of sterilized distilled water, and the sample was shaken thoroughly to mix well. The well-mixed initial solution was allowed to set for 20 mins. One milliliter of the initial solution was transferred to a sterilized test tube or large centrifuge tube containing 9 mL of sterilized distilled water and thoroughly mixed. One milliliter of the diluted solution taken from the first test tube was transferred to a sterilized second test tube containing 9 mL of

sterilized distilled water. Similarly, the soil sample was diluted six times (with sterilized distilled water and sterilized glass wear) from 10^{-1} to 10^{-6}. From each dilution, 0.1-0.5 mL (few drops) of the solution was transferred using a sterilized glass micro pipette into a Petri dish containing antibiotic-supplemented sterilized Potato Dextrose Agar (PDA) medium and uniformly spread on the surface of the medium using a sterilized glass spreader. The plates were closed and incubated at 25 °C for 2-3 days for colony formation. Subsequently, hyphal tips were transferred and further subcultured to get pure fungal colonies using PDA and Malt extract agar (MEA). Oatmeal agar (OA) was used for colony sporulation.

2.2.2 Soil Baiting Method

An appropriate amount of soil (nearly 50 g) was placed on a sterile Petri dish, and the sterilized hair baits and deadwood pieces were placed on the soil. Plates were sealed and incubated for 3 weeks. After a few days of incubation, they were observed for fungal colonization on baits using a microscope, followed by periodic observation every four days. In each observation, fungal propagules were separated from the colonies grown on baits and placed in sterilized antibiotic-supplemeted PDA medium using a sterilized needle to obtain pure fungal colonies. Subculturing was done using MEA and PDA for pure fungal colonies, and OA were used for colony sporulation.

2.3 Morphological Studies

After obtaining pure colonies on the PDA media, cultures were incubated at 25ºC to facilitate sporulation. Reproductive structures bearing mycelium parts were removed with a needle and placed in a drop of distilled water on a slide for morphological observation and were recorded. Photomicrographs of fungal structures were captured using an OLYMPUS SZ61 compound microscope, and images were recorded with a Canon EOS 600D digital camera mounted on a Nikon ECLIPSE 80i compound microscope. Tarosoft (R) Image Frame Work program was used to do the measurements of photos. Photo-plates were made with Adobe Photoshop CS6 Extended version 13.0.1 (Adobe Systems, USA). Living cultures were deposited at Mae Fah Luang University Culture Collection (MFLUCC), Chiang Rai, Thailand, and dried culture specimens at the Mae Fah Luang University

Herbarium (Herb. MFLU). Faces of Fungi numbers were registered as described in Jayasiri et al. (2015).

2.4 DNA Extraction, PCR Amplification, Sequencing, and Phylogenetic Analyses

Scraped fungal mycelia were used for DNA extraction using a Biospin fungus genomic DNA kit (BioFlux®) China, following the manufacturer's protocol. Polymerase chain reactions (PCR) were performed using Small nuclear ribosomal subunit rDNA (SSU), internal transcribed spacer region (ITS), and large nuclear ribosomal subunit rDNA (LSU) regions; that were amplified using primer pairs NS1/NS4 (White et al., 1990), ITS5/ITS4 (White et al., 1990), and LR0R/LR5 (Vilgalys & Hester, 1990), respectively. Protein-coding gene regions, RNA polymerase II second largest subunit (*rpb2*) and Glyceraldehyde-3-Phosphate Dehydrogenase (*gapdh*), were amplified using fRPB2-5F/fRPB2-7cR (Liu et al., 1999) and GDP 1/GDP 2 (Berbee et al., 1999) primers, respectively. The translation elongation factor 1-alpha gene (*tef1-α*) was amplified using two primer pairs, EF1-983F/EF1-2218R (Rehner & Buckley, 2005) and EF1-728F/ EF2 (O'Donnell et al., 1998; Carbone & Kohn, 1999). For β-tubulin (*tub2*) gene region, three primer pairs were used: bt2a/ bt2b, T1/ bt2b (Glass & Donaldson, 1995) and Btub2fd/ Btub4rd (Woudenberg et al., 2009). PCR was carried out in a 25 µL reaction volume containing 12.5 µL of 2 × Power Taq PCR MasterMix (a premixed and ready-to-use solution, including 0.1 Units/µL Taq DNA Polymerase, 500 µM dNTP Mixture each (dATP, dCTP, dGTP, dTTP), 20 mM Tris-HCl pH 8.3, 100 Mm KCl, 3 mM MgCl2, stabilizer and enhancer),1 µL of each primer, 1 µL genomic DNA extract and 8.5 µL double distilled water. The PCR thermal cycles for SSU, LSU, ITS, *tef1*- α (983F/EF1-2218R), *tub2* (Btub2fd/ Btub4rd), and *rpb2* (5F/fRPB2-7cR) gene regions were followed as described in Chen et al. (2015). The PCR thermal cycles, for *gapdh* described in Marin-Felix et al. (2017b), for *tub2* (bt2a/ bt2b) described in Zhang et al. (2021c), and for *tef1*- α (EF1-728F/ EF-2), and *tub2* (T1/ bt2b) described in Zhang et al. (2022e) were followed. The PCR products were purified and sequenced at Biogenomed Co., Ltd. in South Korea. The newly produced sequence data were subjected to BLASTn searches against the non-

redundant GenBank nucleotide database (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to determine the reference sequences for phylogenies. Raw forward and reverse sequences were assembled using BioEdit v.7.2.5 (Hall, 2004). Based on BLASTn search results and recently published data, the reference sequences were downloaded and aligned using the MAFFT v.7.110 online program (http://mafft.cbrc.jp/alignment/server/) (Katoh & Standley, 2013) and further were refined by BioEdit 7.2.3 (Hall, 1999). Single and/or multi-gene phylogenetic analyses were performed to determine the taxonomic placements of newly generated isolates. Thereby, new species and host, geographical records were determined (Jayawardena et al., 2021; Jeewon & Hyde, 2016; Senanayake et al., 2020)

The obtained sequence data were subjected to BLAST searches against the non-redundant GenBank nucleotide database (https://blast.ncbi.nlm.nih.gov/Blast.cgi) to get the reference sequences for comparisons. Raw forward and reverse sequences were assembled using BioEdit v.7.2.5 (Hall, 2004). Based on BLAST search results and recently published data, the reference sequences were downloaded and subjected to alignment using the MAFFT v.7.110 online program (http://mafft.cbrc.jp/alignment/server/) (Katoh & Standley, 2013) and further were refined by BioEdit 7.2.3 (Hall, 1999). Single and/or multigene phylogenetic analyses were performed to determine the correct taxonomic placement of newly generated sequences.

Phylogenetic trees were obtained from maximum likelihood (ML) and Bayesian analyses. Maximum likelihood analyses were performed using two web-based platforms, the CIPRES Science Gateway platform (Miller et al., 2010) and IQ-Tree web server. In the CIPRES Science Gateway platform (Miller et al., 2010), Maximum likelihood trees were generated using the RAxML-HPC2 on XSEDE (8.2.8) (Stamatakis et al., 2008; Stamatakis, 2014) using the GTR+I+G model of evolution. Further, Maximum likelihood (ML) trees that were generated using IQ-Tree web server (http://iqtree.cibiv.univie.ac.at/) with bootstrap support obtained from 1,000 pseudoreplicates (Chernomor et al., 2016; Nguyen et al., 2015). The best evolutionary models for phylogenetic analyses were selected independently for each locus using MrModeltest v. 3.7 (Posada & Crandall, 1998) under the Akaike Information Criterion (AIC). Bayesian analyses were conducted with MrBayes v. 3.2.7a (Huelsenbeck & Ronqvist, 2001) to evaluate posterior probabilities (PP) (Rannala & Yang, 1996; Zhaxybayeva & Gogarten, 2002), with four simultaneous Markov Chain Monte Carlo (MCMC) runs with predefined generations. The convergence of the PP for

each dataset will be assessed by visualizing log files with Tracer version 1.7 (Rambaut et al., 2018). The first twenty-five percent of the trees, representing the burn-in phase of the analyses, will be discarded. The remaining trees were used to calculate posterior probabilities in the majority rule consensus tree. Phylograms were visualized with FigTree v1.4.0 (Rambaut, 2012), and trees were edited by Microsoft PowerPoint. After the phylogenetic placement, newly generated sequence data were deposited in the NCBI and GenBank.

Table 2.2 Partial gene regions and primers that will be used in the study

Gene	Forward primer	Reverse primer	Reference
Internal transcribed spacer (ITS)	ITS5	ITS4	White et al. (1990)
Large subunit nuclear ribosomal DNA region (LSU)	LROR	LR5	Vilgalys and Hester (1990), Rehner and Samuels (1994)
Small subunit nuclear ribosomal DNA region (SSU)	NS1	NS4	White et al. (1990)
Translation elongation factor 1-α tef1-α (EF 1-α)	EF1-728F	EF1- 986R	Carbone and Kohn (1999)
Second largest subunits of RNA polymerase II (RBP2)	fRPB2-5F	fRPB2-7cr	Liu et al. (1999)
Beta (β) tubulin (TUB)	Bt2a	Bt2b	Glass and Donaldson (1995)
Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	gpd	1gpd2	Berbee et al. (1999)

2.5 Writing the Outline and the Generic Notes of Soil *Ascomycota* and Providing the Drawings for Genera

The taxonomic outline and comprehensive notes for soil-inhabiting Ascomycota genera worldwide are provided. These notes cover 270 genera and include morphological descriptions, updated phylogenies, and ecological data. The species reported from the soil are listed under each note. Line drawings are provided for selected genera to illustrate their morphological characteristics. The scattered information is gathered from journal articles, books, and credible websites. The total number of species in each genus is obtained from recently updated articles, Index Fungorum (2025), Species Fungorum (2025), or the recent outline by Hyde et al. (2024c). Based on the previous publications, the sexual or asexual morph characteristics of the type species of selected genera are drawn.

CHAPTER 3

VALUE OF CULTURING SOIL *ASCOMYCOTA* IN THE MODERN MOLECULAR ERA AND EMPHASIS ON TWELVE ISOLATION METHODS

3.1 History and the Development of Soil *Ascomycota* Investigations

A holistic understanding of microbial diversity and taxonomy relies on knowing the functions of the taxa involved and how they interact with the ecosystem (Biswas & Sarkar, 2018; Maharachchikumbura et al., 2021). Thus, the correct naming will help link the versatile knowledge of taxa worldwide. Due to technological and methodological limitations in sampling and resolution of detection techniques, the awareness of belowground fungi is limited, and integrating a reliable and effective method for assessing their taxonomy and diversity is an emergent challenge. Each method contains advantages and disadvantages (Hibbett et al., 2011; Orgiazzi et al., 2016; Cameron et al., 2018; Hongsanan et al., 2018; Wu et al., 2019; Semenov et al., 2019). Conventionally, a polyphasic approach based on morphology, physiology, biochemistry, or reactions to chemical tests has been used to distinguish species (Senanayake et al., 2020). Currently, soil fungal research is based on culture-dependent and culture-independent methods (Tedersoo et al., 2017; Dissanayake et al.; 2018; Jayawardena et al., 2018; Wu et al., 2019; Wijayawardene et al., 2021). The culture-independent methods use genomic technology to generate, analyse and interpret data from environmental samples. These data are extracted and analyzed using metagenetic, metagenomics (DNA-based) and metatranscriptomics (RNA-based) approaches (Gutleben et al., 2018; Semenov et al., 2021). Metagenomics is used for functional profiling, and metagenetic is used for taxonomic community profiling using High-throughput sequencing (HTS) technology. High-throughput sequencing features next-generation sequencing (NGS) and third-generation sequencing (TGS) methodologies to determine fungal DNA data (O'Brien et al., 2005; Carvalhais et al., 2012; Schmidt et al., 2013; Raja et al., 2017; Sudhakar et al., 2018; Wu et al., 2019). This has spurred rapid advancements in recent years and is used for obtaining whole-genome

sequences, delineating higher taxonomic levels, identifying closely related fungal species, describing the evolution of chemical gene clusters, and prioritizing industrially productive strains for bioactive compounds (among taxonomically related strains) discovery (Schmidt et al., 2013; Tedersoo et al., 2014, 2017, 2020, 2021; Raja et al., 2017; Sudhakar et al., 2018; Yang et al., 2019; Wu et al., 2019; Semenov et al., 2021) From a taxonomic perspective, HTS is effective for revealing the unculturable soil taxa. However, these methods are still limited in classifying fungi to family or genus level (Tedersoo et al., 2017; Frac et al., 2018; Vu et al., 2019; Jurburg et al., 2021) as identification based on OTUs with short reads that lack a physical specimen cannot presently be used to accurately identify novel species (Tedersoo et al., 2017; Nagler et al., 2018, 2021; Hongsanan et al., 2018; Jurburg et al., 2021).

Culture-based techniques are essential to understanding taxonomy at the species level (Chambergo & Valencia, 2016; Gutleben et al., 2018; Wu et al., 2019; Senanayake et al., 2020). This is where morphological illustrations and multigene phylogenies are integrated through living and dried cultures (Jeewon & Hyde, 2007; Hongsanan et al., 2017; Chethana et al., 2020; Hyde et al., 2020c; Aime et al., 2021). Protocols to isolate and analyse soil-living species are found in numerous publications. Few recent soil studies have combined culture-based methods with HTS methods (Stefani et al., 2015; Selbmann et al., 2021). Different researchers have also used various methods, making it problematic to compare the results. For example, studies from 20–30 years ago have limited taxonomic information, and high-throughput sequencing (HTS) methods have made information readily available and pertinent to initiate fungal culturing (Gutleben et al., 2018; Wu et al., 2019; Hyde et al., 2020a, 2020b). Thus, the collection and standardization and freely available publication of protocols are needed. At the same time, it is also necessary to establish universal standards for the collection, transportation, and storage of soil samples (Gutleben et al., 2018; Wu et al., 2019; Senanayake et al., 2020). This is particularly important because a great deal of current taxonomic information has been obtained, which helps study the characteristics of miscellaneous soil fungal taxa and culture them (Wu et al., 2019; Hyde et al., 2020a, 2020b).

This chapter will provide a review of the importance of soil fungal-culturing methods in the genomic era and provide an account of existing culturing methods for studying soil fungal diversity, taxonomy, and other applications. I have provided the status

of investigative methods for soil fungi, including modern genomics methods in fungal taxonomy and their pros and cons. The value of fungal isolation methods and considerations in terms of modern soil fungal taxonomy is also addressed. In addition, the results of

Importance of isolating and culturing fungi in modern taxonomy

Cultures (living or dry) of fungi provide physical samples that can be linked to the physiology and ecology of a species (Collado et al., 2007; Jeewon & Hyde, 2007; Tedersoo et al., 2017; Aime et al., 2021). Unlike environment sequences, cultures can be stored, reproduced, and verified by molecular sequencing. Cultures are valuable for linking sexual and asexual morphs, understanding functional guilds, and can be preserved as isolates (as dry and living) in reference collections. Cultures are also essential for screening biological activities, elucidating structures for biosynthesis and obtaining successful inoculants (Mueller et al., 2004; Guimarães et al., 2006; Kaewchai et al., 2009; Dorhout et al., 2011; Qiu et al., 2012; Rao et al., 2013; Knudsen & Dandurand, 2014; Chambergo & Valencia, 2016; Sena et al., 2018; Ramesh et al., 2019; Gurusinghe et al., 2019; Satyanarayana et al., 2019; Hyde et al., 2020b). In addition, due to the lack of cultivation, it has been predicted that 80% of fungal taxa in the soil are unidentified at the species level, and 20% cannot be assigned to an order (Tedersoo et al., 2017; Libor et al., 2019; Chethana et al., 2020; Senanayake et al., 2022).

3.2 Isolation and Culturing Methods for Fungi

The employment of culture-dependent methods involves a series of steps, which can be summarized as follows: (i) a pure colony is isolated; (ii) the isolate is characterized by morphological and phylogenetic analysis; and (iii) morpho-molecular evidence is combined, providing evidence to identify the species (Hawksworth & Rossman, 1997; Stefani et al., 2015; Wu et al., 2019; Chethana et al., 2020; Aime et al., 2021). Growth media is essential as morphological characteristics can be produced in vitro (Hawksworth & Rossman, 1997; Stefani et al., 2015). The morphology is based on macroscopic characteristics (form, size, colour, and growth rates of cultures) and microscopic characteristics of reproductive structures of asexual and/or sexual morphs

(Jeewon & Hyde, 2007; Rosas-Medina et al., 2019). Cultures help observe and describe specific structures not present in natural states, such as synasexual morphs, different conidia (alpha, beta, or gamma), and chlamydospores, which help document the taxa (Domsh et al., 1993; Wijayawardene et al., 2021). Morphology is illustrated through images, drawings, and descriptions (Raja et al., 2017; Rosas-Medina et al., 2019; Senanayake et al., 2020).

Some taxa (*Xylariales* and macrofungi) produce fruiting bodies on plant litter or the surface of the earth that are easy to observe. Fast-growing strains can also easily be isolated and grown in artificial media (Jeewon & Hyde, 2007). However, many species are present in soils without forming visible phenotypic characteristics, dwell in uncommon or extreme conditions, and some are remarkably slow-growing (Bridge & Spooner, 2001; Stefani et al., 2015; Senanayake et al., 2022). Furthermore, soil-inhabiting strains are exclusively adapted to their substrates; hence, the *in vitro* conditions of isolation limit their growth. Therefore, selecting isolation methods is critical for isolation success (Bridge & Spooner, 2001). Inducing in vitro conditions similar to the original edaphic conditions enhances the isolation frequency and growth (Grossbard et al., 1952; Kazerooni et al., 2017).

Recovering unculturable species is a major challenge in culture-dependent methods as artificial media can inhibit growth (Grossbard et al., 1952; Kazerooni et al., 2017). Symbiotic relationships cannot be maintained in vitro, precluding the growth of these organisms (Jeewon & Hyde, 2007; Kazerooni et al., 2017). Fast-growing species overgrow slow-growing taxa (Jeewon & Hyde, 2007). Some species release antibiotics, inhibiting the germination and growth of other strains (Grossbard et al., 1952).

The following section provides an overview of currently available isolation techniques for investigating soil fungi (Table 3.1).

Table 3.1 Available methods to isolate different fungal taxa from soil

Fungal isolation method	Isolated fungal group	References
Baiting method	*Ascomycota* and basal fungi	Butler (1907), Simpanya and Baxter (1996), Giudice et al. (2012), Abu-Mejdad (2013), Altayyar et al. (2016), Masoudi et al. (2020), Senanayake et al. (2020)
Dilution series method (Serial dilution)	*Ascomycota*, *Basidiomycetes*, and basal fungi	Waksman (1922), Brierley et al. (1928), Kutateladze et al. (2016), Das et al. (2019, 2020), Park et al. (2020), Santos et al. (2020), Senanayake et al. (2020), Yasanthika et al. (2020)
Soil Plate method	*Ascomycota*	Warcup (1950), Parkinson and Thomas (1965), Kazerooni et al. (2017), Senanayake et al. (2020)
Chemical pasteurization (Alcohol treatment method, and Acid treatment)	*Coprophilous, Ascomycota*, ascosporic, and sclerotia-producing *Eurotiales* and cleistothecial and perithecial *Ascomycota*	Kuehn and Orr (1962), Warcup and Baker (1963), Bills et al. (2004)
Heat treatment method	*Ascomycota*	Warcup and Baker (1963), Ali et al. (2009)
Soil steaming method	*Ascomycota*	Warcup et al. (1951)

Table 3.1 (continued)

Fungal isolation method	Isolated fungal group	References
Soil immersion tube	*Ascomycota*	Chesters (1948), Mueller and Durrell (1957), Garrett (1981), Mukerji (2002), Senanayake et al. (2020)
Isolation of fungal hyphae attached to soil particles	*Ascomycota*	Warcup (1955)
Soil washing technique	Mycorrhizal fungi, *Ascomycota*, *Mucorales* and *Basidiomycota*	Parkinson and Williams (1960), Azaz (2003), Pacioni et al.1991
Wet sieving and decanting method	Mycorrhizal fungi and endogenous fungi	Gerdemann and Nicolson (1963)
The Mankau method for isolation of nematophagous fungi in soil	*Ascomycota*	Mankau (1975)
Fungal highway columns method	Arbuscular mycorrhizal fungi	Simon et al. (2015)

3.3 Baiting Method

Baiting, initiated by Butler (1907), is one of the most effective methods for isolating soil fungi (Meyling et al., 2007). The method aids in isolating substrate-specific taxa (cellulophilic fungi, keratinophilic fungi, and entomopathogenic fungi) and estimates their trophic nature (Mueller et al., 2004; Giudice et al., 2012; Abu-Mejdad, 2013). In this method, sterilized organic substances are placed in soil samples and incubated. The growth of fungi on the substrates is observed, and propagules are transferred to sterilized nutrient media. Different baits provide various nutrient sources, and therefore, it is possible to isolate a wide range of fungal taxa (Meyling et al., 2007). Table 2 lists the various organic substrates that were used in previous studies. The general steps involved in the baiting method for isolating soil fungi are given in Figure 3.1. Below-ground fungi have numerous adaptations that allow them to thrive on different substrates, depending on their nutrient

preferences (Marano et al., 2012; Yasanthika et al., 2022). As a result, they can utilize various sources of carbon, nitrogen, and sulphur, and possibly coexist in the same environment (Marchisio, 2000; Marano et al., 2012). Baiting is a selective technique for isolating fungi that are associated with selected nutrient sources (Marano et al., 2012; Marchisio, 2000; Yasanthika et al., 2022). Various baits can be used to isolate keratinophilic and cellulophilic species, allowing us to obtain a general understanding of their substrate preferences and contributions to the degradation process (Caretta & Piontelli, 1997; Bojanich et al., 2015). However, categorizing soil fungi based on substrates is challenging due to the overlapping characteristics of their occurrences (Dick, 1992; Marchisio, 2000). The baiting technique is suitable for isolating soil-, dust- and water-inhabiting fungal groups (Marano et al., 2012; Overy et al., 2019; Greco et al., 2020; Hamada et al., 2024). Furthermore, to examine the biocontrol activity of taxa against target hosts, weed leaves, other fungi, insects, and nematodes can be used as baits (Meyling et al., 2007). For example, *Galleria mellonella* and *Tenebrio molitor* larvae are commonly used to isolate entomopathogenic fungi from soil (Tuininga et al., 2009; Sharma et al., 2018). For this, larvae are placed in a sealed plastic container filled with a soil sample and the resulting larvae carcass is dissected and placed on culture media to observe mycelial growth (Tuininga et al., 2009; Sharma et al., 2018). In addition, to examine the biocontrol activity, the baiting methods have successfully been used as a microcosm to recover real-time interactions of fungi and bacteria under natural soil conditions. (Ballhausen et al., 2015; Ghodsalavi et al., 2017) Bait can be treated with an antibiotic solution (20% Clorox, 0.2 g/mL chloramphenicol or streptomycin or penicillin at 1000 IU/mL) to avoid bacterial contamination (Manoch, 1998; Pakshir et al., 2013).

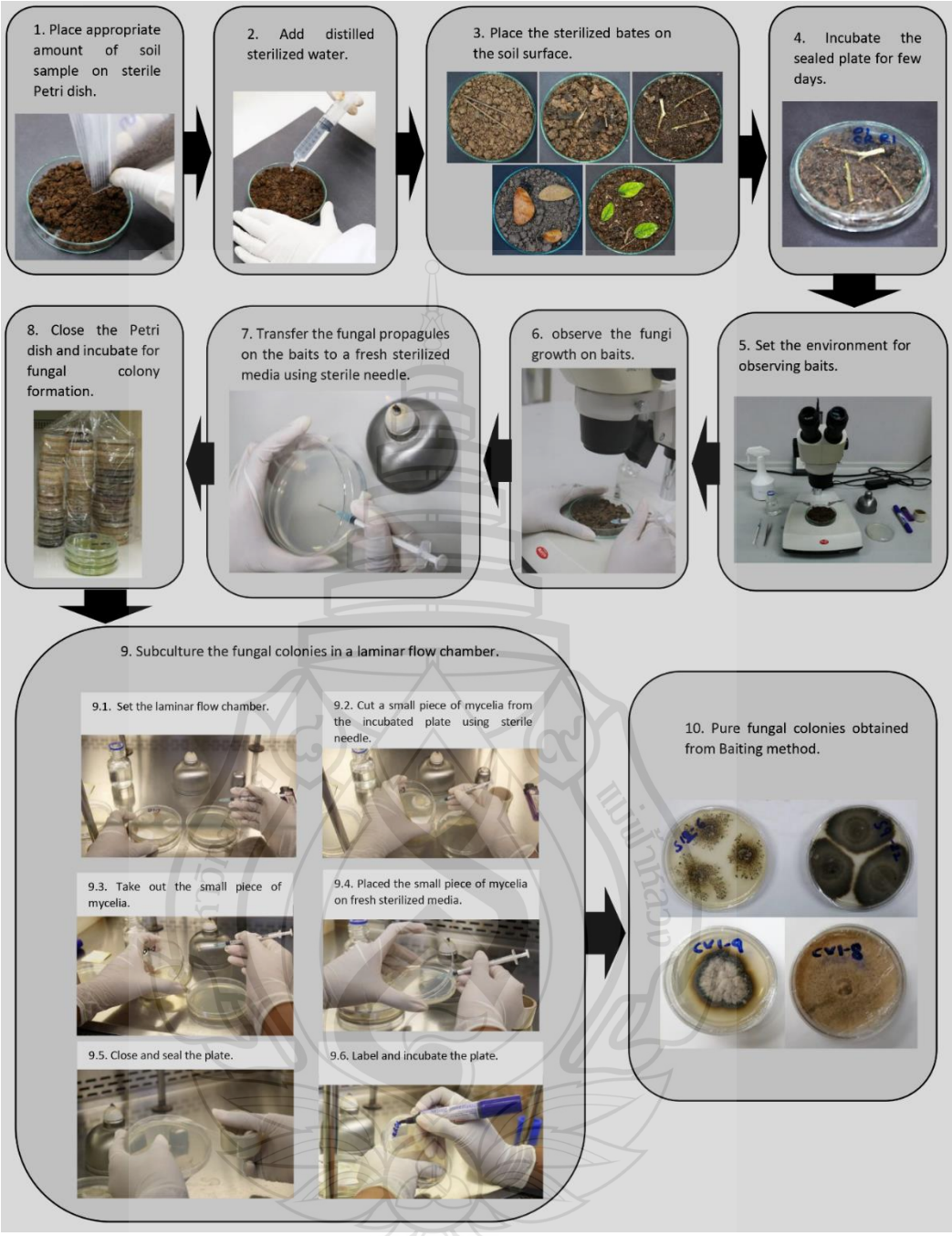


Figure 3.1 Baiting technique for the isolation of soil fungi

Table 3.2 The different types of baits used for fungal isolations from soil (ND=Not determined)

Baits	Fungal genera/ groups	Incubation period	Reference
Hair	*Mycrosporum* (Kerotinophillic fungi)	Poultry farm soil for 3 weeks	Shukia et al. (2003)
Hair	*Aspergillus*, *Acremonium*, *Chrysosporium*, *Microsporum*, *Trichoderma*	3–4 weeks	Altayyar et al. (2016)
Corn leaf, snake skin, pine pollen, and hemp seed	*Catenaria*, *Rhizoptrydiums*	ND	Sundaram et al. (1977)
Human hair and Fowl's feather Wool	*Aspergillus*, *Chrysosporium*, *Microsporum*	ND	Sundaram et al. (1977)
vegetable pieces, rice, and pine	89 fungal genera		Manoch (1998)
Apple, Black pepper leaves, Black pepper leaf discs, and castor seeds	*Phytophthora*	ND	Holliday and Mowat (1963), Kueh and Khew (1982), Ramachandran et al. (1986), Sastry and Hegde (1988)
Sterilized wood pieces (at least 2 cm^2)	*Ramophialophora sp.*	ND	Calduch et al. (2004)
Hair	*Chrysosporium* sp.	ND	Călin et al. (2017)

Table 3.2 (continued)

Baits	Fungal genera/ groups	Incubation period	Reference
Goat hair-baiting	*Alternaria, Aspergillus, Candelabrella, Chaetomium, Chaetomium, Cladosporium, Cunninghamella, Drechslera, Emericella, Eurotium, Fusarium, Fonsecaea, Geotrichum, Geotricum, Graphium, Gliocladium, Giodianichiella, Haplosporangium, Helmithosporium, Macrophomina, Monocillium, Neosartoria, Paecilomyces, Penicillium, Phoma, Pythium, Scytalidium, Stemphylium, Sclerotium, Syncephalastrum, Tetracoccosporium, Thermoascus, Tricladium, Trichosporium, Verticillium, Rhizomucor,* and Yeasts	14 days on sterilized Petri dishes	Ramadan and Ismael (2011)

3.3.1 Isolation Keratinophilic and Cellulophilic *Ascomycota* from the Baiting Method

The baiting method is useful in identifying substrate preferences of fungi in soil. Keratinophilic species are natural colonizers of keratin substrates that have the ability to partially invade keratinized substrates, such as hair, wool, feathers and nails (Marchisio, 2000; Tridico et al., 2014). Keratinophilic fungi that inhabit the soil can be isolated via keratin baits, such as human and animal hair, nails and bird feathers (Marchisio, 2000; Abu-Mejdad, 2013; Yasanthika et al., 2022). *Aspergillus*, *Chaetomium*, *Clonostachys*, *Fusarium, Humicola, Lecanicillium, Paecilomyces*, *Scopulariopsis*, and *Trichoderma*

species have been isolated using hair baits (González et al., 2000; Sharma et al., 1997; Spychała et al., 2024). In addition, some of the clinically important keratinophilic fungi, such as *Curvularia* and *Alternaria*, have also been isolated by this method (Marchisio, 2000). They are dermatophytes that cause systemic and superficial infections in humans (Marchisio, 2000; Meenakshi et al., 2022). However, *Curvularia ramosa* and *Alternaria* sp. have exhibited mildly keratinophilic characteristics (English, 1963, 1965; Tridico et al., 2014). These species can also be isolated from other substrates like decaying plant materials (Bohacz & Korniłłowicz-Kowalska, 2019; Marchisio, 2000). Studies by De Vries (1962) and Griffin (1960) identified the succession of fungi on hair and soil and discovered chytrids as preliminary colonizers. Subsequently, *Fusarium*, *Penicillium*, and *Mucor* species occupy the substrate, and later, *Chaetomium*, *Gliocladium*, and *Humicola* species colonize the hair substrates that are involved in the degradation of resistant substances. In the final stages of decomposition, microsporum-like and trichophyton-like species colonized the substrate (Marchisio, 2000).

Most *Ascomycota* fungi have the ability to colonize and thrive in cellulosic materials (Bucher et al., 2004). They can degrade cellulose and hemicellulose material, while some have the potential to degrade lignin in decaying wood materials (Bucher et al., 2004; Sánchez, 2009; Kuhad et al., 2011). Thus, the cellulophilic fungal groups present in soil have been isolated from baiting methods (Greco et al., 2020), using cellulosic substrates like pollen grains, corn leaves, pine pollen, hemp seed (Sundaram, 1977), vegetable substrates, rice (Manoch, 1998), sterilized wood pieces (Calduch et al., 2004) and *Albizia falcafaria* leaflets (Anandaraj & Sarma, 1990). The baiting technique has been used to isolate numerous lower fungal groups such as *Achlya*, *Dictyuchus*, *Pythium* and *Saprolegnia* from soil (Yasanthika et al., 2022b). Calduch et al. (2004) introduced soil-associated *Ramophialophora* from wood baits. Moreover, *Aspergillus tubingensis*, *A. westerdijkiae*, *Penicillium solitum*, *P. solitum* and *Trichoderma longibrachiatum* have been isolated from marine water using wooden baits (Greco et al., 2020).

3.3.2 Taxonomy and Phylogeny of Soil *Ascomycota* Isolated from Baiting Method in Thailand

In Thailand, several studies have applied the baiting method to isolate soil fungi. For example, *Chaetomium* species have been recovered from agricultural soils using straws, filter paper, tissue paper and pineapple leaves (Pornsuriya et al., 2008, 2011), and

Manoch (1998) isolated *Achlya* and *Pythium t*axa from forest soil using vegetable, pine and rice substrates. The hair-baiting technique has been employed to isolate *Mucor*, *Pythium* and *Sclerotium* species from urban soils (Mar Htun et al., 2021). Compared to other countries, this method has been rarely applied in fungal studies in Thailand. Most studies isolating soil fungi in forests have primarily used the soil dilution plate method (Manoch, 1998; Puangsombat et al., 2010; Liamthong et al., 2017; Yasanthika, 2020; Yasanthika et al., 2022a; Chethana et al., 2023). Thailand's tropical climate and high biodiversity have led to extensive studies on above-ground fungi, while the diversity of below-ground fungal species remains largely unexplored (Osono et al., 2009; Amma et al., 2018; Hyde et al., 2024a). This research provides morpho-molecular illustrations of the newly identified cellulophilic fungus *Neptunomyces soli* and document a host record of the keratinophilic fungus *Curvularia dactylocteniicola*, both belonging to *Pleosporales* That have been isolated from the forests soils in Thailand.

3.4 Dilution Plate Method

Different soil samples might contain miscellaneous densities of fungal propagules. Low densities of colonies in culture media minimize inter-colony interactions, favouring obtaining pure fungal strains (Bills et al., 2004). The soil: water ratio is adjusted to obtain several colonies (5–30) in a 100 mm Petri-dish plate in the dilution plate method. Waksman (1922) introduced the dilution plate technique for soil bacteria isolation, and Brierley et al. (1928) modified it for fungal isolations from the soil. Most of these taxa are saprobes and can withstand microbial antagonism (Ramakrishnan, 1955). This technique is widely used for quantitative and qualitative estimations of the species (e.g., Aziz & Zainol, 2018; Marin-Felix et al., 2019; Alotaibi et al., 2020; Alidadi et al., 2020; Guevara-Suarez et al., 2020). The steps of the method vary according to the study objectives (Aghamirian & Ghiasian, 2013; Aziz & Zainol, 2018). The basic steps of the dilution method are illustrated in Figure 3.2.

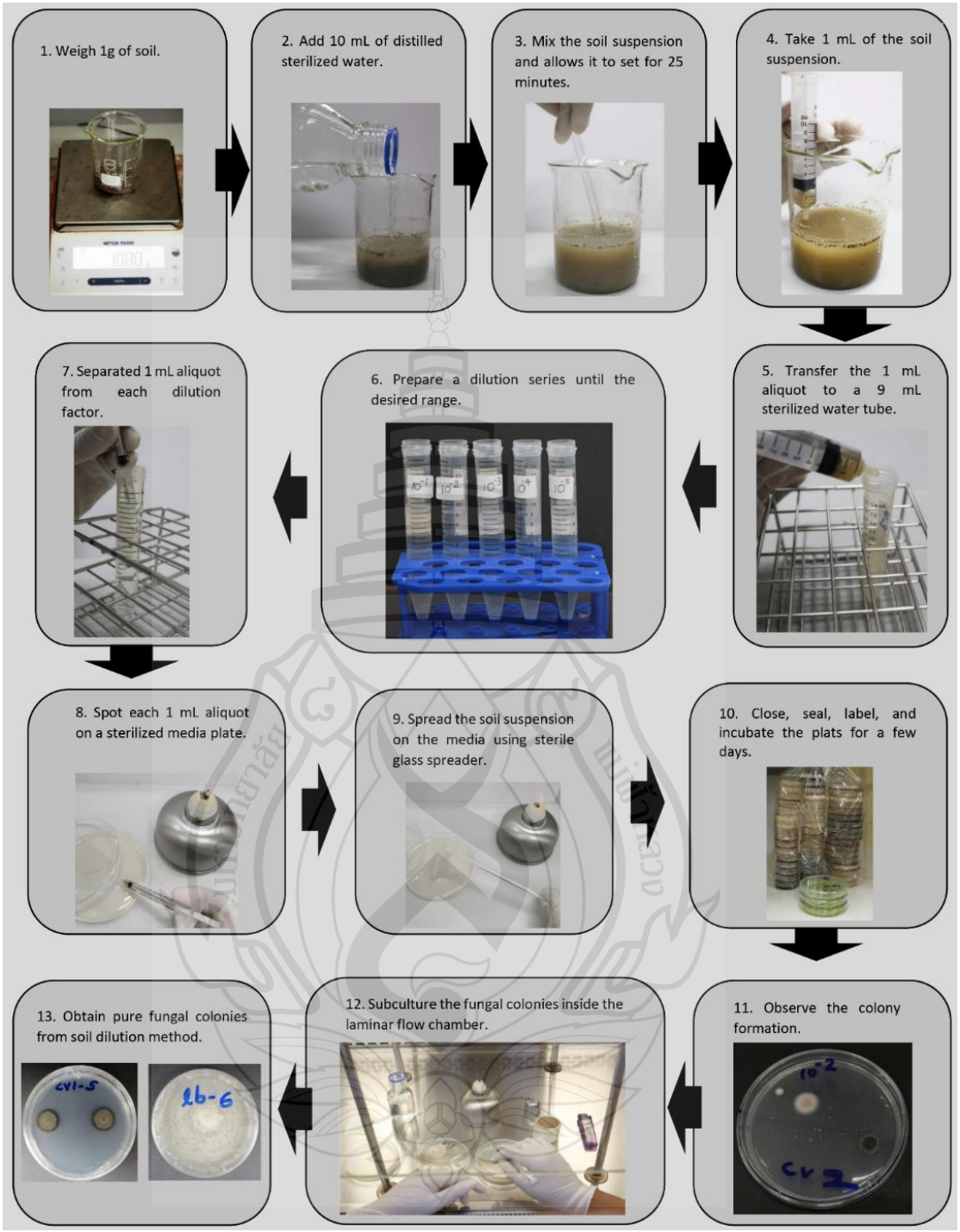


Figure 3.2 Dilution method for the isolation of soil fungi

Taxonomy and phylogeny of soil *Ascomycota* isolated from dilution method in Thailand

Most of the soil fungal isolation studies in Thailand have been carried out using the serial dilution method. However, many of those studies recovered common *Ascomycota* species belong to *Aspergillus*, *Penicillium*, *Fusarium* and *Talaromyces* like genera. During this study, 37 *Ascomycota* species were investigated from Thai soils that have been isolated using soil dilution method.

3.5 Soil Plate Method

The plating method for isolating soil-inhabiting species was introduced by Warcup (1950). In this method, the soil is placed directly beneath the growth media to obtain cultures. Soil samples are weighed to 0.015 g and placed in the sterile Petri-dish, and a thin layer of sterile warm melted Czapek-Dox + yeast extract, pH 5.0 agar, or glucose ammonium nitrate (GAN) media is poured over the soil layer. Plates are incubated at room temperature, preferably for 3–5 days, for colony growth (Warcup, 1950; Manoch, 1998). In his experiment, the author obtained hyphomycetes, *Pythium*, and *Mortierella* species using this method. This method was successfully used, with minor modifications, by Parkinson and Thomas (1965) to isolate rhizosphere fungi. The steps for utilizing the soil plate method are illustrated in Figure 3.3.

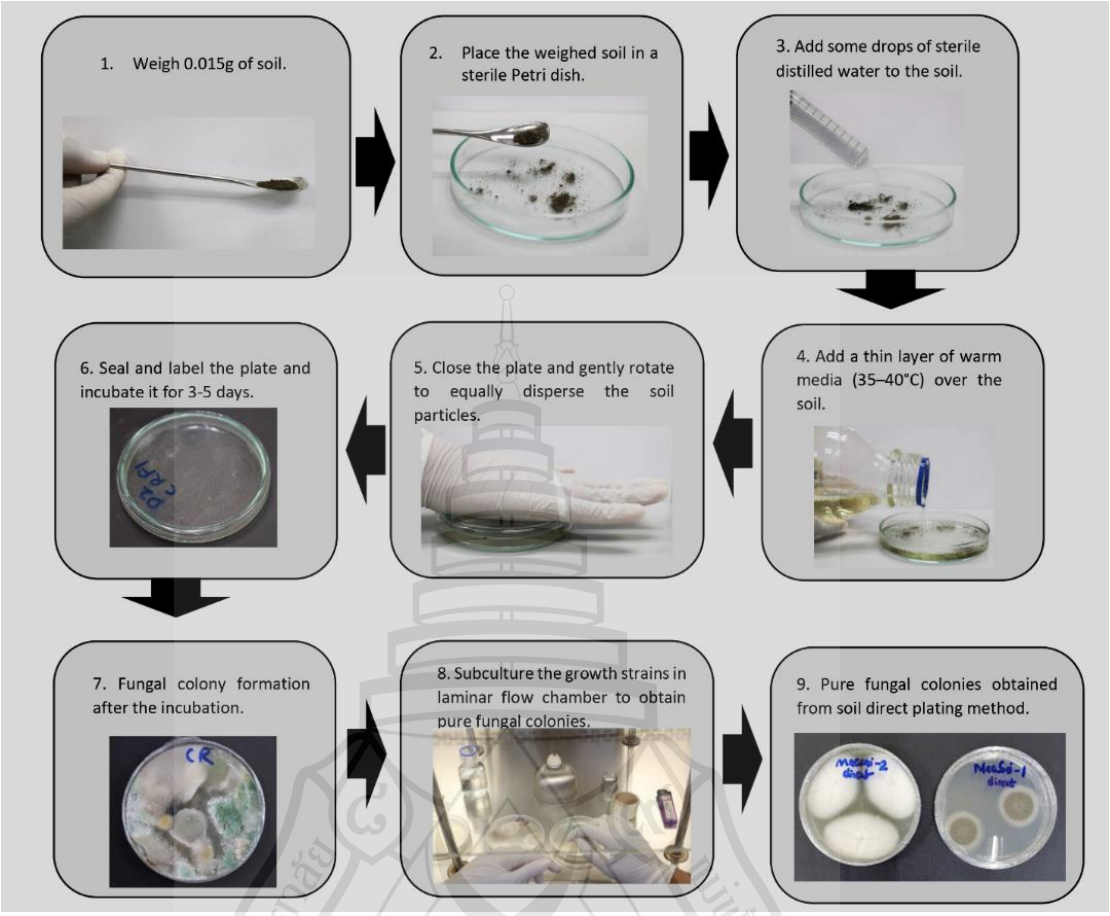


Figure 3.3 Soil plating method for the isolation of soil fungi

3.6 Alcohol Treatment Method (Chemical Pasteurization)

This method was first described by Warcup and Baker (1963). It consists of weighing approximately 0.3 g of soil, placing it in an 18 mm sterilized dry test tube, and adding 65–70% ethanol. After that, the solution is shaken thoroughly and left for 10–15 minutes to settle. The excess alcohol is removed, and the soil is transferred to the sterile Petri-dish using a spatula. A thin layer of warmed GAN (glucose-ammonium nitrate) media at 45°C is then poured over the soil layer. Petri dishes are shaken gently until soil particles are distributed well across the bottom. Plates are incubated for 3–5 days at 26–28°C. Once the hyphal growth is obtained, its tips are transferred into the potato dextrose agar (PDA) slants and kept at 26–28°C for two weeks to allow culture growth (Warcup & Baker, 1963; Abdullah & Saadullah, 2013).

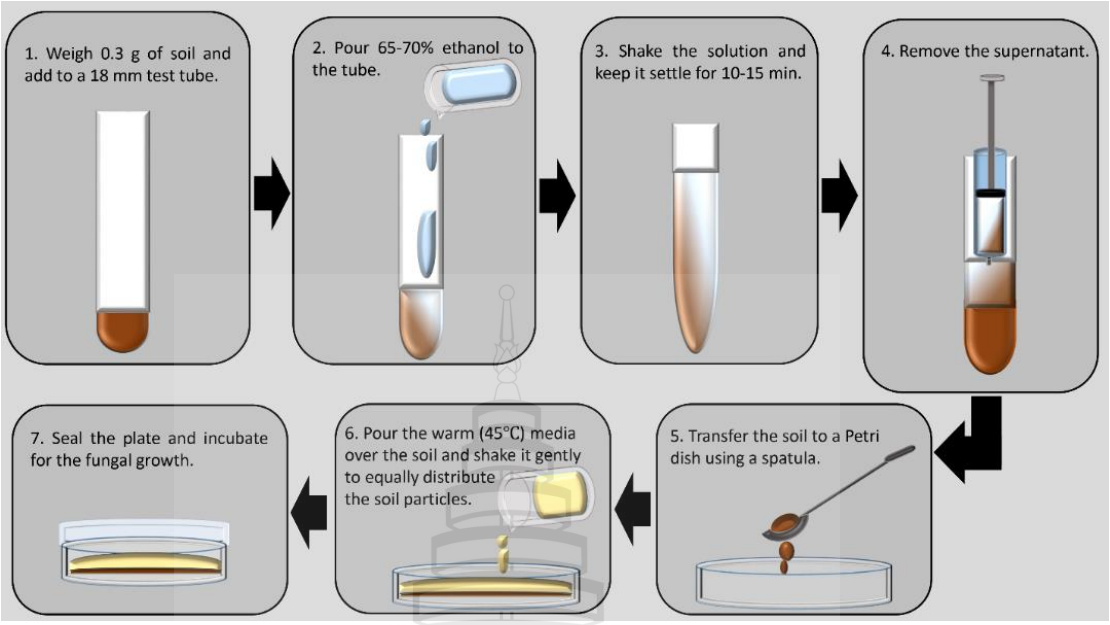


Figure 3.4 Alcohol treatment method for the isolation of soil fungi

3.7 Acid Treatment (Chemical Pasteurization)

In a study by Kuehn and Orr (1962), acid was added in 0.00015, 0.0005, and 0.00075 mg/mL into melted PDA and poured onto the Petri-dish. A small amount of soil was added to the media and incubated for 3–5 days. After obtaining the hyphal growth, the hyphal tips were transferred to PDA slants using a sterile needle. Finally, PDA plates were incubated at 26–28°C for two weeks until fungal colonies were obtained. The method was later adapted by Furuya and Naito (1979), in which 3 g of soil were weighed and mixed with 5% acetic acid in a glass tube. The mixture settles for 20 minutes, and the surface acid layer is discarded. Next, the soil is washed with 10 mL of sterilized distilled water, and 1 mL of soil suspension is poured over the sterilized malt-extract agar (MEA) media (Figure 3.5).

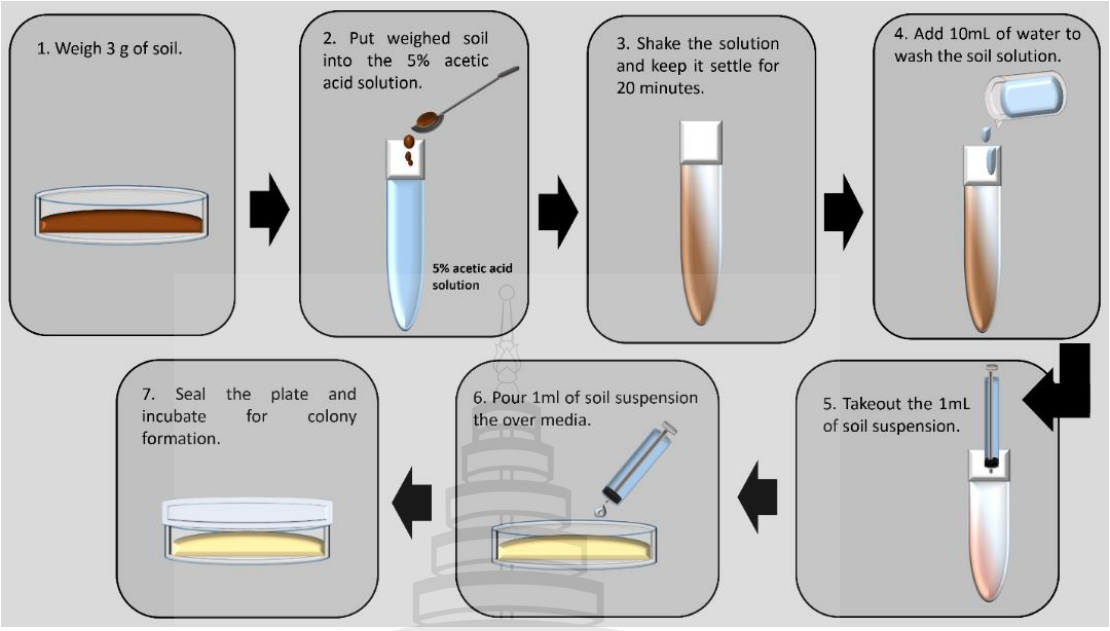


Figure 3.5 The acid treatment method for the isolation of soil fungi

3.8 Heat Treatment Method

Warcup and Baker (1963) introduced the heat treatment method to isolate fungi from the soil. Many heat-resistant ascomycetes demand heat activation before germination of ascospores (Katan, 1985; Ali et al., 2009); thus, this method can isolate heat-resistant strains (Ali et al., 2009). Heat inactivates the vegetative parts and less heat-resistant sexual spores of fungi but suppresses the activities of bacteria (Beuchat & Pitt, 1992). In this method, 0.3 g of soil is placed in a sterile 18 mm test tube, and sterile distilled water is added. The soil solution is kept in a water bath at 60–80°C for 10–15 minutes. Once the soil settles, excess water is removed, and the soil is placed in a sterile Petri dish. GAN (glucose-ammonium nitrate) media is poured over the soil layer and gently rotated to distribute the soil in the bottom of the Petri-dish. The Petri dishes are then incubated for 30 days between 26–30°C. The colonization begins after the fifth day, maturing after 14 days. Hence, observation of colony growth generally occurs between days 7 and 14. Once the grown hyphae are observed, their tips are transferred to the new PDA medium to obtain isolates (Warcup & Baker, 1963; Abdullah & Saadullah, 2013).

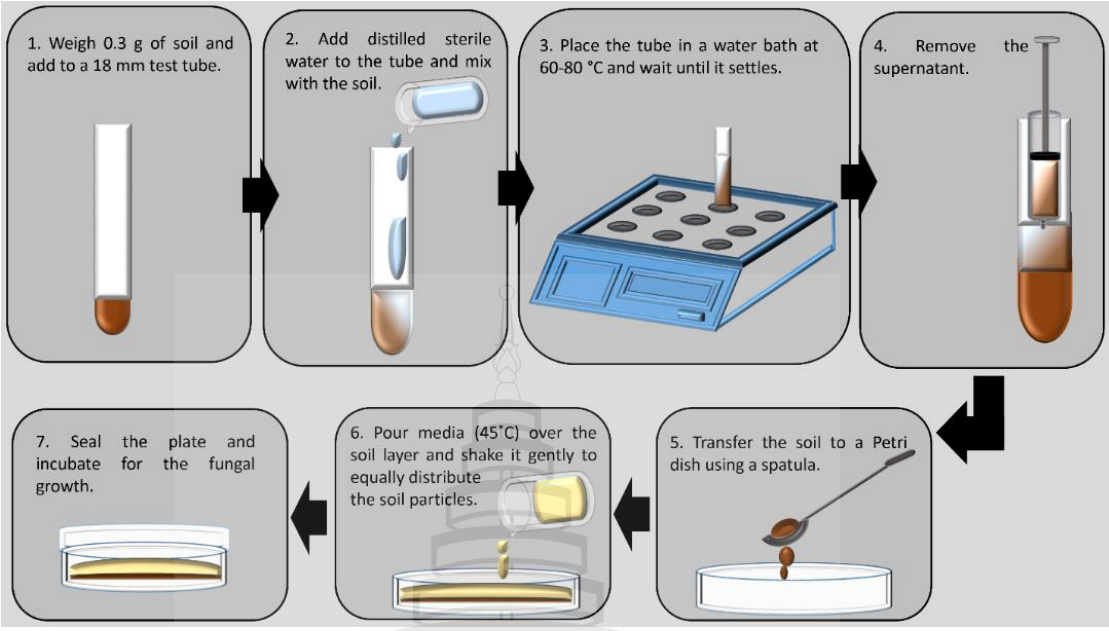


Figure 3.6 The heat treatment method for the isolation of soil fungi

3.9 Soil Immersion Tube

This method was first used to isolate other microorganisms from soils (Chesters et al. 1940; Chester et al., 1948) and has been characterized as highly selective for isolating species that can tolerate low oxygen levels (Chesters & Thornton, 1956). The method was later modified by Gochenaur (1964) and several other authors to reduce selectivity and permit the isolation of a broader range of species (Thornton, 1952; Parkinson, 1957). A tube with 4–6 spirally arranged mini-holes containing nutrient agar is placed in the soil, separated by an air gap. After 5–8 days, the tubes are brought to the laboratory, where the agar core is taken out and cut into pieces. Pieces with mycelia are placed in sterilized media, and subsequently, colonies can be sub-cultured in selective media (Mueller & Durrell, 1957; Mukerji, 2002). The basic steps of the method are illustrated in Figure 3.7. When using the original method, the core of the agar tube contains less aeration, which makes it suitable for isolating low oxygen-tolerant, fast-growing fungi. This method also isolates non-sporulating fungi such as *Rhizoctonia solani* (Chester et al., 1940, 1948; Garrett, 1981).

3.10 Soil Steaming Method

Soil steaming is a selective method for isolating slow-growing ascomycetes and hyphomycetes from the soil (Warcup et al., 1951) that are likely to be overgrown by fast-growing groups such as *Absidia*, *Mortierella*, *Mucor*, *Trichoderma*, and *Zygorhynchus*. The method consists of weighing 125 g of soil into a glass tumbler and steaming it for 2, 4, 6, 8, and 10 minutes at 100 °C. One cm from the surface soil layer in each tumbler is removed and transferred separately to 10 Petri-dishes containing Dox+yeast extract agar media (acidified with phosphoric acid to pH 4). This is then steamed for four minutes. The most efficient duration is four minutes to reduce fast-growing taxa, and ascomycetes resistant to a short steam treatment can also be isolated. This is favoured by the small number of colonies grown on the plates (Warcup et al., 1951). Heavy soils or soils with a high proportion of humus may require more extended steaming periods. However, over-steaming can inactive colony formation (Warcup et al., 1951).

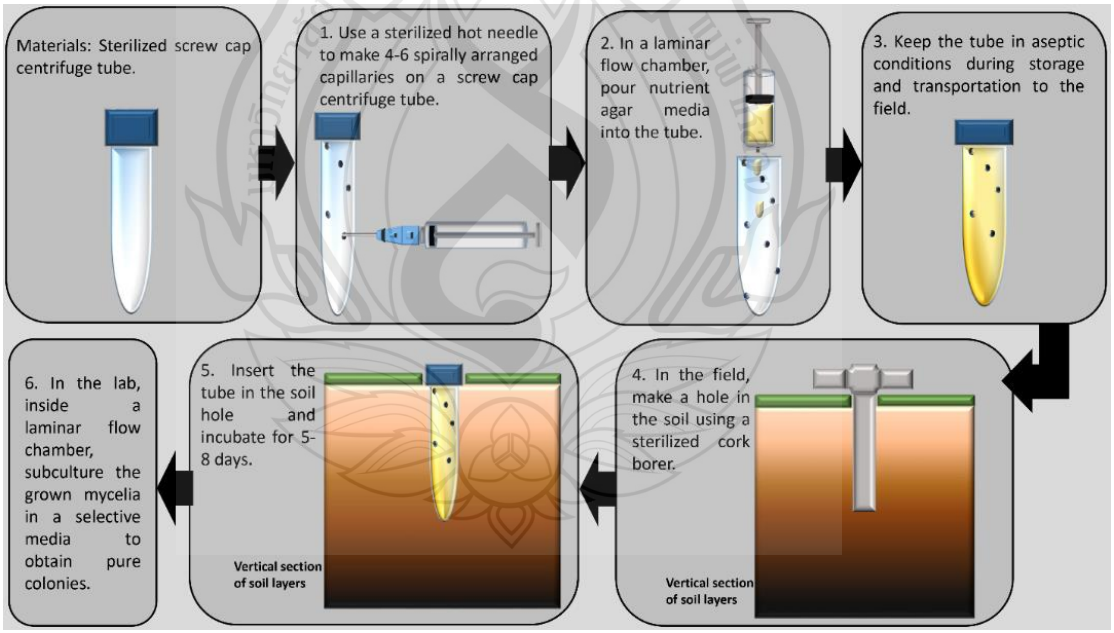


Figure 3.7 Chester's soil immersion tube method for the isolation of soil fungi

3.11 Isolation of Fungal Hyphae Attached to Soil Particles

Most fungal mycelia in soil are attached to larger particles, and removing fine particles eases their observation and isolation from the soil (Warcup, 1955). For the procedure, 1–1.5 g of soil is placed in sterilized water in a part-filled beaker for 4–5 minutes. After that, the crumbled soil particles are broken using a water jet, and the suspension is left to settle for 60–90 seconds. After sedimentation is completed, the excess suspension is removed, and the process is repeated several times until the suspension becomes clear. Finally, a small amount of water is added to the soil sedimentation to create a soil solution, and the solution is distributed across three sterile Petri-dishes. The presence of hyphae attached to the soil is observed using a stereomicroscope. The hyphal masses or parts of hyphae are removed using fine forceps. Then it is deposited on the sterile water drop placed on sterile Petri-dishes, and melted cooled agar is poured over the hyphal water solution. After incubation for a few days at room temperature, hyphae grown on media are transferred to a new sterilized Dox+agar media plate. Ammonium salt, peptone, soil extract, or hydrolysed casein yeast extract can also be added to the medium to stimulate hyphal growth (Warcup, 1955).

3.12 Isolation of Rhizosphere and Mycorrhizal Fungi

Wet sieving and decanting method

Plant nematologists commonly use wet sieving and decanting techniques to extract nematode cysts and larvae from the soil (Triffitt, 1935). Gerdemann and Nicolson (1963) used this method to obtain fungal *Endogone* spores from the soil. This technique consists of suspending 100 g of soil in litre of water, waiting some seconds for the heavier particles to settle, and sieving the suspension by passing it through a 1 mm sieve to remove larger particles of organic matter. The suspension that passes through is stirred to re-suspended. After the heavier particles settle for a few seconds, the decanted liquid is filtered in a sieve fine enough (1–40 µm) to retain the spores. Finally, retained content of all the sieves is transferred to a Petri-dish and examined with a stereoscopic microscope. The spores and

sporocarps identified in the mixture are individually picked up using a flattened needle and placed in a small concave dish of water for further use (Gerdemann & Nicolson, 1963; An et al., 1990; Srinath et al., 2003). Several modifications were introduced, such as the optimal ratio as 1:10 in the soil: water proportion, stirring the suspension by a magnet stir using a water-driven stirrer without heat for 10 minutes, the addition of 0.1–0.5% of Tween 80 and 0.1 M of sodium pyrophosphate if the soil is clay (Pacioni, 1991).

3.13 The Method to Isolate Nematophagous Soil Fungi

Mankau (1975) introduced this method to quantify soil-borne nematophagous fungal colonies. Ten grams of soil are weighed, sieved using a 2 mm mesh, soaked in distilled water for 10 minutes, and suspended in 500 mL of distilled water. The suspension is sieved through graded sieves of 500 µm, 125 µm, and 35 µm. The residue on each sieve is collected into a flask and allowed to stand briefly for the heavy mineral particles to settle, and the remaining suspension is discarded. The residual materials are vacuum-filtered on filter paper discs. The filter paper disks are removed, cut into halves, and each half is placed on a cornmeal agar or water agar plate to obtain colonies (Mankau, 1975; Bailey & Gray, 1989).

3.14 Novel Techniques Introduced to Isolate Soil Fungi

Fungal highway columns method

Fungi and bacteria are involved in many soil interactions. Fungal highways are one such interaction in which bacteria disperse along fungal mycelium. These interactions are still poorly studied (Simon et al., 2015). Simon et al. (2015) introduced this method to identify fungal and bacterial species involved in fungal highway interactions. In the pilot study, Simon et al. (2015) isolated and verified the associations between *Chaetomium globosum* × *Acinetobacter* sp., *Fusarium oxysporum* × *Ochrobactrum* sp. and *Stenotrophomonas maltophilia*, and *Fusarium equiseti* × *Achromobacter spanius*, and *Stenotrophomonas humi*.

The fungal highway column separates coexisting fungi and bacteria in their associations (Simon et al., 2015). The device contains columns with two agar plugs containing culture media (Figure 3.8). The interior of the column is designed to be the nutritional habitat for both fungal and bacterial growth. Within the column, the culture media is separated into two compartments. Filamentous fungi are separately isolated into the top, and bacteria and some other fungi are separated into the underneath compartment (Figure 3.8) (See Simon et al., 2015 for more details). The diversity of isolated fungi depends on the nutrient composition of the media in the column.

For using the fungal highway column, the bottom cap is removed, and the column is placed on the desired substrate and left for 4–10 days. After removing the substrate, the column is immediately closed with another sterilized bottom cap. Directly, or after 8–15 days of incubation, the cap on the top of the column is removed in a sterile environment, and the target culture medium is plated for the isolation of cultivable organisms or directly used for nucleic acids extraction (Simon et al., 2015). Junier et al. (2021) modified this method to isolate soil bacterial-fungal associations.

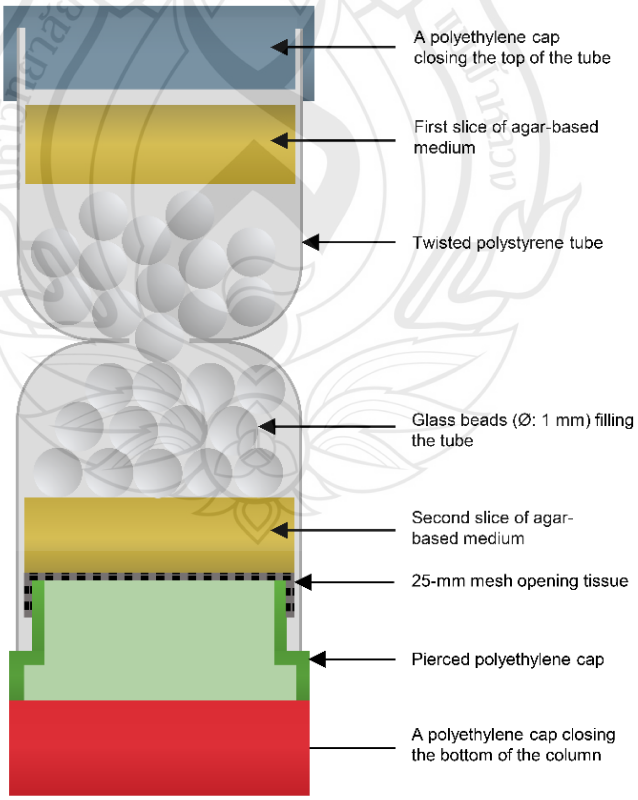


Figure 3.8 Design and parts of the fungal highway column

3.15 A Brief Comparison of Different Isolation Methods

Each culture-dependent method consists of specific procedures and presents unique benefits (Katateladze et al., 2016). Kumar et al. (2015) obtained higher species diversity and abundant sporulation in the dilution plate method over the soil plate method using the same soil samples. Abdullah and Saadullah (2013) stated that the dilution plate method isolates more colonies than the alcohol treatment method. Several *Ascomycota* (*Apisordaria, Chaetomium, Gelasinospora, Neosartoria, Sordaria*, and *Talaromyces*) were obtained using heat and alcohol treatments (Manoch, 1998). The selective isolation of soil *Ascomycota* can be done by heat and chemically pasteurized soils (Warcup, 1951; Warcup & Baker, 1963; Samson & Luiten, 1975; Furuya & Naito, 1979, 1980). Moreover, heat, ethanol, or other organic solvent treatments limit fungal isolations from thin-walled conidia or hyphal fragments and facilitate isolating strains from ascospores, sclerotia, and thick-walled conidia or hyphae (Furuya & Naito, 1980). Furuya and Naito (1980) and Bills et al. (2001) suggested that pre-treating soil with heat or small organic molecules can facilitate ascospore germination in some taxa.

3.16 Sample Collection, Media Selection, Growth Conditions, and Preservation of Cultures from Soil Studies

3.16.1 Soil Sample Collection

Sample collection is the first step in soil fungal studies. Generally, the A1 horizon is collected for biological diversity studies. Before collecting, litter or non-soil materials should be removed from the surface of the collection site. Depending on the purpose, tools such as a shovel, auger, knife, spatula, or spoon can be used (Mueller et al., 2004; Senanayake et al., 2020). The tool of choice and gloves must be sterilized with 70% ethanol and dried before use. Usually, 10–30g of soil is collected from each location; however, this depends on the study objectives. Samples can be separately analysed or homogenized to represent a large study area. Ziploc bags or sterilized bags can store the samples, which should be maintained at 0–10°C during transportation and short-term storage. It is advisable to isolate fungi immediately from the fresh samples

within a few days. Otherwise, soil samples can be air-dried in sterile conditions (laminar flow hood can be used) at 25°C and placed in cold storage or freezers. Temperate soil samples can be stored at -10 to -20°C to eliminate the effects of temporal changes (Mueller et al., 2004).

3.16.2 Media Selection and Growth Conditions

The culture media are critical when growing fungi *in vitro*, mainly because the growth requirements (nutrients, pH, osmotic conditions, and temperature) and patterns differ among taxa (Basu et al., 2015). They can be present as mycelia, non-mycelial spores (chlamydospores), and sexual/asexual spores on the soil that can have different sensitivity to growth media (Tsao & Ocana, 1969). As fungi are substrate-specific, previous knowledge of the sampling location (climate, soil type, soil temperature, and vegetation) is vital for selecting and preparing ideal media (Basu et al., 2015; Kumar et al. 2015).

Both natural media and synthetic media are used for isolation. Because of the low cost and ease of production, the natural media, corn meal agar (CMA), potato dextrose agar (PDA), and dung agar are widely used. However, the nutritional composition range in natural media is undetermined, while synthetic media are produced using precise amounts of ingredients, finely controlled temperature, and pH conditions. However, media selection depends considerably on research objectives and resource availability (Bills et al., 2004; Kumar et al., 2015). Most soil studies use PDA, which is suitable for mycelia growth and facilitates a wide range of taxa (Kumar et al., 2015). Calduch et al. (2004) used potato-carrot and oatmeal agar to grow propagules isolated from the baiting technique. Agar medium has been used as the isolation medium for coexisting fungi and bacteria in the fungal highways method (Simon et al., 2015). Manoch (1998) used GAN in the dilution plate method to obtain cultures, followed by subculturing on PDA and Czapek-Dox agar medium to obtain *Aspergillus* and *Penicillium*. Warcup (1950) mentioned that Czapek-Dox +0.5% yeast extract agar with Phosphoric acid (pH 5.0) is a suitable medium for sporulating and isolating soil fungi.

The pH of the media is critical for inducing the growth of certain taxa while inhibiting others (Chesters & Thornton, 1956). For acidification, sulphur, citric, lactic, and phosphoric acids and alkalization, NaOH are added to the medium (Warcup, 1950; Azaz, 2003; Kazerooni et al., 2017). Antibiotics (penicillin, streptomycin, chloramphenicol, chlortetracycline, oxytetracycline, tetracycline, kanamycin, pimaricin, and vancomycin)

and antimicrobial chemicals (sodium propionate, rose Bengal, crystal violet, malachite green, gallic acid, pentachloronitrobenzene and phenols) are used to exclude and control for unwanted organisms in the media (Tsao, 1970; Hunter et al., 1974). Fungicides or antifungal compounds can select specific taxa and help obtain pure fungal colonies (Tsao & Ocana, 1969; Tsao, 1970; Hunter et al., 1974; Bills et al., 2004). Tsao and Ocana 1969 mentioned that 100 ppm (parts per million) pimaricin and 200 ppm pentachloronitrobenzene could delay or prevent germinating non-pythiaceous taxa, and vancomycin 100 ppm can suppress actinomycetes and bacterial growth in the media, which can successfully isolate soil-dwelling *Phytophthora* species. Dodine has been used to selectively isolate entomopathogenic hyphomycetes from soil, including some of Metarhizium and Beauveria (Fernandes et al., 2010). For isolation of entomopathogenic fungi, glucose, Oxgall, and peptone have been added to the media with antibiotics such as rose Bengal, chloramphenicol, and cycloheximide (Veen & Ferron, 1966). *Trichoderma* selective medium was introduced by Elad et al. (1981), which was developed using chloramphenicol for bacterial inhibition and pentachloronitrobenzene, p-dimethylaminobenzenediazo sodium sulfonate, and rose Bengal for fungal inhibition.

Incubation conditions and storage environment of the isolates need to be set according to the thermo-sensitivity and the photo-sensitivity of the media and the antimicrobial/chemical substances (Tsao & Ocana, 1969). Most polyene antibiotics are photosensitive, and media containing those substances necessary to store/incubate under dark conditions.

Nevertheless, constraints are more critical when isolating and growing extremophiles because many media are unstable above 70°C (Tsudome et al., 2009; Basu et al., 2015). In some successful cases, Durán et al. (2019) isolated psychrotrophic soil fungi that grow above 20°C and psychrophilic soil fungi that grow below 20°C. Carreiro and Koske (1992) used different temperature conditions (0 and 25°C) for isolating extremophiles. At 0°C, many psychrotrophic and some psychrophiles *(e.g.*, *Mortierella* and *Mucor* sp.) were isolated, while mesophiles were isolated at 25°C. Satyanarayana et al. (2019) isolated thermophilic soil fungi at 41–122°C. A porous solid plate made of nano-fibrous cellulose media can be stable at 260°C in 25 MPa, which has the potential for *in vitro* fungi isolation from extreme soils (Tsudome et al., 2009; Basu et al., 2015).

3.16.3 Preservation of Soil Fungal Cultures

Fungal strains can be preserved as fresh materials, dried cultures, and permanent slides (Mueller et al., 2004). Dried cultures and permanent microscope slides are stored at fungaria (Mueller et al., 2004; Senanayake et al., 2020). These preserved strains are labelled with specific numbers with taxonomic and biogeographical data and other metadata such as host, substrate, collector's name, and collected date (Dentinger et al., 2016).

For the preparation of dried cultures, the fungal strains are grown in a water agar medium (2.5% glycerol). Properly labelled strains are subjected to warm air drying or drying in a desiccator. Dried cultures can be stored in wax paper bags with silica gel, paper envelopes, or thin Petri dishes for deposit in the herbarium (Mueller et al., 2004; Silva et al., 2011). These materials can be used for DNA extractions and later morphological studies (Senanayake et al., 2020).

To preserve fungal structures, tissues containing them are mounted on microscopic slides, which can be reused for a long time. This method is beneficial for preserving fungal-type specimens with rare or important morphological structures (Foster et al., 2011). Kohlmeyer and Kohlmeyer (1972) state that the steps involved in this technique are fixation, dehydration, clearing, and mounting. For fixation, 70% alcohol, Bouin's fluid, or formalin is used, and glycerin can be used as the mounting agent. Finally, the slide is sealed using a coverslip and colorless nail polish (Kohlmeyer & Kohlmeyer, 1972; Senanayaka et al., 2020). Fresh culture preservations can be submerged in 70% ethanol, Kew mixture, or Copenhagen solution with glycerol to preserve their living phase (Mueller et al., 2004).

3.17 The Value and Potential of Culturing Soil Fungi

There are significant benefits stemming from culture-dependent methods (Jeewon & Hyde, 2007; Rao et al., 2013). Genomic DNA extractions from pure cultures, sequence data, and phylogenetic analyses enhance the identification accuracy. Currently, DNA extraction from cultures is done by DNA extraction kits (Sanger sequencing) and CTAB methodology (Cetyl trimethylammonium bromide) (Rao et al., 2013; Dissanayake et al., 2020; Wijayawardene et al., 2021). Thus, cultures represent a source of fungal DNA and help to preserve the DNA of the species (Rao et al., 2013;

Rincon-Florez et al., 2013; Wu et al., 2019; Chethana et al., 2020; Wijayawardene et al., 2021). Some culture methods, such as baiting and the "Fungi highway column method," help study the nutritional modes inherent among soil groups. Using different growth media and in vitro conditions is beneficial for detecting slow-growing taxa and observing various cultural characters. Hence, isolation methods are evidence-based research techniques that cannot be overlooked from the toolbox of techniques used for soil fungi identification (Tuininga et al., 2009; Gutleben et al., 2018; Libor et al., 2019).

Therefore, several factors must be considered when designing soil isolation experiments: the number of soil samples and horizons, collection and isolation protocol(s), isolation media(s), culture observations, and suitable preservation methods. Furthermore, the incorporation of expert knowledge and skills of taxonomists is also an essential factor for thorough investigations (Bills et al., 2004). A balance of the above factors will help ensure accuracy in results and minimize human errors (Mueller et al., 2004). In addition, understanding the limitations and challenges of the culture-dependent methods encourages researchers to develop traditional static methods in novel ways. Finally, advanced culture-dependent methods should be initiated more in unusual niches (Kazerooni et al., 2017; Wu et al., 2019).

3.18 New Trends in Soil *Ascomycota* Taxonomy: The Use of HTS in Soil Fungal Studies

Metagenetics uses metabarcoding sequencing to examine the community composition of microorganisms. The nuclear ribosomal internal transcribed spacer (ITS) region is used as the primary barcode marker for fungi, followed by the small (SSU) and large subunit ribosomal ribonucleic acid (LSU) and their combinations (Taberlet et al., 2012; Ji et al., 2013; Chambergo & Valencia, 2016; Gutleben et al., 2018; Nilsson et al., 2019; Tedersoo et al., 2020; Semenov et al., 2021). Numerous sequences are derived from a single sample in the analysis and are present as OTUs (Schoch et al., 2012; Lindahl et al., 2013; Nilsson et al., 2019; Tedersoo et al., 2020). As a result, the HTS approach has been widely used in studies in the most diverse soil biomes (Tedersoo et al., 2014; Prosser, 2015; Thompson et al., 2017; Tedersoo et al., 2020). Specifically, HTS methods have become

affordable and capable of recovering soil fungi from large land areas, specifically in habitats with extreme environmental conditions (Tedersoo et al., 2020), because organisms from oligotrophic soils in Antarctica, dry valleys, glaciers in polar regions, salty lands, and hypersaline microbial mats are difficult to recover *in vitro* (Semenov et al., 2021). Therefore, HTS can reveal fungi, including rare to cryptic taxa, uncultivable fungi, including *Archaeorhizomycetes*, *Cryptomycota*, *Zygomycotina*, and uncultivable symbiotic fungi such as mycorrhizal fungi and nematophagous fungi (Blackwell, 2011; Rosling et al., 2011; Sota et al., 2014; Wu et al., 2019). HTS-generated data can also be used in ecological studies to map the diversity and distribution patterns of soil communities from different environmental conditions and land uses (Lumini et al., 2010; Salvioli & Bonfante, 2013; Franzosa et al., 2015; Tedersoo et al., 2014; Wang et al., 2015; Asemaninejad et al., 2018; Kazerooni, 2017; Schlatter et al., 2018; Bonito et al., 2019; Egidi et al., 2019).

3.18.1 Latest HTS Findings - The Global Soil Mycobiome Consortium Dataset and Endemicity of Soil Fungi

The Global Soil Mycobiome consortium (GSMc) dataset is a ready-to-use fungal HTS dataset derived from global soil sampling (Tedersoo et al., 2021). It provides an overview of the worldwide soil fungal diversity and distribution patterns, supplemented with macroecological metadata. Of all the recently published HTS data, the GSMc dataset is the largest in the number of samples and geographical breadth. It recovered 1,157,667 OTUs and revealed the richness of the fungal kingdom. As per GSMc, belowground fungal functional guilds determined 124,616 OTUs of ectomycorrhizal (EcM), 75,530 OTUs of saprotrophs, 49,521 OTUs of unspecified saprotrophs, and 43.758 OTUs of unspecified pathotrophs (Tedersoo et al., 2021). In the most recent GSMc publication, Tedersoo et al. (2022) used the dataset to study the endemicity and vulnerability of soil fungal species. It revealed that belowground taxa are most vulnerable to droughts and high temperatures, resulting in the prevalence of lifestyle shifts among the pathogenic, mutualistic, and free-living fungal groups. Biotrophic pathogens and EcM species can be highly vulnerable in case of loss of biotic niche due to environmental changes (Tedersoo et al., 2022). The authors suggested the need for habitat conservation, the inclusion of fungi in conservation frameworks to protect the endemic groups, and encouraged soil diversity assessment using HTS technology (Tedersoo et al., 2022).

3.18.2 Limitations of the HTS Methods for Soil Fungal Studies

Despite its wide application, HTS has several drawbacks. Chemical contaminations, such as soil-inherent humic and fulvic acids, can potentially inhibit enzymatic reactions affecting PCR-based DNA amplification or cloning procedures (Lombard et al., 2011; Lindahl et al., 2013). In the studies using HTS, the extraction aims to obtain a total DNA containing extracellular (exDNA) and intracellular DNA (iDNA). However, iDNA provides more reliable genetic information concerning the microbial communities than exDNA (Taberlet et al., 2012; Nagler et al., 2018; Nagler et al., 2021). exDNA can mask genetic information from the iDNA as the DNA portion from intact cells within the total DNA pool is undetermined. Therefore, HTS methods cannot distinguish living and dead materials or active and dormant organisms (Tuininga et al., 2009), thus reducing the reliability of data interpretation for the taxonomic composition of soil microbes (Nagler et al., 2021).

The lack of reference information and sequences in public databases, available bioinformatics tools, and higher error rates (5–13%) are the main limitations of HTS (Tedersoo et al., 2017; Mafune et al., 2019). Likewise, short-read sequences from environmental samples generated by HTS are challenging to align, assign and annotate for further study (Wu et al., 2019; Chethana et al., 2020), making it tough to assign fungal OTUs to lower taxonomic levels, resulting in numerous OTUs named under unclassified taxa (Hongsanan et al., 2018; Wu et al., 2019; Chethana et al., 2020). Comparing the Global Fungi dataset (Větrovský et al., 2020) by Baldrian et al. (2022) and GSMc by Tedersoo et al. (2021), the richness of *Zoopagomycota*, *Entomophthoromycota*, *Blastocladiomycota*, and *Kickxellomycota* showed greater levels of contradictions as a result of different sampling strategies and analytical biases such as the use of different primers for metabarcoding and lack of properly annotated reference sequences (Tedersoo et al., 2021).

In taxonomic assignments, as sequences from environmental samples cannot be correlated to a physical specimen, reproduced, or verified, there is thus a higher possibility for erroneous sequences or dark taxa (Tedersoo et al., 2017; Chethana et al., 2020). In addition, the storage, processing, integration, and interpretation of data using bioinformatics analysis for HTS are all considerably complex, requiring computer power and specialized personnel (Rincon-Florez et al., 2013; Sota et al., 2014; Nilsson et al., 2019; Wu et al., 2019).

3.18.3 Integrating Culture and "Genomics" Techniques to Understand the Taxonomy and Biodiversity of Soil Fungi

Combining culture-based results with molecular-based data can reduce inherent technical errors in HTS and data interpretations and reduce bias in culturing methods (Rincon-Florez et al., 2013; Dissanayake et al., 2018; Jayawardena et al., 2018; Wu et al., 2019; Wijayawardena et al., 2021). Genomics methods recover hidden unculturable diversity and thus can potentially help predesign isolation methodologies to obtain cultures of these taxa (Stefani et al., 2015; Chambergo & Valencia, 2016; Gutleben et al., 2018). HTS can be used to identify fungal secondary metabolite biosynthesis gene clusters from environmental samples, but the cultivation of these strains is essential to obtain the products (Chambergo & Valencia, 2016). Thus, a combination of methods can improve the characterization of taxa for biotechnological use. Bioactive compounds produced by soil fungi are used in bioremediation, food production, and pharmaceutical industries (Muller et al., 2013; Stefani et al., 2015; Gutleben et al., 2018; Hyde et al., 2019). In this regard, Stefani et al. (2015) used HTS to recover strains able to degrade hydrocarbons, of which most were unculturable and thus could not test their hydrocarbon degradation capacity (Stefani et al., 2015). Therefore, the combination of culture-dependent and -independent approaches may provide better insights (Anderson & Cairney, 2014).

CHAPTER 4

THE GENERA OF SOIL *ASCOMYCOTA* WORLDWIDE AND ACCOUNT ON TAXONOMY AND PHYLOGENY OF SOIL-INHABITING SPECIES ISOLATED FROM THAILAND WITH THE EMPHASIS ON UNCOMMON SPECIES

4.1 Introduction

Soil is a heterogeneous medium that is composed of diverse biological, chemical, and physical processes. Thus, it becomes a dynamic living ecosystem, providing niches for a wide range of inhabitants (Bridge & Spooner, 2001; Wagg et al., 2019; Thies & Grossman, 2023). Fungi, one of the dominant colonizers in soil, are eukaryotic microorganisms that play a key role in functional and structural stability in edaphic habitats (Finlay & Thorn, 2019; Niego et al., 2023a; Tedersoo et al., 2021). They function as pathogens, saprobes, and mutualists, contributing to nutrient cycling, plant nutrition, and disease dynamics (Niego et al., 2023b). Their filamentous growth enhances soil aggregation, and they secrete hydrophobic compounds that influence water infiltration (Ritz & Young, 2004; Tedersoo et al., 2014; Wu et al., 2019). The value of fungi to the global economy has been estimated at 54.57 trillion USD based on the major individual products and services of fungi (Niego et al., 2023b).

Identifying and naming fungal groups is important for estimating their numbers, diversity, and functions in soil. The global fungal number is estimated to be around 11.7–13.2 million (Wu et al., 2019), yet only 3–8% have been described at the species level (Blackwell, 2011; Tedersoo et al., 2020; Hyde et al., 2024b) Soil provides a habitat for approximately 59 ± 15% of the species on the earth, where fungi represent the second most species-rich group, accounting for 90% of the total fungal numbers (Anthony et al., 2023). *Ascomycota* is the most widely distributed fungal group in global soils (Tedersoo et al., 2021).

Detecting soil fungi is, however, challenging. Two primary methods are available: culture-dependent and culture-independent approaches (Yasanthika et al., 2022b). Culture-independent methods utilize high-throughput sequencing (HTS) technology to identify taxonomic groups, abundance, community compositions, and unculturable fractions in soil (Wu et al., 2019; Tedersoo et al., 2020). However, HTS identifications are typically limited to higher taxonomic levels. In contrast, culture-dependent methods are integral in identifying the species, as they provide morphological evidence along with living and dry cultures for further studies (Chethana et al., 2020; Senanayake et al., 2020; Yasanthika et al., 2022b). The soil dilution series, direct plating, and baiting methods have commonly been used in recent studies (Senanayake et al., 2020). Using suitable soil fungal isolation methods along with appropriate growth conditions is vital to obtain a diverse collection of fungal strains. Most current research relies on HTS methods, and the potential of culture-dependent methods is often overlooked (Frąc et al., 2018; Mueller et al., 2004; Wijayawardene et al., 2021). As a result, the proportion of cultured fractions remains comparatively low (Wu et al., 2019; Chethana et al., 2020). During the past two decades, new species and genera have been discovered using morpho-molecular studies (Chethana et al., 2020; Wijayawardene et al., 2021; Yasanthika et al., 2022b). However, compiled information on soil fungal genera has not been recently updated (Yasanthika et al., 2022b). Thus, in this study, we provide an updated taxonomic outline and in-depth account of 270 soil-associated *Ascomycota* genera worldwide.

Based on current data, we can predict that soil is a potential substrate for studying fungal taxonomy and diversity (Frąc et al., 2019; Tedersoo et al., 2021). However, below-ground fungi are distributed diversely across various ecosystems worldwide, each with distinct nutritional levels and structures to which fungi have uniquely adapted (Garrett, 2016; Tedersoo et al., 2014, 2021, 2022). They are sensitive to changes in soil ecosystems that are influenced by natural and human activities such as drought, heat, land cover change, and human population pressures (Baldrian et al., 2022a; Tedersoo et al., 2022; Zhang et al., 2023d). Recent studies have predominantly focused on global soil fungi, while country-specific studies are relatively limited (Tedersoo et al., 2021, 2022; Yasanthika et al., 2023). Above-ground fungi are well-studied in regions, such as Australia, China, Europe, North America, South Africa and

Thailand, whereas below-ground fungi are less explored in these areas (Hyde et al., 2020b, 2024a). Different countries have diverse ecosystems, with the tropical regions exhibiting particularly high soil fungal diversity (Hawksworth, 2001; Tedersoo et al., 2022).

Thailand has a tropical climate rich in biodiversity (Baimai, 2010). Current estimates indicate that 55–96% of fungi from northern Thailand are new to science (Hyde et al., 2018), suggesting a high potential for soil fungal diversity (Amma et al., 2018). A HTS-based study by Farias et al. (2023) collected soil samples from different land use types in Thailand, revealing 18,209 fungal operational taxonomic units (OTUs), with Ascomycota being the dominant group, comprising 9,529 OTUs. Hyde et al. (2018) emphasized the need for proper sampling strategies and exploration of the understudied hosts/substrates to discover the missing fungal diversity in Thailand (Hyde et al., 2018). Despite extensive studies on aboveground fungi, the fungal species present in Thai soil remains poorly explored (Tedersoo et al., 2014; Amma et al., 2018; Hyde et al., 2018).

Most research has focused on agricultural lands or forest ecosystems, identifying common fungal groups, such as *Aspergillus*, *Chaetomium*, *Cladosporium*, *Curvularia*, *Fusarium*, *Penicillium*, *Trichoderma*, and *Talaromyces* (Manoch, 1987; 1998; Pornsuriya et al., 2008, 2011; Puangsombat et al., 2010; Eamvijarn et al., 2013; Manoch et al., 2013; Liamthong et al., 2017; Seephueak et al., 2019; Wingfield et al., 2021; Maneeboon et al., 2023). However, there is a shortfall in studying the uncommon groups inhabiting the soil. Given its tropical climate, Thailand has a diverse range of disturbed and undisturbed ecosystems that could harbor rare species (Amma et al., 2018; Farias et al., 2023). Therefore, we selected three understudied soil-based ecosystems in Thailand, forests, caves and urban environments, to identify their uncommon *Ascomycota* groups.

Thailand has significant forest cover that receives high to moderate precipitation. There are mainly two forest types: evergreen and deciduous, both characterized by dense vegetation that retains favorable amounts of water and organic matter (Pomoim et al., 2022; Limsakul et al., 2023; Kruasilp et al., 2024). Those soils replenish the nutritional requirements of fungi, i.e., organic carbon, nitrogen, phosphorus and potassium, contributing to high fungal diversity (Bridge & Spooner,

2001; Tsai et al., 2007; Tedersoo et al., 2022). It is believed that higher soil fungal diversity is found in tropical and deciduous forests, shrubs, and grasslands (Taylor & Sinsabaugh, 2015; Satyanarayana et al., 2019). In global tropical forest soils, *Ascomycota* are prevalent, with *Archaeorhizomycetes*, *Dothideomycetes*, *Eurotiomycetes*, *Orbiliomycetes*, and *Sordariomycetes* classes being highly abundant (Taylor & Sinsabaugh, 2015; Tedersoo et al., 2014). While Ascomycota dominate the phyllosphere, data on soil-dwelling taxa in the tropical forest in Thailand are lacking (Izuno et al., 2016). Some studies have identified species belonging to *Aspergillus*, *Penicillium*, and *Fusarium*, highlighting the need to explore uncommon groups (Amma et al., 2018). Thus, we studied uncommon *Ascomycota* from undisturbed forests in northern and southern regions of Thailand.

Natural caves are widely spread in Thailand (Martin & Ritchie, 2020). Karst cave ecosystems are characterized by dark, relatively cool, humid, nutrient-limited conditions, where fungi have adapted to extreme oligotrophic environments (Preedanon et al., 2023; Suetrong et al., 2023) (Preedanon et al., 2023). Typically, these caves contain thin layers of soil and exhibit extensive spatial heterogeneity (Suetrong et al., 2023). Natural caves can be disturbed by farming, tourism, and changes in water flow, which can negatively impact the highly adapted cave organisms (Bai et al., 2020; Ren et al., 2021). Species of *Allophoma*, *Arthroderma*, *Aspergillus*, *Fusarium*, *Penicillium*, *Pyrenochaetopsis*, *Trichoderma*, and *Tritirachium* have been isolated from cave soils globally (Castrillón et al., 1976; Taylor et al., 2013; Cunha et al., 2020; Zhang et al., 2021; Preedanon et al., 2023). However, studies on cave-dwelling fungi remain scarce globally (Ren et al., 2021). Although new animal and insect species have been discovered in Thai caves (Bolger & Ellis, 2015; Preedanon et al., 2023; Deharveng et al., 2023), studies on associated fungal species are limited (Preedanon et al., 2023). Thus, we have investigated soil *Ascomycota* from undisturbed and disturbed cave ecosystems in Thailand.

Soils affected by rapid urbanization, industrialization, and agriculture undergo nutritional fluctuations, which in turn affect their fungal inhabitants (Zhang et al., 2019b; Rusterholz & Baur, 2023). Thailand is rapidly urbanizing, but the fungi inhabiting urban areas remain poorly studied. Simmons (2004) reported that urban soils in Thailand may contain significant amounts of organic and inorganic pollutants.

Fungal groups that can thrive in these conditions are beneficial for maintaining soil health (Zhang et al., 2019b). Previous studies have indicated that cultivated and urban soil ecosystems generally have low species richness (Taylor & Sinsabaugh, 2015; Satyanarayana et al., 2019). Thus, we have selected urban areas in northern Thailand to study below-ground *Ascomycota*.

During our study of *Ascomycota* species inhabiting soils, we have focused on three distinct soil-based localities (forests, caves and urban areas) in Thailand. To obtain a more diverse fungal collection, we aimed to collect samples from both disturbed and undisturbed habitats within these ecosystems. This study provides a comprehensive taxonomic investigation of 30 *Ascomycota* fungal species.

2.1 Outline of *Ascomycota* from Soil

The outline follows the latest *Outline of Fungi and fungus-like organisms* in Hyde et al. (2024c)

Phylum:	***Ascomycota*** Caval.-Sm
Subphylum:	***Pezizomycotina*** O.E. Erikss. & Winka
Class:	***Dothideomycetes*** O.E. Erikss. & Winka
Subclass:	***Dothideomycetidae*** P.M. Kirk, P.F. Cannon, J.C. David & Stalpers ex C.L. Schoch, Spatafora, Crous & Shoemaker
Order:	***Cladosporiales***
Family:	***Cladosporiaceae*** Chalm. & R.G. Archibald
	Cladosporium Link
Order:	***Mycosphaerellales*** (Nannf.) P.F. Cannon
Family*:*	***Dissoconiaceae*** Crous & de Hoog
	Ramichloridium Stahel ex de Hoog
Family:	***Extremaceae*** Quaedvl. & Crous
	Pseudoramichloridium Cheewangkoon & Crous
Family*:*	***Mycosphaerellaceae*** Lindau
	Neoceratosperma Crous & Cheew.

Family:	***Piedraiaceae*** Viégas ex Cif., Bat. & S. Camposa
	Piedraia Fonseca & Leão
Family*:*	***Saccotheciaceae*** Bonord.
	Aureobasidium Viala & G. Boyer
Family:	***Teratosphaeriaceae*** Crous & U. Braun
	Acidiella Hujslová & M. Kolařík
	Devriesia Seifert & N.L. Nick
Subclass:	***Pleosporomycetidae*** C.L. Schoch, Spatafora, Crous & Shoemaker
Order:	***Pleosporales*** Luttrell ex M.E. Barr
Family*:*	***Acrocalymmaceae*** Crous & Trakun.
	Acrocalymma Alcorn & J.A.G. Irwin
Family*:*	***Amorosiaceae*** Thambug. & K.D. Hyde
	Amorocoelophoma Jayasiri, E.B.G. Jones & K.D. Hyde
Family*:*	***Anteagloniaceae*** K.D. Hyde, J.K. Liu & A. Mapook
	Anteaglonium Mugambi & Huhndorf
Family*:*	***Astrosphaeriellaceae*** Phook. & K.D. Hyde (=Caryosporaceae) Huang Zhang, K.D. Hyde & Ariyaw.)
	Pithomyces Berk. & Broome
Family*:*	***Coniothyriaceae*** W.B. Cooke
	Coniothyrium Corda
Family:	***Corynesporascaceae*** Sivan.
	Corynespora Güssow
Family*:*	***Cucurbitariaceae*** G. Winter (= *Fenestellaceae* M.E. Barr)
	Neocucurbitaria Wanas., E.B.G. Jones & K.D. Hyde
Family*:*	***Dictyosporiaceae*** Boonmee & K.D. Hyde
	Neodendryphiella Iturrieta-González

Family*:* ***Didymellaceae*** Gruyter, Aveskamp & Verkley
(=*Microsphaeropsidaceae* Qian Chen et al.)
Ascochyta Lib. (= *Heracleicola* Tibpromma, Camporesi & K.D. Hyde)
Cumuliphoma Valenz.-Lopez, Stchigel, Crous, Guarro & Cano
Didymella Sacc. ex D. Sacc.
Ectophoma Valenz.-Lopez, Cano, Crous, Guarro & Stchigel
Epicoccum Link
Juxtiphoma Valenzuela-Lopez, Cano, Crous, Guarro & Stchigel
Neoascochyta Q. Chen & L. Cai
Neodidymelliopsis Q. Chen & L. Cai
Nothophoma Q. Chen & L. Cai
Paraboeremia Q. Chen & L. Cai
Pseudoascochyta Valenz.-Lopez, Stchigel, Cano-Canals, Guarro & Cano
Remotididymella Valenz.-Lopez, Crous, Cano, Guarro & Stchigel
Stagonosporopsis Died.
Vandijckomycella Hern.-Restr., L.W. Hou, L. Cai & Crous
Xenodidymella Q. Chen & L. Cai

Family*:* ***Didymosphaeriaceae*** Munk
Alloconiothyrium Verkley, Göker & Stielow
Bimuria D. Hawksw
Didymocrea Kowalski
Neptunomyces M. Gonçalves, T. Vicente & A. Alves
Paraconiothyrium Verkley
Phaeodothis Syd. & P. Syd.
Pseudopithomyces Ariyaw. & K.D. Hyde
Spegazzinia Sacc.

Family*:* ***Latoruaceae*** Crous

Latorua Crous

Matsushimamyces Rahul Sharma & Rohit Sharma

Multiverruca H.Y. Wang, Y.F. Han & Z.Q. Liang

Polyschema H.P. Upadhyay

Family*:* ***Lentimurisporaceae*** N.G. Liu, J.K Liu & K.D. Hyde

Bahusandhika Subram

Family*:* ***Leptosphaeriaceae*** M.E. Barr

Leptosphaeria Ces. & De Not.

Family*:* ***Neocamarosporiaceae*** Wanas., Wijayaw., Crous & K.D. Hyde

Neocamarosporium Crous & M.J. Wingf.

Family*:* ***Nigrogranaceae*** Jaklitsch & Voglmayr

Nigrograna Gruyter, Verkley & Crous

Family*:* ***Phaeosphaeriaceae*** M.E. Barr

Paraleptospora Mapook & K.D. Hyde

Setophoma Gruyter, Aveskamp & Verkley

Family*:* ***Pleosporaceae*** Nitschke

Alternaria Nees

Bipolaris Shoemaker

Curvularia Boedijn

Pyrenophora Fr.

Family: ***Pseudopyrenochaetaceae*** Valenz.-López, Crous, Stchigel, Guarro & J.F. Cano

Pseudopyrenochaeta Valenzuela-López, Crous, Stchigel, Guarro & Cano

Family*:* ***Pyrenochaetopsidaceae*** Valenz.-López, Crous, Cano, Guarro & Stchigel

Neopyrenochaeta Valenz.-Lopez, Crous, Stchigel, Guarro & Cano

Pyrenochaetopsis Gruyter, Aveskamp & Verkley

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

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

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

Roussoella Sacc.

Family*:* ***Sporormiaceae*** Munk

Preussia Fuckel

Westerdykella Stolk

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

Tetraploa Berk. & Broome

Family*:* ***Torulaceae*** Corda

Torula Pers.

Pleosporales genera incertae sedis

Setophaeosphaeria Crous & Y. Zhang ter

Dothideomycetes* orders *incertae sedis

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

Family: ***Botryosphaeriaceae*** Theiss. & H. Syd. (=

Endomelanconiopsidaceae Tao Yang & Crous**)**

Lasiodiplodia Ellis & Everh.

Order: ***Eremomycetales*** Crous, Spatafora, Haridas & I.V. Grig.

Family*:* ***Eremomycetaceae*** Malloch & Cain

Arthrographis G. Cochet ex Sigler & J.W. Carmich

Rhexothecium Samson & Mouch

Order: ***Muyocopronales*** Mapook, Boonmee & K.D. Hyde

Family*:* ***Muyocopronaceae*** K.D. Hyde

Arxiella Papendorf

Leptodiscella Papendorf

Order: ***Phaeotrichales*** Ariyaw., Jian K. Liu & K.D. Hyde

Family*:* ***Phaeotrichaceae*** Cain

Phaeotrichum Cain & M.E. Barr

Order: ***Trypetheliales*** Lücking Aptroot & Sipman.

Family*:* ***Trypetheliaceae*** Zenker (= *Arthopyreniaceae* Walt. Watson)

Aptrootia Lücking & Sipman

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

Family*:* ***Sympoventuriaceae*** Y. Zhang ter, C.L. Schoch & K.D. Hyde

Guizhoumyces T.P. Wei & Y.L. Jiang

Matsushimaea Subram.

Scolecobasidium E.V. Abbott

Verruconis Samerp., H.J. Choi, van den Ende, Horré & de Hoog

Dothideomycetes families incertae sedis

Family*:* ***Pseudorobillardaceae*** Crous

Pseudorobillarda M. Morelet

Dothideomycetes genera incertae sedis

Bahusakala Subram.

Monodictys S. Hughes

Class: ***Eurotiomycetes*** Tehler ex O.E. Eriksson & K. Winka

Subclass: ***Chaetothyriomycetidae*** Doweld

Order: ***Chaetothyriales*** M.E. Barr

Family*:* ***Herpotrichiellaceae*** Munk

Cladophialophora Borelli

Exophiala J.W. Carmich.

Phialophora Medlar

Rhinocladiella Nannf.

Veronaea Cif. & Montemart.

Subclass: ***Eurotiomycetidae*** Geiser & Lutzoni

Order: ***Eurotiales*** G.W. Martin ex Benny & Kimbr.

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

Aspergillus P. Micheli ex Haller

Hamigera Stolk & Samson

Penicillium Link

Family*:*	***Thermoascaceae*** Apinis
	Paecilomyces Bainier
	Thermoascus Miehe
Family*:*	***Trichocomaceae*** E. Fisch.
	Sagenomella W. Gams
	Talaromyces C.R. Benj.
Order:	***Onygenales*** Cif. ex Benny & Kimbr.
Family*:*	***Ajellomycetaceae*** Unter., J.A. Scott & Sigler
	Blastomyces Gilchrist & W.R. Stokes (=*Ajellomyces* McDonough & A.L Lewis; Emmonsia Cif. & Montemart.)
	Emergomyces Dukik, Sigler & de Hoog
	Emmonsiellopsis Y. Marín, Stchigel
Family*:*	***Arthrodermataceae*** Currah
	Arthroderma Curr. & Berk.
	Ctenomyces Eidam
	Microsporum Gruby
	Nannizzia Stockdale
	Trichophyton Malmsten
Family*:*	***Gymnoascaceae*** Baran.
	Arachniotus J. Schröt
	Gymnascella Peck
	Gymnoascoideus G.F. Orr, K. Roy & G.R. Ghosh
	Gymnoascus Baran.
	Kraurogymnocarpa Udagawa & Uchiyama
	Narasimhella Thirumalachar & Mathur.
	Pseudoarachniotus Kuehn
	Sporendonema Desm

Family*:*	***Malbrancheaceae*** Kandemir & de Hoog
	Malbranchea Sacc.
Family*:*	***Neogymnomycetaceae*** Kandemir & de Hoog
	Auxarthronopsis Sharma
	Canomyces Rahul Sharma & Shouche
	Currahmyces Rahul Sharma & Shouche
	Renispora Sigler & J.W. Carmich.
Family*:*	***Onygenaceae*** Berk.
	Amauroascus J. Schröt.
	Aphanoascus Zukal
	Brunneospora Guarro & Punsola
	Coccidioides G.W. Stiles
	Keratinophyton Randhawa & Sandhu
	Pectinotrichum Varsavsky & G.F. Orr
	Pseudoamauroascus Cano, M. Solé & Guarro
Family*:*	***Spiromastigoidaceae*** Guarro, Cano & Stchigel.
	Pseudospiromastix Guarro, Stchigel & Cano
	Spiromastigoides Doweld
Class:	***Lecanoromycetes*** O.E. Erikss. & Winka
Subclass	***Ostropomycetidae*** V. Reeb, Lutzoni & Cl. *Roux*
Order:	***Graphidales*** Bessey
Family:	***Diploschistaceae*** Zahlbr.
	Diploschistes Norman
Class:	***Leotiomycetes*** O.E. Erikss. & Winka
Order:	***Helotiales*** Nannf. ex Korf & Lizoň (= *Cyttariales* Luttr. ex Gamundí**)**
Family*:*	***Amorphothecaceae*** Parbery
	Amorphotheca Parbery
Family:	***Discinellaceae*** Ekanayaka & K.D. Hyde

Acidea Hujslová & M. Kolařík

Family: ***Hyphodiscaceae*** Ekanayaka & K.D. Hyde

Soosiella Hujslova & M. Kolarık

Family*:* ***Myxotrichaceae*** Currah

Byssoascus Arx

Myxotrichum Kunze

Oidiodendron Robak

Family*:* ***Sclerotiniaceae*** Whetzel ex Whetzel

Botrytis P. Micheli ex Pers.

Sclerotinia Fuckel

Helotiales* genera *incertae sedis

Cadophora Lagerb. & Melin

Scytalidium Pesante

Class: ***Lichinomycetes*** V. Reeb, Lutzoni & Cl. Roux

(= *Candelariomycetes* Voglmayr & Jaklitsch;

= *Coniocybomycetes* M. Prieto & Wedin; = *Geoglossomycetes*

Zheng Wang, C.L. Schoch &

Spatafora; *Sareomycetes* Beimforde, A.R. Schmidt, Rikkinen

& J.K. Mitch.

Order: ***Geoglossales*** Zheng Wang, C.L. Schoch & Spatafora

Family*:* ***Geoglossaceae*** Corda

Hemileucoglossum Arauzo

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

Order: ***Orbiliales*** Baral, O.E. Erikss., G. Marson & E. Weber

Family*:* ***Orbiliaceae*** Nannf.

Arthrobotrys Corda

Class: ***Pezizomcetes*** O.E. Erikss. & Winka

Order: ***Pezizales*** J. Schröt.

Family*:* ***Ascodesmidaceae*** J. Schröt.

Cephaliophora Thaxt.

Family*:* ***Pezizaceae*** Dumort. (= *Carbomycetaceae* Trappe)

Peziza Dill. ex Fr.

Family*:* ***Pyronemataceae*** Corda (= *Otideaceae* Eckblad)

Lotinia Pérez-Butrón

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

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

Order: ***Calosphaeriales*** M.E. Barr

Family: ***Calosphaeriaceae*** Munk

Jattaea Berl.

Family*:* ***Pleurostomataceae*** Réblová, L. Mostert, W. Gams & Crous

Pleurostoma Tul. & C. Tul

Order: ***Diaporthales*** Nannf.

Family*:* ***Diaporthosporellaceae*** C.M. Tian & Q. Yang

Diaporthosporella C.M. Tian & Q. Yang

Order: ***Magnaporthales*** Thongk., Vijaykr. & K.D. Hyde

Family*:* ***Magnaporthaceae*** P.F. Cannon

Falciphoriella M. Hern.-Restr. & Crous

Order: ***Myrmecridiales*** Crous

Family*:* ***Myrmecridiaceae*** Crous

Myrmecridium Arzanlou, W. Gams & Crous

Order: ***Ophiostomatales*** Benny & Kimbr.

Family*:* ***Ophiostomataceae*** Nannf.

Leptographium Lagerb. & Melin (= *Grosmannia* Gold.)

Sporothrix Hektoen & C.F. Perkins

Diaporthomycetidae families incertae sedis

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

Brunneochlamydosporium Giraldo López & Crous

Chordomyces Bilanenko, Georgieva & Grum-Grzhim

Furcasterigmium Giraldo López & Crous

Fuscohypha Giraldo López & Crous

Gibellulopsis Bat. & H. Maia

Lectera P.F. Cannon

Paramusicillium Giraldo López & Crous

Phialoparvum Giraldo López & Crous

Plectosphaerella Kleb.

Sayamraella Giraldo López & Crous

Sodiomyces A.A. Grum-Grzhim

Stachylidium Link, Mag. Gesell. naturf. Freunde

Summerbellia Giraldo López & Crous

Verticillium Nees

Trichosphaeriaceae genera incertae sedis

Acrostalagmus Corda

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

Order: ***Coronophorales*** Nannf.

Family: ***Ceratostomataceae*** G. Winter

Dactylidispora Y. Marín, Stchigel

Echinusitheca Y. Marín

Vittatispora Chaudhary P.

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

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

Colletotrichum Corda

Order: ***Hypocreales*** Lindau

Family*:* ***Acremoniopsidaceae*** M. Li, M. Raza & L. Cai

Acremoniopsis A. Giraldo, Gené & Guarro

Family*:* ***Bionectriaceae*** Samuels & Rossman

Acremonium Link

Amphichorda Fr.

Clonostachys Corda

Emericellopsis J.F.H. Beyma

Family*:* ***Clavicipitaceae*** (Lindau) Earle ex Rogerson

Keithomyces Samson, Luangsa-ard & Houbraken

Marquandomyces Samson, Houbraken & Luangsa-ard
Metapochonia Kepler, S.A. Rehner & Humber
Metarhizium Sorokīn (= *Chamaeleomyces* Sigler; = *Metacordyceps* G.H. Sung, J.M. Sung, Hywel Jones & Spatafora; = *Nomuraea* Maubl.; = *Stereocrea* Syd. & P. Syd.)
Pochonia Bat. & O.M. Fonseca
Romanoa Thirum.

Family*:* ***Cordycipitaceae*** Kreisel ex G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora
Beauveria Vuill.
Cordyceps (Fr.) Link (= *Isaria* Pers.; = *Microhilum* H.Y. Yip & A.C Rath)
Gamszarea Z.F. Zhang & L. Cai
Lecanicillium W. Gams & Zare
Simplicillium W. Gams & Zare

Family*:* ***Hypocreaceae*** De Not.
Kiflimonium Summerb., J.A. Scott, Guarro & Crous
Trichoderma Pers.

Family*:* ***Myrotheciomycetaceae*** Crous
Trichothecium Link

Family*:* ***Nectriaceae*** Tul. & C. Tul.
Calonectria De Not.
Cylindrocladiella Boesew.
Fusarium Link
Mariannaea G. Arnaud ex Samson
Nectria (Fr.) Fr.
Neocosmospora E.F. Sm.
Paracremonium L. Lombard & Crous

Family*:* ***Ophiocordycipitaceae*** G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora
Purpureocillium Luangsa-ard, Hywel-Jones, Houbraken & Samson

Ophiocordyceps Petch

Tolypocladium W. Gams

Family: ***Polycephalomycetaceae*** G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

Polycephalomyces Kobayasi

Family*:* ***Stachybotryaceae*** L. Lombard & Crous

Brevistachys L. Lombard & Crous

Didymostilbe Henn.

Memnoniella Höhn.

Myrothecium Tode

Stachybotrys Corda

Order: ***Microascales*** Luttr. ex Benny & Kimbr.

Family*:* ***Ceratocystidaceae*** Locq. ex Réblová, W. Gams & Seifert

Ceratocystis Ellis & Halst.

Family*:* ***Graphiaceae*** De Beer

Graphium Corda

Family*:* ***Microascaceae*** Luttr. ex Malloch

Acaulium Sopp

Cephalotrichum Link

Gamsia M. Morelet

Lomentospora Hennebert & B.G. Desai

Microascus Zukal

Petriella Curzi

Pseudallescheria Negroni & I. Fisch.

Scopulariopsis Bainier

Scedosporium Sacc. ex Castell. & Chalm.

Wardomyces F.T. Brooks & Hansf.

Wardomycopsis Udagawa & Furuya

Yunnania H.Z. Kong

Triadelphiaceae Y.Z. Lu, J.K. Liu, Z.L. Luo & K.D. Hyde

Triadelphia Shearer & J.L. Crane

Subclass:	***Sordariomycetidae*** O.E. Erikss & Winka (= *Meliolomycetidae* P.M. Kirk & K.D. Hyde)
Order:	***Cephalothecales*** Maharachch. & K.D. Hyde
Family*:*	***Cephalothecaceae*** Höhn.
	Victoriomyces D. Davolos, B. Pietrangeli, A.M. Persiani & O. Maggi
Order:	***Chaetosphaeriales*** Huhndorf, A.N. Mill. & F.A. Fernández
Family*:*	***Chaetosphaeriaceae*** Réblová, M.E. Barr & Samuels
	Caligospora Réblová
	Chaetosphaeria Tul. & C. Tul.
	Chloridium Link (*Chloridium=Gonytrichum*)
	Dinemasporium Lév.
	Kionochaeta P.M. Kirk & B. Sutton
	Menispora Pers.
	Thozetella Kuntze
	Verhulstia Hern.-Restr.
Order:	***Coniochaetales*** Huhndorf, A.N. Mill. & F.A. Fernández (= *Cordanales* M. Hern.-Rest. & Crous)
Family*:*	***Coniochaetaceae*** Malloch & Cain
	Coniochaeta (Sacc.) Cooke
Family*:*	***Cordanaceae*** Nann.
	Cordana Preuss
Order:	***Sordariales*** Chad. ex D. Hawksw. & O.E. Erikss.
Family*:*	***Chaetomiaceae*** G. Winter
	Achaetomium J.N. Rai, Tewari & Mukerji
	Arxotrichum A. Nováková & M. Kolařik
	Chaetomium Kunze
	Humicola Traaen
	Staphylotrichum J.A. Mey. & Nicot
	Stellatospora T. Ito & A. Nakagiri
	Thielavia Zopf

Trichocladium Harz

Family: ***Diplogelasinosporaceae*** Y. Marin & Stchigel

Diplogelasinospora Cain

Family: ***Naviculisporaceae*** Y. Marin & Stchigel

Naviculispora Stchigel, Y. Marín, Cano & Guarro

Family*:* ***Podosporaceae*** X. Wei Wang & Houbraken

Cladorrhinum Sacc. & Marchal

Podospora Ces.

Triangularia Boedijn (= *Apiosordaria* Arx & W. Gams)

Family: ***Schizotheciaceae*** Y. Marin & Stchigel

Jugulospora N. Lundq.,

Lundqvistomyces Y. Marin & Stchigel

Family*:* ***Sordariaceae*** G. Winter

Boothiella Lodhi & Mirza

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

Pseudoneurospora Dania García, Stchigel & Guarro

Sordaria Ces. & De Not.

Sordariales* genera *incertae sedis

Eosphaeria Höhn.

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

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

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

Arthrinium Kunze

Nigrospora Zimm.

Family*:* ***Beltraniaceae*** Nann.

Beltraniella Subram.

Family*:* ***Sporocadaceae*** Corda

Bartalinia Tassi

Broomella Sacc.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous

Robillarda Sacc.

Order: ***Xylariales*** Nannf.

Family*:* ***Coniocessiaceae*** Asgari & Zare

Coniocessia Dania García, Stchigel, D. Hawksw. & Guarro

Family*:* ***Hansfordiaceae*** Crous

Hansfordia S. Hughes

Family*:* ***Microdochiaceae*** Hern.-Restr., Crous & J.Z. Groenew.

Idriella P.E. Nelson & S. Wilh. (=*Monographella* Petr.)

Microdochium Syd.

Family*:* ***Xylariaceae*** Tul. & C. Tul.

Ascotricha Berk.

Coniolariella Asgari & Zare

Xylaria Hill ex Schrank

Sordariomycetes orders incertae sedis

Order: ***Amplistromatales*** M.J. D'souza, Maharachch. & K.D. Hyde

Family*:* ***Amplistromataceae*** Huhndorf, A.N. Mill., Greif & Samuels

Acidothrix Hujslová & M. Kolařík

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

Class: ***Dipodascomycetes*** M. Groenew., Hittinger, Opulente & A. Rokas

Order: ***Dipodascales*** M. Groenew., Hittinger, Opulente & A. Rokas

Family ***Trichomonascaceae*** Kurtzman & Robnett

Trichomonascus H.S. Jackson emend. Kurtzman & Robnett

Zygoascus M.T. Sm.

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

Order: ***Pichiales*** M. Groenew., Hittinger, Opulente & A. Rokas

Family: ***Pichiaceae*** Zender

Ogataea Y. Yamada, K. Maeda & Mikata

Pichia E.C. Hansen

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

Order: ***Ascoideales*** J.H. Schaffner

Family*:* ***Saccharomycopsidaceae*** Arx & Van der Walt

Saccharomycopsis Schiønning

Order: ***Saccharomycodales*** M. Groenew., Hittinger, Opulente & A. Rokas

Family*:* ***Saccharomycodaceae*** Kudryavtsev

Hanseniaspora Zikes

Ascomycota* genera *incertae sedis

Effetia Bartoli, Maggi & Persiani

Heterocephalum Thaxt.

Gilmaniella G.L. Barron

Phaeotrichoconis Subram.

Solosympodiella Matsush.

4.2 Genera Notes and the Taxonomy of Soil *Ascomycota*

Phylum: ***Ascomycota*** Caval.-Sm.

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

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

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

Order: ***Cladosporiales*** Abdollahz. & Crous

Family: ***Cladosporiaceae*** Chalm. & R.G. Archibald

Cladosporium Link, Mag. Gesell. naturf. Freunde, Berlin 7: 37 (1816) [1815].

Figure 4.1

For synonyms, see Species Fungorum (2025)

Index Fungorum number: IF 7681; Facesoffungi number: FoF 06967

Link (1816) introduced *Cladosporium*, with *C. cladosporioides* as the type species. The genus comprises three major complexes: *C. cladosporioides*, *C. herbarum*, and *C. sphaerospermum* (Dugan et al., 2008; Bensch et al., 2012). Currently, around 200 species are listed in the Species Fungorum (2025). The asexual morph is hyphomycetous, having coronate conidiogenous loci and catenate conidia with hila,

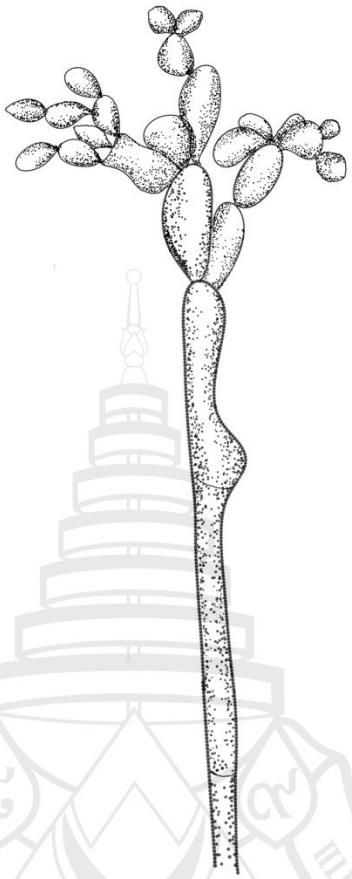
consisting of a convex central dome surrounded by a raised periclinal rim (Bensch et al., 2012). Arrangements of conidial chains facilitate the mass spreading of conidia over long distances. Species can be found as plant endophytes, human and plant pathogens, and also as hyper-parasites on other fungi (Bensch et al., 2012; Schubert & Braun, 2005). They have a worldwide distribution, including air, animals, food, sludge, soil, and water (Bensch et al., 2012; Domsch et al., 1993; Ma et al., 2017). Species exhibit halotolerance, osmotolerance, thermotolerance, and psychrophilic properties (Ma et al., 2017).

Table 4.1 *Cladosporium* species isolated from soil

Species	Country	Habitat or soil type	References
Cladosporium cladosporioides	Denmark	Pea field soil	Bensch et al. (2012)
C. cladosporioides	Brazil	ND	
C. longissimum	Papua New Guinea	Soil along the coral reef coast	
C. oxysporum	China	Terracotta sculpture site	
C. pseudocladosporioides	Chile	ND	
C. sphaerospermum	Antarctic	Ornithogenic soil near a lake	
C. tenuissimum	Indonesia	Bat cave	
C. cladosporioides	China	Plateau soils	Ma et al. (2017)
C. herbarum			
C. neopsychrotolerans			
C. paralimoniforme			
C. prolongatum			
C. sinuatum,			
C. tianshanense,			
C. verruculosum			
C. fuscoviride	Spain	Garden soil	Iturrieta-González et al. (2021)
C. pseudotenellum			
Cladosporium sp.	Papua New Guinea	Coral reef coast soil	Zalar et al. (2007)
C. sphaerospermum	Canada	ND	
C. speluncae	Brazil	Cave soil	Dutra et al. (2023)

Note ND= The information is not available

a



Note Redrawn from Domsch et al. (1993)

Figure 4.1 *Cladosporium cladosporioides* a. Conidiophores and conidia

Order: ***Mycosphaerellales*** (Nannf.) P.F. Cannon

Family: ***Dissoconiaceae*** Crous & de Hoog

Ramichloridium Stahel ex de Hoog, Stud. Mycol. 15: 59. 1977.

Figure 4.2

Index Fungorum number: IF 9690; Facesoffungi number: FoF 06941

Hoog (1977) introduced *Ramichloridium* and typified by *R. apiculatum*. Species Fungorum (2025) lists 23 species under this genus, while seven species have molecular data (Hongsanan et al., 2020a). Arzanlou et al. (2007) provided a morphological and phylogenetic revision (based on LSU and ITS gene regions) for *Ramichloridium* with a key to ramichloridium-like genera. This is an anamorphic genus with a hyphomycetous asexual morph. It is characterized by having dark brown, straight, unbranched or rarely branched, thick-walled conidiophores with continuous or several

additional thin septa. Conidiogenous cells are polyblastic, terminal, integrated, smooth, thick-walled, golden-brown, apical part sub-hyaline with sympodial proliferation, straight or flexuous, geniculate or nodose, conspicuous; scars are crowded or scattered, unthickened, unpigmented to faintly pigmented, or slightly prominent denticles. Conidia are solitary, 0–1-septate, sub-hyaline to pale brown, smooth to coarsely verrucose, thin-walled, obovate, obconical or globose to ellipsoidal, fusiform with a somewhat prominent, slightly pigmented hilum and conidial secession is schizolytic (de Hoog, 1977). Species are found in various habitats, including air, plants and soil, as endophytes, saprobes and plant and human pathogens recorded in Saudi Arabia, China, Denmark, UK, India, Malaysia and Seychelles (Arzanlou et al., 2007; Hongsanan et al., 2020a; Salvatore et al., 2022). *Ramichloridium apiculatum* is known for producing a rapicone that leads to post-harvest losses in apples and pears (Salvatore et al., 2022).

Table 4.2 *Ramichloridium* species isolated from soil

Species	Country	Habitat or soil type	References
Ramichloridium apiculatum	Georgia	Forest soil	Arzanlou et al. (2007)
R. apiculatum	Pakistan	ND	

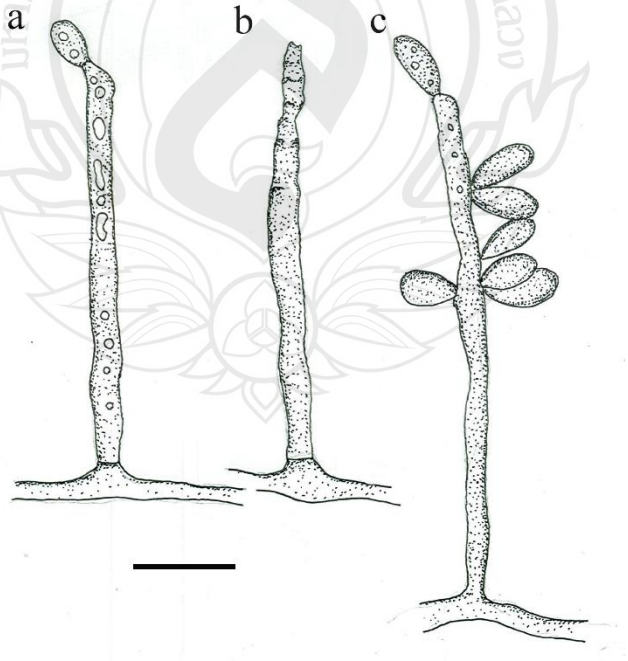


Figure 4.2 *Ramichloridium apiculatum* (CBS 156.59)

a–c Conidiophores with sympodial proliferating conidiogenous cells and conidia. Scale bar: a–c = 10 μm. Redrawn from Arzanlou et al. (2007).

Family: *Extremaceae* Quaedvl. & Crous

Pseudoramichloridium Cheewangkoon & Crous, Persoonia 23: 75 (2009).

Figure 4.3

Index Fungorum number: IF 513854; Facesoffungi number: FoF 06851

Pseudoramichloridium was established by Cheewangkoon et al. (2009) with *P. henryi* as the designated type. Currently, three species are listed under *Pseudoramichloridium* (Species Fungorum, 2025); two species with molecular data. Cheewangkoon et al. (2009) provided the phylogenetic analyses based on LSU to infer its placement in *Teratosphaeriaceae*. The genus was subsequently transferred to *Extremaceae* based on the phylogenetic revision of Quaedvlieg et al. (2014). The asexual morph is hyphomycetous and characterized by unbranched, slightly thick-walled, *darker* conidiophores with sympodially proliferating, polyblastic, integrated, terminal, conidiogenous cells. Conidia are subhyaline to pale brown, aseptate, obovoid to fusiform, smooth to verruculose, thin-walled and smooth to slightly verruculose. The sexual morph of the genus is not determined yet. These species have been recorded from plants and soil from Australia, Brazil and China (Arzanlou et al., 2007; Cheewangkoon et al., 2009; Jiang et al., 2017b).

Table 4.3 *Pseudoramichloridium* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudoramichloridium brasilianum	*Brazil*	*Forest soil*	Arzanlou et al. (2007), Cheewangkoon et al. (2009)
P. xinjiangens	China	Park soil	Jiang et al. (2017b)

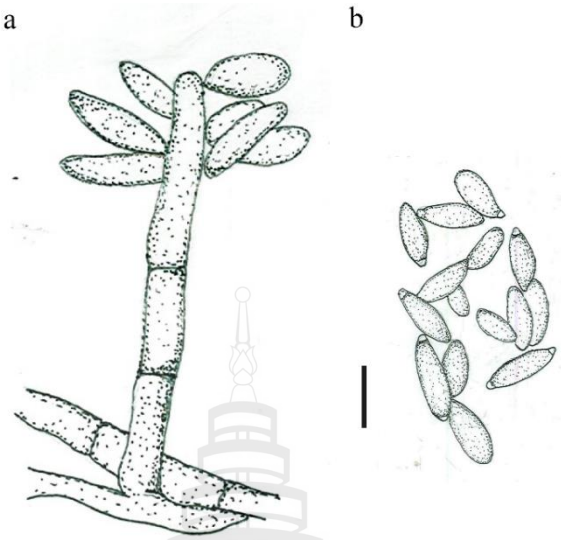


Figure 4.3 *Pseudoramichloridium henryi* (CBS 124775)

Figure 4.3, a Conidiophores. b Conidiogenous cells and conidia. Scale bar: a, b = 10 μm. Redrawn from Cheewangkoon et al. (2009).

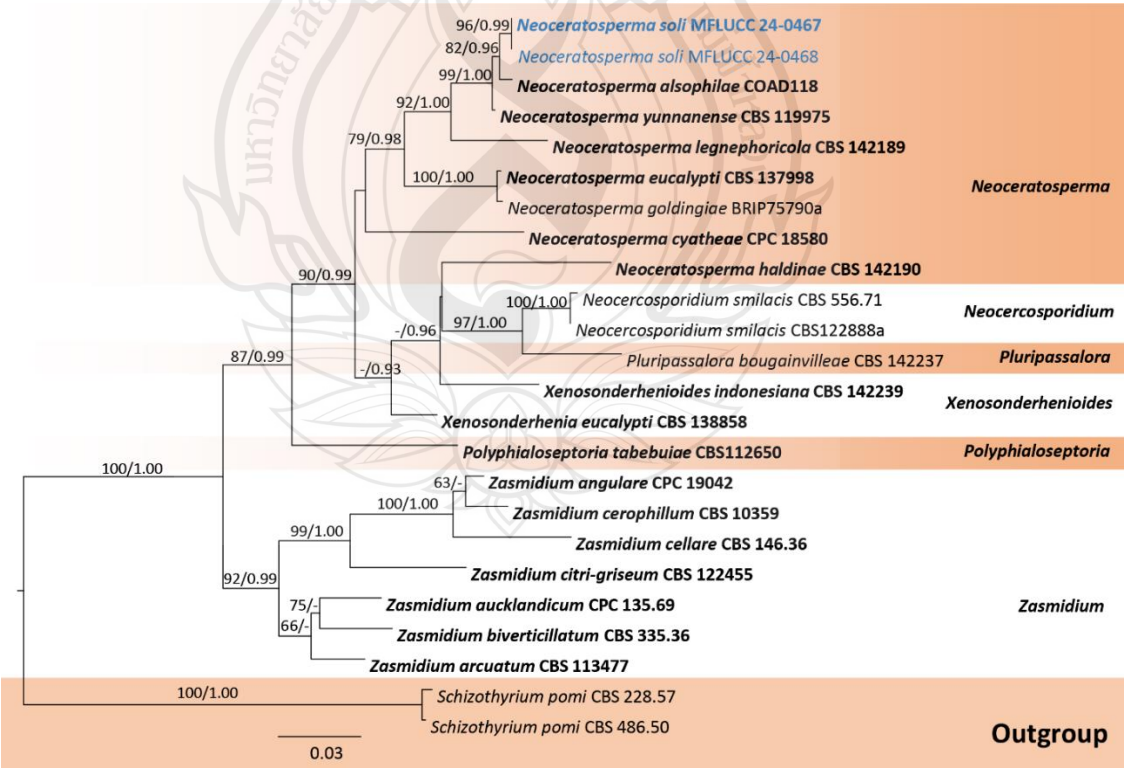


Figure 4.4 The best-scoring maximum likelihood tree generated of the combined LSU and ITS sequence data for selected species in *Mycosphaerellaceae*

Note Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Schizothyrium pomi* (CBS 228.57 and CBS 468.50). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 1344 bp, and single gene alignments are ITS: 503 bp, and LSU: 841 bp. A final ML optimization likelihood value of - 7424.047814. The matrix had 383 distinct alignment patterns with 8.5% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.236, C = 0.249, G = 0.295, T = 0.220; substitution rates AC = 1.00000, AG = 1.74503, AT = 1.00000, CG = 1.00000, CT = 5.60171, GT = 1.00000; gamma distribution shape parameter α = 0.407.

Family: ***Mycosphaerellaceae*** Lindau

Neoceratosperma Crous & Cheew., Persoonia 32: 257. 2014.

Index Fungorum number: IF 808935

Crous et al. (2014) introduced *Neoceratosperma* with the type species, *N. eucalypti*. The genus is comprised of seven species (Species Fungorum, 2025), and all of them have molecular data. The asexual morph consists of conidiophores that are reduced to brown, verruculose, sub-cylindrical conidiogenous cells, and conidia that are solitary, rarely in unbranched chains, subcylindrical, medium brown to dark brown, verruculose, warty, distoseptate with an obtuse apex and a truncate base (Crous et al., 2014a). The species have been reported from Australia, Brazil, China, Laos and Thailand associated with living and dead leaves (Videira et al., 2017). The genus has not been reported from soil previously.

Neoceratosperma soli Yasanthika & K.D. Hyde, sp. nov.

Figure 4.5.

Index Fungorum number: IF903421

Etymology – The specific epithet "*soli*", from Latin, refers to the soil, the substrate of which the holotype was collected.

Holotype – MFLUCC 24-0467Sexual morph: Undetermined. Asexual morph: *Conidiophores* 6–8 × 4–6 μm ($\bar{x}$ = 7 × 4.5 μm, n = 15), solitary, erect, semi- to macronematous, straight, hyaline to pale brown, septate, branched, smooth. *Conidiogenous cells* terminal in conidiophores, intercalary in prostrate hyphae, smooth,

sometimes verruculose, monoblastic, rarely polyblastic, sympodially proliferating through rim-like previous conidiogenous loci, thick-walled, pale brown. *Conidia* 5–16 × 3–8 μm ($\overline{x}$ = 10 × 6 μm, n = 25) solitary or occasionally in chains, sub-cylindrical to dumbbell-shaped, hyaline to sub-hyaline, smooth to verruculose, rounded to thin at apex, rounded or enlarged at base, 0–3-distoseptate, constricted at septa with an inconspicuous hilum at base.

Culture characteristics – *Colonies* on PDA at 25°C become 2–2.5 cm diam. after seven days, appearing in olive-brown to dark brown surface, reverse dark brown, flat, irregular filiform margin. *Mycelium* 2–3 μm ($\overline{x}$ = 2.5 μm, n = 25), immersed to superficial, hyaline to sub-hyaline or pale brown, smooth to course-surfaced, thick-walled, septate, branched hyphae, sporulated after 4 weeks.

Material examined – Thailand, Chiang Rai, Buddha Cave (What Tham Phra), on soil, 99.788928N, 19.9175247E, 425m, 21 June 2021, W.A. Erandi Yasanthika, cv8-64 (MFLU25-0126, holotype); ex-type 48-cv8-64 = MFLUCC 24-0467. *ibid*. (MFLU25-0127, isotype); living culture 48b-cv8-64b = MFLUCC 24-0468.

GenBank numbers – MFLUCC 24-0467: LSU: PQ578016, ITS: PQ578006; MFLUCC 24-0468 LSU: PQ590756, ITS: PQ590758

Notes – Based on morpho-molecular results, *Neoceratosperma soli* (MFLUCC 24-0467 and MFLUCC 24-0468) has been introduced as a new species. The multi-gene phylogeny (Figure 4.4) shows that this species produced an independent clade sister to *Neoceratosperma alsophilae* with 82% ML and 0.96 BYPP statistical support. We compared the nucleotides across the ITS (+5.8S) region of *N. soli* with *N. alsophilae*, resulting in 8/469 (1.7 %) (including gaps) differences. However, only sexual morph has been reported in *N. alsophilae*; thus, comparing the morphology of our species was not possible (Guatimosim et al., 2016). The other two adjacent species have asexual morphs; of these, *N. yunnanensis* has cylindrical to long obclavate, filiform, 0–6 -eu- or distoseptate conidia with a short-obconical, truncate base and rounded apex (Guatimosim et al., 2016), and *N. legnephoricola* has cylindrical, straight or curved, 0–10-distoseptate conidia with obconically truncate base and conically truncate apex (Videira et al., 2017). In contrast, our species has sub-cylindrical to dumbbell-shaped, hyaline to sub-hyaline, 0–3-distoseptate conidia with a rounded to thin apex and a rounded, enlarged base. Considering the multi-gene phylogeny and the distinct

morphology, we confirm *N. soli* as a new species isolated from disturbed cave soil. This is the first report of a *Neoceratosperma* species from soil, as this genus was previously found associated with plants (Crous et al., 2014a; Guatimosim et al., 2016; Videira et al., 2017).

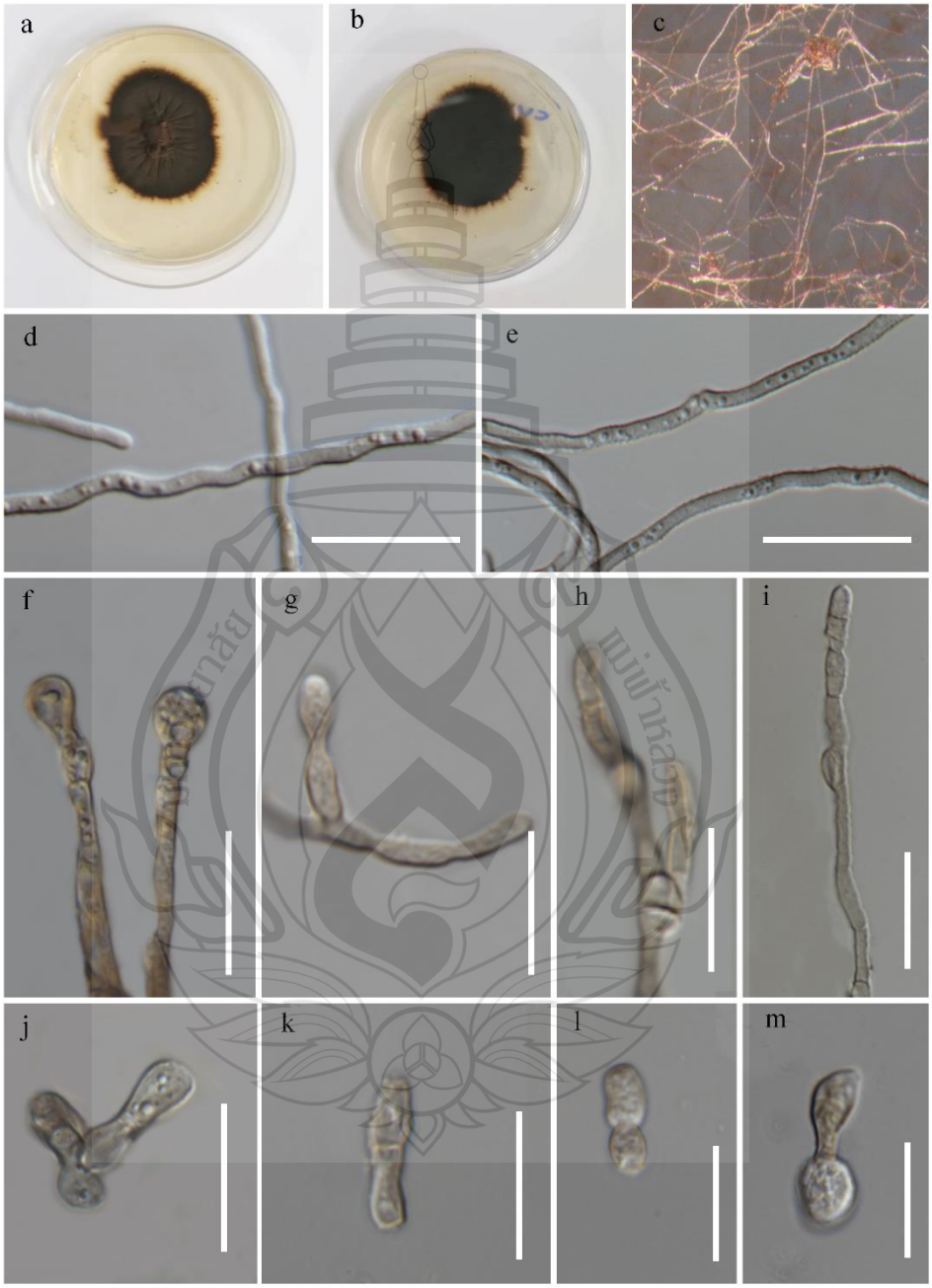


Figure 4.5 *Neoceratosperma soli* (MFLUCC 24-0467, Holotype)

Figure 4.5, a, b Culture characters on PDA (b = reverse). c Sporulated colony with conidial attachments on the mycelium. d Immature hyphae. e Mature hyphae. f–i Conidiophores with conidiogenous cells. j–m Conidia. Scale bars: d–m = 20 μm.

Family: *Piedraiaceae* Viégas ex Cif., Bat. & S. Camposa

Piedraia Fonseca & Leão, Memórias do Instituto Oswaldo Cruz 21 (suppl. 4): 125 (1928).

Figure 4.6

Index Fungorum number: IF 4098; Facesoffungi number: FoF 06139

Fonseca and Areakio (1928) introduced *Piedraia*, with *P. hortae* as the type species. Currently, two species are present in the genus (Species Fungorum, 2025), and both of them have molecular data. Initially, the genus was placed in *Piedraiaceae* (Ciferri et al., 1956), but based on phylogeny, Crous et al. (2009) placed it under *Teratosphaeriaceae*. However, Hongsanan et al. (2020a) and other subsequent studies suggested *Piedraia* in *Piedraiaceae.* The sexual morph of *P. hortae* is described as having ascostroma singly or in groups with loculi containing asci that contain 1–8 protunicate oval asci, whose wall disappears with spore maturity. Asci bear fusiform, sometimes straight, but usually curved or S-shaped, aseptate, and hyaline to slightly dark pigmented ascospores with a filiform appendage at both ends (Takashio & Vanbreuseghem, 1971). *Piedraia* have human pathogens that can infect the scalp and hair. The genus is distributed in Brazil, Indiniesia, Surinam and Venezuela and have been isolated from crops, dead *Homo sapiens*, mammalian hair, soil and stagnant water (Hongsanan et al., 2020a; Muggia et al., 2008).

Table 4.4 *Piedraia* species isolated from soil

Species	Country	Habitat or soil type	References
Piedraia hortae	Nigeria	A market	Nwokeoma et al. (2017)

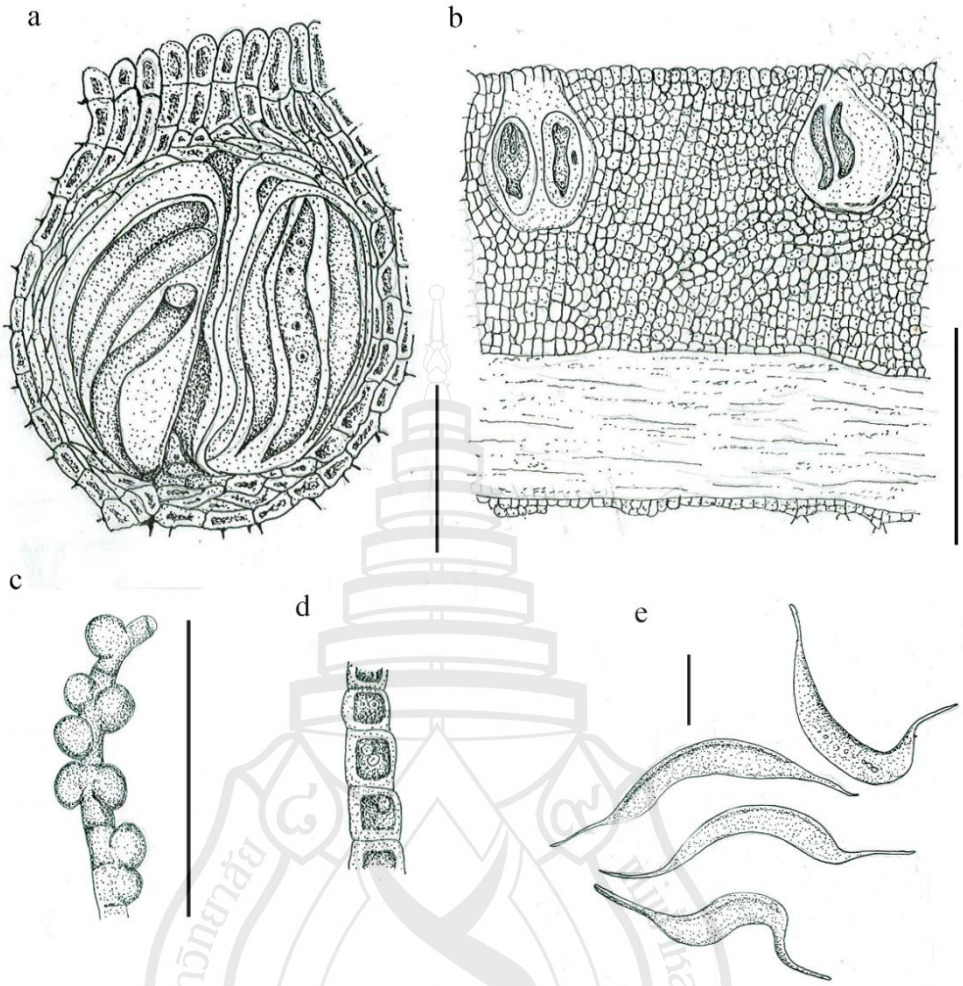


Figure 4.6 *Piedraia hortae*

Figure 4.6, a Vertical section of an ascoma. b Stroma on human hair. c Peripilar nodules grown on hypha. d Hypha on the culture. e Ascospores. Scale bars: a–e = 20 μm. Redrawn from Hongsanan et al. (2020a).

Family: *Saccotheciaceae* Bonord.

Aureobasidium Viala & G. Boyer, Rev. gén. Bot. 3: 371(1891).

Index Fungorum number: IF 7297; Facesoffungi number: FoF 00098

Aureobasidium was introduced by Viala and Boyer (1891) with *Aureobasidium vitis* as the type species. Currently, there are 36 species listed in Species Fungorum (2025), while 28 have molecular data (Tan & Steinrucken, 2024). Thambugala et al. (2014) placed *Aureobasidium*, *Saccothecium* and five other genera in *Aureobasidiaceae*, which was introduced by Ciferri (1958). Based on phylogeny, later studies have placed *Aureobasidium* in *Dothioraceae* (Jones et al., 2019; Lee et al.,

2021), however, some studies have shown that *Aureobasidiaceae* was introduced earlier by Bonorden (1864) as *Saccotheciaceae* to accommodate *Saccothecium*. As a result, *Aureobasidium* is currently placed in *Saccotheciaceae* (Calabon et al., 2023; Hongsanan et al., 2020a). The asexual morph is characterized by acervular to sporodochial, amphigenous, substomatal conidiomata with hyaline, cylindrical, clavate or globose, holoblastic, and polyblastic conidiogenesis cells. Conidia are hyaline to dark brown, ellipsoidal to spherical, reniform to sickle-shaped, aseptate with cylindrical and obtuse ends (Thambugala et al., 2014). *Aureobasidium* has been identified as an endophyte, saprobe and a pathogen associated with plants and human pathogens recorded from air, clinical laboratory samples, glass, marine sediments, marshland, soil, stone and water (Arzanlou, 2012; Wu et al., 2023; Zain et al., 2009). They have been reported from several countries, including China, the Czech Republic, India, Korea, Romania, Spain, the Netherlands and the USA. These species are utilized as biocontrol agents and for producing biodegradable extracellular polysaccharides (Arzanlou, 2012; Wu et al., 2023).

Table 4.5 *Aureobasidium* species isolated from soil

Species	Country	Habitat or soil type	References
Aureobasidium Pullulans	Egypt	Valley area-Wadi Houf	Zain et al. (2009)

Family: *Teratosphaeriaceae* Crous & U. Braun

Acidiella Hujslová & M. Kolařík, Fungal Diversity 58: 39 (2013). Figure 4.7

Index Fungorum number: IF 564518; Facesoffungi number: FoF 06992

Hujslová et al. (2013) erected *Acidiella* based on the LSU phylogeny and morphological characters, with *A. bohemica* as the type species. Currently, five species are listed in the Species Fungorum (2025), all of them with molecular data. The asexual morph is hyphomycetous, producing velvety black colonies, consisting of septate, branched, hyaline, or pale brown hyphae. Conidial formation occurs through fragmentation, resulting in oblong or swollen arthroconidia with truncated ends (Hujslová et al., 2013). The sexual morph is presently unknown. These species have been recorded from mine spoil, soil, and the wall of a cooling tower in the Czech

Republic, Poland and the USA (Crous et al., 2017b; Hujslová et al., 2014; Kolařík et al., 2021).

Table 4.6 *Acidiella* species isolated from soil

Species	Country	Habitat or soil type	References
Acidiella bohemica	Czech Republic	Acidic soil in a Kaolin quarry	Hujslová et al. (2013)

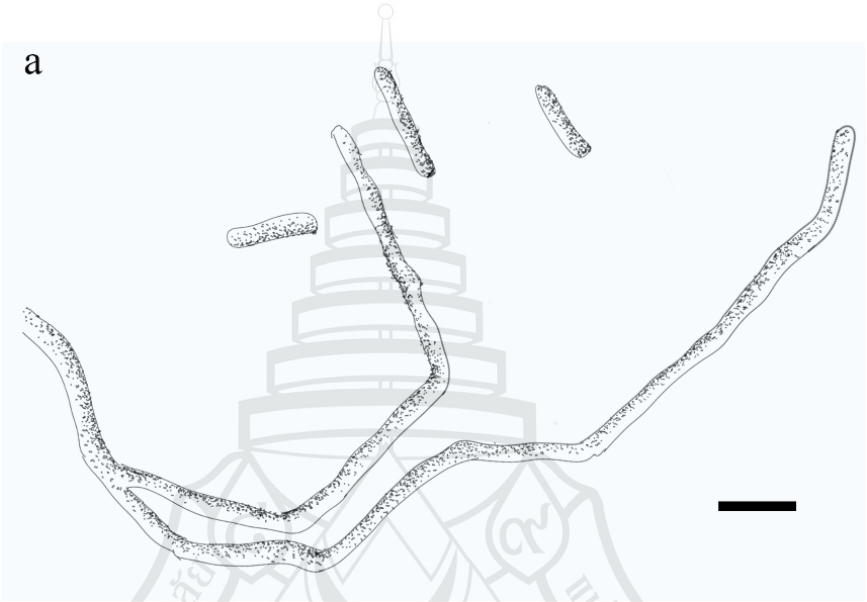


Figure 4.7 *Acidiella bohemica.* (CBS 132721)

Figure 4.7, a Conidiogenesis and the arthroconidia. Scale bar: a = 10 μm. Redrawn from Hujslová et al. (2013).

Devriesia Seifert & N.L. Nick., Can. J. Bot. 82(7): 919 (2004)

Figure 4.8

Index Fungorum number: IF 28865; Facesofungi number: FoF 07006

Devriesia was established by Seifert et al. (2004) based on the ITS phylogeny, accommodating the type species *D. staurophora*. Currently, 12 species have been listed in the genus while eight species have molecular data (Species Fungorum, 2025). The asexual morph is hyphomycetous with mononematous, pale brown, unbranched or sparingly branched conidiophores with a stipe, and holoblastic, polyblastic, or sometimes monoblastic conidiogenous cells. *Devriesia* has two types of conidia: ramoconidia that are slightly pigmented with a cylindrical to fusiform base, and the septate, subhyaline conidia arranged in dry acropetal chains (Seifert et al., 2004). The

sexual morph has not yet been discovered. Species have been isolated from dead plant leaves, house dust, rocks and soils in Baleares, Canada, Japan and the UK (Seifert et al., 2004).

Table 4.7 *Devriesia* species isolated from soil

Species	Country	Habitat or soil type	References
Devriesia acadiensis	Canada	Heat-treated soil in blueberry fields	Seifert et al. (2004)
D. shelburniensis			
D. thermodurans			
D. chlamydospora	Japan	Garden soil	

Figure 4.8 *Devriesia staurophora* (DAOM 230744)

Figure 4.8, a Conidiophores and ramoconidia. Redrawn from Seifert et al. (2004).

Order: *Pleosporales* Luttrell ex M.E. Barr

Family: *Acrocalymmaceae*

Acrocalymma Alcorn & J.A.G. Irwin, Trans. Br. mycol. Soc. 88(2): 163 (1987)

Index Fungorum number: IF 11008; Facesoffungi number: FoF 07097

Acrocalymma was established by Alcorn and Irwin (1987), assigning *A. medicaginis* as the type species. Based on morphology coupled with ITS and LSU-based phylogeny, Trakunyingcharoen et al. (2014) introduced *Acrocalymmaceae* to accommodate *Acrocalymma*. Recently, Tennakoon et al. (2021) and Liu and Zeng (2022)

provided phylogenetic and morphological analyses for this genus. Currently, 18 species have been listed in the Species Fungorum (2025), and all of them have molecular data. The asexual morph possesses solitary, papillate, globose pycnidia that bear holoblastic conidiogenous cells and aseptate, hyaline, cylindrical conidia with a helmet-shaped mucilaginous appendage at each end (Alcorn & Irwin, 1987; Jayasiri et al., 2019). Sexual morph has ostiolate ascomata, 8-spored asci containing fusiform ascospores with hyaline sheath (Shoemaker et al., 1991). *Acrocalymma arengae, A. chuxiongense, A. hongheense, A. pterocarpi* and *A. walker* have been reported as sexual morphs (Liu & Zeng, 2022). *Acrocalymma* species are recorded as pathogens and saprobes from terrestrial and aquatic plants and soil in Australia, China, Korea and Thailand (Das et al., 2020c; Tennakoon et al., 2021; Konta et al., 2023).

Table 4.8 *Acrocalymma* species isolated from soil

Species	Country	Habitat or soil type	References
Acrocalymma guizhouense	China	Rhizosphere soil of Perilla frutescens	Shao et al. (2022)
A. pterocarpi	Korea	Field soil	Das et al. (2020a)

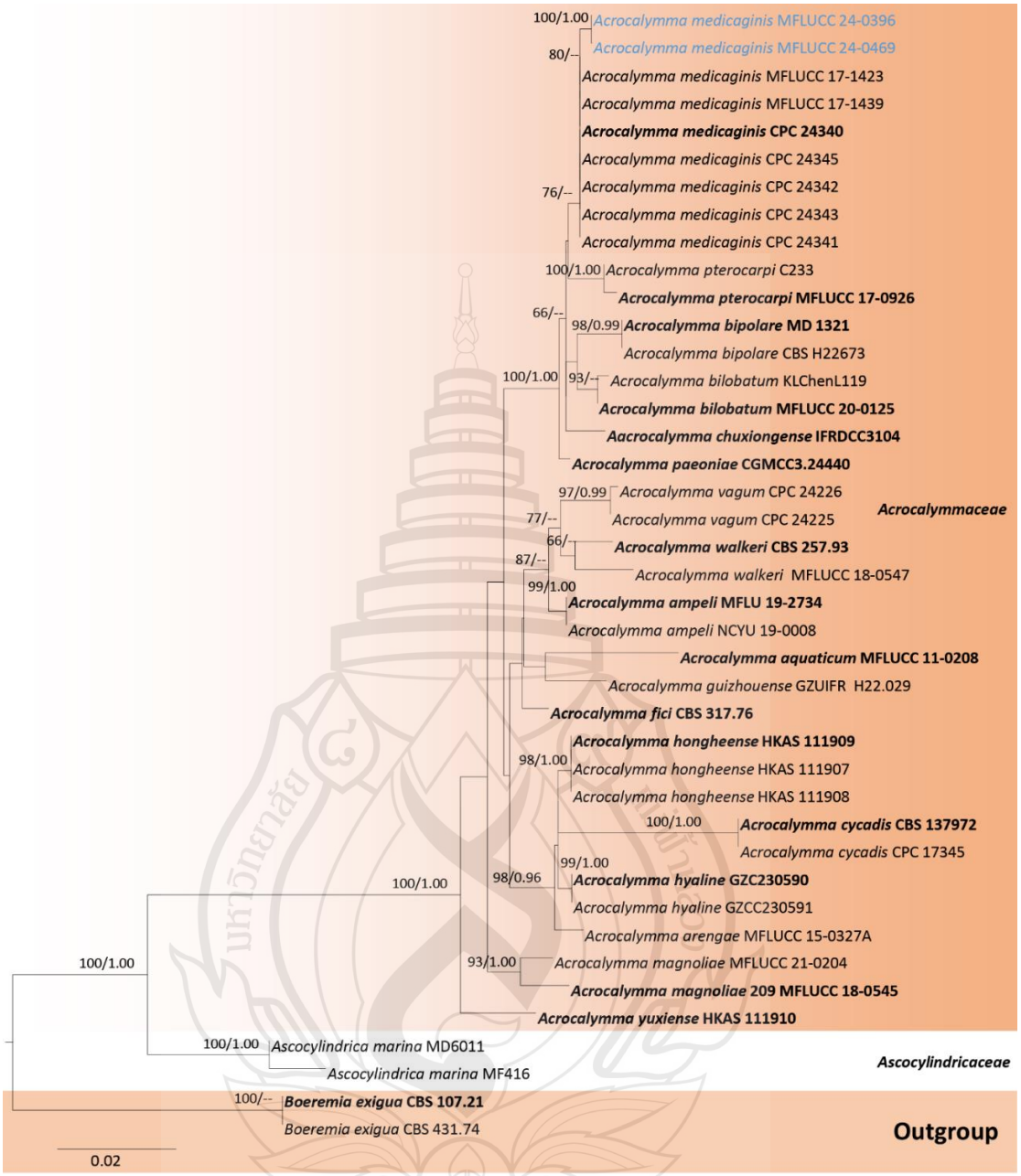


Figure 4.9 The best-scoring maximum likelihood tree generated of the combined SSU, LSU and ITS sequence data for selected genera in *Acrocalymmacea*

Figure 4.9, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Boeremia exigua* (CBS 431.74 and CBS 431.74) and *B. foveata* (CBS 341.67). The topology and clade stability of the combined gene tree are compared with the single

gene analyses. The approximate length of the combined alignment is 1327 bp, and single gene alignments are ITS: 497 bp, and LSU: 830 bp. A final ML optimization likelihood value of - 7424.047814. The matrix had 272 distinct alignment patterns with 16.86% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 3.55168, AG = 3.55906, AT = 3.55168, CG = 1.00000, CT = 11.54762, GT = 1.00000; gamma distribution shape parameter α = 0.738.

Acrocalymma medicaginis Alcorn & J.A.G. Irwin, Trans. Br. mycol. Soc. 88(2): 163 (1987).

Figure 4.10

Index Fungorum number: IF 130085, Faces of Fungi number: FoF 07099

Sexual morph: Ascomata: 47–150 × 52–91 µm ($\overline{x}$ = 82 × 67 µm, n = 10), semi-immersed to erumpent, solitary or in groups, *obpyriform* to ovoid. *Peridium* 7–12 µm ($\overline{x}$ = 9 µm) wide, inner subhyaline to golden-brown cell layers and hyaline outer cell layers, composed of *textura angularis* cells. *Asci* 52–39 µm × 8–12 µm ($\overline{x}$ = 45 × 9 µm; n = 20), fissitunicate, clavate, hyaline, curved to straight, 8-spored, short-stalked. *Ascospores* 8–16.5 µm × 3–5 µm ($\overline{x}$ = 11 × 4.5 µm; n = 20), biseriate, fusiform, hyaline, straight to slightly curved, 1-septate, constricted at the septum, thick-walled. Asexual morph: Undetermined.

Culture Characteristics – Colonies grew on PDA at 25°C reached 4 cm in diam. within 14 days, circular, flat, entire-margined, white surface became whitish red when mature, reverse white, became crimson at the center with yellowish-red outer ring when mature. Mycelium superficial to semi-immersed, hyaline, smooth-walled, septate 1.5–3 µm ($\overline{x}$ = 2 µm, n = 25), sporulated after three weeks.

Material examined – Thailand, Chiang Mai Province, Mae On District, Tham Muang On cave, on soil, 99.238054 N, 18.7862964 E, 496 m, 9 May 2022, W.A. Erandi Yasanthika,58 (MFLU25-0116); living culture 58-cv20-17= MFLUCC 24-0396. *ibid.* (MFLU25-0117); living culture 58b-cv20-17b=MFLUCC 24-0469

GenBank numbers –MFLUCC 24-0396: SSU: PQ559869, LSU: PQ559854, ITS: PQ559850; MFLUCC 24-0469: LSU: PQ572138, ITS: PQ570529

Notes – *Acrocalymma medicaginis* was introduced by Alcorn and Irwin (1987) from root and crown rotting of *Medicago sativa* (*Fabaceae*) in Australia. It has later been isolated from dead stems of *Chromolaena odorata* in Thailand (Mapook et al., 2020) and dead culms of herbaceous plants in China (Zhang et al., 2024b). In the phylogenetic analyses (Figure 4.9), our strains (MFLUCC 24-0396 and MFLUCC 24-0469) grouped with *A. medicaginis* with 76% ML statistical support. However, the baysean value was less than 0.90. Our isolates (MFLUCC 24-0396 and MFLUCC 24-0469) are morphologically similar to *A. medicaginis* by having 8-spored, fissitunicate, cylindric-clavate, straight or slightly curved, short stalked asci and ascospores with 1–2-seriate, hyaline, straight or slightly curved, and two-celled constricted at the septum (Alcorn & Irwin, 1987). However, our strain is slightly different from the type species by having thick-walled ascospores. Thus, based on morphology and multi-gene phylogeny, we confirmed our collection isolated from disturbed-cave soils in Thailand as *A. medicaginis*. Based on the GlobalFungi website, *A. medicaginis* has been reported from forest soils, and this is the first *A. medicaginis* strain reported from Thai soil habitats and the first member of this genus associated with the cave environment.

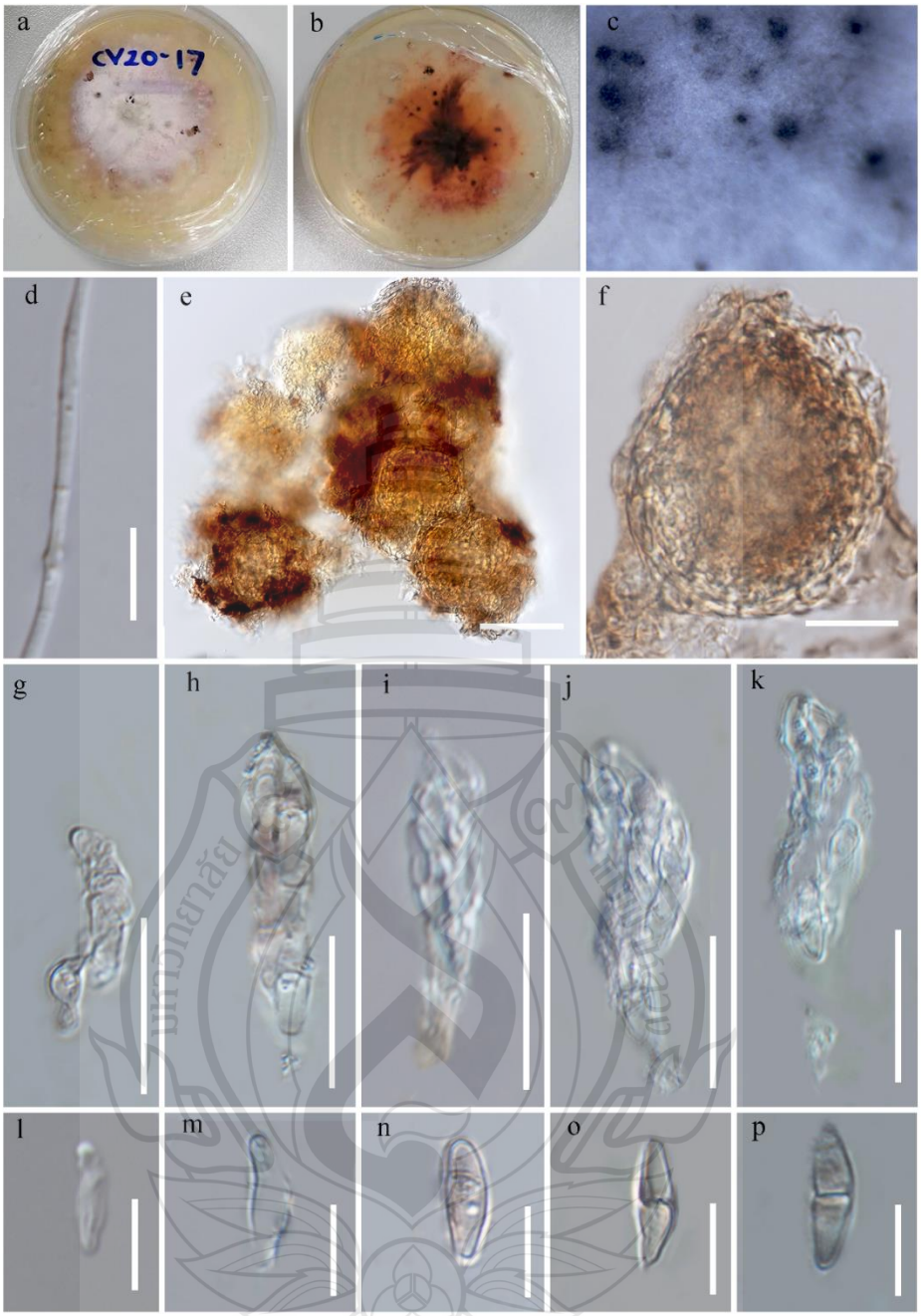


Figure 4.10 *Acrocalymma medicaginis* (MFLU25-0116, new habitat and geographical record)

Figure 4.10, a, b Culture characters on PDA (b = reverse). c Sporulated colony with ascomata. d Mature hyphae. e Ascomata. f Ascomatal wall. g–k Asci. l–p Ascospores. Scale bars: e = 50 µm, f, g–k = 20 µm, d, l–p = 10 µm, k–o = 5 µm.

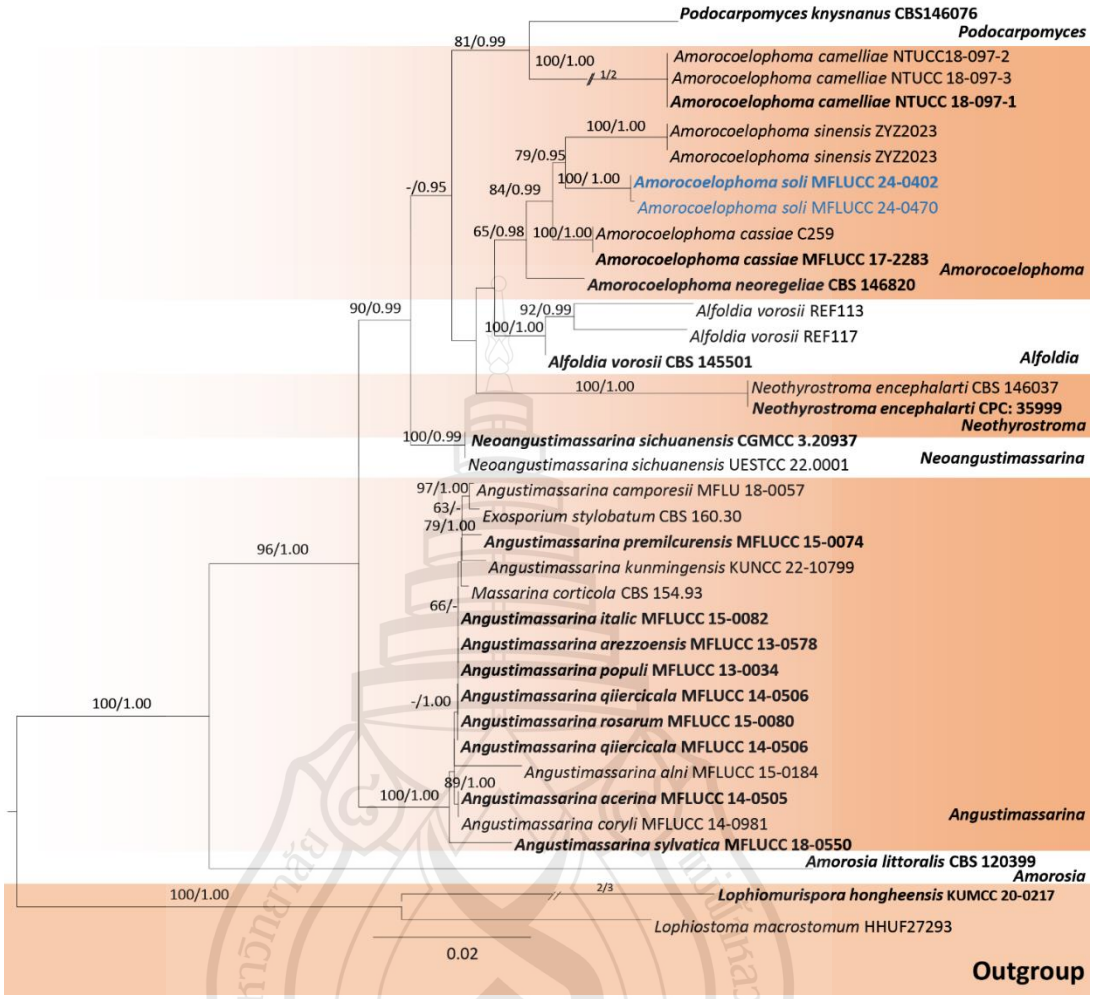


Figure 4.11 The best-scoring maximum likelihood tree generated of the combined SSU, ITS and LSU sequence data for selected genera in *Amorosiaceae*

Figure 4.11, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Lophiomurispora hongheensis* KUMCC 20-0217 and *Lophiostoma macrostomum* HHUF27293. The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 2430 bp, and single gene alignments are SSU: 1018 bp, ITS: 552 bp, and LSU: 860 bp. A final ML optimization likelihood value of - 7424.047814. The matrix had 585 distinct alignment patterns with 22.01% % undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.253032, C = 0.219699, G = 0.273895, T = 0.253374,

substitution rates AC = 2.142025, AG = 3.315365, AT = 2.376966, CG = 1.013124, CT = 10.058142, GT = 1.000000; gamma distribution shape parameter α = 0.678674.

Family: *Amorosiaceae* Thambug. & K.D. Hyde

Amorocoelophoma Jayasiri, E.B.G. Jones & K.D. Hyde, Mycosphere 10(1): 25 (2019)

Index Fungorum number: IF 555529

Amorocoelophoma was introduced by Jayasiri et al. (2019) based on SSU, ITS, LSU and *tef1-α* sequences and the morphological evidence. Currently, four *Amorocoelophoma* species are listed in the Species Fungorum (2025), and they are supported with molecular data. The asexual morph is characterized by the solitary to gregarious, ovoid to globose, brown, pycnidia covered with hyaline to pale brown, septate, branched hyphal growth as a layer with outer brown layer and the pycnidia wall having thick, two layers, inner hyaline, *textura angularis*, 1–2 cell layers, outer *textura angularis*, brown, 1–2 cell layers. Conidiogenous cells are phialidic, doliform, hyaline, smooth-walled and hyaline, cylindrical, aseptate, smooth- and thin-walled conidia with guttules that are concentrated at the ends (Jayasiri et al., 2019). Most of the species are recorded from leaf spots, associated with leaf lesions, fallen pods and soil from China, New Zealand and Thailand (Jayasiri et al., 2019; Ariyawansa et al., 2020; Crous et al., 2021b).

Table 4.9 *Amorocoelophoma* species isolated from soil

Species	Country	Habitat or soil type	References
Amorocoelophoma sinensis	China	Guizhou Wildlife Park	Zhang et al. (2024b)

Amorocoelophoma soli Yasanthika & K.D. Hyde, sp. nov.

Figure 4.12

Index Fungorum number: IF903040; Faces of Fungi number: FoF 16702

Etymology – The specific epithet "*soli"*, from Latin, refers to the soil, the substrate of which the holotype was collected.

Holotype – MFLU25-0121

Sexual morph: Ascomata 80–150 × 100–480 µm ($\overline{x}$ = 108 × 257 µm, n = 5), mostly solitary, *globose to subglobose*, immersed or semi-immersed, light brown, *pseudoparenchymatous-walled.* Asci 15–30 × 3–7.5 µm ($\overline{x}$ = 20 × 4.5 µm, n = 10), 8-

spored, bitunicate, fissitunicate, cylindrical to clavate, slightly curved, pedicellate, rounded at the apex. Ascospores 6–8 × 3–4 µm ($\overline{x}$ = 7 × 3.5 µm, n = 15), bi-seriate to tri-seriate, partially overlapping, hyaline, aseptate, ellipsoidal to reniform, thick-walled. Asexual morph: Undetermined.

Culture Characteristics – Colonies on PDA at 25℃ reached 3.5 cm in diam. within 14 days, circular, flat, irregularly margined, brownish gray surface, became grayish brown center and whitish to ivory at periphery when mature, reverse yellowish brown, dark brown center, yellow middle ring and whitish yellow periphery. Mycelium superficial to semi-immersed, hyaline to pale brown, septate, smooth-walled, 1–3.5 µm ($\overline{x}$ = 2.5 µm), sporulated after 4 weeks on PDA.

Material examined – Thailand, Chiang Rai, What Tham Pha Tong cave, on soil, 99.9038925 N, 20.0918488 E, 430 m, 28 Aug 2022, W.A. Erandi Yasanthika (MFLU25-0121, holotype); ex-type 88-cv23-12= MFLUCC 24-0402. *ibid*. (MFLU25-0122, isotype); living culture 88b-cv23-12b= MFLUCC 24-0470.

GenBank numbers – MFLUCC 24-0402: SSU: PQ573489, LSU: PQ570690, ITS: PP993906; MFLUCC 24-0470: SSU: PQ576457 LSU: PQ576474, ITS: PQ576414.

Notes – In this study, we introduce *Amorocoelophoma soli* from undisturbed cave soils in Thailand. According to the phylogeny (Figure 4.11), our species (MFLUCC 24-0402 and MFLUCC 24-0470) cluster with *Amorocoelophoma cassiae* (MFLUCC 17-2283, C259), *A. neoregeliae* (CBS 146820) and *A. sinensis* (CGMCC 3.25499), and forms a sister lineage to *A. sinensis* (CGMCC 3.25499) with 79% ML and 0.95 BYPP statistical support. However, in our tree, *A. camelliae* does not group with other *Amorocoelophoma* species, similar to Zhang et al. (2024). We compared the nucleotides across the ITS (+5.8S) gene region of *Amorocoelophoma soli* (MFLUCC 24-0402 and MFLUCC 24-0470) with *A. cassiae* and *A. neoregeliae*. There are 23/ 465 (4%) (including gaps) differences between *Amorocoelophoma soli* and *A. cassiae*, while 27/ 376 (7%) (including gaps) with *A. neoregeliae* and 31/ 472 (6%) (including gaps) with *A. sinensis*. *Amorocoelophoma cassiae, A. neoregeliae* and *A. sinensis* have been recorded from their asexual morphs, and our collection reported the first sexual morph in this genus (Jayasiri et al., 2019; Ariyawansa et al., 2020). *Amorocoelophoma camelliae* was recorded on leaves of *Camellia sinensis* in China (Taiwan) (Ariyawansa

et al., 2020), *A. cassiae* on fallen pods in Thailand (Jayasiri et al., 2019) and *A. neoregeliae* on leaf spots in New Zealand (Crous et al., 2021b), while *A. sinensis* has been reported from soil in China (Zhang et al., 2024b). Thus, based on both morphology and multi-gene phylogeny, *Amorocoelophoma soli* is introduced as a new species, and interestingly, it's the first *Amorocoelophoma* species documented from soils in Thailand.

Figure 4.12 ***Amorocoelophoma soli*** (MFLU25-0121)

Figure 4.12, a, b Culture characters on the PDA (b = reverse). c Sporulated colony with ascomata. d, e Hyphae. f Ascomata. g. Vertical cross section of Ascomata. h Asci. l, m Ascospores. Scale bars: f, g = 100 µm, e = 20 µm, d, h = 10 µm, i, j = 5 µm.

Family: *Anteagloniaceae* K.D. Hyde, J.K. Liu & A. Mapook

Anteaglonium Mugambi & Huhndorf, Syst. Biodiv. 7(4): 460 (2009)

Index Fungorum number: IF 541631

Anteaglonium was introduced with the type species, *A. abbreviatum*, which was previously known as *Glonium abbreviatum*as (Mugambi & Huhndorf, 2009). Based on the phylogenetic revision of Hyde et al. (2013), *Anteagloniaceae* was erected while accommodating *Anteaglonium* as the type genus. There are 11 species listed in the Species Fungorum (2025), and all of them have molecular data. Both asexual and sexual morphs have been identified in *Anteaglonium*, and the genus was initially distinguished by its smaller ascomata, elongate or globose-shaped, small ascospores that are less than 8 μm long except for *A. latirostrum* (22–28 μm) (Jaklitsch et al., 2018; Mugambi & Huhndorf, 2009). However, the subsequent species discovered in the genus have globose ascomata, often with raised, laterally compressed apices that are absent in the initially identified members (Carneiro de Almeida et al., 2014). Species are found on dead wood and leaves collected in Greece, Kenya, Pennsylvania, Spain, Thailand and the USA. There is no previous record of the genus from soil habitats (Zhang et al., 2023a).

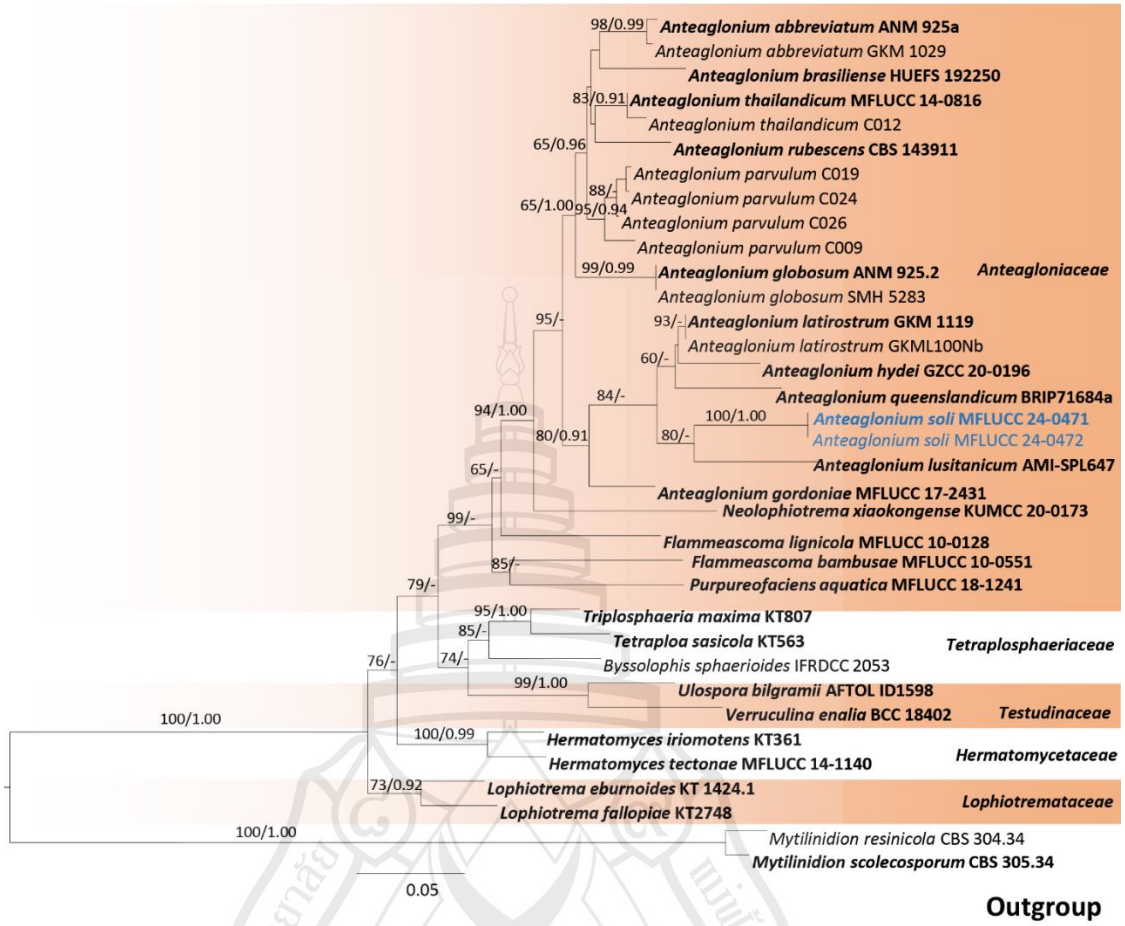


Figure 4.13 The best-scoring maximum likelihood tree generated of the combined ITS, SSU, LSU, *tef1-α* and *rpb2* sequence data for *Anteagloniaceae* and selected genera in adjacent families

Figure 4.13, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Mytilinidion resinicola* (CBS 304.34) and *Mytilinidion scolecosporum* (CBS 305.34). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 3784 bp, and single gene alignments are SSU: 976bp, ITS: 537 bp, LSU: 645 bp, tef1-α:726bp, RPB2: 900bp. A final ML optimization likelihood value of -16854.010. The matrix had 585 distinct alignment patterns with 42.65% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250, substitution rates

AC = 1.00000, AG = 3.66088, AT = 1.00000, CG = 1.00000, CT = 8.41951, GT = 1.000000; gamma distribution shape parameter α = 0.502.

Anteaglonium soli Yasanthika & K.D. Hyde, sp. nov.

Figure 4.14

Index Fungorum number: IF903422; Facesoffungi number: FoF 16703

Etymology – The specific epithet "*soli*", from Latin, refers to the soil, the substrate of which the holotype was collected.

Holotype – MFLU25-0165

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 30–75× 25–65 μm ($\overline{x}$ = 50 × 40 μm, n = 10), pycnidial, dark brown to black, globose, aggregated or rarely solitary, superficial to semi-immersed. *Conidiomata wall* consists of *texura angularis* cells. *Conidiogenous cells* 1.5–3 × 1–2.5 μm ($\overline{x}$ = 2 × 2 μm, n = 15), hyaline, phialidic, ampulliform, smooth-walled. *Conidia* 1–3 × 1–2.5 μm ($\overline{x}$ = 2 × 1.5 μm, n = 25), hyaline, aseptate, thick-walled, rough, ellipsoidal to globose or obovoid, occasionally rounded apex, tapering at the base, sometimes with 1–2 lateral protuberances.

Culture Characteristics – Colonies on the PDA at 25℃ reached 3.5 cm in diam. within 14 days, circular, flat, entire-margined, initially greyish white, becoming brown to greyish brown, reverse dark brown center, light brown middle rind and dark brown periphery. Mycelium superficial to semi-immersed, hyaline to pale brown, septate, thick-walled, 1–2.5 μm ($\overline{x}$ = 1.5 μm, n = 25), sporulated after six weeks on PDA.

Material examined –Thailand, Chiang Mai, Mae On District, Tham Muang On cave, on soil, 99.238054 N, 18.7862964 E, 496 m, 9 May 2022, W.A. Erandi Yasanthika (MFLU25-0165, Holotype); ex-type 62-cv20-14= MFLUCC 24-0471. *ibid*. (MFLU25-0166, isotype); living culture 62b-cv20-14b = MFLUCC 24-0472.

GenBank numbers – MFLUCC 24-0471: LSU: PQ578018, ITS: PQ578017; MFLUCC 24-0472: LSU: PQ590757, ITS: PQ590759

Notes –The combined ITS, SSU, LSU, *tef1-α* and *rpb2* phylogenetic tree in Figure 4.13 shows that our species (MFLUCC 24-0471 and MFLUCC 24-0472) clustered within *Anteaglonium*, producing a distinct branch sister to *A. lusitanicum* with 80% ML statistical support, but its BYPP value was less than 0.90. The nucleotides across the ITS (+5.8S) gene region of our species was compared with *A. lusitanicum*, which showed 66/537 (12.29%) (including gaps) basepair differences. However, only the sexual morph was

reported for *A. lusitanicum*. Thus, morphological comparison with our species was not possible (Tan et al., 2022). Mostly, other *Anteaglonium* species were also reported as sexual morphs, while *A. rubescens*, *A. parvulum* and *A. thailandicum* were reported in their asexual morphs (Jayasiri et al., 2016; Jaklitsch et al., 2018). *Anteaglonium thailandicum* and *A. parvulum* have globose conidiogenous cells and globose conidia that are rounded at both ends (Jayasiri et al., 2016), and *A. rubescens* has lageniform to ampulliform or subglobose conidiogenous cells and subglobose to globose or ellipsoid conidia with 1–2(3) guttules (Jaklitsch et al., 2018). Our species is different from the above three by having ampulliform conidiogenous cells and ellipsoidal to globose or obovoid, aguttulate conidia, occasionally with a rounded apex and tapering at the base. Along with multi-gene phylogeny and morphology, we introduce *Anteaglonium soli* from disturbed-cave soils in Thailand. This genus has mainly been isolated as plant saprobes (Boehm et al., 2009; Jayasiri et al., 2016; Jaklitsch et al., 2018; Tan et al., 2022), hence, this becomes the first member isolated from soil habitats.

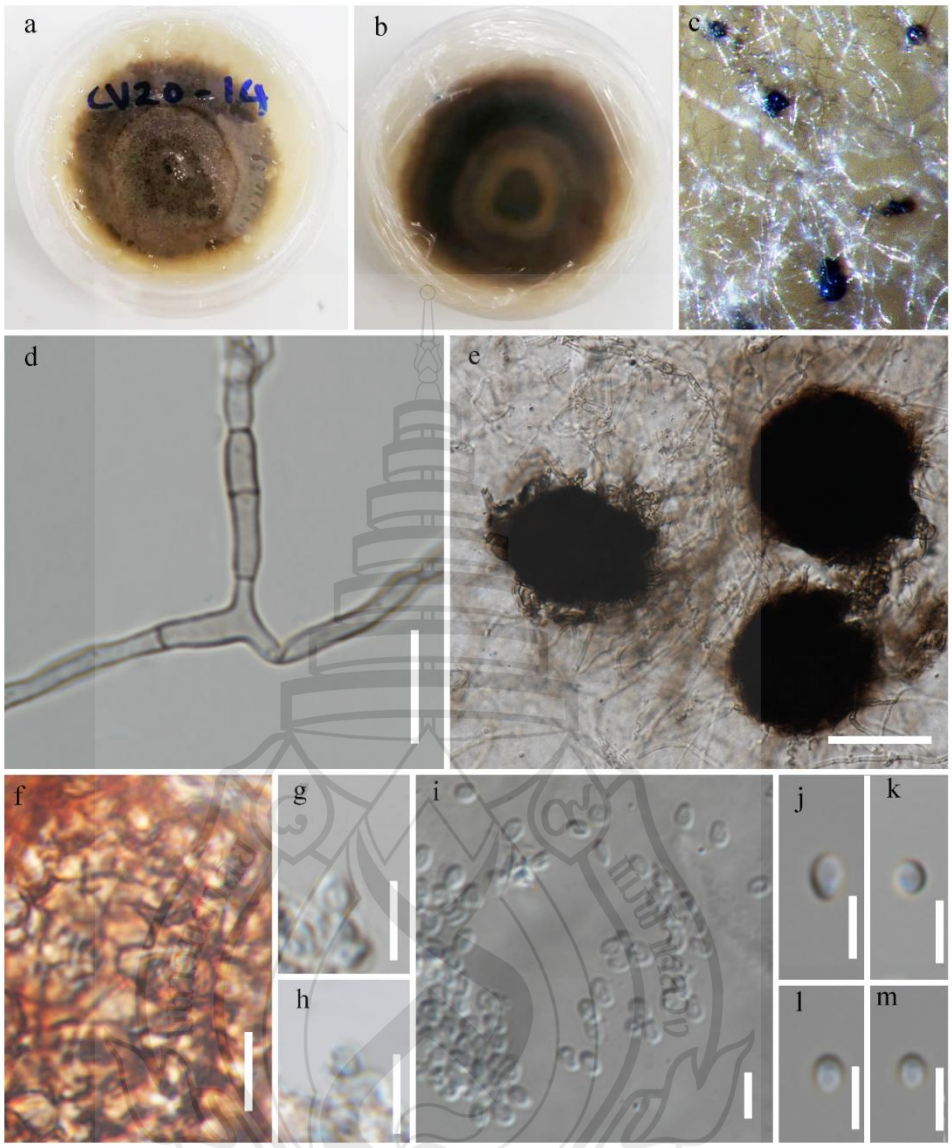


Figure 4.14 ***Anteaglonium soli*** (MFLU25-0165, Holotype)

Figure 4.14, a, b Culture characters on the PDA (b = reverse). d. Hypha e. Pycnidia f. Pycnidia wall g, h Conidiogenous cells. i–m. Conidia. Scale bars: e =20 µm, d = 10 µm, f–m =5 µm.

Family: ***Astrosphaeriellaceae*** Phook. & K.D. Hyde (=Caryosporaceae Huang Zhang, K.D. Hyde & Ariyaw.)

Pithomyces Berk. & Broome, J. Linn. Soc., Bot. 14: 100 (1873).

Index Fungorum number: IF 9412; Facesoffungi number: FoF 03611

Pithomyces was introduced by Berkeley & Broome (1873), typified with *Pithomyces flavus*. There are 45 species listed in the Species Fungorum (2025), and six

of them have molecular data (Hongsanan et al., 2020a). The asexual morph is hyphomycetous, comprising mononematous, micronematous conidiophores, mostly intercalary, sometimes denticulate, producing mono or polyblastic, hyaline to light brown, aseptate conidiogenous cells. Conidia are solitary, brown to black, obovate to oblong, verruculose, with transverse, dark septa. The sexual morph is characterized by solitary to gregarious, erumpent to superficial ascomata, with a *textura angularis* to *textura prismatica* wall, and bitunicate, fissitunicate, 8-spored asci, with overlapping bi-seriate, pale brown to brown, fusiform ascospores. Species are globally reported, including China, Cuba, India, Thailand and the USA, that are associated with aquatic, soil and terrestrial habitats as saprobes (Wanasinghe et al., 2018a).

Table 4.10 *Pithomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Pithomyces longiclavisporus	China	Warm temperate area	Liu and Zhang (2007)
P. pallidus			
P. pavgii			

Family: *Coniothyriaceae* W.B. Cooke

Coniothyrium Corda, Icon. fung. (Prague) 4: 38 (1840).

Index Fungorum number: IF 7765; Facesoffungi number: FoF 08171

Coniothyrium was introduced by Corda (1840) and is typified with *C. palmarum*. Currently, 457 species are included in this genus, but only 6 with the molecular data (Hongsanan et al., 2020). By providing a comprehensive phylogeny of the combined LSU and ITS sequence data, de Gruyter et al. (2013) accommodate *Coniothyrium* in *Coniothyriaceae*, while erecting this as the type genus of the family. The asexual morph is characterized by pycnidial conidiomata that have broadly, flask-shaped conidiogenous cells and light to dark brown, two-celled conidia. This genus is known as saprobes or plant pathogens, and some have been found in air and soil habitats with worldwide distribution (de Gruyter et al., 2013).

Table 4.11 *Coniothyrium* species isolated from soil

Species	Country	Habitat or soil type	References
Coniothyrium multiporum	India	Saline soil	de Gruyter et al. (2013)

Family: *Corynesporascaceae* Sivan., Mycological Research 100: 786 (1996).

Corynespora Güssow, Zeitschrift für Pflanzenkrankheiten und Pflanzenschutz 16: 10 (1906).

Index Fungorum number: IF 7795; Facesofungi number: FoF 06663

Corynespora was introduced by Güssow (1906) with *C. cassiicola* as the type species. Studies have identified *Corynespora* as a polyphyletic genus (Crous et al., 2015c; Hyde et al., 2016; Voglmayr & Jaklitsch, 2017), while the phylogenetic revision of Voglmayr and Jaklitsch (2017) transferred several *Corynespora* species to *Helminthosporium.* There are 129 valid species in the genus, however, 13 species have molecular data (Liu et al., 2023a). Thus, more collections are required to build an in-depth phylogeny in the genus. Most of the species have been identified based on the morphological characteristics (Hongsanan et al., 2020a). Mostly species occur on plant leaves, roots, stems, dead twigs and trunks and have also been reported from human skin, nematode cysts and soils, where they can be saprobes or pathogens (Dixon et al., 2009). Pathogenic mode causes leaf spots, and is a significant plant pathogenic genus that causes target spot disease worldwide (Koenning et al., 2006; Schlub et al., 2009; Fulmer et al., 2012).

Table 4.12 *Corynespora* species isolated from soil

Species	Country	Habitat or soil type	References
Corynespora cassiicola	Thailand	Agricultural field	Kamolmanit et al. (2013)

Family: *Cucurbitariaceae* G. Winter (= Fenestellaceae M.E. Barr)

Neocucurbitaria Wanas., E.B.G. Jones & K.D. Hyde, Mycosphere 8(3): 408 (2017).

Index Fungorum number: IF 552832; Facesoffungi number: FoF 02902

Neocucurbitaria was introduced by Wanasinghe et al. (2017a) with morpho-molecular (LSU, SSU and ITS) analyses while accommodating *N. unguis-hominis* as the type species. The genus comprises 29 species (Species Fungorum 2025), and all

have been supported with molecular data. Coelomycetous asexual morph is pycnidial, globose to sub-globose, with hyaline, septate, doliiform to cylindrical conidiogenous cells, and hyaline, aseptate, cylindrical or ellipsoidal, smooth-walled conidia. The sexual morph is characterized by black, superficial to semi-immersed, globose, ostiolate ascomata with a peridium comprised of *textura angularis* cells. Asci are 8-spored, bitunicate, fissitunicate, cylindrical, short-pedicellate, comprising muriform, mostly ellipsoidal ascospores with 6−8 transverse septa and a longitudinal septum (Sutton, 1980; Wanasinghe et al., 2017a). Species have been isolated from Australia, Italy, Spain, the Netherlands and the USA. In addition, they have been recorded as saprobes on leaves and wood, from human lungs, corneal scrapings and wounds, sea water and one species from soil (Wanasinghe et al., 2017a; Valenzuela-Lopez et al., 2018).

Table 4.13 *Neocucurbitaria* species isolated from soil

Species	Country	Habitat or soil type	References
Neocucurbitaria cava	Germany	ND	Valenzuela-Lopez et al. (2018)

Family*: Dictyosporiaceae* Boonmee & K.D. Hyde

Neodendryphiella Iturrieta-González, Dania García & Gené, MycoKeys 37: 25 (2018)

Figure 4.15

Index Fungorum number: IF 824664; Facesoffungi number: FoF 08214

Iturrieta-González et al. (2018) introduced *Neodendryphiella* based on morpho-molecular analyses (ITS and LSU), with the type species, *N. tarraconensi* (Iturrieta-González et al., 2018). *Neodendryphiella* presently comprises four species Species Fungorum (2025), and all of them have molecular data. The asexual morph is hyphomycetous and has conidiophores that are subhyaline to brown, smooth to verrucose, semi-macronematous to macronematous, mononematous, erect or slightly flexuous, cylindrical, septate and unbranched or branched towards the apical region. Conidiogenous cells are integrated, terminal or intercalary and produce conidia in acropetal branched chains. Of these, ramoconidia are pale brown, aseptate or septate, smooth to verruculose cylindrical or subcylindrical, while conidia are blastocatenate, pale brown, aseptate or septate, verruculose to verrucose, ellipsoidal, doliiform and

clavate. The sexual morph remains undiscovered. Species have been reported from dung, dead stems, leaves and soil in China, Italy, Mexico and Spain (Iturrieta-González et al., 2018; Dong et al., 2023).

Table 4.14 *Neodendryphiella* species isolated from soil

Species	Country	Habitat or soil type	References
Neodendryphiella michoacanensis	Mexico	City area	Iturrieta-González et al.
N. tarraconensis	Spain	Garden	(2018)

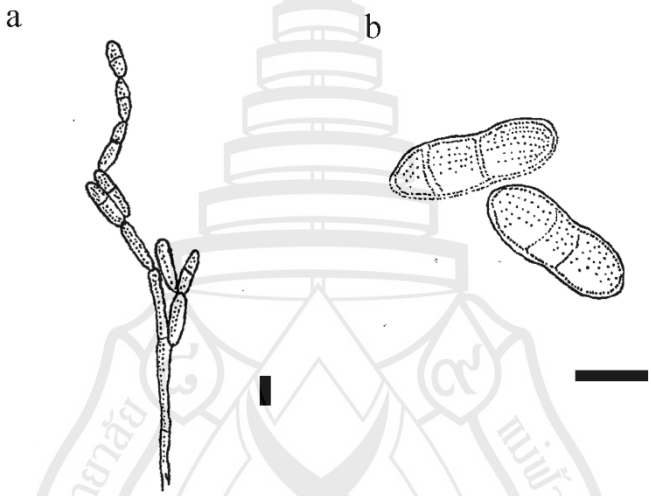


Figure 4.15 *Neodendryphiella tarraconensi* (FMR 16234)

Figure 4.15, a Conidiophores. b Conidia. Scale bars: a, b =10 μm. Redrawn from Iturrieta-González et al. (2018).

Family: *Didymellaceae* Gruyter, Aveskamp & Verkley (=*Microsphaeropsidaceae* Qian Chen et al.)

Ascochyta Lib., Plantae Cryptogamae, quas in Arduenna collegit Fasc. 1: 8 (1830).

Index Fungorum number: IF 7239; Facesoffungi number: FoF 07121;

Ascochyta was introduced by Klotzsch (1830), and *A. pisi* is designated as the type species (Boerema & Bollen, 1975). Currently, 25 species are valid under the genus, and all of them have molecular data (Gomzhina & Gasich, 2024). The asexual morph of this genus has pycnidial, subglobose or ampulliform to mammiform, superficial or

immersed, solitary or confluent conidiomata with an ostiolate or poroid opening. Conidiogenous cells are annellidic or phialidic, and conidia are hyaline or slightly coloured (yellow to pale brown), variably shaped (ovoid, oblong, subcylindrical, ellipsoidal, cymbiform or allantoid), mostly uniseptate, sometimes 2–3-septate, eguttulate or guttulate. The sexual morph has pseudothecial, immersed or erumpent, subglobose to flattened, or irregular, solitary or confluent, and ostiolate ascomata. Asci are bitunicate, 8-spored, subcylindrical to subclavate, or saccate. Pseudoparaphyses present but disappear at maturity, and ascospores are ovoid to ellipsoidal, slightly biconic, hyaline to yellowish and become brown after release, 1–3-septate, constricted at the septum (Chen et al., 2015; Mel'nik, 2000). Some *Ascochyta* species are plant pathogens of cereal crops and legumes, and several species show host specificity on *Campanulaceae, Chenopodiaceae, Leguminosae, Poaceae, Solanaceae* and *Umbelliferae* (Hongsanan et al., 2020a; Valenzuela-Lopez et al., 2018). It is an ubiquitous genus with a global distribution, occurring in aquatic and terrestrial environments including dead stems, leaves and soils (Hou et al., 2020a).

Table 4.15 *Ascochyta* species isolated from soil

Species	Country	Habitat or soil type	References
Ascochyta clinopodiicola	USA	Canyonlands National Park	Hou et al. (2020b)
A. benningiorum	The Netherlands	Garden soil	Hou et al. (2020a)
A. syringae			

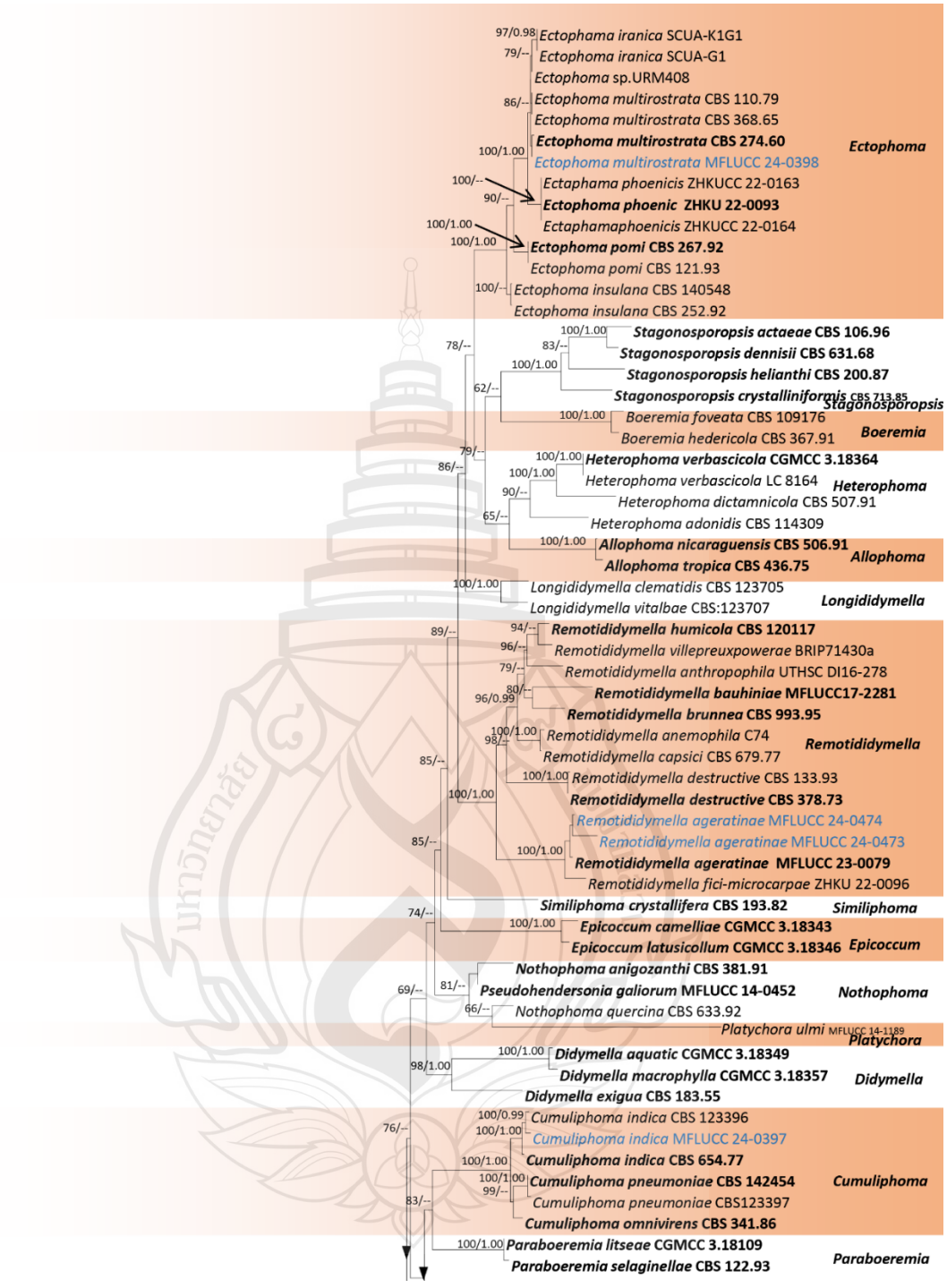


Figure 4.16 The best-scoring maximum likelihood tree generated using the combined, ITS, LSU, *rpb2 and tub2* sequence data of *Didymellaceae* taxa

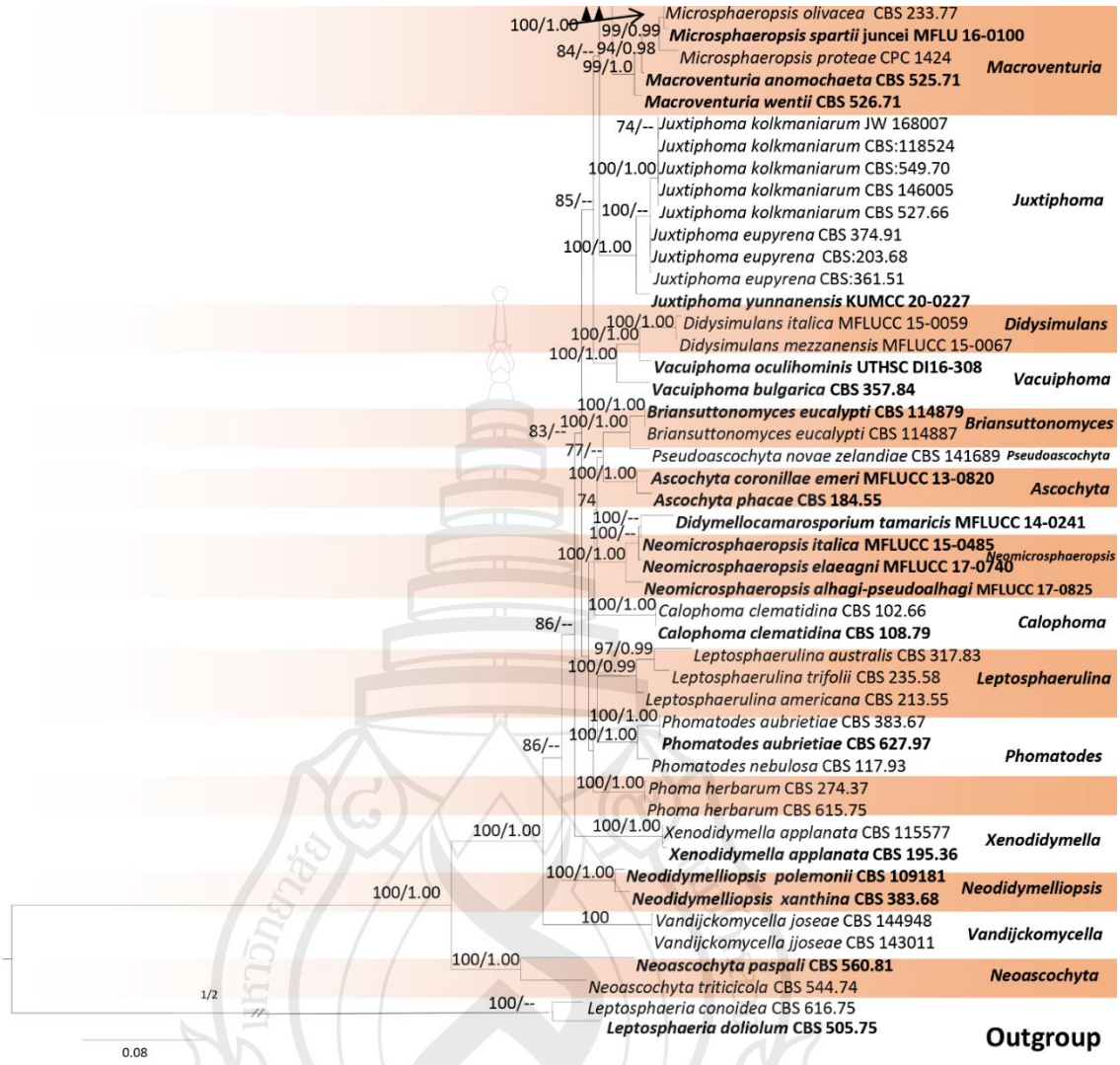


Figure 4.16 (continued)

Figure 4.16, Bootstrap support values of maximum likelihood greater than or equal to 60% and Bayesian posterior probabilities (BYPP) greater than or equal to 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Leptosphaeria conoidea* (CBS 616.75) and *L. doliolum* (CBS 505.75). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 2305 bp, and single gene alignments are ITS: 493 bp, *tub2*: 312, LSU: 904 bp and *rpb2*: 596. The matrix had 1046 distinct alignment patterns, with 24.36% undetermined characters and gaps. Estimated base frequencies were as follows: A = 0.238174, C = 0.244190, G = 0.276056, T = 0.241580; substitution rates AC = 1.788747, AG =

6.334550, AT = 2.067321, CG = 0.907644, CT = 13.561340, GT = 1.000000; gamma distribution shape parameter α = 0.572158.

Cumuliphoma Valenz.-Lopez, Stchigel, Crous, Guarro & Cano, Stud. Mycol. 90: 38 (2017).

Index Fungorum number: IF 819878; Facesoffungi number: FoF 08220;

Cumuliphoma was introduced by Valenzuela-Lopez et al. (2018) with comprehensive multi-loci phylogenetic analyses (LSU, ITS, *tub2* and *rpb2*) and morphology. This genus is typified by *Cumuliphoma omnivirens.* It currently comprises four species (Species Fungorum, 2025), and molecular data is provided for all of them. The asexual morph is characterized by brown, globose pycnidia, glabrous, mostly confluent conidiomata and hyaline, smooth-walled, aseptate and ellipsoidal to cylindrical conidia. The sexual morph is not reported. Chlamydospores are absent in most species and have only been observed in *C. omnivirens*. *Cumuliphoma* is reported from human clinical samples, plant materials and soil habitats in Belgium, China, India and the USA (Valenzuela-Lopez et al., 2018).

Table 4.16 *Cumuliphoma* species isolated from soil

Species	Country	Habitat or soil type	References
Cumuliphoma indica	Papua New Guinea	Varirata National Park	Valenzuela-Lopez et al. (2018)

Cumuliphoma indica Valenz.-Lopez, Stchigel, Crous, Guarro & Cano, Stud. Mycol. 90: 38 (2017)

Index Fungorum number: IF 819880, Faces of Fungi number: FoF 16704,

Figure 4.17

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 110–120 × 100–110 μm ($\bar{x}$ = 113 × 107.5 μm, n = 10), pycnidial, mostly in groups, rarely solitary, superficial to semi-immersed, dark brown to black, globose, glabrous. *Conidiomata wall* 12.5–18 μm ($\bar{x}$ = 15 μm, n = 10), thick, composed of cells of *textura angularis*. *Conidiogenous cells* 3.5–5 × 2–3.5 μm ($\bar{x}$ = 4 × 2.5 μm, n = 10), hyaline, phialidic, ampulliform, smooth-walled. *Conidia* 2.5–4 × 1.5–2.5 μm ($\bar{x}$ = 3.5 × 2 μm, n = 25), hyaline, aseptate, thick-walled, ellipsoidal to sub-cylindrical, guttulate. *Chlamydospores* absent.

Culture characteristics – *Colonies* on PDA become 4–5 cm diam. after seven days at 25°C, appear in dark brown to dark grey, reverse brownish grey at the center and dark brown at the edge, undulate margined, flat powdery surface. *Hyphae* hyaline to pale brown, smooth, thin-walled, septate, 2.5–5 μm ($\overline{x}$ = 4 μm, n = 20) wide.

Material examined – Thailand, Chiang Rai, What Tham Pha Tong cave, on soil, 99.9038925 N, 20.0918488 E, 430 m, 28 Aug 2022, W.A. Erandi Yasanthika (MFLU25-0118); living culture 80-cv23-18 = MFLUCC 24-0397.

GenBank numbers – MFLUCC 24-0397: LSU: PQ560071, ITS: PQ560064

Notes – *Cumuliphoma indica* was introduced by Valenzuela-Lopez et al. (2018) from an unknown substrate in India and soils in Papua New Guinea. Based on the combined LSU, ITS, *rpb2* and *tub 2* phylogeny (Figure 4.17), our strain (MFLUCC 24-0397) grouped with *C. indica* (CBS 654.77) with 100% ML and 1.00 BYPP support. However, *C. lijiangensis* (YMF1.05096) was not included in our analyses as the sequences were not available in the Gene Bank (Chen et al., 2023). When compared each gene region of our strain (MFLUCC 24-0397) with those of the type species (CBS 654.77), they showed 100% similarity. Our isolate also has similar morphological characteristics with the type species, including phialidic, hyaline conidiogenous cells and hyaline, aseptate, guttulate conidia (Valenzuela-Lopez et al., 2018). However, the type species has globose to ampulliform conidiogenous cells and smooth- and thin-walled, ellipsoidal to cylindrical conidia, whereas our strain has only ampulliform conidiogenous cells and thick-walled, ellipsoidal to sub-cylindrical conidia (Valenzuela-Lopez et al., 2018). Based on morphology and multi-gene phylogeny, we confirm our strain as *Cumuliphoma indica.* This study reveals the first record of *Cumuliphoma indica* from Thailand soils associated with undisturbed cave environments.

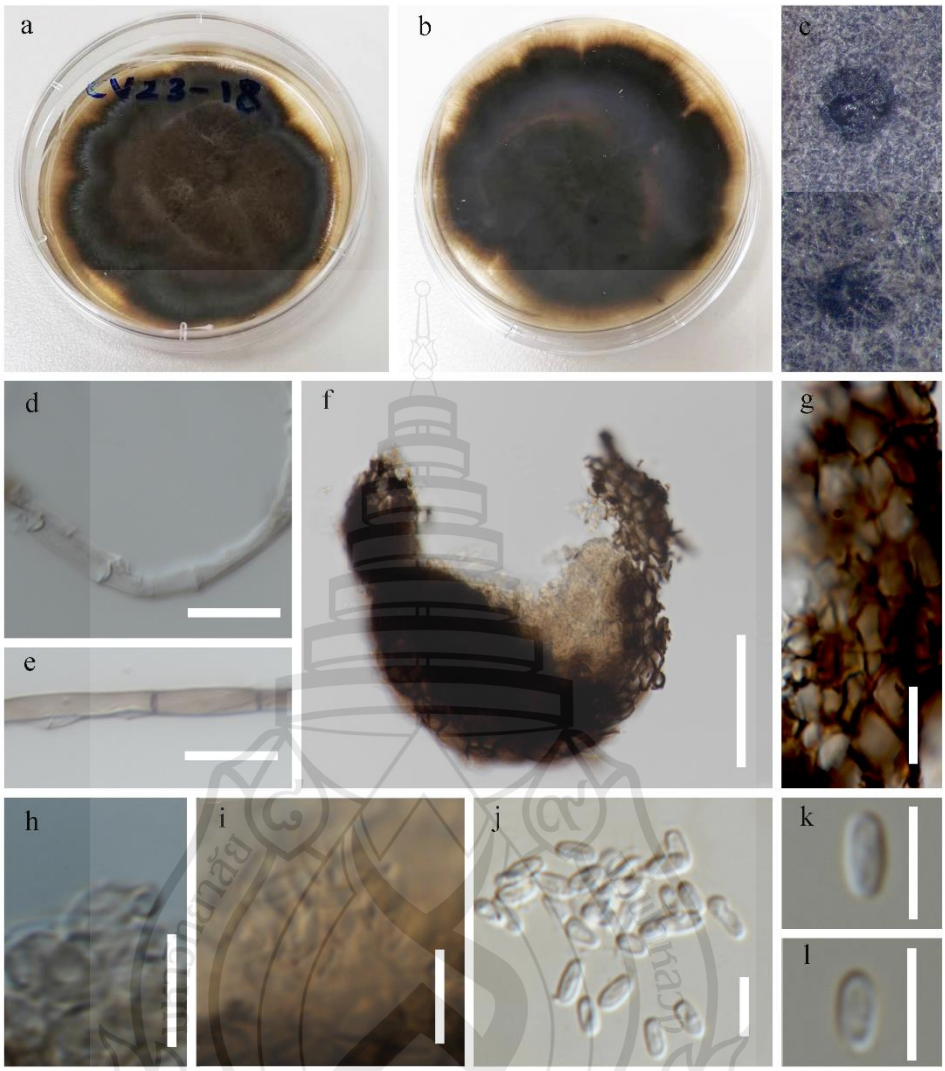


Figure 4.17 *Cumuliphoma indica* (MFLU25-0118)

Figure 4.17, a, b Culture characters on the PDA (b = reverse). d Immature hypha e Mature hyphae. f Pycnidia. g Conidiomata wall h, i Conidiogenous cells. j–l Conidia. Scale bars: d, e =15 μm, f, g = 10 μm, h–k =5 μm.

Didymella Sacc. ex Sacc. Syll. Fung. 1: 545 (1882).

Index Fungorum number: IF 1548; Facesoffungi number: FoF 07278

Saccardo (1882) introduced *Didymella* and accepted *Didymella exigua* as the type species. There are 438 *Didymella* species listed in the Species Fungorum (2025). However, based on the morpho-molecular study of Chen et al. (2015), restricted *Didymella* as a monophyletic genus, which currently includes 87 species. The asexual morph is characterized by pycnidial, subglobose to ellipsoidal or irregular, superficial

or immersed, ostiolate or poroid conidiomata. Conidiogenous cells are phialidic, hyaline, smooth, flask-shaped, ampulliform or doliiform and produce aseptate, hyaline variably shaped (ellipsoidal to subglobose, cylindrical, oblong, ovoid, sometimes allantoid) and mostly guttulate conidia. The sexual morph has pseudothecial, immersed or erumpent, (sub-)globose to flattened, solitary or confluent, ostiolate ascomata with 2–5(–8)-layered, pseudoparenchymatous cell wall. Asci are bitunicate, 8-spored, cylindrical to clavate or saccate, comprising hyaline or brownish, ellipsoidal to cymbiform, uniseptate ascospores that are constricted at the septum (Chen et al., 2015; Jayasiri et al., 2017). Most species produce chlamydospores, allowing them to survive in the soils for several years after the decay of the host tissues (Tivoli & Banniza, 2007; Hou et al., 2020). Most of the species are ubiquitous, and present as pathogens, endophytes and saprobes in soils and some inorganic substrates, such as asbestos, cement, and paint (Chen et al., 2015; Jayasiri et al., 2017).

Table 4.17 *Didymella* species isolated from soil

Species	Country	Habitat or soil type	References
Didymella degraaffiae	The Netherlands	Garden soil	Hou et al. (2020a)
D. mitis	South Africa	Near a city; Namibia: desert	Hou et al. (2020b)
D. prolaticolla	Namibia	Desert	
D. guttulata	*Zimbabwe*	*Deciduous forest*	
D. calidophila	Egypt	*ND*	Chen et al. (2015)

Ectophoma Valenz.-Lopez, Cano, Crous, Guarro & Stchigel, Stud. Mycol. 90: 34 (2017).

Index Fungorum number: IF 819952; Facesoffungi number: FoF 08221

Ectophoma was introduced by Valenzuela-Lopez et al. (2018) based on morphology and multi-gene phylogeny (LSU, ITS, *tub2* and *rpb2*) in *Didymellaceae* to accommodate two species, *E. multirostrataas* and *E. pomi*. The type species is *Ectophoma multirostrata*, which was previously known as *Phoma multirostrata* (Aveskamp et al., 2010; Valenzuela-Lopez et al., 2018). Currently, seven *Ectophoma* species are listed in the Species Fungorum (2025), and all have molecular data. The sexual morph is unknown, and the asexual morph is characterized by pycnidial, brown to dark brown conidiomata with one or more short necks and phialidic, hyaline conidiogenous cells that produce aseptate, hyaline, oblong to ellipsoidal, smooth-

walled, guttulate conidia. Species have been isolated from soil and different woody and herbaceous plants and fruits as saprobe, endophyte, or opportunistic plant pathogens from Greece, India, Iran, South Africa, and the Netherlands, and one species has been reported from soil (Valenzuela-Lopez et al., 2018; Larki et al., 2019; Kularathnage et al., 2023).

Table 4.18. *Ectophoma* species isolated from soil

Species	Country	Habitat or soil type	References
Ectophoma multirostrata	India	Poultry farm	Valenzuela-Lopez et al. (2018)

Ectophoma multirostrata (P.N. Mathur, S.K. Menon & Thirum.) Valenz.-Lopez, Cano, Crous, Guarro & Stchigel, Stud. Mycol. 90: 34 (2017)

Figure 4.18

Index Fungorum number: IF 819953, Faces of Fungi number: FoF 11508

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 125–130 ×108–112 μm ($\overline{x}$ = 128 × 110 μm, n =10), pycnidial, solitary and confluent, superficial, brownish-black, globose to subglobose, apapillate, glabrous, with *textura angularis* pycnidial wall. *Conidiogenesis cells* 3–4 ×1.5–3.5 μm ($\overline{x}$ = 3.5 × 2.5 μm, n = 10), hyaline, phialidic, smooth-walled. *Conidia* 4–4.5 × 1–2.5 μm ($\overline{x}$ = 3 × 1.5 μm, n = 25), hyaline, oval, ellipsoidal to subcylindrical, mostly with 1–2 polar guttules or eguttulate, smooth-walled. *Chlamydospores* not present.

Culture characteristics: *Colonies* on PDA become 3–4 cm diam. after seven days at 25°C, whitish grey surface, reverse brown-black, undulate margined, flat woolly surface. *Hyphae* hyaline, aseptate, becoming pale brown and septate, when mature, smooth, thin-walled 1.5–5 μm ($\overline{x}$ = 3 μm, n = 20) wide.

Material examined – Thailand, Chiang Rai city, on soil (near a Café), 19.983438 N, 99.892159 E, 384 m, 17 Oct 2022, W.A. Erandi Yasanthika (MFLU25-0178); living culture 109-u3-1= MFLUCC 24-0398.

GenBank numbers –MFLUCC 24-0398: LSU: PQ559824, ITS: PQ559838, RPB2: **, BUTB: **.

Notes–Multi-gene phylogeny (LSU, ITS, *rpb2* and *tub2*) in Figure 4.16 confirms that our strain (MFLUCC 24-0398) grouped with *Ectophoma multirostrata* with 100% ML and 1.00 BYPP statistical support. In our analyses (Figure 4.16), *E. myriophyllana*

YMF1.05050 (Chen et al., 2023) has not been included as the sequences were unavailable in GenBank. Each gene region showed 100% similarity when compared between our strain (MFLUCC 24-0398) and those of the type species of *Ectophoma multirostrata* (CBS 274. 60). Further, our strain has comparable morphology with the type species, including globose to subglobose, glabrous, solitary and confluent pycnidia and hyaline, oval, ellipsoidal to subcylindrical, mostly 1–2 polar guttules, and sometimes eguttulate conidia (Boerema et al., 2004; Valenzuela-Lopez et al., 2018). By considering the morphology and phylogenetic evidence, we confirm our isolate (MFLUCC 24-0398) as *E. multirostrata.* This species has previously been reported from poultry farm soil in India and the stem of *Cucumis sativus* in the Netherlands (Valenzuela-Lopez et al., 2018). This study investigates the first record of *E. multirostrata* from Thailand from urban soils.

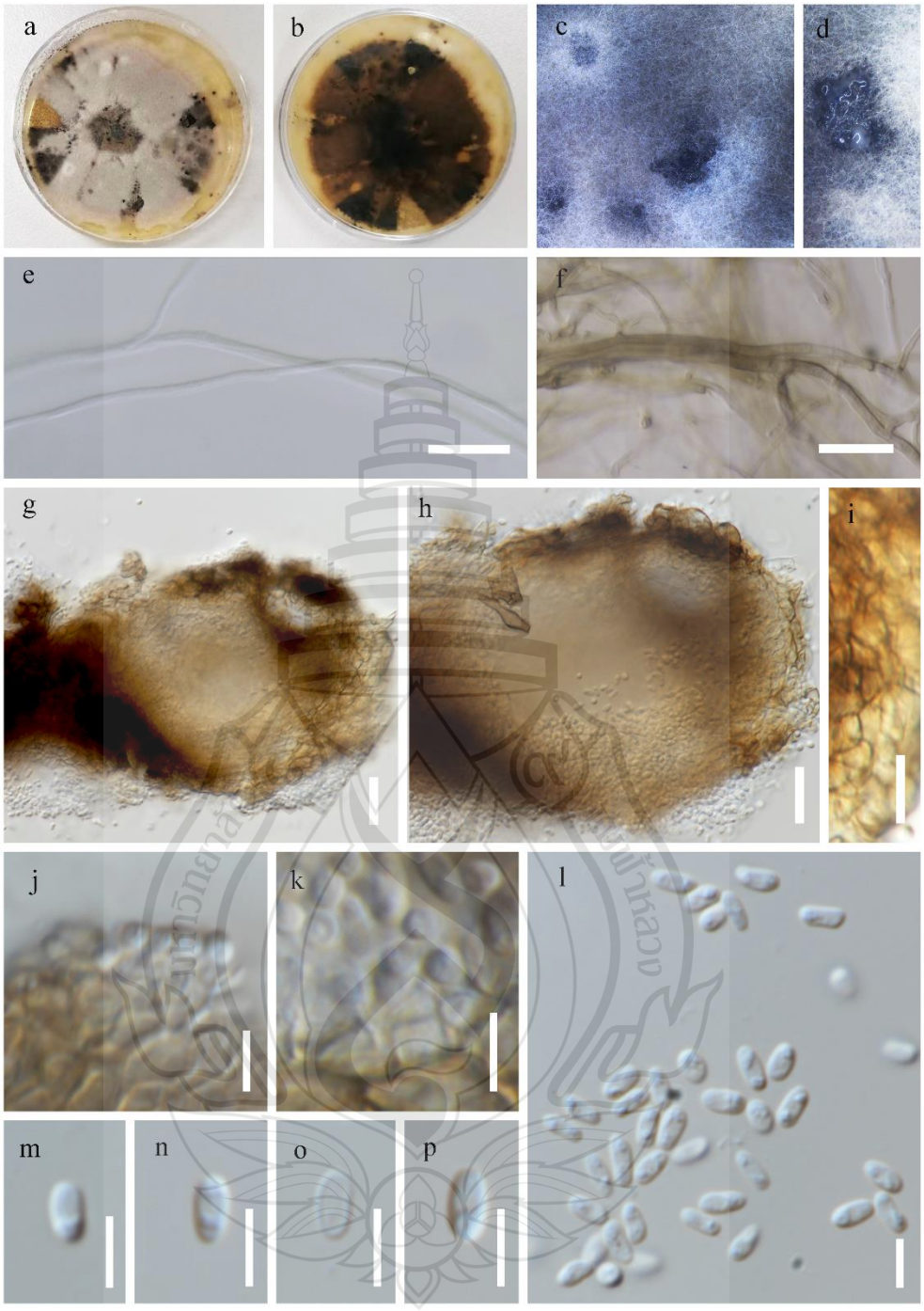


Figure 4.18 *Ectophoma multirostrata* **(**MFLU25-0178)

Figure 4.18, a, b Culture characters on the PDA (b = reverse). c, d. Pycnidia form on the culture. e Immature hypha. f. Mature hyphae. g. Pycnidia. h. Pycnidia with conidial matrix and conidia i. Pycnidial wall. j, k. Conidiogenous cells. l–p.. Conidia. Scale bars: d, e, g = 20 μm, i = 10 μm, j–p = 5 μm.

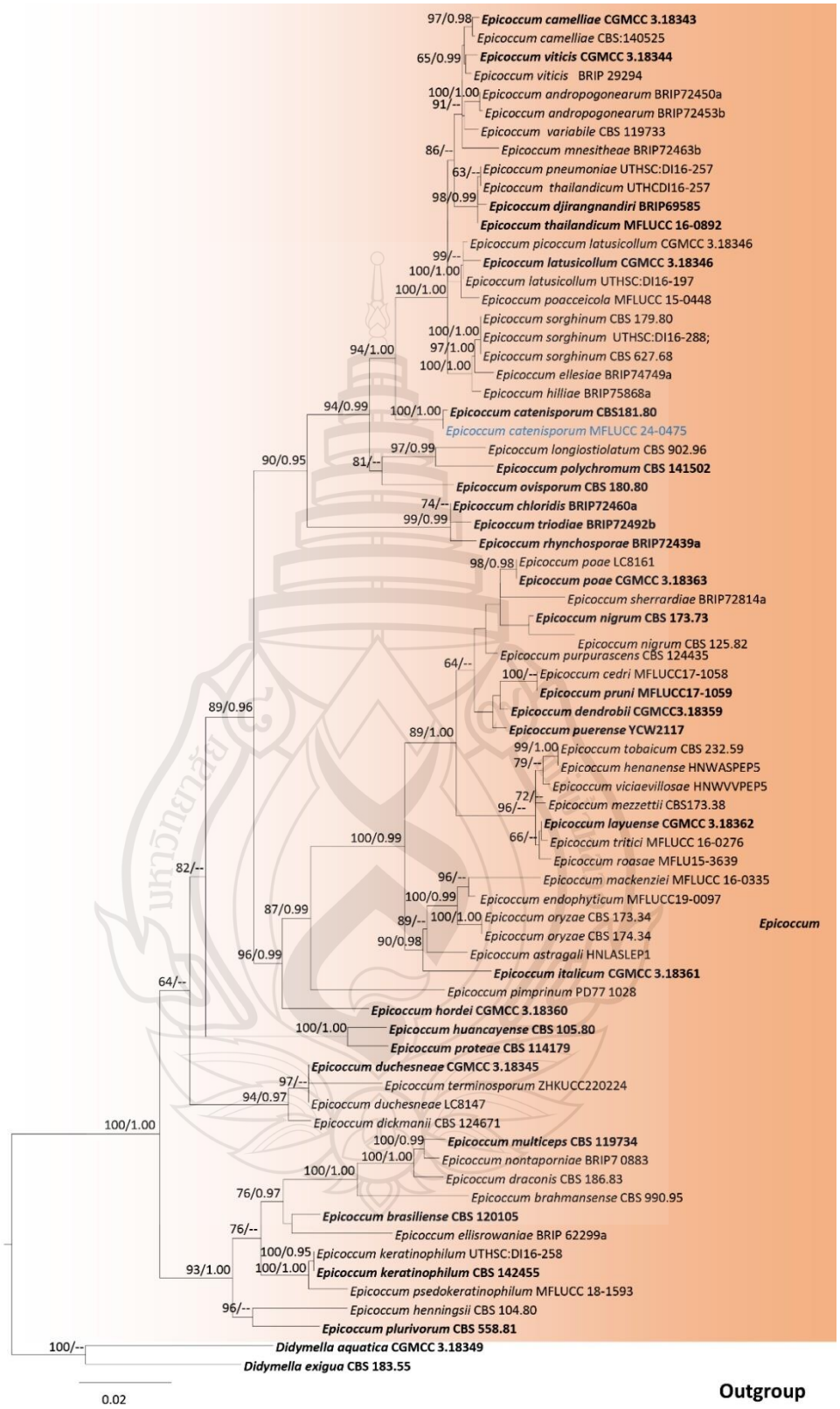


Figure 4.19 The best-scoring maximum likelihood tree generated of the combined LSU and ITS, *rpb2* and *tub2* sequence data for *Epicoccum*

Figure 4.19, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Didymella aquatica* (CGMCC 3.18349) and *Didymella exigua* (CBS 183.55). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 2531 bp, and single gene alignments are ITS: 469 bp, LSU: 871 bp, *tub2*: 306 and *rpb2*: 885 bp. The matrix had 632 distinct alignment patterns with 22.49% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250 G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 4.26929, AT = 1.00000, CG = 1.00000, CT = 9.28992, GT = 1.00000; gamma distribution shape parameter $\alpha = 0.794$.

Epicoccum Link, Mag. Gesell. naturf. Freunde, Berlin 7: 32 (1816) [1815].

Index Fungorum number: IF 8188; Facesoffungi number: FoF 08222;

Epicoccum was introduced by Link (1815) with its type species *E. nigrum.* Currently, 149 species are listed in the Species Fungorum (2025), and there are 43 species with molecular data (Wang et al., 2024c). The asexual morph has sporodochia on cultures and natural substrates. Conidia are globose to pyriform with a funnel-shaped base and broad attachment scar (Domsch et al., 1993). Chen et al. (2015) further specified the morphology as irregular, pycnidial conidiomata and subcylindrical-shaped conidia. Culture sporulation can be induced by black light. Most of the *Epicoccum* species are plant pathogens and can also be endophytes (Chen et al., 2015) and are associated with air, animals, aquatic habitats, humans and soil (Abdel-Azeem et al., 2021). Species are distributed in China, Egypt, Indonesia, Italy, Korea, Romania, Papua New Guinea and the USA (Guiraud et al., 1995; Samiksha & Sanjeev, 2021).

Table 4.19 *Epicoccum* species isolated from soil

Species	Country	Habitat or soil type	References
Epicoccum brahmansense	Papua New Guinea	Tropical forest	Hou et al. (2020b)
E. draconis	Korea	Tobacco field	Ayim et al. (2020)
E. mackenziei	Kashmir valley	Agricultural soil	Amin et al. (2024)
E. nigrum	ND	Dead Sea valley	Guiraud et al. (1995)
E. pimprinum	India	ND	Aveskamp et al. (2010)
E. sorghi	Papua New Guinea	Near a national park	
E. tobaicum	Indonesia	Heath soil	Hou et al. (2020b)

Epicoccum catenisporum Valenz.-Lopez, Stchigel, Crous, Guarro & Cano, Stud. Mycol. 90: 30 (2017)

Figure 4.20

Index Fungorum number: IF 819762, Facesoffungi number: FoF 16706

Sexual morph: Undetermined. Asexual morph: *Chlamydospores* 4.5–11.5 × 4–9 μm ($\overline{x}$ = 8 × 6 μm, n = 25), brown, globose to subglobose or ellipsoidal, terminal or intercalary, produced from mature hyphae, solitary, or simple or branched chains, smooth-walled.

Culture characteristics: *Colonies* on PDA become 3–4 cm diam. after 7 days at 25 °C, appear whitish brown at the center, white at the middle and brownish margined, reverse brownish orange, undulate margined, raised surface. *Hyphae* hyaline and become sub-hyaline to brown when mature, septate, 1.5–4.5 μm ($\overline{x}$ = 3 μm) wide, superficial to semi-immersed and branched, immature hyphae become pale brown septate when mature

Material examined – Thailand, Chiang Rai city, on soil (near a Café), 19.983438N, 99.892159E, 384 m, 17 Oct 2022, W.A. Erandi Yasanthika (MFLU25-0128); living culture 111-u3-7 = MFLUCC 24-0475.

GenBank numbers –MFLUCC 24-0475: LSU: PQ568013, ITS: PQ567558

Notes – According to multi-gene phylogeny (Figure 4.19), our strain (MFLUCC 24-0475) grouped with the type species of the *Epicoccum catenisporum* with 100% ML, 1.00 BYPP statistical support. Each gene region of our strain and the type species showed that they have 100% similarity. *Epicoccum catenisporum* was introduced by Valenzuela-Lopez et al. (2018) from a leaf spot of *Oryza sativa* in Guinea-Bissau, and it has later been isolated from tea plant leaves in China (Wang et al., 2024c). The type species is characterized by brown to dark brown, solitary, superficial and immersed glabrous, subglobose pycnidia and phialidic, hyaline, smooth-walled, doliiform or ampulliform conidiogenous cells and aseptate, hyaline, smooth- and thin-walled, ovoid or ellipsoidal, guttulate conidia (Valenzuela-Lopez et al., 2018). However, our collection only produced chlamydospores without forming other asexual or sexual structures. Comparing the chlamydospore characteristics, we observed that our isolate is similar to the type species by having dark brown, smooth- and thick-walled, ellipsoidal to ovoid chlamydospores singly or in chains (Valenzuela-Lopez et al., 2018).

Based on the results, we confirm our collection (MFLUCC 24-0475) as *Epicoccum catenisporum* collected in an urban area in Thailand. This becomes the first record of the species present in the soil.

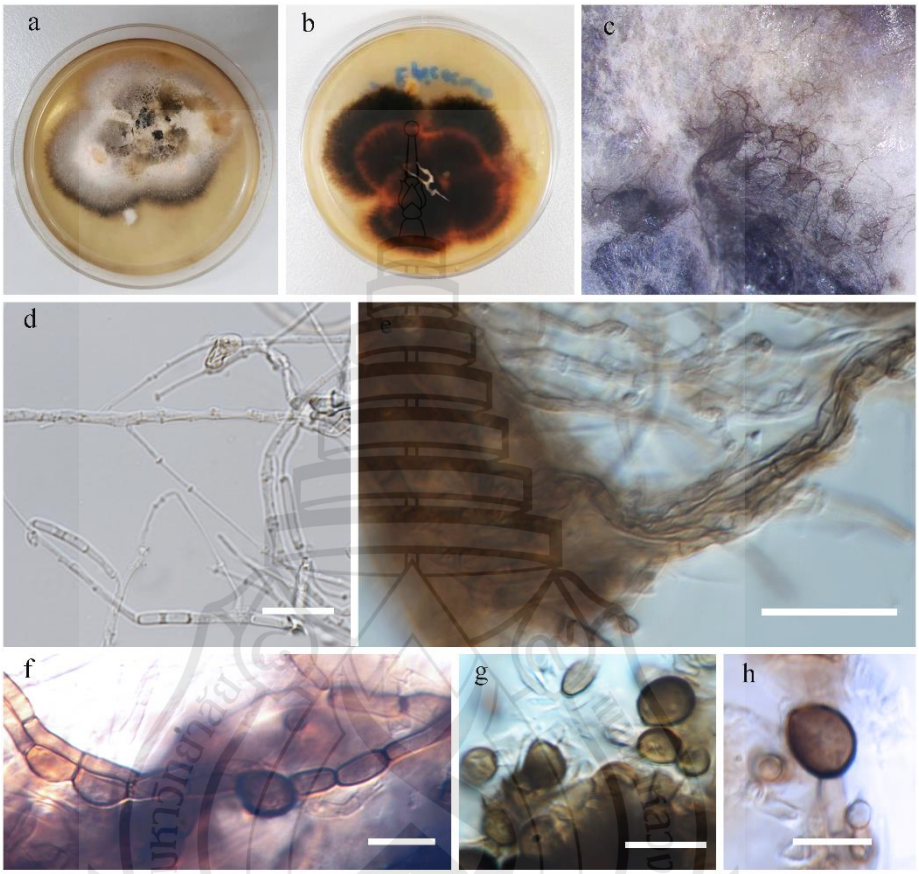


Figure 4.20 *Epicoccum catenisporum* (MFLU25-0128)

Figure 4.20, a, b culture characters on PDA (b = reverse). c Mycelia appear in the colony. d Immature aseptate hyphae e Mature septate hyphae. f Intercalary chained chlamydospores. g Solitary chlamydospores. h Solitary terminal chlamydospores formation. Scale bars: d, e = 20 μm, f–h = 10 μm.

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

Figure 4.21

Index Fungorum number: IF 821111; Facesoffungi number: FoF 08224

Juxtiphoma was erected by Valenzuela-Lopez et al. (2018) using morphology and multi-gene phylogeny (LSU, ITS, *rpb2* and *tub2*). The type species is designated as *J. eupyrena* isolated from *Solanum tuberosum* (Saccardo, 1879). *Juxtiphoma* has three species listed in the Species Fungorum (2025), all of which are supported by

molecular data. The asexual morph is characterized by pycnidial conidiomata, aseptate, hyaline, smooth- and thin-walled, ovoid, ellipsoidal or cylindrical, biguttulate conidia. Chlamydospores are aseptate, ochraceous-brown and single or in chains. Species are recorded from various soils, including volcanic, steam- and formalin-treated soils and activated sludge. These species have been isolated from soils in China, Germany, Iceland, India, Malaysia, the British Isles, the Netherlands, and the USA (Domsch et al., 1993; Valenzuela-Lopez et al., 2018; Hou et al., 2020). *Juxtiphoma eupyrena* inhabits soil, mostly saprobic fungi, but also can cause damping off of seedlings and woody plants (Boerema et al., 2004).

Table 4.20 *Juxtiphoma* species isolated from soil

Species	Country	Habitat or soil type	References
Juxtiphoma eupyrena	Germany	Wheat field soil	Domsch et al. (1993)
J. kolkmaniorum	Canada	Cave	Hou et al. (2020a),
J. kolkmaniorum	Germany	Wheat field soil	Valenzuela-Lopez et al.
J. kolkmaniorum	The Netherlands	Garden soil	(2018)
J. yunnanensis	China	Contaminated soil	Yasanthika et al. (2021)

Figure 4.21 *Juxtiphoma eupyrena*

Figure 4.21, a Chlamydospores. Redrawn from Domsch et al. 1980

Neoascochyta Q. Chen& L. Cai, Stud. Mycol. 82: 198. 2015.

Figure 4.2

Index Fungorum number: IF 814064; Facesoffungi number: FoF 07462

Neoascochyta was introduced by Chen et al. (2015) based on LSU, ITS, *rpb2* and *tub2* phylogeny and morphological support, accommodating *N. exitialis* as the type species. The genus comprises 21 species (Species Fungorum 2025), and all of them are supported by molecular data. *Neoascochyta* and *Ascochyta* have similar morphology but are phylogenetically distinct (Chen et al., 2015). The asexual morph is characterized by pycnidial, globose to subglobose, or irregular, superficial or immersed, ostiolate conidiomata, and pseudoparenchymatous pycnidial walls. Conidiogenous cells are phialidic, globose to flask-shaped, short obpyriform, or ampulliform to doliiform and produce variably shaped (fusoid to cylindrical, obclavate-ovoid to ellipsoidal), hyaline, smooth- and thin-walled, uniseptate or aseptate, eguttulate or guttulate conidia. The sexual morph has pseudothecial immersed or erumpent, solitary or confluent, globose to subglobose, and ostiolate ascomata. Asci are cylindrical to subclavate, slightly curved, short pedicellate or sessile, 8-spored, bitunicate, and cylindrical to ovoid, ellipsoidal, hyaline, 1-septate ascospores that are constricted at the septum (Chen et al., 2015). *Neoascochyta* species occur in clinical samples, dead and living plant materials and two species from soil in Argentina, China, Germany, Italy, New Zealand, Norway and the USA (Chen et al., 2015; Valenzuela-Lopez et al., 2018).

Table 4.21 *Neoascochyta* species isolated from soil

Species	Country	Habitat or soil type	References
Neoascochyta humicola	USA	Near a city	Hou et al. (2020b)
N. soli	China	Kuankuoshui National Geopark	Valenzuela-Lopez et al. (2018)

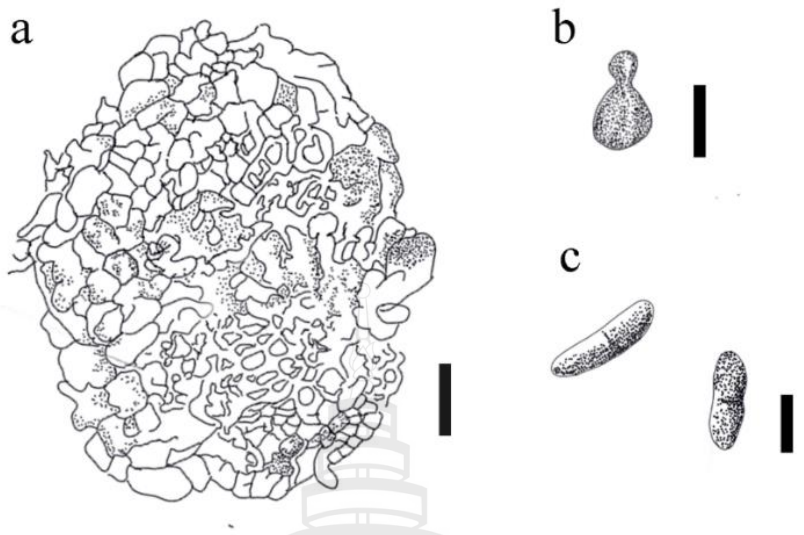


Figure 4.22 *Neoascochyta exitialis* (CBS 389.86)

Figure 4.22, a Pycnidial section. b Conidiogenous cell. c Conidia. Scale bars: a = 20 μm, b, c = 10 μm. Redrawn from Chen et al. (2015).

Neodidymelliopsis Qian Chen & L. Cai, Stud. Mycol. 82: 207 (2015).

Figure 4.23

Index Fungorum number: IF 814066; Facesoffungi number: FoF 07518

Chen et al. (2015) introduced *Neodidymelliopsis* with its type species *N. cannabis*, based on LSU, ITS, *rpb2* and *tub2* phylogeny and morphological support. *Neodidymelliopsis* comprises 15 species (Species Fungorum 2025), and all of them have molecular data. The asexual morph has pycnidial, globose to subglobose, superficial or immersed, ostiolate, conidiomata with an elongated neck and pseudoparenchymatous wall. Conidiogenous cells are phialidic, hyaline, smooth, flask-shaped, ampulliform to short cylindrical, that produce smooth- and thin-walled, hyaline to pale brown, or pale yellowish, 0–1-septate, guttulate conidia in variable shapes (ovoid to ellipsoidal, cylindrical, allantoid). The sexual morph has pseudothecial, immersed or erumpent, subglobose to pyriform, solitary or confluent, ostiolate ascomata having filamentous, 0(–3) -septate pseudoparaphyses. Asci are cylindrical to clavate, sessile or stipitate, 8-spored, bitunicate and sub-ovoid to oblong, ellipsoidal, hyaline, smooth, 1(–3)-septate, ascospores constricted at the septum. Chlamydospores that are globose to oval, single or in chains can also be present (Chen et al., 2015). The species have been reported from clinical samples (human

eye and respiratory tract), dead plant materials and one species from soil, which are found in Canada, Israel, the Netherlands, the UK, and the USA (Valenzuela-Lopez et al., 2018).

Table 4.22 *Neodidymelliopsis* species isolated from soil

Species	Country	Habitat or soil type	References
N. longicolla	Israel	A desert	Chen et al. (2017)

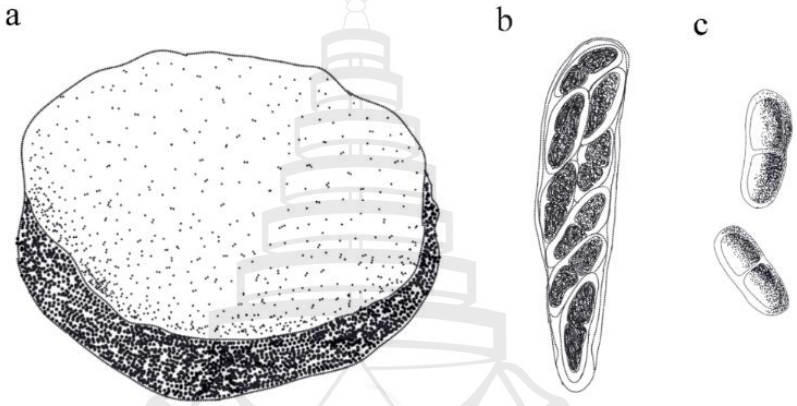


Figure 4.23 *Neodidymelliopsis cannabis*

Figure 4.23, a Conidiomata. b. Ascus and ascospores. c. Conidia. Redrawn from McPartland (1994).

Nothophoma Qian Chen & L. Cai, Stud. Mycol. 82: 212 (2015).

Index Fungorum number: IF 814060; Facesoffungi number: FoF 08227

Chen et al. (2015) introduced *Nothophoma* to accommodate several *Phoma* species based on morpho-molecular (LSU, ITS, *rpb2* and *tub2*) support, with *Nothophoma infossa* being accepted as the type species. The genus currently comprises 23 species (Species Fungorum, 2025), while all of them have molecular data. The asexual morph is characterized by pycnidial, superficial or immersed, globose to elongated, or irregular conidiomata, with phialidic, hyaline, smooth, ampulliform to doliiform conidiogenous cells. Conidia are hyaline, sometimes brown, aseptate, smooth- and thin-walled, with variable shapes (ovoid, oblong to ellipsoidal), eguttulate or guttulate. The sexual morph remains undetermined. These species include saprobes and pathogens that occur on plants, the human body, litter and soil detected in India,

the Netherlands, the USA and Ukraine (Chen et al., 2015; Valenzuela-Lopez et al., 2018).

Table 4.23 *Nothophoma* species isolated from soil

Species	Country	Habitat or soil type	References
Nothophoma brennandiae	The Netherlands	Garden	Hou et al. (2020a)
N. raii	India	Industrial area	Crous et al. (2017a)

Paraboeremia Qian Chen & L. Cai, Stud. Mycol. 82: 183 (2015).

Figure 4.24

Index Fungorum number: IF 814061; Facesoffungi number: FoF 08228

Paraboeremia was erected by Chen et al. (2015) and typified with *P. selaginellae.* This genus has 11 species (Species Fungorum 2025), all of which are available with molecular data. Morphologically, *Paraboeremia* is similar to *Boeremia* but has a distinct phylogeny (Chen et al., 2015). The asexual morph has pycnidial, globose to subglobose, irregular-shaped conidiomata. Conidiogenous cells are hyaline, phialidic, globose to flask-shaped and produce hyaline or sometimes greenish, ellipsoidal or curved, smooth- and thin-walled, aseptate, guttulate conidia. The sexual morph has pseudothecial, subglobose to pyriform, ostiolate ascomata, containing 8-spored, bitunicate asci. Ascospores are hyaline, subcylindrical, 1-septate, and constricted at the septum (Chen et al., 2015; Hongsanan et al., 2020a). Species have been isolated from plant materials and soil in China, the Netherlands and the USA (Hou et al., 2020a).

Table 4.24 *Paraboeremia* species isolated from soil

Species	Country	Habitat or soil type	References
Paraboeremia litseae	The Netherlands	Garden soil	Hou et al. (2020a)
P putaminum			
*P. rekker*i			
P. truiniorum			

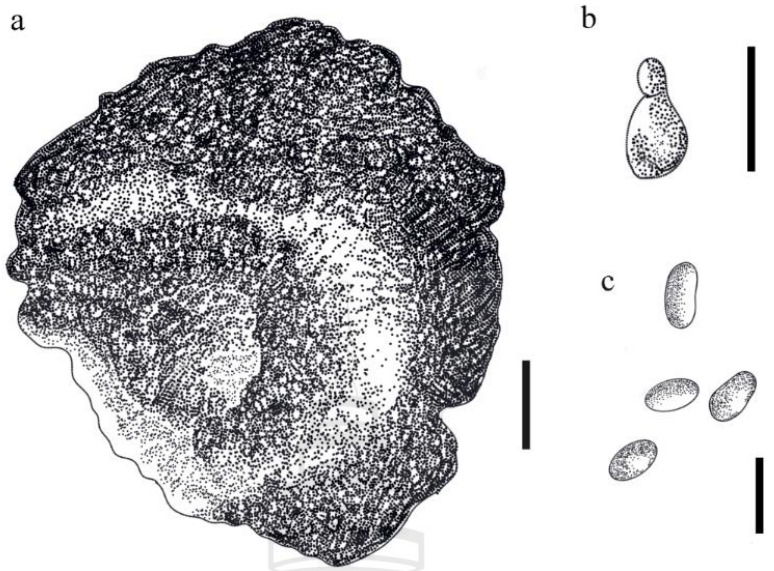


Figure 4.24 *Paraboeremia selaginellae* (CBS 122.93)

Figure 4.24, a Pycnidium. b Conidiogenous cell. c Conidia. Scale bars a= 100 μm, b = 10 μm, c = 5 μm. Redrawn from Chen et al. (2015).

Pseudoascochyta Valenzuela-Lopez, Stchigel, Cano-Canals, Guarro & Cano, Persoonia 37: 255 (2016).

Figure 4.25

Index Fungorum number: IF 817646; Facesoffungi number: FoF 08232;

Crous et al. (2016) introduced *Pseudoascochyta* based on LSU, ITS, *rpb2* and *tub2* with morphological illustrations, and *P. pratensis* is accommodated as the type species. Two species are currently listed in this genus (Species Fungorum, 2025), and both are supported with molecular data. The asexual morph has brown to dark brown, globose, solitary pycnidia with textura angularis walls. Conidiogenous cells are hyaline, enteroblastic, phialidic, globose to flask-shaped, thin-walled and produce hyaline, cylindrical, 1-septate, guttulate conidia. The sexual morph is unreported (Crous et al., 2016; Hongsanan et al., 2020a). This genus has been found in plant material, and one species has been reported from soil (Crous et al., 2016).

Table 4.25 *Pseudoascochyta* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudoascochyta pratensis	Spain	ND	Crous et al. (2016)

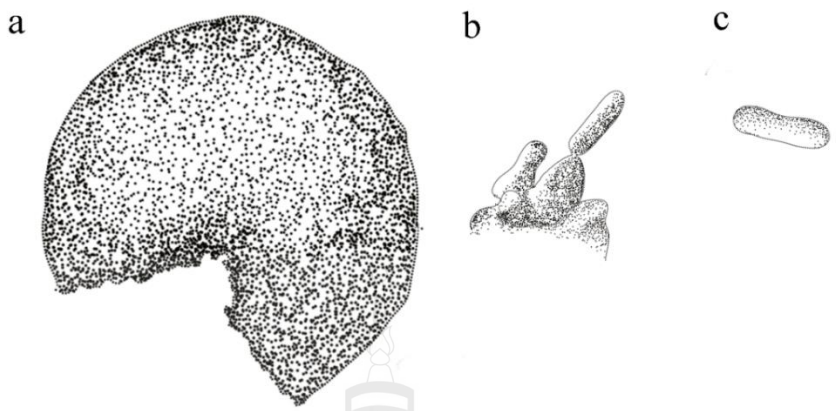


Figure 4.25 *Pseudoascochyta pratensis* (CBS H-22735)

Figure 4.25, a Pycnidium. b Conidiogenous cells. c Conidium. Redrawn from Crous et al. (2016)

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

Index Fungorum number: IF 819990

Remotididymella was introduced by Valenzuela-Lopez et al. (2018) with the multigene phylogenetic analyses in *Didymellaceae*, and *Remotididymella destructiva* is accepted as the type species. The Species Fungorum (2025) lists 11 species under *Remotididymella*, and all are supported by molecular data. The asexual morph is characterized by the pycnidial conidiomata with brown to dark brown, mostly glabrous, globose or irregularly-shaped, with *textura angularis* pycnidial wall. It has phialidic, hyaline, smooth-walled conidiogenous cells and hyaline, aseptate, allantoid or cylindrical, guttulate conidia. The sexual morph is characterized by immersed or superficial, scattered or aggregated, globose, conical, globose to lenticular ascomata and 8-spored, bitunicate, fissitunicate, clavate to short cylindrical asci, that contain hyaline, overlapping 2–3-seriate, fusiform, 1–3-septate ascospores. C*hlamydospores* appear in intercalary or terminal, verruculose or incidentally tuberculate in subhyaline to dark brown (Hou et al., 2020b; Valenzuela-Lopez et al., 2018). ***Remotididymella*** has been recorded as plant saprobes and pathogens from *Ageratina adenophora*, *Bauhinia* sp., *Capsicum annuum*, *Lycopersicon* sp., and *Solanum* sp., human clinical samples and soil (Valenzuela-Lopez et al., 2018; Yang et al., 2021; Kularathnage et al., 2023). These species are distributed in China, Guadeloupe, Papua New Guinea, Thailand, the

Republic of Fiji and the USA (Hou et al., 2020b; Yang et al., 2021a; Kularathnage et al., 2023).

Table 4.26 *Remotididymella* species isolated from soil

Species	Country	Habitat or soil type	References
Remotididymella brunnea	**Papua New Guinea**	Tropical forest	Hou et al. (2020b)
R. humicola	**Puerto Rico**	Onion field	

Remotididymella ageratinae H.B. Zhang, A.L. Yang & L. Chen

Figure 4.26

Index Fungorum number: IF 833832; Facesoffungi number: FoF 16705,

Sexual morph: *Ascomata* 80–100 ×125–132 μm ($\overline{x}$ = 88 × 128 μm, n = 10), globose to subglobose, brown to dark brown, papillate, aggregated, with *textura angularis* wall. *Asci* 32–43 × 5–10 μm ($\overline{x}$ = 37 × 8 μm, n = 15), hyaline, bitunicate, clavate to short cylindrical. *Ascospores* 11–14 × 4–6 μm ($\overline{x}$ = 12 × 5 μm, n = 25), biseriate, hyaline, smooth, ellipsoidal, slightly curved, pointed apex and a broadly pointed to curved base, 1-septate, constricted at the septum, sometimes guttulate. *Chlamydospores* 10–20 × 7–17 μm ($\overline{x}$ = 13 × 11 μm, n = 20), hyaline, become brown when mature, intercalary, branched chains, verruculose, rough, globose to subglobose or cylindrical, thick-walled. Asexual morph: Undetermined.

Culture characteristics – *Colonies* on PDA become 2–3 cm diam. after seven days at 25 °C, appear whitish brown to grey, reverse brownish orange to dark brown, undulate margined, raised surface. *Hyphae* hyaline to pale brown, thick-walled, septate become brown when mature 1.5–3.5 μm ($\overline{x}$ = 2.5 μm) wide.

Material examined – Thailand, Chiang Rai Province, Chiang Rai, Fish cave temple (Wat Tham Pla), on soil in a cave, 99.863679 N, 20.328605 E, 440m, 8 February 2021, W.A. Erandi Yasanthika (MFLU25-0132); living culture 32-cv4-72= MFLUCC 24-0473. *ibid*. a public roadside, 19.909030 N, 99.835183E, 398m, 17 Oct 2022, W.A. Erandi Yasanthika (MFLU25-0133); living culture 3-Rd7=MFLUCC 24-0474

GenBank numbers – MFLUCC 24-0473: LSU: PQ568011, ITS: PQ567556, RPB2: PV523930; MFLUCC 24-0474: LSU: PQ568012, ITS: PQ567557, RPB2: PV523928, BUTB: PV523929.

Notes –Based on the combined LSU, ITS, *rpb2* and *tub2* phylogeny in Figure 4.16, our strains (MFLUCC 24-0473 and MFLUCC 24-0474), grouped with *Remotididymella ageratinae* (MFLUCC 23-0079) with 100% ML, 1.00 BYPP statistical support. We were unable to include *R. hydrillana* (YMF1.05022) (Chen et al., 2023) in the phylogenetic analyses as the sequences were unavailable in GenBank. The comparison of each gene region between our strain and the type of *R. ageratinae* (MFLUU 23-0079) showed that they have 100% similarity. Our isolates are morphologically similar to *R. ageratinae* (MFLUCC 23-0079) by having aggregated, globose or irregular, papillate ascomata, clavate to cylindrical asci and ellipsoidal, 1-septate, ascospores that are slightly constricted at the septum (Yang et al., 2021a). In contrast to the type species, we observed guttulate ascospores and chlamydospores in our isolate. *Remotididymella ageratinae* was introduced by Yang et al. (2021) from leaf spots in *Ageratina adenophora* in China and has also been reported from dead leaves of *Nayariophyton zizyphifolium* in Thailand (Karunarathna et al., 2024). Based on morphology and phylogeny, we confirm our collection as *R. ageratinae* from the soil collected from a disturbed cave and public roadsides in Thailand. Thus, this accounts for its first record from soil habitats.

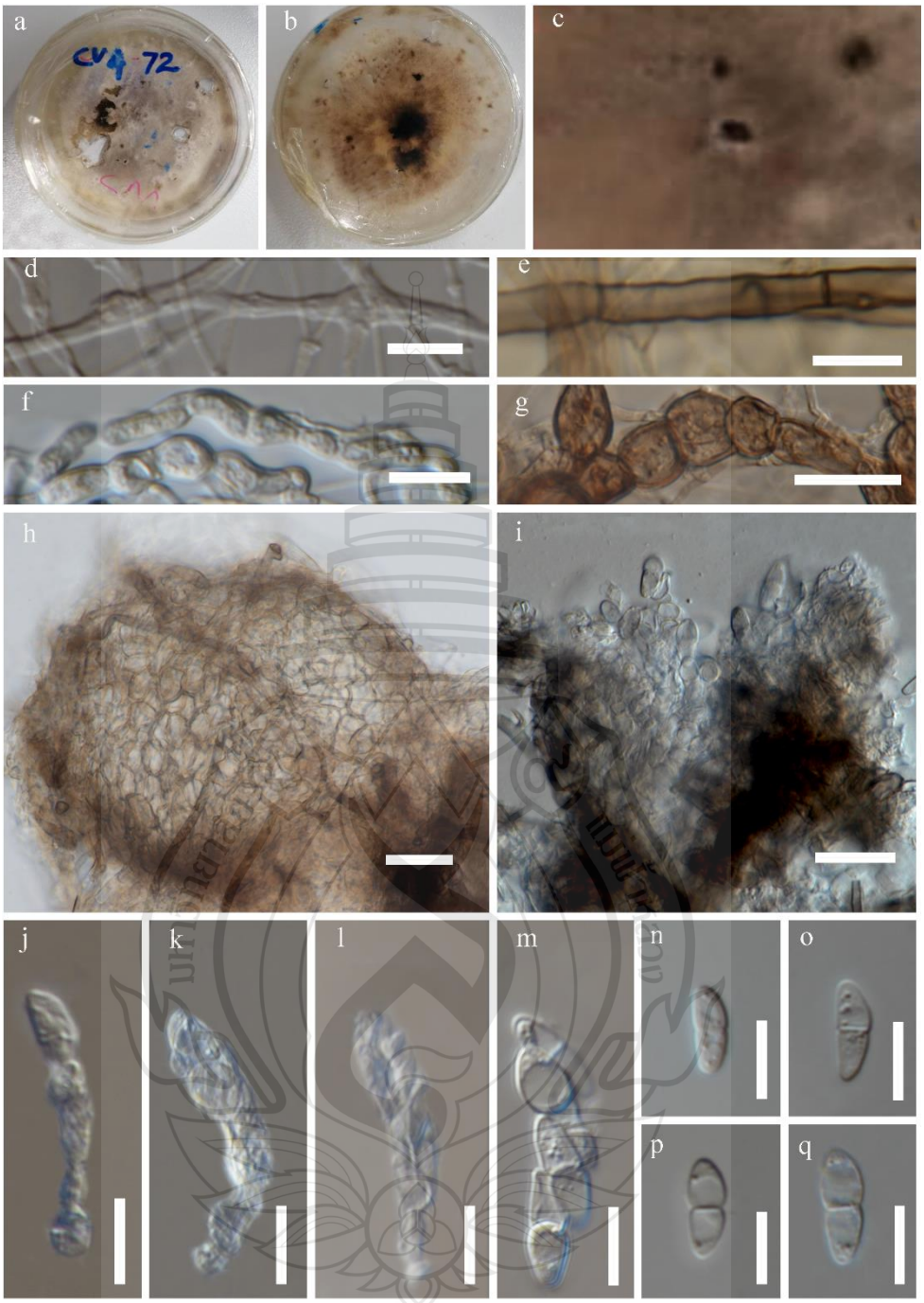


Figure 4.26 *Remotididymella ageratinae* (MFLUCC 24-0473)

Figure 4.26, a, b Culture characters on the PDA (b = reverse). c Ascomata forming on culture. d Immature hypha. e. Mature, pigmented hyphae. f, g. Chlamydospores. h, i Ascomata and wall j–m Asci. n–q Ascospores. Scale bars: g–i = 20 µm, d–f, j–q = 10 µm.

Stagonosporopsis Died. emend. Aveskamp et al., Stud. Mycol. 65: 44. 2010.

Index Fungorum number: IF 10059; Facesoffungi number: FoF 00160;

Stagonosporopsis was introduced by Diedicke (1912) with the type species, *S. hortensis*. Its placement in *Didymellaceae* was confirmed using phylogenetic analyses (LSU, ITS and *tub2*) by Aveskamp et al. (2010). There are 43 *Stagonosporopsis* species in the Species Fungorum (2025), while 32 have molecular data (Chen et al., 2023). The asexual morph possesses conidiomata that are pycnidial, superficial or immersed, globose to subglobose, ostiolate or poroid with a pseudoparenchymatous pycnidial wall. Conidiogenous cells are phialidic, hyaline, ampulliform or doliiform and produce dimorphic conidia, of which the majority are hyaline, smooth-walled, aseptate and ellipsoidal to subglobose. The sexual morph occurs only in culture and is characterized by pseudothecial ascomata having a globose to subglobose shape and sometimes with a conical neck. Asci are cylindrical or subclavate, 8-spored, biseriate, containing ellipsoidal, fusiform or obovoid, 1-septate, guttulate ascospores (Chen et al., 2015; Hongsanan et al., 2020a). Species exist as pathogens and saprobes on plant materials and soil in Germany, New Zealand, Sweden and the Netherlands (Chen et al., 2015; Hou et al., 2020a).

Table 4.27 *Stagonosporopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Stagonosporopsis rhizophilae	China	Rhizospheric soil	Wei et al. (2021)
S. stuijvenbergii	The Netherlands	A garden soil	Hou et al. (2020a)
S. weymaniae			

Vandijckomycella Hern.-Restr., L.W. Hou, L. Cai & Crous, in Hou et al., MycoKeys 65: 86 (2020)

Figure 4.27

Index Fungorum number: IF 833205; Facesoffungi number: FoF 08849

Vandijckomycella was erected by Hou et al. (2020a) based on the multi-loci phylogeny of ITS, LSU, *rpb2* and *tub2* genes, and *V. joseae* is designated as the type species. The genus has two species (Species Fungorum, 2025) and is supported by molecular data. Both of these were isolated from soil (Hongsanan et al., 2020a; Hou et al., 2020a). The asexual morph is characterized by pycnidial conidiomata with longer

whitish hyphal outgrowths. Conidiogenous cells are phialidic, giving rise to hyaline, smooth and thin-walled, aseptate, ovoid, oblong or ellipsoidal conidia. The sexual morph has not been observed (Hongsanan et al., 2020a; Hou et al., 2020a).

Table 4.28 *Vandijckomycella* species isolated from soil

Species	Country	Habitat or soil type	References
Vandijckomycella joseae	The Netherlands	A garden soil	Hou et al. (2020a)
V. snoekiae			

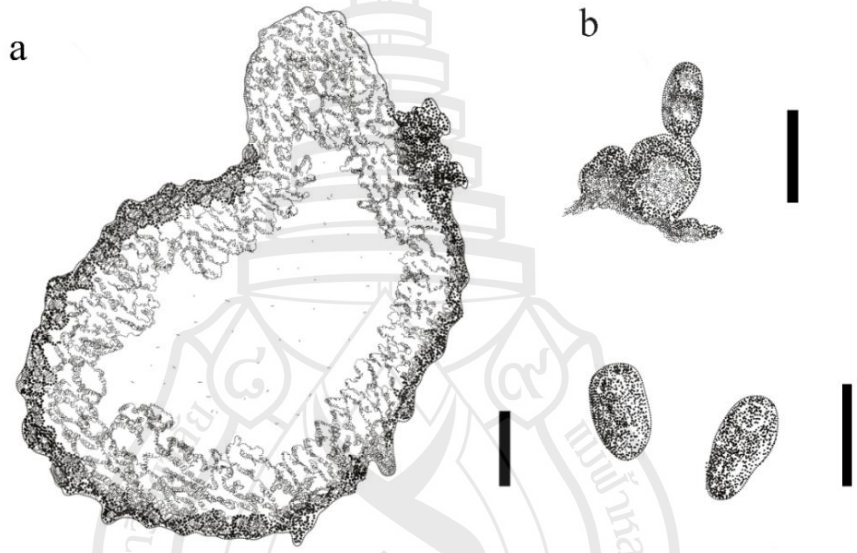


Figure 4.27 *Vandijckomycella joseae* (CBS 143011)

Figure 4.27, a Section of pycnidium. b Conidiogenous cell. c Conidia. Scale bars a = 10 μm, b, c = 5 μm. Redrawn from Hou et al. (2020a)

Xenodidymella Qian Chen & L. Cai, Studies in Mycology 82: 205 (2015)

Index Fungorum number: IF814065; Facesoffungi number: FoF08236;

Figure 4.28

Chen et al. (2015) erected *Xenodidymella* with morpho-molecular (LSU, ITS, *rpb2* and *tub2*) evidence while accommodating the type species, *X. applanata* (Chen et al., 2015). The Species Fungorum (2025) lists 12 species under *Xenodidymella*, and all of them have molecular data. The asexual morph is characterized by pycnidial, globose to subglobose, superficial or immersed, solitary or confluent, and ostiolate conidiomata. Conidiogenous cells are phialidic, hyaline, globose to flask-shaped, or ampulliform, and

conidia are variably shaped, hyaline, ellipsoidal to allantoid, subcylindrical, oblong, pyriform, and usually 0–1-septate, mostly guttulate. The sexual morph is pseudothecial, immersed or erumpent, globose to subglobose, ostiolate or poroid ascomata. Asci are cylindrical to sub-clavate, 8-spored, bitunicate, and ascospores are hyaline, obovoid to oblong, clavate, ellipsoidal, 1-septate, and constricted at the septum. Chlamydospores are brown, intercalary, unicellular, globose to subglobose, and arranged in spiral chains (Chen et al., 2015; Hongsanan et al., 2020a). Several species cause plant diseases, and some have been investigated from living and dead plant parts, while two species were found associated with soil. *Xenodidymella humicola* has been found in soil and has also been found as an opportunistic pathogen on roots (Boerema et al., 2004). The members are distributed in France, Italy, the Netherlands and the USA (Hongsanan et al., 2020a).

Table 4.29 *Xenodidymella* species isolated from soil

Species	Country	Habitat or soil type	References
Xenodidymella humicola	India	Forest	Kayang (2006)
X. weymaniae	The Netherlands	A garden	Hou et al. (2020a)

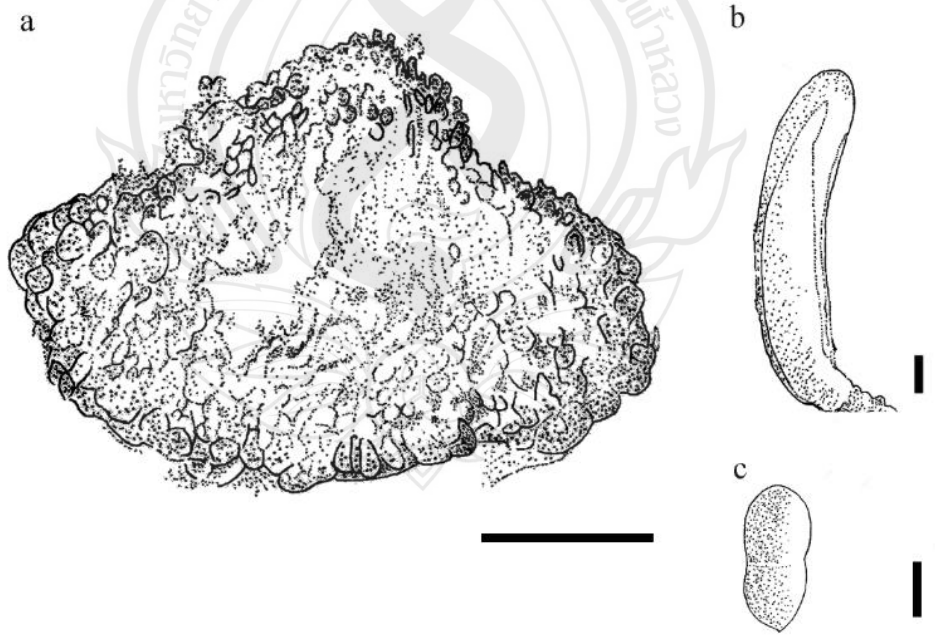


Figure 4.28 *Xenodidymella applanata* (M0275818)

Figure 4.28, A Section of pseudothecium. b. Asci. c. Ascospore. Scale bars: a = 50 μm, b, c =5 μm. Redrawn from Chen et al. (2015).

Family: *Didymosphaeriaceae* Munk

Alloconiothyrium Verkley, Göker & Stielow, Persoonia 32: 33 (2014)

Index Fungorum number: IF800756; Facesoffungi number: FoF 00028*;* Figure 4.29

Alloconiothyrium was erected by Verkley et al. (2014), and *A. aptrootii* was designated as the type species. Currently, three species are listed under *Alloconiothyrium* (Species Fungorum 2025), and all of them have molecular data. The sexual morph is still undetermined. The asexual morph is characterized by pycnidial or eustromatic conidiomata, with holoblastic and annellidic conidiogenous cells. Conidia are olivaceous-brown and irregular in outline with a roughened surface. Species have been isolated from *C. sinensis* and *Encephalartos* leaves, and one species from soil (Ariyawansa et al., 2020; Verkley et al., 2014).

Table 4.30 *Alloconiothyrium* species isolated from soil

Species	Country	Habitat or soil type	References
Alloconiothyrium aptrootii	Papua New Guinea	A park	Verkley et al. (2014)

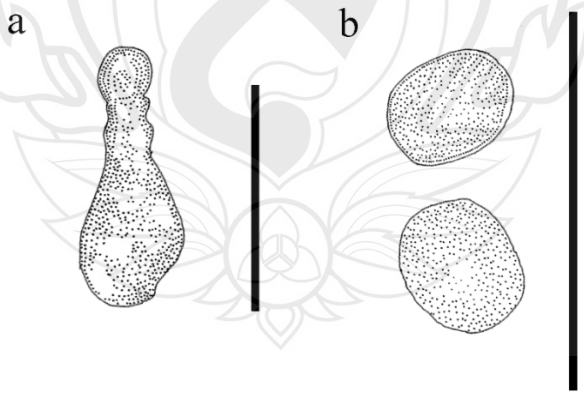


Figure 4.29 *Alloconiothyrium aptrootii* (CBS 980.95)

Figure 4.29, a Conidiogenous cell. b Conidia. Scale bar: a, b = 10 μm. Redrawn from Verkley et al. (2014).

Bimuria D. Hawksw., Chea & Sheridan, N.Z. Jl Bot. 17(3): 267 (1979) Figure 4.30

Index Fungorum number: IF574; Facesoffungi number: FoF 00032

Bimuria was introduced by Hawksworth et al. (1979) and typified by *B. novae-zelandiae*. Presently, *Bimuria* has two species (Species Fungorum, 2025), and both of them with molecular data. Initially, the genus was placed in *Pleosporaceae* and Barr (1987) transferred it to *Phaeosphaeriaceae*. Then, Lumbsch and Huhndorf (2007) placed this genus in *Melanommataceae,* and subsequently, Schoch et al. (2009) transferred it to *Montagnulaceae*. *Montagnulaceae* was synonymized under *Didymosphaeriaceae*, thus, this genus is currently considered a member of *Didymosphaeriaceae* (Phookamsak et al., 2019; Wanasinghe et al., 2016, 2018b). Wijesinghe et al. (2020) provided a combined ITS, LSU, and *tef1-α* phylogeny and morphological characterization while introducing a second species to this genus. The asexual morph is characterized by pycnidial conidiomata that are superficial to semi-immersed with a thick wall comprising textura angularis cells. Conidiogenous cells are enteroblastic, phialidic, and produce pale brown to hyaline, oblong to cylindrical, 1-septate, smooth and thin-walled conidia. The sexual morph has singular, globose ascomata, comprising 2-spored, bitunicate, clavate asci, with dark brown, verrucose ascospores. (Hawksworth, 1979; Wijesinghe et al., 2020). Species have been found in soil and decaying leaves from New Zealand and Oman (Hawksworth et al., 1979; Wijesinghe et al., 2020).

Table 4.31 *Bimuria* species isolated from soil

Species	Country	Habitat or soil type	References
Bimuria novae-zelandiae	New Zealand	Arable soil	Gonçalves et al. (2020)

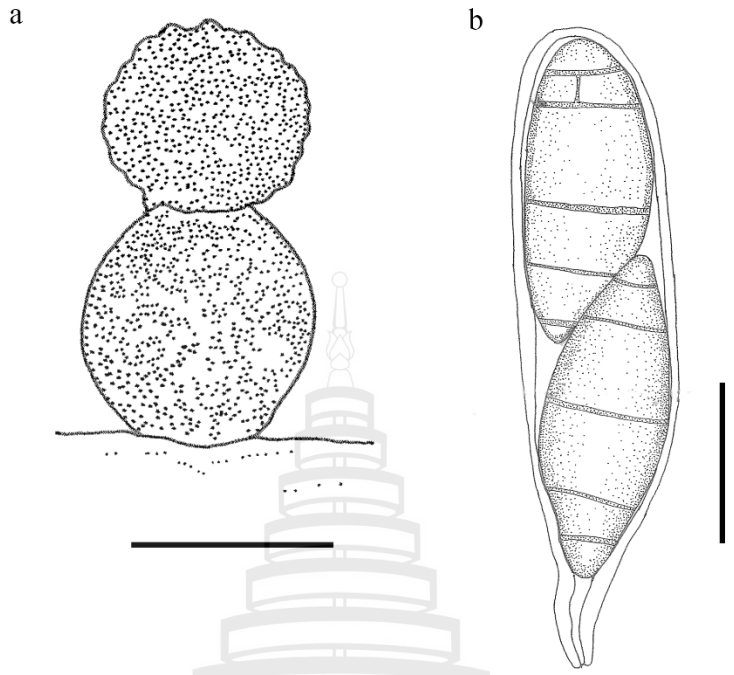


Figure 4.30 *Bimuria novae-zelandiae* (CBS 107.79)

Figure 4.30, a Ascoma. b Asci with ascospores. Scale bars a= 200 μm, b = 25 μm. Redrawn from Hawksworth et al. (1979).

Didymocrea Kowalski, Mycologia 57(3): 405 (1965).

Index Fungorum number: IF 1552; Facesoffungi number: FoF08238

Kowalski (1965) introduced *Didymocrea* by accommodating *D. sadasivanii* as the type species, which was previously known as *Didymosphaeria sadasivanii*. There are two species listed in the Species Fungorum (2025), and they have molecular data. Based on SSU and LSU and *tef1-α* gene regions and morphology, Ariyawansa et al. (2014b) placed this genus in *Didymosphaeriaceae,* which was previously placed in *Zopfiaceae* (Aptroot, 1995). Jayasiri et al. (2019) introduced the asexual morphology of this genus, which is hyphomycetous. The sexual morph is characterized by perithecia that are deep brown or black with a brown or black wall of parenchymatous cells. Pseudoparaphyses are septate, and asci are unitunicate, short-pedicellate, with no apical pore. Ascospores are two-celled, rounded and wide upper cell, a more true-spiked lower cell, hyaline, become brownish-yellow. Species have been reported from soil and saprobes on dead plant parts in India and Thailand (Jayasiri et al., 2019; Kowalski, 1965).

Table 4.32 *Didymocrea* species isolated from soil

Species	Country	Habitat or soil type	References
Didymosphaeria sadasavanii	India	ND	Kowalski (1965)

Neptunomyces M. Gonçalves, T. Vicente & A. Alves, MycoKeys 60: 37 (2019)

Index Fungorum number: IF 831436

Neptunomyces was introduced by Gonçalves et al. (2019) based on ITS and *tef1-α* and *tub2* single and multigene phylogeny analyses and morphological evidence, while accommodating *Neptunomyces aureus* as the type species. The genus comprises four species (Species Fungorum 2025), all of which have molecular data. The type species has an asexual morph with the solitary or aggregated, globose to subglobose, dark brown, immersed or rarely superficial conidiomata with a pseudoparenchymatous wall. Conidiophores are reduced to ampulliform to subcylindrical, hyaline, smooth conidiogenous cells that produce aseptate, golden yellow, smooth, subcylindrical conidia with rounded apices. The sexual morph remains undetermined (Gonçalves et al., 2019b). Species have been isolated from algae, dead plants, and two of them were from soil substrates distributed in Australia, Portugal and Thailand (Gonçalves et al., 2019b; Yasanthika et al., 2024).

Table 4.33 *Neptunomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Neptunomyces litoralis	Australia	Sand	Austin et al. (2004)
N. soli	Thailand	Forest soil	Yasanthika et al. (2024)

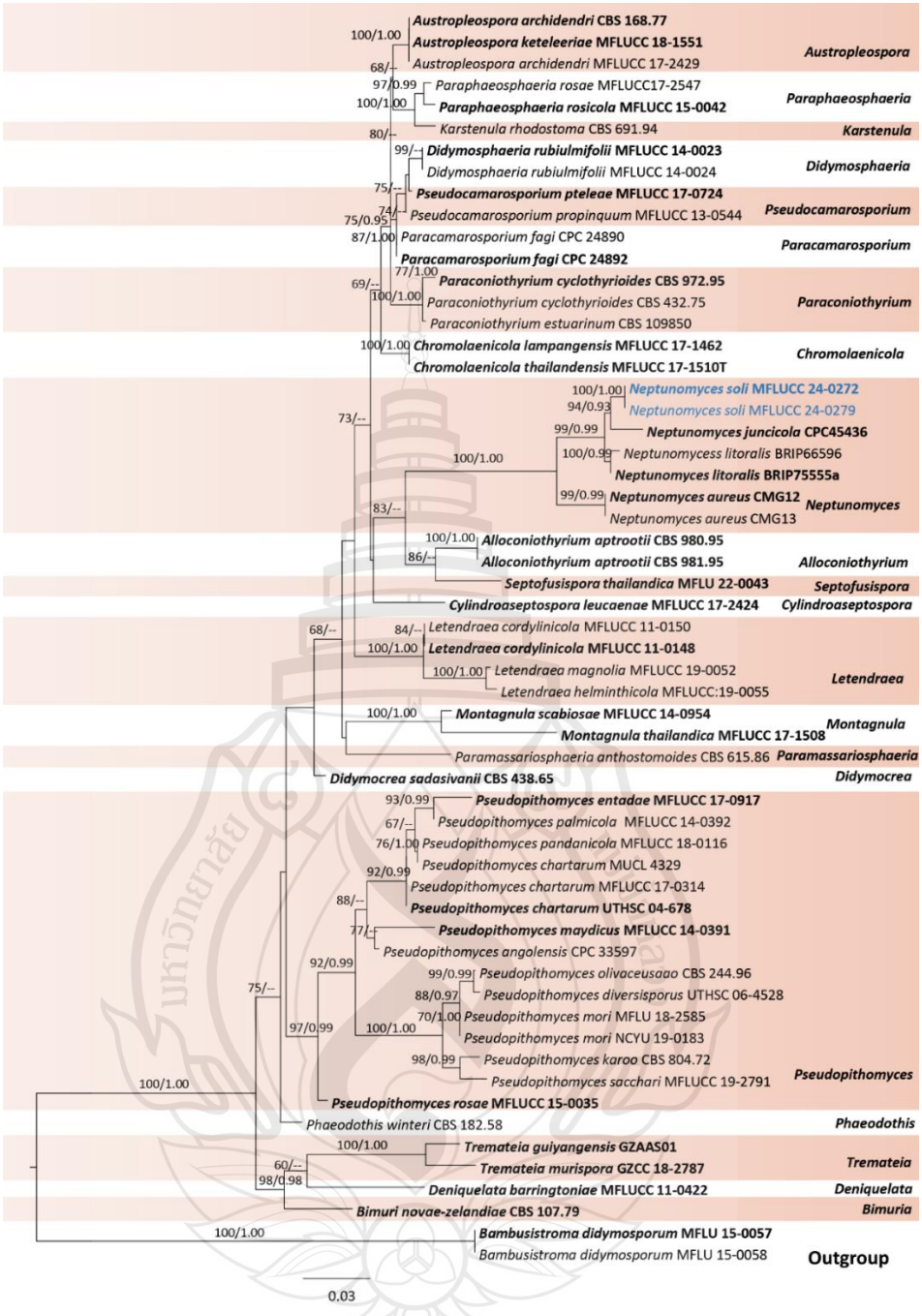


Figure 4.31 Maximum likelihood phylogenetic tree generated based on the combined ITS-LSU sequence data for *Didymosphaeriaceae* taxa

Figure 4.31, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Bambusistroma didymosporum* (MFLU 15-0057T, MFLU 15-0058).

The combined ITS and LSU alignment comprised 63 strains of Didymosphaeriaceae belonging to 21 genera, and Bambusistroma didymosporum (MFLU 15-0057 and MFLU 15-0058) strains were used as outgroup taxa. The combined alignment has 1414 bp, comprising ITS: 630 bp, LSU: 784 bp. A best-scoring ML tree resulting from the combined alignment is shown (Figure 4.31), which has a final ML optimization likelihood value of – 6463.451. The matrix had 438 distinct alignment patterns, with 28.78% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 1.68636, AT = 1.00000, CG =1.00000, CT = 4.38173, GT = 1.00000; proportion of invariable sites I = 0.505; gamma distribution shape parameter $\alpha = 0.510$. Both trees of ML and BYPP analyses were similar in topology at the generic relationships, and also the tree topology is comparable to previous studies (Gonçalves et al., 2019). Strains (MFLUCC 24-0272 and MFLUCC 24-0279) formed a distinct cluster with 94% ML and 0.93 BYPP statistical support, sister to Neptunomyces juncicola (CPC23456), *N. litoralis* (BRIP 75555a) and N. aureus (CMG 12, CMG 13). Phylogenetic placement shows our strains (MFLUCC 24-0272 and MFLUCC 24-0279) form a new lineage.

Neptunomyces soli Yasanthika & K.D. Hyde, ***sp. nov.***

Figure 4.32

Index Fungorum number: IF902620, Faces of Fungi number: FoF 16493

Etymology:–*soli*, soil in Latin, substrate from which the holotype was collected.

Holotype:– MFLU24-0379

Sexual morph: Undetermined. Asexual morph: *Conidiomata* scattered throughout the media, globose to subglobose, brown to dark brown, superficial to semi-immersed, pseudoparenchymatous-walled. *Conidiogenous cells* 7–3 × 7–2.5 μm ($\overline{x}$ = 5 × 4.5 μm, n = 10), hyaline to subhyaline, doliiform to obovoid, smooth. *Conidia* 5–6.5 × 3–5 μm ($\overline{x}$ = 5.8 × 3.8 μm, n = 25), initially hyaline, becoming golden yellow, ellipsoidal to fusiform, 0.5–1.5 μm ($\overline{x}$ = 1 μm) thick-walled, slightly pointed apex and rounded base.

Culture characteristics: —*Colonies* on PDA at 25 ℃, become 3–4 cm diam., appear white after seven days, become yellowish-white when mature, reverse whitish-orange to yellow, cottony flat surface with filiform margin. *Mycelium* immersed to

semi-immersed, hyaline, smooth-walled hyphae, aseptate when immature, become septate at maturity, 2–4 μm ($\bar{x}$ = 2.3 μm) wide, sporulated after two weeks.

Material examined:—THAILAND. Chiang Rai: tropical forest soil, on woody baits, 20°4'35"N, 100°5'43"E, 450 m, 7 January 2020, W.A. Erandi Yasanthika (MFLU24-0379, holotype); ex-type MFLUCC 24-0272 (CRL5-120); *ibid*., (MFLU24-0380); MFLUCC 24-0279 (CRL5b-120b).

Notes:– According to the multi-gene phylogenetic analyses, our isolates (MFLUCC 24-0272 and MFLUCC 24-0279) formed an independent lineage sister to *Neptunomyces juncicola* (CPC 45436) with 94% ML and 0.93 BYPP bootstrap support. A comparison of the 557 nucleotides of the ITS (+5.8S) gene region of *N. soli* revealed 39/378 bp (10%) differences (including gaps) with *N. aureus* (CMG12), 20/545 bp (3.6%) differences (including gaps) with *N. juncicola* (CPC 45436) and 18/534 bp (3%) (including gaps) differences with *N. litoralis* (BRIP75555a). Morphologically, our isolate MFLUCC 24-0272 is characterized by doliiform to obovoid conidiogenous cells and ellipsoidal to fusiform conidia with a slightly pointed apex and a rounded base. *N. aureus* has ampulliform to subcylindrical conidiogenous cells and subcylindrical conidia with rounded apices (Gonçalves et al., 2019), while *N. juncicola* has ampulliform conidiogenous cells and subcylindrical to fusoid-ellipsoid conidia with subobtuse apices (Crous et al., 2024). Conidial sizes of our species are relatively shorter and broader (5–6.5 × 3–5 μm) compared to *N. aureus* (7.0 × 2.7 μm) and *N. juncicola* (7–8× 2–2.5 μm) (Gonçalves et al., 2019; Crous et al., 2024). However, we were not able to compare the morphology of *N. litoralis*, as its data were unavailable. *N. aureus* recorded from macroalgae in Portugal (Gonçalves et al., 2019), *N. litoralis* from sands in Australia (Austin et al., 2004) and *N. juncicola* from culms of *Juncus maritimus* in the Netherlands (Crous et al., 2024). We used a polyphasic approach based on morphology and multigene phylogeny (Maharachchikumbura et al., 2021) to introduce *Neptunomyces soli* as a new species isolated from forest soil in Thailand. This is the first record of the genus from soil and is the first record of *Neptunomyces* from Thailand. We isolated this species from wood pieces using the baiting technique. Thus, we suggest that this species has an affinity to lingo-cellulosic substrates and introduce it as a cellulophilic species. However, future biochemical analyses are required to confirm this and define its contribution to lignocellulose degradation in soil.

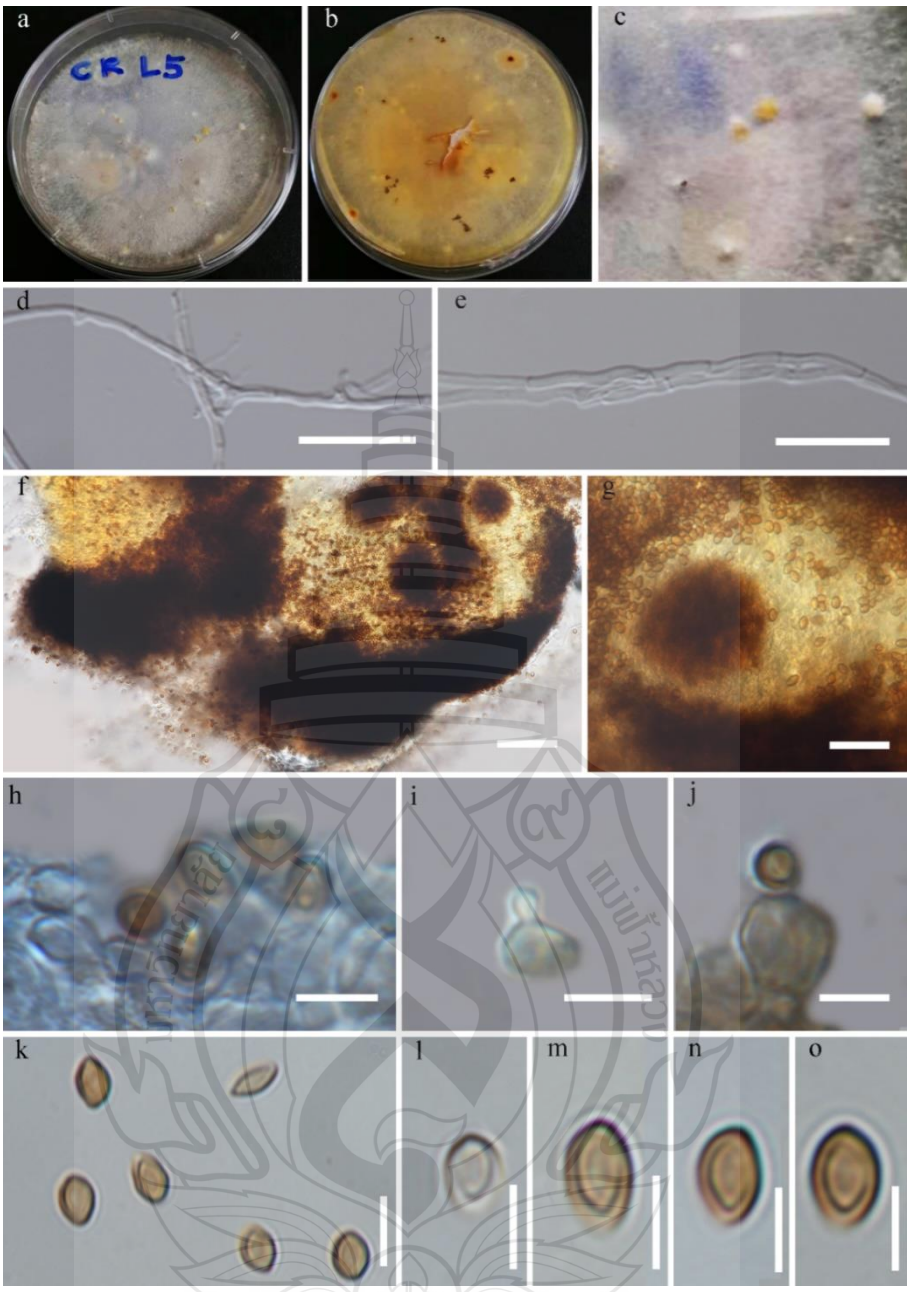


Figure 4.32 *Neptunomyces soli* (MFLU24-0379, holotype)

Figure 4.32, a, b. Colony on PDA (top and reverse). c. Pycnidia forming on culture. d Immature aseptate hyphae. e. Mature septate hyphae. f. Pycnidia. g. Pycnidial matrix. h–j. Conidiogenous cells with developing conidia. k–o. Conidia. Scale bars: d, e, g = 20 µm, f = 75 µm, h–o = 5 µm.

Paraconiothyrium Verkley, Stud. Mycol. 50(2): 327 (2004).

Index Fungorum number: IF 500080; Facesoffungi number: FoF 00053;

Verkley et al. (2004) erected *Paraconiothyrium* and typified it with *P. estuarinum.* Currently, 28 species are listed under *Paraconiothyrium* (Species Fungorum 2025), and all of them have molecular data. Ariyawansa et al. (2014) provided a comprehensive phylogeny for this genus and new species have been identified by subsequent studies using morpho-molecular evidences (Wang et al., 2021). The asexual morph is characterized by the eustromatic to pycnidial conidiomata with phialidic or annellidic conidiogenous cells. Conidia are smooth-walled or minutely warted and hyaline, becoming brown at the latter stages. The sexual morph is unknown. They have several trophic modes as opportunistic human pathogens, phytopathogens, plant endophytes or saprobes (Ibrahim et al., 2024). The species have been isolated from fungicolus fungi, human samples, leaf spots, leaves, saline water, sediment from estuarine habitats, skin, soil, wood and wounds in Australia, Brazil, China, Papua New Guinea, South Africa, Thailand and the USA (Gonçalves et al., 2020; Verkley et al., 2004). Around 147 secondary metabolites have been investigated from *Paraconiothyrium* species and 95 of them are new (Wang et al., 2021).

Table 4.34 *Paraconiothyrium* species isolated from soil

Species	Country	Habitat or soil type	References
Paraconiothyrium brasiliense	Malaysia	Virgin peatland	Noman et al. (2023)
P. cyclothyrioides	Papua New Guinea	A national park	Gonçalves et al. (2020)
P. kelleni	Korea	ND	Yadav et al. (2023)

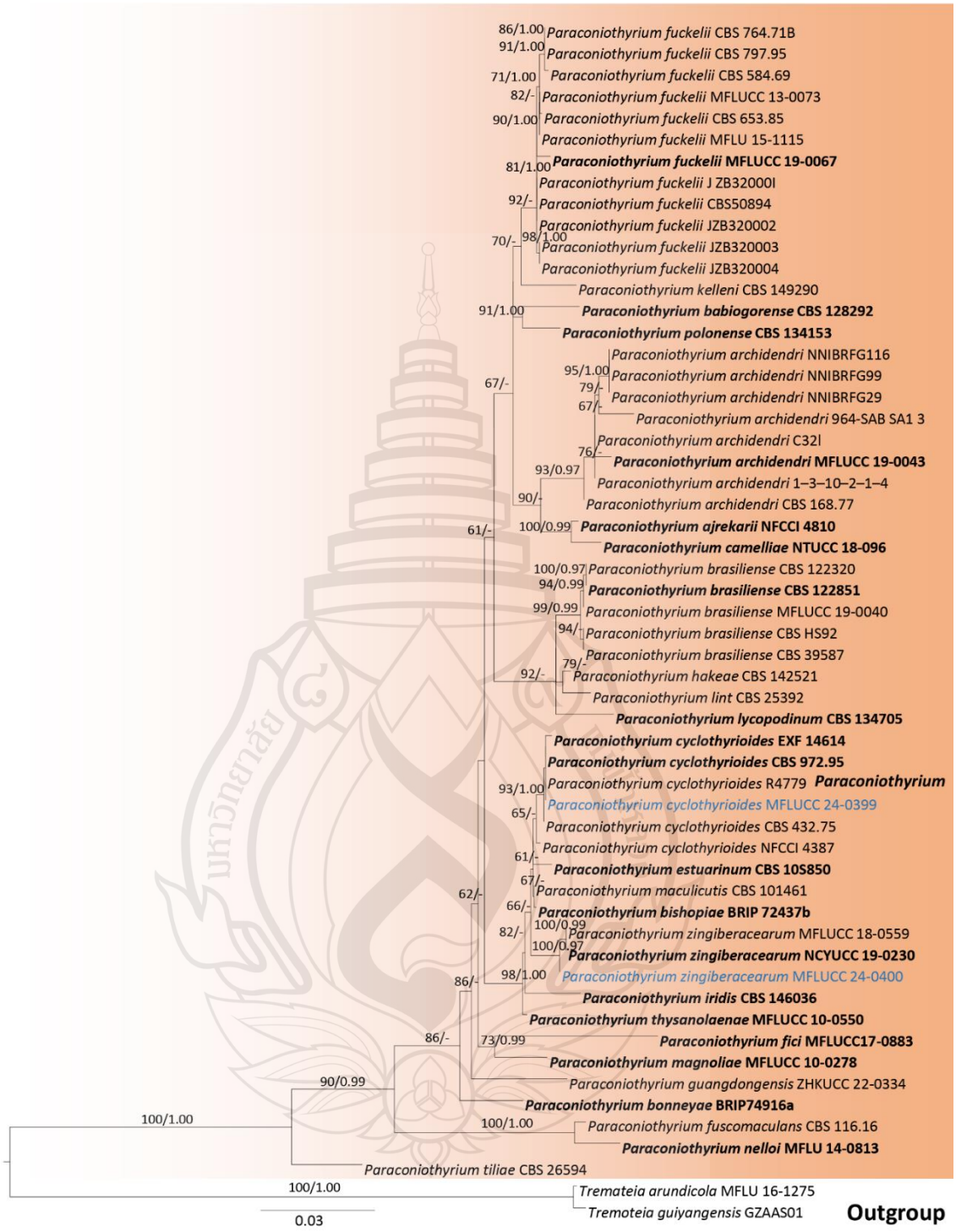


Figure 4.33 The best-scoring maximum likelihood tree generated of the combined ITS and LSU sequence data for *Paraconiothyrium*

Figure 4.33, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.95 are indicated above the

nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Trematei arundicola* (MFLU 16-1275) and *Trematei guiyangensis* (GZAAS01). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 1658 bp, and single gene alignments are ITS: 750 bp, and LSU: 908 bp. The matrix had 1371 distinct alignment patterns with 26.34% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 1.70814, AT = 1.00000, CG = 1.00000, CT = 6.85743, GT = 1.00000; gamma distribution shape parameter α = 0.690.

Paraconiothyrium cyclothyrioides Verkley Stud. Mycol. 50(2): 330 (2004)

Figure 4.34

Index Fungorum number: IF 500083

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 300–350 × 225–250 μm ($\bar{x}$ = 315 × 242 μm, n=10), pycnidial, superficial to semi-immersed on PDA, brown to reddish brown, solitary or confluent with *textura angularis* wall, 8–15 μm ($\bar{x}$ = 11 μm, n=10) thick. *Conidiogenous cells* 7.5–3 × 7–2.5 μm ($\bar{x}$ = 5 × 4.5 μm, n=10), phialidic, subhyaline to pale-brown, ampulliform to subcylindrical, indeterminate. *Conidia* 3.5–5.5 × 1.5–2.5 μm ($\bar{x}$ = 3.5 × 2 μm, n = 25), hyaline, aseptate, cylindrical to globose, straight, rounded at both ends, smooth-walled.

Culture characteristics – *Colonies* on PDA at 25°C, become 4–5 cm diam. after seven days, appearing in white, become olive-brown to white when mature, reddish-brown at the center, brownish orange middle ring and yellow preiphery, raised, undulate margin. *Mycelium* superficial, aseptate, hyaline, smooth when immature, become sub-hyaline to brown, thick-walled 1.5–3 μm ($\bar{x}$ = 2, n = 30), sporulated after 4 weeks.

Material examined – Thailand, Chiang Mai, Omkoi District, Sop Khong, forest, on soil, 17.7145N, 98.2619E, 1388m, 16 October 2019, W. A. Erandi Yasanthika (MFLU25-0160); living culture 24-pin4= MFLUCC 24-0399.

GenBank numbers – MFLUCC 24-0399: LSU: PQ565569, ITS: PQ565453.

Notes – Based on the phylogenetic analyses of *Paraconiothyrium* shown in Figure 4.31, our strain (MFLUCC 24-0399) clusters with *P. cyclothyrioides* 93% ML, 1.00 BYPP statistical support. Our isolate has a similar morphology with *P. cyclothyrioides* by having irregularly globose or flattened, reddish brown to black conidiomata and phialidic,

subhyaline to pale-brown, ampulliform to subcylindrical, conidiogenous cells and 1-celled, hyaline, both ends rounded conidia. However, the type species has short-cylindrical, straight, or slightly curved conidia, whereas our isolate has cylindrical to globose, straight conidia. Further, the type species has one or two very small, polar guttules in conidia and becomes yellow when mature, which is absent in our isolate. Morphology and phylogeny analyses confirm that our strain is *P. cyclothyrioides*. This species was introduced by Verkley et al. (2004) from soil in Papua New Guinea and has later been found in human specimens in the USA (Gonçalves et al., 2020). We document the first record of *P. cyclothyrioides* from soil collected in Thailand.

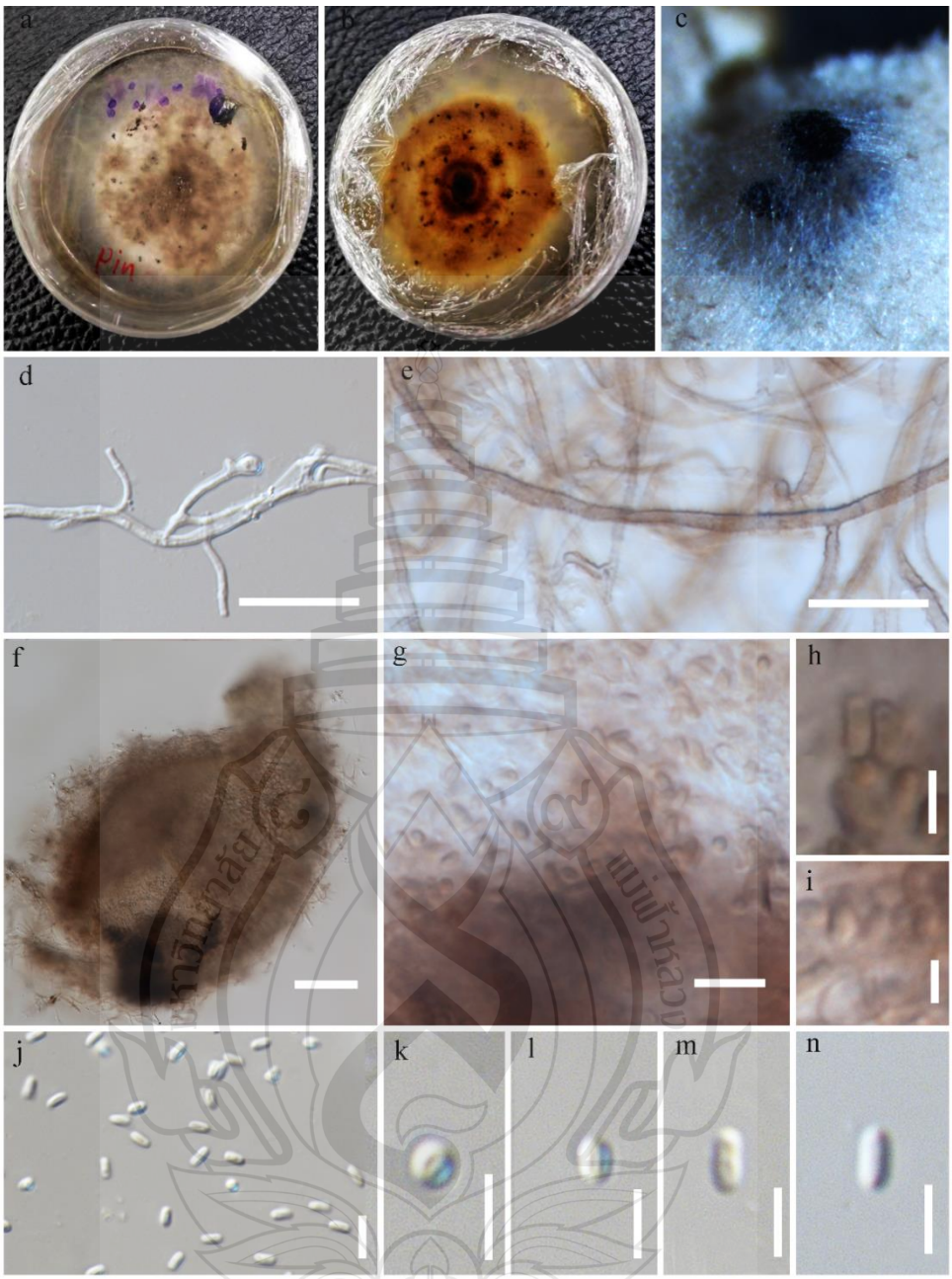


Figure 4.34 *Paraconiothyrium cyclothyrioides* (MFLU25-0160)

Figure 4.34, a, b Culture characters on PDA (b = reverse). c Pycnidia forming on culture. d Immature hypha e. Mature hyphae. f Pycnidia. g Pycnidia matrix h, i Conidiogenous cells. j–n Conidia. Scale bars: f = 75 d, e = 10 μm, f, g, j = 10 μm, h,i, k–n =5 μm

Paraconiothyrium zingiberacearum Tennakoon & S. Lumyong, Frontiers in Microbiology 13(101628): 16 (2023)

Figure 4.35

Index Fungorum Number: IF559600; Facesoffungi number: FoF 10802

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 200–250 μm ($\bar{x}$ = 230 μm, n = 10) diam., pycnidial, superficial to semi-immersed on PDA, brown to dark brown, sub-globose, ostiole indistinct, *pycnidial* wall cells of *textura angularis*. *Conidiogenous cells* 2–3 × 1.5–3 μm ($\bar{x}$ = 2.5 × 2 μm, n=10), sub-hyaline, ampulliform, thick-walled. *Conidia* 3.5–4.5 × 1–2 μm ($\bar{x}$ = 4 × 1.5 μm, n = 25), hyaline, aseptate, fusiform, rarely ellipsoidal to oval, thick-walled.

Culture characteristics – *Colonies* on PDA at 25°C, become 3–4 cm diam. after 7 days, whitish-yellow, becoming Ivory at the center and brown-beige outer rind when mature, reverse brown at the center, middle rind brownish-orange, brown-beige outer rind, raised, undulate filiform margined. *Mycelium* superficial to semi-immersed, hyaline, becoming subhyaline to pale brown when mature, septate, smooth to verrucose 1.5–4 μm ($\bar{x}$ = 3), sporulated after 8 weeks.

Material examined – Thailand, Chiang Rai, Bandu, Market place, on soil, 19.967000 N, 99.855912E, 393m, 17 October 2022, W.A. Erandi Yasanthika, (MFLU25-0161); living culture 91-u4-2 = MFLUCC 24-0400.

GenBank numbers –MFLUCC 24-0400: LSU: PQ565570, ITS: PQ565454.

Notes– Based on the multi-gene phylogenetic analyses in Figure 4.31, our strain (MFLUCC 24-0400) clusters with *Paraconiothyrium zingiberacearum* with 100% ML, 0.97 BYPP statistical support. When compared each gene region between our strain and the type species (NCYUCC 19-0230), they showed 100% similarity. *Paraconiothyrium zingiberacearum* was introduced by Tennakoon et al. (2022) from a dead stem of *Hedychium coronarium* in China. Only the sexual morph has previously been reported in this species (Tennakoon et al., 2022), but we observed the asexual morph in our isolate. By considering morphology and phylogeny, we suggest that our collection is the asexual morph of *P. zingiberacearum* isolated from an urban area in Thailand. It is the first soil record of this species, and it appears to adapt to a variety of habitats.

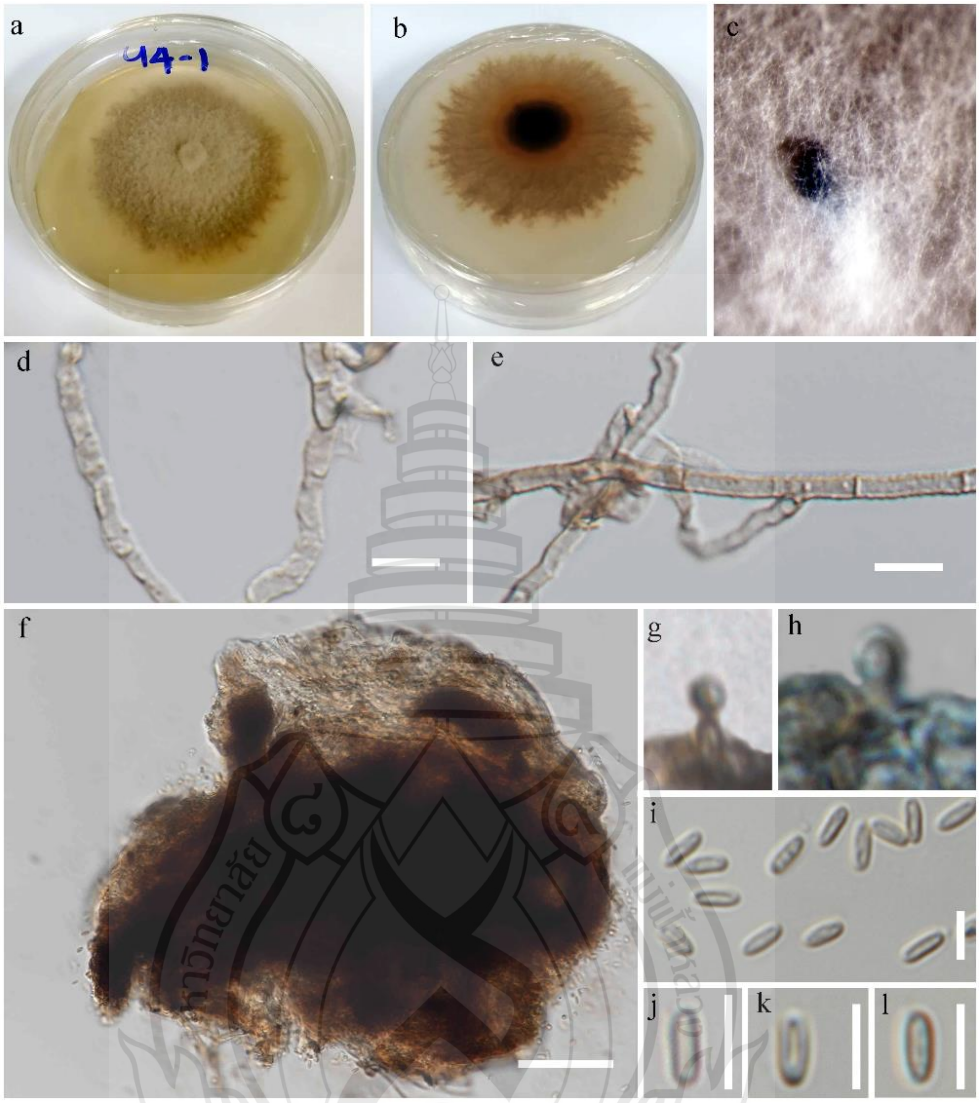


Figure 4.35 *Paraconiothyrium zingiberacearum* (MFLU25-0161)

Figure 4.35, a, b Culture characters on PDA (b = reverse). c Pycnidia forming on culture. d Immature hyphae e Mature hyphae. f Pycnidia. g, h Conidiogenous cells. i–l Conidia. Scale bars: f = 50 µm, d, e =10 µm, g–l = 5 µm.

Phaeodothis Syd. & P. Syd., Annls mycol. 2(2): 166 (1904).

Index Fungorum number: IF 3914; Facesoffungi number: FoF 00059

Phaeodothis was established by Sydow and Sydow (1904); the type species is accepted as *Phaeodothis tricuspidis*. There are 22 species listed in the Species Fungorum (2025), however, only three have molecular data. Von Niessl (1875) transferred *Phaeodothis* to *Didymosphaeriacea,* and subsequently, Aptroot (1995)

placed *Phaeodothis* in *Phaeosphaeriaceae*. However, based on morphology and the multigene phylogeny, this genus is currently placed in *Didymosphaeriaceae* (Ariyawansa et al., 2014b; Tennakoon et al., 2020). The asexual morph is unreported and the sexual morph is characterized by the subglobose to hemispherical, immersed, scattered to gregarious, dark brown to black ascostromata. Hamathecium has pseudoparaphyses often in a gelatinous matrix. *Asci* are 8-spored, bitunicate, fissitunicate, cylindrical, short pedicellate with olivaceous brown ascospores that are fusiform with rounded ends (Ariyawansa et al., 2014b). The species are present in saprobic or parasitic mode on dead wood, grasses and soil in terrestrial environments in Australia, Austria, Congo, India, Japan, Germany, Nigeria, Pakistan, Philippines, Sri Lanka, Thailand, Sweden and Uganda (Kamolmanit et al., 2013; Ariyawansa et al., 2014b; Tennakoon et al., 2020).

Table 4.35 *Phaeodothis* species isolated from soil

Species	Country	Habitat or soil type	References
Phaeodothis ribesiella	Congo	ND	Aptroot (1995)
P. winteri	Thailand	Agricultural field	Kamolmanit et al. (2013)

Pseudopithomyces Ariyaw. & K.D. Hyde, Fungal Divers. 75: 64 (2015).

Index Fungorum number: IF 551392; Facesoffungi number: FoF 00937

Pseudopithomyces was established by Ariyawansa et al. (2015) by providing multigene phylogenetic analyses (ITS and LSU) and morphological descriptions. The type species is *Pseudopithomyces chartarum,* which was previously known as *Sporidesmium chartarum*. There are 13 species in the Species Fungorum (2025), and all of them have molecular data. The asexual morph has micronematous or semi-macronematous, thin-walled, hyaline to subhyaline, aseptate, smooth conidiophores, monoblastic or blastic, closely aggregated, globose or subglobose, integrated, terminal conidiogenous cells and dark fuligineous, septate to multi-septate, fusiform or subglobose, verruculose to echinulate, acrogenous conidia with ornamented walls (Ariyawansa et al., 2015a). *Pseudopithomyces* is morphologically similar to *Pithomyces* species, but can be distinguished by chinulate or fusiform, verruculose, dark conidia. The sexual morph of the genus is still unknown. The genus is recorded as saprobes or plant and human pathogens that are found in animal specimens, dead leaves and stems, freshwater and marine

environments, leaf spots, humans and soil in Africa, China, Korea and Thailand (Ariyawansa et al., 2015a; Wahdan et al., 2022; Mitra et al., 2024).

Table 4.36 *Pseudopithomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudopithomyces chartarum	Brazil	ND	Oliveira et al. (2013)
P. karoo	China	Warm temperate area	Liu and Zhang (2007)

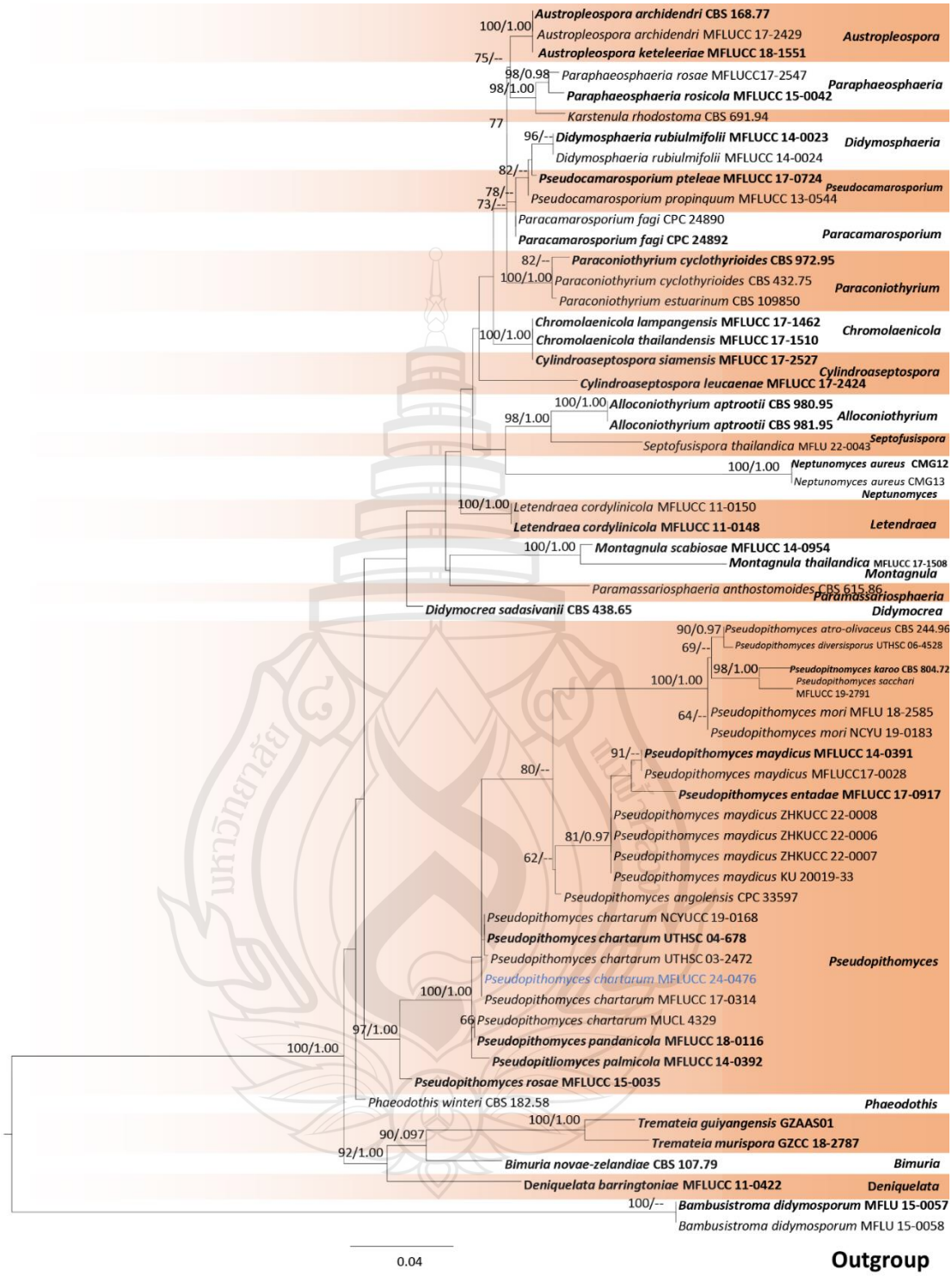


Figure 4.36 The best-scoring maximum likelihood tree generated based on the combined LSU, ITS and *tef1-α* sequence data for *Didymosphiraceae*

Figure 4.36, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Bambusistroma didymosporum* (MFLU 15-0057 and MFLU 15-0058). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 1333 bp, and single gene alignments are ITS: 632 bp, and LSU: 701 bp. The matrix had 1740 distinct alignment patterns with 23.54% % undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.225334, C = 0.250694, G = 0.286607, T = 0.237365; substitution rates AC = 1.166020, AG = 2.057124, AT = 1.892820, CG = 1.203646, CT = 5.719619, GT = 1.000000; gamma distribution shape parameter α = 0.505971.

Pseudopithomyces chartarum (Berk. & M.A. Curtis) Jun F. Li, Ariyaw. & K.D. Hyde, in Ariyawansa et al., Fungal Diversity: 10.1007/s13225-015-0346-5, [40] (2015)

Figure 4.37

Index Fungorum number: IF551393; Facesoffungi number: FoF00938

Sexual morph: Undetermined. Asexual morph: *Conidiophores* macronematous, mononematous, branched, anastomosing, subhyaline to pale brown, smooth to verruculose 11.5–20.5 × 3.5–7.5 μm ($\bar{x}$ = 14.5 × 5 μm, n=10). *Conidiogenous cells* 5–11 × 6.5–10 μm ($\bar{x}$ = 8 × 7.5 μm), globose to subglobose, integrated, holoblastic, terminal, smooth. *Conidia* 12.5–22.8 × 8.8–13 μm ($\bar{x}$ = 18.2 × 16.2 μm, n = 25), pleurogenous, broadly ellipsoid, 3–4 transverse septa and usually middle septum (septa) divided by longitudinal septum, middle brown to dark brown, apical and basal septa pale brown, often constricted at the septa, smooth to verruculose and rhexolytic.

Culture characteristics – *Colonies* on CMA at 25 °C become 2–3 cm diam. in 7 days. Initially white, becoming pale yellow to yellowish brown, flat surface, entire- margin, reverse dark brown at the center with pale brown rind at the edge. *Hyphae* hyaline to pale brown, superficial, smooth to verruculose and septate, 1.5–4 μm ($\bar{x}$ = 3 μm). *Chlamydospore* hyaline to sub-hyaline, verruculose.

Material examined – Thailand, Chiang Rai Province, Chiang Rai, forest, 20°4'35"N, 100°5'43"E, on soil, 7 January 2020, W.A. Erandi Yasanthika, (MFLU25-0129); living culture 7-gl01a = MFLUCC 24-0476.

GenBank numbers – MFLUCC 24-0476: LSU: PQ568014, ITS: PQ567559

Notes – As shown in Figure 4.34, our isolate (MFLUCC 24-0476) clusters with *Pseudopithomyces chartarum* strains with 100% ML, 1.00 BYPP statistical support. Comparing the LSU, ITS and *tef1-α* regions of our strain with the type species (UTHSC04-678), showed that they have 100% similarity. Our isolate (MFLUCC 24-0476) shares a similar morphology with the type species by having mononematous, branched, and anastomosing conidiophores, integrated conidiogenous cells, and conidia with 3–4 transverse septa and usually with a middle septum (septa) divided by a longitudinal septum. According to the phylogeny and morphological analyses, we suggest that our species is *P. chartarum* (Ariyawansa et al., 2015a). The species have previously been isolated as saprobes on decaying pods, leaves, twigs, leaf spots and soil in Brazil, China and Thailand and found pathogenic on human or sheep skin (Oliveira et al., 2013; Ariyawansa et al., 2015; de Silva et al., 2022). Herein, we provide the first report of *P. chartarum* from Thai soils that was collected from forest habitats.

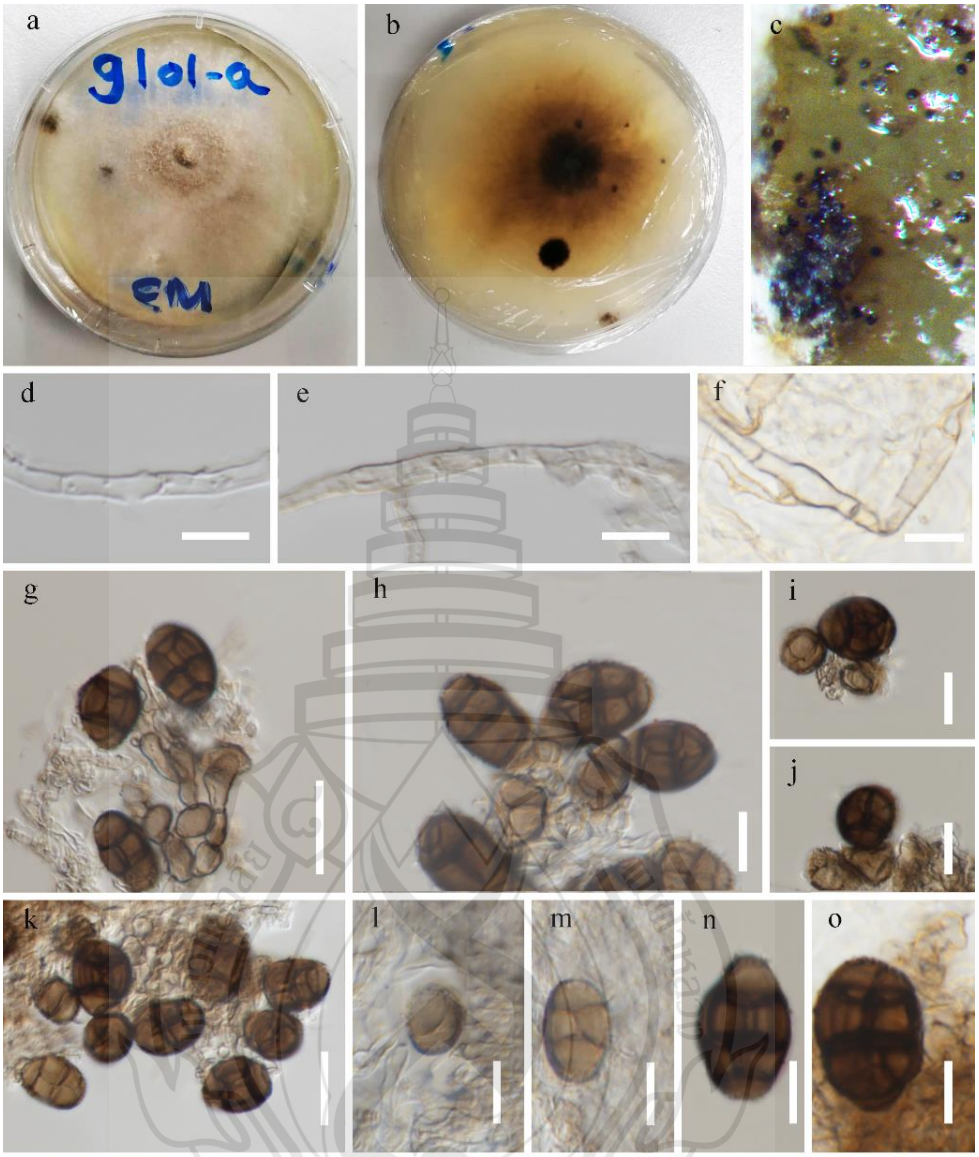


Figure 4.37 *Pseudopithomyces chartarum* (MFLU25-0129)

Figure 4.37, a, b Culture characters on PDA (b = reverse). c Sporulated colony with conidial attachments on the mycelium. d Immature hyphae. e Mature hyphae. f Chlamydospore. g–j Conidiogenous cells attached with conidia. k–n Conidia. Scale bars: g, k = 20 µm, d–f, h–j, l–o = 10 µm

Spegazzinia Sacc., Michelia 2 (6): 37 (1880).

Index Fungorum number: IF 9963; Facesoffungi number: FoF 08241

Saccardo (1880) introduced *Spegazzinia*, accommodating *Spegazzinia ornata* as the type species. The genus comprises 19 species (Index Fungorum 2025), but only 11 species have molecular data. Previously, *Spegazzinia* was classified in *Apiosporaceae* (*Sordariomycetes*) by Hyde et al. (1998). But, based on SSU, LSU, ITS and *tef1-α* sequence data of *S. deightonii* and *S. tessarthra*, Tanaka et al. (2015) placed the genus in *Didymosphaeriaceae.* Hughes (1953) mentioned this as a hyphomycetous genus, with a unique basauxic conidiophore ontogeny (conidiophores that arise and elongate from a cup-shaped basal cell called a conidiophore mother cell). It shows pleomorphism, where species produce two types of conidia in the same mycelium: α conidia are composed of 4–8 subglobose, very dark cells with very long spines, and have a very similar morphology and size in almost every species; while β conidia is characterized by subspherical or broadly ellipsoid, in general, flattened in one plane, cruciately septate or muriform, frequently pale brown and smooth, with short spines or lobed (Mena-Portales et al., 2017). Species are found as endophytes and saprobes in tropical, subtropical and temperate regions. Their hosts can be dead and living stems and leaves, fruits, lichens, marine and brackish estuary sediments and soils (Borut & Johnson, 1962; Ellis, 1971; Leão-Ferreira & Gusmão, 2010).

Table 4.37 *Spegazzinia* species isolated from soil

Species	Country	Habitat or soil type	References
Spegazzinia parkeri	Australia	Wheat rhizosphere	Sivasithamparam (1974)
S. tessarthra	Thailand	ND	Manoch (1998)

Family: *Latoruaceae* Crous

Latorua Crous, IMA Fungus 6(1): 175 (2015).

Figure 4.38

Index Fungorum number: IF 812791; Facesoffungi number: FoF 07743

Crous et al. (2015) introduced *Latorua*, based on morpho-molecular (ITS and LSU) analyses, with two species accepted, and *L. caligans* is designated as the type. However, Crane and Miller (2016) synonymized *Latorua* with *Bahusandhika* based on the development of conidiogenous cells and conidia and the conidial morphology. But *Latorua* was reinstated subsequently, and it currently remains as a monotypic genus

with molecular data (Liu et al., 2018). The asexual morph is hyphomycetous, that is solitary, erect, clavate, pale brown and polyblastic. conidiogenous cells that produce acrogenous, brown, fusoid-ellipsoidal, septate conidia that are constricted at the septa. Conidia appear in conidial chains, where secondary conidia are produced via the apical cells of conidia. The sexual morph is unknown (Crous et al., 2015; Crane & Miller, 2016).

Table 4.38 *Latorua* species isolated from soil

Species	Country	Habitat or soil type	References
Latorua caligans	Brazil	Soil sample taken in A soil horizon	Crane & Miller (2016)
Latorua caligans	India	ND	

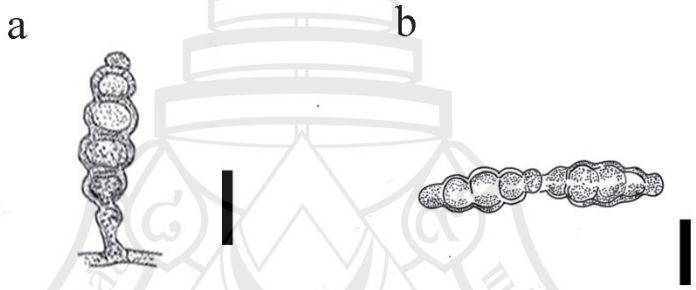


Figure 4.38 *Latorua caligans* (CBS 576.65)

Figure 4.38, a Conidiogenensis. b. Conidia. Scale bars a,b = 10 μm. Redrawn from Crous et al. (2015b).

Matsushimamyces Rah. Sharma & Roh. Sharma, IMA Fungus 6(2): 338 (2015)

Figure 4.39

Index Fungorum number: IF 810895; Facesoffungi number: FoF 07744

Sharma et al. (2015) erected *Matsushimamyces,* and *M. bohaniensis* is designated as the type species. Currently, two species are listed in *Matsushimamyces* (Species Fungorum 2025), and both of them have molecular data. The asexual morph is hyphomycetous and bears solitary, erect, rarely branched macronematous, mononematous conidiophores that produce pale brown, coarsely verruculose, monoblastic, terminal conidiogenous cells and solitary, sub-hyaline to brown, fusoid to broadly ellipsoid, straight or curved, multi-septate conidia (Sharma et al., 2015). The genus was reported from soil and decaying leaves of unidentified trees in India and Cuba (Sharma et al., 2015).

Table 4.39 *Matsushimamyces* species isolated from soil

Species	Country	Habitat or soil type	References
Matsushimamyces bohaniensis	India	Soil in a village	Sharma et al. (2015)

Figure 4.39 *Matsushimamyces bohaniensis* (CBEC 001)

Figure 4.39, a Conidiophore with a conidium. Scale bar: a = 20 μm. Redrawn from Sharma et al. (2015).

Multiverruca H.Y. Wang, Y.F. Han & Z.Q. Liang, Int. J. Syst. Evol. Microbiol. 73(no. 005734): 6 (2023)

Figure 4.40

Index Fungorum number: IF 843849; Facesoffungi number: FoF 16007

Wang et al. (2023a) introduced *Multiverruca* based on morpho-molecular analyses using ITS and LSU gene regions. Currently, the genus is comprised of one species (Species Fungorum, 2025). *Multiverruca sinensis*, the type species, has been isolated from soil under vegetation in China. The asexual morph is hyphomycetous with conidiophores which are reduced to conidiogenous cells. Conidiogenous cells are solitary, erect, mostly globose, smooth and produce conidial chains. Conidia are characterized by acrogenous, mostly solitary or in short, branched chains, brown, verruculose, mostly cymbiform, septate, more thick-walled at the septa, and obtusely rounded basal and apical cells produced directly on the mycelium or on conidiogenous cells. Secondary conidia are arising from the apical cells, and further, they form additional conidia. The sexual morph is still undetermined. (Wang et al., 2023a). The species have only been reported from soil habitats (Wang et al., 2023a).

Table 4.40 *Multiverruca* species isolated from soil

Species	Country	Habitat or soil type	References
Multiverruca sinensis	China	Land with vegetation near a hospital	Wang et al. (2023a)

a

Figure 4.40 *Multiverruca sinensis* (HMAS 351940)

Figure 4.40, a Conidiogenous cell and conidia. Scale bar: a = 10 μm. Redrawn from Wang et al. (2023a).

Polyschema H.P. Upadhyay, Mycopath. in Mycol. Appl. 30(3-4): 278 (1966).

Figure 4.41

Index Fungorum number: IF 9506; Facesoffungi number: FoF 07745

Polyschema was introduced by Upadhyay (1966) and erected *P. terricola* as the type species. Currently, 20 species are available under the genus (Hyde et al., 2024c), but only four species have molecular data. The asexual morph is hyphomycetous with lateral, short or long, erect, simple, torulose, 0–3 septate conidiophores. Conidiogenous cells are mono- or polytretic and globose to clavate. Conidia are borne singly at hyphal tips, directly along sides, or on short pedicels, septate, smooth-walled, verrucose or tuberculate and pigmented (Hongsanan et al., 2020a). Species inhabiting decaying woods and leaves, human clinical specimens and soil habitats have been found from Brazil, Cuba, India and the USA (Upadhyay, 1966; Hongsanan et al., 2020a).

Table 4.41 *Polyschema* species isolated from soil

Species	Country	Habitat or soil type	References
Polyschema chambalensis	India	ND	Joshi et al. (1983)
P. congolense	Congo	Forest	Reisinger and Kiffer (1974)
P. queenslandicum	Australia	Forest	Mota et al. (2008)
P. sagari	India	Forest	Pandeya and Saksena (1978)
P. terricola	Brazil	ND	Upadhyay (1966)
P. variabile	India	ND	Tiwari et al. (1977)
P. yakuense	Japan	Forest soil	Matsushima (1975)

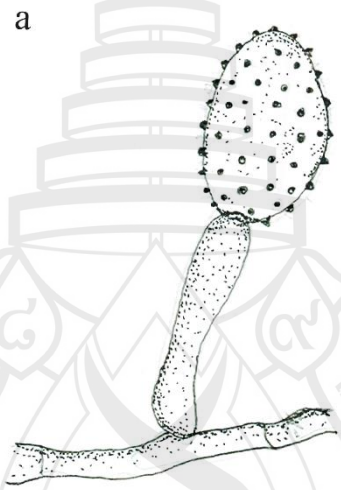


Figure 4.42 *Polyschema terricola*

Figure 4.42, a. Conidiophore. Redrawn from Upadhyay (1966)

Family*: Lentimurisporaceae* N.G. Liu, J.K Liu & K.D. Hyde

***Bahusandhik*a** Subram., Journal of the Indian Botanical Society 35(4): 469 (1956)

Figure 4.43

Index Fungorum number: IF 7319; Facesoffungi number: FoF 07231

Subramanian (1956) introduced *Bahusandhik*a by accommodating *B. indica* as the type species. Currently, seven species are accepted in this genus, and only one has molecular data (Hyde et al., 2024c). Pratibha et al. (2014) suggested this genus in *Pleosporales* with ITS and LSU phylogeny. Crane and Miller (2016) synonymized several *Latorua* species under *Bahusandhika* based on morphological characteristics. Hyphomycetous asexual morph possesses conidiophores that are brown, borne terminally

or laterally, septate, sometimes constrictions at the septa, occasionally reduced to a stalk cell, and sometimes lacking conidiophores. Monoblastic or polyblastic, spherical and ovoid conidiogenous cells produce light or dark brown, fusiform, cylindrical or rhomboidal, smooth or verrucose conidia present in simple or branched chains. The sexual morph is unknown (Pratibha et al., 2014). Most of the species are saprobes occupying woods or soil from India, Mexico, New Zealand, Panama and Venezuela (Crane & Miller, 2016).

Table 4.42 *Bahusandhik*a species isolated from soil

Species	Country	Habitat or soil type	References
Bahusandhika grootfonteinensis	Namibia	Brown sandy soil	Crous et al. (2015a)
B. terrestris	India	*Shorea robusta* forest	Crane and Miller (2016)

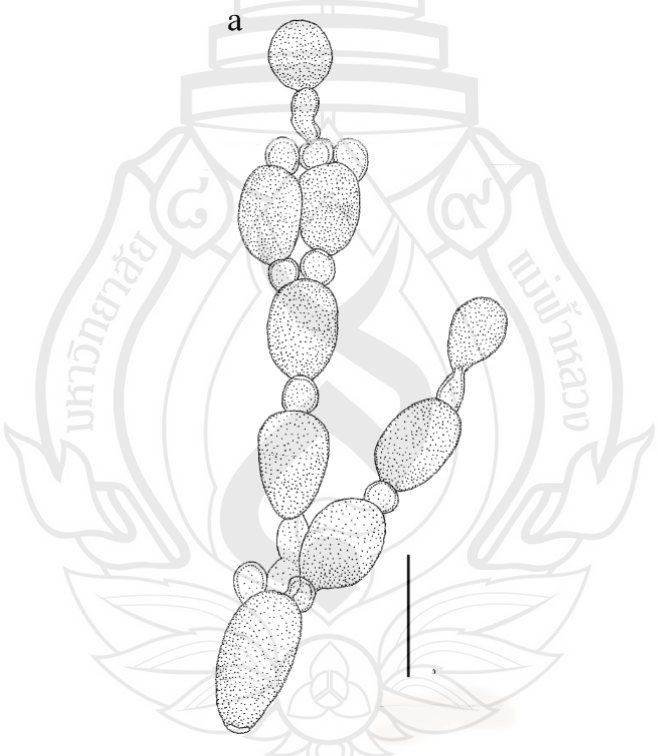


Figure 4.43 *Bahusandhik*a *indica* (HCIO 51509)

Figure 4.43, a. Conidiogenous cells with conidial chains. Scale bar: a = 20. Redrawn from Pratibha et al. (2014).

Family: *Leptosphaeriaceae* M.E. Barr

Leptosphaeria Ces. & De Not. (1863).

Figure 4.44

Index Fungorum number: IF 550958; Facesoffungi number: FoF 00454

Leptosphaeria was introduced by Cesati and De Notaris (1863), and the type species is *L. doliolum*, which was previously known as *Sphaeria doliolum* (Barr, 1987a; Shearer et al., 1990). Based on the ITS, LSU and *actin* gene regions, Ariyawansa et al. (2015) have provided an in-depth phylogenetic revision for this genus, including the *L. doliolum* species complex. The asexual morph is coelomycetous with depressed globose conidiomata, and ellipsoidal to subcylindrical conidia. The sexual morph has solitary, scattered ascomata in small groups, erumpent to superficial, globose to subglobose, broadly conical, black, coriaceous, and ostiolate. Asci are 8-spored, bitunicate, fissitunicate, cylindrical, pedicel furcate, rounded at the apex, with an ocular chamber, and having ascospores that are uni- or bi-seriate, partially overlapping, reddish to yellowish brown, 3-septate and constricted at each septum (Ariyawansa et al., 2015b). The species are saprobic or pathogenic and mostly harbour on herbaceous or woody plants in terrestrial habitats, while a few species are associated with soil. Species show a wide geographical distribution, including American, Asian and European regions (Ariyawansa et al., 2015b).

Table 4.43 *Leptosphaeria* species isolated from soil

Species	Country	Habitat or soil type	References
Leptosphaeria saccharicola	The Netherlands	ND	Hou et al. (2020a)

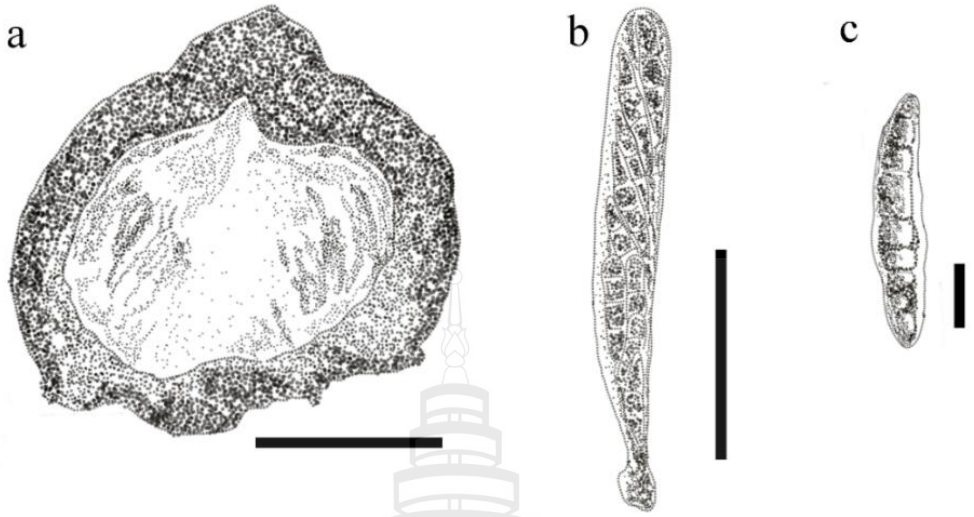


Figure 4.44 *Leptosphaeria doliolum* (MFLU 15-1875)

Figure 4.44, a Section of Ascoma. b Ascus. c Ascospore. Scale bars a= 200 μm, b = 60 μm, c = 10 μm. Redrawn from Ariyawansa et al. (2015b).

Family: ***Neocamarosporiaceae*** Wanas., Wijayaw., Crous & K.D. Hyde

Neocamarosporium Crous & M.J. Wingf., Persoonia 32: 273 (2014).

Figure 4.45

Index Fungorum number: IF 808949; Facesoffungi number: IF 808949

Neocamarosporium was introduced by Crous et al. (2014a), with *N. goegapense* as the type species. There are 24 species in the Index Fungorum (2025) and all of which are supported with molecular data. Initially, the genus was treated under *Pleosporaceae* (Crous et al., 2014a, 2014b), and then Wanasinghe et al. (2017b) established *Neocamarosporiaceae* based on the combined ITS, LSU, SSU, and *tef1-α* phylogeny and designated *Neocamarosporium* as the type genus (Gonçalves et al., 2019a). The asexual morph is characterized by pycnidial conidiomata, hyaline conidiogenous cells that produce brown, smooth, muriform conidia, similar to *Camarosporium*. However, these two genera are phylogenetically distinguishable (Crous et al., 2014a; Gonçalves et al., 2019a). The sexual morph is characterized by superficial to semi-immersed, confluent, gregarious, globose, ostiolate ascomata with peridium comprised of loosely packed cells of *textura angularis*. Asci are 8-spored, bitunicate, fissitunicate, cylindrical-clavate to cylindrical, with muriform, mostly ellipsoidal, 5–7-transversely septate, 1–2-longitudinal septate ascospores

that are constricted at the septum (Wanasinghe et al., 2017b). *Neocamarosporium* species are discovered from deserts, hypersaline soils, salt marshes, seawater habitats and some are associated with leaf spots, plant debris, living leaves, roots, seedlings and stems. They can be potentially useful in agriculture in drought and salinity-affected soils (Crous et al., 2014b; Wanasinghe et al., 2017b; Gonçalves et al., 2019). Species are distributed in Africa, America, Asia and Europe (Crous et al., 2021a).

Table 4.44 *Neocamarosporium* species isolated from soil

Species	Country	Habitat or soil type	References
Neocamarosporium chichastianum	Iran	ND	Crous et al. (2014b)
N. jorjanensis	Iran	Saline soil	Papizadeh et al. (2018)
N. persepolisi			
N. solicola			

a

Figure 4.45 *Neocamarosporium goegapense* (CBS 138008)

Figure a Conidiogenesis and conudium. Redrawn from Crous et al. (2014a)

Family: *Nigrogranaceae* Jaklitsch & Voglmayr

Nigrograna Gruyter, Verkley & Crous, Stud. Mycol. 75: 31 (2012) [2013]

Index Fungorum number: IF 564794

Nigrograna was introduced by de Gruyter et al. (2013) by using LSU phylogeny and morphology, accommodating *Nigrograna mackinnonii* (≡*Pyrenochaeta mackinnoni*) as the type species. Currently, Species Fungorum (2025) has listed 43 species under the genus. The asexual morph of the type species is characterized by pycnidial conidiomata that are solitary or rarely confluent, superficial to immersed, globose to subglobose or pyriform, with dark brown, septate mycelial outgrowths, having papillate ostioles, olivaceous to olivaceous-black and with pseudoparenchymatous cell wall. Conidiogenous cells are hyaline, phialidic and discrete and produce subhyaline, aseptate, ellipsoidal

conidia that appear brown in mass (de Gruyter et al., 2013). Subsequent studies have reported that the sexual morph is characterized by the black ascomata, clavate, short pedicellate asci and pale to chocolate brown, asymmetric, fusoid to narrowly ellipsoid, septate ascospores (Wanasinghe et al., 2020; Zhang et al., 2020). The Sexual morph is reported from *N. chromolaenae*, *N. impatitentis* and *N. hydei* (Mapook et al., 2020; Zhang et al., 2020). Species have a wide distribution as endophytes, saprobes, or human pathogens and are associated with dead wood, hive-stored pollen, marine environments and soil in Austria, China, Italy, Norway, Thailand and Venezuela (Kolařík et al., 2017; Tibpromma et al., 2017; Kolařík, 2018; Dayarathne, 2020; Zhang et al., 2020).

Table 4.45 *Nigrograna* species isolated from soil

Species	Country	Habitat or soil type	References
Nigrograna carollii	Kenya	Sediments and soils of a lake	Orwa et al. (2020)

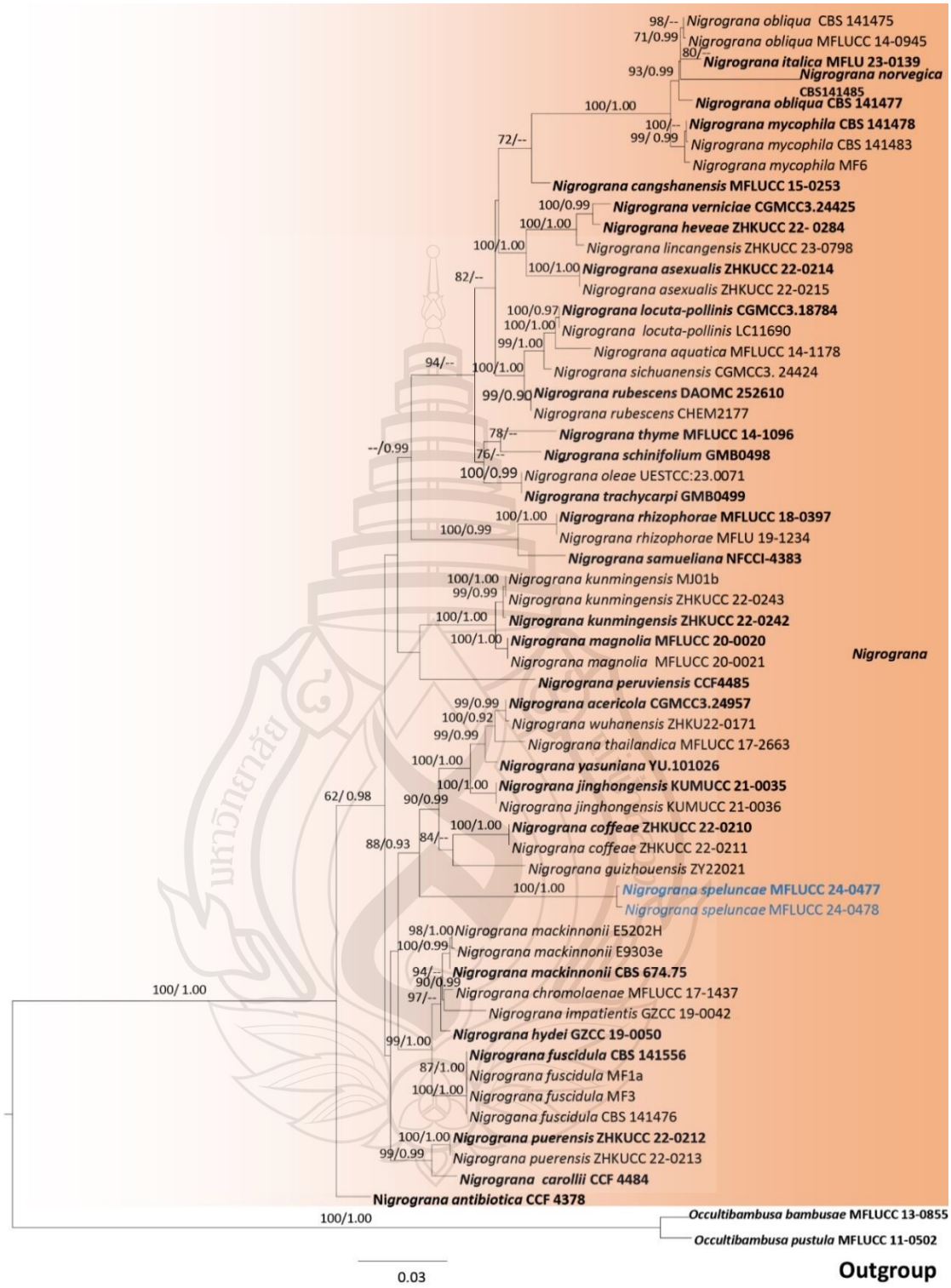


Figure 4.46 The best-scoring maximum likelihood tree generated of the combined LSU, ITS and *tef1-α* sequence data for *Nigrograna*

Figure 4.46, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Occultibambusa bambusae* (MFLUCC 13-0855) and *Occultibambusa pustula* (MFLUCC 11-0502). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 3974 bp, and single gene alignments are ITS: 1745 bp, LSU: 786 bp and tef1-α: 1443. The matrix had 1026 distinct alignment patterns with 19.98% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.62417, AT = 1.00000, CG = 1.00000, CT = 6.47412, GT = 1.00000; gamma distribution shape parameter α = 0.700.

Nigrograna speluncae Yasanthika & K.D. Hyde, sp. nov.

Figure 4.47

Index Fungorum number: IF903041; Facesoffungi number: FoF 16707

Etymology – The specific epithet "*speluncam*", from Latin, refers to the cave, the location of which the holotype was collected.

Holotype – MFLU25-0130

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 190–350 × 230–290 μm ($\overline{x}$ = 248 × 254 μm, n=10), pycnidial, mostly confluent, superficial on PDA, brown to dark brown or black, globose, unilocular, pycnidial wall pseudoparenchymatous. *Conidiophores* 2.5–6 × 1–2 μm ($\overline{x}$ = 4.5 × 1.7 μm), formed from the pycnidial wall, cylindrical to filliform, erect or flexuous, septate, hyaline to subhyaline or pale brown, simple to sparsely branched, with pegs, terminally phallidic. *Phialides* 2.5–3.5 × 2.5–5 μm, ($\overline{x}$= 3 × 3.5 μm), discrete, ampulliform to lageniform. *Conidia* 2.5–3.5 μm × 1.5–2.5 μm ($\overline{x}$ = 3 × 2 μm, n = 25), yellowish in groups, singly hyaline, aseptate, oval to ellipsoidal, thick-walled.

Culture characteristics – *Colonies* on PDA at 25°C, become 3–4 cm diam. after seven days, whitish-brown when immature, become brown to pale brown when mature, reverse brown, dark brown, raised, entire margined. *Mycelium* superficial, hyaline, becomes subhyaline to pale brown when mature, septate, smooth-walled, 1.5–3 μm ($\overline{x}$ = 2, n=30), sporulated after 8.5 weeks.

Material examined – Thailand, Chiang Rai, from What Tham Pha Tong cave, on soil 99.9038925N, 20.0918488E, 430m, 28 August 2022, W.A. Erandi Yasanthika (MFLU25-0130, holotype); ex-type 90-cv23-1=MFLUCC 24-0477. *ibid.* (MFLU25-0131); living culture 77-cv23-19 = MFLUCC 24-0478.

GenBank numbers –MFLUCC 24-0477: LSU: PQ587532, ITS: PP994670; MFLUCC 24-0478: ITS: PQ577713

Notes – According to the Figure 4.43, our collection (MFLUCC 24-0477 and MFLUCC 24-0478) clusters within *Nigrograna* producing an independent clade adjacent to *Nigrograna acericola* (CGMCC3.24957), *N. coffeae* (ZHKUCC 22-0210, ZHKUCC 22-0211), *N. jinghongensis* (KUMUCC 21-0035, KUMUCC 21-0036), *N. thailandica* (MFLUCC 17-2663), *N. wuhanensis* (ZHKU 22-0171) and *N. yasuniana* (YU.101026), with 88 % ML and 0.93 BYPP statistical support. We compared the nucleotides across the ITS (+5.8S) gene region of our species (90-cv23- MFLUCC 24-0477) with each sister species, given that 71/ 451(15 %) (including gaps) difference with *Nigrograna acericola* CGMCC3.24957, while having 66/ 486 (13.5 %) (including gaps) *N. coffeae* (ZHKUCC 22-0210), 73/ 479 (15 %) (including gaps) *N. jinghongensis* (KUMUCC 21-0035), 82/ 476 (17 %) (including gaps) *N. thailandica* (MFLUCC 17-2663), 75/ 487 (15 %) (including gaps) *N. wuhanensis* (ZHKU 22-0171) and 59/417 (14 %) (including gaps) and *N. yasuniana* (YU.101026). Only sexual morph has been observed in *N. acericola, N. thailandica, N. jinghongensis, N. coffeae* and *N. wuhanensis* and no sexual or asexual morph reported for *N. yasuniana* YU.101026 (Boonmee et al., 2021; Kolařík et al., 2017; Li et al., 2023; Lu et al., 2022; Senanayake et al., 2023). Therefore, comparing the morphology of our species with the sister species was difficult. *Nigrograna thailandica* has been isolated from Thailand (Senanayake et al., 2023) and *N.acericola, N. coffeae, N. jinghongensis,* and *N. wuhanensis,* reported as plant saprobes in China (Boonmee et al., 2021; Li et al., 2023; Lu et al., 2022) while *N. yasuniana* was reported as an endophyte in Ecuador (Kolařík et al., 2017). Based on phylogenetic and morphological analyses we introduce our species (MFLUCC 24-0477 and MFLUCC 24-0477) as *N. speluncae* isolated from undisturbed-cave soils in Thailand.

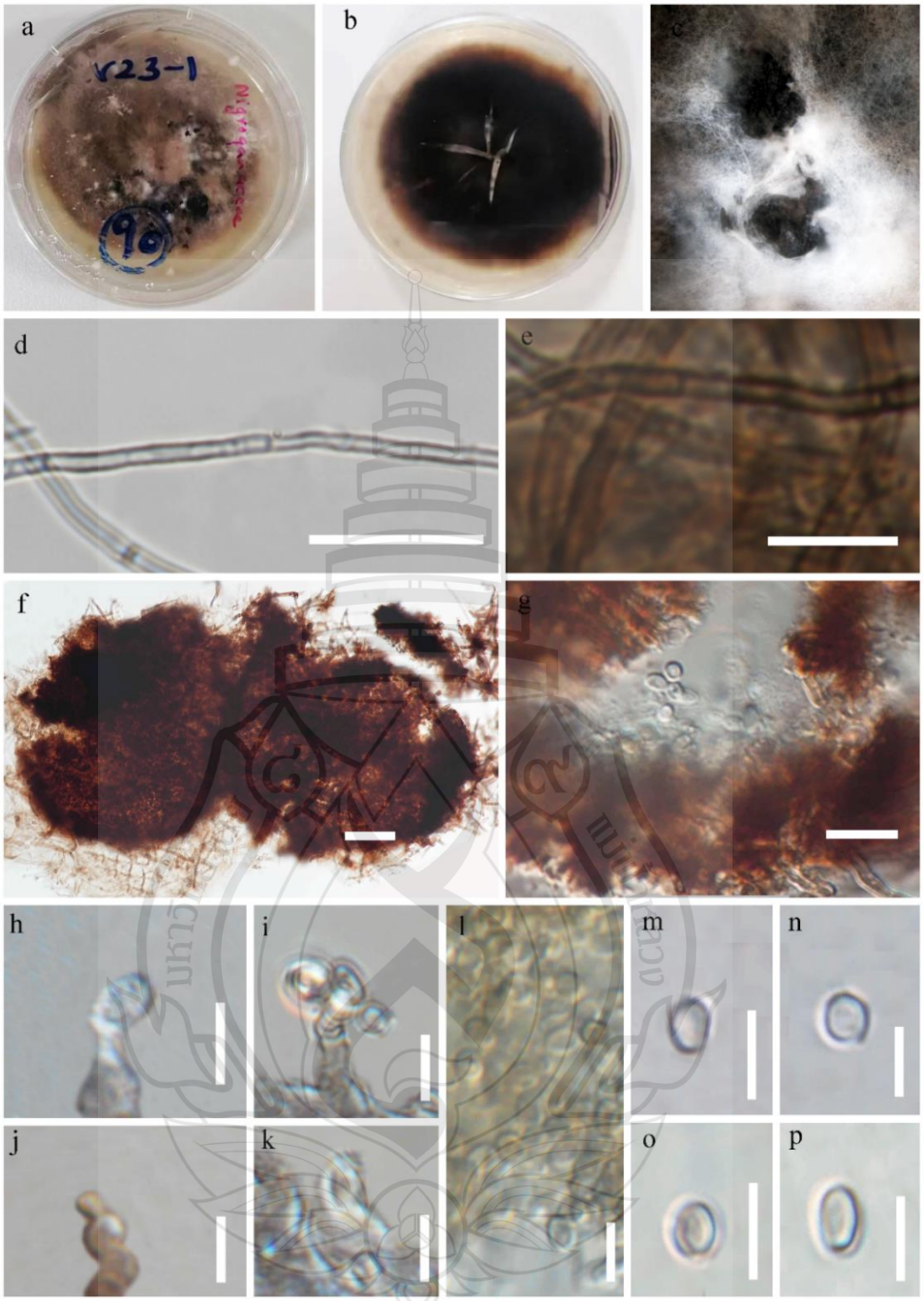


Figure 4.47 *Nigrograna speluncam* (MFLU25-0130, Holotype)

Figure 4.47 a, b Culture characters on PDA (b = reverse). c Pycnidia forming on culture. d Immature hypha e Mature hyphae f. Pycnidia. g pycnidia wall and matrix h–k Conidiophores with phialidic conidiagenous cells. l–p Conidia. Scale bars: f = 50 µm, d = 20 µm, e,g = 10 µm, h–p =5 µm.

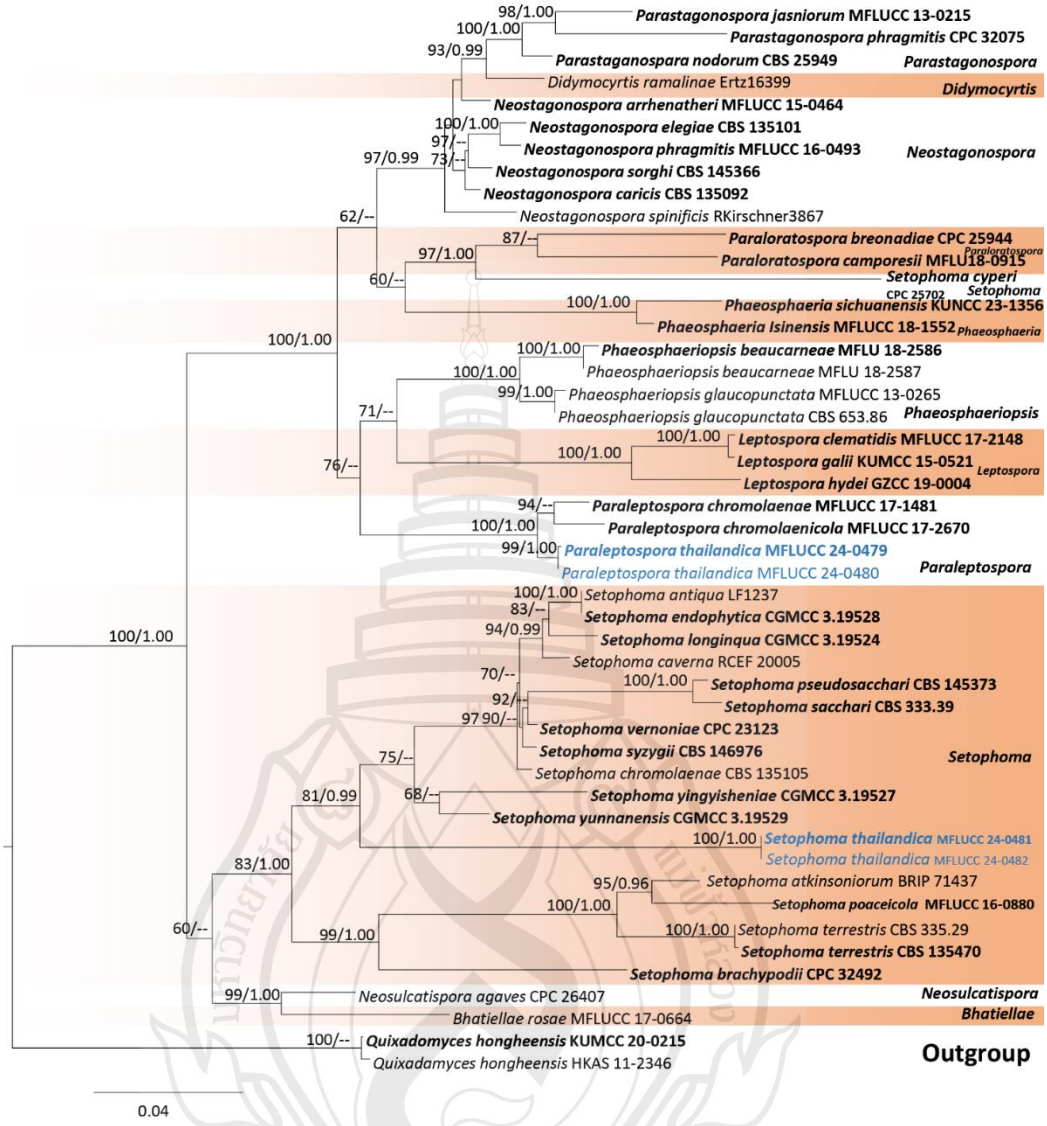


Figure 4.48 The best-scoring maximum likelihood tree generated of the combined LSU and ITS sequence data for *Phaeosphaeriaceae*

Figure 4.48, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Quixadomyces hongheensis* (KUMCC 20-0215 and HKAS 11-2346). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 1312 bp, and single gene alignments are ITS: 540 bp, and LSU: 772 bp. The matrix had 341 distinct alignment patterns with 3.56% undetermined characters and gaps. Estimated base

frequencies were as follows; A = 0.242, C = 0.215, G = 0.273, T = 0.269; substitution rates AC = 1.27505, AG = 3.36886, AT = 3.09631, CG = 0.30167, CT = 7.23013, GT = 1.00000; gamma distribution shape parameter α = 0.391.

Family: *Phaeosphaeriaceae* M.E. Barr

Paraleptospora Mapook & K.D. Hyde, Fungal Diversity 101: 75 (2020)

Index Fungorum number: IF 557347; Facesoffungi number: FoF 07810

Mapook et al. (2020) introduced *Paraleptospora* based on phylogeny and morphology, accommodating *P. chromolaenae* as the type species. Currently, two species are accepted in the genus, both of which were introduced with molecular data (Mapook et al., 2020). The sexual morph consists of immersed to semi-immersed, solitary or scattered, globose or subglobose to ampulliform, brown to dark brown ascomata with a short papillate ostiole, and the peridium is composed of several layers of thick-walled, pseudoparenchymatous, *textura angularis* cells. Asci are 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-subclavate, straight or slightly curved, pedicellate, apically rounded, with an ocular chamber, containing overlapping 1–3-seriate, hyaline or pale yellow to yellowish brown, cylindric-fusiform ascospores, (5–)6–7(–8)-septate, broader at the center and slightly constricted at septa, straight to slightly curved, guttulate, with or without polar appendages. Species have been reported as saprobes of dead stems of *Chromolaena odorata* in Thailand (Mapook et al., 2020). The genus has not been previously reported from soil.

Paraleptospora thailandica Yasanthika & K.D. Hyde, sp. nov.

Figure 4.49

Index Fungorum number: IF903042; Facesoffungi number: FoF 16708.

Etymology – The specific epithet "*thailandica*", from Latin, refers to Thailand, the country of which the holotype was collected.

Holotype – MFLU25-0169

Sexual morph: not observed. Asexual morph: not observed.

Culture characteristics —*Colonies* on PDA reach 4–5 cm diam. after 14 days at 25 °C, appear yellowish brown to grayish brown with brown periphary, raised cottony surface, reverse black brown center, yellowish middle rind and black to brown outer rind. *Mycelium* hyaline to subhyaline smooth-walled to thick-walled, septate, 1–3.5 µm ($\bar{x}$ = 2.1 µm, n=30) wide. *Chlamydospores* 4.5–12 × 3.5–6 µm ($\bar{x}$ = 7 × 5 µm, n = 20),

produced from mature hyphae, mostly intercalary, sometimes terminal, solitary, or in simple or branched chains, globose to ellipsoidal or sub-cylindrical, sub-hyaline to pale brown, thick-walled, Sexual morph: not observed. Asexual morph: not observed.

Material examined – Thailand, Chiang Mai, Mae Taeng District, Mushroom Research Centre, from forest, on soil, 19.2145N, 98.5953E, 1440m, 17 February 2019, W.A. Erandi Yasanthika, (MFLU25-0169, holotype); ex-type 69-fo5= MFLUCC 24-0479. *ibid*. (MFLU25-0170); living culture 69b-fo5b= MFLUCC 24-0480.

GenBank numbers – MFLUCC 24-0479: LSU: PQ590753, ITS: PQ012928; 69b-fo5b= MFLUCC 24-0480: LSU: PQ590755, ITS: PQ590754.

Notes – Our isolates (MFLUCC 24-0479 and MFLUCC 24-0480) cluster in *Paraleptospora* clade (Figure 4.45), however, made a distinct clade from *P. chromolaenae* (MFLUCC 17-1481) and *P. chromolaenicola* (MFLUCC 17-2670) with 99 % ML and 1.00 BYPP statistical support. The base pair difference of ITS (+5.8S) gene region in *P. thailandica* and *P. chromolaenicola* (MFLUCC 17-2670) is 20/473 (4.2%) (including gaps), and for *P. chromolaenae* (MFLUCC 17-1481), it is 17/473 (3.5%). Only sexual morph has been discovered previously (Mapook et al., 2020). Because there were no reproductive structures produced in MFLUCC 24-0479, we were unable to compare its morphology with sister species. However, chlamydospore production was observed in MFLUCC 24-0479. Based on our results, *Paraleptospora thailandica* was introduced, which was isolated from forest soil in Thailand. However, more specimens are needed for identifying its sexual and asexual characteristics. Both *P. chromolaenae* MFLUCC 17-1481 and *P. chromolaenicola* have been isolated from the dead stem of *Chromolaena odorata* from Thailand (Mapook et al., 2020). This is the first species of *Paraleptospora* associated with soil habitats.

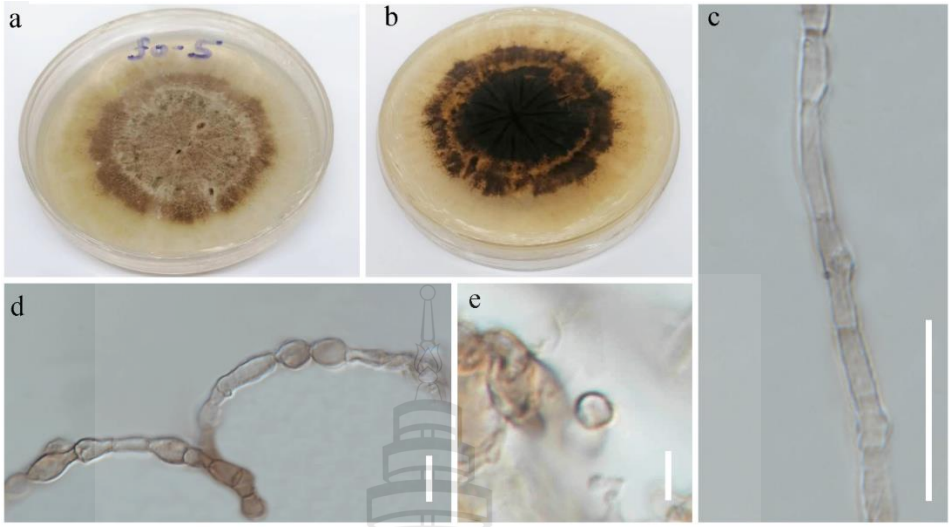


Figure 4.49 *Paraleptospora thailandica* (MFLU25-0169, Holotype)

Figure 4.49, a, b Culture characters on PDA (b = reverse). c Hyphae. d, e Chlamydospores. Scale bars: c = 20 µm, d = 10 µm, e = 5 µm.

Setophoma Gruyter, Aveskamp & Verkley, Mycologia 102(5): 1077 (2010)

Index Fungorum number: IF 514658

de Gruyter et al. (2010) introduced *Setophoma,* accommodating *Setophoma terrestris* as the type species. The genus comprises of 17 species (Species Fungorum 2025), and all of them are supported with molecular data. The asexual morph is characterized by pycnidia covered by setae, phialidic conidiogenous cells, and hyaline, ellipsoidal to subcylindrical, aseptate and guttulate conidia (de Gruyter et al., 2010). Most of the species can be found on living and dead leaves and associate with leaf spots. *Setophoma terrestris* is a cosmopolitan species harbours in roots and soils, and also a root pathogen causing pink root rot (Boerema et al., 2004; de Gruyter et al., 2010; López-López et al., 2020). Species are distributed in Australia, Belgium, Brazil, China, France, Japan and Thailand (Crous et al., 2021b; Liu et al., 2019b).

Table 4.46 *Setophoma* species isolated from soil

Species	Country	Habitat or soil type	References
Nigrograna carollii	Argentina	Onion rhizosphere soil	Albarracín Orio et al. (2016)

Setophoma thailandica Yasanthika & K.D. Hyde, sp. nov.

Figure 4.50

Index Fungorum number: IF903044; Facesoffungi number: FoF 16709

Etymology – The specific epithet "*thailandica*", from Latin, refers to Thailand, the country of which the holotype was collected.

Holotype – MFLU25-0135 Sexual morph: not observed. Asexual morph: not observed.

Culture characteristics —*Colonies* on PDA reach 4–5 cm diam. after 14 days at 25°C, appear yellowish brown to brown, become brownish grey with brown periphery when mature, raised cottony surface, reverse black brown center, yellowish brown outer ring. *Mycelium* hyaline, smooth, becoming subhyaline to thick-walled, septate, 1–4 µm ($\bar{x}$ = 3 µm) wide. *Chlamydospores* 5–10 × 4–9 µm ($\bar{x}$ = 7 × 6 µm, n = 20), produced from mature hyphae, terminal or intercalary, solitary, or in simple chains, globose to sub-globose or cylindrical, pale yellow to pale brown, thick-walled, guttultate or aguttulate.

Material examined – Thailand, Chiang Rai city, public area, on soil, Chiang Rai, 19.983438N, 99.892159E, 384m, 17 October 2022, W.A. Erandi Yasanthika, (MFLU25-0135, holotype); ex-type living culture 94-u3-4= MFLUCC 24-0481. *ibid*. 19.82714926N, 99.7574546E, 407m, 28 October 2022, W.A. Erandi Yasanthika (MFLU25-0136); living culture u4-2 110= MFLUCC 24-0482.

GenBank numbers –MFLUCC 24-0481: LSU: PQ577781, ITS: PP993943; MFLUCC 24-0482: ITS: PQ577782.

Notes –Based on the multi-gene phylogeny in Figure 4.45, our isolates (MFLUCC 24-0481 and MFLUCC 24-0482) cluster within *Setophoma,* producing an independent branch with 81% ML, 0.99 BYPP statistical support. However, we have not observed the sexual or asexual morphology in our species. But, chlamydospores were produced in our culture. This genus has members that produce chlamydospores. *Setophoma terrestris,* which is a common soil inhabitant, is characterized by producing globose to subglobose, terminal or intercalary, solitary or aggregated chlamydospores with guttules, which are similar to our species (Ikeda et al., 2012; Yoshida, 2022). Whereas, in our species, they can occasionally be in simple chains, cylindrical in shape and agglutinated. However, it is necessary to collect more specimens to identify its

sexual and asexual morphology. Based on morphology and multi-gene phylogeny, we introduce *Setophoma thailandica* which is isolated from urban soil in Thailand.

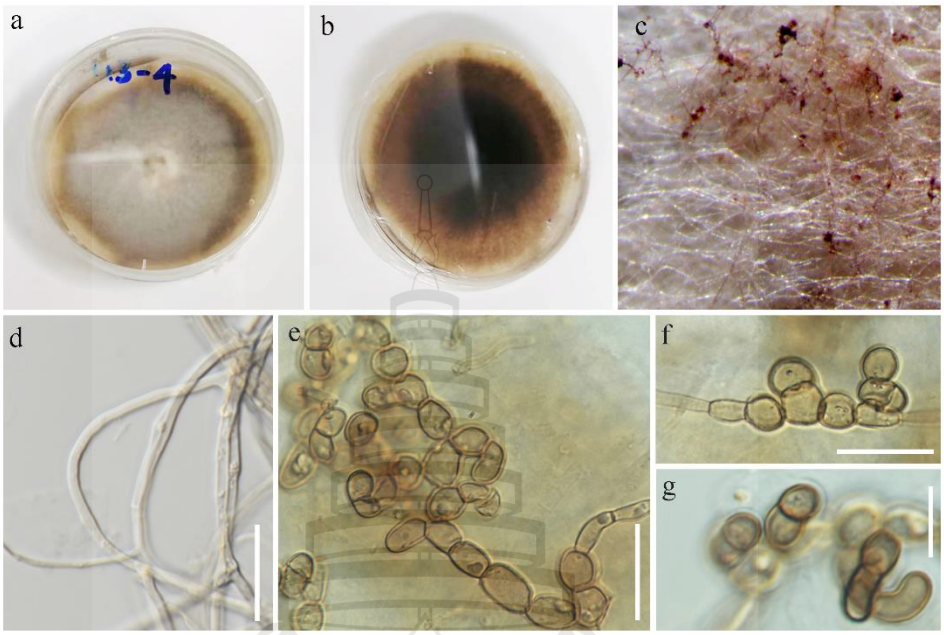


Figure 4.50 *Setophoma thailandica* (MFLU25-0135)

Figure 4.50, a, b Culture characters on PDA (b = reverse). C Chlamydospore formations d Hyphae. E–g Chlamydospores. Scale bars: d–g = 20 µm.

Family: *Pleosporaceae* Nitschke

Alternaria Nees, Syst. Pilze (Würzburg): 72 (1817).

Figure 4.51

Index Fungorum number: IF 7106; Facesoffungi number: FoF 00501

Alternaria was originally described by Nees von Esenbeck (1816), accommodating *A. tenuis* as the only species. Based on phylogeny, *Alternaria* is currently considered a complex comprised of non-monophyletic genera within the *Alternaria* complex. Phylogenetic revision for the *Alternaria* complex is provided by recent studies, and currently it is comprised of 27 sections (Lawrence et al., 2016; Woudenberg et al., 2013). The type species is accommodated as *Alternaria alternata* (Woudenberg et al., 2013). The asexual morph in the species has dark-coloured multi-celled conidia with longitudinal and transverse septa (phaeodictyospores), and a beak of tapering apical cells (Hongsanan et al., 2020a). This is an ubiquitous genus, having saprobic, endophytic and pathogenic modes that are associated with agricultural

products, air, animals, plants, seeds and soil. Some of them are serious plant pathogens leading to major crop and postharvest losses (Lawrence et al., 2016; Woudenberg et al., 2013).

Table 4.47 *Alternaria* species isolated from soil

Species	Country	Habitat or soil type	References
Alternaria alternata	Mexico	Spinach cultivation	Heredia et al. (1988)
A. angustiovoidea	Egypt	A Botanical garden	Ismail et al. (2020)
A. arborescens			
A. chlamydospora			
A. tenuissima			
A. arborescens	Switzerland	Peat soil	Norphanphoun et al.
A. indefessa	USA	ND	(2021)
A. phragmospora		ND	
A. soliaridae		ND	
A. carotiincultae	USA	ND	Park et al. (2008)
A. limaciformis	UK	ND	Woudenberg et al. (2013)
A. kulundii	Russia	Soda soil in steppe and a lake	Grum-Grzhimaylo et al. (2016)
A. petuchovskii		Soda/chloride soil in a lake	
A. shukurtuzii		Soda/chloride/sulfate soil in a lake	
A. radicina	USA	Carrot fields	Pryor et al. (1998)
Alternaria sp.	Thailand	ND	Manoch (2004)

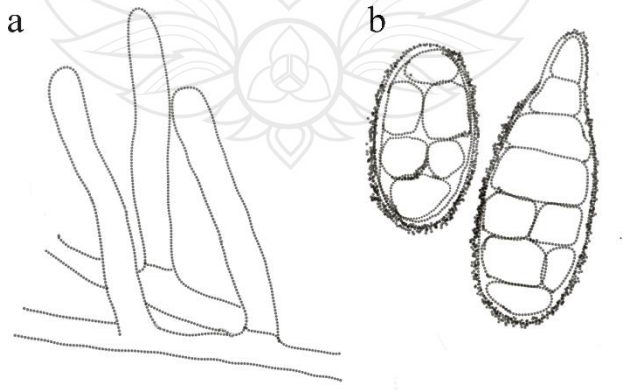


Figure 4.51 *Alternaria alternata* (CBS 326.65)

Figure 4.51, Redrawn from Domsch et al. (1993).

Bipolaris Shoemaker, Can. J. Bot. 37(5): 882 (1959).

Index Fungorum number: IF 7375; Facesoffungi number: FoF 00503

Shoemaker (1959) introduced *Bipolaris*, and the type species is *Bipolaris maydis*. Currently, 76 species are listed in the Species Fungorum (2025). During the taxonomic refinements in *Helminthosporium*, the species were segregated into several genera including *Bipolaris*, *Curvularia*, *Drechslera*, *Exserohilum*, *Johnalcornia* and *Porocercospora* (Sivanesan, 1987). Manamgoda et al. (2014) provided a phylogenetic revision for this genus, and the recent phylogenetic revision was provided by Bhunjun et al. (2020), while addressing various taxonomic misidentifications of the *Bipolaris* species and suggesting *gapdh* as the best single marker for the genus. The asexual morph is hyphomycetous, having conidiophores that are pale to dark brown, single, branched, sometimes arranged in small groups, straight to flexuous or geniculate. Conidiogenous nodes are smooth to slightly verruculose and produce conidia mostly curved, canoe-shaped, fusoid or obclavate, rarely straight, 3–14-distoseptate, hyaline, pale to dark brown, reddish brown or pale to deep olivaceous (Manamgoda et al., 2014). The sexual morph is not common in nature; however, it can be produced in laboratory conditions. The sexual morph is characterized by the brown or black, immersed, erumpent ascomata and the peridium is comprised of pseudoparenchymatous cells. Asci are 2–8-spored, clavate, cylindrical-clavate or broadly fusoid, bitunicate, fissitunicate and short pedicellate, with fasciculate, filiform or flagelliform, hyaline to pale yellow or pale brown, septate ascospores (Manamgoda et al., 2014). The genus is globally reported, and has pathogens, saprobes and endophytes inhabiting various hosts, including plants and soil. Some species are important plant pathogens that manifest diseases over 60 host genera, and associate with leaf spots, foliar blights and root rots (Bhunjun et al., 2020; Manamgoda et al., 2014). *B. sorokiniana* is widely distributed in soil, which is known as a root pathogen (Manamgoda et al., 2014).

Table 4.48 *Alternaria* species isolated from soil

Species	Country	Habitat or soil type	References
Bipolaris oryzae	Thailand	Rice field	Reanprayoon and Pathomsiriwong (2012)
B. australiensis	China	Yellow River Delta	Huimei and Tianyu (2004)
B. hawaiiensis			
B. spicifera			
B. sorokiniana	Japan	Rice field	Manamgoda et al. (2014)

Curvularia Boedijn, Bulletin du Jardin Botanique de Buitenzorg 13 (1): 123 (1933)

Index Fungorum: IF, Facesoffungi Number: FoF

Curvularia was introduced by Boedijn (1933) with its type species *C. lunata*. There are 196 species listed in the Species Fungorum (2025), and around 129 of them are supported with molecular data. Recent studies (Manamgoda et al., 2015; Marin-Felix et al., 2017a, 2017b; Tan et al., 2018) provided multi-gene phylogenetic analyses for *Curvularia* and introduced new species. Both asexual and sexual morphs have been observed; however, mainly asexual morph is used to distinguish this genus. Due to the morphological overlapping with other genera, multi-gene phylogenetic analyses are essential in species delineation in *Curvularia*. Asexual morph is characterized by brown, curved, disto- or eu-septate conidia with inordinately enlarged intermediate cells (Marin-Felix et al., 2017a, 2020a; Shoemaker, 1959). The sexual morph is characterized by black, globose ascomata, bitunicate, cylindrical asci and filiform, hyaline ascospores (Manamgoda et al., 2015). Nelson (1964) mentioned it is difficult to observe the sexual morph in the natural environment but in cultures. The genus has worldwide distribution recorded from air, clinical samples, household environments, plants, soil and water habitats in various life modes such as saprobes, endophytes and pathogens They can be pathogenic on animals, humans and plants (Manamgoda et al., 2015; Marin-Felix et al., 2017a; Tan et al., 2018). *Curvularia* infections have been observed in rice, maize, wheat and sorghum crops.

Table 4.49 *Curvularia* species isolated from soil

Species	Country	Habitat or soil type	References
Curvularia affinis	China	Yellow River Delta	Huimei and Tianyu (2004)
C. intermedia			
C. lunata			
C. brachyspora	Java	ND	Manamgoda et al. (2014)
C. inaequalis	France	Sand dune soil	
C. neergaardii	Chile	Desert soil	
C. spicifer	Spain	ND	
C. chiangmaiensis	Thailand	Forest soil	Yasanthika et al. (2023)
C. deserticola	Namibia	Desert soil	van Vuuren et al. (2024)
C. maraisii			
C. moringae			
C. namibe			
C. prasadii			
C. rouhanii			
C. stipagrostidicola			
C. tribuli			
C. eragrostidis	Thailand	Forests and cultivated lands	Seephueak et al. (2019)
C. lunata			
C. pallescens			

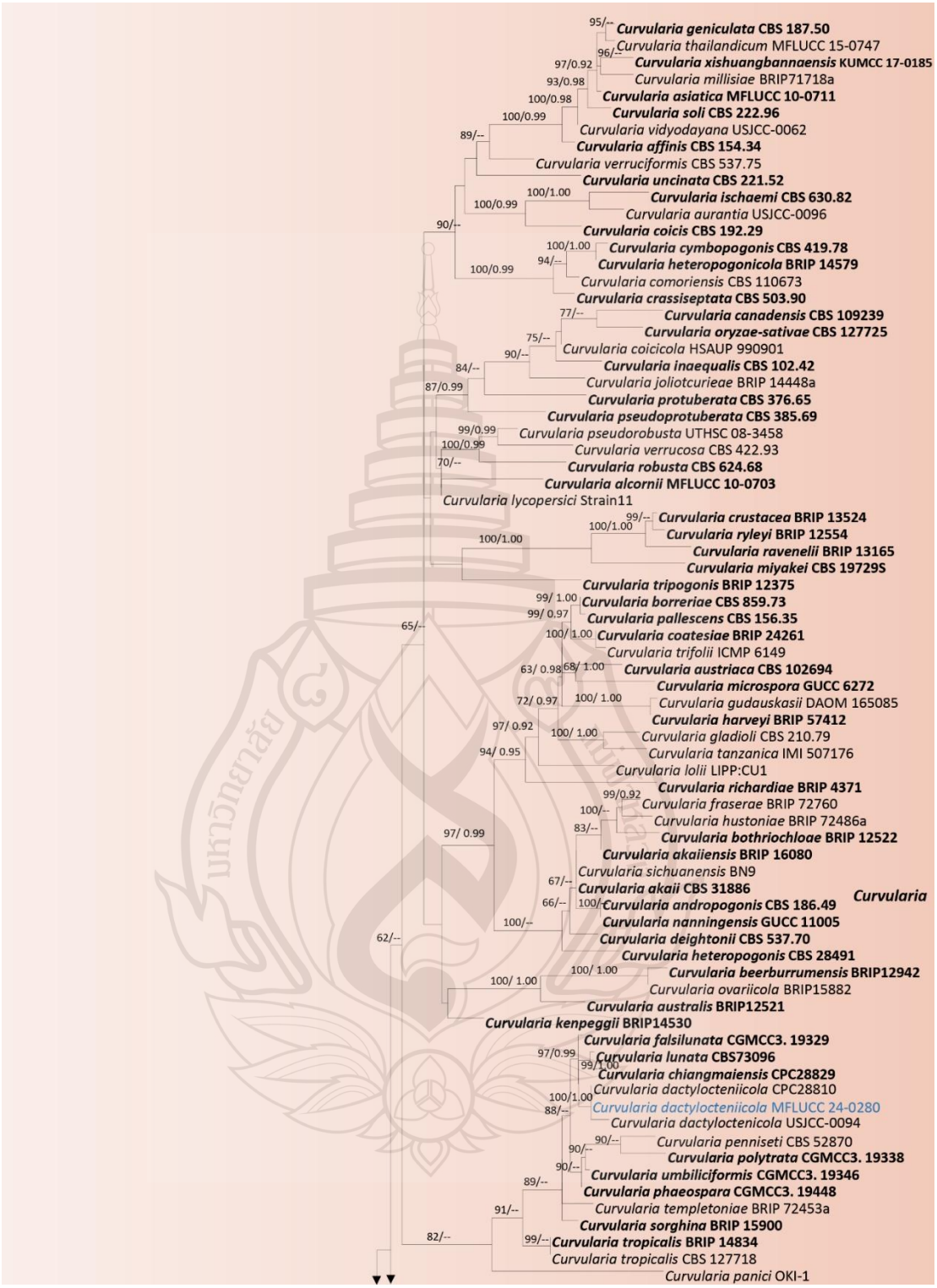


Figure 4.52 Maximum likelihood phylogenetic tree generated based on the combined ITS-*GAPDH*- *tef1-α* sequence data for *Curvularia* taxa

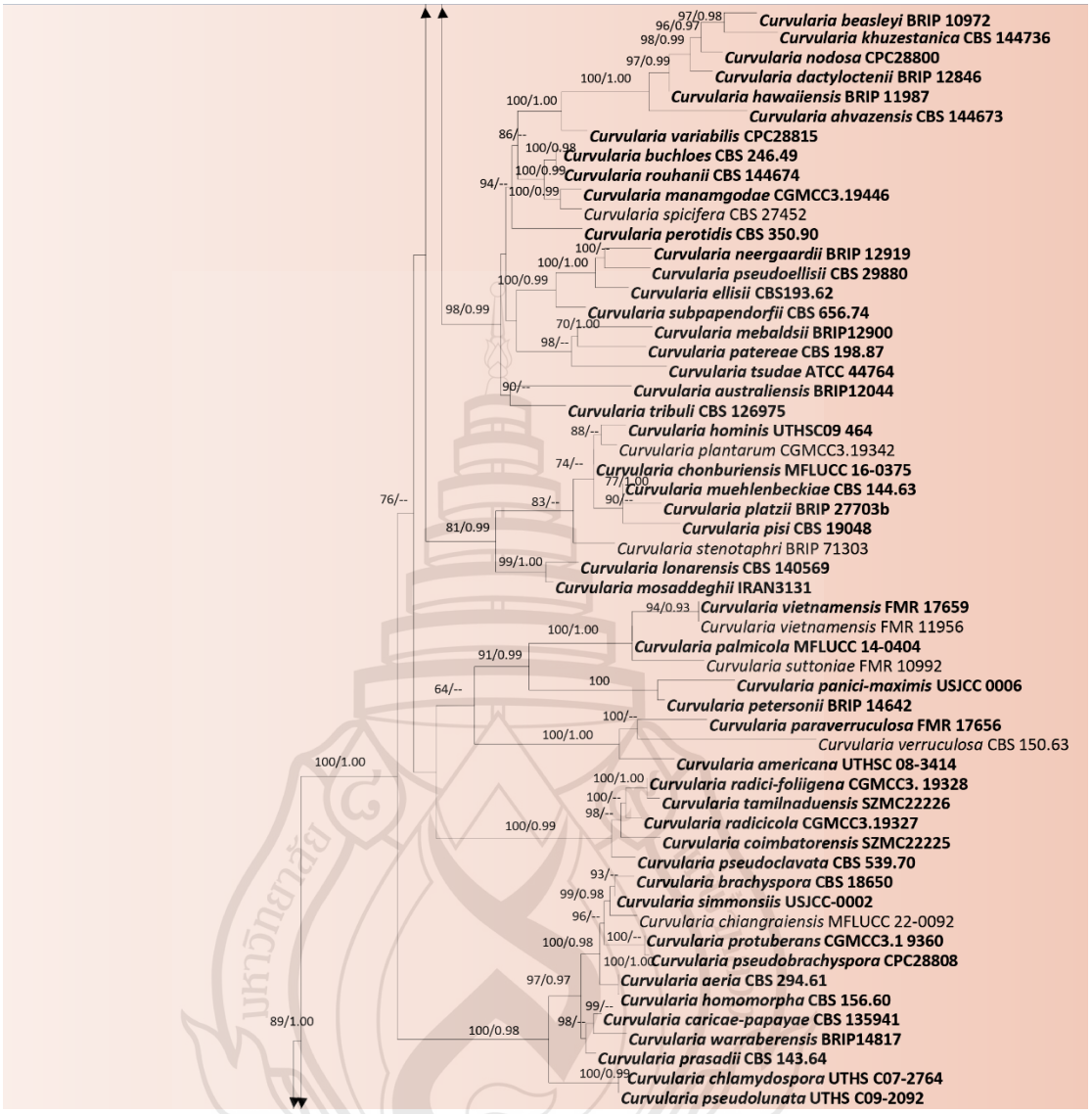


Figure 4.52 (continued)

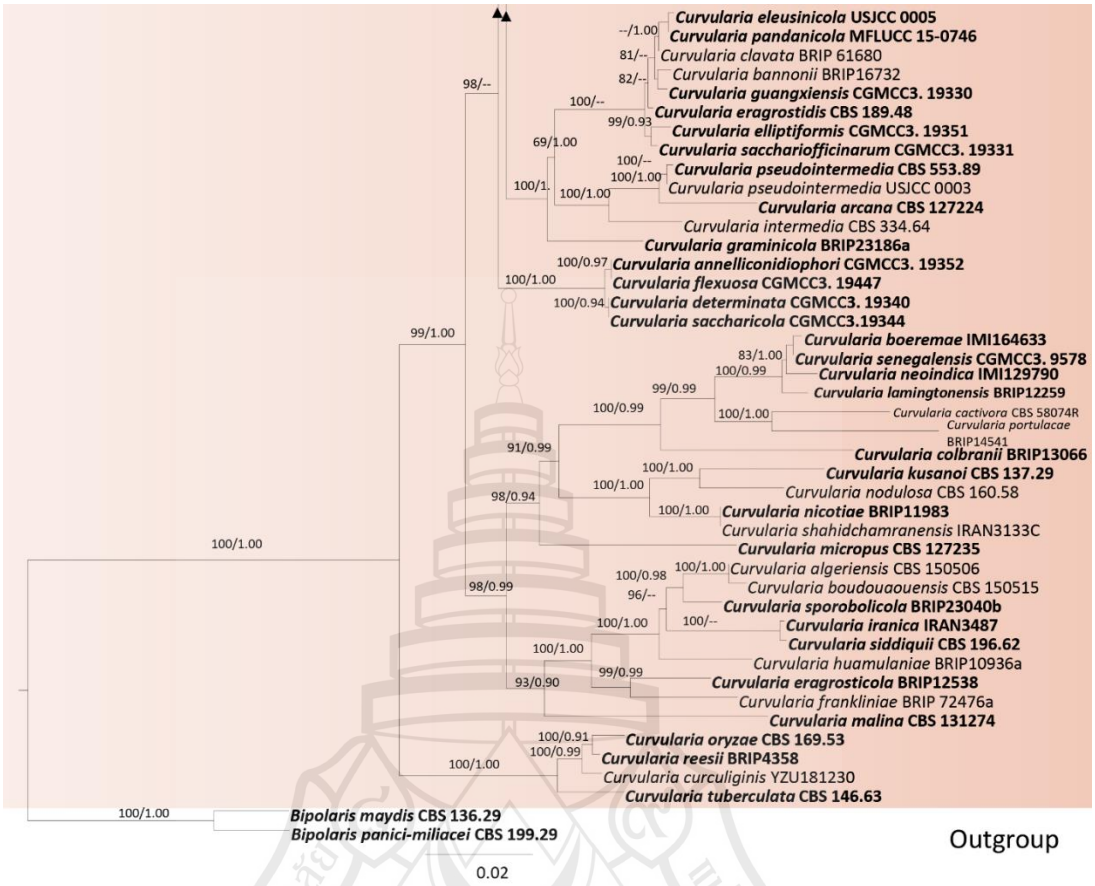


Figure 4.52 (continued)

Figure 4.52, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Bipolaris maydis* (CBS136.29) and *B. panici-miliacei* (CBS 199.29).

A best-scoring ML tree is shown (Figure 3.12), resulting from the combined ITS-*GAPDH-tef1-α* alignment comprising 158 strains, including *Curvularia* taxa and *Bipolaris maydis* (CBS 136.29) and *B. panici-miliacei* (CBS 199.29) as the outgroup taxa. The tree resulted in a final ML optimization likelihood value of – 16902.911. The matrix had 732 distinct alignment patterns, with 18% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.230, C = 0.308, G = 0.243, T = 0.220; substitution rates AC = 0.80851, AG = 3.44094, AT = 0.80851, CG =1.00000, CT = 6.12954, GT = 1.00000; proportion of invariable sites I = 0.607; gamma distribution shape parameter α = 0.665. Single-gene trees and multi-gene ML

and Bayesian (BYPP) analyses showed similar topologies, and there were no significant differences in tree topology compared to previous publications (Marin-Felix et al., 2017, 2020; Ferdinandez et al., 2021). The approximate length of the combined alignment is 1700 bp, and single gene alignments are ITS: 375 bp, *GAPDH*: 490 bp, and *tef1-α*: 835 bp. Our strain, MFLUCC 24-0280, grouped with *C. dactyloctenicola* with 77% ML and 1.00 BYPP statistical support. *Curvularia dactyloctenicola* is adjacent to *C. chiangmaiensis* (CPC 28829), *C. falsilunata* (CGMCC 3.19329, LC 11983) and *C. lunata* (CBS 73096).

Curvularia dactylocteniicola Y. Marín, Senwanna & Crous [as '*dactyloctenicol'*], Mycosphere 8(9): 1567 (2017)

Figure 4.53

Index Fungorum number: IF 822083, Faces of Fungi number: FoF 16494.

Sexual morph: Undetermined. Asexual morph: *Conidiophores* 150–200 × 6.5–3 μm ($\overline{x}$ = 172.5 × 5 μm, n = 10), single or often in groups, mononematous, macronematous, subhyaline, becoming hyaline towards apices, septate, straight or flexuous, geniculate in the upper part, size of cells not decreasing towards apex, sometimes branched, thick-walled. *Conidiogenous cells* 4–11 × 3–7.5 μm ($\overline{x}$ = 7.2 × 5 μm, n = 10), hyaline to subhyaline, smooth-walled, terminal or intercalary, sympodially proliferating, subcylindrical to swollen. *Conidia* 14–20 × 6.5–12 μm ($\overline{x}$ = 17 × 9.5 μm, n = 25), thick-walled, verrucose, straight to slightly curved, middle cells sometimes unequally enlarged, ellipsoidal to obovoid or sometimes subglobose, pale brown, 2–3-distoseptate, hila inconspicuous to slightly conspicuous.

Culture characteristics: —*Colonies* reach 4–5 cm diam. after seven days at 25°C on PDA, brownish-orange to black-brown, cottony, with moderate aerial mycelium, irregular margin, reverse black. *Mycelium* hyaline to subhyaline to pale brown, branched, smooth-walled to verrucose, thick-walled, septate, 2–7 μm ($\overline{x}$ = 3.6 μm) μm wide.

Material examined: —THAILAND. Chiang Mai: Omkoi District, Yang Piang, tropical forest soil, on hair baits, 17.7145N, 98.4286E, 935 m,16 October 2019, W.A. Erandi Yasanthika (MFLU24-0381); living culture MFLUCC 24-0280 (CM21-1).

Notes – Soil-inhabiting *Curvularia* species have previously been isolated from forests (Yassanthika et al., 2023) and rice fields in Thailand (Leewijit et al., 2016;

Marin-Felix et al., 2017b). In the multi-gene (ITS-GAPDH-*tef1-α*) phylogenetic analyses of *Curvularia* species (Figure 4.52), our strain (MFLUCC 24-0280) grouped with *C. dactylocteniicola* (CPC 28810, USJCC-0094) with 100% ML and 1.00 BYPP statistical support. *Curvularia dactylocteniicola* was introduced by Marin-Felix et al. (2017) associated with a leaf spot of *Dactyloctenium aegyptium* in Doi Saket, Chiang Mai, Thailand. *Curvularia dactylocteniicola* has been reported from *Saccharum officinarum*, *Sorghum* sp. and *Zea mays* in China, Indonesia and Sri Lanka (Ferdinandez et al., 2024; Hidayat & Ramadhani, 2019; Raza et al., 2019). It has also been isolated from the phylloplane of xerophytic plants (Bhanot et al., 2024). Our isolate is morphologically similar to the type species (CPC 28810) in having straight or flexuous, occasionally branched, mononematous, semi- to macronematous conidiophores that are sometimes geniculate in the upper part, terminal or intercalary, sympodial proliferating, subcylindrical to swollen conidiogenous cells and verruculose, mostly curved, occasionally unequally enlarged middle-celled, ellipsoidal to obovoid conidia (Marin-Felix et al., 2017b). Our isolate (MFLUCC 24-0280) differs from the type species (CPC 28810) in having thick-walled, verrucose, straight to slightly curved, ellipsoidal to obovoid or sometimes subglobose, pale brown, 2–3-distoseptate conidia and inconspicuous to slightly conspicuous hila, in contrast to the smooth- to slightly verruculose-walled, mostly curved, ellipsoidal to obovoid, 3-distoseptate with flat to slightly protruding, darkened conidia with thickened hila of the latter (Marin-Felix et al., 2017b). Based on the morphology and phylogeny, we confirmed our collection as *C. dactylocteniicola* isolated from forest soils in Thailand; this is the first time this species has been reported from soil. *Curvularia dactylocteniicola* was isolated using the hair-baiting technique, and we suggest that it is a keratinophilic species. Further biochemical analyses are necessary to confirm and identify its contribution to the hair degradation process.

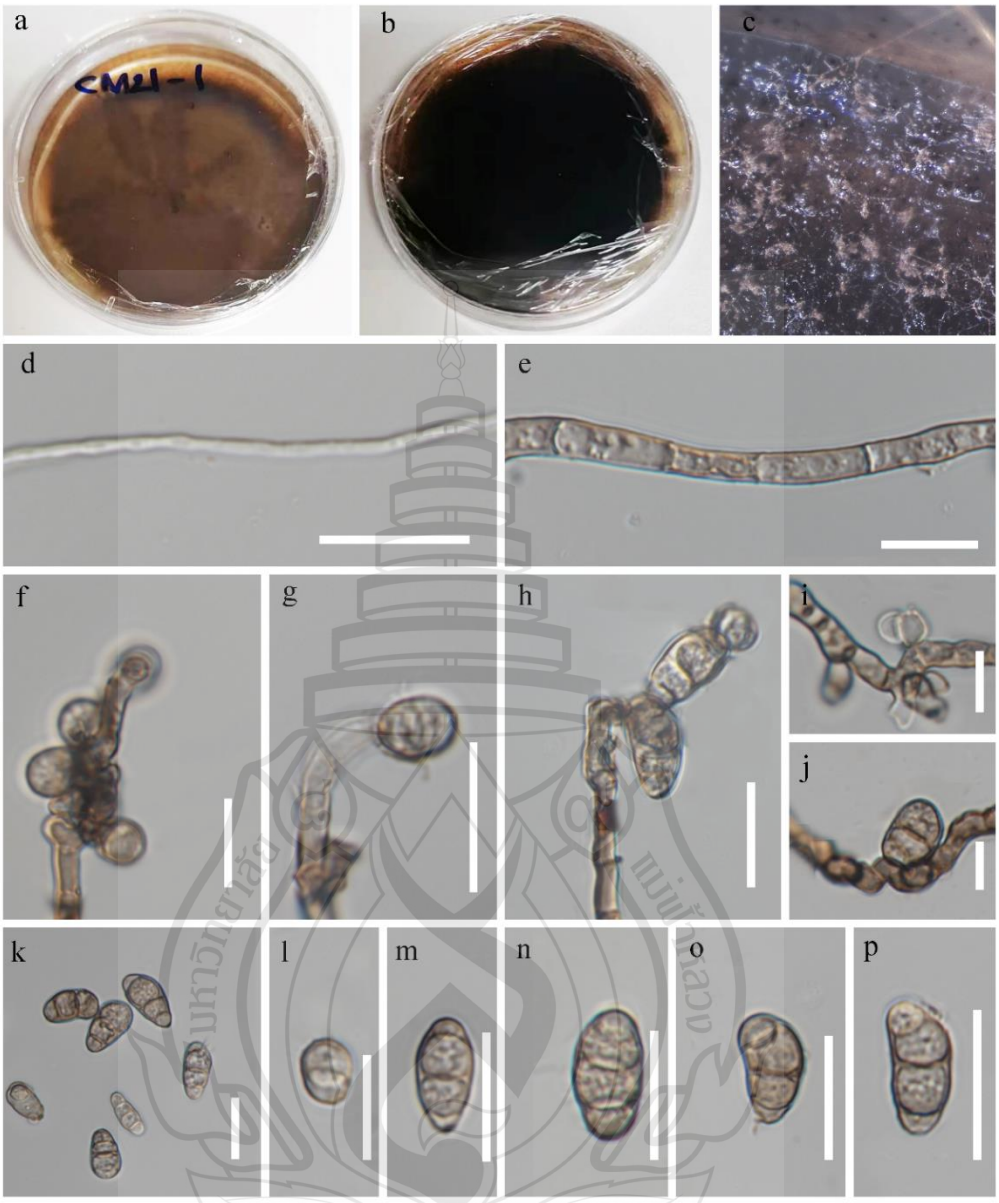


Figure 4.53 *Curvularia dactylocteniicola* (MFLU24-0381)

Figure 4.53, a. Colony from above on PDA. b. Colony from below on PDA. c. Sporulating colony with conidial attachments on the mycelium. d. Immature hyphae e. Mature melanized hypha. f–j Conidiogenesis on the conidiophore. k–p. Conidia. Scale bars: d–h, k–p = 20 µm, i, j =10 µm.

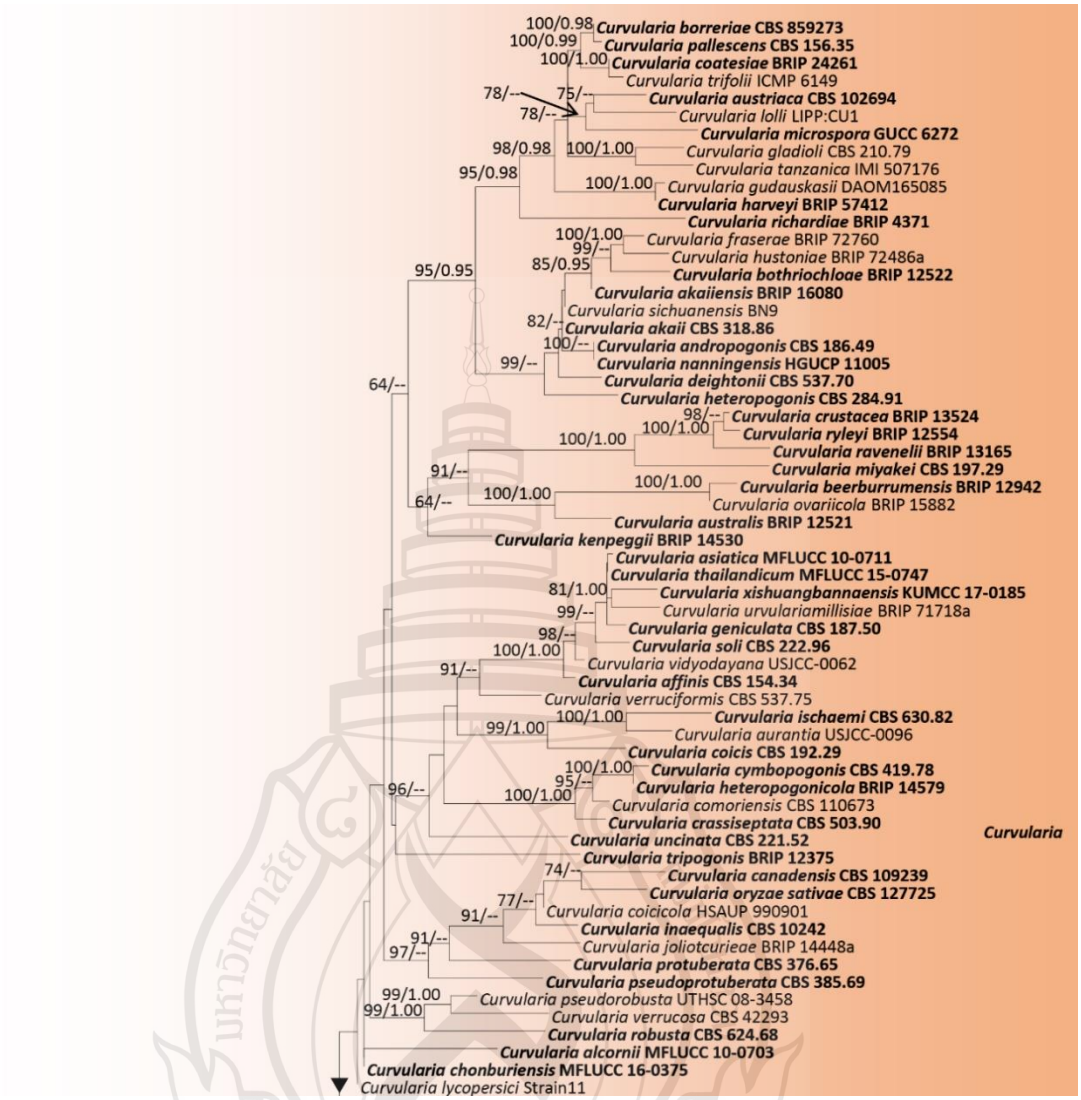


Figure 4.54 The best-scoring maximum likelihood tree generated based on the combined ITS, *gapdh*, and *tef1-α* sequence data for *Pleosporaceae*

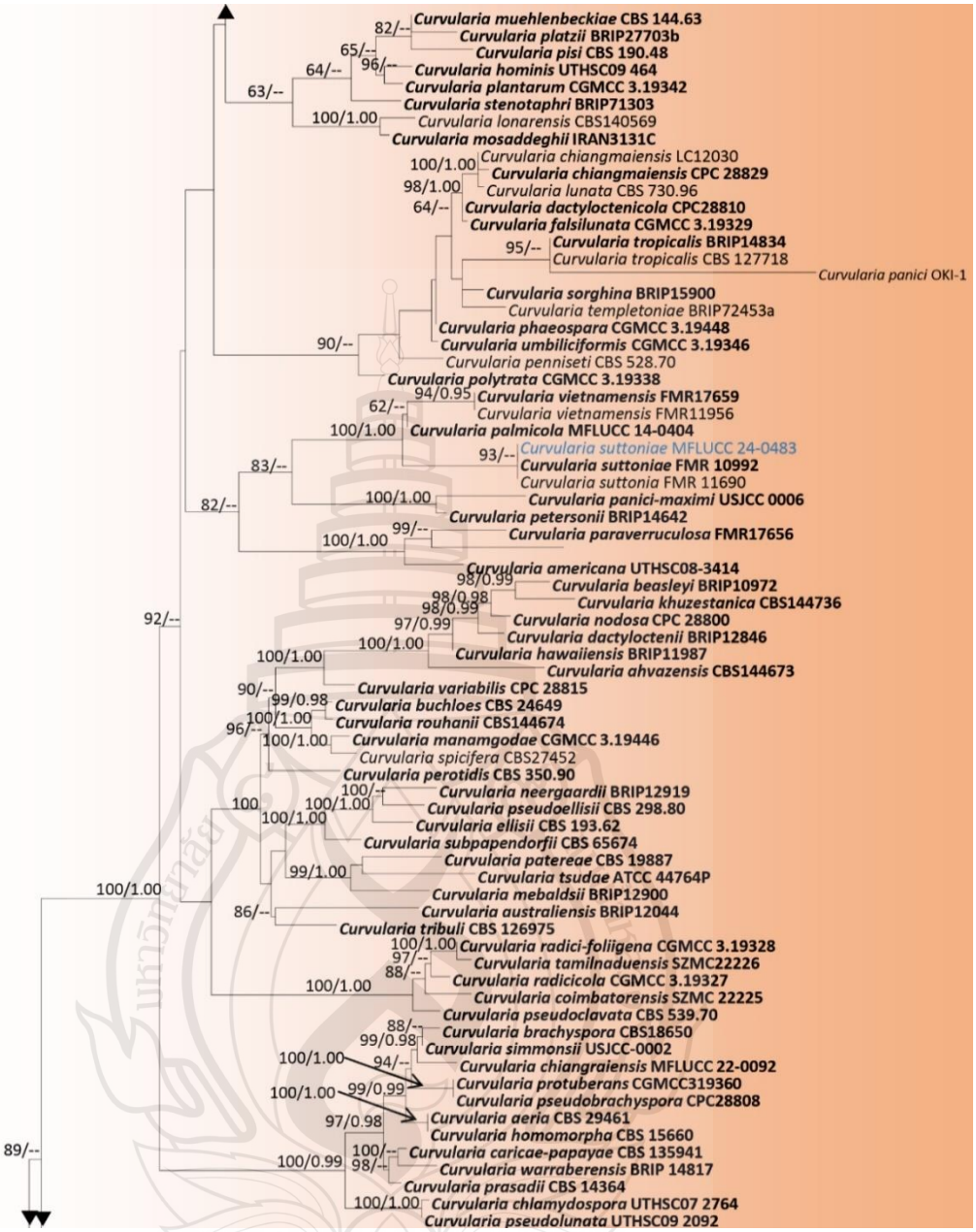


Figure 4.54 (continued)

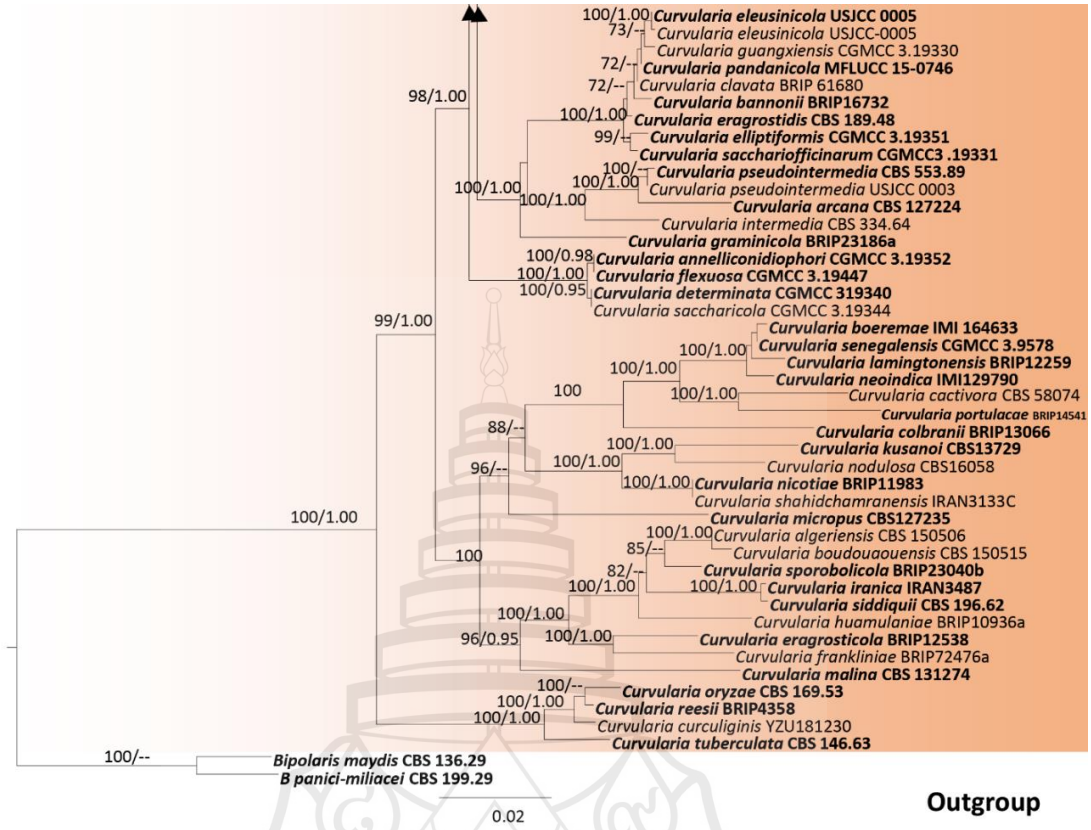


Figure 4.54 (continued)

Figure 4.54, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted in *Bipolaris maydis* (CBS 13629) and *Bipolaris panici-miliacei* (CBS 19929LT). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 1820 bp, and single gene alignments are ITS: 377 bp, *tef1-α*: 906 bp, *GAPDH*: 537 bp. The matrix had 674 distinct alignment patterns with 16.84% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.230, C = 0.308, G = 0.243, T = 0.219; substitution rates AC = 1.00000, AG = 4.00737, AT = 1.00000, CG = 1.00000, CT = 6.66178, GT = 1.00000; gamma distribution shape parameter α = 0.674.

Curvularia suttoniae Iturrieta-González, Wiederhold, Gené & Dania García, MycoKeys 68: 13 (2020)

Fig. 4.55

Index Fungorum number: IF 833025; Facesoffungi number: FoF 16710

Sexual morph: not observed. Asexual morph: *Conidiophores* 2–5.5 × 1.5–3 μm ($\overline{x}$ = 3.5 × 2.5 μm), mononematous, micronematous, mostly intercalary, smooth-walled, pale brown to brown. *Conidiogenous cells* arise from hyphae or mostly intercalary, polytretic, pale brown, sub-cylindrical. *Conidia* 11.5–20 × 6–9 μm ($\overline{x}$ = 15.5 × 7.5 μm, n = 25), pale brown, straight or slightly curved, smooth-walled, 2–3 septate, the third cell from the base often swollen, apical and basal cells paler than the middle cells, protuberant and thickened at hila. *Chlamydospores* sub-hyaline to brown, globose to sub-globose intercalary, simple or branched chains, smooth to slightly verruculose-walled.

Culture characteristics–*Colonies* become 3–4 cm diam. at 25°C on PDA, appear black-brown velvety, flat, irregularly margined, reverse black. *Mycelium* sub-hyaline to brown, branched, smooth-walled to verruculose, septate, 2.5–6 μm ($\overline{x}$ = 4.5 μm) μm wide.

Material examined – Thailand, Chiang Rai, Public area in the city, 19.82714N, 99.7574546E, 407m,28 October 2022, W.A. Erandi Yasanthika, (MFLU25-0134); living culture 101-U2-3= MFLUCC 24-0483.

GenBank numbers – MFLUCC 24-0483: ITS: PQ567560, *gapdh*: PV523927, *tef1-α:* PV523926

Notes – Our strain (MFLUCC 24-0483) clustered with *Curvularia suttoniae* with 93% ML statistical support and in the phylogenetic tree (Figure 4.49), however, with a BYPP value less than Each gene region was compared between our strain and the type species (FMR 10992), and they showed 100% similarity. Our isolate has a similar morphology to *C. suttoniae* (FMR 10992) by having straight or slightly curved, 2–3 septate conidia with the third cell from the base often swollen and protuberant and thickened hila (Iturrieta-González et al., 2020). However, the type species (FMR 10992) has semi- to macronematous, erect to slightly flexuous conidiophores with geniculated apices, while in our isolate, most of them are intercalary and smooth-walled. In addition, our isolate has produced chlamydospores. Based on morphology

and phylogeny, we confirm our strain as *C. suttoniae.* The species has previously been isolated from human clinical samples in the USA (Iturrieta-González et al., 2020). Herein, we report its first record from soil that was isolated from a public place in Chiang Rai City, Thailand.

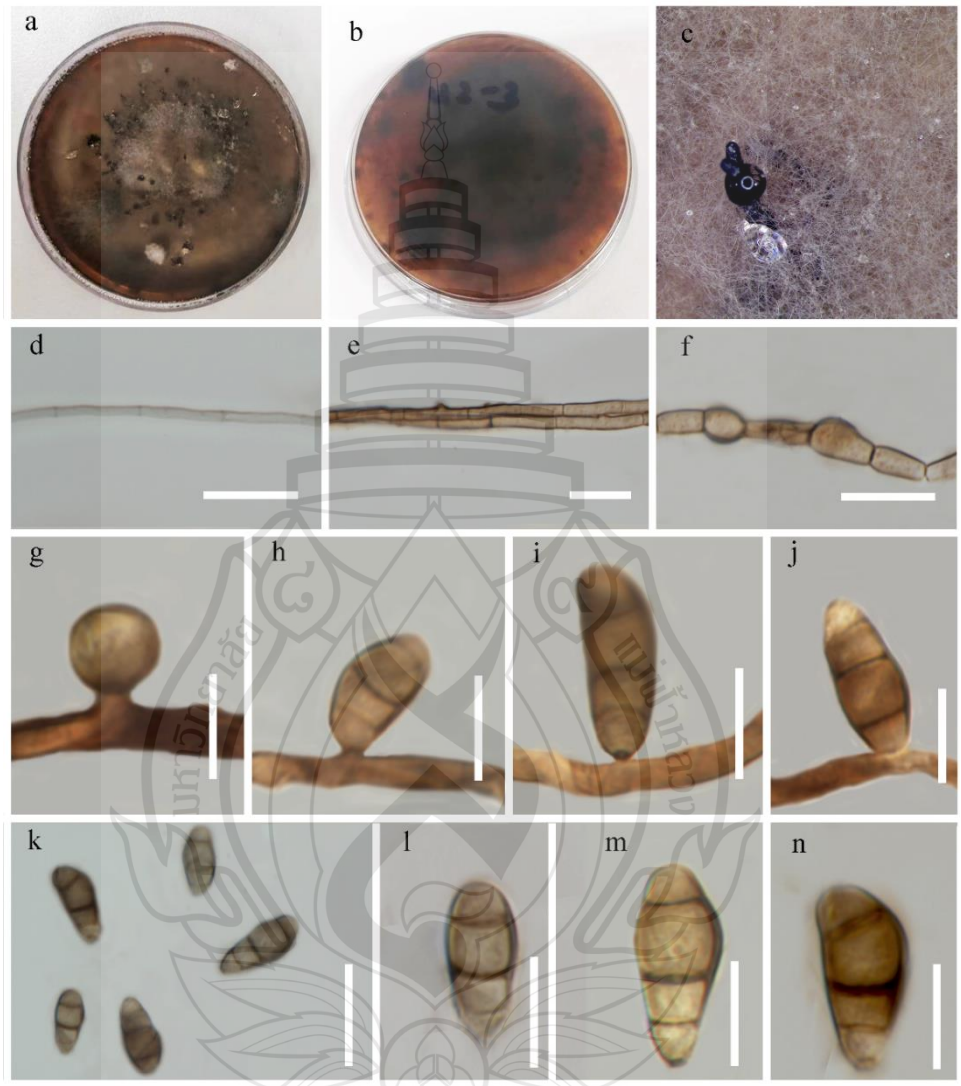


Figure 4.55 *Curvularia suttoniae* (MFLU25-0134MFLU)

Figure 4.55, a, b Culture characters on PDA (b = reverse). c. Sporulated colony with conidial attachments on the mycelium. d. Immature hyphae. e Mature hyphae. f. Clamydospores g–i Conidiogenesis. k–n Conidia. Scale bars: d–f, k = 20 µm, g–j, l–n = 10 µm.

Pyrenophora Fr., Summa veg. Scand., Sectio Post. (Stockholm): 397 (1849)

Index Fungorum number: IF 4596; Facesoffungi number: FoF 000009

Pyrenophora was introduced by Fries (1849) while accommodating the type species, *P. phaeocomes,* which was previously described as *Sphaeria phaeocomes* in *Xylariaceae* (Rebentisch, 1804). However, Fries (1849) placed *Pyrenophora* in *Pleosporales,* and currently, the genus consists of more than 100 species (Hyde et al., 2024c). *Pyrenophora* is linked to asexual morphs in *Drechslera* and the sexual morph is characterized by having ascomata that are immersed to semi immersed, neck covered with brown to reddish-brown setae, lack of pseudoparaphyses, clavate to saccate asci, usually with a large apical ring, and muriform terete (cylindrical, frequently circular in section but narrowing to one end) ascospores (Ariyawansa et al., 2014a). Species can be saprobes or pathogens that have been found in living and dead leaves and stems, seeds, and soil in Australia, Europe, Hungary, India, New Zealand, North America, and Thailand. Further, they are pathogens on many graminicolous hosts that cause serious diseases such as barley stripe and tan spot of wheat (Zhang & Berbee, 2001; Ariyawansa et al., 2014a).

Table 4.50 *Pyrenophora* species isolated from soil

Species	Country	Habitat or soil type	References
Pyrenophora sp.	Thailand	ND	Manoch et al. (2004)
Pyrenophora sp.	India	Arsenic-contaminated soil	Naseem et al. (2024)
P. tritici-repentis	China	North China Plain	Liu et al. (2024)

Family: *Pseudopyrenochaetaceae* Valenz.-López, Crous, Stchigel, Guarro & J.F. Cano

Pseudopyrenochaeta Valenz.-Lopez, Crous, Stchigel, Guarro & Cano, Stud. Mycol. 90: 53 (2017).

Figure 4.56

Index Fungorum number: IF 820427; Facesoffungi number: FoF 08353

Pseudopyrenochaeta was erected by Valenzuela-Lopez et al. (2018), based on a multi-gene phylogenetic analysis (LSU, ITS, *tub2,* and *rpb2*) and the morphological support. It was designated as the type genus of *Pseudopyrenochaetaceae,* with *P. lycopersici* recognized as the type species (Valenzuela-Lopez et al., 2018).

Pseudopyrenochaeta consists of two species (Species Fungorum 2025), and both of them have molecular data. The asexual morph possesses pycnidial, brown to dark brown, solitary, globose to subglobose, setose conidiomata. Conidiophores are hyaline, simple, filiform, and have phialidic, hyaline, and intercalary conidiogenous cells. Conidia are hyaline, cylindrical to allantoid, aseptate, smooth- and thin-walled. The sexual morph remains undetermined. Members are soil-borne fungal pathogens that can cause corky disease in tomatoes, leading to significant yield losses in tomato crops, and infect cucumber, eggplant, melon, pepper, safflower, spinach, and tobacco, found in Korea, Russia, and the Netherlands (Aragona et al., 2022).

Table 4.51 *Pseudopyrenochaeta* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudopyrenochaeta lycopersici	Italy, Korea, and Russia	Soil in tomato cultivations	Bubici (2018)
P. terrestris	The Netherlands	Greenhouse soil	Valenzuela-Lopez et al. (2018)

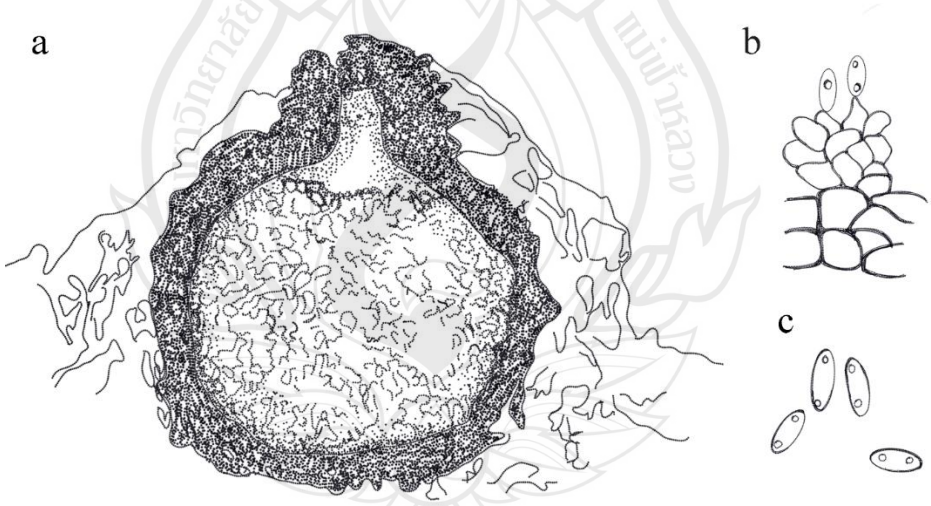


Figure 4.56 *Pseudopyrenochaeta lycopersici*

Figure 4.56, a Conidiomata. b Conidiogenesis c Conidia. Redrawn from Schneider and Gerlach (1973)

Family: *Pyrenochaetopsidaceae* Valenz.-López, Crous, Cano, Guarro & Stchigel

Neopyrenochaeta Valenz.-Lopez, Crous, Stchigel, Guarro & Cano, Stud. Mycol. 90: 54 (2017)

Index Fungorum number: IF 820313; Facesoffungi number: FoF 07389

Valenzuela-Lopez et al. (2018) introduced *Neopyrenochaetaceae* based on LSU, ITS, *tub2*, and *rpb2* gene regions and accommodated *Neopyrenochaeta* as a new genus with its type species, *N. acicula*. The genus comprises 16 species (Species Fungorum 2025), all supported with molecular data. The asexual morph is characterized by the pale brown to brown, solitary ovoid to globose pycnidia and setose, ostiolate, and with textura angularis pycnidial wall. Conidiogenous cells are phialidic, ampulliform, or lageniform and produce aseptate, hyaline, smooth- and thin-walled, ovoid to subcylindrical conidia (Valenzuela-Lopez et al., 2018). Species are reported from dead plant materials, freshwater habitats, mobile phones, and soil in China, Russia, South Africa, Thailand and the Netherlands (Li et al., 2020a; Magaña-Dueñas et al., 2021; Mapook et al., 2020; Valenzuela-Lopez et al., 2018).

Table 4.52 *Neopyrenochaeta* species isolated from soil

Species	Country	Habitat or soil type	References
Neopyrenochaeta acicula	The Netherlands	ND	de Gruyter et al. (2010)

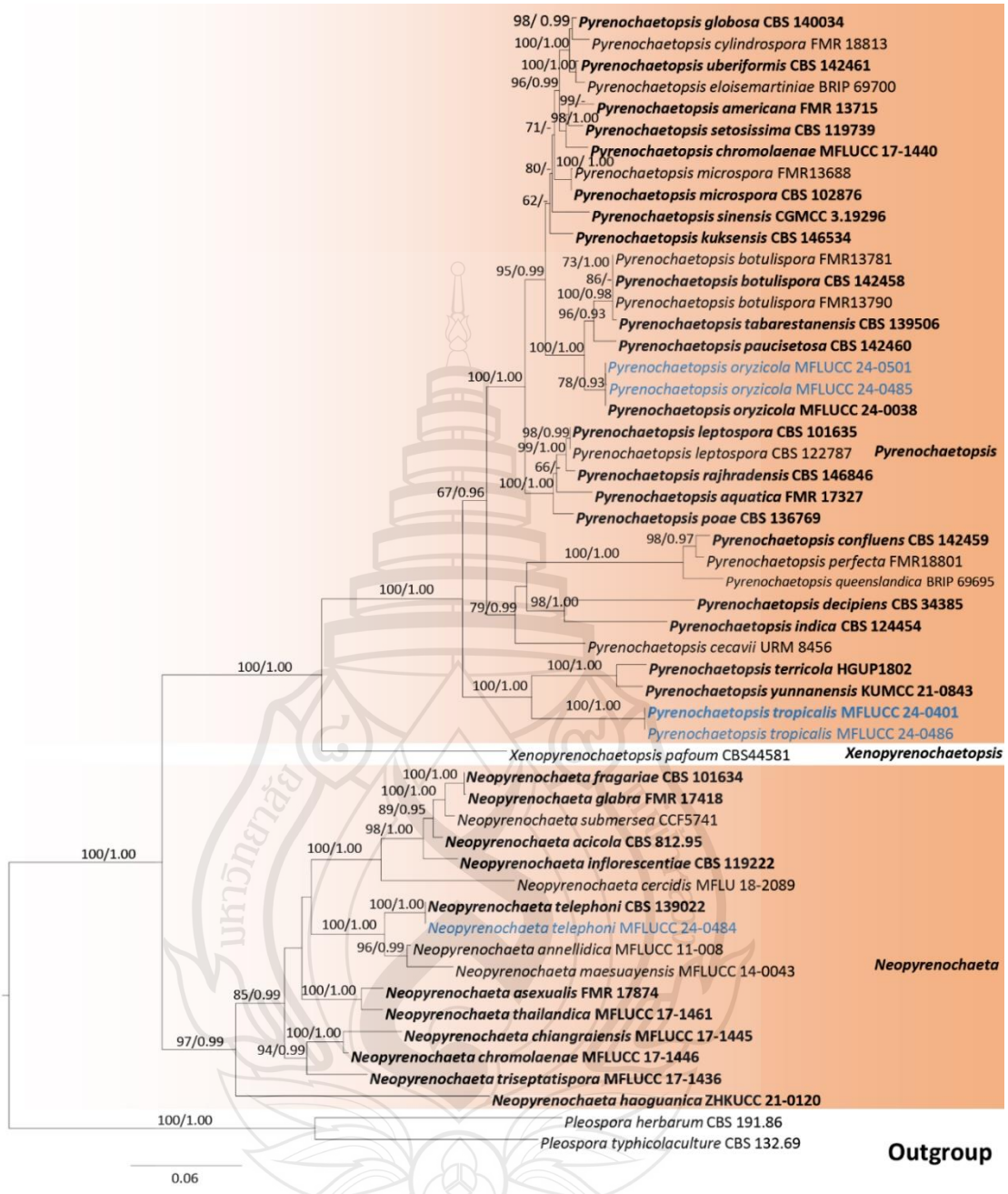


Figure 4.57 The best-scoring maximum likelihood tree generated based on the combined ITS, LSU, and *rpb2* sequence data for *Pyrenochaetopsidaceae*

Figure 4.57, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Pleospora herbarum* (CBS 19186) and *Pleospora typhicolaculture* (CBS 13269). The topology and clade stability of the combined gene tree are compared with the single gene

analyses. The approximate length of the combined alignment is 2827 bp, and single gene alignments are ITS: 535 bp, LSU: 1340 bp, and *rpb2*: 952 bp. The matrix had 993 distinct alignment patterns with 21.21% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.76273, AG = 5.14987, AT = 1.76273, CG = 1.00000, CT = 8.82768, GT = 1.00000; gamma distribution shape parameter α = 0.488.

Neopyrenochaeta telephoni (Roh. Sharma, Kurli, Sonawane, Shouche & Rahi) Valenz.-Lopez, Crous, Stchigel, Guarro & Cano, Stud. Mycol. 90: 56 (2017)

Figure 4.58

Index Fungorum number: IF 833025

Sexual morph: not observed. Asexual morph: not observed.

Culture characteristics —*Colonies* on PDA reach 3–4 cm diam. after 14 days at 25°C, yellowish brown, becomes ivory-brown center and greyish periphary, flat, irregularly-margined, reverse black brown. *Mycelium* hyaline, becoming sub-hyaline to pale brown when mature, smooth-walled to thick-walled, septate, 1.5–3 µm ($\bar{x}$ = 2 µm, n=30) wide. *Chlamydospores* 3.5–4.5 × 3–4 µm ($\bar{x}$ = 4 × 3 µm, n = 20), produced from mature hyphae, mostly intercalary, solitary, globose to subglobose, hyaline, thick-walled.

Material examined – Thailand, Tham Tu Pu Cave (Buddha image cave), Chiang Rai, 99.802962N, 19.925411E, 424m, 21 June 2021, W.A. Erandi Yasanthika (MFLU25-0171); living culture 44-cv10-98=MFLUCC 24-0484.

GenBank numbers – MFLUCC 24-0484: ITS: PQ567561, RPB2: PV611065

Notes–According to the phylogenetic analyses (Figure 4.52), our strain (MFLUCC 24-0484) clusters with *Neopyrenochaeta telephoni* CBS 139022 with 97% ML, 0.99 BYPP statistical support. Comparing the LSU, ITS, and *rpb2* gene regions of our strain with those type species (UTHSC04-678) showed 100% similarity. We have not observed sexual or asexual morphs in our culture. Thus, we were not able to compare the morphology with the type species (CBS 139022). The chlamydospores were observed in our isolate. The type species (CBS 139022) has been isolated from a mobile phone screen in India (Crous et al., 2015c). Herein, we report the first *N. telephoni* strain from soil in a disturbed cave in Thailand.

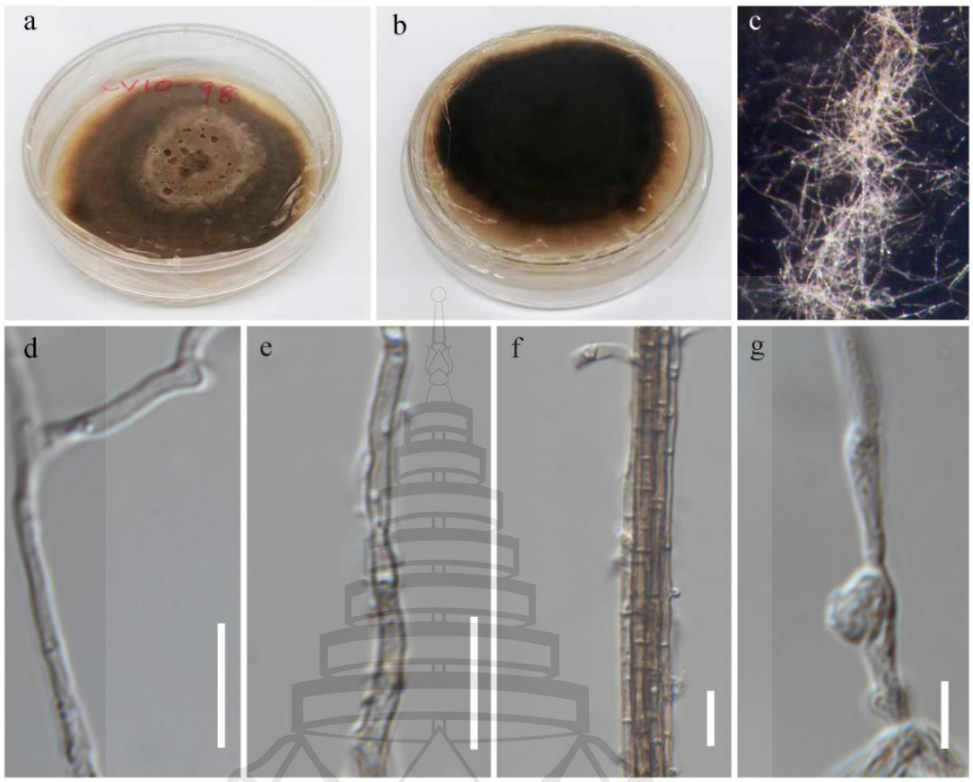


Figure 4.58 *Neopyrenochaeta telephoni* (MFLU25-0171)

Figure 4.58, a, b Culture characters on PDA (b = reverse). c, e Immature hyphae e. mature hyphae. f, g Chlamydospores. Scale bars: d, e, f = 10 μm. g = 5 μm

Pyrenochaetopsis Gruyter, Aveskamp & Verkley, Mycologia 102(5): 1076 (2010).

Index Fungorum number: IF 514653; Facesoffungi number: FoF 08356

Pyrenochaetopsis was introduced by de Gruyter et al. (2010) based on the LSU and SSU gene regions while revising the *Phoma* section. *Pyrenochaetopsis leptospora* (≡*Pyrenochaeta leptospora*) is designated as the type species. Currently, the genus comprises 27 species (Species Fungorum, 2025) and all of them have molecular data. The asexual morph is characterized by the solitary to confluent, superficial or immersed, globose to subglobose, honey/citrine to olivaceous/olivaceous-black pycnidia that are setose, with non-papillate or papillate ostioles and the wall with pseudoparenchymatal cells. Conidiogenous cells are hyaline, phialidic, discrete, or integrated in septate, acropleurogenous conidiophores and aseptate, cylindrical/ellipsoidal to allantoid, guttulate conidia (de Gruyter et al., 2010). Species have been found as plant pathogens, saprobes,

and endophytes from human clinical samples, leaves, marine environments, stems, and soil in China, India, New Zealand, North America, Thailand, and the Netherlands. These species have been studied for their ability to produce bioactive compounds (da Silva et al., 2019; Fan et al., 2020; Špetík et al., 2021).

Table 4.53 *Pyrenochaetopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Pyrenochaetopsis decipiens	Europe	Rhizosphere soil	Boerema et al. (2004)
P. leptospora		ND	
P. microspora		ND	
P. tabarestanensis	Iran	Rice field	Papizadeh et al. (2017)
P. terricola	China	Mountain soil	Wang et al. (2019a)

Pyrenochaetopsis oryzicola S. Absalan, S. Lumyong & K. D. Hyde, J. Fungi 10(no. 763): 22 (2024)

Figure 4.59

Index Fungorum number: IF 902535; Faces of Fungi number: FoF 16749

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 21–35 × 23–40 μm ($\bar{x}$ = 21 × 31 μm), pycnidial, mostly confluent, sometimes solitary, superficial on OA, translucent to pale brown, globose to ovoid, unilocular, pycnidial wall *textura angularis*. *Conidiogenous cells* 2–3 μm × 1–2 μm ($\bar{x}$ = 2.5 × 1.5 μm), phialidic, hyaline to pale brown, sub-globose, thick-walled, difficult to distinguish from the pycnidial wall. *Conidia* 4–3 μm × 1–2 μm ($\bar{x}$ = 3.5 × 1.5 μm, n = 25), aseptate, hyaline, obovoid to ellipsoidal or cylindrical, slightly guttulate, smooth-walled.

Culture characteristics – *Colonies* on the PDA at 25°C, become 4–5 cm diam. after seven days, pale brown to greyish, becoming brownish grey at the center, grayish to whitish gray middle ring with pale brown periphery when mature, reverse brown to black at the center, greyish brown outer rind, flat, circular, filiform margined. *Mycelium* semi-immersed to superficial, hyaline, aseptate, becoming subhyaline to pale brown, septate when mature, 1.5–3 μm ($\bar{x}$ = 2).

Material examined – Thailand, Chiang Rai, Bandu, outdoor market, on soil, 19.967000N, 99.855912E, 393m, 17 October 2022, W.A. Erandi Yasanthika (MFLU25-0119, holotype); ex-type 108-u3-4=MFLUCC 24-501. *ibid.* (MFLU25-0120); living culture 108b-u3-4b=MFLUCC 24-485

GenBank numbers – MFLUCC 24-501: LSU: PQ577865, ITS: PP998348, RPB2: PV618261; 108b-u3-4b= MFLUCC 24-485: ITS: PQ577885, RPB2: PV618262

Notes–The multigene phylogenetic tree (Figure 4.52) shows that our isolates (MFLUCC 24-501 and MFLUCC 24-485) grouped with the type species of *Pyrenochaetopsis oryzicola* (MFLUCC 24-0038) with 78% ML, 0.93 BYPP statistical support. *Pyrenochaetopsis oryzicola* was originally isolated from the dead panicle of *Oryza sativa* in Chinag Rai, Thailand (Absalan et al., 2024). Comparing the LSU, ITS, and *rpb2* gene regions of our strain with those type species (MFLUCC 24-0038) resulted in 100% similarity. Our isolate is morphologically comparable to the type species by having globose to ovoid conidiomata, hyaline, guttulate, aseptate, and cylindrical to ellipsoid conidia, and phialidic conidiogenous cells that are difficult to distinguish from the pycnidial wall. However, our isolate has hyaline to pale brown conidiogenous cells and relatively smaller conidia ($\overline{x}$ = 3.5 × 1.5 μm), which are distinct from the type species that has hyaline conidiogenous cells and larger conidia ($\overline{x}$ = 3.5 × 1.5 μm) (Absalan et al., 2024). Based on the morphology and molecular results, we confirm our strain is *P. oryzicola* from urban soil in Chiang Rai, Thailand. Thus, it confirms the occurrence of this species in the Chiang Rai region. Further, this is the first record of the species reported in soil habitats. The morphological variances of our isolate from the type species can be influenced by the host's differences (Yasanthika et al., 2022a).

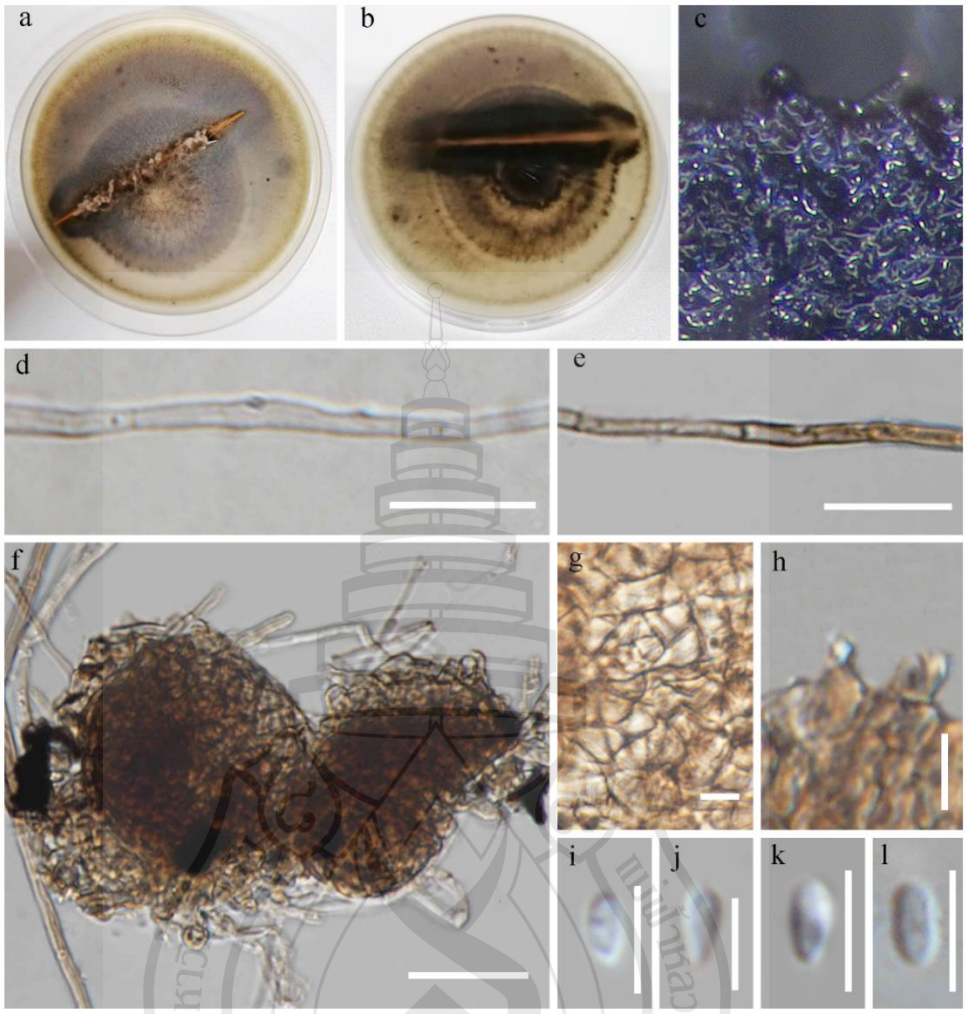


Figure 4.59 *Pyrenochaetopsis oryzicola* (MFLU25-0119)

Figure 4.59, a, b culture characters on PDA (b = reverse). c Pycnidia forming on culture. d Immature hyphae e Mature hyphae. f Pycnidia. g Pycnidia wall h Conidiogenous cells. i–l Conidia. Scale bars: f = 25 μm, d, e = 10 μm, g–i =5 μm.

Pyrenochaetopsis tropicalis Yasanthika & K.D. Hyde, sp. nov.

Index Fungorum number: IF903047; Facesoffungi number: FoF 16711

Figure 4.60

Etymology – The specific epithet "*tropicalis*", from Latin, refers to the tropical, the ecological condition from which the holotype was collected.

Holotype – MFLU25-0162

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 73–130 μm × 91–160 μm ($\bar{x}$ = 106 × 127 μm, n=10), pycnidial, mostly confluent, rarely solitary, semi-immersed

on OA, brown to black, pyriform to subglobose, unilocular. *Conidiomatal wall* cells *textura angularis*, 7–18 µm ($\bar{x}$ = 11) thick. *Conidiogenous cells*, 2.5–5 µm × 1–2 µm ($\bar{x}$ = 4 × 1.5 µm, n=5), annalidic, hyaline, smooth-walled, determinate, ampulliform to cylindrical. *Conidia* 3–4 µm × 1–2 µm ($\bar{x}$ = 3.5 × 1.5 µm, n = 25), aseptate, hyaline, cylindrical or subglobose to reniform, sometimes with small guttules, thick-walled.

Culture characteristics – *Colonies* on PDA at 25°C, become 3–4 cm diam. after seven days, whitish to ivory, becoming brown at the center, ivory to white middle ring and brown to pale brown outer ring when mature, reverse brown to dark brown, flat, entire margined. *Mycelium* superficial, hyaline, aseptate, becoming subhyaline to pale brown, septate when mature, 1–2 µm ($\bar{x}$ = 1.5, n=30). *Chlamydospores* present, subhyaline to brown.

Material examined – Thailand, Chiang Mai, Omkoi District, Sop Khong, from forest, on soil, 17.7145N, 98.2619E, 1388m, 16 October 2019, W.A. Erandi Yasanthika (MFLU25-0162, holotype); ex-type 19-pin3=MFLUCC 24-401. *ibid.* (MFLU25-0163); living culture 19b-pin3b=MFLUCC 24-486.

GenBank numbers – MFLUCC 24-401: LSU: PQ568244, ITS: PP998344,; MFLUCC 24-486: LSU: PQ577866, ITS: PQ577864,

Notes– Based on morpho-molecular analyses, *Pyrenochaetopsis tropicalis* (MFLUCC 24-401 and MFLUCC 24-486) is introduced as a new species here. The multi-gene phylogeny of *Pyrenochaetopsidaceae* (Figure 4.52) shows that our isolates (MFLUCC 24-401) formed an independent clade sister to *P. terricola* (HGUP1802) and *P. yunnanensis* (KUMCC 21-0843) with 100% ML and 1.00 BYPP statistical support. We compared the base pair difference in the ITS (+5.8S) gene region, comparison of *P. tropicalis* (MFLUCC 24-401) with *P. yunnanensis* showed 10/490 (2%) (including gaps) differences and with *P. terricola*, it was 19/478 (3.9%) (including gaps). Our collection (19) and *P. yunnanensis* share similar conidial size ranges (3–4 µm × 1–2 µm), while *P. terricola* having relatively smaller conidia (2–3×1–2µm). However, our isolate has cylindrical or subglobose to reniform conidia whereas *P. yunnanensis* having subglobose to oblong and *P. terricola* have ovoid to cylindrical conidial shapes (Phookamsak et al., 2022; Wang et al., 2019a). *Pyrenochaetopsis terricola* has been isolated from soil and *P. yunnanensis* from dead bamboo stem in China (Phookamsak et

al., 2022; Wang et al., 2019a). Our data confirms, this collection (MFLUCC 24-401 and MFLUCC 24-486), as a new species from forest soil in Thailand.

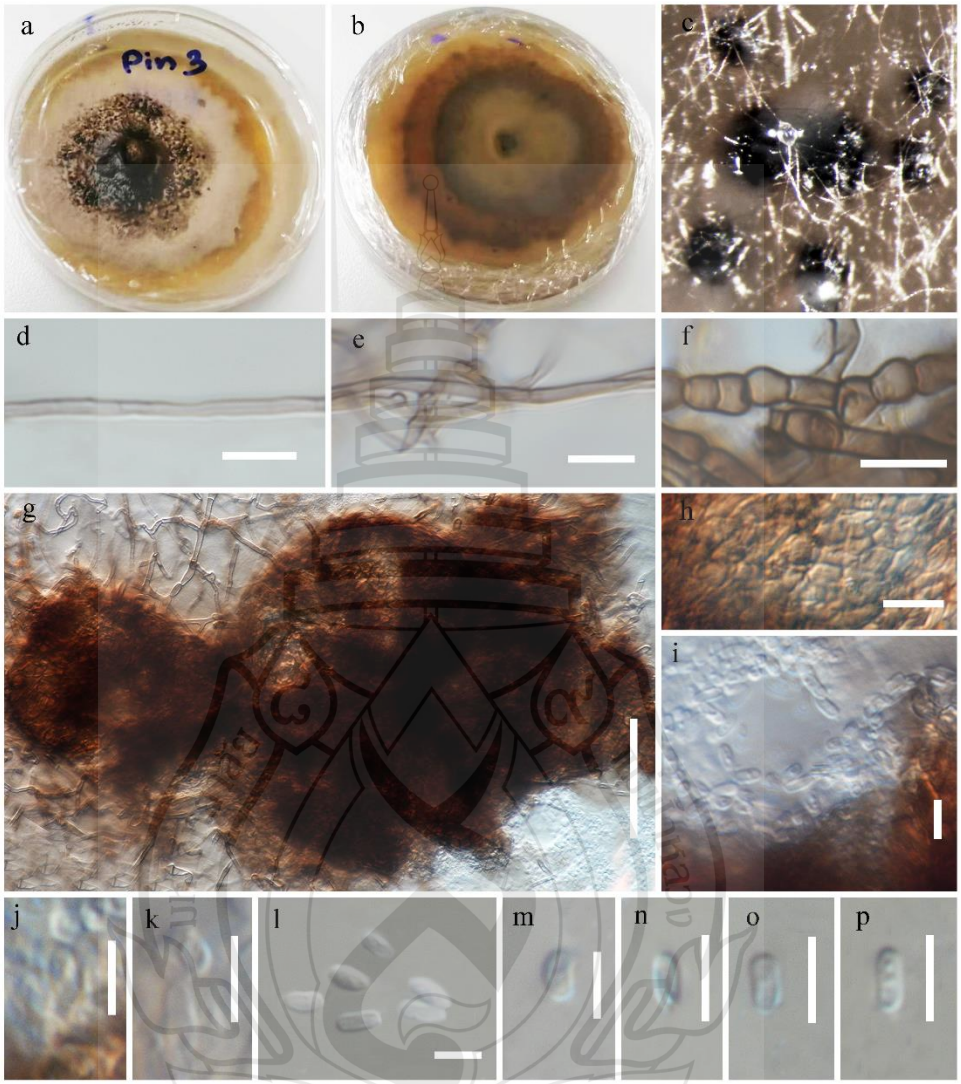


Figure 4.60 *Pyrenochaetopsis tropicalis* (MFLU25-0162, Holotype)

Figure 4.60, a, b Culture characters on PDA (b = reverse). c Pycnidia forming on culture. d immature hypha e Mature hyphae. f Chlamydospores g Pycnidia. h Pycnidia wall i Pycnidia matrix. j, k Conidiogenous cells. l–p Conidia. Scale bars: g = 50 µm, e, f, h = 10 µm. g = 50 µm, d, i–l = 5 µm.

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

Neoroussoella Jian K. Liu, Phookamsak & K.D. Hyde, Phytotaxa 181(1): 21 (2014).

Index Fungorum number: IF 550668; Facesoffungi number: FoF 08363

Liu et al. (2014) introduced *Neoroussoella* with its type species *N. bambusae* in *Roussoellaceae* based on the combined ITS, LSU, *tef1*-α, and *rpb2* phylogeny. Currently, 15 species are listed in the Species Fungorum (2025), and all of them are introduced with molecular data. The asexual morph is characterized by superficial to immersed pycnidia, uni to multi-loculate, globose to subglobose or irregular shape, scattered or clustered, solitary or gregarious, indistinctly ostiolate conidiomata with the cell wall having several layers of cells of *textura angularis*. Conidiophores are unbranched, aseptate, and have annellidic, unbranched, ampulliform or lageniform, or cylindrical, or cylindric-clavate conidiogenous cells. Conidia are oblong to ellipsoidal, hyaline, smooth-walled, aseptate with two guttules. The sexual morph is characterized by ascostromata that are coriaceous, solitary to gregarious, black, central ostiolate, and the peridium is composed of 2–3 layers of thin-walled cells of *textura angularis*, and the hamathecium comprises numerous, anastomosing, cellular pseudoparaphyses, which are branching at the apex, often constricted at the septum, embedded in a gelatinous matrix. Asci are 8-spored, bitunicate, cylindrical, short to long pedicellate, apically rounded with an ocular chamber containing ellipsoidal to fusiform, 2-celled, pale brown to brown or yellowish brown, rough-walled, longitudinally ribbed ascospores that are constricted at the septum and surrounded by a mucilaginous sheath. (Liu et al., 2014). Species have been isolated from brown algae in the sea and dead wood in terrestrial habitats in China, the Mediterranean Sea, and Thailand (Karunarathna et al., 2019; Poli et al., 2020; Liu et al., 2014).

Table 4.54 *Neoroussoella* species isolated from soil

Species	Country	Habitat or soil type	References
Neoroussoella solani	China	ND	Shi et al. (2021)

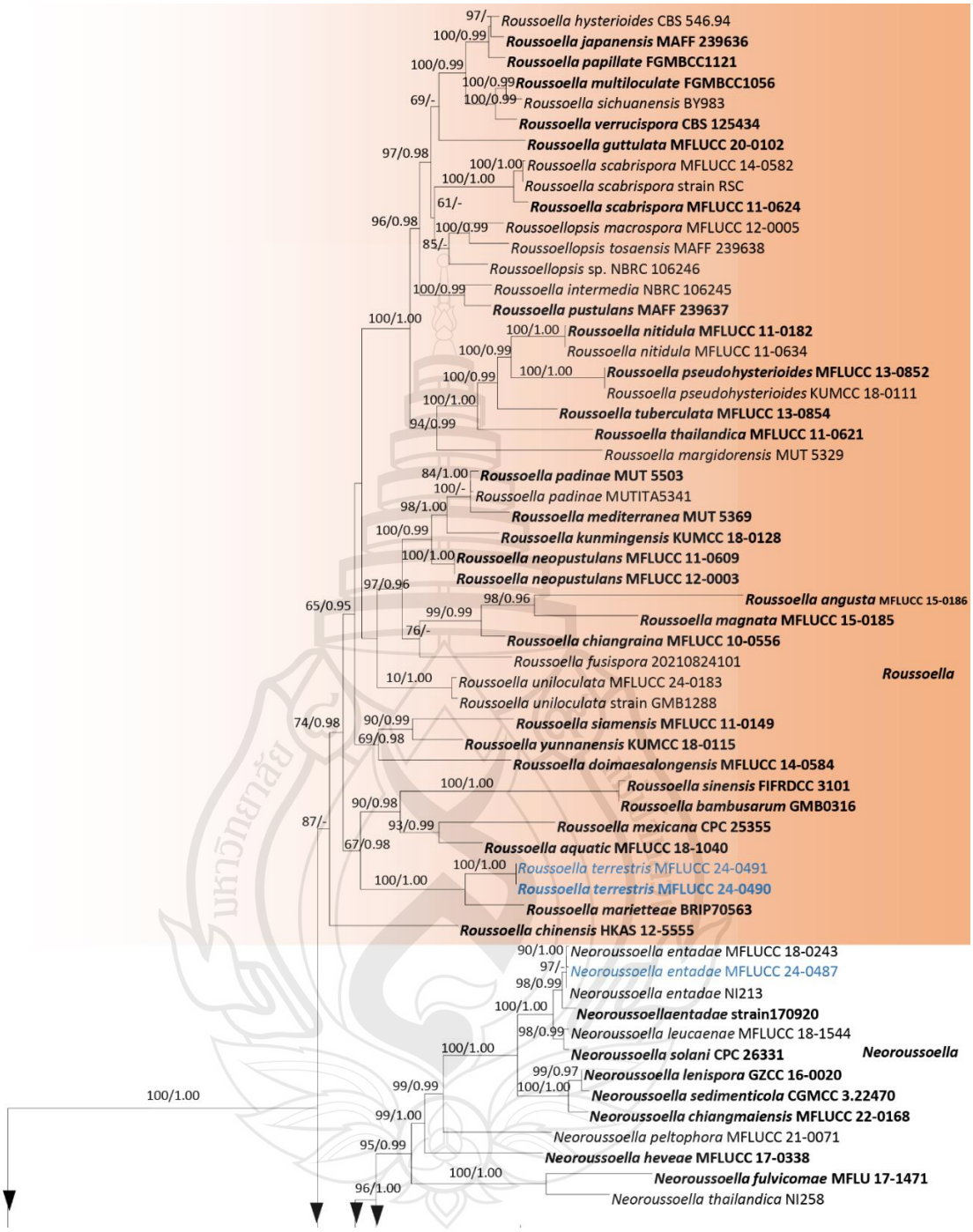


Figure 4.61 The best-scoring maximum likelihood tree generated based on the combined ITS, LSU, *tef1-α,* and *rpb2* sequence data for *Roussoellaceae*

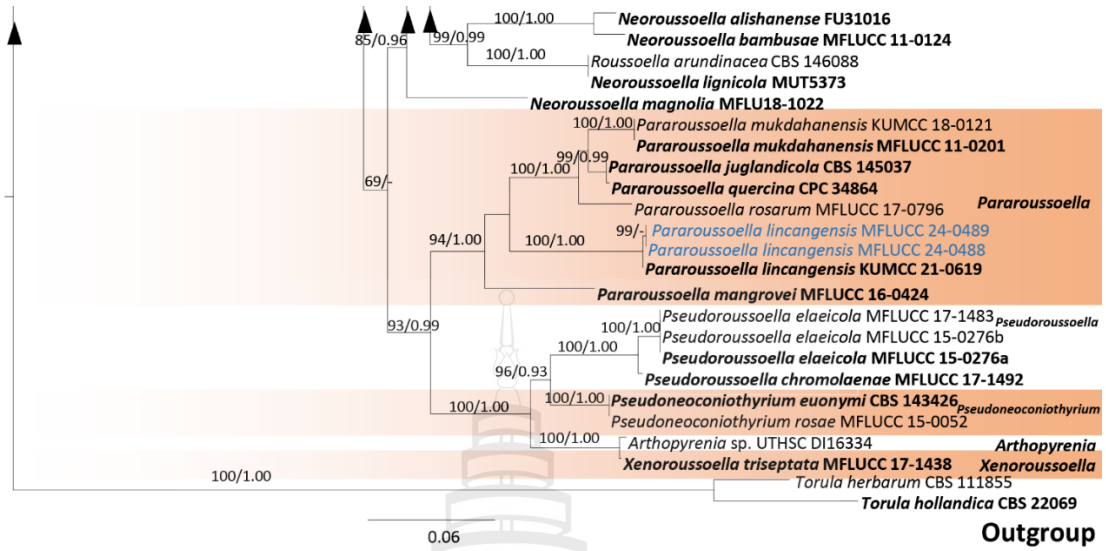


Figure 4.61 continued

Figure 4.61, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue, and ex-type strains are in bold. The tree is rooted to *Torula herbarum* (CBS 111855) and *T. hollandica* (CBS 22069). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 3216 bp, and single gene alignments are ITS: 518 bp, LSU: 886 bp, *tef1-α*: 939 bp, and *rpb2*: 873 bp. The matrix had 1353 distinct alignment patterns with 30.25% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.239, C = 0.267, G = 0.272, T = 0.222; substitution rates AC = 1.62721, AG = 4.01951, AT = 1.62721, CG = 1.00000, CT = 8.33564, GT = 1.00000; gamma distribution shape parameter α = 0.569.

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

Figure 4.62

Index Fungorum number: IF 555568

Sexual morph: not observed. Asexual morph: not observed.

Culture characteristics – *Colonies* on PDA reach 3–4 cm diam. after 14 days at 25°C, ivory to whitish brown, becoming grayish brown, raised, irregularly margined, reverse whitish yellow, becoming brownish yellow when mature. *Mycelium* hyaline, becoming sub-hyaline when mature, septate, thick-walled, verruculose, 1.5–4 µm

($\bar{x}$ = 3 µm, n = 10) wide. Sexual morph: not observed. Asexual morph: not observed.

Material examined – Thailand, Yang Piang, Chiang Mai, Omkoi District, from the forest, on soil 17.7145N, 98.4286E, 935m, 16 October 2019, W.A. Erandi Yasanthika (MFLU25-0139); living culture 37-s9-20= MFLUCC 24-487.

GenBank numbers –37-s9-20= MFLUCC 24-487: ITS: PQ570519, RPB2: PV611064

Notes – According to the multi-gene phylogeny (Figure 4.56), our strain (MFLUCC 24-487) clusters with *Neoroussoella entadae* strains (MFLUCC 18-0243, NI213, MFLUCC 17-0920) with a 98% ML and 0.99 BYPP support. The ITS (+5.8S) gene region of our isolate was compared with the type species of *Neoroussoella entadae* that showed 100% similarity. We have not observed the sexual or asexual sporulation in our culture. The type species (MFLU 18–2106) is characterized by pycnidia that are solitary to gregarious, occasionally confluent, immersed, formed in uni- or multi-loculate stromata. Pycnidia are papillate, central, circular ostiole and have dark brown cells of *textura angularis* with a thin, hyaline inner layer. Conidiophores are reduced to conidiogenous cells with phialidic, ampulliform to cylindrical, hyaline, smooth-walled conidiogenous cells that produce initially hyaline, becoming pale brown when mature, oblong to ovoid, straight, both ends broadly rounded, aseptate conidia (Jayasiri et al. 2019). Species have been isolated as saprobes from *Entada phaseoloides*, *Leucaena* sp. and *Magnolia candolli* hosts in Thailand (Jayasiri et al., 2019; de Silva et al., 2022). We report the first record of *N. entadae* from Thailand forest. This is also the first record of this genus associated with soil-habitats.

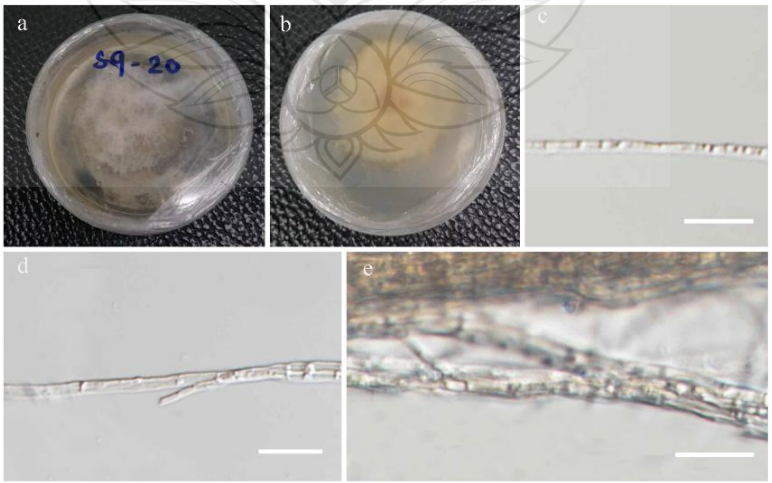


Figure 4.62 *Neoroussoella entadae* (MFLU25-0139)

Figure 4.62, a, b Culture characters on PDA (b = reverse). c–e. Hypha. Scale bars: d, e=20 µm, c=10 µm.

Pararoussoella Wanas., E.B.G. Jones & K.D. Hyde, Fungal Divers. 89: 169 (2018).

Index Fungorum number: IF 554218

Wanasinghe et al. (2018) introduced *Pararoussoella* using multi-gene phylogenetic analyses based on the combined LSU, ITS, *tef1-α* and *rpb2* sequences, with *P. rosarum* as the type species. Currently, Species Fungorum (2025) has listed six species under this genus and all of them have molecular data. The sexual morph is characterized by scattered or aggregated ascomata, arranged in groups. These ascomata are immersed, globose with a papillate ostiole. Ascomatal walls are comprised of small and thin-walled cells that tend to thicken towards the ostiole, and a pigmented outer layer with cells *textura angularis*. Hamathecium is comprised of numerous filamentous, branched pseudoparaphyses. Asci are 8-spored, bitunicate, fissitunicate, and cylindrical, with a stipe and containing uniseriate to overlapping uniseriate ascospores that are narrowly ellipsoid, straight to slightly curved, and 1-septate. The ascospores are hyaline to pale brown at first, turning dark brown when mature, guttulate, rough, and exhibit irregular longitudinal striations, with or without a sheath (Wanasinghe et al., 2018b). Species have been reported from dead and living leaves and stems in China, England, Germany, and Thailand (Crous et al., 2020; Wanasinghe et al., 2018b). It has not been previously reported from soil.

Pararoussoella lincangensis G.C. Ren & K.D. Hyde, Mycosphere 15(1): 1044 (2024)

Figure 4.63

Index Fungorum number: IF 901359; Facesoffungi number: IF901359

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 55–85 × 102–124 µm µm ($\bar{x}$ = 74 × 115 µm, n=5), superficial on PDA, brown to black, sub-globose solitary, unilocular, pycnidial wall cells *textura angularis*, 5.5–13.5 µm ($\bar{x}$ = 11, n=10) wide. *Conidiogenous cells* 1.5–4.5 × 1–3 µm ($\bar{x}$ = 3 × 12 µm, n=10), hyaline to sub hyaline to pale brown, phialidic, smooth, ampulliform to doliiform. *Conidia* 3–4.5 × 2–3 µm ($\bar{x}$ = 3 × 2.5 µm, n = 20), hyaline to pale brown, aseptate, ellipsoidal or to sub-cylindrical, rounded at both ends, thick-walled.

Culture characteristics– *Colonies* on PDA at 25 ℃, become 3–4 cm diam. after seven days, white becoming reddish white to whitish grey when mature, reverse reddish yellow to reddish brown at the center with white periphery, raised, irregular, filiform margined. *Mycelium* superficial hyaline, thick-walled, septate, verrucose, 1.5–5 μm ($\bar{x}$ = 3.2 μm, n = 30), sporulated after eight weeks on the PDA.

Material examined – Thailand, Chiang Mai, Omkoi District, Yang Piang, from forest, soil, 17.7145N, 98.4286E, 935m, 16 October 2019, W.A. Erandi Yasanthika (MFLU25-0140); living culture 73-s9-32=MFLUCC 24-089. *ibid.* (MFLU25-0167), living culture 33-s9-321=MFLUCC 24-088.

GenBank numbers –MFLUCC 24-089: LSU: PQ572134, ITS: PQ570520,; MFLUCC 24-088: LSU: PQ572135, ITS: PQ570521

Notes – *Pararoussoella lincangensis* was introduced by Ren et al. (2024) from dead twigs of *Heliciopsis terminalis* in China. In the phylogenetic analyses (Figure 4.56), our strains (MFLUCC 24-089 and MFLUCC 24-088) group with *P. lincangensis* with 100% ML and 1.00 BYPP statistical support. When comparing the ITS (+5.8S) gene region of our strain with the type species of *Pararoussoella lincangensis* (KUMCC 21-0619), it showed 100% similarity. Our isolate has similar morphology to the type species (KUMCC 21-0619) by having phialidic, smooth, ampulliform to doliiform conidiogenous cells and aseptate conidia (Ren et al., 2024). It has hyaline to pale brown, aseptate, ellipsoidal or sub-cylindrical conidia, whereas the type species has hyaline conidia, yellowing at maturity (Ren et al., 2024). Morpho-molecular evidence confirms that the strain in this study is *P. lincangensis* isolated from forest soil in Thailand. This genus has mostly been reported as plant-associated fungi (Phukhamsakda et al., 2020; Ren et al., 2024; Wanasinghe et al., 2018b). Herein, we report the first *Pararoussoella* member present in soil which confirms its survival in alternative substrates.

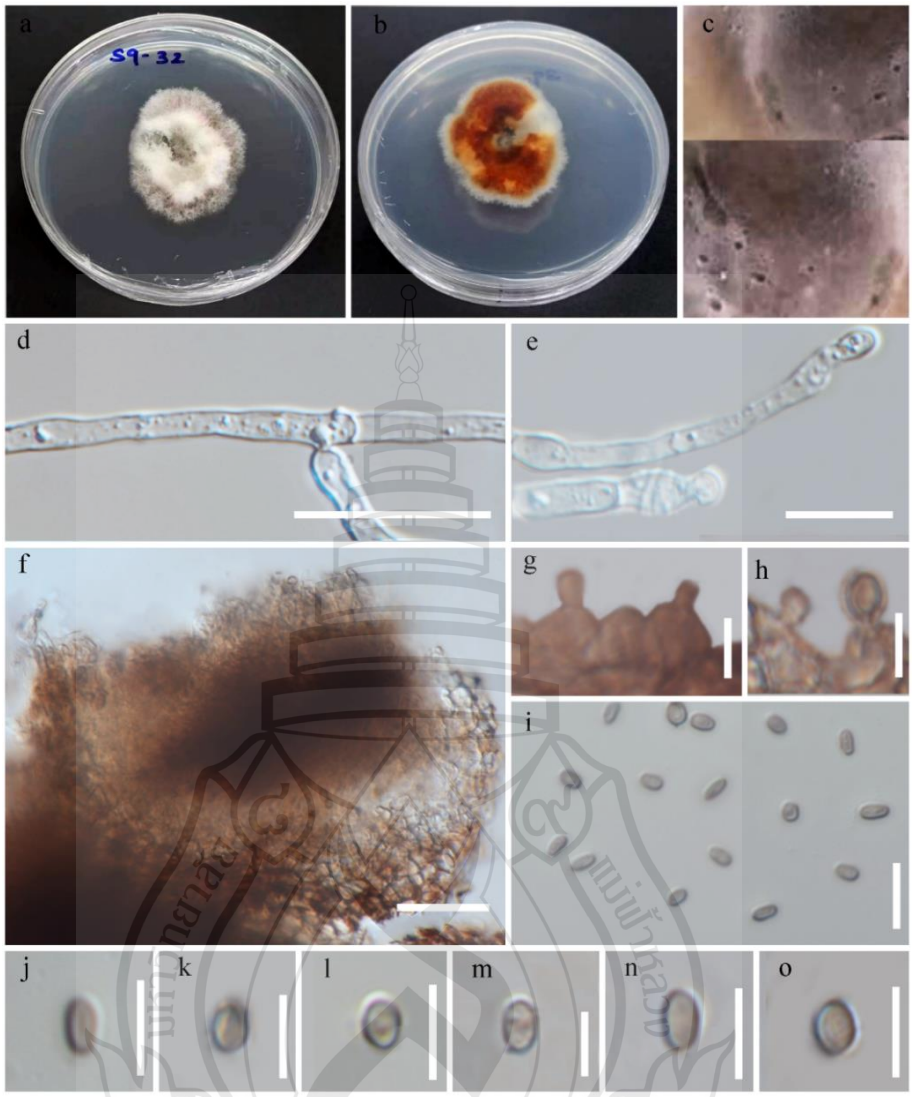


Figure 4.63 *Pararoussoella thailandensis.* (MFLU25-0140)

Figure 4.63, a, b Culture characters on PDA (b = reverse). c Pycnidia forming on culture. d Immature hyph, a e Mature hyphae. f Pycnidia and pycnidia wall. g, h Conidiogenous cells. i-o Conidia. Scale bars: f = 25µm, d = 20 µm, e = 10 µm, g–o = 5 µm.

Roussoella Sacc., Sér. 6 6: 410 (1888)

Index Fungorum number: IF 4799; Facesoffungi number: FoF 01689

Saccardo & Paoletti (1885) introduced *Roussoella* with its type species *R. nitidula*. Currently, the genus accommodates 42 species (Species Fungorum, 2025). *Roussoella* is considered polyphyletic however, *Neoroussoella*, *Pararoussoella* and *Pseudoroussoella* are established to accommodate some species in *Roussoella sensu lato* (Jaklitsch & Voglmayr, 2016; Jayasiri et al., 2019). *Roussoella sensu stricto* is

characterized by cytoplea-like asexual morphs and uni- to multi-loculate ascostromata, immersed in a clypeus, visible as raised, black dome-shaped or elongate linear on the host surface, bitunicate, cylindrical to subcylindrical asci, with brown, 2-celled ornamented ascospores (Hongsanan et al., 2020a). Species are inhabiting on living and dead leaves and branches (mostly gramineous plants), human clinical samples from Africa, Mexico, China, Malaysia, Ecuador and Thailand (Dai et al., 2022).

Table 4.55 *Roussoella* species isolated from soil

Species	Country	Habitat or soil type	References
Roussoella sp.	Trinidad	Oil contaminated soil	Ramdass and Rampersad (2021)

Roussoella terrestris Yasanthika & K.D. Hyde, sp. nov.

Figure 4.64

Index Fungorum number: IF903045; Facesoffungi number: FoF 16715

Etymology – The specific epithet " *terrestris*", , refers to the terrestrial environment from Latin, of which the holotype was collected.

Holotype – MFLU25-0141

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 175–300 × 220–337 μm ($\bar{x}$ = 220 × 337 μm, n=10), pycnidial, unilocular to multilocular, mostly confluent, superficial on MEA, dark brown to black, subglobose, *Conidiomatal wall* of cells *textura angularis*. *Conidiogenous cells* 2–4 × 2–3 μm ($\bar{x}$ = 3 × 2.5 μm, n = 20), phialidic, determinate, discrete, globose to subglobose, hyaline, thick-walled. *Conidia* 2–5 × 1–3 μm ($\bar{x}$ = 3 × 2 μm, n = 20), hyaline, broadly obovoid to globose or filiform, aseptate, sometimes granular, thick-walled.

Culture characteristics – *Colonies* on PDA at 25°C, becoming 3–4 cm diam. after seven days, initially white, becoming yellowish white when mature, reverse yellowish white at the center, white rind, flat, entire margined. *Mycelium*, immersed to semi immersed, hyaline, 1–4 μm ($\bar{x}$ = 2 μm, n=30), aseptate, thick-walled, sporulated after nine weeks on the MEA. *Chlamydospores* hyaline to sub-hyaline, globose, thick-walled.

Material examined – Thailand, Krabi, from forest, soil, 2, 8°4'11 "N, 98°53'25" E, 181m, 28 October 2019, W.A.Erandi Yasanthika (MFLU25-0141, holotype); ex-type 68-kr003=MFLUCC 24-0490. *ibid*. (MFLU25-0168); living culture 68b-kr003b=MFLUCC 24-0491.

GenBank numbers – MFLUCC 24-0490: LSU: PQ577819, ITS: PP993960, RPB2: PV624713, *tef1-α*: PV624715; MFLUCC 24-0491: LSU: PQ577821, ITS: PQ577820, RPB2: PV624715, *tef*-1: PV624714Notes – Our collection (MFLUCC 24-0490 and MFLUCC 24-0491) clusters within *Roussoella* (Figure 4.56), producing a distinct branch sister to *R. marietteae* with 100% ML and 1.00 BYPP statistical support. When compared the base pair difference of ITS (+5.8S) gene region of our species with *R. mariettea*, it resulted in having 11/468 (2.3%) (including gaps) differences. *Roussoella marietteae* has been isolated from *Sporobolus elongates* stem in Australia and introduced only based on molecular evidence LSU, ITS, *tef1-α* and *rpb2* (Steinrucken et al., 2022; Tan & Steinrucken, 2024). Thus, morphological comparison was not possible. Our culture (MFLUCC 24-0490) only produced an asexual morph, and sexual morph has not been observed. Based on our molecular and morphological data we introduced *R. terrestris* as a new speceis which is isolated from forest soils from Thailand. It is the first species of the genus that has been isolated in Thai soils.

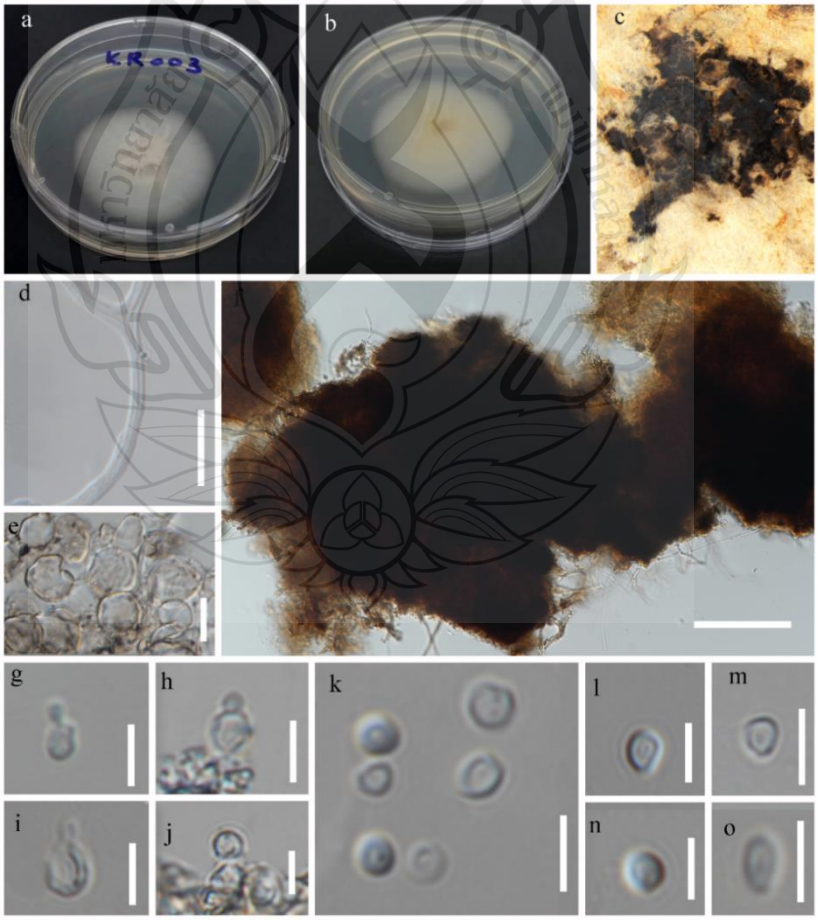


Figure 4.64 *Roussoella terrestris* (MFLU25-0168, Holotype)

Figure 4.64, a, b Colony on PDA (front and reverse). c Pycnidia forming on culture. d Hypha e Chlamydospores. f Pycnidia. g–j Conidiogenous cells. k–o Conidia. Scale bars: f = 100µm, d,e = 10 µm, g–o = 5 µm.

Family: *Sporormiaceae* Munk

Preussia Fuckel, Hedwigia 6: 175 (1867).

Figure 4.65

Index Fungorum number: IF 4363; Facesoffungi number: FoF 06568.

Preussia was introduced by Fuckel (1866) with the type species, *P. funiculate*. There are 64 species present under *Preussia* (Species Fungorum, 2025), while 40 species have molecular data. The sexual morph is associated with dark brown to black, immersed to semi-immersed, scattered or aggregated, ostiolate or non-ostiolate ascomata, fasciculate, clavate to cylindrical, short or elongated -stalked, inconspicuously biunicate, 8- spored asci and dark brown, 3 to many septate ascospores. Species are isolated as endophytes from plant leaves, saprobes or coprophilous on dung, decaying wood, seeds, submerged plant debris and soil habitats found in Argentina, Germany, Japan, Iran, Nepal, Spain, the Netherlands and the USA (Hongsanan et al., 2020a).

Table 4.56 *Preussia* species isolated from soil

Species	Country	Habitat or soil type	References
Preussia fleischhakii	Belgium	ND	Domsch et al. (1993)
Preussia fleischhakii	Poland	ND	
P. flanaganii	Mexico	Sandy soil	Gonzalez-Menendez
P. isomera	Nepal	ND	et al. (2017)
Preussia sp.	Spain	ND	
Preussia sp.	India	Frozen soil in Himalaya Mountain	Youn et al. (2018)
P. aemulans	Netherlands	Greenhouse soil	Asgari and Zare
P. fleischhakii	Germany	Wheat field soil	(2010)
Preussia sp.	Czech Republic	ND	
Preussia globose	Japan	Paddy field	Ito and Nakagiri (1995)

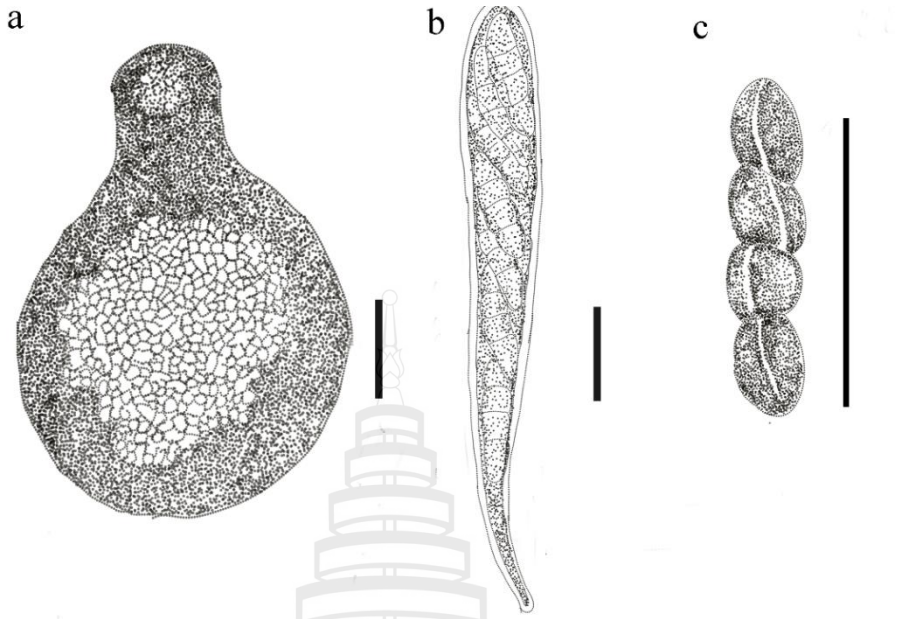


Figure 4.65 *Preussia sp.*

Figure 4.65, a Ascomata b. Ascus. *P. funiculate* c. Ascuspore. Scale bars a = 50 μm, b, c = 25 μm. Redrawn from Guarro et al. (2012).

Westerdykella Stolk, Trans. Br. Mycol. Soc. 38 (4): 422 (1955).

Figure 4.66

Index Fungorum number: IF 5772; Facesoffungi number: FoF 06570

Stolk (1955) introduced *Westerdykella* to accommodate *W. ornata* as the type species. Currently, 17 *Westerdykella* species are available in the Species Fungorum (2025) and 12 species have molecular data. The asexual morph produces sub-cylindrical, aseptate and hyaline conidia (Crous et al., 2017b; Sue et al., 2014). The sexual morph has cleistothecioid ascomata and short-pedicellate asci. Ascospores are one-celled, verruculose but without germ slits (Kruys & Wedin, 2009). Most of the species are coprophilous fungi and have also been found in mud, plant material and soil distributed in France, India, Japan, the USA and Ukraine (Crous et al., 2017; Ito & Nakagiri, 1955).

Table 4.57 *Westerdykella* species isolated from soil

Species	Country	Habitat or soil type	References
Westerdykella angulata	India	Soil in *Oryza sativa* field	Das (1962)
W. capitulum	India	Saline soil	de Gruyter et al. (2013)
W. minutispora	India	Saline soil	
W. centenaria	Kuwait	Saline soil	Crous et al. (2017b)
W. ornate	Mozambique	ND	Stolk (1955)
W. reniformis	Korea	Agricultural fields	Adhikari et al. (2019)
W. dispersa	Armenia	Salt-marsh soil	Asgari and Zare (2010)
W. dispersa	The Netherland	Greenhouse soil	

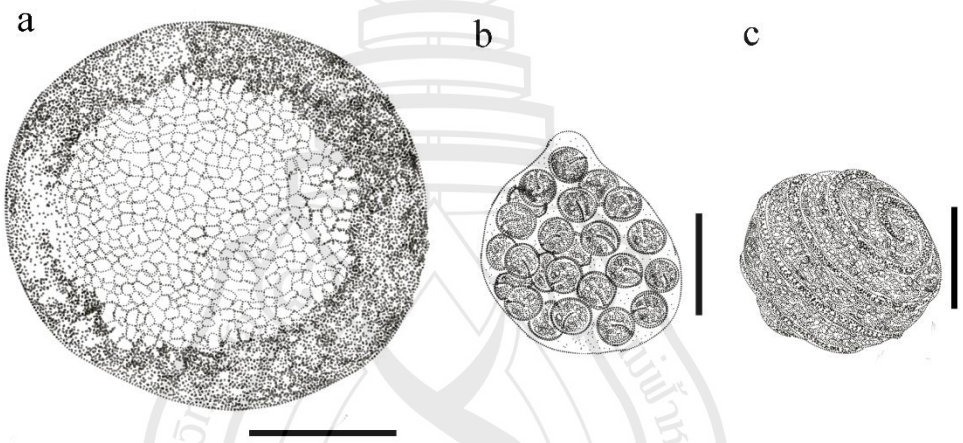


Figure 4.66 *Westerdykella* sp.

Figure 4.66, a. Ascomata. b. Ascus. *W. ornate*. c. Ascospore. Scale bars a = 100 μm, b = 10 μm, c = 2.5 μm. Redrawn from Guarro et al. (2012).

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

Tetraploa Berk. & Broome, Ann. Mag. nat. Hist., Ser. 2 5: 459 (1850). = *Tetraplosphaeria* Kaz. Tanaka & K. Hirayama, Studies in Mycology 64: 177 (2009).

Figure 4.67

Index Fungorum number: IF 10199; Facesoffungi number: FoF 06666

Berkeley and Broome (1850) introduced *Tetraploa* and typified it with *T. aristata.* Species Fungorum (2025) lists 38 species under *Tetraploa*, while 27 of them have molecular data. The asexual morph is hyphomycetous and has micronematous conidiophores, monoblastic conidiogenous cells and brown, short-cylindrical conidia with four setose appendages at the apex (Ellis, 1971; Tanaka et al., 2009). The sexual

morph has globose to subglobose, glabrous ascomata, fissitunicate, cylindrical to clavate, short-stalked, 8-spored asci, and ascospores that are fusiform, hyaline, 1-septate with a mucilaginous appendage-like sheath (Tanaka et al., 2009). These species are found from the saprobic or endophytic mode in herbaceous plants or wood while several have been found from freshwater habitats, raindrops and soil, and some species can rarely be human pathogens (Karpinska-Kolaczek et al., 2010). Species are reported in China, Germany, India, Java, Thailand, the Netherlands and the USA (Dong et al., 2020; Ellis, 1949; Karpinska-Kolaczek et al., 2010; Révay, 1993; Zhao et al., 2024a).

Table 4.58 *Tetraploa* species isolated from soil

Species	Country	Habitat or soil type	References
Tetraploa setifera	ND	ND	Markovskaja (2007)

Figure 4.67 *Tetraploa aristata*

Figure 4.67, a Young and mature conidia. Redrawn from Ellis (1949)

Family: ***Torulaceae*** Corda

Torula Pers., Ann. Bot. (Usteri) 15: 25 (1795

Figure 4.68

Index Fungorum number: IF 10248; Facesoffungi number: FoF 01740

Persoon (1795) introduced *Torula*, accomodating the type species, *Torula herbarum*. Crane and Miller (2016) provided the generic key to differentiate *Torula* species from its seven allied hyphomycete genera but without DNA sequences. Crous et al. (2015a) provided DNA sequences for *Torula* species and discussed about the phylogenetic relationships of *Torulaceae* based on ITS and LSU phylogeny. There are 60 *Torula* species (Species Fungorum, 2025), but 24 species have molecular data. The asexual morph is characterized by the conidiophores, which are reduced to conidiogenous cells or with one brown supporting cell. Conidiogenous cells are solitary on mycelium, erect, doliiform to ellipsoid or clavate, brown, mono- to polyblastic, and producing conidia that are phragmosporous, in branched chains, acrogenous, brown, pale brown apex, dry, constricted at septa. In conidial chains, the conidiogenous cell and the fertile cell (where branching occurs) are darker brown than other cells (Crous et al., 2015a). Some species can be plant pathogens while several are associated with dead wood and soil habitats in China, Cuba, India, Italy, Thailand, the Netherlands and the UK (Crane & Miller, 2016; Li et al., 2017; Crous et al., 2015a).

Table 4.59 *Torula* species isolated from soil

Species	Country	Habitat or soil type	References
Torula brunnea	China	ND	Jiang and Zhang (2008)
T. herbarum	Canada	Forests	Domsch et al. (1993)
T. herbarum	The Neterlands	Arable soil	

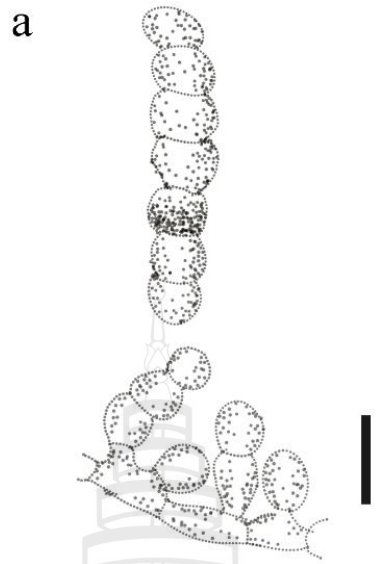


Figure 4.68 *Torula herbarum* (CBS 220.59)

Figure 4.68, a Conidiogenous cells and Conidia. Scale bars: a = X500. Redrawn from Domsch et al. (1993).

Pleosporales genera incertae sedis

Setophaeosphaeria Crous & Y. Zhang ter

Figure 4.69

Index Fungorum number: IF 808945; Facesoffungi number: FoF 00305

Setophaeosphaeria was established by Crous et al. (2014a) with morpho-molecular (ITS and LSU) evidence, and the type is *S. hemerocallidis* (Crous et al., 2014a). There are seven species in the genus (Species Fungorum, 2025), and all of which are supported with molecular data. The asexual morph has pycnidial, brown, globose, and ostiolate conidiomata. Conidiophores are reduced to ampulliform, hyaline, smooth conidiogenous cells that produce hyaline, smooth, subcylindrical, guttulate, and aseptate conidia. The sexual morph has pseudothecial, immersed, globose ascomata. Asci are narrowly ellipsoid, bitunicate, 8-spored, 2–3-seriate, rostrate, short-stipitate, with inconspicuous apical chamber and ascospores that are pale brown, fusoid to ellipsoid, guttulate, 5-septate, with mucoid caps at each end (Crous et al., 2014a). Species have been recorded from leaves, stems and soil in China, Italy and New South Wales (Crous et al., 2014a; Zhang et al., 2021c).

Table 4.60 *Setophaeosphaeria* species isolated from soil

Species	Country	Habitat or soil type	References
Setophaeosphaeria microsporai	China	Cave soil	Zhang et al. (2021c)

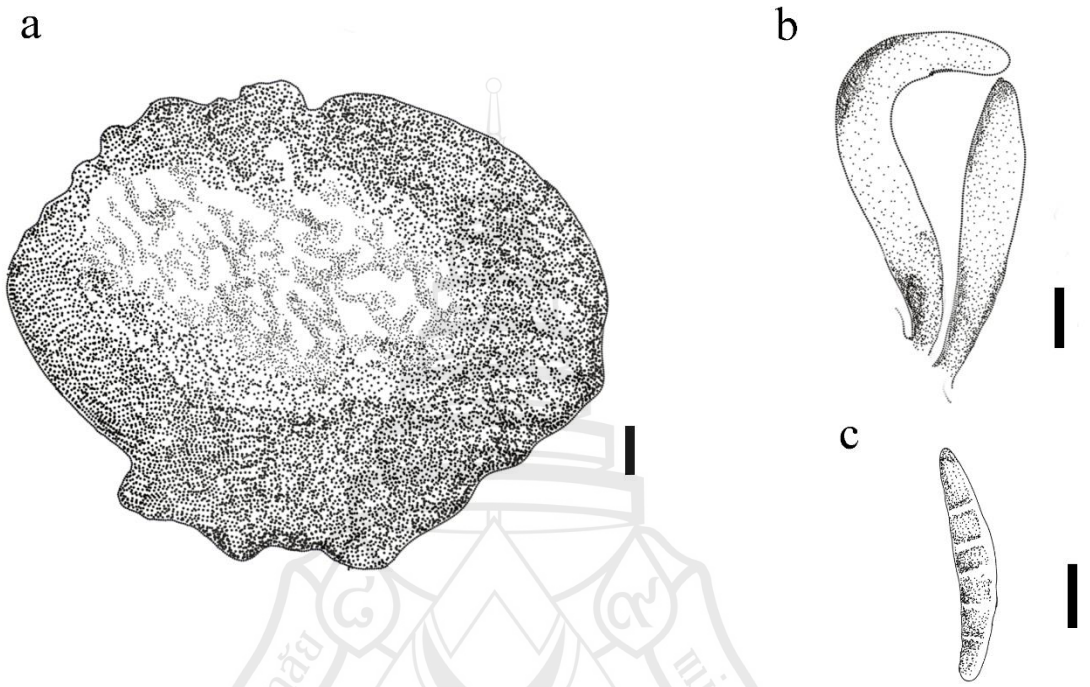


Figure 4.69 *Setophaeosphaeria hemerocallidis* (CBS 138006)

Figure 4.69, a Section of ascomata. b Asci. c Ascospore. Scale bars a–c= 10 μm. Redrawn from Crous et al. (2014a).

Dothideomycetes* orders *incertae sedis

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

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

Lasiodiplodia Ellis & Everh., Bot. Gaz. 21: 92 (1896).

Index Fungorum number: IF 843626; Facesoffungi number: FoF 12936

Ellis and Everhart (1894) introduced *Lasiodiplodia* with its type species *L. tubericola*; however, the generic description was provided by Clendenin (1896). Subsequently, Grifon and Maublanc (1909) suggested to synonymize *Botryodiplodia theobromae,* and the epithet *theobromae* (1892) is older than *tubericola* (1896); thus *L. theobromae* is considered the type species afterward. Currently, 85 species are listed

in the Species Fungorum (2025), while 57 of them have molecular data. Due to overlapping morphological characteristics, multi-locus sequence data is more suitable for identifying the *Lasiodiplodia* species, particularly in the *L. theobromae* species complex, where the morphology is inadequate for species delineation (El-Ganainy et al., 2022). The genus has pathogens and endophytes from various plants, including *Fabaceae*, *Magnolia*, *Mangifera*, *Moraceae* and *Pandanaceae* found worldwide (El-Ganainy et al., 2022; Salvatore et al., 2020), while some have been reported from clinical samples and soil habitats as well (Salvatore et al., 2020; Zhang et al., 2021a). *Lasiodiplodia pseudotheobromae* is identified as soil born root pathogen (Özkaya et al. 2024). Species have been isolated from China, Ecuador, Georgia, Indonesia, Jawa, Laos and Thailand (El-Ganainy et al., 2022). Several species are tested for bioactive compounds that have antifungal, anti-inflammatory and antibacterial activities (Salvatore et al., 2020).

Table 4.61 *Lasiodiplodia* species isolated from soil

Species	Country	Habitat or soil type	References
Lasiodiplodia parva	USA	Cassava field	El-Ganainy et al. (2022)
L. pseudotheobromae	Turkey	Peanut fields	Özkaya et al. (2024)

Order: *Eremomycetales* Crous, Spatafora, Haridas & I.V. Grig.

Family: *Eremomycetaceae* Malloch & Cain

Arthrographis G. Cochet ex Sigler & J.W. Carmich., Mycotaxon 4(2): 359 (1976)

Figure 4.70

Index Fungorum number: IF 7222; Facesofungi number: FoF 16646

Arthrographis was initially proposed by Cochet (1939), but it was not accepted due to an incompatibility with the International Code of Botanical Nomenclature (ICBN). Subsequently, Sigler and Carmichael (1976) validated *Arthrographis* and transferred *Oididendron kalrae* as the type species, while naming it as *A. kalrae.* Giraldo et al. (2014) provided LSU based phylogeny for *Eremomycetaceae* and confirmed the phylogenetic placement of *Arthrographis.* Currently, ten species are available in Species Fungorum (2025) and nine species with molecular data. The asexual morph is hyphomycetous, and has dendritic conidiophores with 1-celled, hyaline, smooth-walled, cylindrical arthroconidia. In addition, it has trichosporiella-like

synasexual morph that has solitary, globose to subglobose conidia which produce laterally and sessile on undifferentiated vegetative hyphae (Sigler & Carmichael, 1976; Giraldo et al., 2014). Species have been identified in air, bark, dead wood, human clinical specimens, marine sediments and soil in Australia, Canada, China, Spain, the Netherlands, the USA (Sigler & Carmichael, 1976; Giraldo et al., 2014, Li et al., 2022).

Table 4.62 *Arthrographis* species isolated from soil

Species	Country	Habitat or soil type	References
Arthrographis grakistii	the Netherlands	A garden	Hernández-Restrepo et al. (2020)
A. kalrae			
A. longispora			
A. multiformispora	China	Soil beside a road in a city area	Li et al. (2022c)

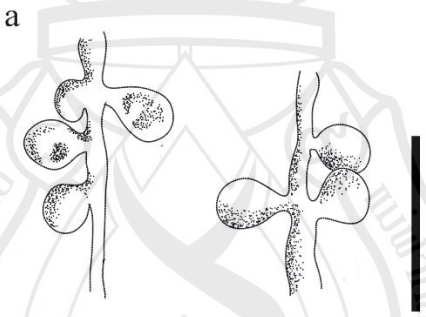


Figure 4.70 *Arthrographis kalrae* (UTHSC 05-17)

Figure 4.70, a Conidia. Scale bars a= 10 μm. Redrawn from Giraldo et al. (2014).

Rhexothecium Samson & Mouch., Can. J. Bot. 53(16): 1637 (1975).

Figure 4.71

Index Fungorum number: IF 4699; Facesofungi number: FoF 06699

Rhexothecium was introduced by Samson and Mouchacca (1975), with the type species; *Rhexothecium globosum.* Currently, it remains a monotypic genus (Species Fungorum 2025). This genus was accepted in *Eremomycetaceae* by Lumbsch and Huhndorf (2010). Asexual morph is hyphomycetous, and it is trichosporiella-like and has solitary lateral conidia. The sexual morph has dark, globose or ellipsoidal, non-ostiolate ascomata with pseudoparenchymatous walls. Asci are eight-spored, obovoidal to clavate, thin-walled, evanescent in clusters with one-celled, globose to subglobose, pale yellow ascospores (Samson & Mouchacca, 1975; Hongsanan et al., 2020b).

Table 4.63 *Rhexothecium* species isolated from soil

Species	Country	Habitat or soil type	References
Rhexothecium globosum	Egypt	Western Desert	Samson and Mouchacca (1975)

a

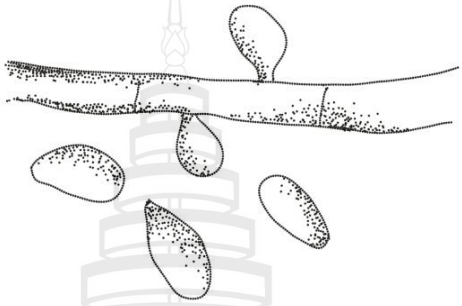


Figure 4.71 *Rhexothecium globosum*

Figure 4.71, a Conidiogenesis and conidia. Redrawn from Samson & Mouchacca (1975)

Order: ***Muyocopronales*** Mapook, Boonmee & K.D. Hyde

Family: ***Muyocopronaceae*** K.D. Hyde

Arxiella Papendorf, Trans. Br. mycol. Soc. 50(1): 73 (1967).

Figure 4.72

Index Fungorum number: IF 7233; Facesofungi number: FoF 08091;

Arxiella was established by Papendorf (1967), and *A. terrestris* is accepted as the type species. Previously, the genus was treated as *incertae sedis* (Crous et al., 2014b) and Crous et al. (2018b) placed *Arxiella* within *Muyocopronaceae* based on the LSU phylogeny. Subsequently, Hernández-Restrepo et al. (2019) confirmed its placement in *Muyocopronaceae* using the combined ITS, LSU, *rpb2*, and *tef1* phylogenetic analyses. Currently, four species are listed under *Arxiella* (Species Fungorum, 2025), all of them are supported by the molecular data. Both coelomycetes and hyphomycetes asexual morphs have been recorded in the genus (Hongsanan et al., 2020b). The asexual morph is characterized by septate, branched hyphae that are hyaline to slightly olivaceous. Conidiophores are 1- to multi-celled, with all cells being conidiiferous. Conidia are hyaline to slightly coloured, 1-septate, and reniform, with

obliquely cornute ends. They are borne on short or elongate, sterigma-like projections, and occur singly, in short chains, or in small irregular groups (Papendorf, 1967). The coelomycetous asexual morph has sporodochial, brown conidiomata with globose to somewhat elongated, phialidic, brown conidiogenous cells that produce reniform, medianly 1-septate conidia with guttules and horn-like appendages at the ends (Hongsanan et al., 2020b; Tennakoon et al., 2021). Species have been recorded in leaves and soil from India, the Netherlands and South Africa (Tiwari, 1976; Crous et al., 2014b; Tennakoon et al., 2021).

Table 4.64 *Arxiella* species isolated from soil

Species	Country	Habitat or soil type	References
Arxiella terrestris	India and South Africa	ND	Papendorf (1967), Tiwari (1976)

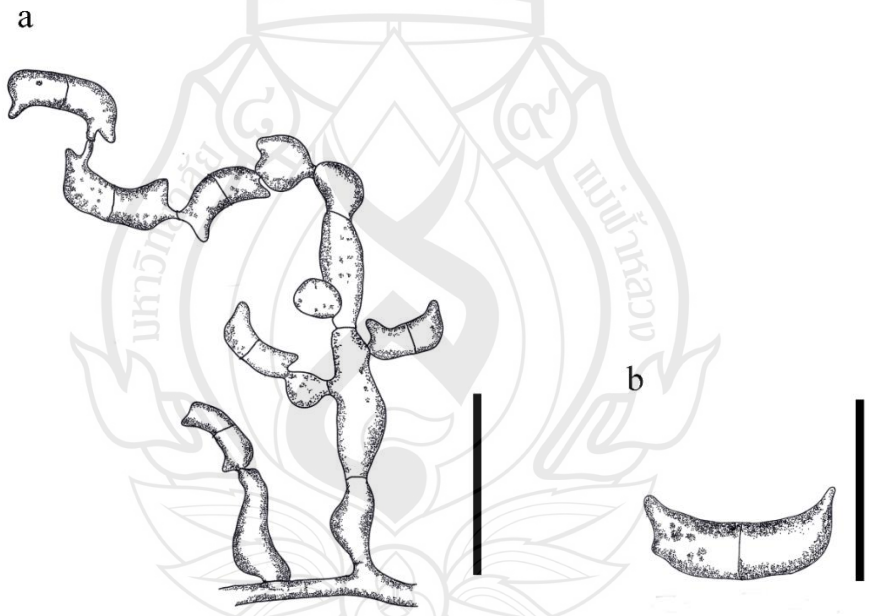


Figure 4.72 *Arxiella terrestris*

Figure 4.72, a Conidiophores. b Conidia. Scale bars a= 20 μm, b = 15 μm. Redrawn from Papendorf (1967).

Leptodiscella Papendorf, Trans. Br. mycol. Soc. 53(1): 146 (1969).

Figure 4.73

Index Fungorum number: IF 8743; Facesofungi number: FoF 08092.

Papendorf (1969) introduced *Leptodiscella* and *L. africana* is designated as the type species. The genus comprises six species (Species Fungorum 2025), and all of which are supported by molecular data. The asexual morph is hyphomycetous and has solitary or aggregated, mono- or polyblastic, sympodial conidiogenous cells, with solitary, hyaline, cylindrical to oblong, 1-septate, conidia with a subpolar, filiform appendage at each cell. Three *Leptodiscella* species have been found in soil and some are associated with house dust, leaves and plant litter in Africa, China, Japan and the Netherlands (Barbosa et al., 2015; Crous et al., 2018c).

Table 4.65 *Leptodiscella* species isolated from soil

Species	Country	Habitat or soil type	References
Leptodiscella brevicatenata	Spain	Forest soil	Madrid et al. (2012)
L. japonica	Japan	Forest soil	Matsushima (1975)
L. rintelii	The Netherlands	ND	Crous et al. (2018c)

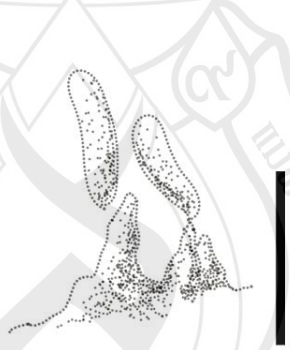


Figure 4.73 *Leptodiscella Africana* (URM 86557)

Figure 4.73, a Conidiogenesis. Scale bar a=10 μm. Redrawn from Barbosa et al. (2015).

Order: *Phaeotrichales* Ariyaw., Jian K. Liu & K.D. Hyde

Family: *Phaeotrichaceae* Cain

Phaeotrichum Cain & M.E. Barr, Can. J. Bot. 34: 676 (1956).

Figure 4.74

Index Fungorum number: IF 3967; Facesofungi number: FoF 08132

Phaeotrichum was introduced by Cain (1956), with to accommodate *P. hystricinum* as the type species (Cain, 1956). The genus was previously placed in *Sporormiaceae* (Munk, 1957), however, subsequently Barr (2000) placed it in *Phaeotrichaceae*. Currently, the genus

accommodates five species (Species Fungorum, 2025), but only two have molecular data. The sexual morph is characterized by superficial, cleistothecial, globose ascomata, covered by long hairy appendages and eight-spored, broadly clavate, stipitate asci. Ascospores are dark-brown and opaque, thick-walled and deeply constricted at the single median transverse septum (Cain, 1956). Species are coprophilous isolated from dung and one species have been isolated from soil in Canada, Japan, Québec and the USA (Cain, 1956; Hongsanan et al., 2020b).

Table 4.66 *Phaeotrichum* species isolated from soil

Species	Country	Habitat or soil type	References
Phaeotrichum setosum	Japan	ND	Hongsanan et al. (2020b)

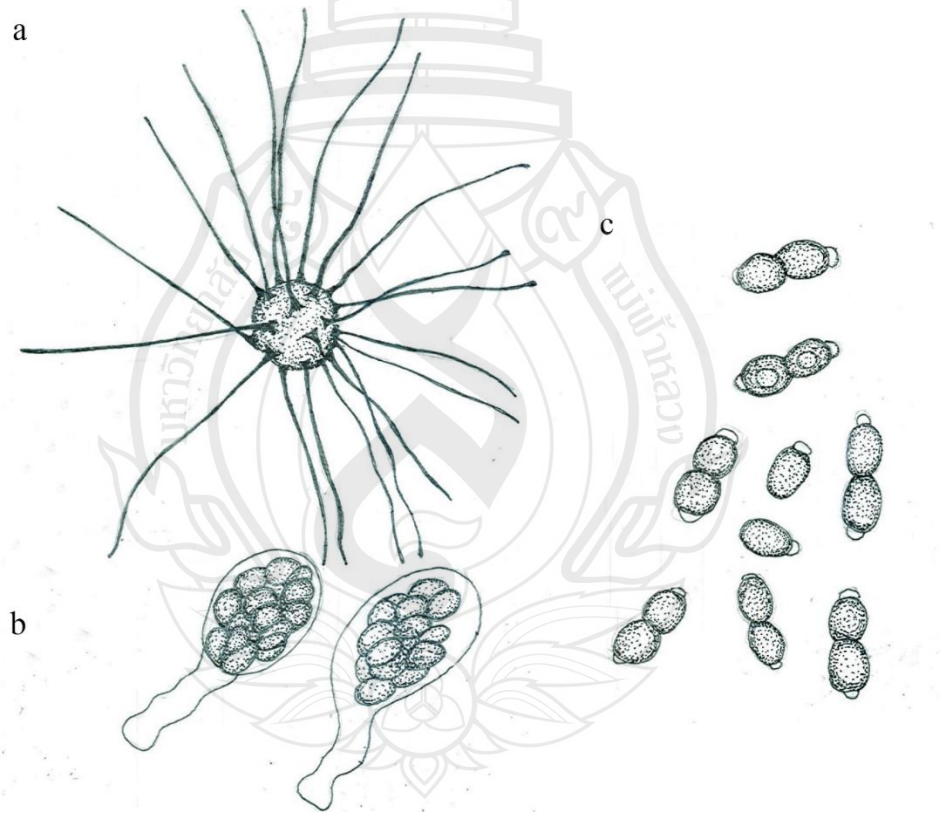


Figure 4.74 *Phaeotrichum hystricinum*

Figure 4.74, a Ascomata. b Asci. c Ascospores. Redrawn from Cain (1956)

Order: *Trypetheliales* Lücking Aptroot & Sipman

Family: *Trypetheliaceae* Zenker (= *Arthopyreniaceae* Walt. Watson)

Aptrootia Lücking & Sipman, Lichenologist 39: 188 (2007).

Figure 4.75

Index Fungorum number: IF 29134; Facesofungi number: FoF 08786

Aptrootia was introduced by Lücking et al. (2007); based on morphology and SSU phylogeny, while *A. terricola* is designated as the type species. *Aptrootia* has four species listed in the Species Fungorum (2025), and all are introduced with molecular data. Thallus appear distinctly corticate, yellow-brown to mostly green, or ecorticate and greyish (Hongsanan et al., 2020b). The asexual morph is unknown. Sexual morph is characterized by solitary, brown-black, globose to pear-shaped or ovoid, coriaceous to carbonaceous, ostiolate ascomata that is usually covered by a thick thallus layer except for the ostiolar area. Asci are 1(–2)-spored, bitunicate, fissitunicate, oblongellipsoid, short pedicellate. Ascospores are oblong-ellipsoid, initially hyaline, becoming dark brown, muriform, weakly distoseptate, with a gelatinous sheath, initially hyaline and I+ amyloid, becoming dark brown (Lücking et al., 2007; Hongsanan et al., 2020b). These species have been found lichenized on bark, on bryophytes in terrestrial tropical forest habitats and two species have been found from soil-substrates in Costa Rica, New Zealand and Thailand (Hongsanan et al., 2020b).

Table 4.67 *Aptrootia* species isolated from soil

Species	Country	Habitat or soil type	References
Aptrootia terricola	Seychelles	Soil on a granitic rock	Diederich et al. (2017)
A. robusta	Tasmania	Soil in rock crevices in alpine heathland	McCarthy and Kantvilas (1993)

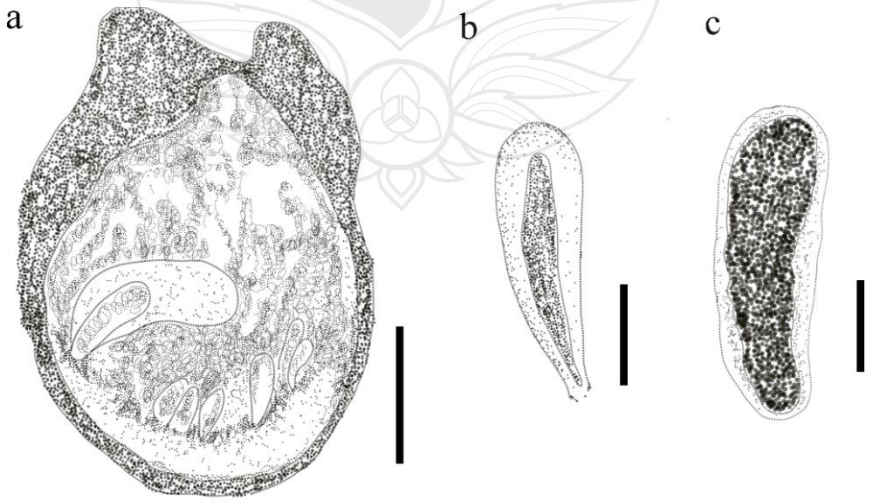


Figure 4.75 *Aptrootia terricola* (*Lücking* 17211)

Figure 4.75, a Ascomata. b Immature ascus. c Mature ascospores. Scale bars: a = 200 μm, b, c = 50 μm. Redrawn from Lücking et al. (2007).

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

Family: ***Sympoventuriaceae*** Y. Zhang ter, C.L. Schoch & K.D. Hyde

Guizhoumyces T.P. Wei & Y.L. Jiang, Persoonia 48: 230 (2022)

Figure 4.76

Index Fungorum number: IF 840922; Facesofungi number: FoF 16647

Guizhoumyces is a monotypic genus that was established by Wei et al. (2022) based on morpho-molecular (SSU, ITS, LSU, Actin, *tef1-α*) analyses and typified with *G. aciculaea*. The asexual morph is characterized by subcylindrical, simple, branched, straight or slightly geniculate, pale brown, septate conidiophores and sometimes reduced to conidiogenous cells and polyphialidic, sympodially proliferating conidiogenous cells with rhexolytic conidial secession. Conidia are enteroblastic, subhyaline to pale brown, solitary, acicular to obclavate or cylindrical, septate, with thick and dark hilum; anastomosis between mature conidia. The sexual morph is still undetermined (Wei et al., 2022a).

Table 4.68 *Guizhoumyces* species isolated from soil

Species	Country	Habitat or soil type	References
Guizhoumyces aciculaea	China	Fodingshan National Nature Reserve	Wei et al. (2022a)

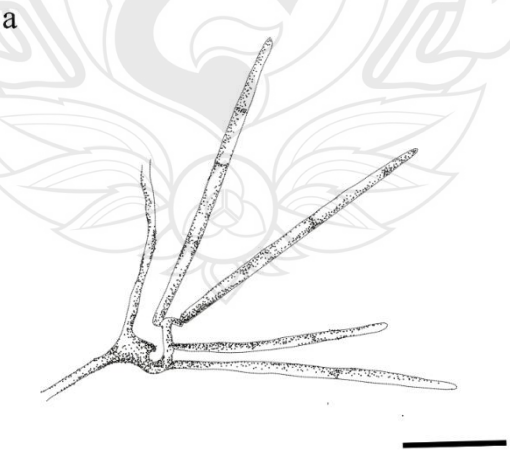


Figure 4.76 *Guizhoumyces aciculaea* (GUCC 18195)

Figure 4.76, a Conidiophores and conidia. Scale bars a = 10 μm. Redrawn from Wei et al. (2022b).

Matsushimaea Subramanian, Kavaka 5: 96. 1977 '1978'

Index Fungorum number: IF8865; Facesofungi number: FoF 08831

Matsushimaea was erected by Subramanian (1977) with the type, *M. fasciculate*. Currently, it accommodates four species (Species Fungorum, 2025), while three of them have molecular data. Crous et al. (2018a) and Wei et al. (2022) provided phylogeny for this genus based on the combined ITS, LSU, *tef1-α*, *rpb2* and *tub2* data while introducing new species in the genus. The asexual morph is characterized by sessile, branched conidia, producing directly from vegetative hyphae, with polyblastic sympodial conidiogenous cells (Subramanian 1977). *Matsushimaea* has been isolated from forest litter and two species from the soil in China, Cuba, Japan and Spain (Crous et al., 2018b; Wei et al., 2022a).

Table 4.69 *Matsushimaea* species isolated from soil

Species	Country	Habitat or soil type	References
Matsushimaea monilioides	Spain	Garden soil	Crous et al. (2018b)
M. fasciculate	China	Land in a resort	Wei et al. (2022a)

Scolecobasidium E.V. Abbott, Mycologia 19: 30. 1927 Synonym. Ochroconis de Hoog & Arx, Kavaka 1: 57. 1974 '1973'.

Figure 4.77

Index Fungorum number: IF9840; Facesofungi number: FoF 09214

Scolecobasidium was described by Abbott (1927) with the type species, *S. terreum.* Shen et al. (2020) placed this genus in *Sympoventuriaceae* as it has slow growing olivaceous colonies. Wei et al. (2022) used the combined SSU, ITS, LSU, *actin*, *tub2* and *tef*1-α molecular data to infer its phylogenetic placement and suggested that *Ochroconis* can be synonymized under *Scolecobasidium*. *Scolecobasidium* currently comprises 77 species (Species Fungorum, 2025) and 51 of them have molecular data. The asexual morph is hyphomycetous, and conidiophores possess one to three conidium-bearing denticles at the apex, ampulliform conidiogenous cells and T- or Y-shaped or bilobed, two- to multi-celled conidia (Hongsanan et al., 2020b; Wei et al., 2022a). Genus exhibit thermophilic properties and it has human and animal pathogens while some of the species harbor in litter and soil substrates. They are geographically distributed in Australia, China, Georgia, India, Malaysia, Spain and the USA (Samerpitak et al., 2014, 2019; Wei et al., 2022a).

Table 4.70 *Scolecobasidium* species isolated from soil

Species	Country	Habitat or soil type	References
Scolecobasidium constrictum	USA	ND	Abbott (1927)
S. terreum		ND	
S. globale	China	Lawn soil	Wei et al. (2022a)
S. tshawytschae		Lawn soil	
S. spiralihyphum		ND	
S. tuberculatum		ND	
S. crassihumicola	Papua New Guinea	ND	
S. icarus	Canada	Forets soil	
S. verrucosa	India	ND	
S. coiledmyces	China	Lawn soil	
S. echinulatum		ND	
S. ellipsoideum		ND	
S. guangxiensis		ND	
S. humicola	Canada	peat soil	
S. icarus	Canada	Forest soil	
S. leishanicola	China	ND	
S. minimum	India	ND	
S. ramosum	China	ND	
S. terreum	USA	ND	
S. tshawytschae	Ireland	peat bog soil	
S. variabile	Canada	ND	
S. verrucaria	China	ND	
S. verrucosum	India	ND	
V. terricola	China	ND	

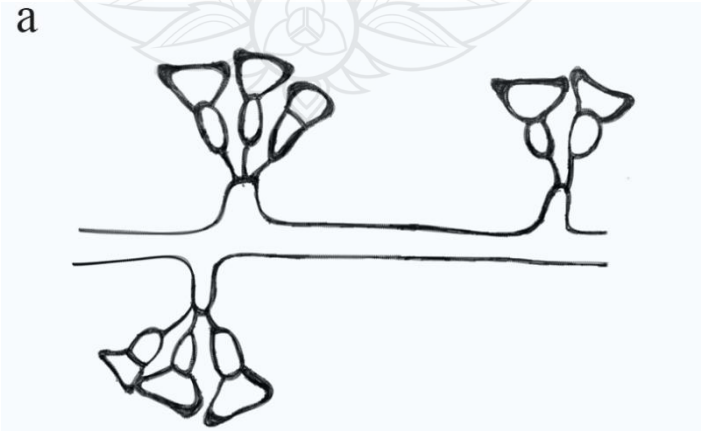


Figure 4.77 *Scolecobasidium terreum*

Figure 4.77 a. Conidiogenesis on the conidiophores and conida. Redrawn from Abbott (1927)

Verruconis Samerp. & de Hoog, Fungal Diversity 65: 117 (2013)

Figure 4.78

Index Fungorum number: IF519169; Facesofungi number: FoF 06351

Samerpitak et al. (2014) established *Verruconis* and designated *V. gallopava* as the type species. Currently, 15 species are listed in the Species Fungorum (2025), and all of which have molecular data. Initially, this genus was established to accommodate thermophilic species that have unbranched conidia. Later, mesophilic species have been discovered within the genus (Samerpitak et al., 2014; Zhang et al., 2018). Samerpitak et al. (2016) used the concatenated dataset of SSU, ITS, LSU, *actin*, *tub2* and *tef1*-α for species delineation in *Sympoventuriaceae*. Subsequently, species delineation is mainly based on molecular analyses coupled with morphological characterization (Wei et al., 2022a). *Verruconis* species are characterized by melanized hyphomycetes, brown to olivaceous colonies, and clavate to cylindrical, two-celled conidia (Zhang et al., 2018; Huanraluek et al., 2019). Later, Y- or T-shaped conidia were also described from this genus (Wei et al., 2022a). The first sexual morph of this genus was recorded from *V. mangrovei*, which has superficial to semi-immersed, globose to sub-globose, pale brown to dark brown ascomata, and dictyosporous, ellipsoidal to oblong, 4–5 transverse septate ascospores (Hyde et al., 2020a). Species can be endophytes, saprobes in plants and opportunistic pathogens in animals and humans (Giraldo et al., 2014b). *Verruconis* have been found in hot springs, humans, industrial effluents, plants and soil in India, Thailand and the USA (Yasanthika et al., 2023).

Table 4.71 *Verruconis* species isolated from soil

Species	Country	Habitat or soil type	References
Verruconis guizhouensis	China	Rhizosphere soil	Shao et al. (2022b)
V. soli	Thailand	Forest soil	Yasanthika et al. (2023)
V. thailandica			
V. terricola	China	ND	Ren et al. (2013)
V. verruculosa	India	ND	Samerpitak et al. (2014)

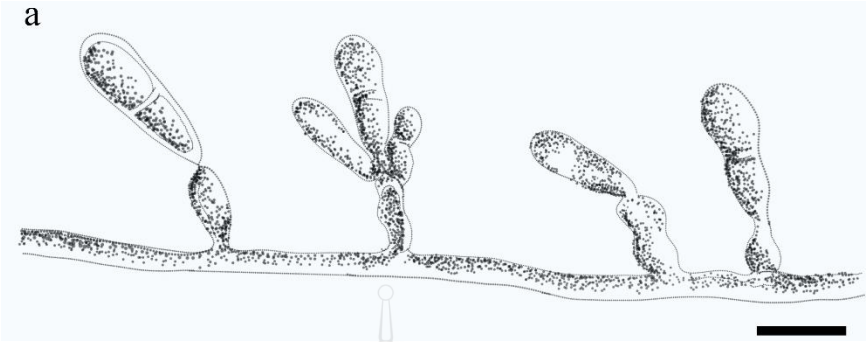


Figure 4.78 *Verruconis gallopava* (CBS 437.64)

Figure 4.78, a. Conidial apparatus and conidia. Scale bar: a = 10 μm. Redrawn from Samerpitak et al. (2014).

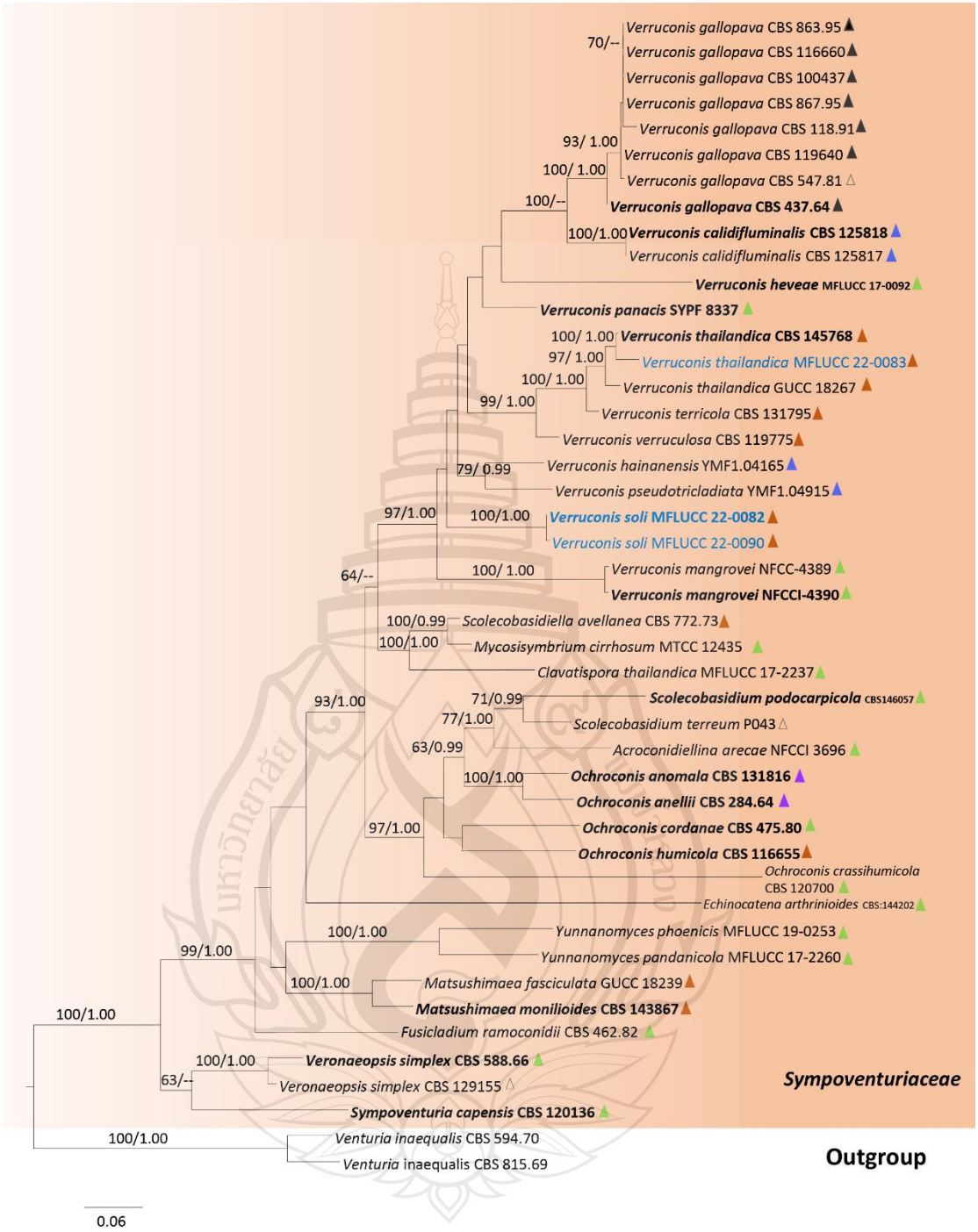


Figure 4.79 Phylogenetic tree generated from the maximum likelihood analysis based on combined SSU-ITS-LSU gene sequences data for the selected genera in the family *Sympoventuriaceae*

Figure 4.79, The concatenated ITS, LSU, and SSU alignment contained 51 strains of *Sympoventuriaceae* with *Venturia inaequalis* (CBS 594.70 and CBS 815.69)

as the outgroup taxon. The ollections (MFLUCC 22-0082 and MFLUCC 22-0090) formed a distinct lineage, however with bootstrap supports less than 60% ML and 0.95 BYPP sister to the several subclades; the sub-clade containing *Verruconis hainanensis* (YMF1-04165) and *V. pseudotricladiata* (YMF1-04915), and sub-clade containing *V. mangrovei* (NFCCI 4390, NFCCI-4389). This topology agrees with that of Zhang et al. (2018), Qiao et al. (2019), and Hernández-Restrepo et al. (2020). Since these studies used different gene combinations and did not include all the available species, several inconsistencies and topological dissimilarities are observed compared to our study. Therefore, we introduce our collections (MFLUCC 22-0082 and MFLUCC 22-0090) as new species in this genus. Another one of our isolates (MFLUCC 22-0083) grouped with *V. thailandica* (CBS 145768, GUCC 18267) with 97% ML bootstrap and 1.00 BYPP, separated from *V. terricola* (CBS131795), and thus identified as *V. thailandica*.

Verruconis soli Yasanthika & K.D. Hyde, sp. nov.

Index Fungorum number: IF 558479, Faces of Fungi number: FoF 12888, Figure 4.80

Etymology – The specific epithet "soli", from Latin, refers to the soil, the substrate of which the holotype was collected.

Holotype –MFLU22-0257

Asexual morph: Conidiophores 20–62 × 1–3.5 µm ($\bar{x}$ = 39 × 2 µm, n = 20), micronematous, mononematous, solitary, unbranched, cylindrical to sub-cylindrical, straight to slightly flexuous, hyaline to brown, smooth. Conidiogenesis cells holoblastic, determinate, and rarely intercalary. Conidia 5–11 × 3–4.5 µm ($\bar{x}$ = 8 × 3.5 µm, n = 20), hyaline, obovoid, smooth becoming sub-cylindrical or ellipsoidal, slightly verruculose thick and sometimes pale brown, 1-septate and constricted at the septum at maturity. Sexual morph: Undetermined.

Culture characteristics — Colonies on PDA at 25°C after 7 days become 3.5 cm diam., irregular margined, velvety, dark brown, raised, grayish brown at center, reverse dark brown. Mycelium hyaline, become pale brown to brown at maturity, 1–3 µm ($\bar{x}$ = 1.5 µm), smooth to verruculose, septate.

Material examined: — Thailand, Chiang Rai, 20°4'35"N,100°5'43"E, 450 m, from forest soil, 7 January 2020, W.A.E. Yasanthika (MFLU22-0257, holotype); ex-type living

culture MFLUCC 22-0082; (MFLU22-0253, paratype), ex-paratype living culture MFLUCC 22-0090.

Notes– *Verruconis* is aggregated with thermophilic species, and several have been reported from the soil, viz., *V. gallopava* from thermal soils, *V. verruculosa* from grassland soils, and V. thailandica from soils near the waterfall (Zhang et al., 2018; Hernández-Restrepo et al., 2020; Shen et al., 2020). Herein, we introduce V. soli from soil in Thailand with morpho-molecular justifications. *Verruconis* soli is phylogenetically adjacent to *V. hainanensis* (YMF 1.04165), *V. pseudotricladiata* (YMF 1.04915), and V. mangrovei (NFCCI 4390, NFCCI-4389) (FIGURE 2). Though V. soli has low bootstrap support in the phylogenetic tree, and pairwise comparisons of LSU and ITS sequences of closely related species showed significant differences that are higher than 1% in each scenario, which is common to many species in this genus. Further, they differ ecologically from V. soli as *V. hainanensis* and *V. pseudotricladiata* have been reported from freshwater habitats (Qiao et al., 2019) while V. mangrovei reported from marine habitats (Hyde et al., 2020). *Verruconis hainanensis*, *V. pseudotricladiata*, and *V. soli* (MFLUCC 22-0082) are mainly distinguishable by their conidiophores and conidial morphology. *Verruconis hainanensis* and *V. pseudotricladiata* have macronematous conidiophores, whereas V. soli (MFLUCC 22-0082) has micronematous conidiophores (Qiao et al., 2019). In addition, V. soli (MFLUCC 22-0082) has sub-cylindrical or ellipsoidal, 1-septate mature conidia and obovoid immature conidia, while *V. hainanensis* has fusiform, 3-septate conidia that are rostrate at the apical cell (Qiao et al., 2019). *Verruconis pseudotricladiata* has staurosporic, branched or unbranched conidia (cylindrical-clavate and 2–4-septate while branched conidia are Y-, or T-shaped) (Qiao et al., 2019). Furthermore, the conidia of *V. hainanensis* and unbranched conidia in *V. pseudotricladiata* have a slight constriction at the median septum, but V. soli (MFLUCC 22-0082) have a prominent constriction at the septum and septation is absent at immature stages in conidia. *Verruconis mangrovei* has been recorded as a sexual morph (Hyde et al., 2020); therefore, we could not compare the morphological characteristics with our collection. The base pair differences of ITS sequences between V. *mangrovei* and *V. soli* were 31% (with gaps). Therefore, we accommodate *V. soli* (MFLUCC 22-0082) isolated from forest soils in Thailand as a new species with morpho-molecular support.

Figure 4.80 *Verruconis soli* (MFLU22-0257, holotype)

Figure 4.80, a. Colony from above (on PDA). b. Colony from below (on PDA). c. Sporulated colony. d. Melanized hyphae. e. Hyaline hyphae f–l. Conidiogenesis. m–r. Conidia. Scale bars: e = 15 μm, d, f–k = 10 μm, l–r = 5 μm

Verruconis thailandica Giraldo López & Crous, Fungal Systematics and Evolution 6: 21 (2020)

Figure.4.81

Index Fungorum number: IF833679, Facesoffungi number: FoF09618,

Asexual morph: Conidiophores 1–2 μm ($\bar{x}$ = 1.8 μm, n=20) wide, macronematous, mononematous and synnematous, erect, straight, or slightly bent, simple, sub-cylindrical, hyaline to pale brown, smooth-walled, conidiogenesis terminal or intercalary, sympodial.

Conidiogenesis cells 2–3.5 × 1.5–3 μm ($\bar{x}$ = 3 × 1.8 μm, n = 20), monoblastic, discrete, sub-cylindrical to ampulliform. Conidia 5–7 × 2.2–3.1 μm ($\bar{x}$ = 5.8 × 2.6 μm, n = 20), broadly ellipsoidal or rarely oval, hyaline to pale brown, 1-septate, constricted at the septum, verrucose, thick-walled, protuberant hilum. Sexual morph: Undetermined.

Culture characteristics: — Colonies on PDA at 25°C after 7 days become 4 cm diam., filamentous margined, hairy, and raised, brown to grayish brown at centre, flat, glabrous, dark brown at periphery, reverse dark brown, diffusible brownish pigment. Mycelium hyaline, aseptate, smooth at immature become septate, pale brown, 1–3 ($\bar{x}$ = 2.5) μm diam. hyphae.

Known hosts and substrates: — soil (Hernández-Restrepo et al. 2020, this study).

Known distribution: — Thailand (Hernández-Restrepo et al. 2020, this study)

Material examined: — Thailand, Chiang Rai Province, 19°53'2" N, 100°5'37" E, 440m, from forest soil, 7 January 2020, W.A.E. Yasanthika (MFLU22-0258); living culture, MFLUCC 22-0083.

Notes– *Verruconis thailandica* (CBS 145768) was first isolated from soil near a waterfall in Nakhon Nayok Province, Thailand (Hernández-Restrepo et al., 2020). *Verruconis thailandica* has a closer phylogenetic affinity to *V. verruculosa* and *V. terricola* (Hernández-Restrepo et al., 2020) (Figure 4.79). Our collection is grouped with V. *thailandica* isolates (CBS 145768, GUCC 18267) in a well-supported clade with 100% ML, 1.00 BYPP support, and related to the isolate CBS 145768 with 97% ML and 1.00 BYPP. Our strain morphologically resembles *V. thailandica* (CBS 145768) by having erect, straight or slightly bent, sub-cylindrical conidiophores and broadly ellipsoidal or rarely oval, 1-septate conidia (Hernández-Restrepo et al., 2020). We observed mononematous and synnematous conidiophores in our isolate (MFLUCC 22-0083), which were missing in the type species (CBS 145768). This morphological variation can be due to the environmental adaptations of the organism (Francisco et al., 2019). Therefore, with morpho-molecular justifications, we present the second report of *V. thailandica* from forest soils in Thailand.

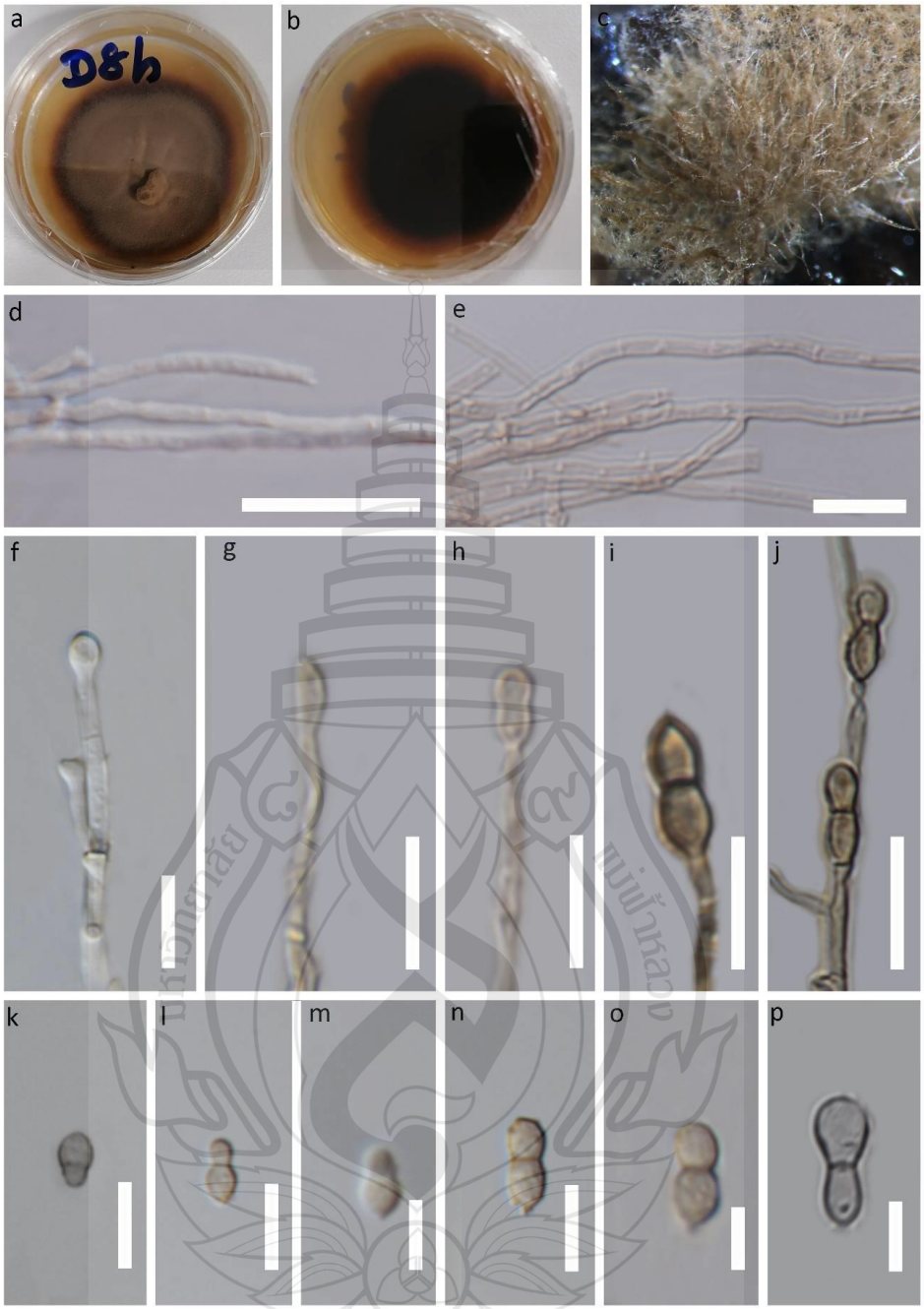


Figure 4.81 *Verruconis thailandica* (MFLU22-0258, new record)

Figure 4.81, Colony from above (on PDA). b. Colony from below (on PDA). c. Sporulated colony with conidial attachments on the mycelium. d. Immature hyphae e. Mature septate hyphae. f. Conidiogenesis synnematous. g–j. Conidiogenesis mononematous conidiophores. k–p Conidia. Scale bars: d, e = 20 µm, f–l, n = 10 µm, m, o, p = 5 µm.

Dothideomycetes families incertae sedis

Pseudorobillarda M. Morelet, Bull. Soc. Sci. nat. Arch. Toulon et du Var 175: 5 (1968).

Figure 4.82

Index Fungorum number: IF 9607; Facesofungi number: FoF 07559

Pseudorobillarda was erected by Morelet (1968) with the type species *P. phragmitis*. It has 20 species listed in the Species Fungorum (2025), while 10 have been supported with molecular data. The asexual morph has pycnidial conidiomata, phialidic or annellidic conidiogenous cells and subcylindrical to fusiform, 0–4-septate conidia with appendages at one end Hongsanan et al. (2020b). There is no sexual morph linked to *Pseudorobillarda* Hongsanan et al. (2020b). Many endophytes and saprobic species are found on both living and dead leaves and stems, respectively, and can also be found on soil in Belgium, Canada, China, Germany, India, Russia, Nigeria, Thailand and the USA. *Pseudorobillarda* species are known as one of the ten most abundant soil fungi and has a significant impact on nutrient cycling in the saprobic state (Tangthirasunun et al., 2014; Hongsanan et al., 2020b; Song et al., 2022).

Table 4.72 *Pseudorobillarda* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudorobillarda asparagis	Canada	Asparagus field	Kadowaki et al. (2014)
Pseudorobillarda texana	ND	ND	

Figure 4.82 *Pseudorobillarda phragmitis*

Figure 4.82, a Conidiogenesis in pycnidium. b Conidium. Scale bars a = 200 μm, b = 10 μm. Redrawn from Raj et al. (1972)**.**

Dothideomycetes genera incertae sedis

Bahusakala Subram., J. Indian bot. Soc. 37: 63 (1958)

Index Fungorum number: IF 7318; Facesoffungi number: FoF09031

Subramanian (1958) introduced *Bahusakala* and its type species, *B. olivaceonigra.* Currently, there are four species listed in the Species Fungorum (2025) and two of them have molecular data. Its asexual morph is characterized by conidiophores that branch at irregular intervals to produce brown conidiogenous hyphae at the terminal and intercalary positions and brown to dark brown conidia that originate from random disarticulation of the main conidiophore axes and conidiogenous hyphae (Bundhun et al., 2021; Pem et al., 2019). Based on the phylogenetic analyses of Bundhun et al. (2021), suggested that *Parasympodiella* and *Bahusakala* are congeneric and to accommodate *Bahusakala* taxa in *Parasympodiella,* however, due to the lack of molecular data in the type species the exact phylogenetic placement of *Bahusakala* remains undetermined (Bundhun et al., 2021). The species are recorded from dead plants and soil while several members are reported as human and plant pathogens in Cuba, India, Japan, Sri Lanka and Thailand (Pem et al., 2019).

Table 4.73 *Bahusakala* species isolated from soil

Species	Country	Habitat or soil type	References
Bahusakala australiensis	Australia	ND	Domsch et al. (1993)
Bahusakala sp.	USA	Desert soil	Bhatnagar and Bhatnagar (2005)

Monodictys S. Hughes, Canad. J. Bot. 36: 785. 1958

Index Fungorum number: IF 8979; Facesoffungi number: FoF12305

Hughes (1958) introduced *Monodictys* and the type species is designated as *M. putredinis*. There are more than 60 species listed in Species Fungorum (2025); however, most of them including the type species lack the sequence data. Thus, their phylogenetic placement is currently unresolved. Based on the previous studies, Tanaka et al. (2015) mentioned that some *Monodictys* species are segregated in *Dothideomycetes*, *Leotiomycetes* and *Sordariomycetes*. Thus, collecting fresh specimens to generate more sequences and conducting a phylogenetic reassessment are timely requirements to infer their true placement (Tanaka et al., 2015; Yeh & Kirschner, 2019). The species are

distributed in China, India, Hungary, Germany, Pennsylvania and Sri Lanka that are associated with plant debris and soil habitats (Tanaka et al., 2015).

Table 4.74 *Monodictys* species isolated from soil

Species	Country	Habitat or soil type	References
Monodictys flucluata	Thailand	ND	Manoch (1987)
M. tuberculate	China	Grassland soil	Wu et al. (2009)
M. clavata			
M. shigatsensis			

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

Subclass: *Chaetothyriomycetidae* Doweld

Order:*Chaetothyriales* M.E. Barr

Family: *Herpotrichiellaceae* Munk

Cladophialophora *Borelli,* Proc. 5th International Conference on Mycoses: 355 (1980)

IndexFungorum: IF 7677; Facesoffungi: FoF 10373

Cladophialophora was initially introduced by de Hoog and de Hoog (1974), and *Cladophialophora carrionii* is designated as the type species (de Hoog, 1974). Subsequently, the genus was revised by Borelli (1980) with significant changes and it was initially erected to accommodate a species exhibiting both *Cladosporium*- and *Phialophora*-like conidiogenesis. There are 67 *Cladophialophora* species in the Species Fungorum (2025), however, Chang et al. (2023) have provided the phylogenetic analyses using 46 species based on ITS, SSU, LSU, *tub2*, and *tef*1-α gene regions. The asexual morph is characterized by blastic, acropetal conidiogenesis, with branched or unbranched conidial chains, and one-celled, ellipsoidal to fusiform conidia (Chang et al., 2023; Das et al., 2019; Sutton et al., 2009). Around eleven species are found pathogenic to humans, with *C. emmonsii* causing human subcutaneous phaeohyphomycosis and skin infections in mammals. Species have been isolated from humans, lichens, plants, processed food and soil in Australia, China, Cuba, Denmark, Germany, Korea, New Zealand, South Africa and Spain (Tang et al., 2017; Torres-Garcia et al., 2023).

Table 4.75 *Cladophialophora* species isolated from soil

Species	Country	Habitat or soil type	References
Cladophialophora chaetospira	Germany	Wheat field	Crous et al. (2007)
C. humicola	Germany	Arable soil	
C. inabaensis	Japan	Forest soil	Chang et al. (2023)
C. lanosa	Korea	Yellowish brown and fine gravelly clay loam soil	
C. multiseptata	Spain	ND	
C. psammophila	the Netherlands	Soil polluted with petroleum	
C. pseudocarrionii	Spain	ND	

Exophiala J.W. Carmich., Sabouraudia 5: 122 (1966)

IndexFungorum: IF 8233; Facesoffungi: FoF 10374

Exophiala was introduced by Carmichael (1966), accommodating its type species as *E. salmonis*. The genus comprises 81 species (Hyde et al., 2024c), and most of them have molecular data. Molecular analyses are essential for species identification in *Exophiala* (Madrid et al., 2023) and exhibit extensive pleomorphism, producing phialophora-like, cladophialophora-like or meristematic synanamorphs in cultures (Crous et al., 2018a; de Hoog & Hermanides-Nijhof, 1977). Moreover, both sexual and asexual morphs have been reported in *Exophiala*; and characterized by the yeast-like budding cells. The asexual morph has annellidic conidiogenous cells and aseptate or transversely septate conidia in slimy masses (Madrid et al., 2023). *Exophiala* species are commonly found on dead or living plant material, indoor spaces, river sediments, rocks, humid surfaces, soil and water in China, Germany, Italy, Japan, Norway, Russia, Spain, Sri Lanka and Thailand (Dög˘en et al., 2013; Madrid et al., 2023; Matos et al., 2002). Several species are pathogenic to animals and humans causing skin and subcutaneous infections (Woo et al., 2013).

Table 4.76 *Exophiala* species isolated from soil

Species	Country	Habitat or soil type	References
Exophiala alcalophila	Japan	ND	Ide-Pérez et al. (2024)
E. atacamensi	Chile	Desert soil	
E. attenuate	Colombia	ND	
E. chapopotensis	Mexico	Oil polluted soil	
E. crusticola	Chile and USA	ND	
Exophiala viscosa	Canada	Biological soil crust	

Phialophora Medlar, Mycologia 7(4): 202 (1915)

Figure 4.83

IndexFungorum: IF 9342, Facesoffungi: FoF 10380

Medlar (1915) erected *Phialophora* with its type species, *P. verrucosa*. There are 37 species listed in Species Fungorum (2025), but only eight of them are supported with molecular data. *Phialophora* is treated with LSU, *tub2* and *tef1-α* phylogeny by Torres-Garcia et al. (2023) while accommodating new species in the genus. Both sexual and asexual morphs are produced, however, the asexual morph is commonly found in nature. The asexual morph is characterized by pigmented conidiophores, solitary or aggregated, flask-shaped phialides with flaring collarettes and one-celled, ellipsoidal or cylindrical conidia (Gams, 2000). Species are inhabiting fresh and polluted water, human skin, plants, paper, straw, soil, wood and wood pulp isolated from Brazil, China, Japan, North America, Peru, the Netherlands and USA (McKemy, 1997; Song et al., 2021). These species can have pathogenic or mutualistic relationships with plant roots (Yuan et al., 2010), while several members like *P. verrucosa* and *P. richardsiae* can cause skin infections, subcutaneous infections, or more systemic diseases in immunocompromised patients (Song et al., 2021).

Table 4.77 *Phialophora* species isolated from soil

Species	Country	Habitat or soil type	References
Phialophora americana	China	ND	Song et al. (2021)
P. chinensis		ND	
P. macrospora		ND	
P. biformis	Japan	Forest soil	Domsch et al. (1993)
P. cinerescens	Sardinia	Soil under oaks	
P. cyclaminis	Germany and the Netherlands	Agricultural soil	

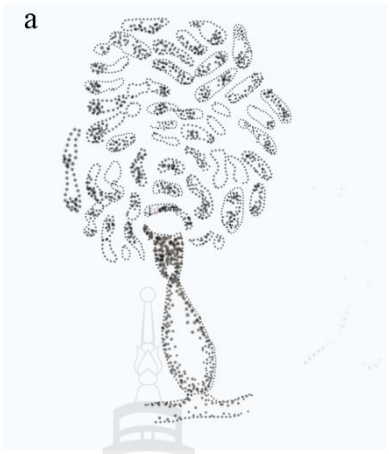


Figure 4.83 *Phialophora verrucosa* (CDC B1757)

Figure 4.83, Redrawn from Zweibel & Wang (1977).

Rhinocladiella Nannf., Svensk Skogsvårdsfören. Tidskr., Häfte 32: 461. 1934.

Figure 4.84

IndexFungorum: IF 9720, Facesoffungi: FoF 10382

Rhinocladiella was established by Melin & Nannfeldt (1934) designating *R. atrovirens* as the type species. *Rhinocladiella* contains 20 species (Hyde et al., 2024c), while 13 have been provided with molecular data. Based on the combined ITS and LSU sequence data, Arzanlou et al. (2007) placed *Rhinocladiella* in *Herpotrichiellaceae*. The asexual morph is characterized by the conidial apparatus, usually branched, olivaceous-brown, consisting of either slightly differentiated tips of ascending hyphae or septa, markedly differentiated conidiophores and intercalary or terminal, polyblastic, cylindrical to acicular, conidiogenous cells. Conidia are sympodially proliferating, solitary, hyaline to subhyaline, aseptate, thin-walled, smooth, subglobose and with subdenticulate rachis (Melin & Nannfeldt, 1934; Arzanlou et al., 2007). *Rhinocladiella* has been found in various hosts including herbaceous and decaying plant parts, human clinical samples, soil and submerged woods. Some members are known as human and plant pathogens. They are distributed in China, Costa Rica, Japan, Madagascar, Russia, Saudi Arabia, Spain, South Africa and Sweden associated with herbaceous and decaying plant parts, human clinical samples, soil and submerged wood (Arzanlou et al., 2007; Roeun et al., 2022).

Table 4.78 *Rhinocladiella* species isolated from soil

Species	Country	Habitat or soil type	References
Rhinocladiella anceps	Canada	soil under *Thuja plicata*	Arzanlou et al. (2007)
R. phaeophora	Colombia	ND	
R. terrigenum	Korea	rhizosphere soil of *Robinia pseudoacacia*	Roeun et al. (2022)
R. tibetensis	China	Everglade soil	Domsch et al. (2007)
R. vesiculosa	Russia	ND	

Figure 4.84 *Rhinocladiella atrovirens*

Figure 4.84, a. Conidia and condiogenous rachids. Scale bars: a = 10 μm. Redrawn from Tsuneda et al. (1986)

Veronaea Cif. & Montemart., Atti Ist. bot. Univ. Lab. crittog. Pavia, sér. 5 15: 68 (1957)

Figure 4.85

IndexFungorum: IF 10387; Facesoffungi: FoF 10386;

Veronaea was established by R. Ciferri and A. Montemartini in 1958, and *V. botryose* is designated as the type species (Ellis, 1971; Arzanlou et al., 2007). Currently, 21 species are listed in the genus (Species Fungorum, 2025), however, only five species have molecular data. Arzanlou et al. (2007) resolved the phylogenetic misconception that remained among *Cladosporium*, *Ramichloridium*, *Rhinocladiella* and *Veronaea* by providing a stable phylogeny with the combined LSU and ITS data. *Veronaea* produces

hyphomycetous asexual morphs, with erect, straight or flexuose, unbranched or occasionally loosely branched, sometimes geniculate, smooth-walled, pale to medium- or olivaceous-brown conidiophores. Conidiogenesis cells are terminally integrated, polyblastic, occasionally intercalary, cylindrical, pale brown, often becoming septate and fertile part subhyaline, and solitary, smooth, pale brown, cylindrical to pyriform, 1(–2)-septate conidia, that are rounded at the apex and truncate at the base. Species have been isolated from India, Japan, and South Africa from dead bamboo clumps and wood materials, leaves, dung soil and submerged wood (Arzanlou et al., 2007).

Table 4.79 *Veronaea* species isolated from soil

Species	Country	Habitat or soil type	References
Veronaea botryose	Egypt	Sandy loam soil	Su et al. (2023)
V. compacta	South Africa	ND	Arzanlou et al. (2007)
V. gobica	China	Yellow River source area	Pan et al. (2008)
V. simplex	South Africa	mixed *Acacia karroo* field	Papendorf (1969b)

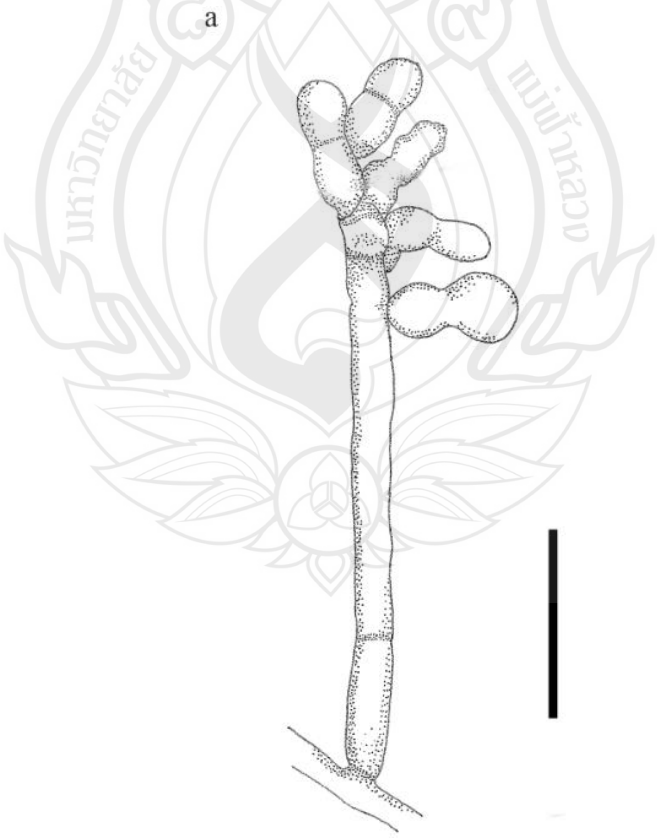


Figure 4.85 *Veronaea botryose* (CBS 254.57)

Figure 4.85, a Conidiogenesis on the conidiophores. Scale bar: a = 10 μm. Redrawn from Arzanlou et al. (2007)

Subclass: *Eurotiomycetidae* Geiser & Lutzoni

Order: *Eurotiales* G.W. Martin ex Benny & Kimbr.

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

Aspergillus P. Micheli, Nov. pl. gen. (Florentiae): 212, tab. 92 (1729)

Figure 4.86

IndexFungorum: IF39019; Facesoffungi: FoF16659

Aspergillus was named by Micheli in 1729. Subsequently, the first major monograph of *Aspergillus* was published by Tom and Church in 1926 (Bennett, 2007). The type species is *Aspergillus flavus* (Raper, 1965), and Visagie et al. (2024) have accepted 453 species within the genus, including 6 subgenera, 28 sections and 88 series, while providing a phylogenetic revision of *Eurotiales* based on ITS, *rpb2*, *tub2*, BenA, cmdA and LSU sequence data. Further, Visagie et al. (2024) suggested that morphology, extrolite (secondary metabolite) profiling, and whole-genome sequencing can be effectively used in resolving this order. Steenwyk et al. (2024) have used phylogenomics to study *Aspergillus* while suggesting to use this method for species identification in the future. Their study also revealed extensive strain misidentification within *Aspergillus*. The asexual morph of the genus is characterized by erect conidiophores that terminate in a palisade-like layer of phialides or subtending cells with whorls of phialides. Subsequently, metulae and phialides are blown out, and biseptal chains of conidia are produced (Domsch et al., 1980). *Aspergillus* species are globally reported across various hosts and substrates, including air, aquatic environments, dung, human tissues, plants and soil, functioning mostly as pathogens and saprobes (Bennett, 2007). These fungi are able to produce useful extracellular enzymes, organic acids and secondary metabolites that are important in medical, agricultural, and biotechnological industries (Bennett, 2007). For example, *Aspergillus fumigatus* and *A. flavus* are pathogenic and produce mycotoxins, while *A. niger* is utilized in industrial applications, and *A. oryzae* is useful in producing fermented foods (Nierman et al., 2005; Steenwyk et al., 2024).

Table 4.80 *Aspergillus* species isolated from soil

Species	Country	Habitat or soil type	References
Aspergillus agricola	USA	ND	Visagie et al. (2024b)
A. alboluteus	Botswana		
A. banksianus	Australia		
A. barbosae	Brazil		

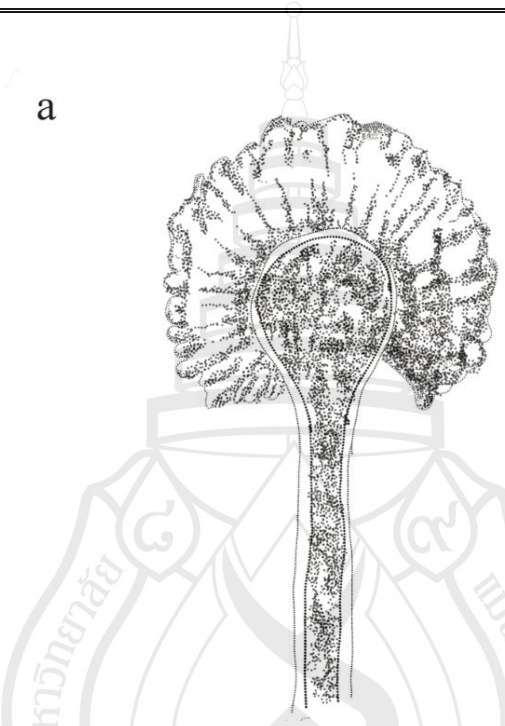


Figure 4.86 *Aspergillus flavus*

Figure 4.86, a Conidiophore with conidial head. Redrawn from Domsch et al. (1993).

Hamigera Stolk & Samson, Persoonia 6(3): 342 (1971)

IndexFungorum: IF 2215; Facesoffungi: FoF16660

Stolk and Samson (1971) introduced *Hamigera* and designated *Hamigera avellanea* as the type species. Subsequently, Peterson et al. (2010) introduced six species using combined morphology and phylogeny. Currently, nine species are listed in the genus (Species Fungorum, 2025) and all of them have molecular data. The asexual morph is *Penicillium*-like, and the sexual morph is soft, globose to subglobose, superficial, discrete and confluent ascomata, covered with interwoven hyphae. Asci are evanescent, 8-spored, subglobose to ellipsoid to clavate, stalked, and formed singly

from croziers, and ascospores are yellowish, ellipsoid with different ornamentations (Stolk & Samson, 1971). Species have been isolated from air, dung, insects, soil and textile materials in Australia, France, Poland and Togo (Peterson et al., 2010).

Table 4.81 *Hamigera* species isolated from soil

Species	Country	Habitat or soil type	References
Hamigera avellanea	USA	ND	Peterson et al. (2010)
H. fusca	Australia and The Comoros	Phenol-treated soil	
H. inflate	Gran Canaria Island	ND	
H. pallida	Togo	Phenol-treated soil	
H. paravellanea	Poland	ND	
H. terricola	France and Equatorial Guinea	Phenol-treated soil	

Penicillium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1-2): 16 (1809)

Figure 4.87

IndexFungorum: IF 9257; Facesoffungi: FoF 12565)

Penicillium was introduced by Link (1809), and the type species is designated as *P. expansum.* Based on the combined ITS, *rpb2, tub2*, BenA, cmdA and LSU phylogeny for *Eurotiales* taxa, Visagie et al. (2024) have accepted 553 species in the genus, classified into two subgenera, 32 sections, and 101 series These species are widely distributed in air, indoors, soil and vegetation; and can be found as saprobes or pre-or post-harvest pathogens on food crops (Frisvad & Samson, 2004; Visagie et al., 2014). Some of them have the ability to produce mycotoxins, whereas several species are exploited for producing cheese, fermented food and medical products (Frisvad & Samson, 2004; Samson et al., 2010; Visagie et al., 2014).

Table 4.82 *Penicillium* species isolated from soil

Species	Country	Habitat or soil type	References
Penicillium umkhoba	South africa	ND	Visagie et al. (2024b)
P. uttarakhandense	India	ND	
P. vaccaeorum	Argentina)	ND	
P. melanosporum	Spain	ND	Rodríguez-Andrade
P. siccitolerans		ND	et al. (2021b)
P. sexuale		ND	
P. aurantioviolaceum	Korea	Rhizosphere soil	Park et al. (2020)
P. bissettii			
P. cairnsense			
P. halotolerans			
P. kananaskense			
P. ortum			
P. radiatolobatum			
P. verhagenii			
P. anatolicum	Turkey	ND	Kirichuk et al.
P. argentinense	Congo	Latosol soil	(2017).
P. atrovenetum	England	ND	
P. attenuatum	Russia	Subaqueous soil	
P. canescens	England	ND	
P. cairnsense	Australia	ND	
P. christenseniae	Costa Rica	Forest	
P. chrzaszczii	Poland	forest)	
P. daleae	Poland	Soil under pine tree	
P. gorlenkoanum	Syria	ND	
P. hetheringtonii	USA	ND	
P. janczewskii	England	ND	
P. melinii	USA	Forest	
P. miczynskii	Poland	Soil under conifer	
P. murcianum	Spain	Sandy soil	
P. neomiczynskii	New Zealand	ND	
P. nothofagi	Chile	Soil under *Nothofagus*	
P. ochotense	Russia	Subaqueous soil	
P. pancosmium	Tunisia	ND	
P. piltunense	Russia	Subaqueous soil	
P. raphiae	Costa Rica	Primary forest	
P. sanguifluum	Spain	Soil under pine tree	

Table 4.82 (continued)

Species	Country	Habitat or soil type	References
P. sumatrense	Syria	Soil under cornel	
P. tropicoides	Thailand	Rainforest, soil	
P. tropicum	India	Soil beneath *Coffea arabica*	
P. ubiquetum	Costa Rica	A botanical garden	
P. waksmanii	Poland	Forest	
P. wellingtonense	New Zealand	ND	
P. westlingii	Poland	Soil under conifer	

Figure 4.87 *Penicillium expansum* (CBS 146.45)

Figure 4.87, a Conidiophore and conidia. Scale bar: X200. Redrawn from Domsch et al. (1993)

Family: *Thermoascaceae* Apinis

Paecilomyces Bainier, Bull. Soc. mycol. Fr. 23(1): 26 (1907)

Figure 4.88

IndexFungorum: IF 9196; Facesoffungi: FoF16661

Bainier (1907) introduced *Paecilomyces* while designating *P. variotii* as the type species. There are 16 species listed in the genus and all are supported with molecular data (Visagie et al. 2024a). The genus has hyphomycetous asexual morphs with verticillate conidiophores that have divergent whorls of phialides, with a cylindrical or inflated base tapering into a long and distinct neck. Conidia are hyaline, one-celled, smooth-walled, and produced in basipetal chains (He et al., 2011). *Paecilomyces* is ubiquitous and found in Australia, Brazil, China, France, Japan, South Africa and the Netherlands from the hosts including air, composts, food products, soil, and wood (Visagie et al., 2024a). They can be pathogenic to plants, animals, insects, and humans or the saprobic mode can be found on plants and food (Dong et al., 2012; Li et al., 2020c; Monpierre et al., 2022; Urquhart & Idnurm, 2023). Some species have industrial uses in agriculture and medical fields (Li et al., 2020c), while others are important as biological control agents (Dong et al., 2012).

Table 4.83 *Paecilomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Paecilomyces formosus	Japan	ND	Visagie et al. (2024a)
P. maximus	Thailand	Pineapple field	
Paecilomyces wawuensis	China	ND	He et al. (2011)

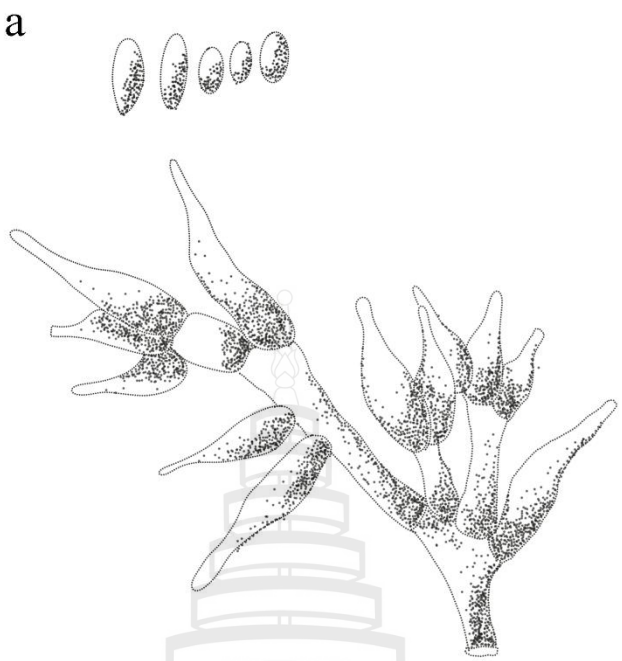


Figure 4.88 *Paecilomyces variotii*

Figure 4.88, a Conidiophore and conidia. Redrawn from Domsch et al. (1993).

Thermoascus Miehe, Selbsterhitz. Heus: 70 (1907)

Figure 4.89

IndexFungorum: IF 5446; Facesoffungi: FoF16662

Miehe (1907) introduced *Thermoascus* with its type species *T. aurantiacus.* The genus comprises seven species Species Fungorum (2025), all of which are supported with molecular data. The asexual morph is characterized by hyaline, clavate to somewhat spindle-shaped, aseptate or septate conidia that are terminal, on shorter or longer branches. The sexual morph has a superficial, cream, orange-yellow to brown, globose to irregular, relatively small, solitary or confluent ascocarp with peridium that has an outer layer of larger, hyaline to yellow-brown pseudoparenchymatous cells and an inner layer of smaller pseudoparenchymatous cells. Asci are formed in small clusters and are enclosed in an irregularly thick peridium, subglobose to oval, evanescent and 8-spored with ascospores that are hyaline or slightly yellow, non-septate and oval or elliptical (Apinis, 1967; Miehe, 1907). *Thermoascus* has been isolated from dead wood, mushroom-compost, sawdust, soil, stored grains and tobacco from Germany, Holland, India, Russia, Netherlands and the USA (Salar & Aneja, 2007).

Table 4.84 *Thermoascus* species isolated from soil

Species	Country	Habitat or soil type	References
Thermoascus aurantiacus	ND	ND	Salar and Aneja (2007)
T. yaguchii	China	ND	Yaguchi et al. (1995)

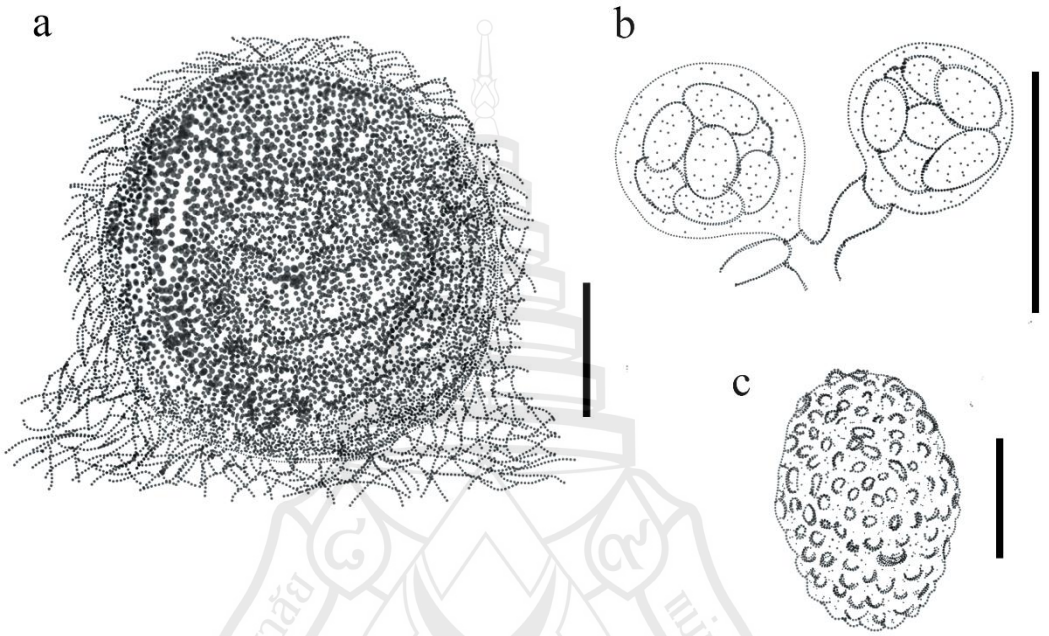


Figure 4.89 *Thermoascus sp.*

Figure 4.89, a Ascoma. b Ascus. *T. aurantiacus* c Ascospore. Scale bars a = 100 μm. b = 10 μm . c = 2.5 μm. Redrawn from Domsch et al. (1993)

Family: *Trichocomaceae* E. Fisch.

Sagenomella W. Gams, Persoonia 10(1): 100 (1978)

Figure 4.90

IndexFungorum: IF 9773; Facesoffungi: FoF16663

Gams (1978) introduced *Sagenomella* and placed *S. diversispora* as the type species. Currently, there are nine *Sagenomella* species included (Species Fungorum 2025), and all of them have been provided with molecular data. The asexual morph is characterized by the micronematous, erect conidiophores, terminal, simple phialides or rarely bearing several whorls of phialides. Phialides are aculeate, often centrally swollen, and in old cultures, they are often sympodially proliferating. Conidia are one-celled, hyaline, or with pigmented incrustations and ornamentations, with long or short

chains, with connectives on both ends (Gams, 1978). *Sagenomella* has been found in fodder, roots, and soil in Canada, Sweden, Spain, the Netherlands and the USA, while some species cause diseases in animals and humans (Gams, 1978; Malewski et al., 2023).

Table 4.85 *Sagenomella* species isolated from soil

Species	Country	Habitat or soil type	References
Sagenomella alba	Sweden	Forest soil	Sigler et al. (2010)
S. humicola	Canada	ND	
S. ocotl	Mexico	Heat-treated soil	
S. griseoviridis	Canada	ND	
S. oligospora	Sweden	agricultural soil	
S. verticillata	Canada	Argentina	Gams (1978)

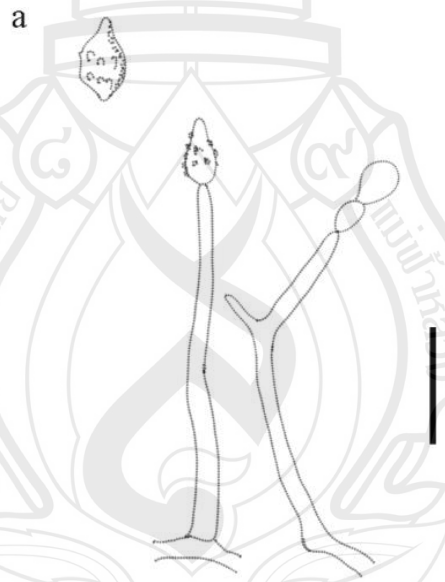


Figure 4.90 *Sagenomella diversispora* (CBS 354.36)

Figure 4.90, a Conidiophores with phialides and conidia. Scale bar: X3000. Redrawn from Domsch et al. (1993)

Talaromyces C.R. Benj., Mycologia 47(5): 681 (1955)

IndexFungorum: IF 5347; Facesoffungi: FoF16664

Benjamin (1955) introduced *Talaromyces* as the teleomorph of the *Penicillium* species and typified with *T. vermiculatus.* Based on the phylogenetic analyses of Visagie et al. (2024), 203 species are accepted in the genus. The asexual morph has

smooth or rough-walled conidiophores, symmetrically bi-verticillate, with a minor proportion having subterminal branches, monoverticillate, or with solitary phialides. They are typically acerose, rarely flask-shaped, with conidiogenous cells that produce aseptate, green masse, in basipetal chains, usually ellipsoidal to fusiform, rarely globose to subglobose, or ovoidal conidia. The sexual morph is characterized by cleistothecial, usually with a distinctly hyphal exterior soft wall, often yellow, occasionally white, creamish, pinkish, orange, reddish or green ascomata. Asci are produced in chains, 8-spored or rarely two-spored, and ascospores are hyaline to yellow, occasionally red, one-celled, ellipsoidal to globose, often with spines and/or less common ridges and rarely smooth-walled (Benjamin, 1955; Yilmaz et al., 2014). They are isolated from decaying wood, house dust, soil and weathering canvas (Yilmaz et al., 2014). Species are widely distributed including Australia, Asia, Europe and American regions. Some species are pathogenic to humans and cause mycosis in immunocompromised individuals, while several species produce mycotoxins in food products (Sigler et al., 1996; Richer et al., 1997; Yilmaz et al., 2014). Besides, *T. flavus* is used as a bio-control agent against soil-borne fungal pathogens, and some species are utilized in producing enzymes and soluble pigments (Gohel et al., 2006; Reyes et al., 1999).

Table 4.86 *Talaromyces* species isolated from soil

Species	Country	Habitat or soil type	References
Talaromyces gaditanus	Denmark	ND	Visagie et al. (2024b)
T. chongqingensis	China	ND	
T. pernambucoensis	Brazil	ND	
T. dimorphus	China	ND	Jiang et al. (2018a)
T. lentulus		ND	
T. mae		ND	
T. thailandensis	Thailand	ND	Manoch et al. (2013)
T. tratensis		ND	
T. purpurogenus	Korea	Soil in agricultural fields	Adhikari et al. (2015)
T. trachyspermus			

Order: *Onygenales* Cif. ex Benny & Kimbr.

Family: *Ajellomycetaceae* Unter., J.A. Scott & Sigler

Blastomyces Gilchrist & W.R. Stokes, J. Exp. Med. 3: 76 (1898) (=*Ajellomyces* McDonough & A.L Lewis; Emmonsia Cif. & Montemart.)

IndexFungorum: IF7389; Facesoffungi: FoF16665

Blastomyces was introduced by Gilchrist and Stokes (1898) with the type species, *B. dermatitidi*. The genus comprises nine species (Species Fungorum, 2025), and six of them have molecular data. Jiang et al. (2018) revised the phylogenetic relationships of the family *Ajellomycetaceae* using the combined ITS, LSU *rpb2, tub2* and *tef*3 phylogeny, while accommodating new species in the *Blastomyces*. The asexual morph of *Blastomyces* has conidiophores that are arising at right angles from the vegetative hyphae, narrow and unbranched; and sometimes with secondary conidiophores, arising from a swollen tip. Conidia form at the tip or on the sides of conidiophores, or sessile on vegetative hyphae with rhexolytic dehiscence and they can be solitary aleurioconidia or irregular alternate athroconidia. The sexual morph is characterized by spherical ascomata with coiled appendages and muricate spherical or oblate ascospores (Guarro et al., 2012; Jiang et al., 2018b; Kandemir et al., 2022). The sexual state of *B. dermatitidis* causes humans and canine blastomycosis and has also been recorded as pathogen in vertebrates. *Blastomyces* is mainly found in human clinical samples, including the brain, lungs and skin (Jiang et al., 2018b), while some of them have been isolated from the soil (Guarro et al., 2012). Species are distributed in Canada, Iraq, South Africa and the USA (Jiang et al., 2018b).

Table 4.87 *Blastomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Blastomyces dermatitidis	USA	ND	Klein et al. (1986)
B. parvus	Canada	ND	Jiang et al. (2018b)
B. silverae	Canada	ND	

Emergomyces Dukik, Sigler & de Hoog, Mycoses 60: 304 (2017)

IndexFungorum: IF818569; Facesoffungi: FoF16666

Emergomyces was established by Dukik et al. (2017) and typified by *E. pasteurianus*. Kandemir et al. (2022) have accepted seven *Emergomyces* species and

all of them are supported with molecular data. The combined ITS, LSU, *rpb2*, *tub*2 and *tef*3, analyses of *Ajellomycetaceae* by Jiang et al. (2018b) have transferred four *Emmonsia* species to this genus. The asexual morph has short and unbranched conidiophores, slightly swollen at the top, arising at right angles from vegetative hyphae; and holothallic on short-stalked conidia. The sexual morph remains unknown (Jiang et al., 2018b). The genus has been recorded as human pathogens isolated from human blood samples, lungs and skin, and some species are occurring on air and soil (Jiang et al., 2018b). They have been found in Canada, China, Germany, Italy and South Africa (Jiang et al., 2020; Kandemir et al.. 2022).

Table 4.88 *Emergomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Emergomyces soli	USA		Jiang et al. (2020)

Emmonsiellopsis Y. Marín, Stchigel, Guarro & Cano, Mycoses 58(8): 455 (2015)

Figure 4.91

IndexFungorum: IF811334; Facesofungi number: FoF16667

Emmonsiellopsis was introduced by Marin-Felix et al. (2015) based on morpho-molecular (ITS and LSU) analyses, and is typified by *E. terrestris*. Currently, three *Emmonsiellopsis* species are listed in the Species Fungorum (2025), and all the species have molecular data. The asexual morph is characterized by hyaline, globose to ovoid or clavate, smooth-walled and verrucose or spinulose, thick-walled, rarely 1-septate, sessile, blastic conidia born laterally or terminally on the hyphae, or on pedicels, solitary or in chains of two conidia, rarely intercalary; and hyaline, short or long, smooth- and thin-walled pedicels inflated at the middle or at the apex. The sexual morph and yeast-like morph are not recorded within the genus. *Emmonsiellopsis* is separable from other family members by the absence of thermal dimorphism (Marin-Felix et al., 2015). These species are found in Spain and USA and they are known for their geophilic nature that have been isolated from sediments and soil (Jiang et al., 2018b; Marin-Felix et al., 2015).

Table 4.89 *Emmonsiellopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Emmonsiellopsis coralliformis	Spain	ND	Jiang et al. (2020)
E. terrestris	USA	ND	Marin-Felix et al. (2015)

Figure 4.91 *Emmonsiellopsis terrestris* (CBS 273.77)

Figure 4.91, a Conidia on inflated pedicels. Scale bar = 5 μm. Redrawn from Marin-Felix et al. (2015)

Family: ***Arthrodermataceae*** Currah

Arthroderma Curr., Outl. Brit. Fung. (London): 357 (1860)

Figure 4.92

IndexFungorum: IF335; Facesofungi number: FoF16676

Arthroderma was introduced in Berkeley (1860) with the type species *A. curreyi.* It was later revised by Currah (1985), and currently, the genus comprises 45 taxa (Hyde et al., 2024c), among which 31 species have molecular data. The asexual morph is *Chrysosporium* like and the sexual morphs have gymnothecia, typically with arched hyphal appendages, slightly curved at the apices. The genus has been discovered in Brazil, Canada, the Czech Republic, Germany, Japan, the Netherlands, the UK and the USA from various hosts including air, animal burrows, caves, fur, hair, clinical materials and soil. Some of the species are known as dermatophytes causing human and animal superficial infections (Hainsworth et al., 2021).

Table 4.90 *Arthroderma* species isolated from soil

Species	Country	Habitat or soil type	References
Arthroderma chinense	China	karst cave	Kandemir et al.
A. curreyi	UK	dune soil	(2022)
A. kuzurovia	Russia	black soil	
A. ciferrii	USA	ND	Moulíková et al.
A. crocatum	Japan and the Netherland	ND	(2023)
A. cuniculi	UK	soil from rabbit burrows	
A. gertleri	Germany	ND	
A. gloriae	USA	ND	
A. insingulare	Canada	farm soil	
A. lenticulare	USA	soil from gopher hole	
A. multifidum	UK	soil from rabbit burrow	
A. simile	USA	soil from bat hibernaculum	
A. terrestre	Australia	ND	
A. tuberculatum	India	ND	
A. uncinatum	USA	ND	

Figure 4.92 *Arthroderma curreyi*

Figure 4.92, a Conidia on inflated pedicels. Scale bar = 5 μm. Redrawn from Guarro et al. (2012)

Ctenomyces Eidam, Beitr. Biol. Pfl. 3: 274 (1880)

Figure 4.93

IndexFungorum: IF1342; Facesofungi number: FoF16677

Eidam (1880) introduced *Ctenomyces*, designating *C. serratus* as the type species. Based on the ITS phylogeny for *Arthrodermataceae*, Kandemir et al. (2022) revised the genus and currently, 11 species are included in the genus (Hyde et al., 2024c), while eight of them have molecular data. The asexual morph has verrucose, thick-walled, and lightly pigmented conidia, typically with ampulliform swelling that are borne terminally and laterally on hyphae (Zhang et al., 2019c). The sexual morph has orange-brown cleistothecia, a peridium formed from a thin layer of densely interwoven hyphae and ctenoid appendages consisting of thick-walled, asperulate cells. This ascomal appendage is considered to be helpful for the attachment to animal surfaces (Currah, 1985). Most of the species are keratinophilic, however, the pathogenic state is not reported. *Ctenomyces* are associated with bird feathers, hair, human speciemens and soil in China, Germany, and India. Some of the species have been isolated by the baiting techniques using chicken feathers and human hair (Currah, 1985; Zhang et al., 2019c).

Table 4.91 *Ctenomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Ctenomyces serratus	Australia	Soils associated with birds	Frey and Griffin (1961)
C. vellereus	Egypt	ND	Kandemir et al. (2022)
C. albus	China	ND	Zhang et al. (2019c)
C. obovatus	China	ND	
C. peltricolor	China	ND	

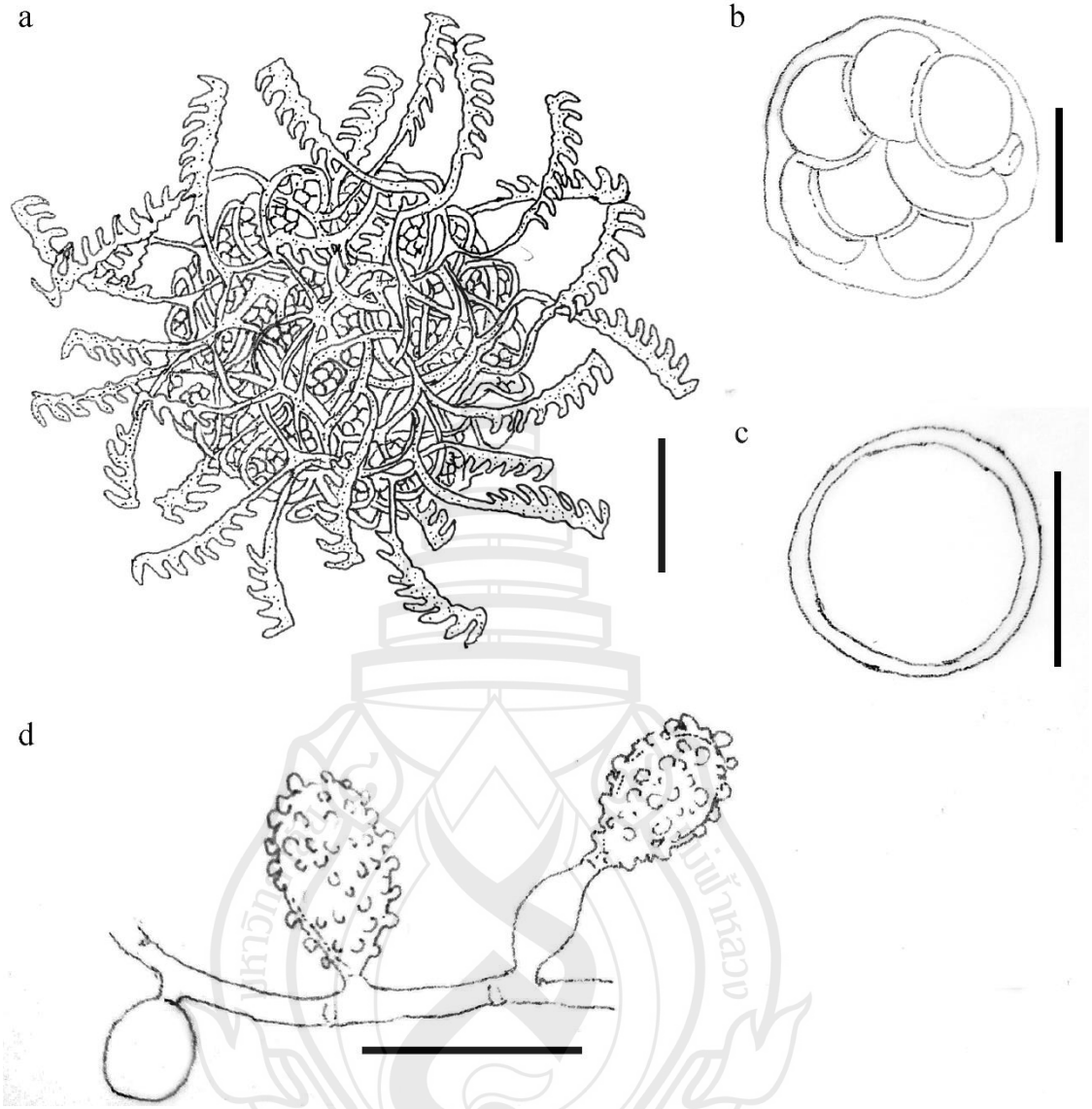


Figure 4.93 *Ctenomyces serratus*

Figure 4.93, a. Ascoma. b.Ascus. c. Ascospore. d. Conidiogensis. Scale bars a = 100 μm, d = 10 μm, b, c = 5 μm. Redrawn from Guarro et al. (2012).

Microsporum Gruby, C. r. hebd. Séanc. Acad. Sci., Paris 17: 302 (1843)

IndexFungorum: IF8939

Microsporum is introduced by Gruby (1843) with the type species *M. audouinii.* It accommodates 19 species (Species Fungorum, 2025), and three have been provided with molecular data. Kandemir et al. (2022) have provided ITS based phylogeny for *Arthrodermataceae* while transferring *Microsporum guizhouense* to *Nannizzia.* These species have been isolated from the skin and scalp of humans and monkeys, while

several species have been reported from dung, freshwater habitats, feathers, nests and soil (de Hoog et al., 2017; Kandemir et al., 2022). *Microsporum canis* has been reported to cause skin infections in cats (Newbury et al., 2015). Geographically they can be found in Czechoslovakia, the Czech Republic, France and India (Newbury et al., 2015; Kandemir et al., 2022).

Table 4.92 *Microsporum* species isolated from soil

Species	Country	Habitat or soil type	References
Microsporum gypseum	ND	ND	Gordon (1953)
M. canis	Iran	Area with a semi-desert climate	Rezaei-Matehkolaei et al.
M. gypseum	Iran		(2017)

Nannizzia Stockdale, Sabouraudia 1: 45 (1961)

Figure 4.94

IndexFungorum: IF3420; Facesofungi number: FoF16678

The genus *Nannizzia* was erected by Stockdale and Phyllis (1961) and typified with *N. incurvata*. The ITS phylogeny of *Arthrodermataceae* provided by Kandemir et al. (2022) includes 14 *Nannizzia* species. Currently, there are 16 species listed in the Species Fungorum (2025), and all of which are supported with molecular data. The asexual morph has multi-septate, thin- to relatively thick-walled, ornamented macroconidia. The sexual morph produces gymnothecia formed by spirally twisted, peridial hyphae, composed of ossiform cells with spherical, evanescent asci, and one-celled, lenticular ascospores. *Nannizzia* is keratinophilic, which can occur on human hair, nails, skin, soil and warm-blooded animals in China, Denmark, India, Somalia and Venezuela (Kandemir et al., 2022).

Table 4.93 *Nannizzia* species isolated from soil

Species	Country	Habitat or soil type	References
Nannizzia sinensis	China	Soil from a hospital	Zhang et al. (2023e)
N. corniculata	Somalia	ND	Dukik et al. (2020)
N. graeserae	India	ND	

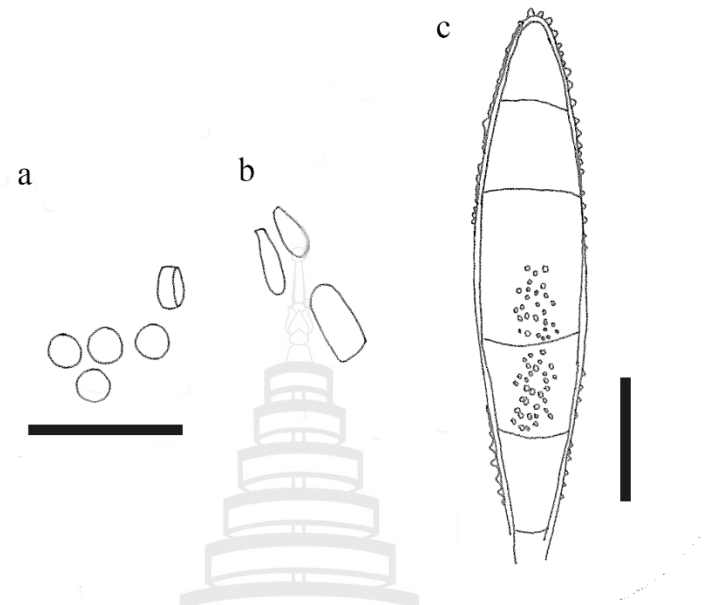


Figure 4.94 *Nannizzia incurvata* (CBS 173.64)

Figure 4.94, a. Ascospores. b. Micro-conidia. c. Macroconidium. Scale bar X1000. The images are redrawn from Domsch et al. (1980).

Trichophyton Malmsten, Arch. Anat. Physiol. Wiss. Med., 1848: 14 (1848)

IndexFungorum: IF 10292; Facesofungi number: FoF16679

Malmsten (1848) introduced *Trichophyton* with its type species, *T. tonsurans*. There are 143 species currently present in *Trichophyton* (Hyde et al., 2024c). It is a keratinophilic genus that has been isolated from human clinical samples and soil habitats (Durie & Frey, 1957) in Australia, Brazil, Canada, Denmark, France, Iran, Japan, Sudan and Venezuela (Čmoková et al., 2021). Species cause superficial and systemic infections in humans and animals as well (Kumar et al., 2023; Pchelin et al., 2016).

Table 4.94 *Trichophyton* species isolated from soil

Species	Country	Habitat or soil type	References
Trichophyton indicum	India		Randhawa and Sandhu (1963)
T. phaseoliforme	Venezuela		

Family: *Gymnoascaceae* Baran.

Arachniotus J. Schröt., Krypt.-Fl. Schlesien (Breslau) 3.2: 210 (1893)

Figure 4.95

IndexFungorum: IF291; Facesofungi number: FoF16668

Arachniotus was erected by Schroeter (1893), accommodating *A. ruber* as the type species. The genus comprises 15 species (Hyde et al., 2024c). Kandemir et al. (2022) analysed the phylogenetic relationships of *Onygenales* based on the LSU phylogeny while placing four species in the genus. The asexual morph of the genus is characterized by arthroaleuriospores (Orr et al., 1977b). Kuehn and Orr (1959) described that this genus produces croziers and lacks conidia on phialides. The sexual morph possesses snow-white or yellowish gymnothecia; peridial elements are thin-walled, more or less uniform in diameter, similar to the vegetative hyphae, completely encasing the asci in a fragile membrane. Asci are ovoid to spherical, hyaline, evanescented, 8-spored and ascospores are hyaline, ovoid to ellipsoid and smooth-walled (Orr et al., 1977b). The genus is characterized by halotolerant members that are highly adapted to high salt contents. Thus, they have been isolated from cheese, marine water-sediment, saline soils, alkaline soils, dog and sheep dung recorded from the Soviet Union, UK and the USA. Further, studies showed that some *Arachniotus* species are unable to grow at 37°C (Kandemir et al., 2022).

Table 4.95 *Arachniotus* species isolated from soil

Species	Country	Habitat or soil type	References
Arachniotus ruber	UK	Alkaline or neutral soils	Orr et al. (1977b)
A. aurantiacus	Soviet Union	ND	Kandemir et al. (2022)
A. confuens	Kuwait	Halomorphic soil	

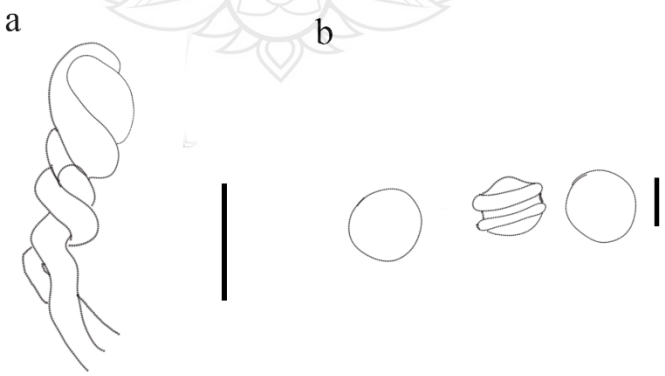


Figure 4.95 *Arachniotus ruber* (CBS 12.69)

Figure 4.95, a Ascogonial coil. b. Ascospores. Scale bar 2000X. Redrawn from Domsch et al. (1993).

Gymnascella Peck, Ann. Rep. N.Y. St. Mus. nat. Hist. 35: 143 (1884)

Figure 4.96

IndexFungorum: IF 2164; Facesofungi number: FoF16670

Peck (1884) accommodated *Gymnascella* with *G. aurantiaca* as the type species. Kandemir et al. (2022) have accepted 11 *Gymnascella* species based on the LSU phylogeny in *Gymnoascaceae.* All the species in the genus have molecular data. The asexual spores in *Gymnascella* are characterized by the arthroaleuriospore type that produces on hyphae (Orr et al., 1977). As described by Currah (1985) and Orr and Kuehn (1971), the sexual morph of *Gymnascella* has discrete ascocarps; coarsely verrucose, loose peridial elements around the asci with subspherical to ovoid, evanescent, 8-spored asci; and smooth, thick-walled, ovoid to oblate ascospores. Most of the species are associated with dung, compost and soil in China, France, India, Japan, the UK and the USA (Kandemir et al., 2022).

Table 4.96 *Gymnascella* species isolated from soil

Species	Country	Habitat or soil type	References
Gymnascella afilamentosa	USA	Clay soil	Currah (1985)
G. dankaliensis	India and USA	ND	
G. devroeyi	Belgium	ND	
Gymnascella citrina	USA	ND	Orr et al. (1977)
G. thermotolerans	China	Corn field soil	Kandemir et al. (2024)
G. udagawae	Japan	ND	Currah (1988)
G. aurantiaca	USA	Clay soil	Orr and Kuehn (1972)

Figure 4.96 *Gymnascella aurantiaca*

Figure 4.96, Ascospores. Redrawn from Orr et al. (1977)

Gymnoascoideus G.F. Orr, K. Roy & G.R. Ghosh, Mycotaxon 5(2): 460 (1977)

Index Fungorum number: IF 2166; Facesofungi number: FoF16671

Gymnoascoideus was introduced by Orr et al. (1977b) with *G. petalosporus* as the type species. Based on the LSU phylogeny treated to *Onygenales* by Kandemir et al. (2022), there are two species included in the genus. Both species have molecular data. *Gymnoascoideus* is distinct by its discrete gymnothecia that has typical elements with branching at right angles, blunt at the apices and covered by asexual spores in and around the ascal clusters. Ascospores are arranged in a petaloid pattern in the asci (Orr et al., 1977b; von Arx, 1971; Kandemir et al., 2022). These species prefer keratin substrates and are associated with feathers, horns, horse skin, human clinical samples and soil. Species have been isolated from Bolivia and India (Orr et al., 1977b; Kandemir et al.; 2022).

Table 4.97 *Gymnoascoideus* species isolated from soil

Species	Country	Habitat or soil type	References
Gymnoascoideus petalosporus	India	ND	Sur and Ghosh (1980)
G. boliviensis	Bolivia	Chicken yard	Kandemir et al. (2022)
G. verrucosus	India	Railway station	Sharma and Singh (2013)

Gymnoascus Baran., Bot. Ztg. 30: 158 (1872)

Figure 4.97

IndexFungorum: IF 2168; Facesofungi number: FoF16669

Baranetzky (1872) introduced *Gymnoascus* accommodating *G.reesii* as the type species. Phylogenetic revision on *Onygenales* based on the LSU gene region by Kandemir et al. (2022) has placed 11 species in the genus, while some of the *Gymnoascus* species were synonymized to *Arachniotus*, *Gymnascella*, *Gymnoascoideus* and *Narasimhella*. There are 11 species with molecular data, and four species do not have molecular data. The asexual morph of *Gymnoascus* produces chrysosporium-like conidia. The sexual morph possesses spherical, yellowish to brownish ascomata, and peridium formed from a loose network of hyaline or pigmented hyphae, with or without appendages, and oblate and pigmented ascospores (von Arx, 1971; Sharma & Singh, 2013; Solé et al., 2002; Zhou et al., 2016). Species have been

found in Guinea pigs and conch shells collected from India and Canada (Kandemir et al., 2022), while some have been isolated from soil habitats in Australia, Bangladesh, Germany, Italy, Japan, Pakistan, and the USA (Kandemir et al., 2022).

Table 4.98 *Gymnoascus* species isolated from soil

Species	Country	Habitat or soil type	References
Gymnoascus flavus	China	Karst cave	Zhang et al. (2021c)
G. longitrichus	USA	Composite soil	Kandemir et al. (2022)
G. intermedius	USA	ND	
G. dugwayensis	USA	Sandy soil	
G. longitrichus	Iran	Soil dune	Kandemir et al. (2024)

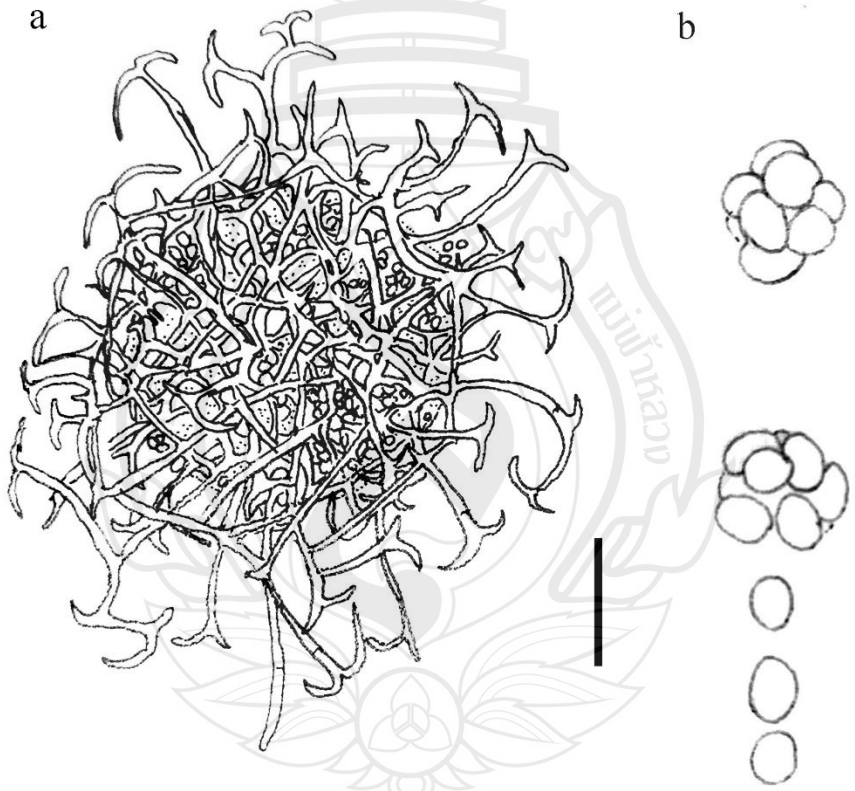


Figure 4.97 *Gymnoascus* sp.

Figure 4.97, a Ascomata Scale bar:a = 100. Redrawn from Guarro et al. (2012). *G.reesii* (CBS 497.64) b Asci and ascospores. Redrawn from Domsch et al. (1980).

Kraurogymnocarpa Udagawa & Uchiy., Mycoscience 40(3): 277 (1999)

Figure 4.98

IndexFungorum: IF28359; Facesoffungi number: FoF16672

Udagawa and Uchiyama (1999) introduced *Kraurogymnocarpa* by designating *K. lenticulospora* as the type species. Currently, only *K. trochleospora* has been accepted in this genus by Kandemir et al. (2022). This genus has been reported from sandy-clay and clay soils, which have higher water-holding capacities than most other soil types (Orr & Kuehn, 1972).

Table 4.99 *Kraurogymnocarpa* species isolated from soil

Species	Country	Habitat or soil type	References
Kraurogymnocarpa trochleospora	USA	ND	Udagawa and Uchiyama (2001)

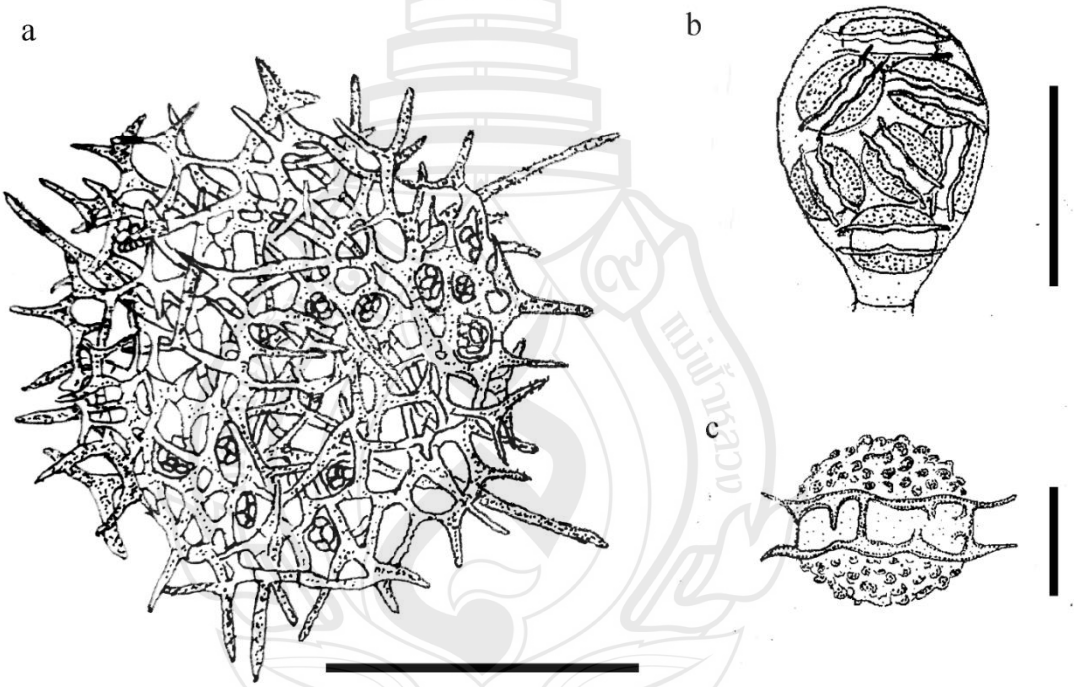


Figure 4.98 *Kraurogymnocarpa lenticulospora*

Figure 4.98, a. Ascomata. b. Ascus. c. Ascospores. a = 100 μm, b = 10 μm, c = 2.5 μm. Redrawn from Guarro et al. (2012)

Narasimhella Thirum. & P.N. Mathur, Sydowia 19(1-6): 184 (1966)

IndexFungorum: IF3425; Facesoffungi number: FoF16674

Narasimhella was introduced by Thirumalachar and Mathur (1966), accommodating *N. poonensis* as the type species. Kandemir et al. (2022) have accepted five species in this genus, and all of them have molecular data (LSU and ITS). The

sexual morph of the genus has well-developed, stipitate fruiting bodies, with a sterile stipe, composed of upwards-growing hyphae and irregularly globular, fertile head-bearing groups of asci (Thirumalachar & Mathur, 1966). It lacks a peridium and shows a crozier formation, similar to the *Pseudoarachniotus* species. von Arx (1971) reported that *Narasimhella* colonies produce synnema- or sporodochium-like structures with yellow, cinnamon or greenish colours. Unlike the other *Gymnoascaceae* members, this genus has been obtained from buried substrates, such as cables and fabrics in dung-enriched soil and rhizosphere soil in India and the USA. Thus, they have the potential to grow on hard-buried substrates in nutrient-rich soils (Kandemir et al., 2022).

Table 4.100 *Narasimhella* species isolated from soil

Species	Country	Habitat or soil type	References
Narasimhella poonensis	India	ND	Kandemir et al. (2022)
N. echinulata	India	Rice-feld	
N. punctata	India	Rice-feld	

Pseudoarachniotus Kuehn, Mycologia 49(5): 694 (1957)

IndexFungorum: IF4411; Facesoffungi number: FoF16673

Pseudoarachniotus was introduced by Kuehn (1957). Based on the LSU and ITS phylogeny of *Onygenales* by Kandemir et al. (2022), it was suggested that previously classified *Pseudoarachniotus* species, including the type species (*P. roseus*), were not related to this genus. As a result, they have been transferred to *Gymnascella,* and only *P. reticulatus* was accepted within *Pseudoarachniotus,* which is phylogenetically close to *Mallochia reticulate* (Kandemir et al., 2022). As suggested by Kandemir et al. (2022), further molecular analyses are required to resolve the remaining taxonomic ambiguities in *Pseudoarachniotus*. The asexual morph is unreported, and the sexual morph of *P. reticulatus* is characterized by absent ascocarps, red-capped hyphae among the tufts of asci, and globose to reticulate ascospores (von Arx, 1971; Kandemir et al., 2022). Studies recorded this species as non-oligotrophic and prefers higher nutritious soils (von Arx, 1971; Orr et al., 1971; Kandemir et al., 2022).

Table 4.101 *Pseudoarachniotus* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudoarachniotus reticulatus	USA	Rhizosphere soil of *Musa sapientum*	von Arx (1971), Kandemir et al. (2022)

Sporendonema Desm., Annls Sci. Nat., sér. 1 11: 246 (1827)

IndexFungorum: IF 10021; Facesoffungi number: FoF16675

Desmazières (1827) introduced *Sporendonema*, accommodating *S. casei* as the type species. The genus was previously subjected to controversies regarding its taxonomic position and the nomenclature. However, Kandemir et al. (2022) suggested its placement in the *Gymnoascaceae* based on the phylogeny. Subsequently, Kandemir et al. (2024) revised the genus using ITS and LSU gene regions while accepting six species in the genus. Species have been found in cheese, soil and dung in China, France, Kuwait and Russia (Kandemir et al., 2024).

Table 4.102 *Sporendonema* species isolated from soil

Species	Country	Habitat or soil type	References
Sporendonema aurantiacum	Russia	Semi-desert (slightly loam) soil	Kandemir et al. (2024)
S. rubrum	The Netherlands	Agricultural soil	
S. rubrum	UK	Alluvial pasture soil	
A. confluens	Kuwait	ND	Kuehn and Orr (1964)
Sporendonema rubrum	UK	ND	

Family: *Malbrancheacea* Kandemir & de Hoog

Malbranchea Sacc., Michelia 2(no. 8): 639 (1882);

Figure 4.99

Saccardo (1882) introduced *Malbranchea* with its type species *M. pulchella.* Rodríguez-Andrade et al. (2021a) revised the genus using combined ITS and LSU phylogeny, and synonymized *Auxarthron* with *Malbranchea*. Later, based on ITS, LSU, *tub2*, *tef*1-*α*, *tef3*, *rpb1*, *rpb2* gene regions and ribosomal protein 60S L10 (L1) (RP60S) sequences phylogeny, Kandemir et al. (2022) established *Malbrancheaceae* in order to accommodate *Malbranchea.* It currently comprises 37 species, and 28 are supported with molecular data. The asexual morph is characterized by the alternate,

hyaline arthroconidia produced in the curved branches from the vegetative hyphae. The sexual morph is originally described under *Auxarthron* (Hyde et al., 2024c; Kandemir et al., 2022) which has globose to less globose ascomata of yellow, orange or brown with thick-walled peridial hyphae, inverted Y-shaped arches produced from peripheral peridium that arise as short or elongate appendages, hyaline, subglobose, globose, or obovate, 8-spored, evanescent asci, and globose or ovoidal and asperulate to echinulate-reticulate ascospores (Orr et al., 1963). Some species are able to degrade keratin substrates and are found in eutrophic environments associated with animal dung and cave soil in Austria, China, France, India, Spain, the UK and the USA (Orr et al., 1963; Sarrocco et al., 2015; Zhang et al., 2021).

Table 4.103 *Malbranchea* species isolated from soil

Species	Country	Habitat or soil type	References
Malbranchea albolutea	USA	ND	Sigler and Carmichael (1976)
M. arcuata		ND	
M.chrysosporioidea		ND	
M. flavorosea		ND	
M. flocciformis	France	Briny soil	

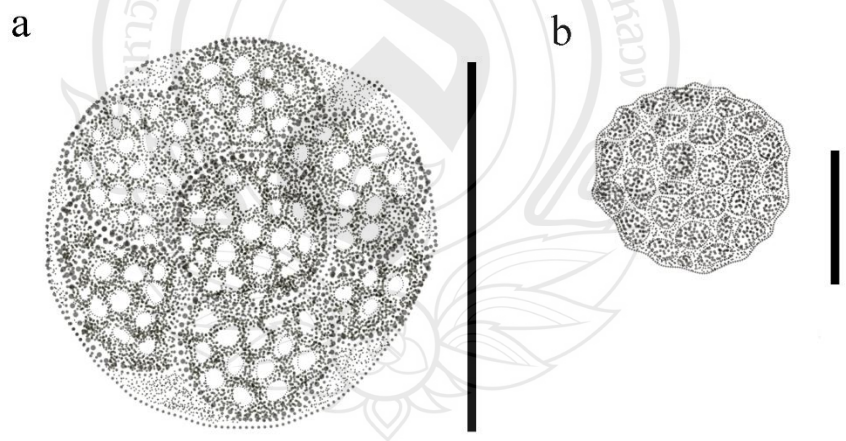


Figure 4.99 *Malbranchea* sp.

Figure 4.99, a Ascus. *M. californiense* b Ascuspore. Scale bars: a = 10 μm, b = 2.5 μm. Redrawn from Guarro et al. (2012)

Family: ***Neogymnomycetaceae*** Kandemir & de Hoog

Auxarthronopsis Rah. Sharma, Y. Gräser & S.K. Singh, IMA Fungus 4(1): 93 (2013)

IndexFungorum: IF563744; Facesoffungi number: FoF16690

Sharma et al. (2013) established *Auxarthronopsis* with its type species *A. bandhavgarhensis.* Previosuly, it was placed in *Onygenaceae* (Sharma et al., 2013), and later, based on the ITS phylogeny, Kandemir et al. (2022) transferred the genus to *Neogymnomycetaceae* with six accepted species. All the species have molecular data (ITS, LSU and *Btub*). The asexual morph has terminal and intercalary, hyaline arthroconidia and aleurioconidia. The sexual morph is characterized by solitary, globose to subglobose, white to pale cream ascomata, peridium made of a mesh of interwoven hyphae with swollen septa, and straight, sometimes branched appendages tapering at the apex, with multiple (≥10) swollen septa. The asci are globose to subglobose, hyaline, evanescent and 8-spored, and unicellular, hyaline, oblate ascospores with finely and regularly punctate walls (Sharma et al., 2013). Most of the species have saprobic life modes, and are distributed in animal dung, rocks, plant debris and soil in China and Thailand (Labuda et al., 2021; Sharma et al., 2013; Zhang et al., 2021c).

Table 4.104 *Auxarthronopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Auxarthronopsis bandhavgarhensis	India	ND	Sharma et al. (2013)
A. globiasca	China	Luotian Cave	Zhang et al. (2021c)

Canomyces Rahul Sharma & Shouche, Mycopathologia 185(1): 76 (2020)

Figure 4.100

IndexFungorum: IF829249; Facesoffungi number: FoF13278

Canomyces was introduced by Sharma & Shouche (2020) and typified by *C. reticulatus*. Kandemir et al. (2022) performed molecular analyses for *Onygenales*, describing this as a monotypic genus and transferring it from *Onygenaceae* to *Neogymnomycetacea*. The species have ITS and LSU molecular data. The asexual morph has narrow, elongated arthroconidia produced from hyphae. The sexual morph is characterized by solitary, globose, cream-coloured ascomata, the peridium formed with

loosely arranged hyphae, pale brown, globose, evanescent, 8-spored asci, and unicellular, pale cream to yellowish, regularly punctate-reticulate ascospores (Kandemir et al., 2022; Sharma & Shouche, 2020).

Table 4.105 *Canomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Canomyces reticulatus	India	ND	Sharma and Shouche (2020)

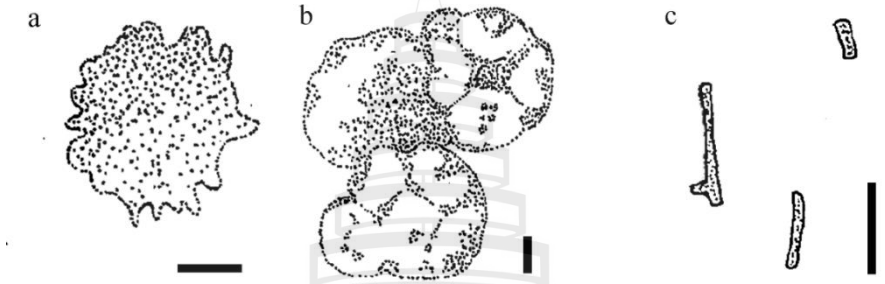


Figure 4.100 *Canomyces reticulatus* (MCC 1486)

Figure 4.100, a Ascomata. b Asci with ascospores. c Narrow elongated arthroconidia. Scale bars: a =100 μm, b = 2 μm, c = 10 μm. Redrawn from Sharma and Shouche (2020).

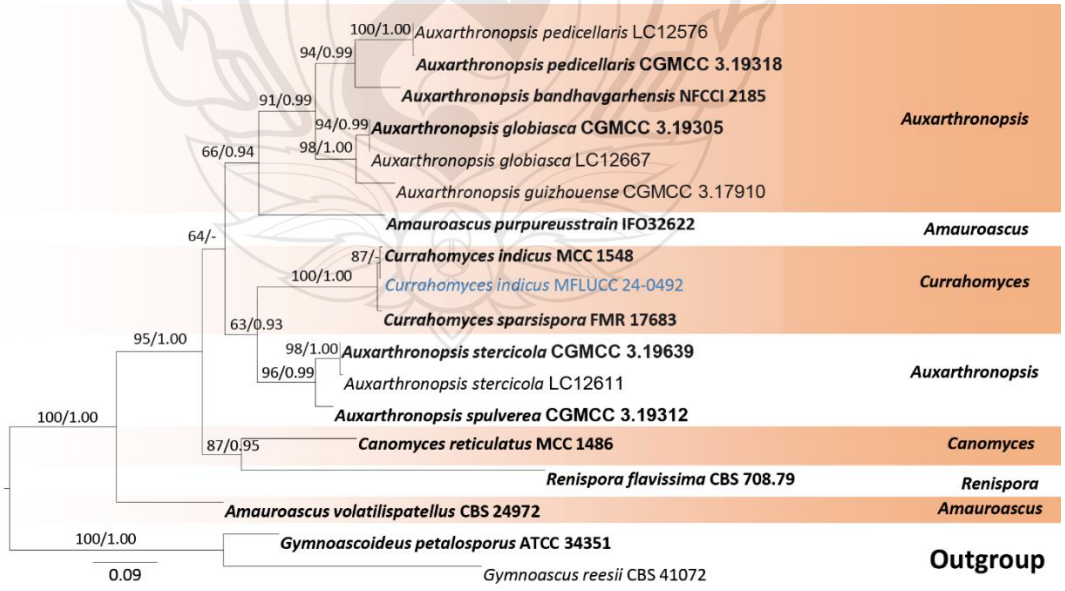


Figure 4.101 The best scoring maximum likelihood tree of the combined ITS sequence data for *Neogymnomycetaceae*

Figure 4.101, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue and ex-type strains are in bold. The tree is rooted to *Gymnoascoideus petalosporus* ATCC 34351 and *Gymnoascus reesii* CBS 41072. The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of ITS alignment is 683 bp. The matrix had 354 distinct alignment patterns with 13.99% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.00000, AG = 2.64528, AT = 2.05543, CG = 2.05543, CT = 5.62234, GT = 1.00000; gamma distribution shape parameter α = 1.131.

Currahomyces Rahul Sharma & Shouche [as 'Currahmyces'], Mycopathologia 185(1): 73 (2019)

Index Fungorum number: IF829247, Facesoffungi number: FoF16689.

Currahomyces was introduced by Sharma and Shouche (2020) based on the ITS and LSU sequences and morphological evidence, the type species is *C. indicus*. The phylogenetic revision using the ITS region conducted by Kandemir et al. (2022) has placed *Currahmyces* in *Neogymnomycetaceae* with two species (Kandemir et al., 2022). Currently, two species are listed in this genus (Species Fungorum 2025), and both have molecular data. The asexual morph has terminal and intercalary slender arthroconidia (Sharma & Shouche, 2020). The sexual morph is characterized by the solitary, globose to subglobose, white on the outer periphery and brown in the centre ascomata with a peridium wall having loosely arranged thin- to thick-walled asperulate, septate hyphae that are densely asperulate, towards margin covered with spine-like crystal structures. Asci are globose, brown, evanescent, 8-spored that contain ascospores characterized by unicellular, pale brown globose, with broadly punctate-reticulate walls (Sharma & Shouche, 2020).

Table 4.106 *Currahomyces* species isolated from soil

Species	Country	Habitat or soil type	References
C. indicus	India	ND	Sharma and Shouche (2020)

Currahomyces indicus Rahul Sharma & Shouche [as 'Currahmyces'], Mycopathologia 185(1): 76 (2019) [2020]

Figure 4.102

Index Fungorum number: IF 835304; Facesoffungi number: FoF 16722

Culture characteristics – *Colonies* on PDA become 2–3 cm diam. after 7 days at 25°C, appear in white, undulate margined, flat, reverse yellow to yellowish orange. *Hyphae* superficial to semi immersed, hyaline, thick-walled, verrucose and aseptate, 0.6–1.5μm ($\overline{x}$ = 1 μm). Sexual morph: Undetermined. Asexual Morph: *Arthroconidia* 3–8 × 1–2 μm ($\overline{x}$ = 5 × 1.5 μm, n = 25), terminal and intercalary.

Material examined – Thailand, Chiang Mai, Chai Prakan District, What Tham Tap Tao, cave, on soil, 99.117570N, 19.662672E, 598m, 9 May 2022, W.A. Erandi Yasanthika (MFLU25-0172); living culture 71-cv-21-21= MFLUCC 24-0492.

GenBank numbers – MFLUCC 24-0492.: ITS: PQ570522

Notes– Multigene phylogeny in Figure 4.93 indicates that our strain (MFLUCC 24-0492) clusters with the type species of *Currahmyces indicus* with 100% statistical support. Morphologically, our isolate has similar characteristics with *C. indicus* by having terminal and intercalary arthroconidia (Sharma & Shouche, 2020). Based on multigene phylogeny and morphology, we confirm our strain as *Currahomyces indicus*. *Currahomyces indicus* was introduced by Sharma and Shouche (2020) from soil in India. We report the first record of *Currahomyces indicus* from soil in Thailand which was isolated from disturbed-cave environment.

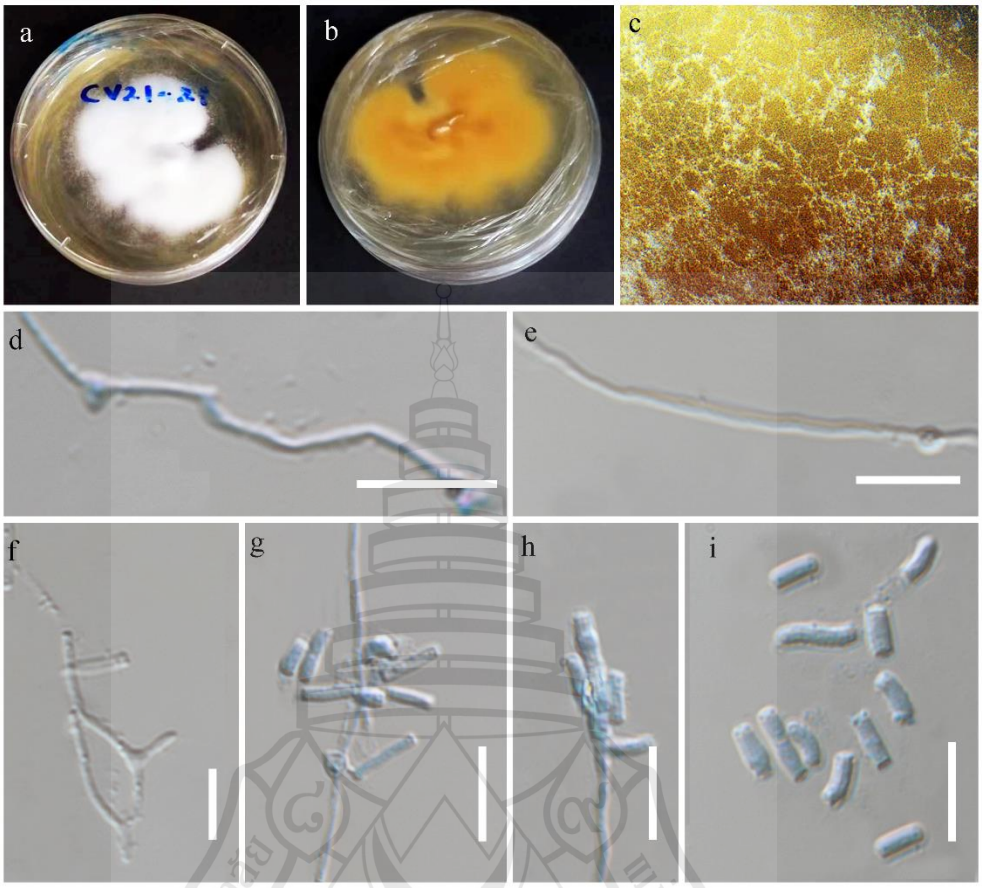


Figure 4.103 *Currahomyces indicus* (MFLU25-0172)

Figure 4.103, a, b culture characters on PDA (b = reverse). c Sporulation. d, e Hyphae. f–l Terminal and intercalary arthroconidia. Scale bars: d–h = 10 μm.

Renispora Sigler & J.W. Carmich., Mycotaxon 10(1): 133 (1979)

Figure 4.104

IndexFungorum: IF 4675; Facesoffungi number: FoF16691

Sigler et al. (1979) introduced *Renispora* by accommodating *R. flavissima* as the type species. Previously, the genus was placed in *Onygenaceae*; however, it has been placed in *Neogymnomycetaceae* by Kandemir et al. (2022) as a monotypic genus. The asexual morph is characterized by one-celled, solitary, terminal or lateral conidia arising from hyphal structures. The sexual morph has heterothallic, gymnotheicial ascomata that appear in yellow and peridial hyphae poorly differentiated from vegetative hyphae. There are unitunicate, 8-spored, clavate asci with one-celled,

reinform bacillum ascospores (Guarro et al., 2012). Species have been isolated from dung and soil in the USA (Sigler et al., 1979).

Table 4.107 *Renispora* species isolated from soil

Species	Country	Habitat or soil type	References
Renispora flavissima	USA	Barn housing	Sigler et al. (1979)

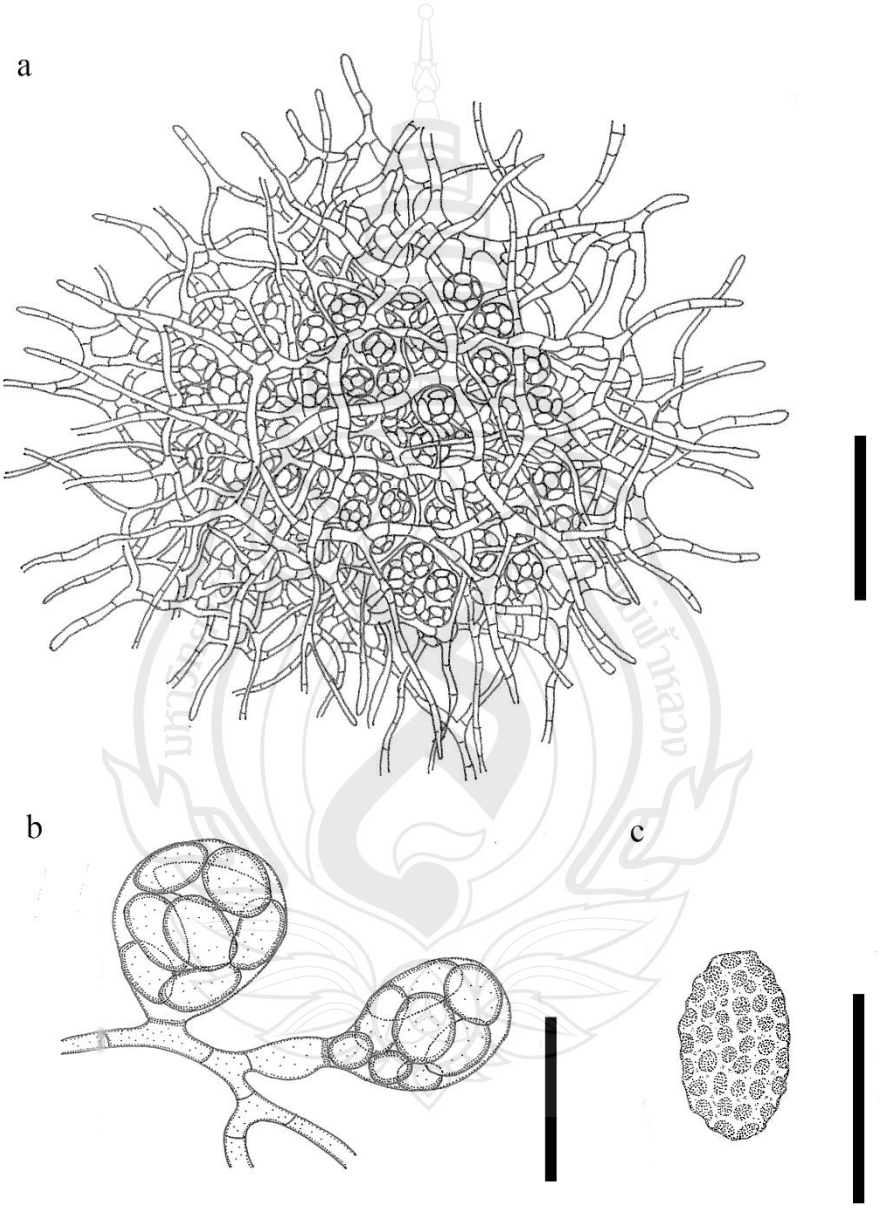


Figure 4.104 *Renispora flavissima*

Figure 4.104, a Ascoma. b Ascus. c Ascospore. Scale bars a = 100 μm, b = 10 μm, c = 5 μm. Redrawn from Guarro et al. (2012).

Family: *Onygenaceae*

Amauroascus J. Schröt., Krypt.-Fl. Schlesien (Breslau) 3.2(1–2): 210, 211 (1893)

Figure 4.105

IndexFungorum: IF152; Facesoffungi number: FoF16680

Schroeter (1893) introduced *Amauroascus*, which was typified by *A. niger*. The ITS phylogeny of *Onygenaceae* conducted by Kandemir et al. (2022) accepted four species in the genus. Species Fungorum (2025) has listed 14 species in the genus while seven have molecular data (ITS and LSU). Guarro et al. (2012) provided a key to the species in *Amauroascus* and further described *Chrysosporium* and *Malbranchea* as the anamorphic genera of *Amauroascus* (Guarro et al., 2012). The sexual morph has gymnotheicial ascomata, solitary or in clusters with dense, peridial hyphae that can be undifferentiated and slightly differentiated from vegetative hyphae, and unitunicate, 8-spored, ovoid to pyriform or spherical to subspherical asci (Guarro et al., 2012). Based on the ascospore morphology, *Amauroascus* species can be differentiated as punctate-reticulate ascospores and irregularly verruculose-punctate ascospores. They have been found in dung, insects and soil collected in Germany, Japan, Poland, Spain and the USA (Sharma & Shouche, 2020).

Table 4.108 *Amauroascus* species isolated from soil

Species	Country	Habitat or soil type	References
Amauroascus javanicus	Jawa	Paddy field soil	Kandemir et al. (2022)
A. malaysianus	Malaysia	Garden soil	
A. niger	USA	ND	
A. purpureus	Japan	Cultivated soil	
A. tropicalis	Cuba	Forest soil	
A. verrucosus	USA	ND	
A. volatilispatellus	USA	Clay soil	

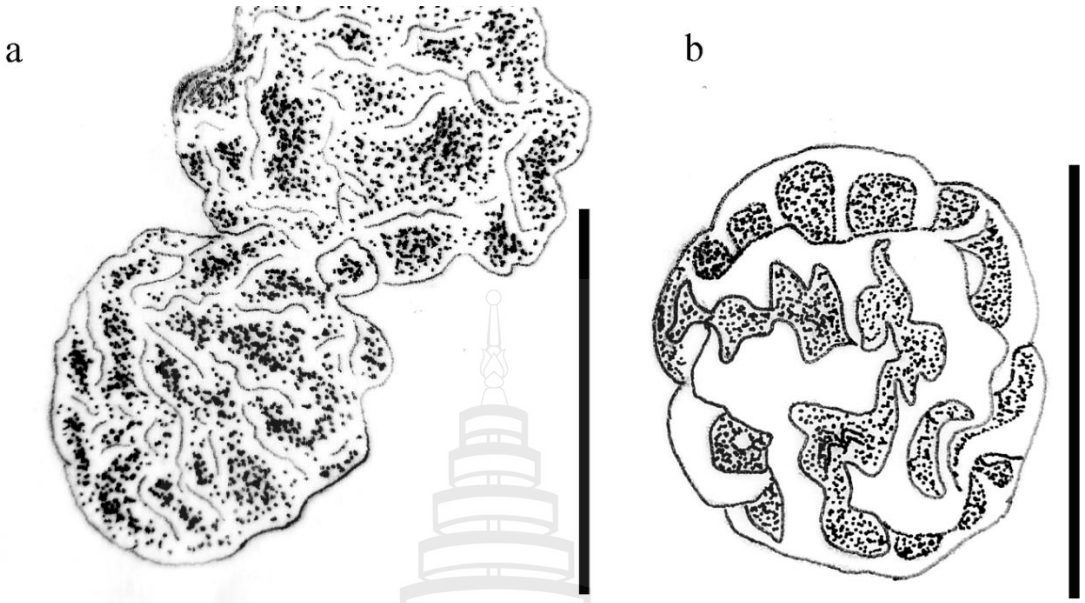


Figure 4.105 *Amauroascus niger*

Figure 4.105, a. Ascomata b. Ascospores. Scale bars: a, b = 5. Redrawn from Guarro et al. (2012)

Aphanoascus Zukal, Ber. Dt. Bot. Ges. 8: 295 (1890)

Figure 4.106

IndexFungorum: IF245; Facesoffungi number: FoF16688

Aphanoascus was introduced by Zukal (1890), accommodating *A. cinnabarinus* in the genus. However, Apinis (1968) suggested a new combination, naming *A. fulvescensas,* while proposing it as the type species in *Aphanoascus.* Subsequently, Labuda et al. (2021) have deposited the neotype and stabilized the current concept of this genus. Based on the phylogeny, Kandemir et al. (2022) confirmed the placement of this genus in *Onygenaceae* and updated the *A fulvescensas* (UAMH 4114) as the neotype, including 13 species in the phylogenetic analyses (Kandemir et al., 2022). There are 19 species in the genus (Hyde et al., 2024c), while 14 of them have molecular data (ITS and LSU). The sexual morph is cleistotheicial, superficial or in clusters, pale to dark brown, ascomata with a thick peridium wall of *textura angularis* or *intricata* cells, unitunicate, 8-spored, subspherical to ellipsoidal asci, and one-celled, subspherical, discoid or obovate or irregular, pale or dark brown ascospores with pitted or verruculose walls. *Aphanoascus* species are distributed in keratinous substrates,

including dung, sediments, and soil in Australia, China, India and Spain (Cano & Guarro, 1990; Kandemir et al., 2022).

Table 4.109 *Aphanoascus* species isolated from soil

Species	Country	Habitat or soil type	References
Aphanoascus fulvescens	Australia	ND	Kandemir et al. (2022)
A. jingzhouensis	China	Farmland soil	
A. pinarensis	Cuba	Forest soil	
A. verrucosus	Spain	Arable soil	

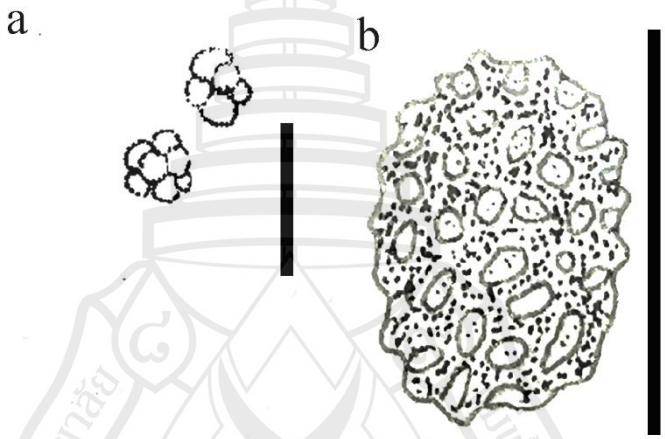


Figure 4.106 *Aphanoascus fulvescens*

Figure 4.106, a. Asci. b. Ascospore. Scale bars: a = 10 μm. b = 5 μm. Redrawn from Guarro et al. (2012)

Brunneospora Guarro & Punsola, Persoonia 13(3): 387 (1987)

Figure 4.107

IndexFungorum: IF25158; Facesoffungi number: FoF16685

Guarro et al. (1987) introduced *Brunneospora* with *B. reticulate* as the type species. Currently, two species are accepted (Kandemir et al., 2022), and both of them have molecular data (ITS, LSU, SSU and *b-tub*). The genus has chrysosporium-like asexual morphs, and the sexual morph has gymnothecia with helical, peridial appendages and pigmented ellipsoidal ascospores. These species are keratinophilic, have been isolated from bird feathers and soil in Australia and Spain, and can infect mammals by inhaling environmental propagules. It has also been reported to have thermal dimorphic characteristics (Kandemir et al., 2022).

Table 4.110 *Brunneospora* species isolated from soil

Species	Country	Habitat or soil type	References
Brunneospora reticulata	Spain	arable soil	(Kandemir et al. (2022)

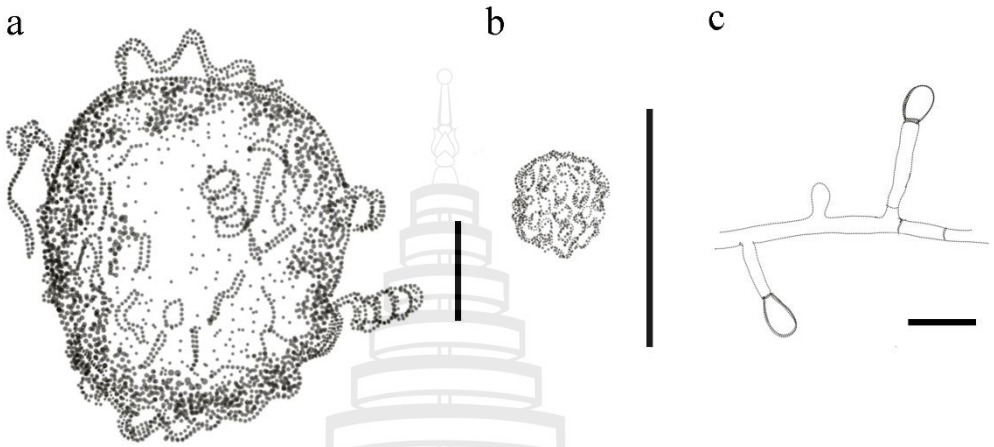


Figure 4.107 *Brunneospora reticulata* (FMR 784)

Figure 4.107, a.Ascomata. b. Ascospore. c. Chrysosporium-like asexual morph. Scale bars: a=100 μm, b, c=10 μm. Redrawn from Guarro et al. (1987).

Coccidioides C.W. Stiles, Rep. Johns Hopkins Hosp. 1: 243 (1896)

Figure 4.108

IndexFungorum: IF7712; Facesoffungi number: FoF16683

Rixford and Gilchrist (1896) introduced *Coccidioides,* designating *C. immitis* as the type species. The phylogenetic study of *Onygenaceae* by Kandemir et al. (2022) revised this genus and accepted two species. Both species have molecular data (ITS). The asexual morph is prominent and can be seen in saprobic and pathogenic life modes. It is hyphomycetous, and produces arthroconidia, and the asexual life cycle in the pathogenic phase produces endospores in mammalian hosts (Lewis et al., 2015). Species cause systemic mycosis in mammals (Van Dyke et al., 2019) while some of them are inhabiting in air and soil. This genus is distinct within *Onygenaceae* because of its keratinophilic properties and thermal dimorphism, where they can thrive in soils with low pH levels and temperatures ranging between -6.5°C and 60.6°C and also tolerate up to 8% NaCl (del Rocío Reyes-Montes et al., 2016).

Table 4.111 *Coccidioides* species isolated from soil

Species	Country	Habitat or soil type	References
Coccidioides immitis	Argentina, Italy and USA	ND	Domsch et al. (1993)

a

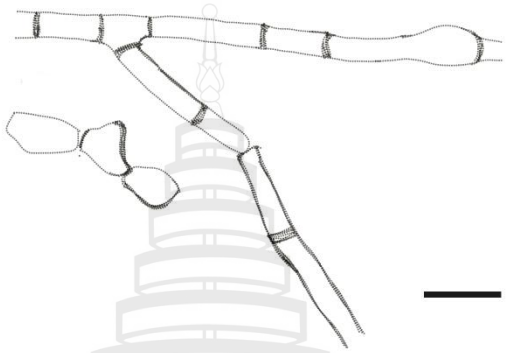


Figure 4.108 *Coccidioides immitis*

Figure 4.108, a. Fragmentig hyphae and arthroconidia. Redrawn from Domsch et al. (1980)

Keratinophyton H.S. Randhawa & R.S. Sandhu, Sabouraudia 3: 252 (1964)

IndexFungorum: IF2559; Facesoffungi number: FoF16687

Randhawa and Sandhu (1964) erected *Keratinophyton*, accommodating *K. terreum* as the type species. Kandemir et al. (2022) revised this genus, suggesting new combinations, and currently, there are 26 species accepted in the genus (Labuda et al. 2024). All the species have molecular data (ITS and LSU). The genus has chrysosporium asexual morphs and the sexual morph has cleistothecia with a pseudoparenchymatic peridium (Labuda et al., 2021; Kandemir et al., 2022). They harbour on keratinous substrates, dung, pollen, and nutrient-rich soil in China, India, Italy and Spain (Kandemir et al., 2022; Labuda et al., 2021; Sutton et al., 2013).

Table 4.112 *Keratinophyton* species isolated from soil

Species	Country	Habitat or soil type	References
Keratinophyton indicum	India	ND	Kandemir et al. (2022)
K. terreum	India	lawn soil	
K. evolceanui	India	ND	
K. linfenense	China	ND	Labuda et al. (2021)
K. chongqingense	China	ND	
K. straussii	Italy	ND	
K. siglerae	Spain	ND	
K. gollerae	Slovakia	Forest soil	
K. hispanicum	Spain	Beach soil	
K. hubeiense	China	Soil under the chicken feather	
K. lemmensii	Austria	Compost soil	
K. linfenense	China	Rhizosphere soil	
K. pannicola	India	ND	
K. straussii	Italy	Garden soil	
K. wagner	Slovakia	Forest soil	
K. turgidum	India	soil near barber shop	
K. sichuanense	China	ND	

Pectinotrichum Varsavsky & G.F. Orr, Mycopath. Mycol. appl. 43(2): 229 (1971)

Figure 4.109

IndexFungorum: IF3784; Facesoffungi number: FoF16686

Varsavsky and Orr (1971) introduced *Pectinotrichum* accommodating *P. llanense* as the type species. Currently, one species is accepted in the genus and it is supported with molecular data (ITS). The asexual morph has thallic, terminal or lateral, one-celled conidia and the sexual morph is characterized by gymnotheicial ascomata, peridium composed of anastomosed hyphae and appendages, unitunicate, 8-spored, spherical asci, and one-celled hyaline, or pale yellow, smooth ascospores (Guarro et al., 2012; Kandemir et al., 2022)

Table 4.113 *Keratinophyton* species isolated from soil

Species	Country	Habitat or soil type	References
Pectinotrichum llanense	Venezuela	Savannah soil	Kandemir et al. (2022)

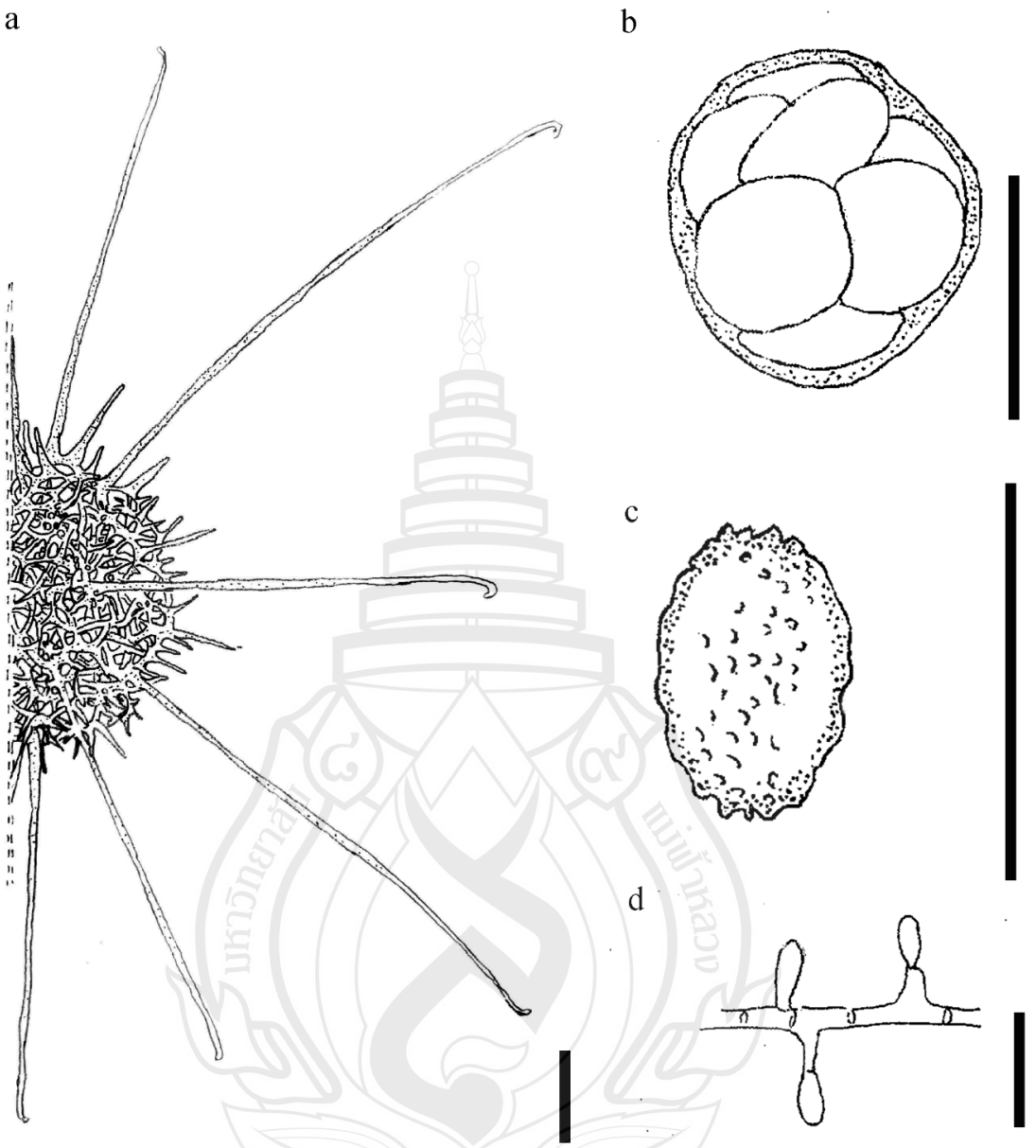


Figure 4.109 *Pectinotrichum llanense*

Figure 4.109, a.Ascomata. b. Ascus. c. Ascospore. d. Asexual morph. Scale bars: a= 100µm, b,c = 5µm. d = 4 µm. Redrawn from Guarro et al. (2012).

Pseudoamauroascus Cano, M. Solé & Guarro, Stud. Mycol. 47: 175 (2002)

Figure 4.110

IndexFungorum: IF28669; Facesoffungi number: FoF16684

Cano et al. (2002) introduced *Pseudoamauroascus* with its type species, *P. australiensis.* It remains as a monotypic genus (Kandemir et al., 2022), supported by molecular data (ITS). The asexual morph has arthroconidia produced on the main hyphae and straight or slightly flexous lateral branches. Sexual morph is gymonothicial, white, peridium possesses an anastomosed network, unitunicate,8-spored asci and one-celled, sub hyaline hyaline to oblate ascospores (Cano et al., 2002).

Table 4.114 *Pseudoamauroascus* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudoamauroascus australiensis	Australia	ND	Guarro et al. (2012)

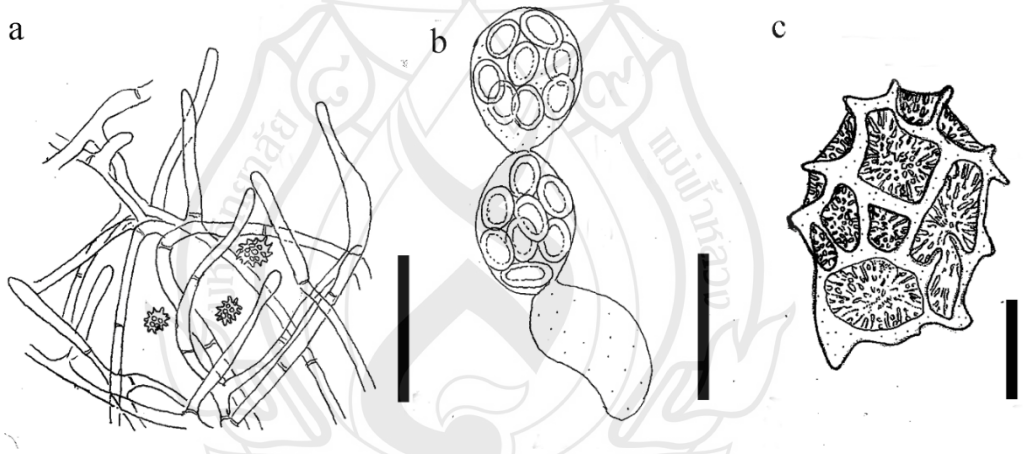


Figure 4.110 *Pseudoamauroascus australiensis*

Figure 4.110, a Part of ascomata b Ascus c Ascospore. Scale bars: a = 20 μm, b = 10 μm, c = 2.5 μm. Redrawn from Guarro et al. (2012).

Family: *Spiromastigoidaceae* Guarro, Cano & Stchigel. ≡ Spiromastixaceae Guarro, Cano & Stchigel—Mycoses 57(7): 425, 2014

Pseudospiromastix Guarro, Stchigel & Cano, Mycoses 57(7): 425 (2014)

IndexFungorum: IF805790; Facesoffungi number: FoF16692

Pseudospiromastix was validated by Hirooka et al. (2016) based on the morphology and ITS phylogeny, while designating *P. tentaculata* as the type species.

It is currently a monotypic genus, supported by molecular data (Hirooka et al., 2016; Kandemir et al., 2022). The asexual morph forms conidiophores on aerial hyphae and sparingly or laterally branched conidiogenous hyphae, producing arthroconidia. Arthroconidia can be septate, cylindrical, cuboid or doliiform. Terminal and single lateral conidia are unicellular, subglobose to clavate or broadly ellipsoidal (Hirooka et al. 2016). In sexual morphs, ascomata can be present or absent based on the species and the asci are globose to ovoid or pyriform, short-stipitate, evanescent, 8-spored, with hyaline, yellowish or pale brown ascospores. (Guarro et al., 1993; Hirooka et al., 2016).

Table 4.115 *Pseudospiromastix* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudospiromastix tentaculata	Somalia	ND	Hirooka et al. (2016)

Spiromastigoides Doweld, Index Fungorum 30: 1 (2013)

IndexFungorum: IF550257; Facesoffungi number: FoF16693

Spiromastigoides was introduced by Doweld (2013) with *S. warcupii* as the type species. Based on the ITS and LSU analyses for *Onygenales,* Kandemir et al. (2022) accepted 15 species in this genus, with all the species having molecular support (SSU, LSU and ITS). The asexual morph shows malbranchea- or chrysosporium-like characteristics (Hirooka et al., 2016; Kandemir et al., 2022), where conidiophores have predominantly unilateral branching patterns. The sexual morph is characterized by discrete or confluent, brown ascomata, curved or twisted appendages, eight-spored, subglobose, ovoid to ellipsoidal in shape asci and smooth-walled, yellowish to pale brown ascospores (Rizzo et al., 2014). The sexual morph in *Spiromastigoides* is found to be unique due to its curved but incompletely coiled peridial appendages (Kuehn & Orr, 1962). Most of the species are cellulolytic and non-keratinolytic, and some are known as pathogens in mammals (Kandemir et al., 2022). They have been isolated from dung, household dust, human clinical samples and soil in Australia, Indonesia, Japan and the USA (Stchigel et al., 2017).

Table 4.116 *Spiromastigoides* species isolated from soil

Species	Country	Habitat or soil type	References
Spiromastigoides gypsea	USA	ND	Stchigel et al. (2017)
S. warcupii	Australia, Indonesia, Japan and the USA	ND	
Spiromastigoides sugiyamae	USA	ND	
Spiromastigoides sphaerospora	Japan	Athletics ground:	
Spiromastigoides princeps	Kenya	ND	

Class: *Lecanoromycetes* *O.E. Erikss. & Winka*

Subclass: *Ostropomycetidae* *V. Reeb, Lutzoni & Cl. Roux*

Order: *Graphidales* Bessey

Family: *Diploschistaceae* *Zahlbr.*

Diploschiste*s* Norman, Conat. Praem. Gen. Lich.: 20 (1852)

Index Fungorum number: IF 1621; Facesoffungi number: FoF16694

Acharius (1852) introduced *Diploschistes,* and the type species is *Diploschistes muscorum.* Currently, the genus comprises 48 species (Mamut et al., 2022). It is known as lichen-forming genus having crustose lichens (Lumbsch & Mangold, 2007). The sexual morph is characterized by three different forms of ascomata, which are perithecioid (ascoma enclosed by a wall and opened only by a small ostiole, disc not visible from above, similar to a perithecium with a well-developed carbonized excipulum), urceolate (ascoma with an exposed, deeply concave disc and well-developed carbonized excipulum), and lecanoroid (ascoma with an exposed flat to moderately concave disc, and reduced hyaline excipulum) (Fernández-Brime et al., 2013). The species can be found in barks, rocks, mosses, other lichens, soil and wood substrates (Ababaikeli et al., 2016; Fernández-Brime et al., 2013) and are distributed in Africa, America, Australia, and Europe (Fernández-Brime et al., 2013).

Table 4.117 *Diploschistes* species isolated from soil

Species	Country	Habitat or soil type	References
Diploschistes diacapsis	Spain	ND	Rubio and Lázaro (2023)

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

Order: *Helotiales* Nannf. ex Korf & Lizoň (= Cyttariales Luttr. ex Gamundí)

Family: *Amorphothecaceae* Parbery

Amorphotheca Parbery

Index Fungorum number: IF161

Amorphotheca was introduced by Parbery (1969), accommodating *A. resinae* as the type species. The genus has only one species, and it is supported by molecular data. The sexual morph is characterized by the submerged or superficial ascocarps that are more or less spherical but often irregular in shape. Asci are pyriform or globose, 8-spored, hyaline. The walls of the ascoid are unitary, disappearing. The ascospores are unicellular, often biguttulate, inner membrane constricted, hyaline, brownish and thick (Parbery, 1969). Some species are utilized for producing industrially important melanin (Oh et al., 2021), and *Amorphotheca resinae* has been identified as having a potential for biodegradation (Ran et al., 2014).

Table 4.118 *Amorphotheca* species isolated from soil

Species	Country	Habitat or soil type	References
Amorphotheca resinae	Germany	ND	Furst et al. (1998)

Family: *Discinellaceae* Ekanayaka & K.D. Hyde

Acidea Hujslová & M. Kolařík, Mycol. Progr. 13(3): 826 (2014)

Index Fungorum number: IF805195; Facesoffungi number: FoF16650

Acidea is a monotypic genus typified with *A. extrema* and was introduced by Hujslová et al. (2014) based on LSU and SSU multi-gene phylogeny. The genus is comprised of a hyphomycetous asexual morph that is sparsely branched, sterile mycelium, that is often fragmenting. The sexual morph is still undetermined (Hujslová et al., 2014).

Table 4.119 *Acidea* species isolated from soil

Species	Country	Habitat or soil type	References
Acidea extrema	Czech Republic	Highly acidic soil	Hujslová et al. (2014)

Family: ***Hyphodiscaceae*** Ekanayaka & K.D. Hyde

Soosiell*a* Hujslová & M. Kolařík, Mycol. Progr. 13(3): 827 (2014)

Index Fungorum number: IF805196; Facesoffungi number: FoF16651

Soosiella is a monotypic genus which was introduced by Hujslová et al. (2014) based on morphology and LSU and SSU phylogeny, and *S. minima* is designated as the type species. The asexual morph is hyphomycetes and the sexual morph remains unknown (Hujslová et al., 2014).

Table 4.120 *Soosiella* species isolated from soil

Species	Country	Habitat or soil type	References
Soosiella minima	Czech Republic	Highly acidic soil	Hujslová et al. (2014)

Family: ***Myxotrichaceae*** *Currah*

Byssoascus Arx, Persoonia 6(3): 377 (1971)

Figure 4.111

Index Fungorum number: IF 699; Facesoffungi number: FoF16698

Von Arx (1971) introduced *Byssoascus* by transferring *Arachniotus striatisporus* as a new combination. Currently, it is a monotypic genus with its type, *B. striatosporus* (Species Fungorum 2025) and supported by molecular data (ITS, LSU and *rpb2*). The asexual morph has cylindrical conidia that are born in chains by fragmentation of branching conidiophores. The sexual morph is characterized by the spherical or irregular, small ascomata with an inconspicuous perdium, composed of loosely arranged hyphal network. Asci are produced from *ascogenous* hyphae with croziers, in clusters, broadly clavate or obovate, thin-walled, and 8-spored. Ascospores are fusiform, striate by longitudinal flutes, and straw-coloured when mature (Von Arx, 1971).

Table 4.121 *Byssoascus* species isolated from soil

Species	Country	Habitat or soil type	References
Byssoascus striatosporus	Canada	ND	Peng et al. (2014)

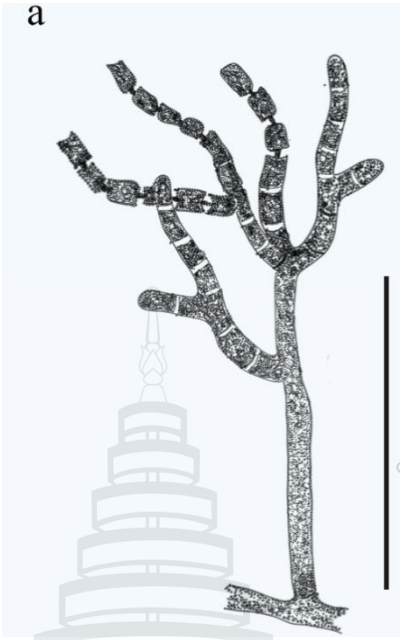


Figure 4.111 *Byssoascus striatosporus*

Figure 4.111, a. Conidiophore. Scale bars: a = 50 μm. Redrawn from redrawn from Guarro et al. (2012)

Myxotrichum *Kunze,* Mykologische Hefte (Leipzig) 2: 108 (1823)

Figure 4.112

Index Fungorum number: IF 3405

Myxotrichum was introduced by Kunze and Schmidt (1823), with the type species accommodated as *M. chatarum*. The genus is comprises of 17 species (Hyde et al., 2024c), and eight of them molecular data. They have been isolated from lichen, litter and soil in Alaska, China, France, Germany, Japan and the USA (Liang et al., 2019; Uchiyama et al., 1995; Yuan et al., 2013).

Table 4.122 *Myxotrichum* species isolated from soil

Species	Country	Habitat or soil type	References
Myxotrichum arcticum	Alaska	Forest soil	Uchiyama et al. (1995)
M. dendromorphum	Pakistan	Coniferous forest soil	
My. ochraceum	Japan	ND	
M. stellatum	Japan	Forest soil	Udagawa and Uchiyama (2000)
M. retardatum	Canada	Forest soil	Udagawa and Uchiyama (1999b)
M. dendromorphum	Pakistan	Coniferous forest soil	
M. deflexum	Canada		Peng et al. (2014)

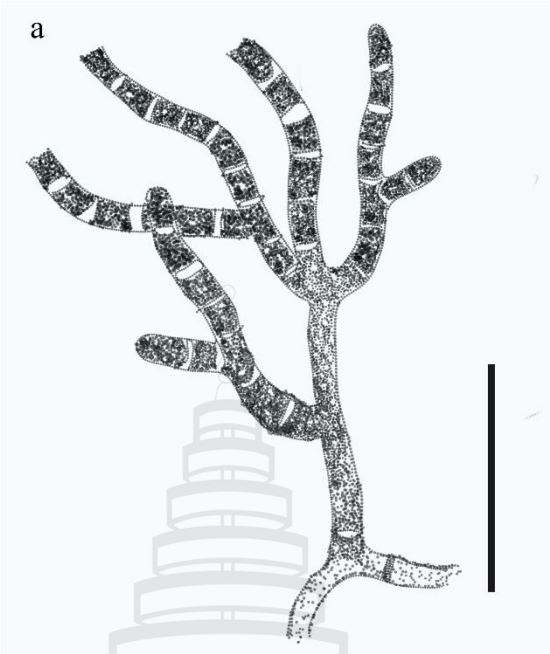


Figure 4.112 *Myxotrichum* sp.

Figure 4.112, a. Conidiophore. Scale bars: a = 25 μm. Redrawn from redrawn from Guarro et al. (2012)

Oidiodendron Robak, Nytt Mag. Natur. 71: 245 (1932)

Index Fungorum number: IF9141; Facesoffungi number: FoF16697

Robak (1932) introduced *Oidiodendron* accommodating *O. fuscum* as the type species. The genus is comprised of 26 species (Hyde et al., 2024c), while 15 of them have molecular data (ITS, LSU and SSU). It is morphologically distinct by having the arborescent conidiogenous apparatus, that has erect conidiophores terminate in a complex branching head of fertile hyphae where they produce arthrospores basipetally. Species can be found in air, bark, decaying wood, humus, insects, lichens, marine sediments, mosses, papers, soil and wood pulp, while some have been reported as mycorrhizal fungi (Hambleton et al., 1998; Lee et al., 2022). The genus is distributed in Austria, Canada, Denmark, Korea, Italy, the Netherlands and the USA (Lee et al., 2022).

Table 4.123 *Oidiodendron* species isolated from soil

Species	Country	Habitat or soil type	References
Oidiodendron chlamydosporicum	USA	ND	Hambleton et al. (1998)
O. citrinum	Canada	Peat soil	
O. echinulatum	Canada	Peat soil	
O. pilicola	Alaska	Soil on human hair	

Family: *Sclerotiniaceae* Whetzel ex Whetzel

Botrytis P. Micheli ex Pers., Neues Mag. Bot. 1: 120 (1794)

Figure 4.113

Index Fungorum number: IF 7435; Facesoffungi number: FoF00142

Micheli (1794) introduced *Botrytis* with the type species, *B cinera*, and the genus was later formally revised by Persoon (1801). As mentioned by Hyde et al. (2024), the genus comprises more than 70 species; however, Garfinkel (2021) mentioned that only 38 species are formally described. For the species delineation in the genus, *g3pdh*, *rpb2*, heat shock protein 60 (HSP60), *nep1*, and *nep2* gene regions have been used (Garfinkel, 2021). Some species of this genus produce highly melanized sclerotia for long-term survival, and subsequently, they produce hyphae with conidiophores or apothecia (Richards et al., 2021). The genus has important plant pathogens that affect a broad range of hosts such as tomatoes, peper, grapes, strawberry, legumes and cut flowers worldwide (Brauna-Morževska et al., 2023; Richards et al., 2021).

Table 4.124 *Botrytis* species isolated from soil

Species	Country	Habitat or soil type	References
Botrytis allii	Israel	Onion field	Kritzman and Netzer (1978)
B. cinerea	Jamaica, Nepal and India	Grassland, Garden, arable, peat land soil, saline, sandy, salt marsh, mangrove, cave and Uranium mine	Domsch et al. (1993)

Figure 4.113 *Botrytis cinera*

Figure 4.113, a. Conidiophore and conidia. Scale bars: a=800X. The images are redrawn from redrawn from Domsch et al. (1980).

Sclerotinia Fuckel, Jb. nassau. Ver. Naturk. 23-24: 330 (1870) [1869-70]

Index Fungorum number: IF 4942; Facesoffungi number: FoF16696

Fuckel (1870) introduced *Sclerotinia* and typified with *Sclerotinia libertiana*. It is comprised of around 103 species (Hyde et al., 2024c; Species Fungorum 2025), and the genus is supported by ITS, *gpdh3*, *rpb2* and HSP60 gene regions (Yin et al., 2024). These species are plant pathogens that infect more than 600 plant species in 75 families, including bean, carrot, pea, lettuce, mustard, canola, lentil and sunflower (Smolińska & Kowalska, 2018). The genus forms sclerotia in soil, plant residues, or seeds during the winter and summer. Around 90% of the life cycle of *Sclerotinia* is spent in the soil as sclerotia (Adams & Ayers, 1979; Yin et al., 2024). Species geographically distribute in China, Germany, Poland, the Netherlands, Venezuela and the USA (Yin et al., 2024)

Table 4.125 *Sclerotinia* species isolated from soil

Species	Country	Habitat or soil type	References
Sclerotinia sclerotiorum	ND	Rhizosphere soil	Domsch et al. (1993)

Helotiales* genera *incertae sedis

Cadophora Lagerb. & Melin, Svensk Skogsvårdsförening Tidskr. 25: 263 (1927)

Index Fungorum number: IF7462; Facesoffungi number: FoF 16649

Lagerberg et al. (1927) established *Cadophora* based on morphological characterization and *C. fastigiata is designated as the type species*. Currently, 44 *Cadophora* species are listed in the Species Fungorum (2025), while 37 of them have molecular data. *The a*sexual morph is hyphomycetes and produces solitary phialides with distinct hyaline collarettes. *Cadophora* has different trophic modes, such as saprobes, plant pathogens, and mutual associations. It is described as one of the most ubiquitous fungal taxa inherent with a higher number of stress-tolerance genes, thus have been isolated from cold, glacial water, marine sediments, soils and submerged woods in Arctic and Antarctic sites, Canada, China, Finland, Germany, Italy, North America and Norway (Zhang et al., 2022a).

Table 4.126 *Cadophora* species isolated from soil

Species	Country	Habitat or soil type	References
Cadophora antarctica	Antarctica	Diesel-contaminated soil	Zhang et al. (2022a)
C. caespitosa	China	Snow mountain	
C. indistincta	China	Glacier soil	
C. inflata	China	Glacier soil	
C. magna	China	Glacier soil	
C. malorum	China	Snow mountain	
C. novi-eboraci	China	Glacier soil	
C. psychrophila	China	Glacier soil	
C. qinghai- tibetana	China	Snow mountain	
C. yulongensis	China	Snow mountain	

Scytalidium Pesante, Annali Sper. agr., N.S. 11(2, Suppl.): cclxiv (1957)

Index Fungorum number: IF 9862; Facesoffungi number: FoF16699

Pesante (1957) introduced *Scytalidium* with its type species *Scytalidium lignicola*. The genus comprises 32 species (Species Fungorum 2025), of which 24 species have molecular data (ITS, LSU and SSU). It is a hyphomycetous genus characterized by small, hyaline fission arthroconidia together with larger, brown conidia (Moore, 1992). Species have a wide geographical distribution including Brazil, China, India, Italy, Malaysia, South Korea and Sweden, associated with air, fruit trees, leaves, soil, timber, and wood (Machouart et al., 2013; Peng et al., 2014). They have been reported as plant and human pathogens (Machouart et al., 2013), while some of them are fungicolous fungi (Goh et al., 2015; Peng et al., 2014)

Table 4.127 *Scytalidium* species isolated from soil

Species	Country	Habitat or soil type	References
Scytalidium chinense	China	Sandy soil	Wu and Zhang (2010)
S. nielamuense	China	Grassland soil	
S. verruculosum	China	Mountain soil	
S. xigazense	China	Mountain soil	
S. flavobrunneum	Georgia	Forest soil	Domsch et al. (1993)

Class: *Lichinomycetes* V. Reeb, Lutzoni & Cl. Roux

Order: *Geoglossales* Zheng Wang, C.L. Schoch & Spatafora

Family: *Geoglossaceae* Corda

Hemileucoglossum Arauzo, Errotari 11: 176 (2014)

Figure 4.114

Index Fungorum number: IF 809532; Facesoffungi number: FoF 16648

Arauzo and Iglesias (2014) introduced *Hemileucoglossum* and designated *H. littorale* as the type species, which was isolated from *Littorela uniflora* plants (Kers & Carlsson, 1996). This genus is comprised of six species (Species Fungorum 2025), and all of them have molecular data (ITS and LSU). The sexual morph is characterized by the setose hairs on the stipe, paraphyses agglutinated by a dense brown amorphous material and hyaline mature ascospores. Most of the species have been isolated from soil in Denmark, Slovakia and the USA (Fadnes et al., 2021).

Table 4.128 *Hemileucoglossum* species isolated from soil

Species	Country	Habitat or soil type	References
Hemileucoglossum pusillum	Slovakia	Gravel soil in fen	Crous et al. (2017a)
H. pusillum	Slovakia	Gravel soil in fen	
H. littorale	Denmark	Sand	Fadnes et al. (2021)
H. intermedium	USA	Swampy soil	

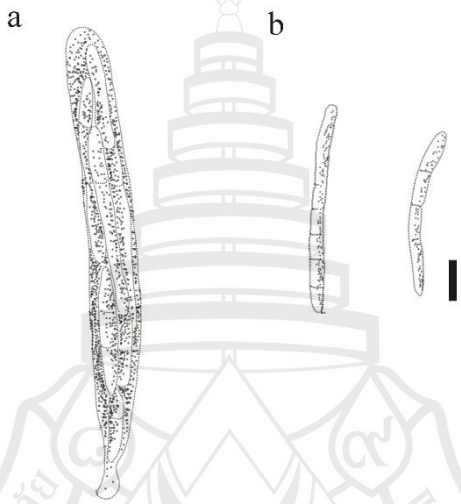


Figure 4.114 *Hemileucoglossum littorale*

Figure 4.114, a. Ascus. b. Ascospores. Scale bar: b = 10 μm. Redrawn from Kučera & Fedosova (2017)

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

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

Family: *Orbiliaceae* Nannf.

Arthrobotrys Corda, Pracht-Fl. Eur. Schimmelbild.: 43 (1839)

Index Fungorum number: IF 7217; Facesoffungi number: FoF 14384

Corda (1839b) introduced *Arthrobotrys*, designating *A. superba* as the type species. There are 59 species accepted in the genus (Zhang et al., 2022b). Zhang et al. (2022b), provided phylogenetic analyses for 54 species using ITS, *tef*, and *rpb2* gene regions. *Arthrobotrys* is considered as the largest genus in *Orbiliaceae*. The genus is characterized by having an asexual morph with the branched or simple conidiophores that asynchronously produce conidia on the nodes or on short denticles, which are obovoid, elliptic, pyriform and 0–3-septate (Chen et al., 2007; Kim et al., 2001;

Subramanian, 1977). Species can be found in animal waste, freshwater, hot springs, sediments, soil and tree trunks. *Arthrobotrys* are saprobes and are also recorded as nematode-trapping fungi (Kim et al., 2001; Zhang et al., 2022b). These species are distributed in Canada, China, Kazakhstan, Poland and the USA (Zhang et al., 2022b).

Table 4.129 *Arthrobotrys* species isolated from soil

Species	Country	Habitat or soil type	References
Arthrobotrys constringens	Canada	ND	Dowsett et al. (1984)
A. jinpingensis	China	ND	Zhang et al. (2022b)
A. luquanensis	China	ND	
A. microscaphoides	China	ND	
A. shuifuensis	China	ND	
A. zhaoyangensis	China	ND	

Class: *Pezizomycetes* O.E. Erikss. & Winka

Order: *Pezizales* J. Schröt.

Family: *Ascodesmidaceae* J. Schröt.

Cephaliophora Thaxt., Bot. Gaz. 35: 157 (1903)

Figure 4.115

Index Fungorum number: IF 7518; Facesoffungi number: FoF16695

Thaxter (1903) introduced *Cephaliophora,* and the type species is accommodated as *Cephaliophora tropica.* The genus is comprised of three species (Species Fungorum, 2025) and two of them have molecular data. The asexual morph is characterized by having conidia that are produced synchronously from a swollen ampulla, arising directly from vegetative hyphae and from a short lateral branch. The sexual morph is unknown (Goos, 1964; Pfister & Healy, 2021). The species have been found as saprobes from dung and soil, and they can cause keratitis in humans and are distributed in China, Jamaica, Jawa, Liberia, India and Puerto Rico (Nguyen et al., 2017; Pfister & Healy, 2021).

Table 4.130 *Cephaliophora* species isolated from soil

Species	Country	Habitat or soil type	References
Cephaliophora sp.	India	ND	Pandey et al. (1990)
C. tropica	Iran	Cucurbitaceae farms	Pordel et al. (2015)

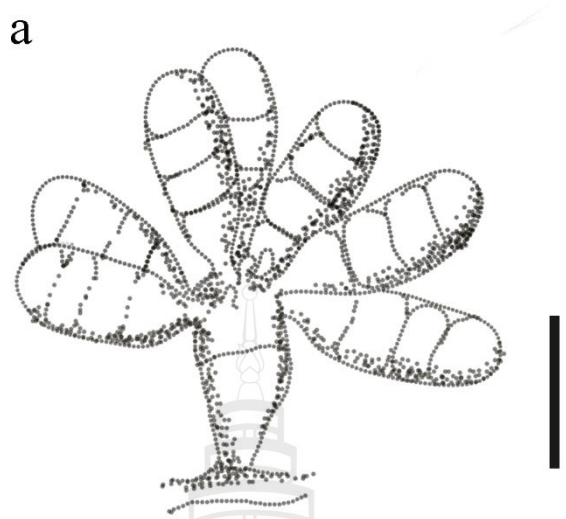


Figure 4.115 *Cephaliophora tropica*

Figure 4.115, a Conidiogenous cells with synchronously forming conidia. Redrawn from redrawn from Domsch et al. (1980).

Family: *Pezizaceae* Dumort. (= *Carbomycetaceae* Trappe)

Peziza Dill. ex Fr., Syst. mycol. (Lundae) 2(1): 40 (1822)

Index Fungorum number: IF 3859; Facesoffungi number: FoF16337

Fries (1822) introduced *Peziza,* and it is considered the largest genus in the *Pezizales,* having more than 100 species (Barseghyan & Solomon, 2011). The sexual morph is characterized by epigeous, sessile or stipitate, cup-shaped, cupulate, turbinate, pulvinate or sparassoid apothecia. Species can be found in different types of soil, dung and wood collected in Austria, Denmark and the USA (Petersen, 1967, 1985).

Table 4.131 *Peziza* species isolated from soil

Species	Country	Habitat or soil type	References
Peziza ammophila	Morocco	ND	Barseghyan and Solomon (2011)
P. ampelina	Denmark	Clayey soil	Hansen et al. (2002)
Peziza aurata	Denmark	ND	
P. arvernensis	Denmark	Disturbed soil	
P. domiciliana	Denmark	Forest	
P. fimeti	Denmark	ND	
P. fimeti	Russia	Clay soil	
P. nivalis	USA	ND	
Peziza varia	Denmark	ND	

Table 4.131 (continued)

Species	Country	Habitat or soil type	References
Peziza varia	USA	Soil with wood debris	
Peziza sp.	Denmark	Calcareous soil	
Peziza sp.	Denmark	Clayey soil	
Peziza sp.	Austria	ND	
Peziza sp.	USA	Soil at the campfire site	
Peziza sp	USA	Disturbed mineral soil	

Family: *Pyronemataceae* Corda (= *Otideaceae* Eckblad)

Lotinia Pérez-Butrón, Fern.-Vic. & P. Alvarado

Figure 4.116

Index Fungorum number: IF 814887; Facesoffungi number: FoF16652

Lotinia is a monotypic genus, introduced by Crous et al. (2015b) and typified with *L. verna*. The species is supported with molecular data (ITS, LSU and *tef*1-α). The asexual morph is unknown. The sexual morph is identified as having brownish, discoidal ascomata, an external surface covered with flexuose hairs from the base to the top. Peridium wall arranged as a *textura prismatica*. Asci are 8-spored, operculate, and non-amyloid, comprising smooth, aguttulate, globose to ellipsoid ascospores (Crous et al., 2015c).

Table 4.132 *Lotinia* species isolated from soil

Species	Country	Habitat or soil type	References
L. verna	Spain	Muddy soil	Crous et al. (2015c)

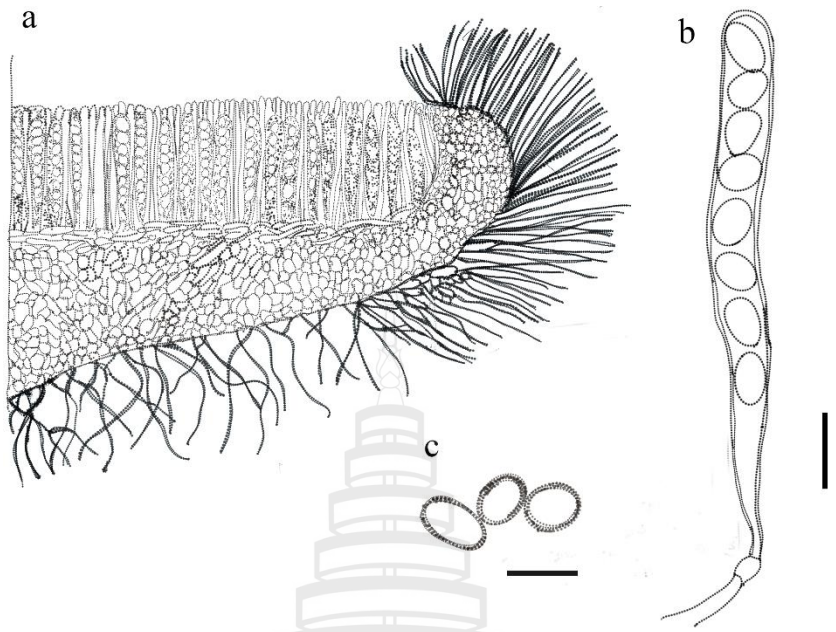


Figure 4.116 *Lotinia verna*

Figure 4.116, a Ascoma. b Ascus. c Ascospores. Scale bars: b = 60 μm, c = 30 μm. The images are redrawn from redrawn from Crous et al. (2015b)

Class: *Sordariomycetes*

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

Order: *Calosphaeriales* M.E. Barr

Family: *Calosphaeriaceae* Munk

Jattaea Berl., Icon. fung. (Abellini) 3(1-2): 6 (1900)

Figure 4.117

IndexFungorum number: IF 2528; Facesoffungi number: FoF07774

Jattaea was introduced by Berlese (1900) without designating the type species, and subsequently, *J. algeriensis* was designated as the lectotype (Clements & Shear, 1931). Currently, the genus has 26 species listed in the Species Fungorum (2025), and 12 of them have molecular data. The phylogenetic revisions for *Jattaea* were provided by Réblová et al. (2015) and Zhang et al. (2021) based on ITS, SSU, LSU, *tub2*, and *rpb2*. *Jattaea* has phialophora-like asexual morphs with short, to elongate, ampulliform phialides or adelo-phialides with funnel-shaped collarettes (Réblová et al., 2015; Zhang et al., 2021c). The sexual morph has non-stromatic perithecial ascomata, clavate and stipitate asci and allantoid, 1-septate and hyaline ascospores. Species can be saprobic

on decaying wood and soil-based substrates in Algeria, Canada, France, Germany, Italy, Sweden, Thailand and the USA (Réblová et al., 2015; Zhang et al., 2021c).

Table 4.133 *Jattaea* species isolated from soil

Species	Country	Habitat or soil type	References
Juttaea reniformis	China	Cave	Zhang et al. (2021c)

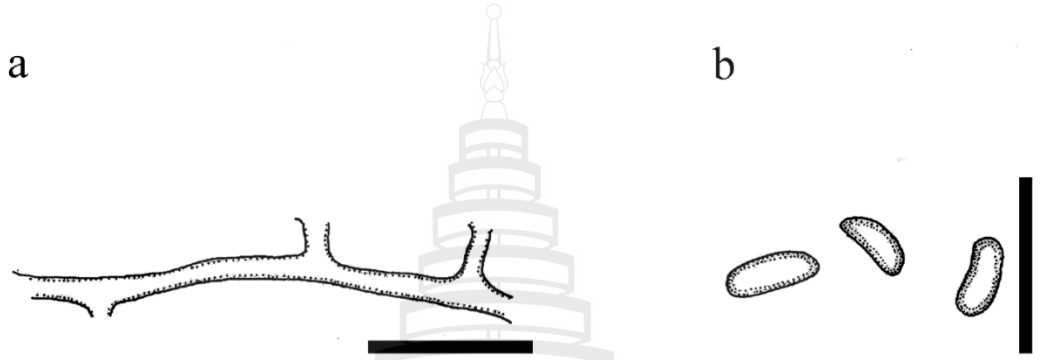


Figure 4.117 *Jattaea algeriensis*

Figure 4.117, a Adelophialides. b Conidia. Scale bars: a, b = 10 μm. Redrawn from Kazemzadeh-Chakusary et al. (2021).

Family: *Pleurostomataceae* Réblová, L. Mostert, W. Gams & Crous

Pleurostoma Tul. & C. Tul., Select. fung. carpol. (Paris) 2: 247 (1863)

Figure 4.118

Index Fungorum number: IF4247; Facesoffungi number: FoF01137.

Pleurostoma was erected by Tulasne and Tulasne (1863), and *P. candollei* is designated as the type species. The genus comprises eight species (Species Fungorum 2025) and only six of them have molecular data (ITS, SSU, LSU and *tub2*). The asexual morph is hyphomycetous, monophialidic, and heavily sporulating, and the collarettes are frequently cupped or slightly rounded. The conidiophore and conidial characteristics among *Pleurostoma* species are highly variable. The sexual morph has globose, black ascomata, reniform to oblong asci, and allantoid, aseptate ascospores (Tulasne & Tulasne, 1863; Maharachchikumbura et al., 2016; Réblová et al., 2015; Tsang et al., 2021). Species are found in contaminated ground wood pulp, dead wood, human clinical samples, sewage and soil. Further, they can be human and plant

pathogens. Species are distributed in China, France, Sweden, Sudan and the USA (Tulasne & Tulasne, 1863; Tsang et al., 2021).

Table 4.134 *Pleurostoma* species isolated from soil

Species	Country	Habitat or soil type	References
Pleurostoma richardsiae	India	Hexachlorocyclohexane dump site	Kaur et al. (2023)

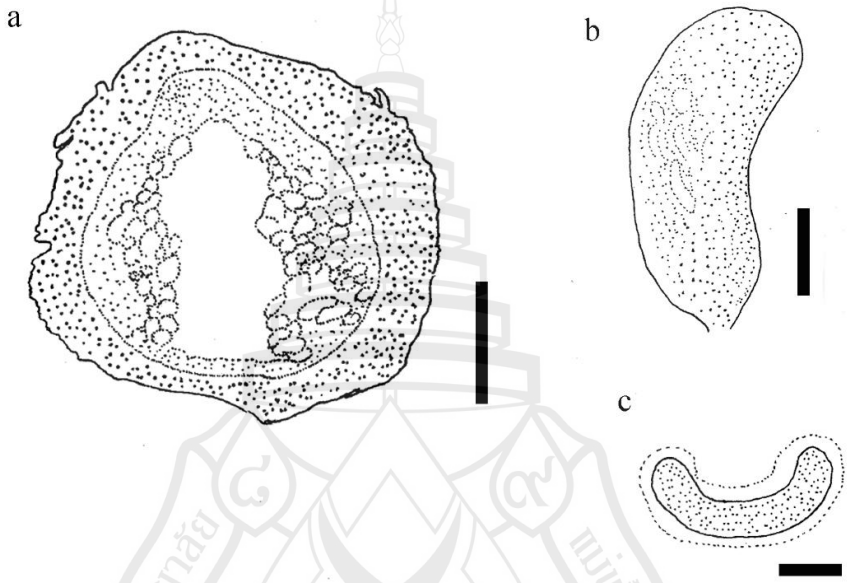


Figure 4.118 *Pleurostoma candollei* (PC 0167640)

Figure 4.118, a Ascoma b Asci. c Ascospore. Scale bars: a = 100, b = 5 μm, c = 1 μm. Redrawn from Hyde et al. (2020c)

Order: *Diaporthales*

Family: *Diaporthosporellaceae*

Diaporthosporella C.M. Tian & Q. Yang; Mycoscience 59: 229–235 (2017)

Index Fungorum number: IF822664

Diaporthosporella was introduced by Yang et al. (2018) based on combined phylogeny (ITS and LSU) and morphological evidence and *D. cercidicola* is accommodated as the type species. There are two species listed in Species Fungorum (2025), with both having molecular data. The asexual morph is phomopsis-like, which is characterized by pycnidial conidiomata, erumpent at maturity with acropleurogenous, branched or sympodial branched, cylindrical, aseptate conidiophores. Conidiogenous cells are enteroblastic, phialidic, cylindrical, terminal, slightly tapering towards the apex that

produce ellipsoidal, aseptate, hyaline, smooth conidia that are bi-guttulate at each end. The sexual morph has perithecial ascomata that are inconspicuous at bark level, surrounding ectostromatic discs, usually irregularly scattered, globose to subglobose, and dark brown to black. Asci are 8-spored, unitunicate, clavate to oblong-clavate, sessile, thin-walled, that contain irregularly uniseriate, allantoid or subreniform, hyaline, aseptate somewhat acute at one end and obtuse at other, 3-4- guttulate ascospores with larger guttules at the center and smaller ones at the ends (Yang et al., 2018b). Species have been isolated as saprobic and pathogenic stages from China (Tennakoon et al., 2021; Yang et al., 2018b). The genus has not previously been reported from soil.

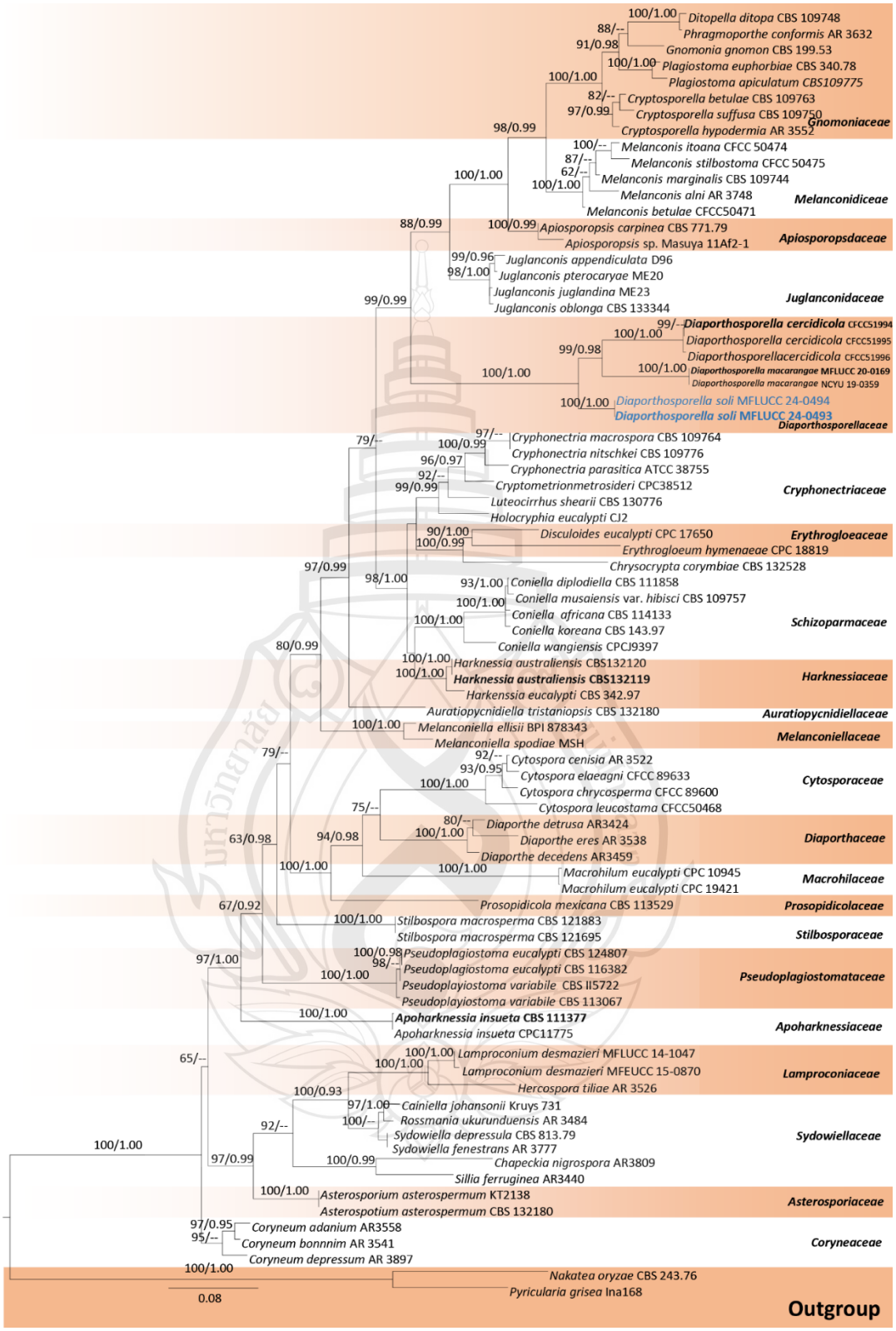


Figure 4.119 The best scoring IQ-tree generated of the combined ITS and LSU sequence data for selected families in *Diapothales*

Figure 4.119, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue and ex-type strains are in bold. The tree is rooted in *Nakatea oryzae* (CBS243.76) and *Pyricularia grisea* (Ina168). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 1589 bp, and single gene alignments are ITS: 750 bp, and LSU: 839 bp. The matrix had 755 distinct alignment patterns with 25.24% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.54849, AG = 2.62794, AT = 2.47465, CG = 1.49097, CT = 6.45856, GT = 1.00000; gamma distribution shape parameter α = 0.654.

Diaporthosporella soli Yasanthika & K.D. Hyde, sp. nov.

Figure 4.120

Index Fungorum number: IF903046

Etymology – The specific epithet "*soli*", refers to the soil in Latin, the location of which the substrate holotype was collected.

Holotype – MFLU25-0137

Sexual morph: Undetermined. Asexual morph: *Conidiomata* 90–120 × 100–135 μm ($\overline{x}$ = 110 × 119 μm, n=10), pycnidial, solitary or confluent, superficial on MEA, reddish brown to black, globose to sub-globose, unilocular, pycnidial wall cells *textura angularis*. *Conidiophores* 2–5 × 2–4 μm ($\overline{x}$ = 3 × 2.5 μm, n=10), formed from the pycnidial wall, acropleurogenous, cylindrical to sub-cylindrical, erect or flexuous, aseptate, hyaline to sub-hyaline, mostly simple, unbranched, terminally phallidic. *Conidiogenous cells* 3.5–5.5 × 2.5–4 μm ($\overline{x}$ = 4.5 × 3 μm, n=10), *p*hialidic, discrete, ampulliform. *Conidia* 3.5–5.5 × 1–2 μm ($\overline{x}$ = 4.5 × 1.5 μm, n = 20), hyaline, obovoid to cylindrical to reniform or ellipsoidal, aseptate or sometimes 1 septate, rough granular surface, thick-walled, verruculose.

Culture characteristics – *Colonies* on PDA at 25℃, become 4–5 cm diam. after seven days of incubation, white becoming brownish red when mature, reverse yellowish white at the center and white at the periphery, become dark brown when mature, flat, irregular margined. *Mycelium* immersed to semi-immersed or superficial, hyaline, becoming pale brown to reddish brown when mature, thick-walled, septate

1.5–4 μm ($\bar{x}$ = 3), sporulated after 1.5 weeks on PDA and MEA. *Chlamydospores* present, intercalary, hyaline to pale reddish-brown, globose to sub globose, in simple or branched chains, thick-walled.

Material examined – Thailand, Chiang Mai, Mae On District, Tham Muang On cave, on soil, 99.238054N, 18.7862964E, 496m 9 May 2022, W.A. Erandi Yasanthika (MFLU25-0137, holotype); ex-type 66-cv20-15=MFLUCC 24-0493; *ibid.* (MFLU25-0177), living culture 59-cv20-12=MFLUCC 24-0494

GenBank numbers – MFLUCC 24-0493: LSU: PQ577822, ITS: PQ012929; MFLUCC 24-0494: LSU: PQ577823, ITS: PQ577824.

Notes – Based on multi-gene phylogeny and the morphological studies, *Diaporthosporella soli* has been introduced as a new species. The phylogenetic analyses in *Diporthales* (Figure 4.110) showed that our species (MFLUCC 24-0493 and MFLUCC 24-0494) clusters within *Diaporthosporella*, producing a distinct clade sister to *D. cercidicola* and *D. macarangae* with 100% ML and 1.0.BYPP statistical support. The base pair difference in the ITS (+5.8S) gene region between *Diaporthosporella soli* and *D. cercidicola* is 108/559 (19%) (including gaps), and with *D. macarangae* is 101/520 (19%) (including gaps). Our collection produced asexual morphs with ampulliform conidiogenous cells and obovoid to cylindrical to reniform or ellipsoidal, aseptate or 1 septate, rough granular surface, thick-walled conidia, which are different from *D. cercidicola* and *D. macarangae* that have cylindrical conidiogenous cells and ellipsoidal, aseptate, hyaline, smooth, biguttulate at each end of the conidia (Yang et al., 2018; Tennakoon et al., 2021). *Diaporthosporella cercidicola* has been found in twigs and branches of *Cercis chinensis* and *D. macarangae* on dead leaves of *Macaranga tanarius* (Tennakoon et al., 2021; Yang et al., 2018b). Based on multi-gene phylogeny and morphology, we introduce our speceis as *Diaporthosporella soli* from disturbed-cave soil in Thailand. This is the first *Diaporthosporella* species found in the soil, denoting its preferences for various habitats.

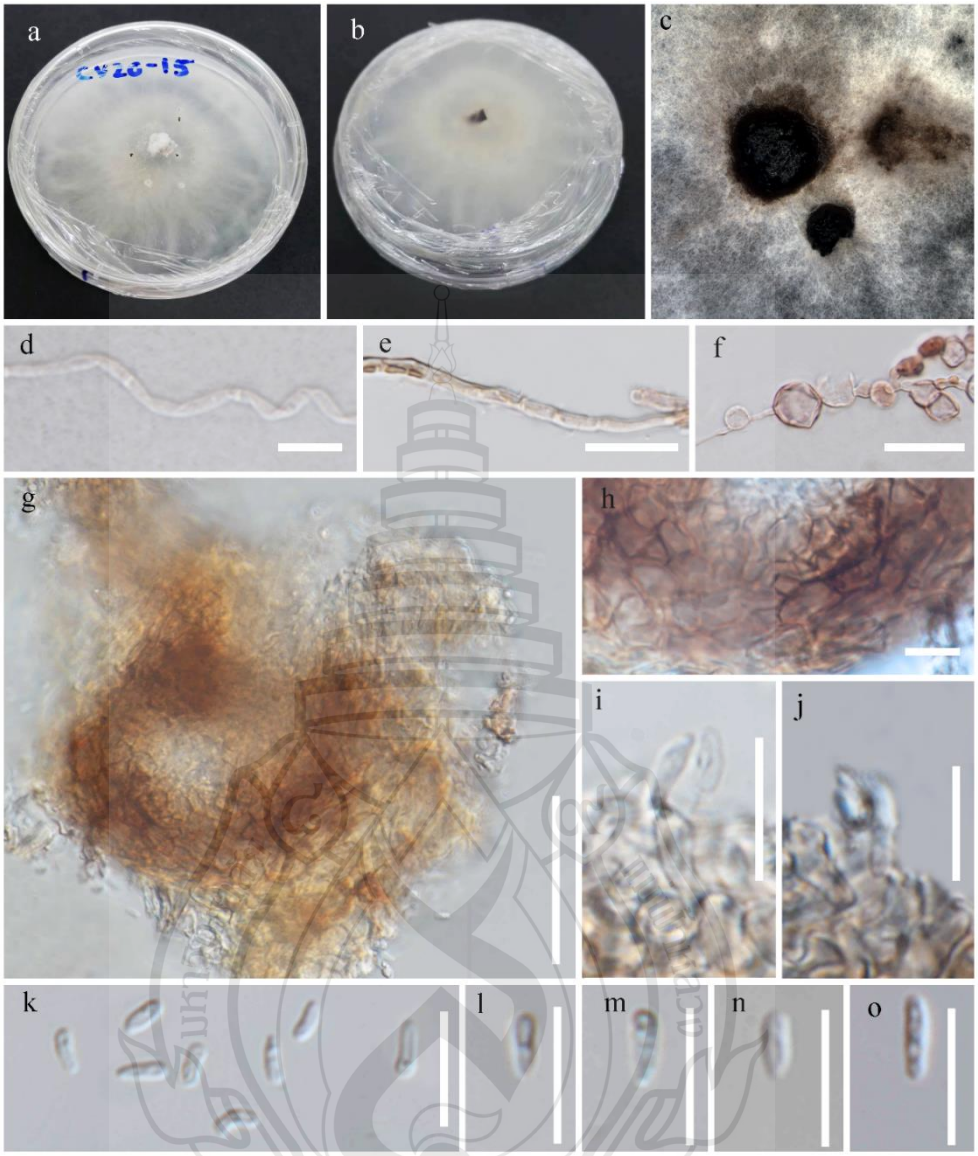


Figure 4.120 *Diaporthosporella soli*. (MFLU25-0137, Holotype)

Figure 4.120, a, b Culture characters on the PDA (b = reverse). c Pycnidia forming on the culture. d Immature hypha. e Mature hyphae. f Chlamydospores g Pycnidia. h Pycnidia wall. i, j Conidiogenous cells k–o Conidia. Scale bars: g = 50 µm, e, f = 20 µm, d, h–o = 10 µm.

Order: ***Magnaporthales*** Thongk., Vijaykr. & K.D. Hyde

Family: ***Magnaporthaceae*** P.F. Cannon

Falciphoriella Hern.-Restr. & Crous, Stud. Mycol. 83: 9 (2016)

Figure 4.121

Index Fungorum number: IF816902; Facesoffungi number: FoF10236

Falciphoriella was introduced by Hernández-Restrepo et al. (2016b) based on multi-gene phylogeny (LSU, ITS, *rpb1* and *tef1-α*), with the type species, *F. solaniterrestris*. The genus is comprised of two species (Species Fungorum, 2025), and both of them have molecular data. The hyphomycetous asexual morph is characterized by hyaline to pale brown, differentiated, indeterminate, and branched conidiophores and phalidic, hyaline to pale brown, terminal or intercalary conidiogenous cells, with hyaline, fusiform, sometimes obovoid, conidia. Species are associated with soil and submerged wood in fresh water and terrestrial habitats located in China and the Netherlands (Hernández-Restrepo et al., 2016b; Wang et al., 2024b).

Table 4.135 *Falciphoriella* species isolated from soil

Species	Country	Habitat or soil type	References
Falciphoriella solaniterrestris	the Netherlands	Potato field	Hernández-Restrepo et al. (2016b)

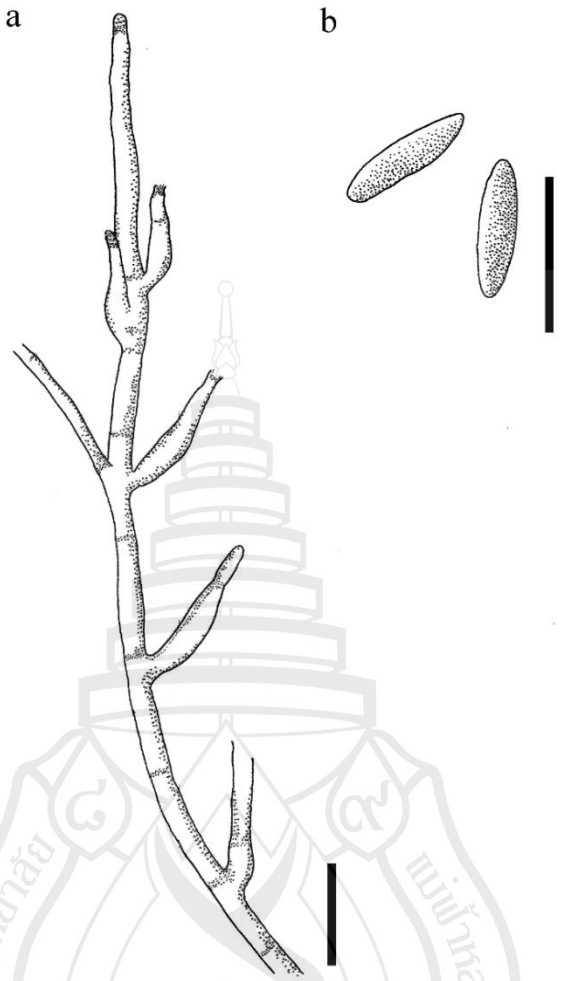


Figure 4.121 *Falciphoriella solaniterrestris* (CBS H-22572)

Figure 4.121, a Conidiophores b Conidia. Scale bars: a, b = 10 μm. Redrawn from Hernández-Restrepo et al. (2016b).

Order: ***Myrmecridiales*** Crous

Family: ***Myrmecridiaceae*** Crous

Myrmecridium Arzanlou, W. Gams & Crous, Stud. Mycol.58: 84 (2007)

Figure 4.122

Index Fungorum number: IF504559; Facesoffungi number: FoF07925

Arzanlou et al. (2007) established *Myrmecridium*, typified by *M. schulzeri* based on LSU and ITS phylogeny. Currently, 23 *Myrmecridium* species are listed in the Species Fungorum (2025) and all of them have molecular data. The genus has a ramichloridium-like asexual morph that is characterized by unbranched, straight or

flexuose, brown conidiophores, and terminally integrated, polyblastic, cylindrical, conidiogenous cells. Conidia are solitary, sub-hyaline, smooth or finely verrucous, obovoidal or fusiform, with a wing-like gelatinous sheath and they are produced from schizolytic conidial secession (Arzanlou et al., 2007). The only known sexual morph is reported from *M. montsegurinum* (Hyde et al., 2020c). *Myrmecridium* species are distributed in both terrestrial and aquatic environments, including leaves, marine sediments, reed litter, soil, stems and submerged wood, while some species are eurypsychrophilic, meaning that they can grow at lower temperatures (Peintner et al., 2016). Species have been found in Australia, China, Indonesia, Thailand and the Netherlands (Jiea et al., 2013; Peintner et al., 2016).

Table 4.136 *Myrmecridium* species isolated from soil

Species	Country	Habitat or soil type	References
Myrmecridium flexuosum	Suriname	ND	Arzanlou et al. (2007)
M. obovoideum	China	ND	Jiea et al. (2013)
M. hiemale	Austria	Snow-covered alpine soil	Peintner et al. (2016)
M. schulzi	Germany	Wheat-field soil	

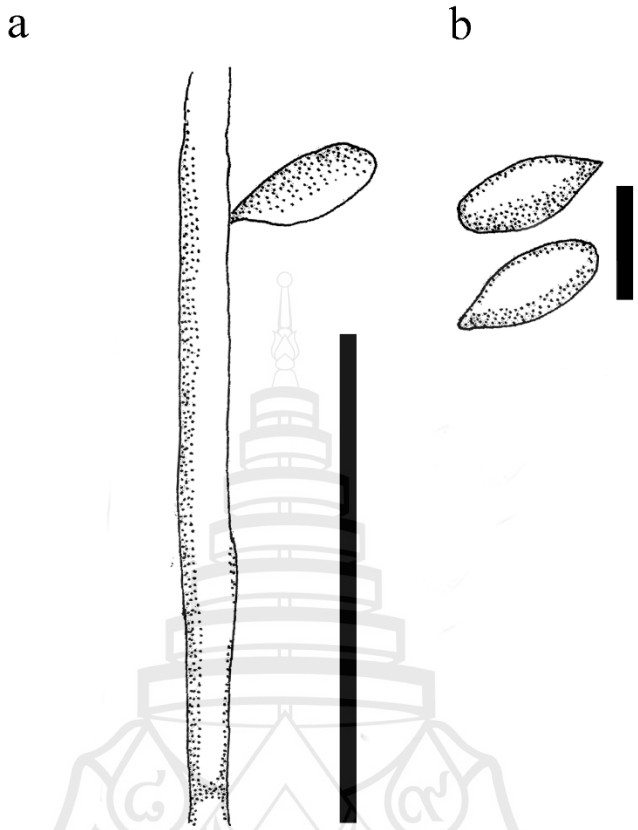


Figure 4.122 *Myrmecridium schulzeri* (CBS 325.74)

Figure 4.122, a Conidiogenesis b Conidio genesis. Scale bars: a, b = 10 μm. Redrawn from Arzanlou et al. (2007).

Order: *Ophiostomatales* Benny & Kimbr.

Family: *Ophiostomataceae* Nannf.

Leptographium Lagerb. & Melin, Svensk SkogsvårdsföreningTidskr. 25: 257 (1927)

Figure 4.123

Index Fungorum number: IF8749; Facesoffungi number: FoF11030

Leptographium was introduced by Lagerberg et al. (1927), and the type species is designated as *L. lundbergii*. The phylogenetic revision of De Beer and Wingfield (2013) described 10 species complexes in *Leptographium sensu lato*. Previously, generic boundaries between *Grosmannia* and *Leptographium* had a controversy; however, currently, they have been recognized as two distinct genera (Wang et al., 2024e). There are 93 species available in the Species Fungorum (2025), and Wang et

al. (2024c) have provided LSU and ITS phylogeny using 63 *Leptographium* species. According to De Beer and Wingfield (2013), *Leptographium sensu lato* was predominantly characterized by leptographium-like asexual morphs, while some smaller lineages had synnematous or raffaelea-like asexual morphs, and they have dark mononematous conidiophore and conidiogenous apparatus that are comprised of a series of apical branches (metulae) with amero-conidia produced in slimy masses (Lagerberg et al., 1927; Weber et al., 1996). The sexual morph has ascomata with long necks and ascospores in slimy masses (Lagerberg et al., 1927). These species are tolerant to high concentrations of cycloheximide in culture, and their cell walls are composed of rhamnose and cellulose (Harrington, 1981). *Leptographium* is associated with dung, insects (bark beetles), decaying plant materials, sediments and soil and some species are root pathogens of conifers (Hyde et al., 2020c; Weber et al., 1996). The genus has been found in Canada, Finland, Great Britain, Mexico, Spain and the USA (Wang et al., 2024e).

Table 4.137 *Leptographium* species isolated from soil

Species	Country	Habitat or soil type	References
Leptographium reconditum	South Africa	Rhizosphere of *Triticum*	Jooste (1978)
L. costaricense	Costa Rica	Rhizosphere of *Talauma sambuensis*	Weber et al. (1996)

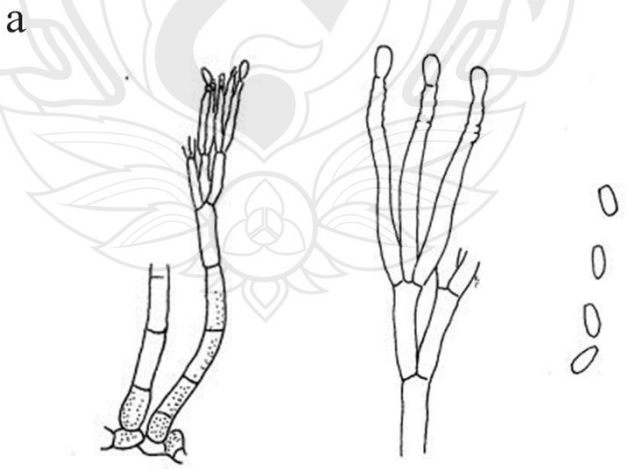


Figure 4.123 *Leptographium lundbergii*

Figure 4.123, a Conidiogenesis on the conidiophores and conidia Redrawn from Seifert et al. (2011)

Sporothrix Hektoen & C.F. Perkins, J. Exp. Med. 5: 80 (1901)

Index Fungorum number: IF10046; Facesoffungi number: FoF10509

Sporothrix was introduced by Hektoen and Perkins (1900), and *S. schenckii* is designated as the type species. Species Fungorum (2025) has listed 98 species in the genus, while 66 species have molecular data (de Beer et al., 2022). Previously, *S. schenckii* and *Ophiostoma stenoceras* were considered a species complex in *Ophiostoma sensu lato* (Berbee & Taylor, 1992). Subsequently, *Sporothrix* was confirmed as a distinct clade from *Ophiostoma sensu stricto* based on multi-gene phylogenetic analyses (LSU, ITS, *tub2* and cmdA) (de Beer et al., 2016). Ostafińska et al. (2021) mentioned that the ITS is the least informative gene region while emphasizing the use of protein genes for the species delineation in the genus. The hyphomycetous asexual morph of *Sporothrix* has sympodially proliferating conidiophores with denticulate conidiogenous cells that produce hyaline or occasionally pigmented conidia. The sexual morph is characterized by dark brown to black, globose, ostiolate ascomata with elongated necks and evanescent, globose to broadly clavate asci, with curved, lunate to reniform, hyaline, aseptate ascospores (De Beer & Wingfield, 2013; Hyde et al., 2020c). Some *Sporothrix* species cause disease in humans and animals. Further, they are mostly found in *Protea* sp. and other forest wood substrates, while several species are associated with ambrosia beetles, basidiocarps, human clinical samples, mites, and soil. The genus is distributed in Africa, America, and Asia regions (Hyde et al., 2020c; Ostafińska et al., 2021).

Table 4.138 *Sporothrix* species isolated from soil

Species	Country	Habitat or soil type	References
Sporothrix pallida	the Netherlands	A garden	de Meyer et al. (2008)
S. dimorphospora	Canada	ND	de Beer et al. (2022)
S. guttuliformis	Malaysia	ND	
S. inflata	Canada	Wheat field soil	
S. albicans	UK	ND	
S. chilensis	Chile	ND	
S. humicola	South Africa	ND	
S. mexicana	Mexico	ND	
S. bragantina	Brazil	Forest	
S. brunneoviolacea	Spain	Forest	

Diaporthomycetidae families incertae sedis

Family: *Trichosphaeriaceae* G. Winter

Brunneochlamydosporium Giraldo López & Crous, Stud. Mycol. 92: 260 (2018)

Figure 4.124

IndexFungorum: IF 828053; Facesoffungi number: FoF13528

Brunneochlamydosporium was established by Giraldo & Crous (2019) based on morphology and the LSU, ITS, *tef1*-α and *rpb2* multigene phylogeny, while accommodating the type species, *B. nepalense*, which was previously known as *Acremonium nepalense*. Giraldo and Crous (2019). Currently, the genus accommodates four species (Species Fungorum 2025), and all of them have molecular data. The asexual morph of the genus is hyphomycetous which is characterized by erect, lateral, simple or poorly branched conidiophores. Conidiogenous cells are enteroblastic, monophialidic, and sometimes polyphialidic and produce hyaline, ellipsoidal, cylindrical, 1-celled, smooth-walled conidia arranged in slimy heads. The sexual morph remains unreported. The species have been discovered from dead wood, leaves, river sediments, sputum and soil in Brazil, France, Nepal, Spain, Switzerland and the Netherlands (Giraldo & Crous, 2019).

Table 4.139 *Brunneochlamydosporium* species isolated from soil

Species	Country	Habitat or soil type	References
Brunneochlamydosporium nepalense	Nepal	Soil under *Pinus* sp.	Giraldo and Crous (2019)
B. nepalense	the Netherlands	Scrub sandy soil	
B. nepalense	the Netherlands	Garden soil	
B. terrestre	France	Soil associated with Manihot	

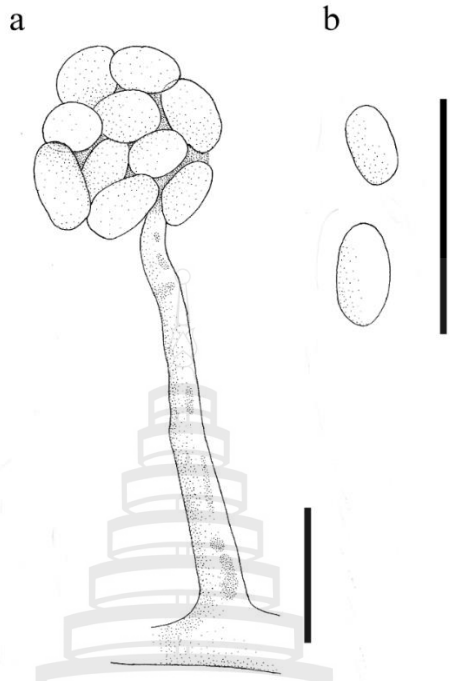


Figure 4.124 *Brunneochlamydosporium nepalense* (CBS 971.72)

Figure 4.124, a Conidiogenesis b Conidia. Scale bar: a = 5μm, b = 10μm. Redrawn from Giraldo and Crous (2019).

Chordomyces Bilanenko, Georgieva & Grum-Grzhim., Fungal Divers. 71(1): 29 (2015)

Figure 4.125

Index Fungorum number: IF811265; Facesoffungi number: FoF13530

Grum-Grzhimaylo et al. (2016) erected *Chordomyces* based on morphology and combined LSU and ITS phylogeny, and *Chordomyces antarcticus* is designated as the type species. There are two species recognized in the genus Species Fungorum (2025), and both of them have molecular data. Hyphomycetous asexual morph is characterized by conidiophores that are solitary or forming in synnemata, having enteroblastic, mono- or polyphialidic sympodially proliferating conidiogenous cells, and hyaline, subglobose, limoniform, ellipsoidal to cylindrical conidia. The sexual morph is unknown (Grum-Grzhimaylo et al., 2016; Giraldo & Crous, 2019). Species are isolated from dead stems, leaf litter and soil habitats (including agricultural fields, gardens,

rhizosphere and soda soils) collected from Belgium, Germany, Mongolia and Russia (Giraldo & Crous, 2019).

Table 4.140 *Chordomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Chordomyces albus	the Netherlands	Garden	Giraldo et al. (2019)
C. antarcticus	Russia	Soda soil	
C. antarcticus	the Netherlands	Garden	

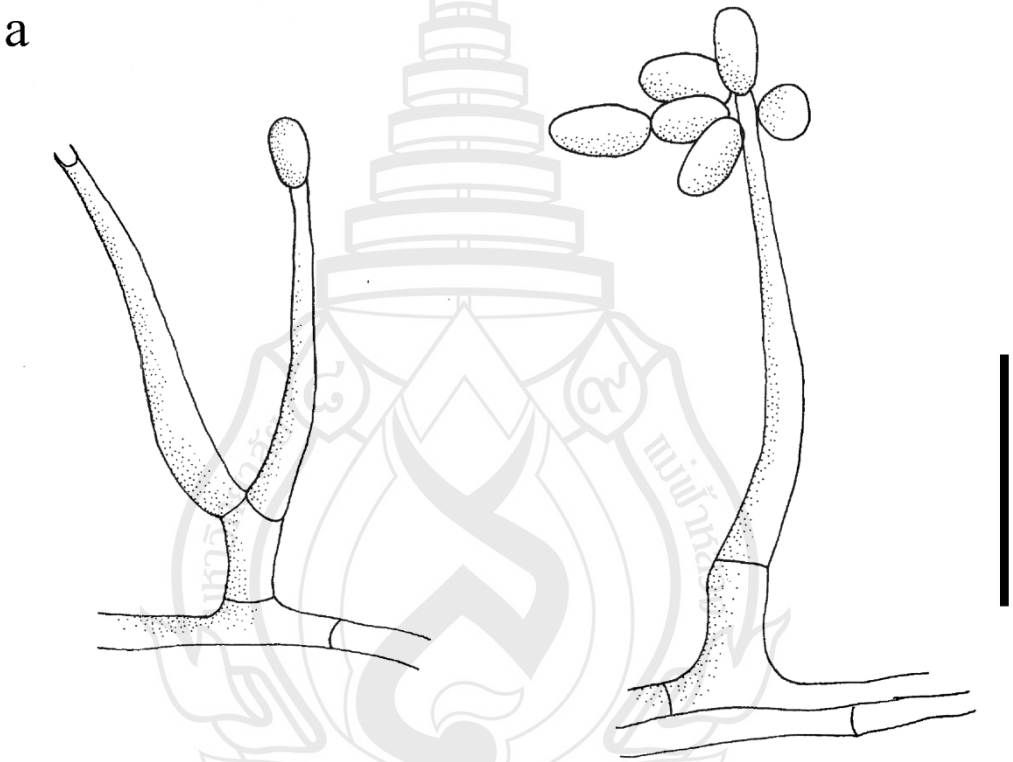


Figure 4.125 *Chordomyces antarcticus* (CBS 120045)

Figure 4.125, a Conidiogenesis on conidiophores. Scale bar: a = 10 μm. Redrawn from Grum-Grzhimaylo et al. (2016)

Furcasterigmium Giraldo López & Crous, Stud. Mycol. 92: 251 (2019)

Figure 4.126

IndexFungorum: IF 828041; Facesoffungi number: FoF13531

Giraldo and Crous (2019) introduced *Furcasterigmium* based on morphology and LSU, ITS, *tef1*-α and *rpb2* combined gene analyses; the type species is designated as *F. furcatum* and only one species is accepted (Species Fungorum 2025). The asexual

morph is hyphomycetous, characterized by erect conidiophores with sympodially proliferating, enteroblastic, mono- and polyphialidic conidiogenous cells and ellipsoidal, 1-celled, hyaline, smooth-walled conidia. Sexual morph is unknown. *Furcasterigmium* species has been found in plants and soil in France, Germany, Iran and Italy (Giraldo & Crous, 2019).

Table 4.141 *Furcasterigmium* species isolated from soil

Species	Country	Habitat or soil type	References
Furcasterigmium furcatum	France	Dune sand under *Calystegia soldanella*	Giraldo and Crous (2019)
F. furcatum	Italy	Agricultural soil	
F. furcatum	The Netherlands	Garden	

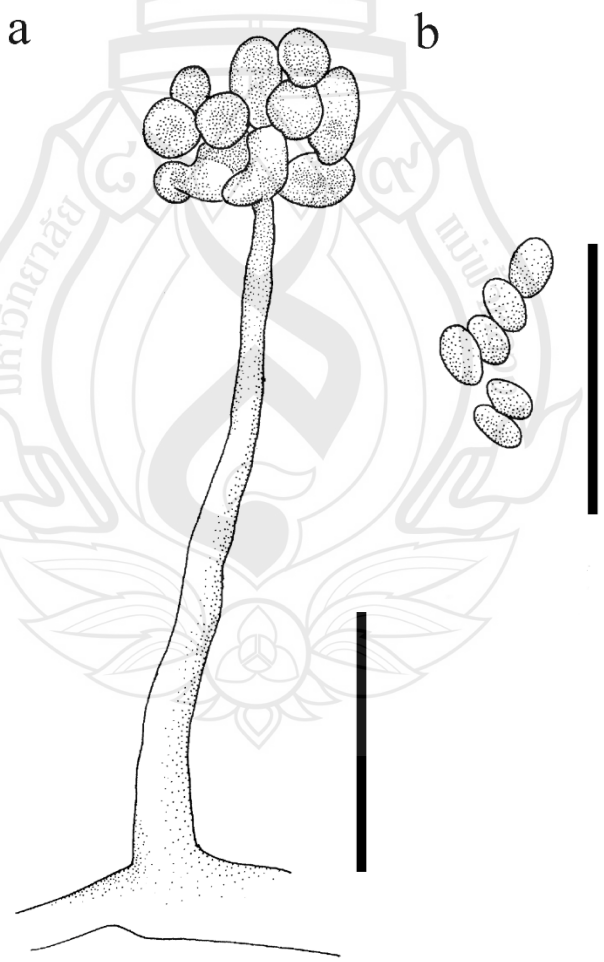


Figure 4.126 *Furcasterigmium furcatum* (CBS 122.42)

Figure 4.126, a Conidiophores and slimy heads b Conidia Scale bar: a, b = 10 μm. Redrawn from Giraldo and Crous (2019).

Fuscohypha Giraldo López & Crous, Stud. Mycol. 92: 264 (2019)

Figure 4.127

Index Fungorum number: IF828058; Facesoffungi number: FoF13532

Fuscohypha was introduced by Giraldo and Crous (2019) based on morpho-molecular (LSU, ITS, *tef*1-α and *rpb2*) analyses and *F. expansa* is placed as the type species. Currently, it remains as a monotypic genus. The genus has a hyphomycetous asexual morph characterized by simple or verticillate conidiophores with enteroblastic, monophialidic conidiogenous cells, and sub-globose or ellipsoidal, 1-celled, hyaline conidia that are arranged in slimy heads. The sexual morph is unknown (Giraldo & Crous, 2019; Hyde et al., 2020c). The genus has been found from soil and the tuber of *Dioscorea* sp. in Brazil and Martinique (Giraldo & Crous, 2019).

Table 4.142 *Fuscohypha* species isolated from soil

Species	Country	Habitat or soil type	References
Fuscohypha expansa	Brazil	ND	Giraldo and Crous (2019)

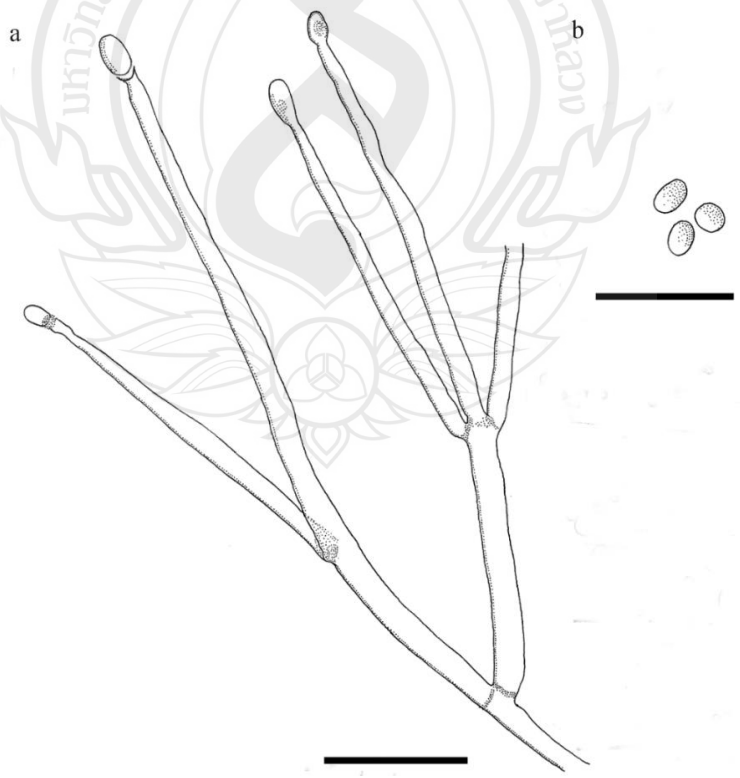


Figure 4.127 *Fuscohypha expansa* (CBS 419.89)

Figure 4.127, a Conidiophores b Conidia Scale bar: a, b = 10 μm. Redrawn from Giraldo and Crous (2019)

Gibellulopsis Bat. & H. Maia, Anais Soc. Biol. Pernambuco 16(1): 153 (1959)

Figure 4.128

Index Fungorum number: IF8331; Facesoffungi number: FoF13533

Gibellulopsis was introduced by Batista and Maia (1959) and typified by *G. piscis*. However, based on LSU, ITS, *tef*1-α and *rpb2* phylogeny and the morphology, Giraldo and Crous (2019) designated *G. serrae* as the type species as a result of a new combination derived from *G. piscis* in their study. In the Species Fungorum (2025), there are seven species listed under the genus. The asexual morph is hyphomyceteous, which comprises erect, mostly terminal conidiophores and conidiogenous cells with collarettes and distinct periclinal thickenings. The conidia are hyaline, elongate, ellipsoidal to cylindrical, 1- or 2-celled, and produced in slimy heads. The species have been isolated from clinical specimens, seeds, soil, wrapping material and wool in Argentina, Canada, Denmark, Finland, France, Germany, Israel, Sweden and the Netherlands (Giraldo & Crous, 2019; Hyde et al., 2020c).

Table 4.143 *Gibellulopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Gibellulopsis fusca	India	ND	Giraldo and Crous (2019)
G. fusca	The Netherlands	Garden	
G. nigrescens	Israel	ND	
G. nigrescens	The Netherlands	Sandy soil	
G. nigrescens	The Netherlands	Soil under lawn	
G. serrae	Israel	ND	
G. serrae	New Zealand	ND	
G. serrae	Argentina	Soil of *Glycine max*	
G. serrae	Israel	Soil in cotton field	

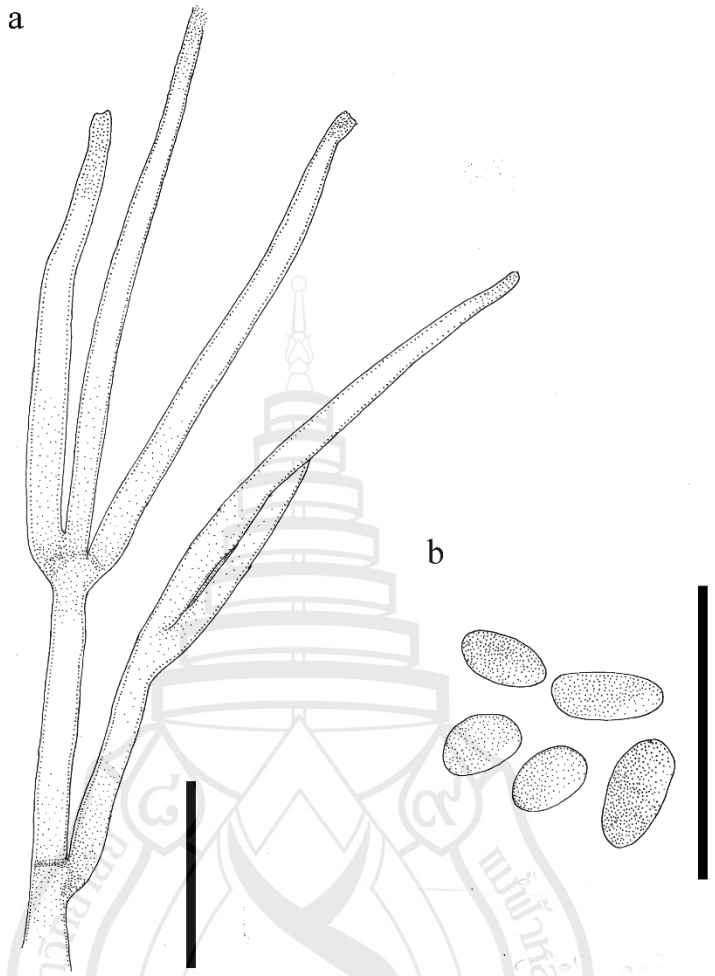


Figure 4.128 *Gibellulopsis serrae* (CBS 101221)

Figure 4.128, a. Conidiophores. (CBS 892.70) b. Conidia. Scale bar: a = 10μm. Redrawn from Giraldo & Crous (2019)

Lectera P.F. Cannon, MycoKeys 3: 28 (2012)

Figure 4.129

Index Fungorum number: IF550041; Facesoffungi number: FoF13534

Lectera was established by Cannon et al. (2012), assigning *L. colletotrichoides* as the type species. Six species are currently accepted in the genus (Cannon et al., 2012a; Species Fungorum, 2025), and all the species are supported by molecular data. *Lectera* was delineated based on the conidial size, and the ITS and *gapdh* genes (Crous et al., 2017b; Hyde et al., 2020c). The asexual morph is characterized by sporodochial or acervular, pink or flesh-coloured, globose to subglobose conidiomata that do not

possess a clear upper wall, and conidiophores are often reduced to conidiogenous cells that produce navicular or fusiform conidia. The sexual morph is unknown (Cannon et al., 2012a; Giraldo & Crous, 2019). Species have been identified as pathogens or saprobes inhabiting plants and soils from Australia, Brazil, Egypt and Malaysia (Cannon et al., 2012a; Giraldo & Crous, 2019).

Table 4.144 *Lectera* species isolated from soil

Species	Country	Habitat or soil type	References
L. colletotrichoides	Brazil	ND	Cannon et al. (2012a)
L. humicola	Brazil	ND	
L. nordwiniana	Garden	The Netherlands	

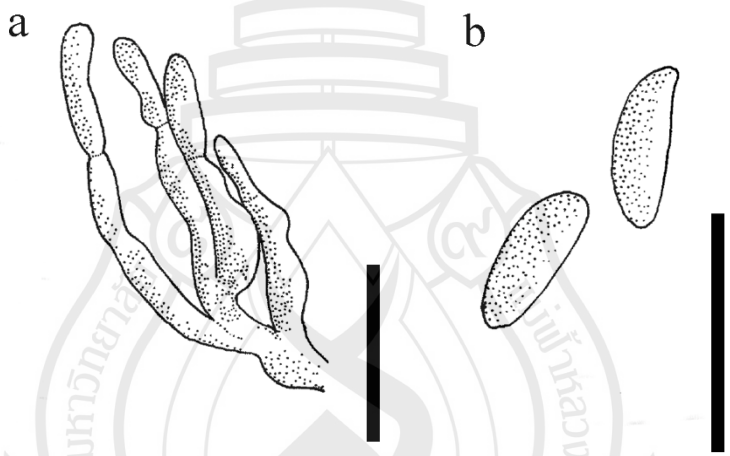


Figure 4.129 *Lectera colletotrichoides* ((IMI 332702)

Figure 4.129, a Conidiogenous cells b Conidia. Scale bar: a = 10μm. Redrawn from Giraldo and Crous (2019).

Paramusicillium Giraldo López & Crous, Stud. Mycol. 92: 269 (2019)

Figure 4.130

Index Fungorum number: IF828067; Facesoffungi number: FoF16638

Paramusicillium is a monotypic genus introduced by Giraldo and Crous (2019) based on morphology and the multi-gene phylogeny (LSU, ITS, *tef*1-α and *rpb2*), *Paramusicillium asperulatum* (= *Musicillium theobromae*) as the type species. Due to

the distant phylogeny and conidiophore morphology, *M. theobromae* was separated from *Musicillium* and established *Paramusicillium* (Giraldo & Crous, 2019; Hyde et al., 2020c). The hyphomycetous asexual morph is characterized by septate, repeatedly verticillate towards the apex, distinctly brown pigmented conidiophores, enteroblastic, monophialidic conidiogenous cells, and ellipsoidal or cylindrical, 1-celled, smooth-walled conidia that are in slimy heads and appear in pale brown when in mass. The sexual morph remains undetermined. *Paramusicillium asperulatum* is identified as a postharvest pathogen in fruits and also inhabiting soil substrates in Argentina, China, Egypt, Sao Tome and Príncipe (Youssef et al., 2020).

Table 4.145 *Paramusicillium* species isolated from soil

Species	Country	Habitat or soil type	References
Paramusicillium asperulatum	Sao Tome and Príncipe	ND	Giraldo and Crous (2019)

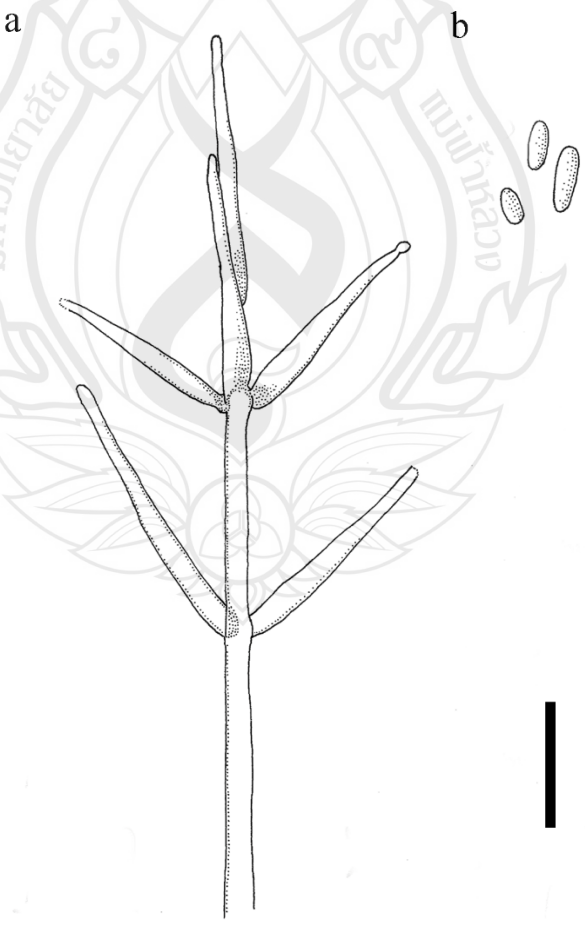


Figure 4.130 *Paramusicillium asperulatum*

Figure 4.130, a. Conidophores. b. Conidia Scale bar: a,b = 10μm. Redrawn from Giraldo and Crous (2019)

Phialoparvum Giraldo López & Crous, Stud. Mycol. 92: 265 (2019)

Figure 4.131

Index Fungorum number: IF828063; Facesoffungi number: FoF13539

Giraldo and Crous (2019) introduced *Phialoparvum* with its type species *P. bifurcatum*, based on morpho-molecular (LSU, ITS, *tef1-α* and *rpb2*) studies. Currently, three *Phialoparvum* species are listed in Species Fungorum (2025) and all of them are supported by molecular data. The asexual morph is hyphomycetous; having erect, unbranched or poorly branched conidiophores and enteroblastic, mono- and polyphialidic conidiogenous cells. Conidia are hyaline, 1-celled, smooth-walled that are arranged in slimy heads. The sexual morph is undetermined (Giraldo & Crous, 2019). The species have been discovered from plant root and soil in Belgium, China and the Netherlands (Giraldo et al., 2019).

Table 4.146 *Phialoparvum* species isolated from soil

Species	Country	Habitat or soil type	References
Phialoparvum rietveltiae	the Netherlands	Garden	Giraldo and Crous (2019)
P. maaspleinense	the Netherlands	Garden	
P. bifurcatum	Belgium	ND	

Figure 4.131 *Phialoparvum bifurcatum* (CBS 299.70B)

Figure 4.131, a Conidiogenesis on conidophores. b Conidia Scale bar: a,b = 10 μm. Redrawn from Giraldo and Crous (2019)

Plectosphaerella Kleb., Phytopath. Z. 1: 43 (1929)

Fig. 4.132

Index Fungorum number: IF4197; Facesoffungi number: FoF01335

Plectosphaerella was introduced by Klebahn (1929), with *P. cucumerina* as the type species. The genus accommodates 25 species (Species Fungorum 2025), while 23 species are supported by molecular data (LSU, ITS, *tef1-α* and *rpb2*). Previously, the genus was placed in *Hypocreaceae* and subsequently in *Sordariaceae* Domsch et al. (1973); however, it is currently placed in *Plectosphaerellaceae* (Zare et al., 2007; Yang et al., 2021b). The asexual morph is hyphomycetous, and has hyaline, simple and poorly branched conidiophores with enteroblastic, mono- and polyphialidic conidiogenous cells. Conidia are hyaline, cylindrical 1- or 2-celled, smooth-walled, and arranged in slimy heads (Giraldo et al., 2019; Klebahn, 1929). The sexual morph is characterized by perithecial, solitary or gregarious, superficial, sub-globose to pyriform, ascomata with dark brown basal part and paler at the neck. Asci are unitunicate, cylindrical, clavate, thin-walled, 8-spored, and containing 2- celled, hyaline, smooth to slightly warted ascospores. Species are present on leaves, papers, plant roots and soil in Brazil, Canada, Italy, Spain, the Netherlands and the USA (Giraldo et al., 2019; Giraldo & Crous, 2019).

Table 4.147 *Plectosphaerella* species isolated from soil

Species	Country	Habitat or soil type	References
Plectosphaerella cucumerina	The Netherlands	Garden	Giraldo and Crous (2019)
P. hanneae	The Netherlands	Garden	
P. humicola	Congo	ND	
P. oligotrophica	Brazil	ND	
P. pauciseptata	The Netherlands	Garden	
P. plurivora	Germany,	ND	
P. plurivora	The Netherlands	Garden	
P. verschoorii	The Netherlands	Garden	

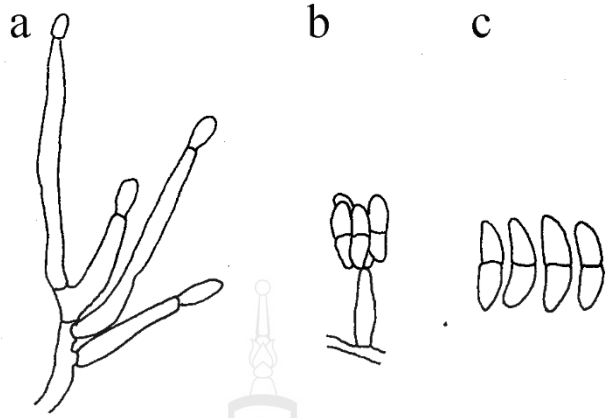


Figure 4.132 *Plectosphaerella cucumerina*

Figure 4.132, a,b Conidophores c Conidia. Redrawn from Domsch et al. (1993)

Sayamraella Giraldo López & Crous, Stud. Mycol. 92: 255 (2019)

Figure 4.133

Index Fungorum number: IF828047; Facesoffungi number: FoF13540

Sayamraella is a monotypic genus, which was introduced by Giraldo and Crous (2019) based on morpho-molecular analyses (LSU, ITS, *tef*1-α and *rpb2*) along with *S. subulata,* isolated from soil, as the type species (Giraldo & Crous, 2019). The asexual morph is hyphomycetous and characterized by sympodially proliferating conidiophores with conidiogenous cells, having minute, cylindrical collarettes and an inconspicuous periclinal thickening at the conidiogenous locus; and hyaline, ellipsoidal, and 1-celled conidia, arranged in slimy heads. The sexual morph is undetermined.

Table 4.148 *Sayamraella* species isolated from soil

Species	Country	Habitat or soil type	References
Sayamraella subulata	Thailand	Soil associated with *Hopea odorata*	Giraldo and Crous (2019)

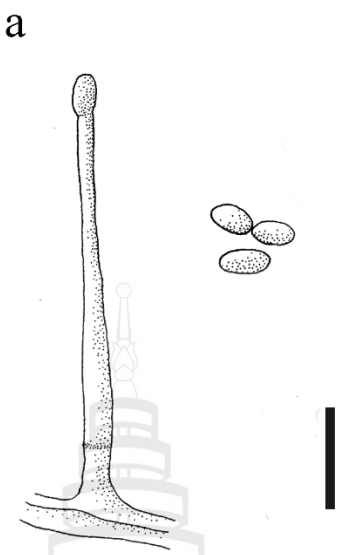


Figure 4.133 *Sayamraella subulata* (BCC 78964)

Figure 4.133, a Simple conidiophore and conidia Scale bar: a = μm. Redrawn from Giraldo and Crous (2019)

Sodiomyces Grum-Grzhim., Debets & Bilanenko ex S.A. Bondarenko, Grum-Grzhim., Debets & Bilanenko, Fungal Diversity 76(1): 52 (2015) [2016]

Figure 4.134

IndexFungorum number: IF92131; Facesoffungi number: FoF13541

Sodiomyces was introduced by Grum-Grzhimaylo et al. (2016) with the type species *S. alkalinus.* The genus was established based on ITS, LSU, SSU, *rpb2* and *tef*1-α phylogeny and morphological support (Grum-Grzhimaylo et al., 2016), and currently, the genus comprises four species (Species Fungorum, 2025), and all of them have molecular data. The asexual morph has weakly branched or penicillate, hyaline conidiophores and enteroblastic, monophialidic conidiogenous cells. Conidia are hyaline, subglobose, cylindrical to oval or allantoid and 1-celled. The sexual morph of the genus has cleistothecial, superficial, globose, dark-brown ascomata and unitunicate, saccate, thin-walled asci without an apical apparatus, and pale brown, ovoid, 2-celled ascospores. *Sodiomyces alkalinus* is known as holomorphic, alkaliphilic species (Grum-Grzhimaylo et al., 2016). Most *Sodiomyces* species are discovered from animal feces, sludge and soil collected from Japan, Kenya, Mongolia and Thailand (Giraldo & Crous, 2019).

Table 4.149 *Sodiomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Sodiomyces alkalinus	Mongolia	Soda soil	Grum-Grzhimaylo et al. (2016)
Sodiomyces magadii	Kenya	Soda soil	
Sodiomyces tronii	Kenya	Soda soil	

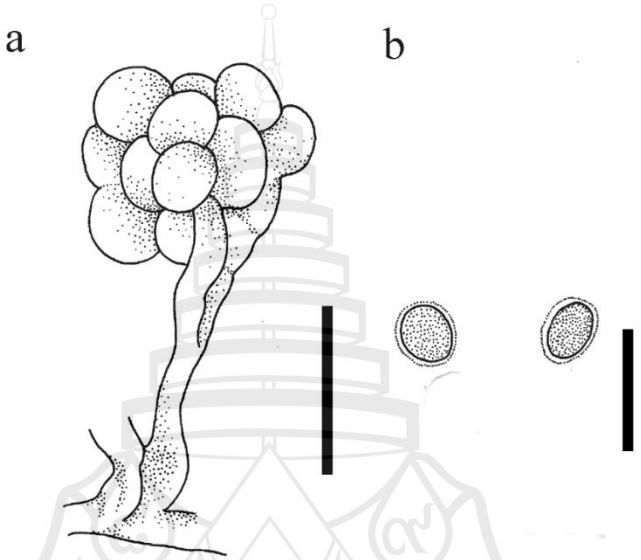


Figure 4.134 *Sodiomyces alkalinus*

Figure 4.134, a. Conidiophore. b. Conidia Scale bar: a, b = 10μm. Redrawn from Grum-Grzhimaylo et al. (2016)

Stachylidium Link, Mag. Gesell. Naturf. Freunde, Berlin 3(1–2): 15 (1809)

Figure 4.135

Index Fungorum number: IF10053; Facesoffungi number: FoF13542

Stachylidium was introduced by Link (1809) without designating a type species (Hughes, 1951). Gams (2017) designated *S. bicolor* (L2923) as the type species of the genus. Subsequently, Giraldo and Crous (2019) have studied the specimens deposited by Link and proposed B700016303 (*S. bicolor*) as the most suitable lectotype. Currently, seven species are listed in the genus (Species Fungorum, 2025), and only two of them have molecular data. The hyphomycetous asexual morph is characterized by septate, verticillate conidiophores arranged singly or in groups, and enteroblastic, hyaline or pale brown, monophialidic conidiogenous cells in whorls, with pale brown to brown, ellipsoidal or cylindrical, 1-celled conidia. The sexual morph is unknown.

The species are distributed in India, Nepal, Spain, Thailand, and Turkey, occurring in decaying plants and soil (Giraldo & Crous, 2019).

Table 4.150 *Stachylidium* species isolated from soil

Species	Country	Habitat or soil type	References
Stachylidium pallidum	Nepal	Soil under *Abies* sp.	Giraldo and Crous (2019)
Stachylidium pallidum	Thailand	ND	

Figure 4.135 *Stachylidium bicolor* (CBS 121802)

Figure 4.135, a Conidiophore and conidiogenous cells b Conidia Scale bar: a, b = 10μm. Redrawn from Giraldo and Crous (2019)

Summerbellia Giraldo López & Crous, Stud. Mycol. 92: 252 (2019)

Figure 4.136

Index Fungorum number: IF828043; Facesoffungi number: FoF13543

Summerbellia is a monospecific genus that was introduced by Giraldo and Crous (2019) based on ITS, LSU, SSU, and *tef*1-α gene regions, accommodating *S. oligotrophica* as the type species. The asexual morph is characterized by erect or

(sub-)erect, unbranched or poorly branched conidiophores and enteroblastic, monophialidic, hyaline conidiogenous cells that produce ellipsoidal or cylindrical, 1-celled, hyaline, smooth-walled conidia arranged in slimy heads. The sexual morph remains undetermined. The species has been isolated from a bath towel, grapefruit juice cans and soil found in Australia, Indonesia, and the USA (Giraldo & Crous, 2019).

Table 4.151 *Summerbellia* species isolated from soil

Species	Country	Habitat or soil type	References
Summerbellia oligotrophica	Indonesia	Alkaline soil	Giraldo and Crous (2019)

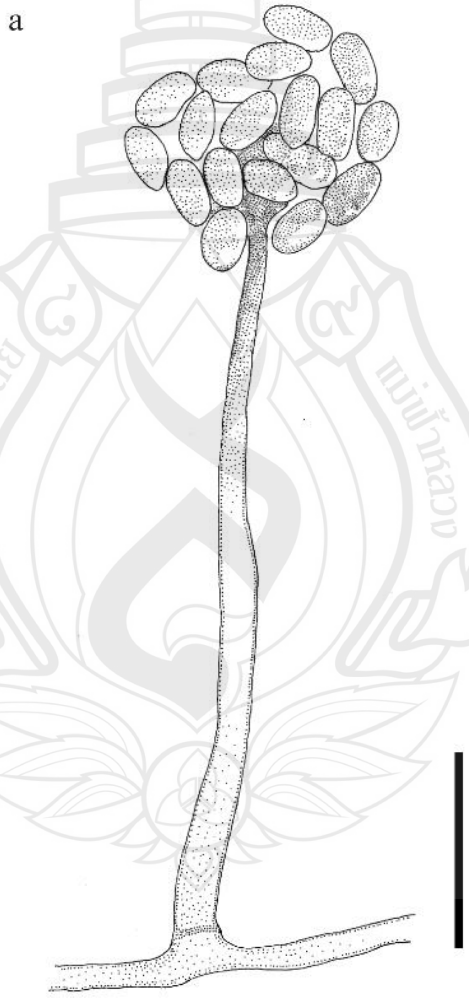


Figure 4.136 *Summerbellia oligotrophica* (CBS 657.94)

Figure 4.136, a Conidiophore and conidia Scale bar: a=10 μm. Redrawn from Giraldo and Crous (2019)

Verticillium Nees, Syst. Pilze (Würzburg): 57 (1816)

Figure 4.137

Index Fungorum number: IF10400; Facesoffungi number: FoF00162

Initially, *Verticillium* was introduced with the type species *V. tenerum*; however, that was later synonymized to *V. luteoalbum* (Subramanian, 1971); but this species was subsequently transferred to *Acrostalagmus* by Zare et al. (2004). As a result, Gams et al. (2005) proposed *V. dahlia* as the type species in *Verticillium* in order to conserve the *Verticillium* generic name. The genus is comprised of 80 species (Species Fungorum 2025), and they are supported by ITS, LSU, SSU, *rpb2* and *tef*1-α molecular data (Giraldo & Crous, 2019). The asexual morph is characterized by mostly verticillate, septate, hyaline to sub-hyaline conidiophores, and enteroblastic, monophialidic, flask-shaped or aculeate conidiogenous cells, with hyaline, ellipsoidal or cylindrical and 1-celled or rarely 2-celled conidia. The sexual morph is unknown. Species are associated with dead and living plant materials, dung and soils, while some of them are plant pathogenic fungi. *Verticillium* is a globally reported genus, including Canada, Japan, New Zealand, the Netherlands, the UK and the USA (Domsch et al., 1993; Giraldo & Crous, 2019).

Table 4.152 *Verticillium* species isolated from soil

Species	Country	Habitat or soil type	References
Verticillium albo-atru	Canada	Soil from potato field	Giraldo and Crous (2019)
V. dahlia	the Netherlands	ND	
V. isaacii	Israel	Soil from potato field	
V. nubilum	UK	ND	
V. tricorpus	New Zealand	ND	
V. tricorpus	Israel	Soil from potato field	

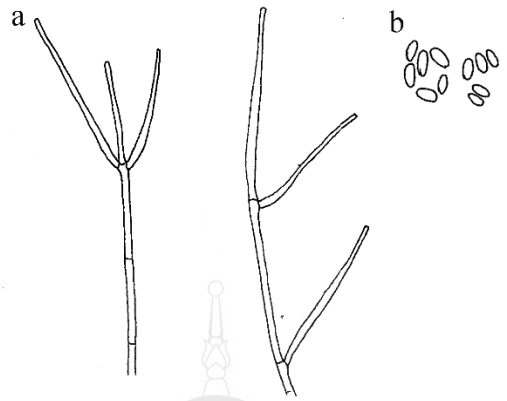


Figure 4.137 *Verticillium dahliae* (CBS205.26)

Figure 4137, a Conidiophore. b Conidia. Redrawn from Domsch et al. (1993)

Trichosphaeriaceae genera incertae sedis

Acrostalagmus Corda, Icon. fung. (Prague) 2: 15 (1838)

Figure 4.138

IndexFungorum number: IF7044; Facesoffungi number: FoF13527

Corda (1838) introduced *Acrostalagmus* with its type species, *A. cinnabarinus*. However, *Sporotrichum luteoalbum*, which was later considered *Verticillium luteoalbum* (Subramanian, 1971), was found to have an identical morphology with *A. cinnabarinus* (Zare et al., 2004). Thus, a new combination, *A. luteoalbus*, and was designated as the type species (Zare et al., 2004). Giraldo and Crous (2019) provided recent phylogeny for this genus based on LSU, ITS, *tef*1-α and *rpb2* gene regions. There are 13 species available in *Acrostalagmus* (Species Fungorum, 2025). The hyphomycetous asexual morph consists of mononematous or synnematous, distinctly bright orange to reddish, branched conidiophores and enteroblastic, sub-hyaline to pale orange, monophialidic, flask-shaped, conidiogenous cells. Conidia are bright orange to reddish, oval, ellipsoidal to oblong-ellipsoidal and 1-celled. The sexual morph is unknown (Zare et al., 2004; Giraldo & Crous, 2019). Some species have cosmopolitan distribution and have been found from bird's feathers and nests, cotton fibres, dung, decaying wood, different types of soil, litter, plant roots, and seeds in Canada, Germany, the Netherlands and the UK (Giraldo & Crous, 2019; Mohammadi, 2015). Species are known for producing bio-active compounds which are utilized for drug development (Shi et al., 2023).

Table 4.153 *Acrostalagmus* species isolated from soil

Species	Country	Habitat or soil type	References
Acrostalagmus luteoalbus	The Netherlands	A Garden	Giraldo and Crous (2019)
Acrostalagmus luteoalbus	Russia	Soda soil	
A. annulatus	Brazil	ND	

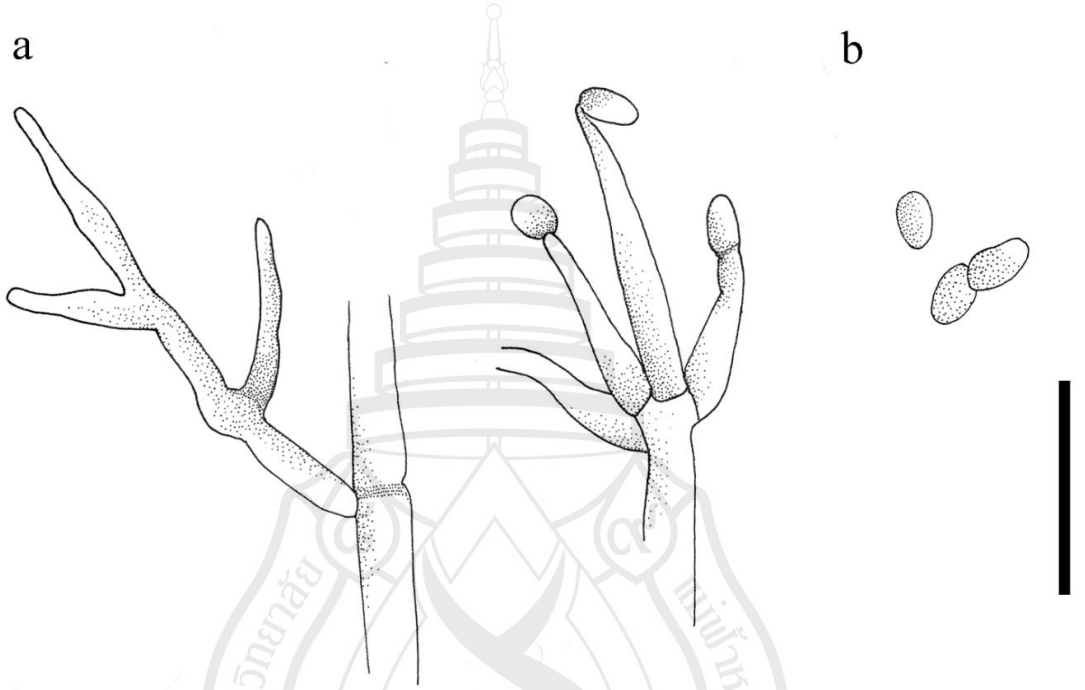


Figure 4.138 *Acrostalagmus luteoalbus* (CBS 121214)

Figure 4.138, a Conidiophore with phialides b Conidia. Scale bar: a, b= 10µm. Redrawn from Giraldo and Crous (2019)

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

Order: ***Coronophorales*** Nannf. (= *Melanosporales* N. Zhang & M. Blackw.)

Family: ***Ceratostomataceae*** G. Winter

Dactylidispora Y. Marín, Stchigel, Guarro & Cano, MycoKeys 44: 89 (2018)

Index Fungorum number: IF812079; Facesoffungi number: FoF10514

Marin-Felix et al. (2018) introduced *Dactylidispora* using multi-gene phylogeny (ITS, LSU, Actin, and *tef*1-α) and the morphology while transferring several *Microthecium* and *Melanospora* species, and the type species is designated as *D. ellipsospora*. Currently, three species are listed in *Dactylidispora* (Species Fungorum, 2025), and all of them have

molecular data. The sexual morph is characterized by globose to pyriform, yellowish-brown to dark brown, glabrous or setose, short, conical ascomata with or without ostiole, and membranaceous, *textura angularis* ascomatal wall, and lacking paraphyses. Asci are characterized by 8-spored, broadly clavate, short-stipitate and evanescent, and containing ascospores that are 1-celled, fusiform or citriform, umbonate initially hyaline becoming brown to dark brown when mature. All the species are isolated from soil substrates (Hyde et al., 2020c; Marin-Felix et al., 2018).

Table 4.154 *Dactylidispora* species isolated from soil

Species	Country	Habitat or soil type	References
Dactylidispora collipora	India	ND	Stchigel et al. (1997)
D. ellipsospora	Papua New Guinea	Forest	Marin-Felix et al. (2018)
D. singaporensis	Singapore	ND	

Echinusitheca Y. Marín, Stchigel, Dania García, Guarro, A.N. Mill. & Cano, MycoKeys 44: 91 (2018)

Index Fungorum number: IF812084; Facesoffungi number: FoF10515

Marin-Felix et al. (2018) introduced *Echinusitheca* based on ITS, LSU, actin and *tef*1-α, and the morphological support, while designating *E. citrispora* as the type species. It is a monotypic genus (Species Fungorum, 2025), supported by molecular data (ITS, LSU, SSU and *tef*1-α). The asexual morph remains undetermined. The sexual morph is characterized by superficial or immersed, solitary to gregarious, globose, non-ostiolate ascomata, 8-spored, globose to subglobose, non-stipitate asci, and hyaline, ellipsoidal, one-celled, smooth-walled ascospores with a depressed germ pore at each end and becoming brown to dark brown when mature (Marin-Felix et al., 2018).

Table 4.155 *Echinusitheca* species isolated from soil

Species	Country	Habitat or soil type	References
Echinusitheca citrispora	USA	Forest	Marin-Felix et al. (2018)

Vittatispora P. Chaudhary, J. Campb., D. Hawksw. & K.N. Sastry, Mycologia 98(3): 461 (2006)

Figure 4.139

Index Fungorum number: IF500705; Facesoffungi number: FoF10525

Vittatispora was introduced by Chaudhary et al. (2006) and typified by *V. coorgii*. Marin-Felix et al. (2018) has suggested the phylogenetic placement of *Vittatispora* within *Coronophorales* using the ITS, LSU, Actin and *tef*1-α multi-gene phylogeny. Subsequently, Huang et al. (2021a) described its placement within *Hypocreomycetidae* while providing the ITS, LSU, SSU, *tef*1-α, *rpb2* and *tub2* phylogeny. Currently, it retains as a monotypic genus. The asexual morph is unreported (Chaudhary et al. 2006, Hyde et al. 2020c) and the sexual morph is characterized by perithecial, solitary or gregarious, globose ascomata with a long cylindrical neck, a membranaceous wall with brown cells of textura angularis, 8-spored, clavate, ellipsoidal to citriform asci, and brown to dark brown ascospores with two apical germ pores surrounded by a raised rim and a thick vertical hyaline ridge running connecting the germ pores (Chaudhary et al., 2006).

Table 4.156 *Vittatispora* species isolated from soil

Species	Country	Habitat or soil type	References
Vittatispora coorgii	India	Plateau of the western Ghats	Chaudhary et al. (2006)

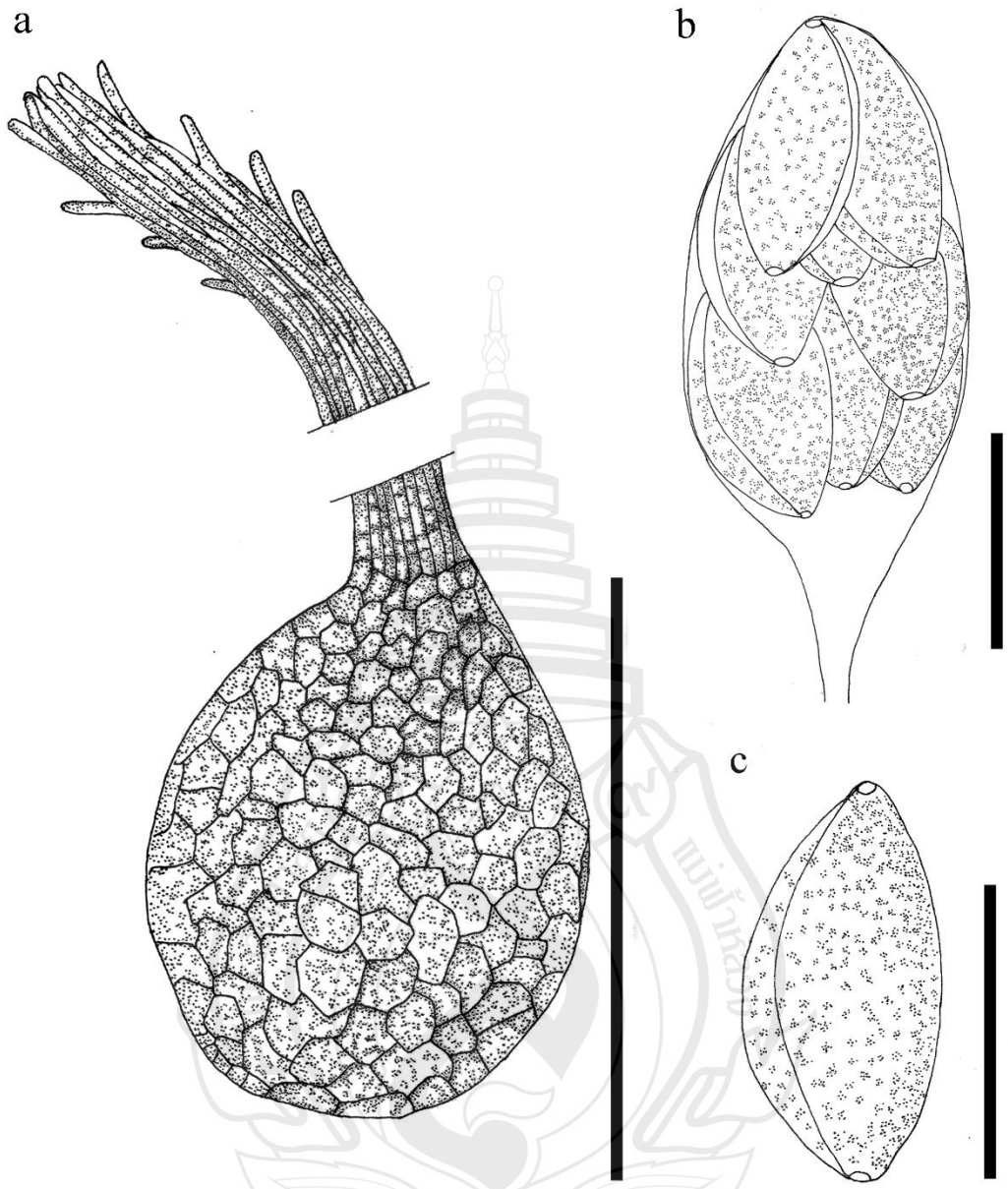


Figure 4.139 *Vittatispora coorgii* (BICC 7817)

Figure 139, a Immature ascoma with cell walls b Ascus. c Ascospore. Scale bars a=200µm, b,c= 5µm. Redrawn from Huang et al. (2021a).

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

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

Colletotrichum Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.)(12): 41 (1831)

Index Fungorum number: IF 7737

Colletotrichum was introduced by Corda (1831) and the type species is designated as *C. lineola*. Based on the combined phylogeny (ITS, *tub2*, *actin*, CHS-1, *gapdh*, cmdA, GS, and SOD2), Cannon et al. (2012b) revised the genus with 113 accepted species and nine species complexes. Recent study of Liu et al. (2022) has accepted 80 species, 16 species complexes, and 15 singleton species in *Colletotrichum*. This is a globally reported genus, as important plant pathogens while some of them are saprobes, endophytes and human pathogens. They have been isolated from air, clinical samples, plant materials and soil (Jayawardena et al., 2020; Liu et al., 2022).

Table 4.157 *Colletotrichum* species isolated from soil

Species	Country	Habitat or soil type	References
Colletotrichum coccodes	ND	ND	Farley (1972)

Order: ***Hypocreales*** Lindau

Family: ***Acremoniopsidaceae*** M. Li, M. Raza & L. Cai

Acremoniopsis A. Giraldo, Gené & Guarro, Persoonia 33: 265 (2014)

Figure 4.140

Index Fungorum number: IF809883; Facesoffungi number: FoF13623

Acremoniopsis was established by Crous et al. (2014) based on the combined morphology and LSU and ITS phylogeny, with *A. suttonii* as the type species. Currently, it has two species (Species Fungorum, 2025) and both of them are supported by molecular data (ITS, LSU, *rpb*2, *tef1-α*). The asexual morph is characterized by erect, simple or poorly branched conidiophores and enteroblastic, monophialidic, sub-hyaline, cylindrical to subulate conidiogenous cells, and hyaline, unicellular, globose or subglobose conidia that are arranged in slimy heads. The sexual morph has not been determined (Crous et al., 2014b). The species have been reported from soil and *Sternorrhyncha* species (Crous et al., 2014b; Tan & Steinrucken, 2024).

Table 4.158 *Acremoniopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Acremoniopsis suttonii	Spain	ND	Crous et al.(2014b)

Figure 4.140 *Acremoniopsis suttonii* (CBS 138708)

Figure 4.140, a Conidiophore and conidia. Scale bar: a = 10μm. Redrawn from Crous et al. (2014b)

Family: *Bionectriaceae* Samuels & Rossman

Acremonium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1–2): 15 (1809)

Index Fungorum number: IF7028; Facesoffungi number: FoF12995

Acremonium was established by Link (1929), and typified by *A. alternatum*. Currently, around 200 species are available in the Index Fungorum (2025) and is one of the largest genera in *Sordariomycetes* (Yang et al., 2019). Studies have analyzed *Acremonium* based on multigene phylogeny (LSU, SSU, ITS and *tef1-α*) and numerous species were synonymized into other genera (Li et al., 2022; Yang et al., 2019). *Acremonium* has a polyphyletic nature and are distributed in two classes: *Leotiomycetes*

and *Sordariomycetes*; however, most of the species including type species belong to *Hypocreales* (Giraldo et al., 2012, 2017; Summerbell et al., 2011; Yang et al., 2019). The genus has simplified and plastic morphologies, thus, morphology is not that informative for the species delimitation (Yang et al., 2019). However, mostly ITS and LSU loci are used in species delineation in *Acremonium*, and the lack of protein sequence data in Genebank is a major constraint (Li et al., 2022; Yang et al., 2019). Currently, the genus comprises more than 100 species (Hyde et al., 2024c). The asexual morph of the genus is characterized by simple or verticillate conidiophores with narrow phialides, solitary and cylindrical, and unicellular, hyaline to light-pigmented, spherical to cylindrical conidia that are arranged in slimy heads or unconnected chains or both. Species occur on various substrates such as air, dung, seawater or deep-sea sediments and soil. They can also be saprobes on dead plant materials, pathogens on humans and animals, parasites on fungi, lichens, insects or arthropods and endophytes on plants, seaweeds or animals (Li et al., 2022; Yang et al., 2019). They have a wide geographical distribution and can be found in Antarctica, China, the Czech Republic, India, Italy, Germany, Korea, Morocco, Ivory Coast, Papua New Guinea, Peru, Sri Lanka and the USA (Li et al., 2022; Yang et al., 2019).

Table 4.159 *Acremonium* species isolated from soil

Species	Country	Habitat or soil type	References
Acremonium variecolor	Korea	A river bank	Park et al. (2017)
A. globosisporum	China	ND	Li et al. (2022b)
A. curvum	China	ND	
A. sclerotiniarum	Worldwide	ND	Wang et al. (2015a)
A. cavaraeanum	Italy	ND	Domsch et al. (1993)
A. borodinense	Japan	Rhizosphere soil of sugarcane	Ito et al. (2000)

Amphichorda Fr., Syst. orb. veg. (Lundae) 1: 170 (1825)

Figure 4.141

Index Fungorum number: IF7134; Facesoffungi number: FoF13119

Amphichorda was introduced by Fries (1825) and typified by *A. felina*. Based on the ITS, *rpb1*, *rpb2* and *tef*1-α gene regions, Zhang et al. (2021) and Liu et al. (2023) provided phylogeny for this genus within *Cordycipitaceae* while introducing new species. However, Guerra-Mateo et al. (2023) and Wang et al. (2024d) have suggested

this genus in *Bionectriaceaea* based on ITS, SSU, LSU, *tef*1-α, *rpb1*and *rpb2* phylogeny, with nine accepted species. The genus is characterized by the hyphomycetous asexual morphs with indeterminate synnemata, branched conidiophores, and sympodial conidiogenous that produce amerosporous and single conidia. The sexual morph remains undetermined (Hyde et al., 2020c). Species discovered from the air, animal and bird faeces, living bats, insects, marine sediments, plant debris and soil collected in Brazil, China, Great Britain and Spain (Hyde et al., 2020c).

Table 4.160 *Amphichorda* species isolated from soil

Species	Country	Habitat or soil type	References
Amphichorda cavernicola	China	Cave soil	Zhang et al. (2021c)

Figure 4.141 *Amphichorda felina*. (CBS 250.34)

Figure 4.141, a Branched conidiophores and conidia. Redrawn from Seifert et al. (2011)

Clonostachys Corda, Pracht-Fl. Eur. Schimmelbild.: 31 (1839)

Index Fungorum number: IF7701; Facesoffungi number: FoF14271

Corda (1839a) introduced *Clonostachys*, designating the type species as *C. araucaria* which is currently known as *C. rosea* (Schroers et al., 1999). Based on ITS, LSU, *btub* and *tef*1-α gene regions, Wang et al. (2023b) revised the phylogenetic placement of the genus in *Bionectriaceae* including 56 species. There are 81 *Clonostachys* species listed in the Species Fungorum (2025). The asexual morph is characterized by the conidiophores that are penicillate, sporodochial, or dimorphic with phialidic conidiogenous

cells and hyaline conidia. The sexual morph is previously linked to *Bionectria,* but subsequently, this genus was accepted as *Clonostachys* which has white, pale yellow, or orange to dark brownish-orange, warted or smooth ascomata formed in pseudoparenchymatous stroma or directly on the substrate. Ascospores are smooth, spinulose, striate or warted (Schroers, 2001; Schroers et al., 1999; Spegazzini, 1919). These species have a cosmopolitan distribution which can be found in bark, dead wood, leaves, roots and soils. *Clonostachys* species are recorded as saprotrophs, endophytes, epiphytes of living plants and mycoparasites found from France, India, Japan, Sri Lanka, Switzerland, the Netherlands and the USA (Kapeua-Ndacnou et al., 2023; Wang et al., 2023b). Species also used as biocontrol agents against various ascomycetes, soil-borne hyphomycetes, and basidiomycetes (Wang et al., 2023b).

Table 4.161 *Clonostachys* species isolated from soil

Species	Country	Habitat or soil type	References
Clonostachys candelabrum	The Netherlands	ND	Abreu et al. (2014)
C. candelabrum	Brazil	ND	
C. chloroleuca	Brazil	Savanna soil	
C. pseudochroleuca	Brazil	ND	
C. chlorina	Brazil	ND	Wang et al. (2023b)
C.chuyangsinensis	China	ND	
C. compactiuscula	China	ND	
C. intermedia	South Korea	ND	
C. kunmingensis	China	ND	
C. rhizophaga	China	ND	
C. rogersoniana	China	ND	
C. divergens	Germany	ND	Schroers (2001)
C. intermedia	The Netherlands	Agricultural soil	
C. parva	The Netherlands	Agricultural soil	
C. rogersoniana	Brazil	Rain forest soil	
C. rosea	USA	ND	
C. solani	Germany	Wheat field soil	

Emericellopsis J.F.H. Beyma, Antonie van Leeuwenhoek 6: 264 (1940)

Figure 4.142

Index Fungorum number: IF1773; Facesoffungi number: FoF13424

Beyma (1940) erected *Emericellopsis* and typified it by *E. terricola*. Species Fungorum (2025) lists 24 species in *Emericellopsis* and 22 of them are supported by molecular data. Based on the LSU phylogeny, Crous et al. (2018b) accommodated this genus in *Myrotheciomycetaceae*. However, based on LSU, SSU, ITS, *tef*1-α and *rpb*2 phylogeny, Bao et al. (2023) transferred this genus to *Hypocreales* genera incertae sedis and suggested that further revisions are needed to confirm its phylogenetic placement. The asexual morph of the genus is characterized by the aerial hyphae and hyaline, 1–2-guttulate, elongate-ellipsoidal conidia (Hyde et al., 2020c). The species have been isolated from freshwater-, estuarine- and marine-mud sediments, rhizomes, peat, prairies and soils that are located in China, Germany, Ireland, Italy, South Korea, Soviet Union and the Netherlands (Bao et al., 2023; Domsch et al., 1980).

Table 4.162 *Emericellopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Emericellopsis alkalina	Russia	Soda soil	Kuvarina et al. (2022)
E. stolkiae	USA	Saline soil	Davidson and Christensen (1971)
E. terricola	The Netherlands	ND	Domsch et al. (1993)

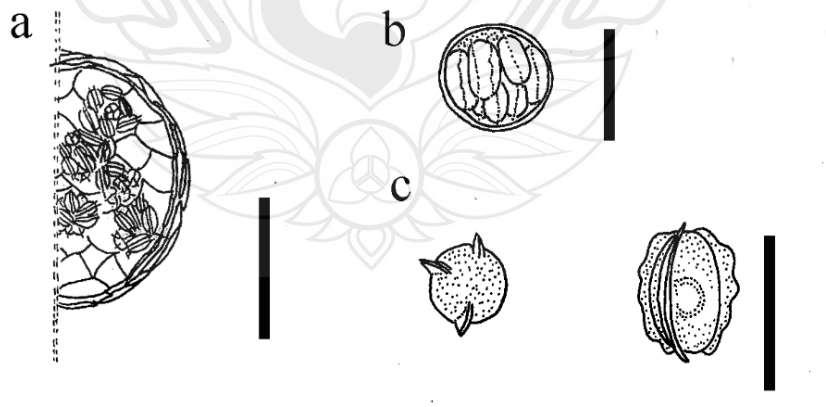


Figure 4.142 *Emericellopsis terricola*

Figure 4.142, a. Section of ascoma b. Asci. c. Ascospore. Scale bars: a = 50μm, b = 20μm, c = 10 μm. Redrawn from Guarro et al. (2012)

Family: *Clavicipitaceae* (Lindau) Earle ex Rogerson

Keithomyces Samson, Luangsa-ard & Houbraken, Stud. Mycol. 95: 186 (2020) Figure 4.143

Index Fungorum number: IF834876; Facesoffungi number: FoF4489

Keithomyces was introduced by Mongkolsamrit et al. (2020) and typified by *K. carneus* based on multi-gene phylogeny (SSU, LSU, *tef*1-α, *rpb1* and *rpb2*) and morphological characterization. Mongkolsamrit et al. (2020) transferred several *Paecilomyces* and *Metarhizium* species to establish *Keithomyces*. There are five species listed in the Index Fungorum (2025), and all of them have molecular data. The asexual morph is characterized by paecilomyces-like asexual morphs with divergent whorls of 2–4 phialides bearing conidiophores and echinulate or aciculate conidial chains. The sexual morph remains undetermined. Species have been isolated from China, France, India and Japan from *Lepidoptera* larvae and soil habitats (Mongkolsamrit et al., 2020; Crous et al., 2022).

Table 4.163 *Keithomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Keithomyces carneus	France	Sandy soil	Mongkolsamrit et al. (2020)
K. acicularis	Japan	soil under *Angelica keiskei*	
K. indicus	India	ND	Crous et al. (2022)
Keithomyces echinosporus	China	Wild life park	Zhang et al. (2024b)

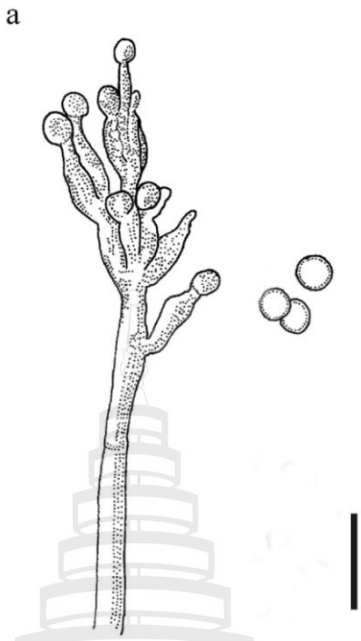


Figure 4.143 *Keithomyces carneus*

Figure 4.143, a Conidiophore and conidia. Scale bar: a = 10μm. Redrawn from Mongkolsamrit et al. (2020)

Marquandomyces Samson, Houbraken & Luangsa-ard, Stud. Mycol. 95: 194 (2020)

Figure 4.144

Index Fungorum number: IF834879; Facesoffungi number: FoF4490

Marquandomyces was established by Mongkolsamrit et al. (2020); the type species is designated as *M. marquandii* (= *Paecilomyces marquandii*). It is a monospecific genus introduced with morphology and the multi-gene (SSU, LSU, *tef*1-α, *rpb1* and *rpb2*) phylogeny (Mongkolsamrit et al., 2020). The asexual morph is characterized by having hyaline, smooth-walled conidiophores bearing whorls of 2–4 phialides and ellipsoidal to fusiform, hyaline conidia in dry divergent chains. Cultures produce chlamydospore-like structures that are solitary, thin-walled, and globose to ellipsoidal cells (Mongkolsamrit et al., 2020). *Marquandomyces marquandii* has been isolated from mushrooms and soil in Russia, the Netherlands, the UK, and the USA (Mongkolsamrit et al., 2020).

Table 4.164 *Marquandomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Marquandomyces marquandii	USA	ND	Mongkolsamrit et al. (2020)

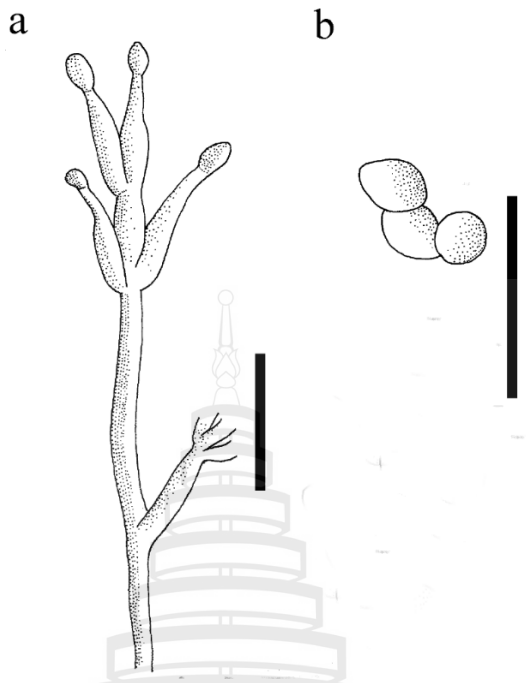


Figure 4.144 *Marquandomyces marquandii*

Figure 4.144, a Conidiophore b Conidia. Scale bars: a = 10m. Redrawn from Mongkolsamrit et al. (2020)

Metapochonia Kepler, Rehner & Humber, Mycologia 106(4): 820 (2014)

Index Fungorum number: IF806070; Facesoffungi number: FoF13083

Kepler et al. (2014) erected *Metapochonia* while accommodating *M. suchlasporia* as the type species, based on morphology and *tub2*, *rpb1*, *rpb2* and *tef1-α* multi-gene phylogeny. The genus is currently comprised of nine species (Hyde et al. 2024c), and all of them are supported by molecular data. *Metapochonia* and *Pochonia* are similar in morphology such as producing dictyochlamydospores, and are parasitic on nematode eggs or cysts (Kondo et al., 2020). Based on morphology and multi-gene phylogenetic (ITS and *tef*1-α) analysis, Kepler et al. (2014) and Labuda et al. (2018) transferred *Pochnia* species to *Metapochonia*. Mongkolsamrit et al. (2020) mentioned that this genus requires further revision. The asexual morph has conidia on slender, awl-shaped phialides, and sexual morph has not been reported (Kepler et al., 2014). These species infect nematodes and rotifers and have also been isolated from insects, such as Coleoptera, Hemiptera and Lepidoptera larvae, plant roots and soil distributed in Canada, China, Denmark and Sweden (Hyde et al., 2020c).

Table 4.165 *Metapochonia* species isolated from soil

Species	Country	Habitat or soil type	References
Metapochonia hahajimaensis	Japan	ND	Kondo et al. (2020)
M. variabilis	China	Karst cave	Zhang et al. (2017b)

Metarhizium Sorokīn, Veg. Parasitenk. Mensch Tieren 2: 268 (1879)

Figure 4.145

Index Fungorum number: IF8912; Facesoffungi: FoF13085

Rombach et al. (1987) amended *Metarhizium* and the type species is designated as *M. anisopliae*. Study of Kepler et al. (2014) prioritized the taxonomic stability of *Metarhizium* while removing *Metacordyceps*, and retaining *Pochonia* and a new genus, *Metapochonia*, however mentioning that several placements have phylogenetic ambiguities. Currently, 78 species have been accepted in this genus (Mongkolsamrit et al., 2020). The asexual morph of the genus is characterized by the variously branched conidiophores without synnemata and hyaline to brown or green conidia (Kepler et al., 2014). The sexual morph is characterized by the predominantly cylindrical or clavate, pale yellow, green to greenish brown or dark purple stromata with immersed to semi-immersed perithecia, and the ascospores are filiform and whole with septation or they can be dissociated into part-spores (Hyde et al., 2020c; Mongkolsamrit et al., 2020). Species have been reported from arthropods, nematodes, plant roots and soil (Kepler et al., 2014; Mongkolsamrit et al., 2020).

Table 4.166 *Metarhizium* species isolated from soil

Species	Country	Habitat or soil type	References
Metarhizium aciculare	Japan	ND	Mongkolsamrit et al. (2020)
M. alvesii	Brazil	soil, associated with *Musa*	
M. anisopliae	Brazil	ND	
M. baoshanense	China	soil, associated with *Angiospermae*	
M. acridum	West Africa	ND	
M. brunneum	Australia	ND	
M. guizhouense	Australia	ND	
M. humberi	Brazil	ND	
M. lepidiotae	Australia	ND	
M. novozealandicum	Australia	ND	
M. robertsii	Australia	ND	

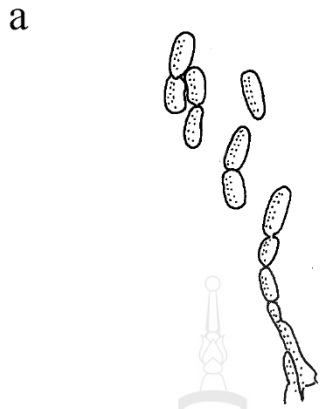


Figure 4.145 *Metarhizium anisopliae*

Figure 4.145, a Conidiophore and conidia. Redrawn from Domsch et al. (1993).

Pochonia Bat. & O.M. Fonseca, Publicações Instituto de Micologia, Recife 462, 4 (1965)

Index Fungorum number: Facesoffungi number: FoF 13104;

Batista and Fonseca (1965) introduced *Pochonia* designating *P. humicola*, as the type species. There are five species accepted in the genus however, only four species have molecular data (SSU, ITS, LSU, *rpb2* and *tef*1-α) (Zhang et al., 2023c). Initial phylogeny was provided by Zare et al. (2001), and several subsequent studies revisited this genus; however, taxonomic ambiguities remained (Kepler et al., 2014; Sung et al., 2007). Sung et al. (2007) introduced *Metacordyceps* transferring several *Metarhizium* and *Pochonia* species. However, Kepler et al. (2014) proposed the suppression of *Metacordyceps* and retained *Pochonia.* A recent taxonomic explanation of *Pochonia* was provided by Mongkolsamrit et al. (2020). *Pochonia* species produce sexual and asexual morphs, while some of them produce dictyochlamydospores or irregularly swollen hyphae (Mongkolsamrit et al., 2020; Zare et al., 2001) Most of the *Pochonia* are nematode parasites, and some have been isolated from soil-based substrates in Brazil, Canada, China, Japan, the Netherlands and Thailand (Chethana et al., 2023; Hyde et al., 2020c; Mongkolsamrit et al., 2020).

Table 4.167 *Pochonia* species isolated from soil

Species	Country	Habitat or soil type	References
Pochonia chlamydosporia	Canada	ND	Mongkolsamrit et al. (2020)
P. chlamydosporia	Thailand	Forest	Chethana et al. (2023)
P. humicola	Brazil	ND	Batista and Fonseca (1965)
P. boninensis	Japan	Cultivated soil under *Livistona chinensis*	Nonaka et al. (2013)
P. sinensis	China	Green belt soil	Zhang et al. (2023a)

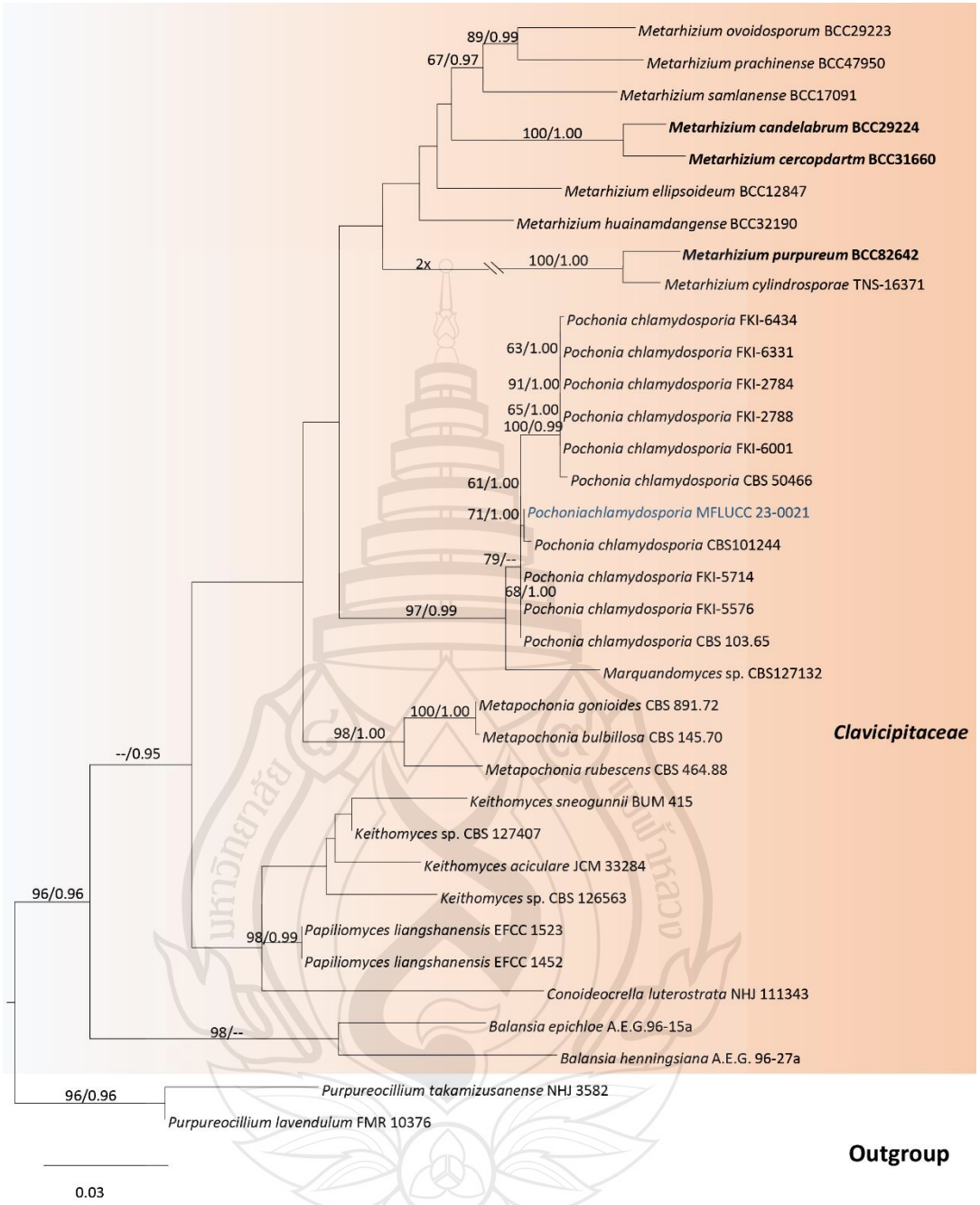


Figure 4.146 Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data of *Clavicipitaceae* taxa

Figure 4.146, Sixty-four strains are included in the combined analyses which comprised 1403 characters (539 characters for ITS and 864 characters for LSU) after aligned. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -11074.502759 is

presented. The matrix had 734 distinct alignment patterns, with 32.93% undetermined characters or gaps. Evolutionary models applied for ITS and LSU are SYM+I+G and GTR+I+G models, respectively. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The tree is rooted with *Purpureocillium takamizusanense* (NHJ 3582), *Cordyceps cylindrica* (CBS 744.73) and *Purpureocillium lavendulum* (FMR 10376). Ex-type strains are in **bold**. The newly generated sequences are indicated in yellow.

Pochonia chlamydosporia (Goddard) Zare & W. Gams, in Gams & Zare, Nova Hedwigia 72(3-4): 334 (2001)

Figure 4.147

Index Fungorum number: IF474783

Hyphae hyaline, aseptate, smooth-surfaced, becoming course-surfaced when mature. **Asexual morph:** *Conidiophores* 12–30 × 1–1.5 μm ($\overline{x}$ = 22 × 1 μm, n = 20), mononematous, micronematous, erect, straight or slightly curved, smooth-walled, unbranched terminal or intercalary. *Phialides* 3–7 × 1–4 μm ($\overline{x}$ = 6 × 2.5 μm, n = 20), solitary on apices of conidiophores, ellipsoid to sub-cylindrical, bearing conidial chains at the apex. *Conidia* 2.5–5.5 × 1.5–4 μm ($\overline{x}$ = 3 × 2 μm, n = 20), globose or sub-globose to ovoid, smooth-walled, hyaline, aseptate. **Sexual morph:** Undetermined.

Culture characteristics — *Colonies* on PDA become 30mm diam. after 14 days at 25℃, appearing in white, becoming yellow to deep-yellow, cottony, slightly raised when mature, entire margined, reverse yellowish-brown at the center and whitish-yellow at the rind.

Material examined — Thailand, Chiang Rai Province, 19°53'2"N, 100°5'37"E, 440 m, on forest soil, 7 January 2020, W.A. E. Yasanthika; living culture, MFLUCC 23-0021.

GenBank: (ITS: OQ690713, LSU: OQ690716)

Known distribution— Canada, Germany, Japan and Thailand (Mensin et al., 2012; Nonaka et al., 2013; Mongkolsamrit et al., 2020; Jaihan et al., 2021)

Known hosts (based on molecular data) — *Nymph of Cicadidae* and soil (Mensin et al., 2012; Nonaka et al., 2013; Kim et al., 2016; Mongkolsamrit et al., 2020; Jaihan et al., 2021)

Notes — *Pochonia chlamydosporia* has been identified as an association of four varieties, which were synonymized under *Pochonia chlamydosporia* based on the latest classification (Nonaka et al., 2013; Species Fungorum, 2022). This species has been subjected to revision in several studies and synonymized recently by Mongkolsamrit et al. (2020). Both sexual and asexual morphs are reported from this species, and the sexual morph is observed in the nymphs of *Cicadidae* in Thailand (Jaihan et al., 2021). This species is commonly found in soils and is a nematode parasite used as a biocontrol agent (Nonaka et al., 2013). Our collection is clustered with other *P. chlamydosporia* with 68 % ML bootstrap support in the combined ITS and LSU phylogenetic tree (Figure 3.41) and also agrees with Mongkolsamrit et al. (2020). Our isolate is morphologically similar to *P. chlamydosporia* (CBS101244) in having globose or sub-globose to ovoid, smooth-walled, hyaline, aseptate conidia produced on phialides (Nonaka et al., 2013). This species produce chlamydospores that help the fungus to survive and establish itself in the soil under adverse conditions as well as provide fungal viability during long-term storage. However, we have not observed chlamydospores in this study (Monteiro et al., 2020). the Based on both morphological characteristics and multigene phylogenetic analyses, current study reports the first collection of *P. chlamydosporia* from the forest soils in Thailand.

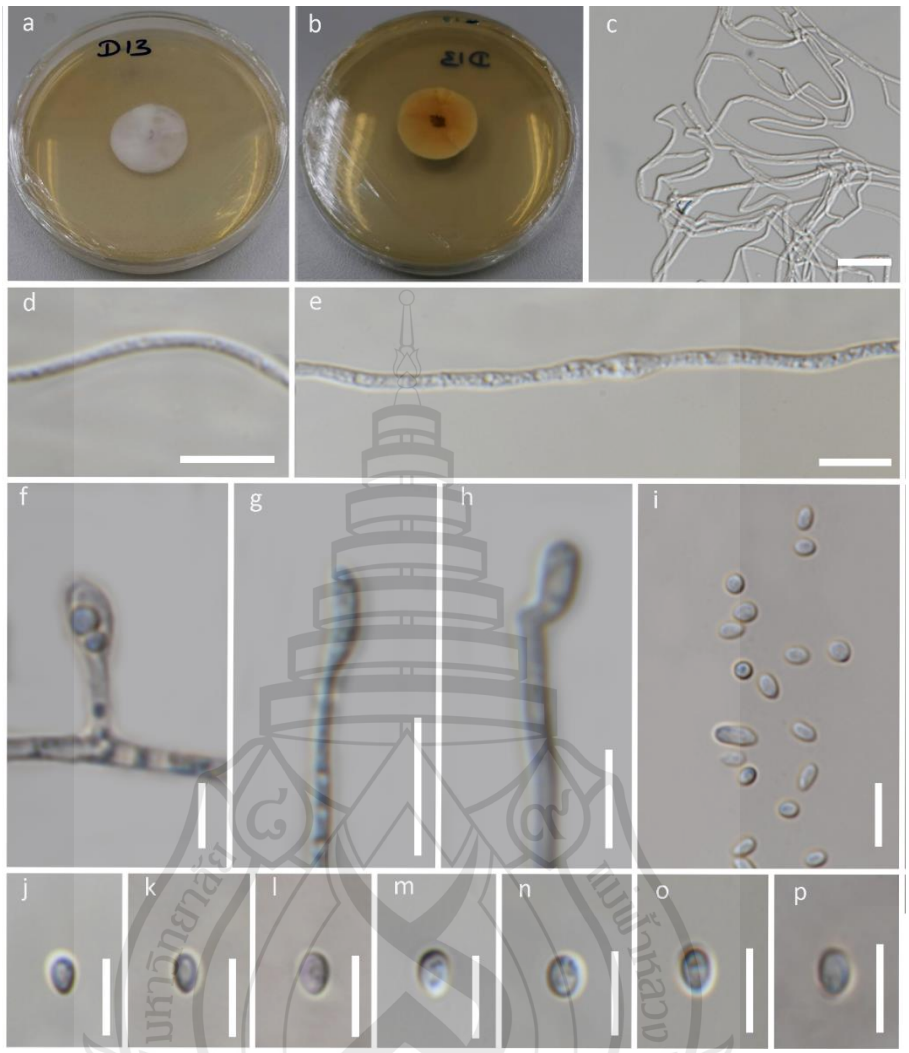


Figure 4.147 *Pochonia chlamydosporia* (MFLUCC 23-0021, new habitat record)

Figure 4.147, a Colony from above (on the PDA). b Colony from below (on the PDA). c–e hyphae. f Conidiogenesis on phialides. g, h Conidiophores. i–p Conidia. Scale bars: c = 20 μm, d, e, h–p = 10 μm, f = 5 μm.

Romanoa Thirum., R.C. Ist. Sup. Sanitä, (Rome) 17: 1326 (1954)

Index Fungorum number: IF4779; Facesoffungi number: FoF13107

Thirumalachar (1954) erected *Romanoa* with its type species, *R. terricola*. Currently, it is a monotypic genus (Hyde et al., 2024c), and does not have molecular data. Species have been recorded from soil (Hyde et al., 2020c).

Table 4.168 *Romanoa* species isolated from soil

Species	Country	Habitat or soil type	References
Romanoa terricola	Italy	ND	Thirumalachar (1954)

Family: *Cordycipitaceae* Kreisel ex G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

Beauveria Vuill., Bull. Soc. bot. Fr. 59: 40 (1912)

Index Fungorum number: IF7346; Facesoffungi number: FoF13121

Beauveria was introduced by Vuillemin (1912), designating *B. bassiana* as the type species. There are around 50 species recognized in the genus (Species Fungorum 2025) and 37 of them are supported with molecular data (SSU, LSU, *tef*1-α, *rpb1*, *rpb2* and Bloc). The asexual morph is characterized by the globose to flask-shaped conidiogenous cells with one-celled, terminal, holoblastic conidia that are produced in sympodial succession on an indeterminate, denticulate rachis and possess cordyceps-like sexual morph (Rehner et al., 2011; Vuillemin, 1912). The genus has saprobes and endophytes residing on plant substrates and soil habitats and some species are pathogens on arthropods. They are cosmopolitan species with a wide geographical distribution (Hyde et al., 2020c; Keller et al., 2003).

Table 4.169 *Beauveria* species isolated from soil

Species	Country	Habitat or soil type	References
Beauveria australis	Chile	ND	Rehner et al. (2011)
B. bassiana	Thailand	ND	Manoch (1998)
B. bassiana	China	ND	Wang et al. (2022b)
B. brongniartii	Switzerland	ND	Keller et al. (2003)
B. caledonica	Australia and Scotland	ND	Rehner et al. (2011)
B. medogensis	China	ND	Imoulan et al. (2016)
B. vermiconia	Chile	ND	Wang et al. (2022b)

Cordyceps Fr., Observ. mycol., Cancellans Edn (Havniae) 2: 316 (1818)

Index Fungorum number: IF1240; Facesoffungi number: FoF01317

Fries (1818) introduced *Cordyceps*, with *C. militaris* as the type species. Being one of the largest genera in *Hypocreales*, it is comprised of around 564 species (Sung et al., 2007; Zhang et al., 2021b). Previously, it was placed in *Clavicipitaceae* (Shrestha et al., 2017), but phylogenetic studies revealed that *Cordyceps sensu lato* is not monophylectic (Sung et al., 2007); thus the genus was circumscribed to *Cordyceps sensu stricto* and new genera were suggested for the species outside this clade. Based on the phylogenetic analyses of Sung et al. (2007) and Kepler et al. (2014), around 180

Cordyceps species were transferred to new genera and *Cordyceps sensu stricto* was placed in *Cordycipitaceae.* However, there are still *Cordyceps* species that remain unresolved within *Hypocreales* (Shrestha et al., 2017). The asexual morph is characterized by evlachovaea-like, isaria-like, lecanicillium-like, mariannaea-like, simplicillium-like phialides or conidia. The sexual morph has bright, stipitate, fleshy stromata, superficial to embedded perithecia, and ascospores that do not break or produce part spores (Hyde et al., 2020c). The genus is considered to have a cosmopolitan distribution, including Brazil, China, India, Indonesia, Japan, Madagascar, Papua New Guinea and Ukraine. Most of the species are entomopathogenic, and some are associated with decaying wood, food and soil as well (Dong et al., 2022; Sung et al., 2007; Zhang et al., 2021b).

Table 4.170 *Cordyceps* species isolated from soil

Species	Country	Habitat or soil type	References
Cordyceps chaetoclavata	China	*Lepidoptera* buried in soil	Wang et al. (2020)
Cordyceps cocoonihabita	China	*Limacodidae in cocoons buried in soil*	
Cordyceps shuifuensis	China	*Lepidoptera buried in soil*	
Cordyceps subtenuipes	China	*Lepidoptera buried in soil*	

Gamszarea Z.F. Zhang & L. Cai

Index Fungorum number: IF556420, Facesoffungi number: FoF08439

Zhang et al. (2021) introduced *Gamszarea* based on the combined ITS, LSU, SSU, *tef1-α, rpb1* and *rpb2* phylogeny and morphology, and typified with *Gamszarea wallacei* (= *Simplicillium wallacei*). Currently, eight species are listed in this genus (Index Fungorum 2025) and all the species have molecular data. The asexual morph is characterized by erect, hyaline conidiophores and discrete aculeate phialides, solitary or verticillate conidiogenous cells, producing less globose, septate macro- or aseptate microconidia with slimy heads. The sexual morph has hyaline, obclavate to naviculate perithecia, 8-spored, narrowly cylindrical asci, and hyaline, filiform ascospores. *Gamszarea* species have been isolated from lepidopteran larvae, spiders, on rocks and soil collected from China, the Czech Republic and Sulawesi (Zhang et al., 2021c).

Table 4.171 *Gamszarea* species isolated from soil

Species	Country	Habitat or soil type	References
Gamszarea humicola	China	Cave soil	Zhang et al. (2021c)

Lecanicillium W. Gams & Zare, Nova Hedwigia 72(3-4): 332 (2001)

Figure 4.148

Index Fungorum number: IF28528; Facesoffungi number: FoF16639;

Zare anf Gams (2001) introduced *Lecanicillium* to accommodate the taxa with aculeate phialides within *Cordycipitaceae* and typified by *L. lecanii*. This genus is polyphyletic in *Cordycipitaceae* (Chiriví-Salomón et al., 2015; Sanjuan et al., 2014; Zhang et al., 2021c). Based on the phylogeny of Kepler et al. (2017), three *Lecanicillium* species were synonymized to *Akanthomyces,* including the type species (*L. lecanii*). Zhang et al. (2021) followed the polyphyletic nature of this genus and four *Lecanicillium* were identified as distinct clade in the combined phylogeny of ITS, LSU, SSU, *tef*1-α, *rpb*1 and *rpb*2 sequences, thus accommodating as the new genus, *Gamszarea.* Currently, 16 species are accepted in the *Lecanicillium* (Hyde et al., 2024c) and all of them have molecular data. However, further phylogeny and updated descriptions are required to resolve the phylogenetic placement of this genus. Both sexual and asexual morphs are present, and asexual morph is hyphomycetous. The species have been observed from animal dung, soil and wood materials as saprobes, endophytes or fungicolous fungi (Yasanthika et al., 2021). They are distributed in Australia, China, Ghana, India, Iran and Sri Lanka (Zhou et al., 2022).

Table 4.172 *Lecanicillium* species isolated from soil

Species	Country	Habitat or soil type	References
Lecanicillium dimorphum	China	Contaminate soil	Yasanthika et al. ((2021)
L. magnisporum	China	Cave	Zhang et al. (2021c)
L. saksenae	India	ND	Sreeja et al. (2023)

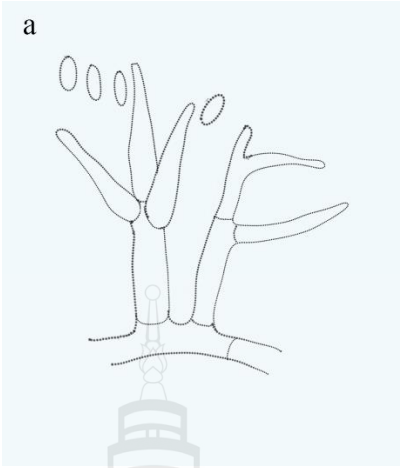


Figure 4.148 *Lecanicillium lecanii* (IMI 327441)

a Conidiophore and conidia. Scale bars: a = 10m. Redrawn from redrawn from Zare and Gams (2001).

Simplicillium W. Gams & Zare

Index Fungorum number: IF28570; Facesoffungi number: FoF13133

Simplicillium was introduced by Zare snd Gams (2001) and typified by *S. lanosoniveum*. Previously, *Simplicillium* species were placed in *Verticillium sect. prostrata Clavicipitaceae* (Zare & Gams, 2001). Based on SSU, LSU and ITS sequences, this was subsequently considered as a separate genus in *Clavicipitaceae* (Zare & Gams, 2001). However, the placement of *Simplicillium* was revised again to *Cordycipitaceae* based on phylogeny (Maharachchikumbura et al., 2016; Wei et al., 2019; Wijayawardene et al., 2018). *Simplicillium* presently accommodates 33 species and all of them are supported by molecular data (Yan et al., 2023a) The genus is considered to have a cordycep-like asexual morph with predominantly solitary phialides, conidial masses either in globose slimy heads, short chains, or in sympodial succession (Zare & Gams, 2001; Zhang et al., 2021c). These species can be found in a variety of environments, including freshwater and marine habitats, human nails and skin, insects, nematodes, plants, mushrooms, cyanobacteria (*Chroococcus* sp.) and distributed soil in China, Germany, Japan and Thailand (Hyde et al., 2020c; Wei et al., 2019; Zhang et al., 2021c). They have various trophic modes, such as mammal- and plant-parasitic, symbiotic, entomopathogenic, fungicolous and nematophagous fungi. Bioactive compounds such as anti-fungal and anti-bacterial profiles have been investigated from some *Simplicillium* species (Wei et al., 2019).

Table 4.173 *Simplicillium* species isolated from soil

Species	Country	Habitat or soil type	References
Simplicillium album	China	Cave	Zhang et al. (2021c)
S. humicola	China	Cave	

Family: *Hypocreaceae* De Not.

Kiflimonium Summerb., J.A. Scott, Guarro & Crous, Microorganisms 6(3, 88): 17 (2018)

Index Fungorum number: IF826819; Facesoffungi number: FoF13218

Kiflimonium was introduced by Summerbell et al. (2018) and designated *K. curvulum* (≡ *Acremonium curvulum*) as the type species based on the ITS phylogeny. Currently, three species are listed in the Index Fungorum (2025), and all of them have molecular data. The asexual morph is characterized by conidiophores arising laterally from somatic hyphae, hyaline, subcylindrical, mostly with 1–4 conidiogenous cells that are phialidic, form singly, laterally on hyphae or on conidiophores. Conidia are 0–1 septate, smooth-walled, lunate to falcate produced on slimy heads (Summerbell et al., 2018). The sexual morph is not reported. Species are identified as saprobes on plants, in rust-infected *Lolium* ryegrass and soil substrates in China, Germany and the Netherlands (Summerbell et al., 2018; Crous et al., 2021).

Table 4.174 *Kiflimonium* species isolated from soil

Species	Country	Habitat or soil type	References
Kiflimonium curvulum	Germany	ND	Summerbell et al. (2018)

Trichoderma Pers., Neues Mag. Bot. 1: 92 (1794)

Index Fungorum number: IF 10282

Persoon (1974) introduced *Trichoderma* with its type species, *T. viride*. The genus comprises more than 500 species (Hyde et al., 2024c), and nearly 300 species are supported by molecular data. The *rpb2* and *tef*1-α gene regions are important for the species identification in *Trichoderma* (Zhao et al., 2024b). The genus is globally reported and most of the species are associated with soil habitats (Zhao et al., 2024b). Some have saprobic or endophytic relationships with dead and living plants while several have been reported as parasites of other fungi (Jaklitsch & Voglmayr, 2015;

Matar et al., 2022; Zhao et al., 2024b). *Trichoderma* can be opportunistic pathogens in humans and also cause diseases in cultivated mushrooms (Sandoval-Denis et al., 2014). This genus has been widely utilized in commercial enzymes and antibiotic production (Zhao et al., 2024b). Members have also been recognized as biocontrol agents, plant growth promoters and bioremediators against some heavy metal ions (Zhang et al., 2023b; Zhao et al., 2024b).

Table 4.175 *Trichoderma* species isolated from soil

Species	Country	Habitat or soil type	References
Trichoderma gongcheniae	China	a rice field	Zhao et al. (2024b)
T. hongkuii		a corn field	
T. hongkuii		a corn field	
T. parapeberdyi		a peach orchard	
T. neoguizhouense		an eggplant field.	
T. parahamatum		a rice field	
T. shaanxiensis		a wheat field	
Trichoderma harzianum	ND	Turkey	Ülker et al. (2011)
Trichoderma guizhouense			Li et al. (2024a)

Family: ***Myrotheciomycetaceae*** Crous

Trichothecium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1-2): 18 (1809) Figure 4.149

Index Fungorum number: IF10303; Facesoffungi number: FoF13427

Link (1809) erected *Trichothecium* with the type species *T. roseum.* Currently, 27 *Trichothecium* species are listed in the Species Fungorum (2024), but only four species have molecular data. Summerbell et al. (2011) suggested that extensive phylogenetic investigations are essential in resolving this genus as some species remain without sequence data, and the recent phylogeny is provided by Hou et al. (2023) with ITS, LSU and *rpb*2 gene regions. Hyphomycetous asexual morph is characterized by simple, unbranched, conidiophores and 1-septate, clavate conidia, with the apical cell being larger than the curved basal cell (Subramanian, 1962; Summerbell et al., 2011; Hyde et al., 2020). The sexual morph is produced on the aerial mycelium, irregularly coiled with spherical or slightly spherical, non-ostiolate, hyaline or slightly pink ascomata, clavate to spherical, evanescent, 8-spored asci, and ellipsoidal or reniform,

smooth or finely striate, hyaline to yellow to pink ascospores (Summerbell et al., 2011). *Trichothecium* has been isolated from decaying plants, grains, seeds, soil and various fruits and vegetables in Algeria, China, Denmark, Egypt, France, Israel, Japan, Poland, Russia, Tanzania, Turkey, and the USA (Hyde et al., 2020c; Perera et al., 2020).

Table 4.176 *Trichothecium* species isolated from soil

Species	Country	Habitat or soil type	References
Trichothecium roseum	China, Denmark, Egypt, France, Israel, Japan, Poland	Forest nurseries, forest soils under beech trees, teak, cultivated soils	Domsch et al. (1993)

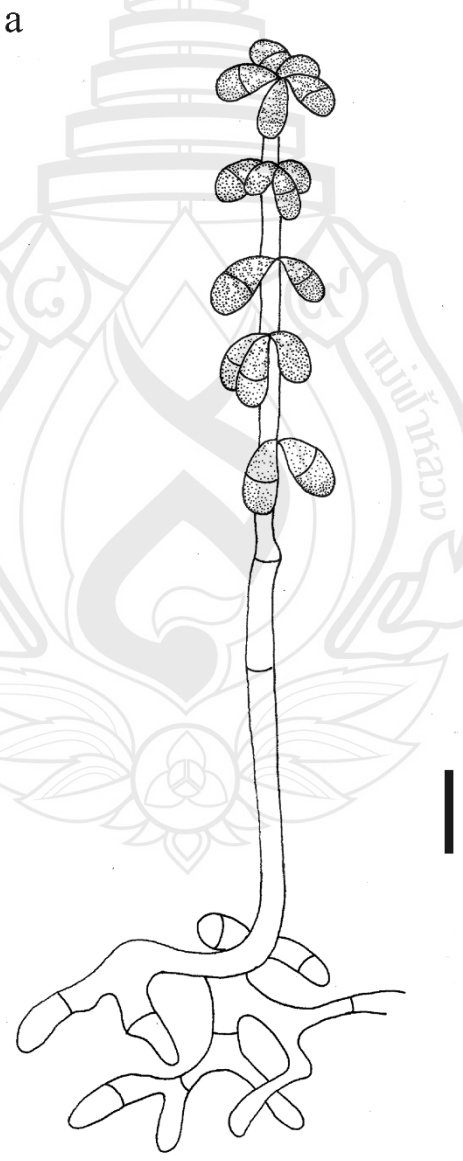


Figure 4.149 *Trichothecium roseum*

Figure 4.149, a. Conidiogenensis on conidiophore. Scale bars: a = 10m. Redrawn from Hyde et al. (2020c)

Family: ***Nectriaceae*** Tul. & C. Tul.

Calonectria De Not., Comm. Soc. crittog. Ital. 2(3): 477 (1867)

Index Fungorum number: IF746; Facesoffungi number: FoF16640

Calonectria was introduced by De Notaris in 1867, with *C. pyrochroa* as the type species (Rossman, 1979). The genus is currently comprised of 127 species, which belong to 13 species complexes with two major groups; the Prolate group, which has clavate to pyriform to ellipsoidal terminal vesicles and the sphaero-naviculate group characterized by sphaeropedunculate and naviculate terminal vesicles (Lombard et al., 2010; Pham et al., 2019). Liu and Chen (2023) have identified *Calonectria* species from soils in southern China based on *tef*1-α, *tub2*, cmdA, his3, *rpb*2 and *Actin* phylogeny. The asexual morph possesses three types of conidia: mega-, micro- and macroconidia. Mega- and microcondia are not common and are not considered informative characters to distinguish between species (Lombard et al., 2010). The sexual morph has yellow to dark red perithecia, with scaly to warty ascocarp walls and long-stalked, clavate asci, and 1-septate to multi-septate ascospores. In the genus, both homothallic and heterothallic mating systems can be found. Some species are recognized as pathogens, affecting 335 hosts across 100 plant families and several have been recorded from soil in South America, South China and Southeast Asia (Lombard et al., 2010).

Table 4.177 *Calonectria* species isolated from soil

Species	Country	Habitat or soil type	References
Calonectria monticola	Thailand	ND	Crous et al. (2015c)
C. densa	Ecuador	ND	Lombard et al. (2010)
C. humicola	Ecuador	ND	
C. orientalis	Indonesia	ND	
C. hongkongensis	China	*Eucalyptus* plantation	Wu and Chen (2021)
C. auriculiformis	Vietnam	*Acacia auriculiformis* plantation	Zhang et al. (2022d)
C. pauciramosa	South Africa	ND	Pham et al. (2018)

Cylindrocladiella Boesew., Can. J. Bot. 60(11): 2289 (1982)

Index Fungorum number: IF7869; Facesoffungi number: FoF13442

Boesewinkel (1982) introduced *Cylindrocladiella* and typified by *C. parva.* The genus comprises 45 species (Liu & Chen, 2024), and 44 of them are supported by molecular data (*his3*, ITS, *tef*1-α, and *tub2*). The asexual morph is hyphomycetous and characterized by the symmetrically branched, penicillate and/or subverticillate conidiophores, producing asymmetrical bundles of small, cylindrical, 1-septate conidia (Lombard et al., 2012). The genus includes soil-born species and can also be found in decayed leaves and wood litter. Some are pathogens, causing leaf spots, and rots of roots, stems and cuttings of agricultural, forestry and horticultural crops in Australia, Brazil, Malaysia, Peru, India, Thailand, the Netherlands and Vietnam (Scattolin & Montecchio, 2007)

Table 4.178 *Cylindrocladiella* species isolated from soil

Species	Country	Habitat or soil type	References
Cylindrocladiella cymbiformis	Australia	ND	Lombard et al. (2012)
C. lanceolata	Australia	ND	
C. longiphialidica	Thailand	ND	
Cy. natalensis	South Africa	ND	
Cy. variabilis	Australia	ND	
C. clavata	Australia	ND	
C. arbusta	Vietnam	*Acacia mangium* plantation	Pham et al. (2018)
C. lageniformis	Vietnam	*Eucalyptus camaldulensis* plantation	
C. malesiana	Malaysia	soil in *A. mangium* plantation	
Cy. obpyriformis	Vietnam	soil in *Acacia* hybrid plantation	
Cy. solicola	Vietnam	soil in *Acacia* hybrid plantation	

Fusarium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1-2): 10 (1809)

Index Fungorum number: IF8284; Facesoffungi: FoF00149

Fusarium was introduced by Link (1809) and typified by *F. roseum*. Currently, around 400 species are listed in this genus, however, most of them lack a proper description (Nikitin et al., 2023). The genus has a cosmopolitan distribution, which can be found in soil, air, water, plants, and insects (Nikitin et al., 2023). The members of

this genus are recorded as pathogens on a wide range of crops, causing rots, blights, wilts, and cankers (Samiksha & Sanjeev, 2021). This is known as soil born genus and has pathogenic, parasitic and saprobic life modes recorded from various substrates. Further, they produce mycotoxins adverse to humans and animals (Samiksha & Sanjeev, 2021, Watanabe et al., 2011). Species are useful in industrial applications such as biofuels, cosmetics, food, and pharmacy (Samiksha & Sanjeev, 2021).

Table 4.179 *Fusarium* species isolated from soil

Species	Country	Habitat or soil type	References
F. solani	Bahrain	Saline soil	Mandeel (2006)
F. oxysporum			
F. chlamydosporum			
F. equiseti			
F. compactum			
F. oxysporum	South Africa	Agricultural soil	Marasas et al. (1988)
F. equiseti			
F. solani			
F. lateritium	Malaysia	Loamy sand	Mohamed Zubi et al. (2021)
F. proliferatum			
F. incarnatum	Malaysia	Sandy loam	
F. rigidiuscula	Malaysia	Silt loam	

Mariannaea G. Arnaud ex Samson, Stud. Mycol. 6: 74 (1974)

Figure 4.150

Index Fungorum number: IF 8846; Facesoffungi number: FoF13445

Mariannaea was established by Samson (1974) and typified by *M. elegans.* There are 23 species listed in the Species Fungorum (2025) and all of them have molecular data. An in-depth revision of *Mariannaea* was provided by Hu et al. (2017) based on ITS and *tub2* phylogeny. The asexual morph is characterized by the branched, septate conidiophores with hyaline and flask-shaped phialides, and hyaline, 1–2-celled conidia mostly forming imbricate chains or in slimy heads, and the sexual morph has solitary, globose, perithecial ascomata with a flat apex and inconspicuous or absent stroma, and cylindrical to narrowly clavate, 8-spored asci, containing 1-septate, hyaline, smooth to spinulose ascospores. Chlamydospores can be present or absent (Bao et al., 2023; Hu et al., 2017; Nonaka et al., 2015). Species are reported from leaves,

soil, terrestrial and submerged wood found in Brazil, China, the Czech Republic, Thailand, the Netherlands, Venezuela and the USA (Bao et al., 2023; Hu et al., 2017).

Table 4.180 *Mariannaea* species isolated from soil

Species	Country	Habitat or soil type	References
Mariannaea atlantica	Brazil	Forest	Hyde et al. (2020a)
M. camptospora	The Neterlands	Forest	Samson (1974)
M. elegans	Japan	ND	Arnaud (1952)
M. humicola	Brazil	ND	Lombard et al. (2015)
M. punicea	Zaire	ND	

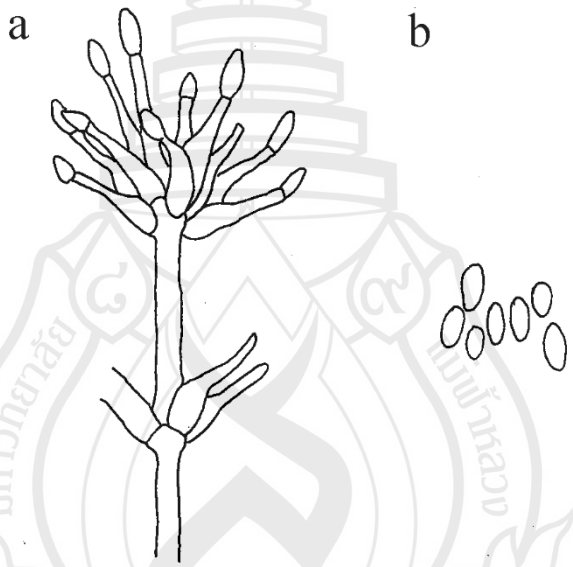


Figure 4.150 *Mariannaea elegans*

Figure 4.150, a Conidiophore. b Conidia. Redrawn from Domsch et al. (1993)

Nectria (Fr.) Fr., Summa veg. Scand., Sectio Post. (Stockholm): 387 (1849)

Index Fungorum number: IF3431; Facesoffungi number: FoF02122

Fries (1849) introduced *Nectria* while designating *N. cinnabarina* as the type species. There were around 800 species accommodated in *Nectria sensu lato*. Subsequently, based on LSU data and morphology, studies have excluded many *Nectria sensu lato* species and placed them in other genera while listing *Nectria* species that are congeneric with type species as *sensu stricto* (Rossman et al., 1999; Yang et al., 2018a). The asexual morphs are coelomycetous (Maharachchikumbura et al., 2016;

Rossman et al., 1999; Yang et al., 2018a), and the sexual morph of *Nectria* has well-developed stromata, subglobose to globose, red to dark red, fleshy, soft-textured, uniloculate, warted perithecia that become cupulate when dry. It has unitunicate, clavate to cylindrical asci, producing hyaline to yellow-brown, broadly ellipsoid to long-fusiform, and non- to multi-septate or muriform ascospores (Fries, 1849). The species are plant pathogens and occur on hardwood trees, leaves, fruits and organic matter, and have also been reported from the soil worldwide (Domsch et al., 1993; Yang et al.; 2018a).

Table 4.181 *Nectria* species isolated from soil

Species	Country	Habitat or soil type	References
Nectria rubicola	Sudan	ND	Lombard et al. (2015)
N. vasinfecta	South Africa	ND	
N. inventa	ND	ND	Domsch et al. (1993)

Neocosmospora E.F. Sm., Bull. U.S. Department of Agriculture 17: 45 (1899)

Figure 4.151

Index Fungorum number: IF 3447; Facesoffungi number: FoF10977

Smith (1899) introduced *Neocosmospora* while designating *N. vasinfecta* as the type species. In the recent revision, Sandoval-Denis et al. (2019) provided the phylogeny (ITS, LSU, *tef1-α* and *rpb*2) and morphology for the genus while introducing new species. As revealed by O'Donnell et al. (2020), some medically important *Fusarium* species had been misplaced in *Neocosmospora,* thus, they have been provided phylogenetic corrections for controversial species. Presently, the genus accommodates 66 species (Species Fungorum 2025), and all of them are supported by the molecular data. The asexual morphs possess distinctive, very long, narrow, acremonium-like, aerial monophialides. The sexual morph is characterized by the orange to red-brown, smooth-walled to coarsely warted perithecia, containing yellow-golden brown, globose to ellipsoidal, 0–1-septate, distinctly ornamented (striate, cerebriform to spinulose) ascospores (Sandoval-Denis et al., 2019). Species present in the air, dead and living plants, human clinical samples, soil and water. Some of them have plant pathogenic nature and several can cause mycotoxicosis in humans and animals (Sandoval-Denis et al., 2019). They can be found in Austria, Belgium, Brazil,

India, Italy, Ivory Coast, Japan, South Africa, Spain, Sri Lanka, Thailand, the Netherlands and the USA (Sandoval-Denis et al., 2019).

Table 4.182 *Neocosmospora* species isolated from soil

Species	Country	Habitat or soil type	References
N. bostrycoides	Honduras	ND	Sandoval-Denis et al.
N. brevis	Belgium	Polluted soil water	(2019)
N. keratoplastica	Belgium	Greenhouse humic soil	
N. lichenicola	Brazil and Tahiti	ND	
N. martii	USA	ND	
N. parceramosa	South Africa	Silty loam soil	
N. pisi	The Netherlands and USA	ND	
N. pisi	Belgium	Greenhouse soil	
N. solani	USA	Soil under Castanea sp.	
N. solani	Japan	Soil on wheat field	
N. stercicola	Belgium	Greenhouse humic soil	
N. striata	Japan	ND	
N. vasinfecta	South Africa	ND	
N. vasinfecta	Ivory Coast	Soil on coffee plantation	

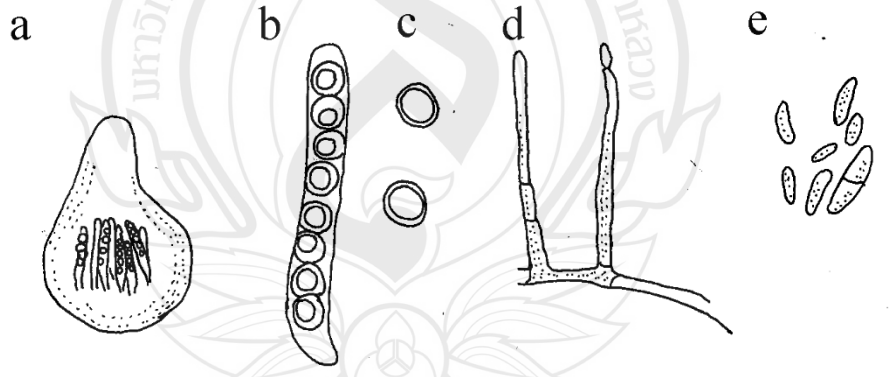


Figure 4.151 *Neocosmospora vasinfecta* (CBS 237.55)

Figure 4.151, a. Ascoma. b. Ascus c. Ascospores. d. Conidiophore. e. Conidia. Redrawn from Domsch et al. (1993)

Paracremonium L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, Stud. Mycol. 80: 233 (2015)

Figure 4.152

Index Fungorum number: IF810267; Facesoffungi number: FoF06584;

While revising *Nectriaceae,* Lombard et al. (2015) introduced *Paracremonium* based on phylogeny using ITS, LSU, *tef1-α,* ATP citrate lyase (*acl1*), *rpb1, rpb2, tub2, cmdA* and *his3* and morphology, accommodating *P. inflatum* as the type species. It presently comprises eleven species (Species Fungorum 2025). The asexual morph is characterized by erect, cylindrical to subcylindrical, hyaline conidiophores, and monophialidic, hyaline, ampulliform or subcylindrical conidiogenous cells, with aseptate, fusiform to ellipsoidal to cylindrical conidia, forming in slimy heads (Lombard et al., 2015). Sometimes mycelium produces sterile coils with conidiophores radiating outwards with inconspicuously swollen septa, which is a significant character for this genus; however, some species do not have this character. The sexual morph is not observed (Lombard et al., 2015; Ming et al., 2021). This genus is recorded as human pathogens and entomopathogenic fungi. They are distributed in air, aquatic habitats, human clinical samples and terrestrial habitats such as alkaline mud samples, cave sewage, soil, stream embankments, submerged wood and water located in Canada, China, Egypt, India, Thailand, the Netherlands and the USA (Ming et al., 2021).

Table 4.183 *Paracremonium* species isolated from soil

Species	Country	Habitat or soil type	References
Paracremonium apiculatum	China	Cave	Ming et al. (2021)
P. bendijkiorum	The Netehrlands	ND	Crous et al. (2021a)
P. binnewijzendii	The Netehrlands	Soil from stream embankment	
P. moubasheri	Egypt	Alkaline mud	Al-Bedak (2019)

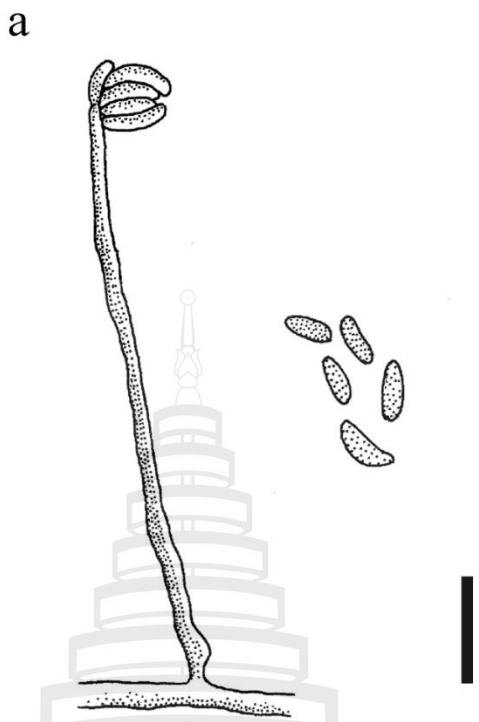


Figure 4.152 *Paracremonium inflatum* (CBS 485.77)

Figure 4.152, a Conidiophores and conidia. Scale bar: a, b = 10 μm. Redrawn from Lombard et al. (2015)

Family: ***Ophiocordycipitaceae*** G.H. Sung, J.M. Sung, Hywel-Jones & Spatafora

Purpureocillium (Thom) Luangsa-ard, Houbraken, Hywel-Jones & Samson, FEMS Microbiol. Lett. 321(2): 144 (2011)

Index Fungorum number: IF519529; Facesoffungi: FoF14520

Luangsa-ard et al. (2011) introduced *Purpureocillium* with the type species *P. lilacinum.* The genus comprises nine species and all of them have molecular data (Chen et al., 2024). The asexual morph is characterized by the mononematous, stiff, verticillate conidiophores and ovate to cylindric phialides. Conidia are in dry divergent chains, purple in mass, straight to slightly curved or ellipsoidal to fusiform and slightly roughened. Species are recorded as saprobes and opportunistic pathogens in humans (Calvillo-Medina et al., 2021; Corrêa-Moreira et al., 2022). *Purpureocillium* has a cosmopolitan distribution and is found from animals, indoor air, humans, insect larvae, nematodes, plant debris and soil in China, Iran, Mexico and Venezuela (Luangsa-ard et

al., 2011). Some have been used for biological control of plant-parasitic nematodes and insects in agricultural practices (Corrêa-Moreira et al., 2022).

Table 4.184 *Purpureocillium* species isolated from soil

Species	Country	Habitat or soil type	References
Purpureocillium lavendulum	Venezuela	ND	Perdomo et al. (2013)
P. lilacinum	ND	ND	Luangsa-ard et al. (2011)
P. sodanum	Iran	ND	
P. jiangxiense	China	ND	Chen et al. (2024)
P. zongqii	China	Sinkhole	

Ophiocordyceps Petch, Trans. Br. mycol. Soc. 16(1): 73 (1931)

Index Fungorum number: IF3598; Facesoffungi: FoF01318

Petch (1931) introduced *Ophiocordyceps* with the type species *O. blattae*. Being the largest genus in *Ophiocordycipitaceae*, it comprises 323 species (Fei et al., 2024). The genus has hirsutella-like asexual morphs with columnar, wart-like, or filamentous, solitary or branched, hyaline to light or dark brown conidiophores, and unicellular, occasionally multicellular, conidia vary in shape; some species have a hyaline or colored mucus layer on the surface of one or more conidia, and several species produce secondary conidia (Fei et al., 2024; Liang, 1990). The sexual morph has hard or flexible, dark-colored, and fibrous stromata with superficial or partially embedded perithecia arranged vertically or obliquely. Ascospores are cylindrical, septate or break into secondary spores (Fei et al., 2024; Luangsa-ard et al., 2018). The genus is pathogenic to a wide range of insects such as *Coleoptera*, *Diptera*, *Hemiptera* and *Lepidoptera*. Species can also be associated with decaying wood, forest plants, leaf litter, mosses, buried host insects, and soils in Brazil, China, Japan, Thailand and Ukraine (Fei et al., 2024).

Table 4.185 *Ophiocordyceps* species isolated from soil

Species	Country	Habitat or soil type	References
Ophiocordyceps sinensis	China	ND	Peng et al. (2013), Xia et al. (2015)
O. highlandensis	China	*Pinus armandi* forest	Xu et al.(2022)

Tolypocladium W. Gams, Persoonia 6(2): 185 (1971)

Figure 4.153

Index Fungorum number: IF10242; Facesoffungi number: FoF10425

Tolypocladium was established by Gams (1971), accommodating *T. inflatum* as the type species. Currently, 52 species are listed in the Species Fungorum (2025), but only around 34 are supported by the molecular data. Previously, the genus was placed in *Clavicipitaceae* (Sung et al., 2007), subsequently, *Tolypocladium* was placed in *Ophiocordycipitaceae* using SSU, LSU, *tef-1α, rpb1* and *rpb*2 phylogeny (Sung et al., 2007). Based on combined SSU, LSU, *tef-1α* and *rpb1* combined phylogeny, Wang et al. (2022) revised the genus, introducing soil inhabiting new species and providing a key to the 48 *Tolypocladium* species. The asexual morph is characterized by solitary or branched conidiophores, cylindrical to conical phialides, and one-celled, cylindrical to globose conidia. The sexual morph has darkly pigmented, stipitate stromata, with semi-immersed to immersed perithecia and cylindrical asci with cylindrical, multi-septate ascospores that disarticulate into part spores, though occasionally they remain articulating (Gams, 1971; Hyde et al., 2020c; Wang et al., 2022c). These species produce metabolites such as cyclosporin A, tolypoalbin, tolypin, and tolyprolinol that can be used in pharmacology and biocontrol products. *Tolypocladium* species have been reported from insects, rotifers, on other fungi or as soil-inhabitants with parasitic, saprobic or plant endophytic life modes in Brazil, Canada, China, Finland, Japan, Mexico, New Zealand, Sri Lanka and the USA (Hyde et al., 2020c; Wang et al., 2022c)

Table 4.186 *Tolypocladium* species isolated from soil

Species	Country	Habitat or soil type	References
Tolypocladium album	Colombia, France, Scotland	ND	Gams (1980)
T. geodes	Austria, Canada, China	ND	Bissett (1983)
T. microsporum	Canada, Germany, the Netherlands	ND	
T. nubicola	Canada and China	ND	
T. tundrense	Canada	ND	
T. inflatum	Japan and U.S.A.	ND	Hodge et al. (1996)
T. terricola	Finland	ND	Weiser et al. (1991)
T. pseudoalbum	China	ND	Wang et al. (2022c)
T. yunnanense	China	ND	

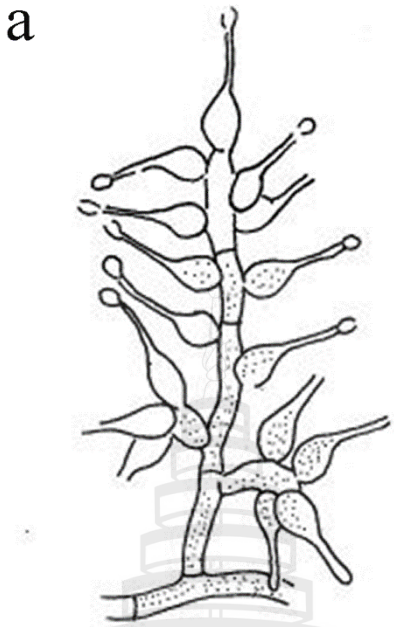


Figure 4.153 *Tolypocladium inflatum*

Figure 153, a Branched conidiophore with conidia. Redrawn from Seifert et al. (2011)

Family: *Polycephalomycetaceae*

Polycephalomyces Kobayasi, Sci. Rep. Tokyo Bunrika Daig., Sect. B 5: 245 (1941)

Index Fungorum number: IF9494; Facesoffungi number: FoF03811

Polycephalomyces was introduced by Kobayasi (1941) and typified by *P. formosus*. It was previously accommodated in *Ophiocordycipitaceae*. Later, in Xiao et al. (2023), *Polycephalomycetaceae* was introduced to accommodate this genus by using the combined SSU, ITS, *tef-1α*, *rpb*1 and *rpb*2 phylogeny. Presently, it comprises 13 species (Species Fungorum, 2025), however only six have molecular data. The asexual morph has branched or unbranched, divergent conidiophores, 1–4 phialides arising from conidiophores and phialidic conidiogenous cells that are intercalary or terminal, giving rise to monomorphic, oblong to cylindrical, hyaline and one-celled conidia. The sexual morph remains undetermined. Species have been identified as insects parasites and also associate with plant leaves and soil in China, Ecuador, France, Japan and Thailand (Xiao et al., 2023)

Table 4.187 *Polycephalomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Polycephalomyces aurantiacus	Thailand	*Ophiocordyceps barnesii* (Ophiocordycipitaceae), buried in the soil	Xiao et al. (2018)
P. marginaliradians	Thailand	Cossidae larva (Lepidoptera), buried in the soil.	

Family: *Stachybotryaceae* L. Lombard & Crous

Brevistachys L. Lombard & Crous, Persoonia 36: 182 (2016)

Figure 4.154

Index Fungorum number: IF815934; Facesoffungi: FoF05536

Brevistachys was introduced by Lombard et al. (2016) based on *B. variabilis*. The genus comprises five species, and all of them are supported by the molecular data (*cmdA*, ITS, *rpb2* and *tub2*) (Lombard et al., 2016). The genus accommodates stachybotrys-like species having distinctly short conidiophores and conidiogenous cells that are born either on conidiophores or directly from vegetative hyphae, features not observed in *Stachybotrys* s. str. (Lombard et al., 2016). They are saprobic fungi and are found on plants (*Musa* sp. and *Zingiber* sp.) and soil in Australia, Georgia, Mexico and Sri Lanka (Lombard et al., 2016).

Table 4.188 *Brevistachys* species isolated from soil

Species	Country	Habitat or soil type	References
Brevistachys globose	Indonesia	Botanical Garden	Rizki and Ilmi (2021)

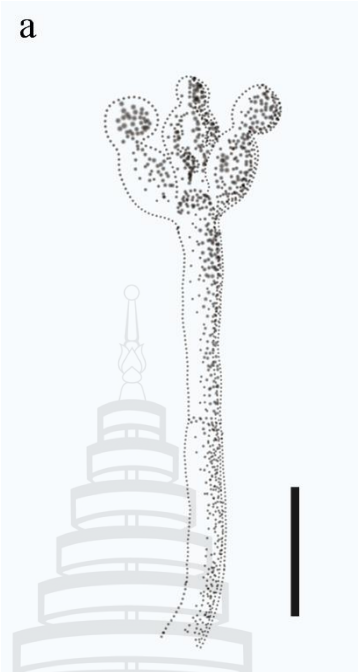


Figure 4.154 *Brevistachys variabilis* (CBS 141057)

Figure 4.154, Conidiogensis on conidiophore. Scale bar a= 10 μm. Redrawn from redrawn from Lombard et al. (2016).

Didymostilbe Henn., Hedwigia 41: 148. 1902 (non *Didymostilbe* Bres. & Sacc. 1902)

Index Fungorum number: IF8021; Facesoffungi: FoF05542

Didymostilbe was introduced by Hennings (1902) with the type *D. coffeae*. Twelve species are accommodated in Species Fungorum (2025) and only three species are supported by molecular data. *Didymostilbe* was previously classified in *Bionectriaceae* (*Hypocreales*, *Hypocreomycetidae*), however, phylogenetic analyses (*cmdA*, ITS, *rpb2*, and *tub2*) by Lombard et al. (2016) showed that this genus belongs to the *Stachybotriaceae*. The asexual morph is characterized by thick-walled, large conidia, with prominent apical and/or basal mammiform protuberances (Seifert, 1985). Species are distributed in Australia, Cuba, Ecuador, Japan, Poland, Thailand and Trinidad that are associated with terrestrial and submerged wood, pods and soil (Lombard et al., 2016).

Table 4.189 *Didymostilbe* species isolated from soil

Species	Country	Habitat or soil type	References
Didymostilbe sp.	Thailand	ND	Manoch (1987)

Memnoniella Höhn., Centbl. Bakt. ParasitKde, Abt. II 60: 16 (1923) [1924]

Index Fungorum number: IF8900; Facesoffungi: FoF05558

Memnoniella was introduced by Von Höhnel (1924) with the type species, *M. aterrima*. Seventeen *Memnoniella* species are listed in Species Fungorum (2025), and all of them have molecular data. The species show a close relationship with *Stachybotrys* and both genera have conidiophores composed of a stipe and a whorl of phialides giving rise to one-celled conidia. Additionally, at least part of the conidiophore or the conidia are pigmented. The confusing taxonomic history of these two genera was deeply discussed by Wang et al. (2015), and they concluded that *Memnoniella* is a synonym of *Stachybotrys*. However, Lombard et al. (2016) resurrected the genus *Memnoniella* and epitypified the type species of the genus, *M. echinate,* based on multi-locus phylogenetic analysis of *cmdA*, ITS, *rpb2* and *tub2* sequence data. The asexual morph is characterized by mononematous, unbranched, septate conidiophores, phialidic conidiogenous cells and ellipsoidal to globose to reniform, aseptate conidia (Ellis, 1971; Lombard et al., 2016). *Memnoniella* can be distinguished from *Stachybotrys* by the formation of mostly smooth, unbranched, thick-walled conidiophores, giving rise to conidia, which are sometimes carried in dry chains (Lombard et al., 2016). They are mostly saprobic species associated with dead plant materials, and soil collected in Austria, China, Nepal, Thailand and Venezuela (Lombard et al., 2016; Tennakoon et al., 2021; Yeh et al., 2023).

Table 4.190 *Memnoniella* species isolated from soil

Species	Country	Habitat or soil type	References
Memnoniella humicola	Suriname	Soil under Elaeis guineensis	Lombard et al. (2016)
M. sinensis	China	ND	

Myrothecium Tode, Fung. mecklenb. sel. (Lüneburg) 1: 25 (1790)

Index Fungorum number: IF9049; Facesoffungi number: FoF05560

Myrothecium was introduced by Tode (1790) with type *M. inundatum*. There are 64 records in the Species Fungorum (2025). Previously, this genus was placed in *Hypocreales* order *incertae sedis* and later, it was accepted in *Stachybotryaceae* (Maharachchikumbura et al., 2015). *Myrothecium* species produce secondary metabolites with strong antifungal and antibiotic activities (Lombard et al., 2016; Ruma

et al., 2015). Phylogenetic analyses of *Myrothecium* species (*Stachybotryaceae*) were constructed based on the combined SSU, LSU, ATP6, *tef*1-α and *rpb2* regions (Chen et al., 2016), *cmdA*, ITS, *rpb2* and *tub2* regions (Lombard et al., 2016), and ITS region (Dai et al., 2017). The asexual morph is characterized by a sporodochial (to occasionally synnematous) conidiomata, phialidic conidiogenesis and variably shaped conidia accumulating in a green mucoid drop (Tulloch, 1972). *Myrothecium* species are mostly saprobes in decaying leaves and soil, and some are weak plant pathogens found in India, the Philippines, Thailand and Venezuela (Chen et al., 2016; Dai et al., 2017; Ellis & Ellis, 1985). Some *Myrothecium* species produce macrocyclic trichothecenes, biochemical compounds being exploited for their strong cytotoxicity towards human and murine lymphocytic leukaemia and solid tumours (Lombard et al., 2016).

Table 4.191 *Myrothecium* species isolated from soil

Species	Country	Habitat or soil type	References
Myrothecium curvisporum	China	Farmland soil	Jiang et al. (2017a)
M. australiense	Australia	Forest soil	

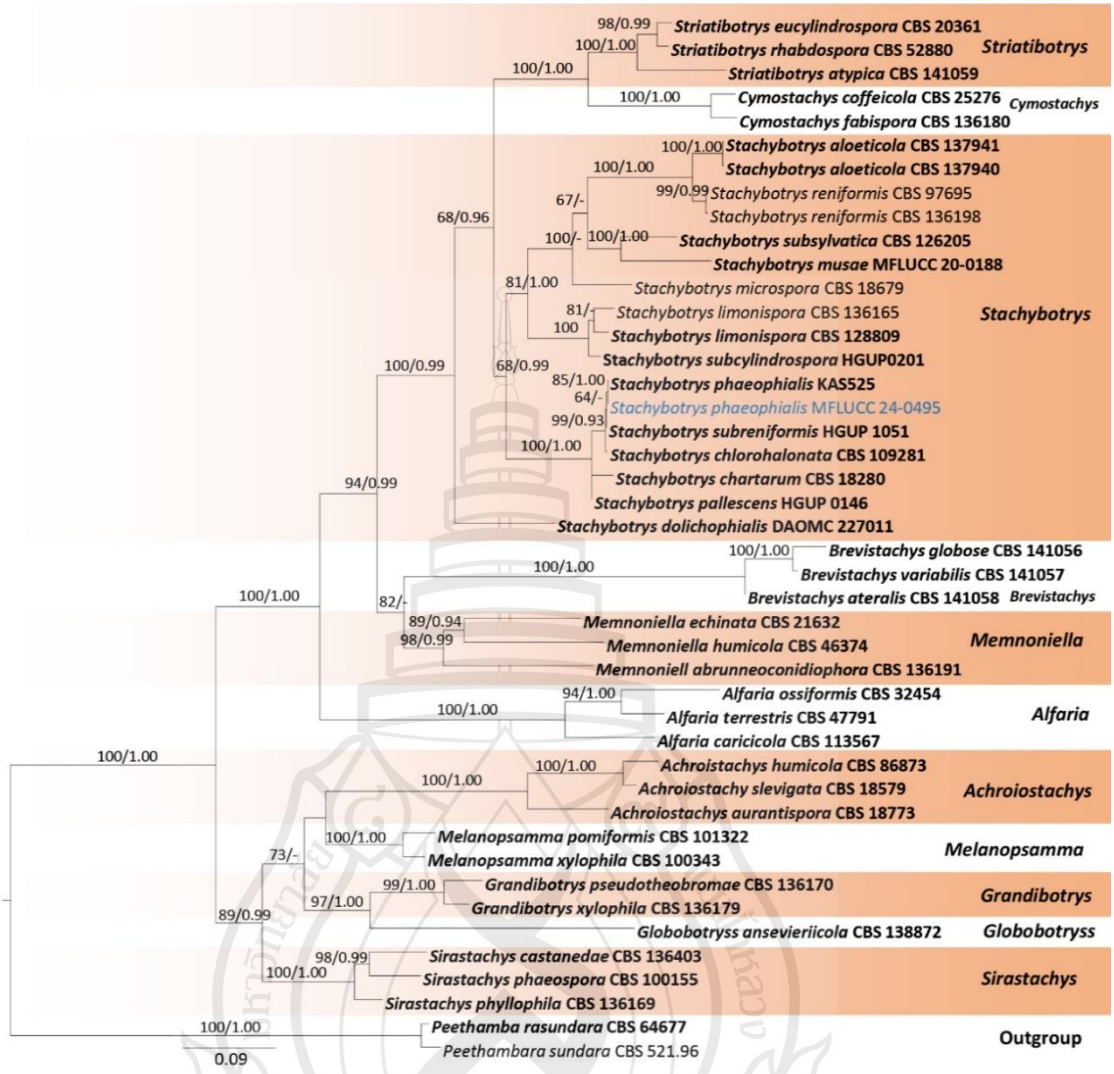


Figure 4.155 The best scoring IQ tree generated of the combined ITS, *tub2*, *tef1-α* and *rpb2* sequence data for *Stachybotryacea*

Figure 4.155, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue and ex-type strains are in bold. The tree is rooted to *Peethambara sundara* (CBS64677 and CBS52196). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 1843 bp, and single gene alignments are ITS: 686 bp, rpb2: 773 and tub2: 384 bp. The matrix had 1318 distinct alignment patterns with 23.66% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.230, C = 0 0.294, G = 0.256, T = 0.220; substitution rates AC =

1.37637 AG = 3.24931, AT = 1.37637, CG = 1.00000, CT = 6.14096, GT = 1.00000; gamma distribution shape parameter α = 0.955.

Stachybotrys Corda, Icon. fung. (Prague) 1: 21 (1837)

Index Fungorum number: IF10052

Stachybotrys was introduced by Corda (1837) with *Stachybotrys atrus* (= *S. chartarum*) as the type species. There are 89 species accommodated in the Species Fungorum (2025), and only 13 have sequence data. Previously, *Memnoniella* and *Stachybotrys* were treated as distinct genera in *Stachybotryaceae* (Bisby, 1945; Jong & Davis, 1976). This idea was further supported by Lombard et al. (2016) using *cmdA*, ITS, *rpb2*, *tef1-α* and *tub2* multi-gene phylogenetic analyses. Conversely, Wang et al. (2015b) suggested *Stachybotrys* as a synonym of *Memnoniella* by indicating morphological and phylogenetic similarities. The asexual morph is characterized by macronematous, mononematous, erect, unbranched or branched, hyaline to olivaceous brown conidiophores, bearing 3–12 conidiogenous cells at the apex with aseptate, initially hyaline, becoming olivaceous brown to dark brown, smooth to verrucose, thick-walled, ellipsoidal to globose to fusiform to limoniform conidia that are rounded at both ends or with an apical hilum. The sexual morph is characterized by ascomata that are perithecial, stromatic, solitary or occasionally in pairs, subglobose to obpyriform, black, surface glabrous, papillate ostiolar region without periphyses, with setae irregularly arranged over the surface and with a single layer of *textura angularis* ascomatal wall. Setae are erect, irregularly flexuous, sometimes developing into fertile conidiophores. Asci are clavate, 8-spored, rounded apex to nearly truncate with refractive apical ring and containing cylindrical, 1-septate, subhyaline, verrucose ascospores that are slightly tapering towards apices and surrounded by a thick mucoid sheath (Lombard et al., 2016). Species are widely distributed as saprobes or pathogens and also can be found on cotton, damp papers, indoor environments, dead and living plant substrates, linen, and soil in Austria, Cuba, Indonesia, Italy, Japan, Thailand, Uganda and the USA (Wang et al., 2015b). *Stachybotrys chartarum* is a soil- born fungus that cause mycotoxicosis in humans and animals and human respiratory diseases (Wang et al., 2015b).

Table 4.192 *Stachybotrys* species isolated from soil

Species	Country	Habitat or soil type	References
Stachybotrys xigazenensis	China	ND	Wu and Zhang (2010)
S. jiangziensis	China	ND	
S. subcylindrospora	China	Tropical primordial rain fores	Jie et al. (2013)
S. terrestris	China	Soil in arable plain (Hexi Corridor)	Kong et al. (2007)
S. subreniformis	China	Forest	
S. chartarum	Belgium, Canada, France and Switzerland	ND	Lombard et al. (2016)
S. chlorohalonata	France	ND	
S. limonispora	USA	ND	
S. microspora	Sudan	ND	
S. pallescens	China	ND	
S. subsylvaticus	Namibia	Woodland of *Colophospermum mopane*	

Stachybotrys phaeophialis L. Lombard & Crous, Persoonia 36: 223 (2016)

Figure 4.156

Index Fungorum number: IF 816033; Facesoffungi number: FoF 16719

Sexual morph: Undetermined. Asexual morph: *Conidiophores* 35–63 × 2–4 μm ($\overline{x}$ = 45 × 3 μm, n=10), single or in groups, mononematous, macronematous, hyaline to sub-hyaline, 1–2 septate, straight to slightly flexuous, smooth to verrucose walled with 3–6 conidiogenus cells. *Conidiogenous cells* 6–10 × 2.5–5.5 μm ($\overline{x}$ = 8 × 4 μm, n=10), phialidic, hyaline to subhyaline, terminal, clavate to subclavate, smooth, with collarette present. *Conidia* 6–10 × 4.5–7.5 μm ($\overline{x}$ = 7.5 × 5.8 μm, n=25), hyaline, ellipsoidal to fusiform or oval, truncate base, thick-walled. *Chlamydospores* sub-globose to globose, intercalary, hyaline.

Culture characteristics – *Colonies* on the PDA become 2–3 cm after 7 days at 25°C, appear in whitish brown, become greyish brown at the center, brown to brownish orange at the edge, undulate margined, flat, reverse brown. *Hyphae* 3.5–2.5 μm ($\overline{x}$ = 3

μm, n = 20), superficial to semi-immersed, hyaline to pale brown, smooth to verrucose and aseptate, become septate at maturity.

Material examined – Thailand, Chiang Rai, Construction site, 20.031269N, 99.880183E, 398m, 17 October 2022, W.A. Erandi Yasanthika, (MFLU25-0138), living culture 96 -u1-6=MFLUCC 24-0495.

GenBank numbers – MFLUCC 24-0495: ITS: PQ570523, *tub2*: PV611463, , rpb2: PV611460

Notes – According to multi-gene phylogeny (Figure 4.145), our strain clusters with *Stachybotrys phaeophialis* with 85%ML and 1.00 BYPP support. *Stachybotrys phaeophialis* was introduced by Lombard et al. (2016) from seeds of unidentified herb imported into Canada from China. Each gene region of our strain was compared with the type species, resulting in 100% similarity. Our strain resembled the type species of *S. phaeophialis* by having macronematous, mononematous conidiophores that are single or in groups, smooth to slightly verrucose, phialidic conidiogenous cells and ellipsoidal to fusiform conidia (Lombard et al., 2016). However, we have observed oval conidia as well. Our phylogeny and morphological results confirm that our strain is *S. phaeophialis.* Herein, we report *S. phaeophialis* from an urban area in Thailand and this is the first record of this species associated with soil.

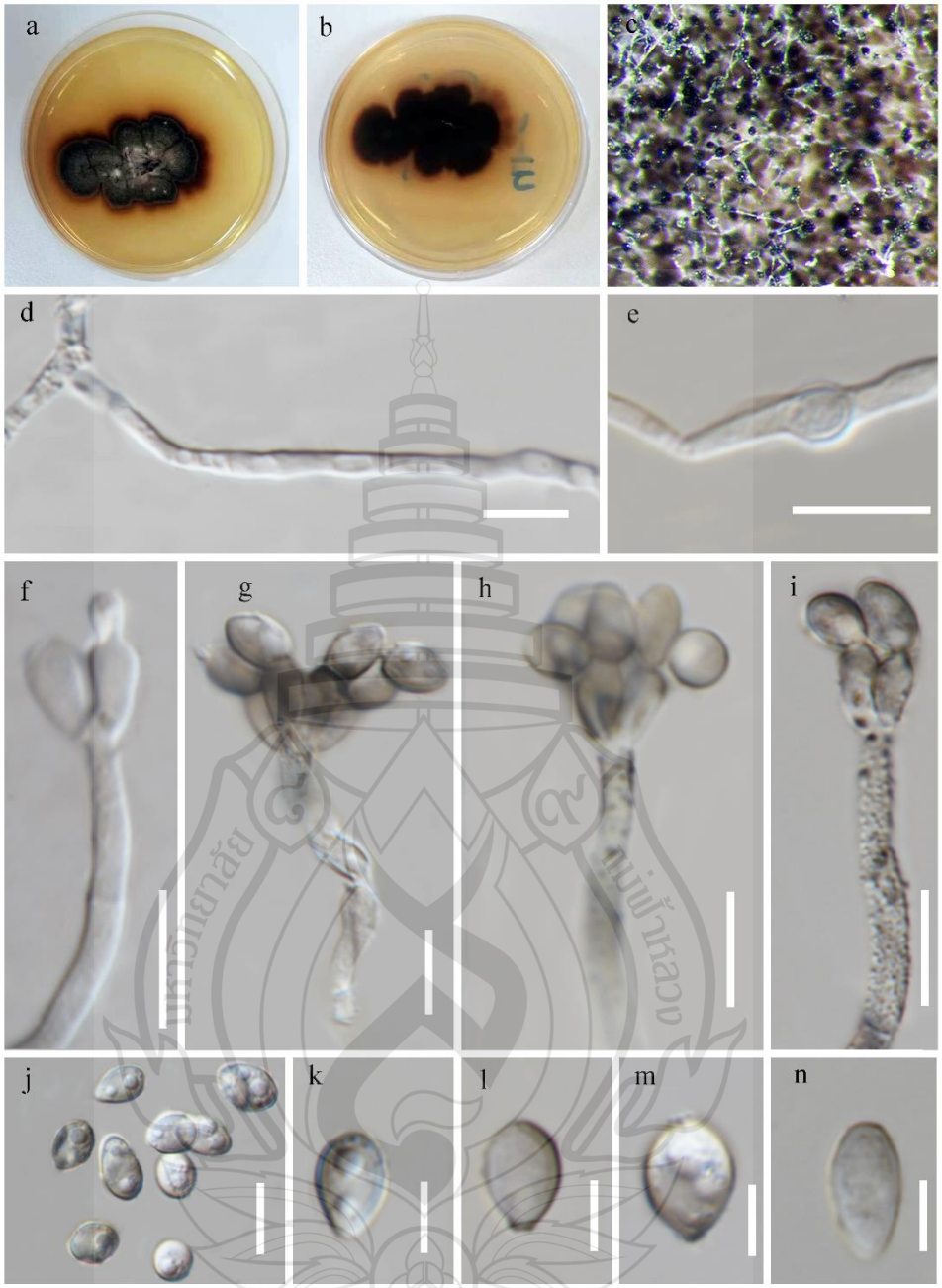


Figure 4.156 *Stachybotrys phaeophialis* (MFLU25-0138)

Figure 4.156, a, b Culture characters on the PDA (b = reverse). c Sporulated colony with conidial attachments on the mycelium. d Mature pigmented hyphae. e Chlamydospore. f–i Conidiophores with phialides. j–n Conidia. Scale bars: d–j = 10 μm, k–n = 5 μm.

Order: ***Microascales*** Luttr. ex Benny & Kimbr.

Family: ***Ceratocystidaceae*** Locq. ex Réblová, W. Gams & Seifert

Ceratocystis Ellis & Halst., New Jersey Agric. Coll. Exp. Sta. Bull. 76: 14 (1890)

Figure 4.157

Index Fungorum number: IF888; Facesoffungi number: FoF01249

Ceratocystis was erected by Halsted (1890), and the taxonomic description was provided by Halsted and Fairchild (1891), confirming the type species as *Ceratocystis fimbriata*. Currently, 106 species are listed in the genus Species Fungorum (2025), and around 45 have molecular data. Marin-Felix et al. (2017) provided a combined ITS, *tub2*, *tef*1-α, *rpb*2 and ms204 phylogeny for *Ceratocystis*, mentioning that morphology is largely insignificant for distinguishing species within the genus. Instead, the *rpb*2 and ms204 gene regions, in combination with ITS, have a high impact on species delineation in this genus. The asexual morph is chalara-like or thielaviopsis-like, and has straight or flexuous, hyaline to pale brown conidiophores, and endophialidic conidiogenous cells, which can be flask-shaped producing various shapes of cylindrical conidia or tubular form producing doliiform conidia (Hyde et al., 2020c; Marin-Felix et al., 2017a). Sometimes secondary, dark, barrel-shaped, thick-walled aleurioconidia are produced that facilitate survival in wood or soil during the dry seasons (Hyde et al., 2020c). The sexual morph of *Ceratocystis* is characterized by brown to black, subglobose to globose or obpyriform, ostiolate, perithecial ascomata, covered with undifferentiated hyphae and having ostiolar necks. The asci are evanescent, and the ascospores are hyaline, 1-celled, ellipsoidal, surrounded by a gelatinous sheath (de Beer et al., 2014; Marin-Felix et al., 2017; Hyde et al., 2020). These species are known as destructive plant pathogens that damage cash crops such as cacao, coffee, eucalyptus and giant taro. Species are distributed in Australia, Colombia, Ecuador, Japan, Russia, Sweden and Venezuela associated with stumps, soils, twigs and wood (Maharachchikumbura et al., 2016; Marin-Felix et al., 2017; Hyde et al., 2020).

Table 4.193 *Ceratocystis* species isolated from soil

Species	Country	Habitat or soil type	References
Ceratocystis fimbriata	Brazil	ND	Harrington (2013)

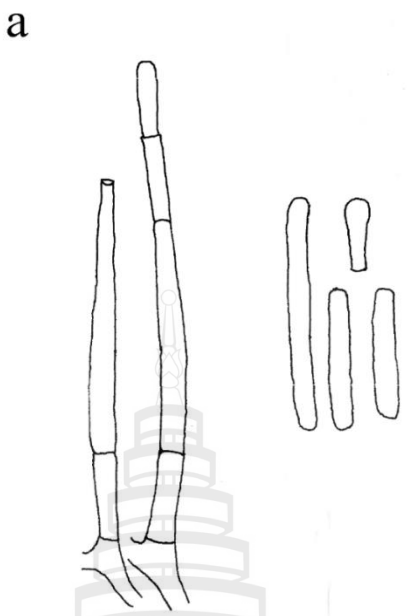


Figure 4.157 *Ceratocystis* sp.

Figure 4.157, a Conidiophores and conidia. The drawings are redrawn from Siefert et al. (2011)

Family: *Graphiaceae* De Beer

Graphium Corda, Icon. fung. (Prague) 1: 18 (1837)

Figure 4.158

Index Fungorum number: IF8398; Facesoffungi number: FoF02143

Corda (1837) introduced *Graphium*, with *G. penicillioides* as the type species. There are 76 species currently listed in Species Fungorum (2025), and 16 are supported by molecular data. de Beer et al. (2013) established *Graphiaceae* (*Microascales*) based on the combined LSU and SSU phylogeny, and species belonged to *Graphium* sensu stricto were classified as *Graphium* with a genus description. Asexual morphology of the genus has synnematous conidiophores and monoblastic, percurrent, subulate or cylindrical conidiogenous cells, producing 1-celled, hyaline, cuneiform or ellipsoidal conidia (Wu et al., 2015; Hyde et al., 2020). These species are reported as plant pathogens and harbor on living leaves, manure, plant debris, polluted water, soil and woody substrates collected from Great Britain, China, Costa Rica, Germany, India, Poland and Romania (de Beer et al., 2013; Hyde et al., 2020).

Table 4.194 *Graphium* species isolated from soil

Species	Country	Habitat or soil type	References
Graphium variabile	China	Forest	Wu et al. (2015b)
G. wuweiense	China	Desert oasis soil	
G. terricola	India	Seashore soil	

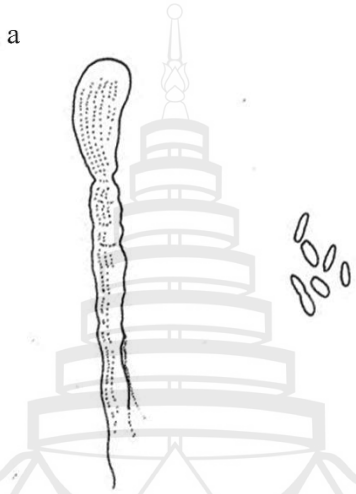


Figure 4.158 *Graphium penicillioides*

Figure 4.158, a Conidiogenesis on synnematous conidiophores and conidia. Redrawn from Crane and Schoknecht (1973).

Family: ***Microascaceae*** Luttr. ex Malloch

Acaulium Sopp, Skr. VidenskSelsk. Christiania, Kl. I, Math.- Natur. 11: 42. 1912.

Figure 4.159

Index Fungorum number: IF7011; Facesoffungi number: FoF06823

Acaulium was introduced by Sopp (1912), and the type species is *A. albonigrescens.* Subsequently, the genus was considered a synonym of *Scopulariopsis* but was re-instated by Sandoval-Denis et al. (2016a; 2016b), based on LSU, ITS, *tef1-α* and *tub2* phylogeny. Later, the placement of *Acaulium* was confirmed by Woudenberg et al. (2017) and Hyde et al. (2020). Currently, 8 species are listed in the genus (Species Fungorum, 2025), and all of them are supported by molecular data (Su et al., 2020). However, morphology is not informative for species delineation in this genus (Hyde et al., 2020c; Sandoval-Denis et al., 2016b). The asexual morph of this genus is characterized by mononematous, rarely synnematous conidiophores and annellidic conidiogenesis with hyaline or subhyaline, smooth- and thick-

walled guttulate conidia with a truncate base (Sandoval-Denis et al., 2016a, 2016b). The sexual morph produces superficial or immersed scattered ascomata; evanescent, 8-spored, subglobose to globose asci, and pale orange to red-brown, 1-celled, lunate ascospores. Cultures can be grown at low temperatures and abundant sporulation can be observed at 15°C. Hyphae have dense fascicles and are abundant with oil drops, which is significant in the genus. Species are distributed in terrestrial habitats worldwide, such as buildings, hair, litter, skin of a horse and soil (Sandoval-Denis et al., 2016b).

Table 4.195 *Acaulium* species isolated from soil

Species	Country	Habitat or soil type	References
Acaulium acremonium	Germany	Wheat field soil	Sandoval-Denis et al. (2016a)
A. pannemaniae	the Netheralnds	ND	
A. peruvianum	Peru	ND	Su et al. (2020)

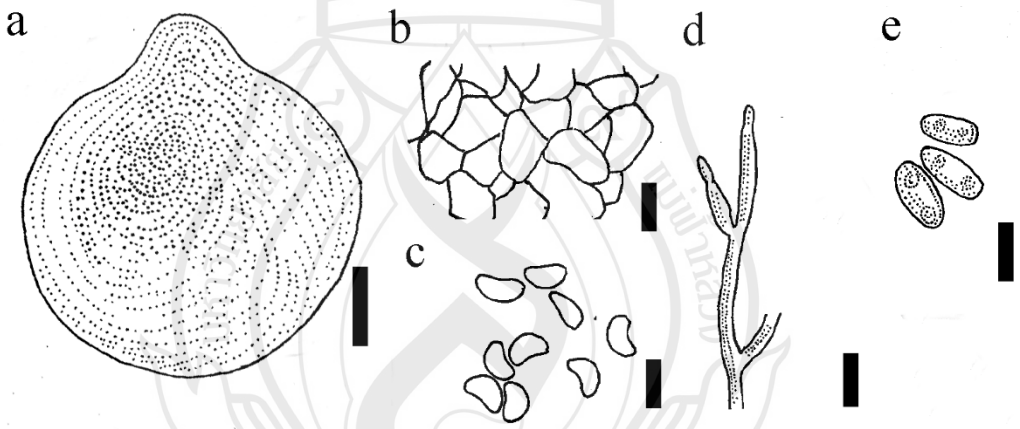


Figure 4.159 *Acaulium albonigrescens* (IHEM 18560)

Figure 4.159 a Ascoma. b Ascomatal peridium. c Ascospores. d Conidiophores and conidiogenous cells. e. Conidia. Scale bars: a = 100μm, b–e = 5 μm. Redrawn from Sandoval-Denis et al. (2016b).

Cephalotrichum Link, Mag. Gesell. naturf. Freunde, Berlin 3(1–2): 20 (1809)

Figure 4.160

Index Fungorum number: IF7527; Facesoffungi number: FoF06826

Cephalotrichum was introduced by Link (1809) and typified by *C. stemonitis*. The genus comprises 42 species (Species Fungorum 2025), and 22 are supported by moelcualr data. The updated phylogeny of *Cephalotrichum* was provided with new

species by Woudenberg et al. (2017) based on LSU, ITS, *tub2* and *tef1-α* multi-gene phylogeny, while studying cultures and herbarium specimens in China. The asexual morph is hyphomycetous, and has branched or unbranched, septate conidiophores that are aggregated in synnemata, penicillately arranged, annellidic conidiogenous cells, producing basipetal, catenate, dry, 1-celled, obovoid, ellipsoidal, globose to subglobose conidia. The echinobotryum-like synasexual morphs produced oval to fusiform, dark brown, verrucose and thick-walled conidia often with a pointed apex (Link, 1809). Sexual morph is unknown. These species are saprobic on dung, indoors, soil and wood with a worldwide distribution including Argentina, China, England, Italy, Japan, the Netherlands and the USA (Sandoval-Denis et al., 2016b; Hyde et al., 2020).

Table 4.196 *Cephalotrichum* species isolated from soil

Species	Country	Habitat or soil type	References
Cephalotrichum asperulum	Argentina	ND	Wei et al. (2024)
Cephalotrichum asperulum	China	Farmland soil	
C. brunneisporum	China	Forest soil	
C. cylindricum	France	ND	
C. dendrocephalum	Iraq	Cultivated soil	
C. domesticum	China	Bamboo forest soil	
C. gorgonifer	China	Forest soil	
C. hinnuleum	South Korea	ND	
C. lageniforme	China	Forest soil	
C. microsporum	Germany	Wheat field soil	
C. nanum	China	Meadow soil	
C. stemonitis	USA	ND	
C. tenuissimum	USA	ND	Woudenberg et al. (2017b)
C. telluricum	Canada	ND	
C. verrucisporum	the Netehrland	sand dune	Sandoval-Denis et al. (2016b)

Figure 4.160 *Cephalotrichum stemonitis*

Figure 4.160, Conidiophores, conidiogenous cells and conidia. Redrawn from Seifert et al. (2011)

Gamsia M. Morelet, Ann. Soc. Sci. Nat. Arch. Toulon et du Var 21: 105 (1969)

Index Fungorum number: IF8306; Facesoffungi number: FoF06831

Gamsia was initially erected by Morelet (1969) with the type species *Gamsia dimera*. The genus accommodates six species (Species Fungorum, 2025), and all of them have molecular data. Sandoval-Denis et al. (2016b) accepted the current placement of *Gamsia* based on the LSU, ITS, *tef*1-α and *tub2* phylogeny and the morphology, particularly the lack of well-differentiated conidiophores and the conidial arrangement with large apical clusters. The asexual morph has unbranched or sometimes branched, septate, hyaline conidiophores, with two types of conidia and conidiogenesis. Polyblastic conidiogenous cells form 1-celled, ovoid to broadly ellipsoidal, brown to black, smooth- and thick-walled conidia, flat at the base and annellidic conidiogenous cells sometimes grouped in sporodochia, producing catenate, 1–2-celled, oval to ellipsoidal, hyaline, smooth- and thin-walled conidia, truncate at the base. Species have been isolated from dung, milled rice, sediments and soil in Austria, China, Germany, Japan and the Netherlands and the USA (Sandoval-Denis et al., 2016b).

Table 4.197 *Gamsia* species isolated from soil

Species	Country	Habitat or soil type	References
Gamsia columbina	the Netherlands	sandy soil	Sandoval-Denis et al. (2016b)
G. dimera	Germany	*Triticum aestivum* field	Morelet (1969b)
Gamsia kooimaniorum	the Netherlands	garden soil	Crous et al. (2017a)

Lomentospora Hennebert & B.G. Desai, Mycotaxon 1(1): 45 (1974)

Index Fungorum number: IF 8790; Facesoffungi number: FoF13422

Lomentospora was introduced by Hennebert & Desai (1974) and typified with *L. prolificans, which* was isolated from soil. Currently, two species are accepted in the genus, and both have molecular data (Hennebert & Desai, 1974; Crous et al., 2018; Hyde et al., 2020). Previously, *Lomentospora* was considered invalid, and the species were transferred to *Beauveria*. Subsequently, the species was synonymized to *Scedosporium inflatum* and later was renamed as *S. prolificans* (Guého & de Hoog, 1991; Malloch & Salkin, 1984). Based on phylogeny (ITS and *tub2*) and morphology, Lackner et al. (2014) re-established *Lomentospora*. Species are distributed in Australia, Europe and the southern USA (Ramirez-Garcia et al., 2018). The species prefer nutrient rich environments and have the ability to inhabit in low aerated and high osmotic substrates, including polluted waters, pond bottoms, sewage, sludge and soil (from agricultural lands, gardens, crude oil contaminated areas, manure of livestock, poultry, or cattle). *Lomentospora prolificans* is known as pathogenic to humans, causing respiratory tract and cutaneous infections and allergic conditions (Huang et al., 2023; Ramirez-Garcia et al., 2018).

Table 4.198 *Lomentospora* species isolated from soil

Species	Country	Habitat or soil type	References
Lomentospora valparaisensis	Chillie	ND	Crous et al. (2018b)
L. prolificans	Belgium	greenhouse	Hennebert and Desai (1974)

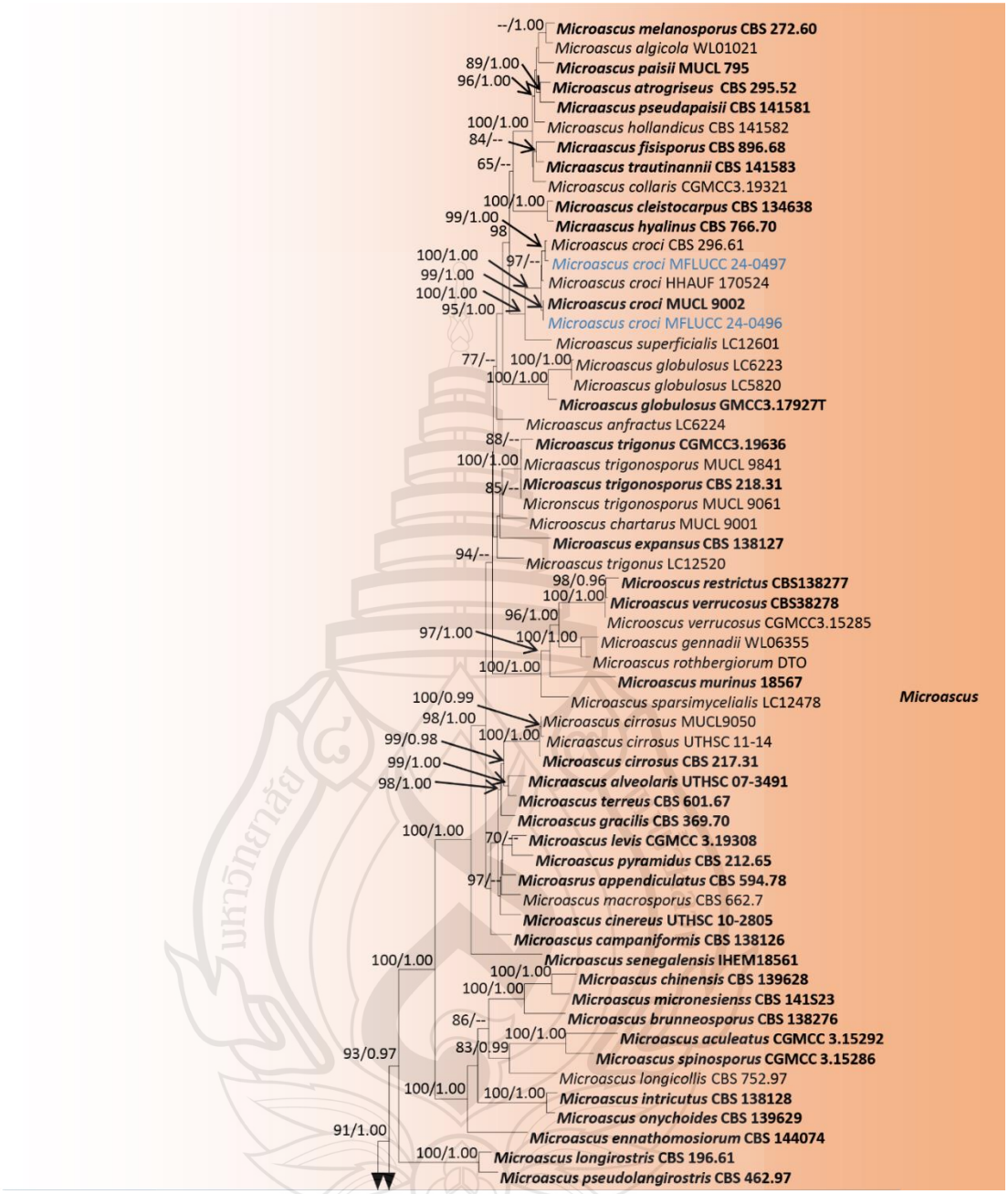


Figure 4.161 The best scoring maximum likelihood tree generated of the combined ITS, LSU, *tef*1-α, *tub2* sequence data for selected genera in *Microascaceae*

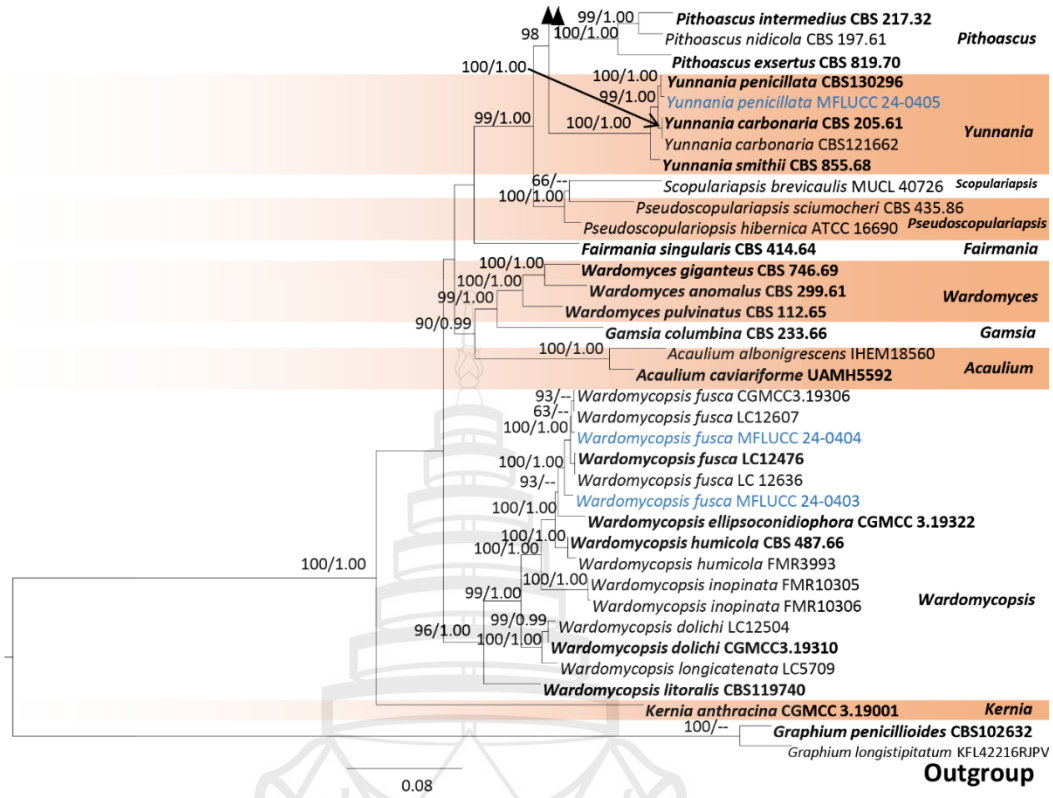


Figure 4.161 (continued)

Figure 4.161, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue and ex-type strains are in bold. The tree is rooted to *Graphium longistipitatum* (KFL42216RJPV) and *Graphium penicillioides* (CBS 102632). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the combined alignment is 3012 bp, and single gene alignments are ITS: 641 bp, and LSU: 880 bp, tef1-α: 962bp, tub2: 529bp. The matrix had 1399 distinct alignment patterns with 24.03% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.216, C = 0.301, G = 0.279, T = 0.203; substitution rates AC = 0.69108, AG = 1.96958, AT = 1.47683, CG = 1.01176, CT = 4.66246, GT = 1.00000; gamma distribution shape parameter α = 0.714.

Microascus Zukal, Verh. Zool.-Bot. Ges. Wien 35: 339 (1885)

Index Fungorum number: IF3153; Facesoffungi number: FoF 12120

Microascus was erected by Zukal (1885), which was previously known as *Masoniella* (Sandoval-Denis et al., 2016a; Zhang et al., 2021c), and is typified with *Microascus longirostris*. This genus comprises 67 species (Species Fungorum 2025), while 48 have molecular data. The genus shows a polyphyletic nature in *Microascaceae* (Zhang et al., 2021c). Sandoval-Denis et al. (2016a, 2016b) suggested that combined ITS, LSU, *tef*1-α and *tub2* regions are required to distinguish species between *Microascus, Scopulariopsis* and other closely related genera. Species are characterized by brown to green-brown mycelia and hyphomycetous asexual state. Conidiogenous cells (annellides) have a long and narrow annelated zone. Conidia are globose to sub-globose, smooth to roughened, pale yellow to dark brown and produced singly or in basipetal dry chains. Sexual morph has perithecial, immersed or superficial, ostiolate ascomata with papillate or long cylindrical necks, unitunicate and 8-spored asci. Ascospores are 1-celled, asymmetrical and reniform (Sandoval-Denis et al., 2016a; Sun et al., 2020; Zhang et al., 2021c). *Microascus* species have been recorded from air, animal dung, plant debris, indoor environments and soils (Sandoval-Denis et al., 2016a, 2016b; Zhang et al., 2021c). Several species have been recorded as human, plant and insect pathogens (Sandoval-Denis et al., 2016a, 2016b; Sun et al., 2020; Zhang et al., 2021c).

Table 4.199 *Microascu*s species isolated from soil

Species	Country	Habitat or soil type	References
Microascus levis	China	Cave	Zhang et al. (2021c)
M. trigonus	China	Cave	
M. aculeatus	China	pig farm	Sun et al. (2020)
M. spinosporus	China	pig farm	
M. cinereus	India	ND	Sandoval-Denis et al. (2016a)
M. gracilis	UK	ND	
M. intricatus	Argentina	ND	
M. longirostris	Japan	ND	
M. macrosporus	the USA	ND	

Microascus croci (J.F.H. Beyma) Sand.-Den., Gené & Guarro, Persoonia 36: 17 (2015)

Figure 4.162

Index Fungorum number: IF809207; Facesoffungi number: FoF 16717

Sexual morph: Undetermined. Asexual morph: *Conidiogenous cells* (*annellophores*) pleurogenous on hyphae, hyaline, solitary or clustered, sometimes branched, ampuliform or obpyriform, inflated base, 2–3 μm ($\overline{x}$ = 2.5 μm, n=10) wide and abruptly tapering. *Conidia* 3.5–4.5 × 2.5–4.5 μm ($\overline{x}$ = 4 × 3.5 μm, n = 25), catenate, globose to sub-globose, rounded at apex, pale brown to hyaline, rough when gelatinous membrane becoming dry.

Culture characteristics – *Colonies* on the PDA at 25℃, attaining 3–4 cm diam. in seven days, with dark brown to brownish black, powdery surface, raised, filiform margin, reverse dark brown at the center, with a pale brown ring at the edge. *Mycelium* mostly superficial. *Hyphae* 2–4.5 μm ($\overline{x}$ = 2.5 μm), hyaline to pale brown, smooth and septate when mature.

Material examined – Thailand, Chiang Rai Province, Chiang Rai, What Tham Pha Tong cave, 99.9038925N, 20.0918488E, on soil, 28 August 2022, W. A. Erandi Yasanthika, (MFLU25-0175); living culture 86-cv23-24 = MFLUCC 24-0496. *ibid*., Thailand, Chiang Mai, Chiang Dao District, Chiang Dao cave, on soil, 98.929366N, 19.400409E, 451m, 9 May 2022, W. A. Erandi Yasanthika (MFLU25-0176); living culture 113-cv22-3= MFLUCC 24-0497.

GenBank numbers – MFLUCC 24-0496: LSU: PQ572136, ITS: PQ570524, *tub2*: PV611066; MFLUCC 24-0497: LSU: PQ572137, ITS: PQ570525, *tub2*: PV611067

Notes– The multigene phylogeny of *Microascaceae* in Figure 4.151 shows that our strains (MFLUCC 24-0496 and MFLUCC 24-0497) cluster with *Microascus croci* with 100% ML and 1.00 BYPP statistical support. Our isolate is morphologically similar to *Microascus croci* in having catenate, globose to sub-globose mature conidia, rounded at apex (van Beyma thoe Kingma, 1944). When compared each ITS, LSU, tef1-α and tub2 gene region of our strain with those of the type spciees of *Microascus croci,* they all are identical with 100% similarity. Based on ITS, LSU, *tef1-α* and *tub2* phylogeny (Sandoval-Denis et al., 2016a) suggested *Microascus croci*

(≡*Scopulariopsis croci*) as a new combination. The species has been isolated from air, aquatic sediments, soil and plants (Sandoval-Denis et al., 2016a). It has previously been reported from air samples from Nerja cave in Spain (Jurado et al., 2021). According to the phylogenetic and morphological evidence, we confirm our strains as *M. croci*. Furthermore, our study reports the first record of this species from Thai soil, isolated from both undisturbed and disturbed caves in Thailand.

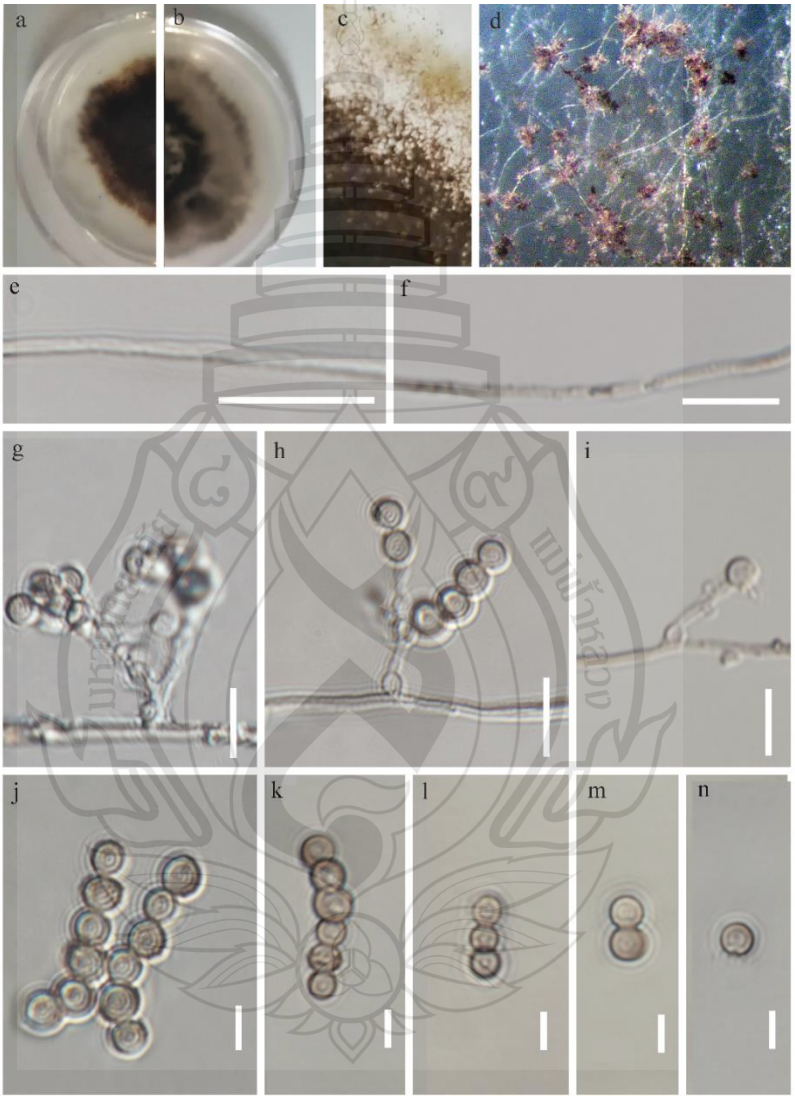


Figure 4.162 *Microascus croci* (MFLU25-0175)

Figure 4.162, a, b Culture characters on the PDA (b = reverse). c, d Sporulated colony with conidial attachments on the mycelium. e Immature hyphae. f Mature hyphae. g–i Conidiogenesis on annellophores. j–n Conidia. Scale bars: f–i = 10 μm, j–n = 5 μm.

Petriella Curzi, Boll. R. Staz. Patalog. Veget. Roma 10: 384 (1930)

Index Fungorum number: IF3852; Facesoffungi number: FoF06834

Petriella was introduced by Curzi (1930) and the type species is designated as *P. asymmetrica.* The genus comprises nine species (Species Fungorum 2025), and five have molecular data (ITS and LSU). Morphologically, *Petriella* is closely resembles to *Microascus*, however different having larger ascopores (Barron et al., 1961). These species have been isolated from bathroom jars, compost, submerged decaying wood, dung, nails and soil in Iran and Thailand (Lackner & de Hoog, 2011)

Table 4.200 *Petriella* species isolated from soil

Species	Country	Habitat or soil type	References
Petriella setifera	Singapore		Lackner and de Hoog (2011)
P. sordida	Germany		

Pseudallescheria Negr. & I. Fisch., Revista Inst. Bacteriol. Dr. Carlos G. Malbrán' 12 (201): 5–9 (1944) I

Index Fungorum number: IF4403; Facesoffungi number: FoF06835

Negroni and Fischer (1944) introduced *Pseudallescheria,* typified by *P. shearii.* The genus comprises eight species (Species Fungorum 2025). Based on the phylogeny of ITS region, Lackner et al. (2014) prioritized *Scedosporium* over *Pseudallescheria* and proposed several *Pseudallescheria* species in *Scedosporium.* However, up to now several studies have accepted *Pseudallescheria* in *Microascaceae* (Kirk et al., 2013; Hyde et al., 2020; Wijayawardene et al., 2022). Hyde et al. (2020) suggested that scedosporium-like and graphium-like taxa are probably linked to the asexual morph of this genus. The sexual morph has cleistothecial ascomata and fusiform or ellipsoidal ascospores (Babu et al., 2014). *Pseudallescheria* species can act as saprobes, and they can grow in very low oxygen substrates and eutrophic environments (Rainer & De Hoog, 2006), where they have been found in the manure of farm animals, polluted water, sewage and soil. In addition to being saprobes, they have also been reported as human and animal pathogens (Hyde et al., 2020c; Kaltseis et al., 2009; Wijayawardene et al., 2017). Species are distributed in Brazil, Korea, Kuwait, Namibia, Panama, Spain, Tajikistan and USA (Rainer & De Hoog, 2006; Babu et al., 2014).

Table 4.201 *Pseudallescheria* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudallescheria africana	Namibia	ND	Rainer and De Hoog (2006)
P. desertorum	*Kwait*	*Salt marsh*	
P. boydi	Brazil, Korea, Panama and Tadzjikistan	ND	Rainer and De Hoog (2006), Babu et al. (2014)

Scopulariopsis Bainier, Bull. Soc. Mycol. Fr. 23: 98 (1907)

Figure 4.163

Index Fungorum number: IF9854; Facesoffungi number: FoF06838

Bainier (1907) established *Scopulariopsis*, typifying with *S. brevicaulis*. This genus comprises 75 species (Species Fungorum, 2025), but only 21 have molecular data. Sandoval-Denis et al. (2016a) accepted this genus in *Microascaceae* based on morpho-molecular (ITS, LSU, *tub2* and *tef1-α*) analyses. Still, there are phylogenetic ambiguities remaining in *Scopulariopsis*. The asexual morph is hyphomycetous and consists of branched, penicillate conidiophores and annellidic conidiogenous cells that produce 1-celled, hyaline, avellaneous or brown, globose to ovate conidia. The sexual morph has perithecial, immersed or superficial, globose to subglobose or pyriform, glabrous, ostiolate ascomata with unitunicate, 8-spored, subglobose, irregularly ovoidal or ellipsoidal, evanescent asci. Ascospores are 1-celled, asymmetrical, short, broadly reniform or lunate, with or without an inconspicuous germ pore (Hyde et al., 2020c; Sandoval-Denis et al., 2016a). *Scopulariopsis* species have a wide distribution, including Austria, Canada, China, France, Italy, and the Netherlands, associated with air, food, human clinical samples, moldy indoor environments, and soil (Hyde et al., 2020c).

Table 4.202 *Scopulariopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Scopulariopsis brevicaulis	China	ND	Yasanthika et al. (2021)
S. asperula	Germany	ND	Sandoval-Denis et al. (2016a)

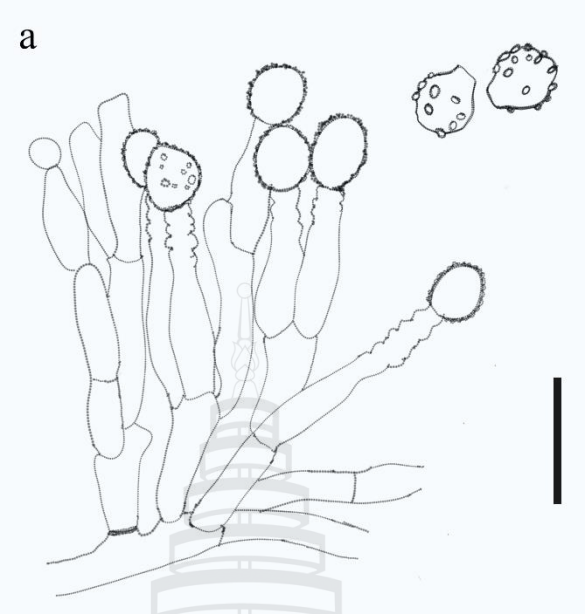


Figure 4.163 *Scopulariopsis brevicaulis.*(CBS273.30)

Figure 4.163, a. Conidiophores and annellidic conidiogenous cells and conidia. Scale bar=500X. The drawings are redrawn from Domsch et al. (1980)

Scedosporium Sacc. ex Castell. & Chalm., Manual of tropical medicine (London): 1122 (1919)

Figure 4.164

Index Fungorum number: IF9794; Facesoffungi number: FoF05201

Saccardo (1911) suggested *Scedosporium* with the type species *S. apiospermum*, and this generic name was validated by Castellani and Chalmers (1919). Using the ITS phylogeny, Lackner et al. (2014) accepted *Scedosporium* over *Pseudallescheria*, and Abrantes et al. (2021) used *tub2*and ITS to provide a phylogenetic revision for this genus while introducing a new species. Currently, 21 species are listed under *Scedosporium* (Species Fungorum, 2025), while 17 are supported by molecular data. Scedosporium-like asexual morph produces annelidic conidiogenous cells with solitary conidia; graphium-like synnematous synanamorph has unicellular sessile conidia; and polycytella-like synanamorph is only produced by *S. apiospermum* that has a sort of "macroconidia". The sexual morph has dark, globose, non-ostiolate ascomata, with a thin peridial wall of *textura epidermoidea*, 8-spored, evanescent asci, and yellowish or reddish brown, broadly fusiform to ellipsoidal

ascospores (Abrantes et al., 2021). This is a ubiquitous filamentous genus that occurs in air, aquatic, human clinical samples, indoor environments and soils found in China, Kuwait, Tajikistan, Thailand and the USA. Some species are pathogenic to humans causing respiratory disease (Abrantes et al., 2021; Wang et al., 2024a).

Table 4.203– *Scedosporium* species isolated from soil

Species	Country	Habitat or soil type	References
Scedosporium apiospermum	China	ND	Huang et al. (2023)
S. boydii		ND	
S. aurantiacum		ND	
S. dehogii		ND	
S. haikouense		ND	
S.desertorum	Kwait	Salt marsh soil	Abrantes et al. (2021)
S. ellipsoideum	Tayikistán	ND	
S. satunense	Thailand	Cave	Preedanon et al. (2023)

Figure 4.164 *Scedosporium apiospermum*

Figure 4.164, a. Conidiogenous cells and conidia. Redrawn from Guarro et al. (2006)

Wardomyces F.T. Brooks & Hansf., Trans. Br. mycol. Soc. 8(3): 137 (1923) Figure 4.165

Index Fungorum number: IF10433; Facesoffungi number: FoF06839

Brooks and Hansford (1923) introduced *Wardomyces*, with *W. anomalus* as the type species. There are eight species in the genus (Species Fungorum, 2025), and seven have sequence data. Sandoval-Denis et al. (2016b) provided the phylogeny (ITS, LSU,

tub2 and *tef1-α*) for *Microascaceae* and showed that this genus does not form a monophyletic clade but and scattered in three closely related lineages. However, there are no significant morphological differences between *senso lato* and *senso stricto.* The asexual morph is hyphomycetous, characterized by branched conidiophores and polyblastic conidiogenous cells. Conidia are solitary, dark 1–2-celled, with a longitudinal germ slit. Some species have secondary annellidic, hyaline, 1-celled conidia, arranged in chains. Sexual morph possesses larger ascomata and dark ascospores with two germ pores (Sandoval-Denis et al., 2016b). Many species are saprobes that live in dung, mud and soil collected from China, Great Britain and the USA (Hyde et al., 2020c; Sandoval-Denis et al., 2016b).

Table 4.204 *Wardomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Wardomyces humicola	Canada	ND	Sandoval-Denis et al. (2016b)
W. ovalis	Germany	ND	
W. inflatus	Belgium	ND	
W. anomalus	China	ND	HaoQin et al. (2012)
W.humicola	China	ND	

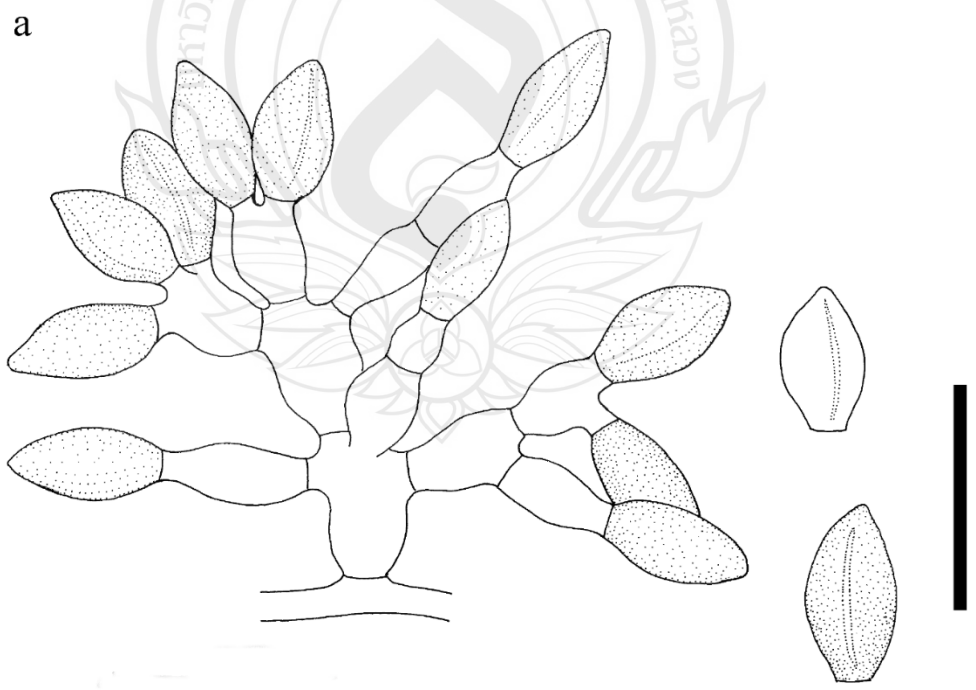


Figure 4.165 *Wardomyces anomalus*

Figure 4.165, a. conidiophores and conidia. Scale bars: a = 10 μm. Redrawn from Hennebert (1962)

Wardomycopsis Udagawa & Furuya, Mycotaxon 7(1): 92 (1978)

Index Fungorum number: IF 10434

Udagawa and Furuya (1978) introduced *Wardomycopsis*, and typified by *Wardomycopsis inopinata*. Currently, the genus has eight species (Species Fungorum 2025), and all with molecular data. The genus is characterized by conidiogenous cells that are annellidic, producing conidial chains that are similar to *Scopulariopsis* and *Fairmani*, featuring globose, darkly pigmented conidia with a single longitudinal germ slit. Sexual morph of the genus has not yet been recorded (Sandoval-Denis et al., 2016b; Silvera-Simón et al., 2008; Zhang et al., 2021c). Based on the combined ITS, LSU, *tef1-α* and *tub2* phylogeny of Sandoval-Denis et al. (2016a) and Zhang et al. (2017b), they revealed *Wardomycopsis* as a monophyletic genus. *Wardomycopsis* has coprophilous and saprobic species that are recorded from air, dung and soil, around the world in saprobic and cor (Sandoval-Denis et al., 2016a; Zhang et al., 2021c).

Table 4.205 *Wardomycopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Wardomycopsis dolichi	China	Cave	Zhang et al. (2021c)
W. fusca	China	Cave	
W. humicola	Canada	ND	Sandoval-Denis et al. (2016a)
W. inopinata	Myanmar	ND	
W. litoralis	Spain	ND	Silvera-Simón et al. (2008)

Wardomycopsis fusca Z.F. Zhang, F. Liu & L. Cai, Fungal Diversity 10.1007/s13225-020-00453-7, (2020)

Figure 4.167

Index Fungorum number: 557752; Facesofungi number: FoF 08461

Sexual morph: Undetermined. Asexual morph: *Conidiophores* 3.5–6.5 × 1.5–4.5 μm ($\bar{x}$ = 3.5 × 2.5 μm, n=15) arising from hyphae, ellipsoidal to globose, often branched, smooth, thick-walled and pale olive-brown to hyaline. *Conidiogenous cells* 3.5–6.5 × 1.5–4 μm ($\bar{x}$ = 4 × 3 μm, n=10) ellipsoidal, clustered on conidiophores, smooth, thick-walled, hyaline to pale olive-brown. *Conidia* 3.5–4.5 × 1.5–3 μm ($\bar{x}$ =

3.8 × 2 μm, n = 25) ellipsoidal, thick-walled, hyaline to pale brown with a truncated base.

Culture characteristics – *Colonies* on PDA at 25℃, become 2–3 cm diam. after seven days, appearing in white, becoming olive-green to dark green at the center, yellowish at the edge when mature, reverse dark brown at the center, with yellowish-white at the edge, and have a slimy to cottony, raised surface with an irregular margin. *Mycelium* immersed, producing immature aseptate, smooth-surfaced hyphae, becoming septate, branched, course-surfaced hyphae, sporulated after three weeks.

Material examined – Thailand, Chiang Mai, Chiang Dao District, Chiang Dao cave, Chiang Dao District, Chiang Mai Province, 98.929366N, 19.400409E, on soil, 9 May 2022, E. Yasanthika (MFLU25-0123), living culture 118-cv22-6= MFLUCC 24-0404. *ibid.*, Thailand, Chiang Rai, Wat Tham Pha Tong cave, on soil, 99.9038925N, 20.0918488E, 430m, 28 August 2022, W.A. Erandi Yasanthika (MFLU25-0124); living culture 87-cv23-15= MFLUCC 24-0403.

GenBank numbers – MFLUCC 24-0404: LSU: PQ565572, ITS: PQ565590, *tef*1-α-: PV611461 *;* MFLUCC 24-0403: LSU: PQ565571, ITS: PQ565589, *tef*1-α: PV615283, tub2: PV615282

Note – Based on the multigene phylogeny study (Figure 4.151), our strains (MFLUCC 24-0404 and MFLUCC 24-0403) clusters with *Wardomycopsis fusca* (CGMCC3.19306, LC12526, LC12607, LC12636) with 100% ML statistical support. Comparison of each ITS, LSU, tef1-α and tub2 gene region of our strain with those of type spcies of *Wardomycopsis fusca* resulted in 100% similarity. Our isolates morphologically resemble to *W. fusca* (HMAS 247997), in having ellipsoidal to globose, often branched conidiophores, ellipsoidal conidiogenous cells and ellipsoidal, thick-walled conidia. However, we observed relatively smaller conidia (3.5–4.5 × 1.5–3 μm) than the type species (4–6.5 × 2.5–3.5 μm) (Zhang et al., 2021c). Aligning to morpho-molecular results, we confirm our strains as *W. fusca* from disturbed and undisturbed caves in Thailand. As the type species has been isolated from soil collected in Guangxi cave, China (Zhang et al., 2021c), our study has become the first record of this species from soil in Thailand.

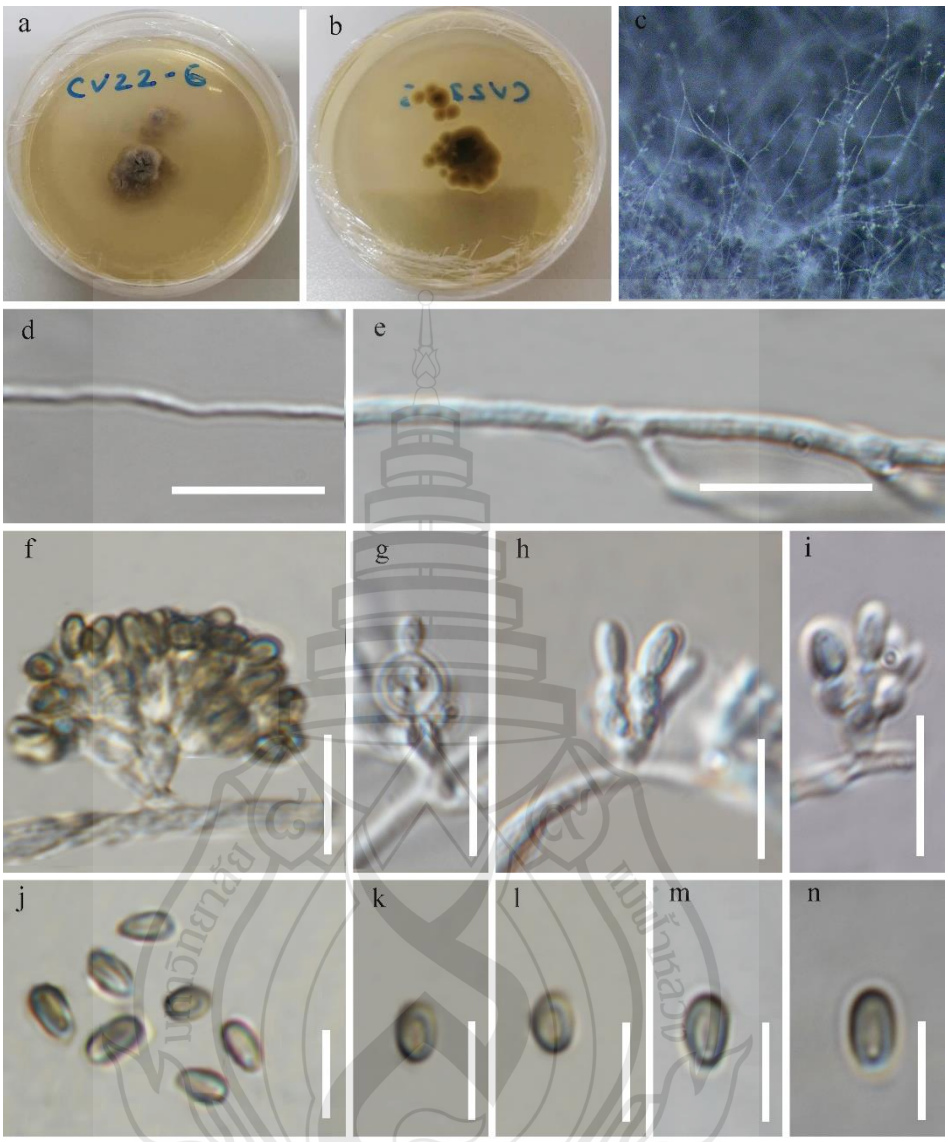


Figure 4.167 *Wardomycopsis fusca* (MFLU25-0123)

Figure 4.167, a, b Culture characters on PDA (b = reverse). c Sporulated colony with conidial attachments on the mycelium. d Immature hyphae. e Mature course-surfaced hyphae. f–i Conidiogenesis on the conidiophores. j–n Conidia Scale bars: d, e = 20 μm, f–i = 10 μm, j–n = 5 μm.

Yunnania H.Z. Kong, Mycotaxon 69: 320 (1998)

Index Fungorum number: IF 27939; Facesoffungi number: FoF 06841

Kong (1998) established *Yunnania* and typified by *Y. penicillata*. Woudenberg et al. (2017) transferred *Fuscoannellis* species to *Yunnania* by providing comprehensive phylogenetic analyses (LSU, ITS, tub2 and *tef1-α*) for *Microascaceae*. *Yunnania* species cannot be delineated based on their ITS sequences (Woudenberg et al., 2017a). Currently, three species are accepted in this genus (Species Fungorum, 2025), and all the species have molecular data. The asexual morph is hyphomycetous. Conidia are truncate and produced by annelids and sexual morph has not yet been discovered (Houbraken & Samson, 2011; Kong, 1998). Species of this genus have been isolated from dead hardwood, molded pork sample and soil, (Woudenber et al., 2017). In addition, some species have been tested for producing useful bioactive compounds, such as *Yunnania penicillata* (von Freiesleben et al., 2019). The species have been found in China, Germany and Panama Woudenberg et al. (2017).

Table 4.206 *Yunnania* species isolated from soil

Species	Country	Habitat or soil type	References
Yunnania carbonaria	Panama	ND	Woudenberg et al. (2017)
Y. smithi	Germany	Garden soil	

Yunnania penicillata H.Z. Kong, Mycotaxon 69: 320 (1998)

Figure 4.168

Index Fungorum number: IF 447022

Sexual morph: Undetermined. Asexual morph: *Conidiophores* septate, frequently branched, discrete, each branch forms terminal group of annellidic conidiogeous cells. *Annellides* ampulliform, 6–10 × 2.5–4 μm ($\overline{x}$ = 8 × 3 μm, n=10), hyaline to pale brown, smooth-walled. *Conidia* in long basipetally developing chains, ellipsoidal to ovoid, with truncate base, sub hyaline to pale brown, smooth, thick-walled, 3.5–4.5 × 2.5–4 μm ($\overline{x}$ = 4 × 3.5 μm, n = 25).

Culture characteristics – *Colonies* on PDA become 2–3 cm after 7 days at 25°C, appear in olivaceous to olivaceous grey at center, yellow ring at the edge, undulate margined, flat powdery surface, reverse olivaceous grey at the center with yellow at the

edge. *Hyphae* 1–2 μm ($\bar{x}$ = 1.5 μm, n=10), superficial, hyaline to pale brown, smooth and mostly aseptate.

Material examined – Thailand, Chiang Rai Province, Chiang Rai, Fish cave temple, Wat Tham Pla cave, 99.863679N, 20.328605E, on soil, 8 February 2021, W.A.E. Yasanthika, (MFLU25-0164), living culture 21-cv2-1= MFLUCC 24-0405.

GenBank numbers – 21-cv2-1 = MFLUCC 24-0405: LSU: PQ565573, ITS: PQ565591, *tef*1-α-: PV611062

Notes–Figure 4.151 shows that our isolate (MFLUCC 24-0405) clusters with *Yunnania penicillata* with 99% ML, 1.00 BYPP statistical support. We compared each gene region (ITS, LSU, *tef1-α* and *tub2*) of our strain with the *Y. penicillata* that showed 100% similarity. Morphologically, our isolate is similar to *Yunnania penicillata* in having frequently branching conididophores with terminal, ampulliform annellides and ellipsoidal to ovoid conidia in long chains. The type species have been isolated from moulded pork in Yunnan, China (Woudenberg et al., 2017a) and it has later been isolated from soil in India (Deshmukh et al., 2018). Herein, we confirm that our species as *Yunnania penicillata* from disturbed-cave; the first record of the species from Thai soil.

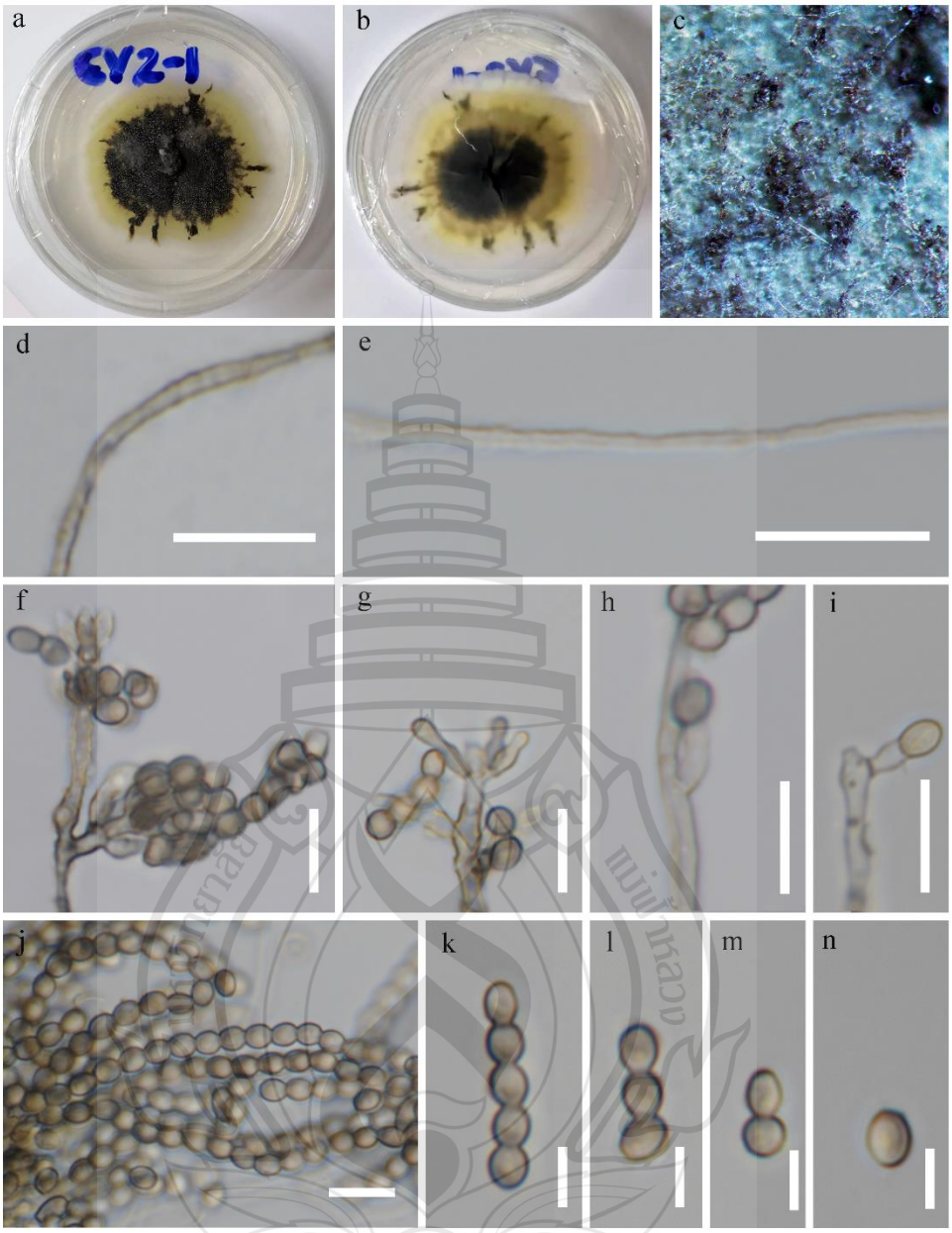


Figure 4.168 *Yunnania penicillata* (MFLU25-0164)

Figure 4.168, a, b Culture characters on PDA (b = reverse). c Sporulated colony with conidial attachments on the mycelium. d Mature pigmented hyphae. e Immature hyphae. f–i Conidiogenesis. j–n Conidia. Scale bars: d–j = 10 μm, k–n = 5 μm

Family: ***Triadelphiaceae*** Y.Z. Lu, J.K. Liu, Z.L. Luo & K.D. Hyde

Triadelphia Shearer & J.L. Crane, Mycologia 63(2): 247 (1971)

Figure 4.169

Index Fungorum number: IF10270; Facesoffungi number: FoF13588

Shearer and Crane (1971) erected *Triadelphia* genus and typified it with *T. heterospora*. Currently, the genus comprises 20 species (Species Fungorum, 2025), and 10 of them have molecular data. The type species is characterized by sporodochial hyphomycete that was isolated from submerged wood blocks and have two different forms of conidia. This genus is characterized by holoblastic, unilocular conidiogenous cells and solitary, pigmented, and pleomorphic (2 to 5) synasexual morphs. However, sexual morph is currently unknown (Chuaseeharonnachai et al., 2020). Species are found in human clinical samples, soil, submerged wood and woody substrates in Australia, Egypt, Saudi Arabia, Thailand and USA (Hyde et al., 2020c).

Table 4.207 *Triadelphia* species isolated from soil

Species	Country	Habitat or soil type	References
T. pulvinata	Saudi Arabia	soil contaminated with bat guano	Bagga and Chattu (2018)

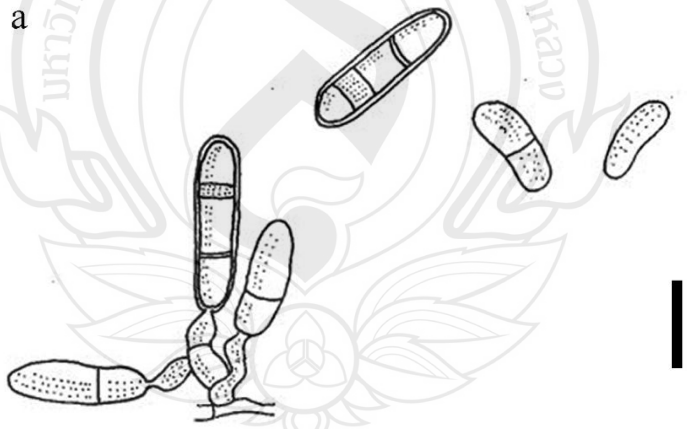


Figure 4.169 *Triadelphia heterospora*

Figure 4.169, a Conidiogenesis and conidia. Scale bar a=10 μm. The drawings are redrawn from Shearer and Crane (1971).

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

Order: *Cephalothecales* Maharachch. & K.D. Hyde

Family: *Cephalothecaceae* Höhn.

Victoriomyces D Davolos, B Pietrangeli, AM Persiani & O Maggi, Int. J. Syst. Evol. Microbiol. 69(4):1099-1110 (2019)

Fig. 4.159

Index Fungorum number: IF823713; Facesoffungi number: FoF13021

Davolos et al. (2019) introduced *Victoriomyces* based on morphology and phylogeny (LSU, SSU and *rpb2*) within *Cephalothecaceae*, placing *V. antarcticus* as the type species. It remains as a monotypic genus supported with molecular data. The asexual morph has *Metarhizium*-like micromorphological characteristics that have conidiophores, develop a palisade layer, rarely simple, mostly branched, immediately below the septum profusely and closely in penicillate with a strongly tapering thick-walled conidiogenous apex Conidia are greyish yellow pigmented, ellipsoidal to ovoid and individual conidium appear in dull yellow. The sexual morph remains unknown (Davolos et al., 2019).

Table 4.208 *Victoriomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Victoriomyces antarcticus	Antarctica	Victoria Land	Davolos et al. (2019)

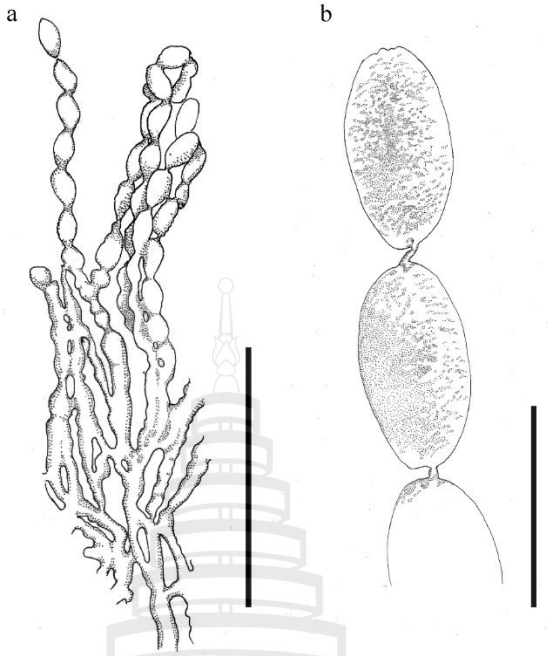


Figure 4.169 *Victoriomyces antarcticus*

Figure 4.169, a. Conidiophores in sporodochium; b. conidia. Scale bars: a= 50μm, b= 5 μm. The drawings are redrawn from Davolos et al. (2019).

Order: *Chaetosphaeriales* Huhndorf, A.N. Mill. & F.A. Fernández

Family: *Chaetosphaeriaceae* Réblová, M.E. Barr & Samuels

Caligospora Réblová, in Réblová & Nekvindová, Stud. Mycol. 106: 219 (2023)

Figure 4.170

Index Fungorum number: IF848560; Facesoffungi number: FoF16641

Caligospora was introduced by Réblová and Nekvindová (2023) based on morphology and combined phylogeny (ITS, LSU and *tef1-α*), with *Caligospora dilabens* (≡ *Chaetosphaeria dilabens*) as the type species. Currently, three species are accommodated in the genus (Réblová & Nekvindová, 2023), and all of them have molecular data. The asexual morph is hyphomycetous and has macronematous, mononematous, solitary conidiophores and terminal, percurrently and sympodially proliferating conidiogenous cells. Conidia are pale brown, aseptate, smooth and adhering in slimy heads. The sexual morph is characterized by perithecial, superficial stroma, globose to subglobose, dark brown, glabrous, papillate ascomata with a two-layered, brittle, carbonaceous wall; persistent, branching, anastomosing paraphyses;

and unitunicate, cylindrical-clavate, short-stipitate, 8-spored asci containing hyaline, fusiform, transversely septate ascospores with the cells separating into part-spores at an early stage within the ascus. The species have been recorded from Brazil and Japan from bamboo stems and culms and soil (Réblová & Nekvindová, 2023).

Table 4.209 *Caligospora* species isolated from soil

Species	Country	Habitat or soil type	References
Caligospora pannosa	Brazil	ND	Réblová and Nekvindová (2023)

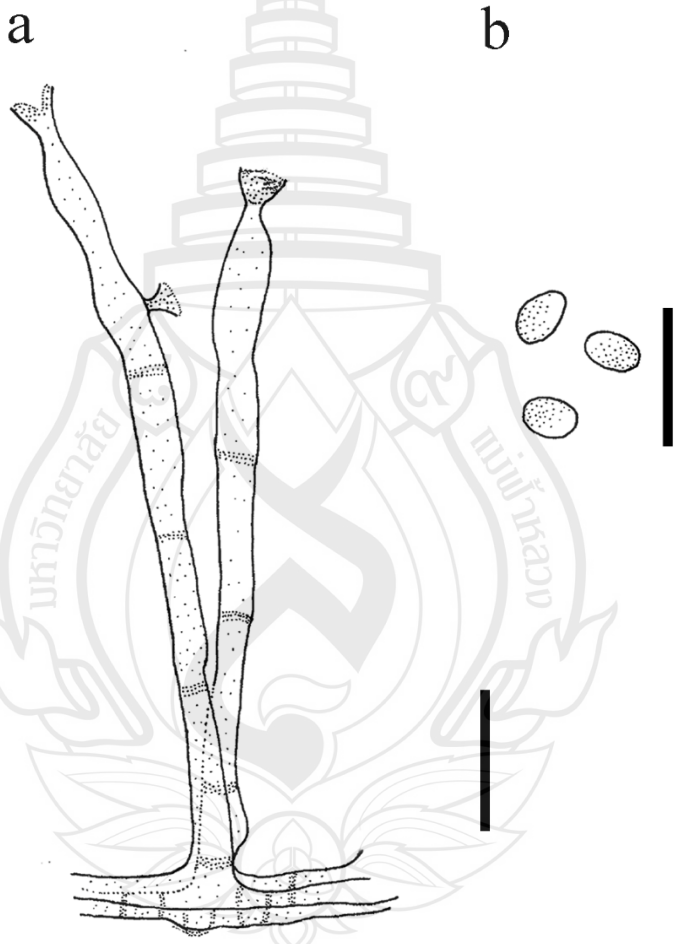


Figure 4.170 *Caligospora dilabens* (CBS 734.83)

Figure 4.170, a Conidiophores b. Conidia. Scale bars: a,b = 10 μm. Redrawn from Réblová and Nekvindová (2023)

Chaetosphaeria Tul. & C. Tul., Select. fung. carpol. (Paris) 2: 252 (1863);

Index Fungorum number: IF970; Facesoffungi number: FoF01140

Chaetosphaeria was introduced by Tulasne and Tulasne (1863) and typified by *Chaetosphaeria innumera*. Locquin (1984) established *Chaetosphaeriaceae* and accommodated *Chaetosphaeria* as the type genus. Over the years, various phylogenetic and morphological studies have synonymized *Chaetosphaeria* species to other genera such as *Cacumisporium*, *Catenularia*, *Chloridium*, *Codinaea*, *Dictyochaeta*, *Exserohilum*, *Gonytrichum* and *Menispora* (Huhndorf & Fernández, 2005, Réblová et al., 2021a, 2021b; Zhang et al., 2022c). Currently, Species Fungorum (2025) has listed 89 species in the genus. The asexual morph is hyphomycetous, characterized by macronematous or mononematous conidiophores, monophialidic or polyphialidic conidiogenous cells, and aseptate to multi-septate, guttulate or eguttulate conidia with or without appendages. The sexual morph consists of black ascomata with surface smooth or covered by setae; 8-spored asci, with small, distinct, refractive, septate, hyaline ascospores (Hyde et al., 2020c). Species are mostly saprobes on plant parts in freshwater and terrestrial habitats located in Austria, China, France, Denmark, Germany, Japan, Malaysia and Mexico (Huhndorf & Fernández, 2005; Hyde et al., 2020c).

Table 4.210 *Chaetosphaeria* species isolated from soil

Species	Country	Habitat or soil type	References
Chaetosphaeria vermicularioides	Worldwide	Beech forest, oak forests, mediterranean brown soil and peat bog soil	Domsch et al. (1980)

Chloridium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1-2): 13 (1809)

Figure 4.171

Index Fungorum number: IF7624; Facesoffungi number: FoF13052

Chloridium was introduced by Link (1809) and typified by *C. virescens*. Currently, the genus comprises 30 species (Réblová et al., 2022; SpeciesFungorum 2025), and all of them are supported with molecular data. Previously, it was accepted as polyphyletic within *Chaetosphaeriaceae.* Based on ITS, LSU, and *tef*1-α phylogeny, Réblová et al. (2022) suggested *Chloridium* as a monophyletic genus. Réblová and

Nekvindová (2023) confirmed placement of *Chloridium* within *Chaetosphaeriaceae* based on morphological and phylogenetic illustrations. The asexual morphology is illustrated in four sections: four types of conidiophores, conidial colour and the shape, presence or absence of chlamydospores and their location in vegetative hyphae (Réblová et al., 2022). Four types of conidiophores are gonytrichum-type, chloridium-type, phialocephala-type and pseudogliomastix-type but they have common phialidic conidiogenesis on multiple loci, percurrently extending phialides with a flaring collarette and relatively small, aseptate conidia accumulating in slimy heads or cirrhi (Réblová et al., 2022). The sexual morph is characterized by perithecial, non-stromatic, ostiolate ascomata, and unitunicate, stipitate asci with hyaline, fusiform, 1-septate ascospores (Réblová et al., 2022). Most of the species are saprobes found in aquatic and terrestrial wood and some soil inhabitants prefer nutrient-rich habitats that have been found in China, France, Japan, Thailand and Venezuela (Réblová et al., 2022).

Table 4.211 *Chloridium* species isolated from soil

Species	Country	Habitat or soil type	References
Chloridium chlamydosporum	France	Forest	Réblová et al. (2022)
C. chlamydosporum	Chile	Volcanic ash soil	
C. chloroconium	Netherlands	ND	
C. costaricense	Costa Rica	Soil, rhizosphere	
C. fuscum	Germany	Wheat field soil	

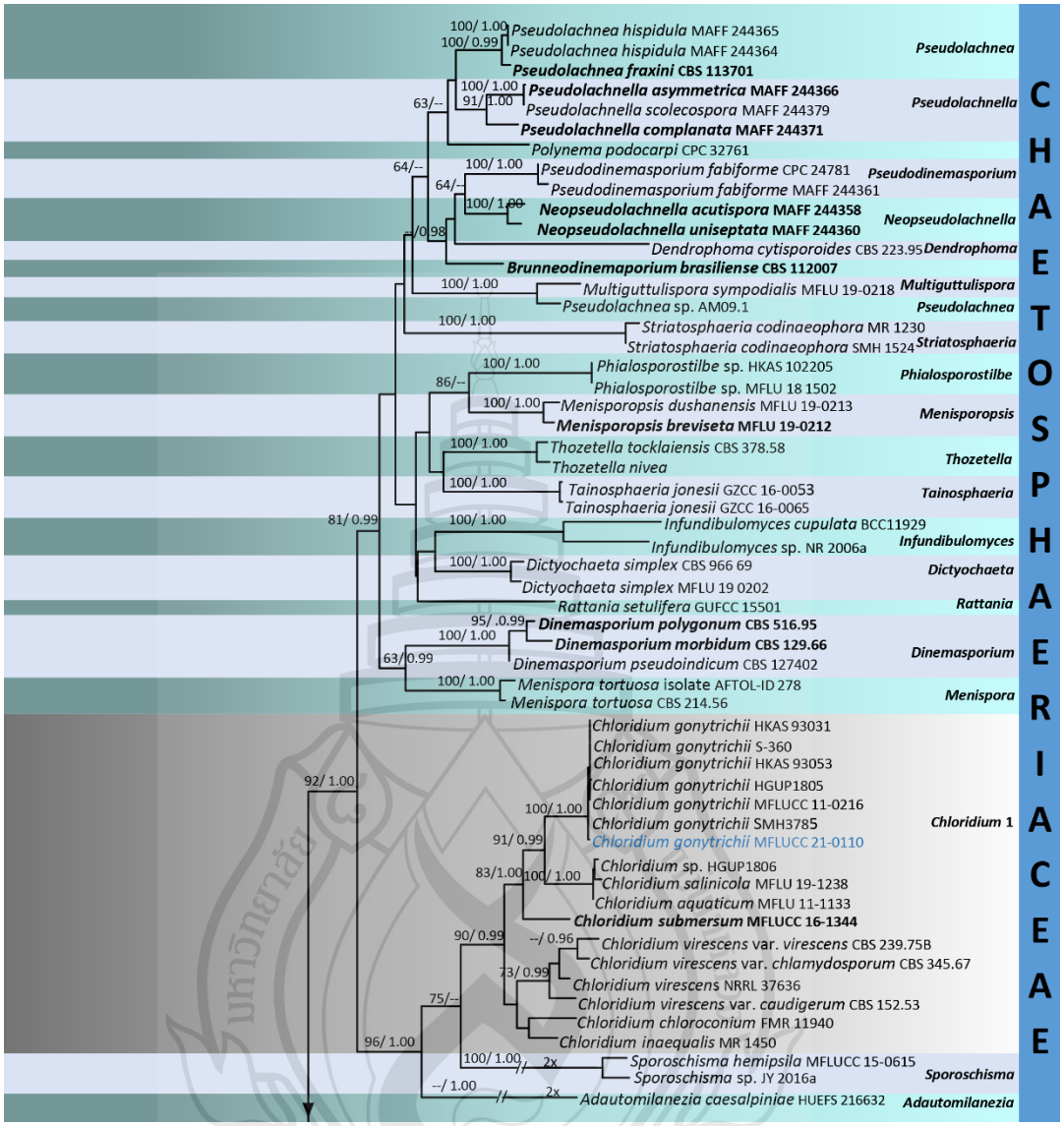


Figure 4.172 Phylogenetic tree generated from the maximum likelihood analysis based on combined LSU and ITS gene sequences data for the selected genera in the family *Chaetosphaeriaceae*

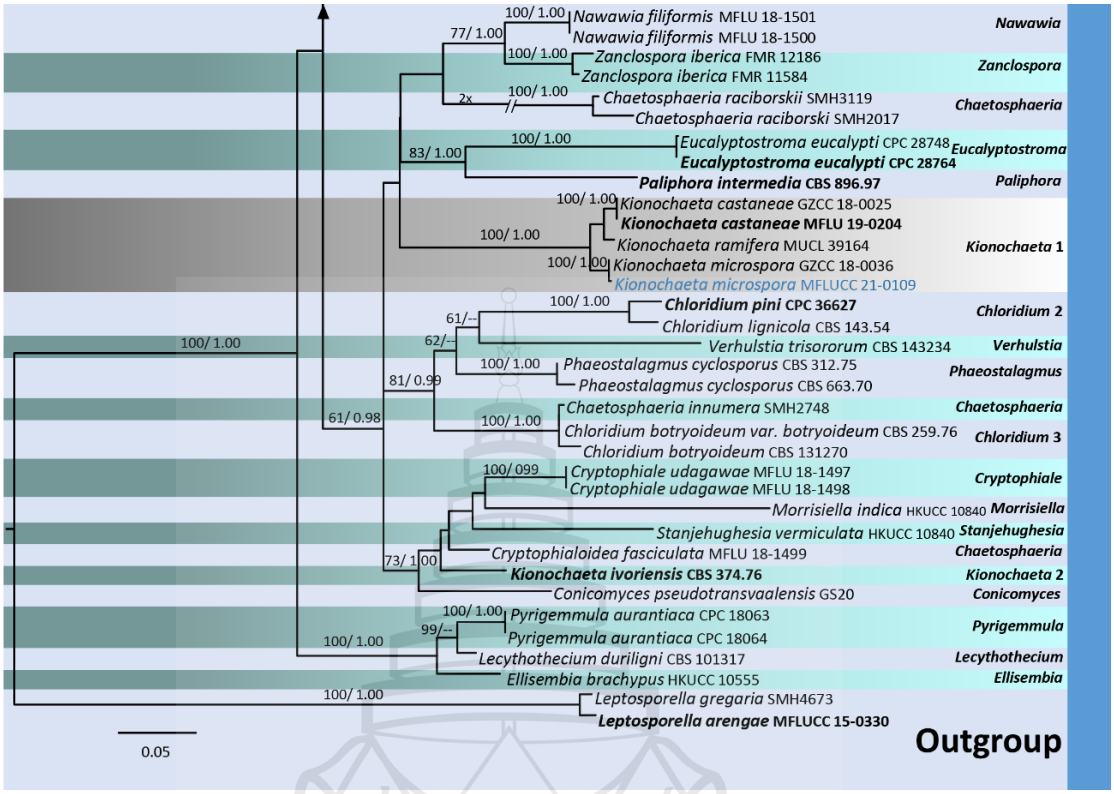


Figure 4.172 (continued)

Figure 4.172, Bootstrap support values for maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.95 are indicated above or below the nodes. Newly added strains are in blue and ex-type strains are in black bold. The tree is rooted with *Leptosporella arengae* (MFLUCC 15-0330) and *L. gregaria* (SMH4673).

The combined LSU and ITS alignment comprised 90 strains of *Chaetosphaeriaceae*. *Leptosporella arengae* (MFLUCC 15-0330) and *L. gregaria* (SMH4673) were selected as the outgroup taxa. A best-scoring ML tree (Figure 4.172) had a final ML optimization likelihood value of -16395.584097. The matrix had 694 distinct alignment patterns, with 13.59% undetermined characters or gaps and estimated base frequencies as follows; A = 0.225233, C = 0.266477, G = 0.310020, T = 0.198270; substitution rates AC = 1.626817, AG = 2.175528, AT = 1.814828, CG = 0.762626, CT = 7.023644, GT = 1.00; proportion of invariable sites I = 0.450438; gamma distribution shape parameter α = 0.535850. Both ML and Bayesian inferences (BYPP) presented similar topology at the generic relationships.

Our phylogenetic analysis indicates that *Chloridium* and *Kionochaeta* are polyphyletic within Chaetosphaeriaceae (Figure 4.172). Their polyphyletic nature has been illustrated in previous taxonomy studies as well (Luo et al., 2019; Hyde et al., 2020; Réblová et al., 2021). Thus, *Chloridium* species are grouped in 3 different clades (*Chloridium* 1–3), and *Kionochaeta* nested in two different clades (*Kionochaeta* 1 and 2) in Chaetosphaeriaceae (Figure 4.172). Comparatively, *Chloridium* clade 1 has a higher number of species (*C. aquaticum, C. caudigerum, C. chlamydosporum, C. chloroconium, C. gonytrichii, C. inaequalis, C. salinicola, C. submersum* and *C. virescens*,), than *Chloridium* clade 2 (*C. lignicola, C. pini*) and clade 3 (*C. botryoideum*). According to Réblová et al. (2016) and Hyde et al. (2020), the type species of *Chloridium, C. viride* is congeneric with the type species of *Melanopsammella*, *Melanopsammella inaequalis*. Thus, Hyde et al. (2020) included *C. inaequalis* in their phylogenetic tree. Our collection, MFLUCC 21-0110 clustered with *C. gonytrichii* isolates (S-360, HKAS:93031, MFLUCC 11-0216, SMH 3785) with 100% ML and 0.99 BYPP support, within *Chloridium* clade 1 (Figure 4.172). *C. gonytrichii* isolates show a sister relationship to *C. aquaticum* (MFLU 19-1238), *C. salinicola* (MFLU 11-1133), and *Chloridium* sp. (HGUP 1806) with 91% ML and 0.99 BYPP support (Figure 4.172). In addition, our other collection (MFLUCC 21-0109) formed a well-supported clade with *K. microspora* (GZCC 18-0036) with 100% ML and 1.00 of BYPP support, which is located in *Kionochaeta* clade 1. In this clade, *K. microspora* is cladded with *K. castaneae* and the generic type, *K. ramifera* (Figure 4.172) (Réblová et al. 2021). *Kionochaeta* clade 2 contains a single species, *K. ivoriensis* (Figure 4.172).

Chloridium gonytrichii Réblová & Seifert, IMA Fungus 7: 134 (2016)

Figure 4.172

Index Fungorum number: IF556708; Facesoffungi number: FoF 05463,

≡ *Melanopsammella gonytrichii* F.A. Ferna´ndez & Huhndorf, Fungal Divers 18: 42 (2005)

Culture characteristics – *Colonies* on PDA, from above: whitish gray in the center with white concentric zones at the initial stage, reaching a diam. of 2–3 cm in 7 days, becoming grayish brown, with reverse becoming grayish brown with grayish center at 25℃ when mature. Colony surface smooth to hairy, effuse, raised, with circular margin, sometimes with gray to black erect, flexuous synnemata. *Mycelium* 2.4–4.4 μm ($\overline{x}$ = 3.2 μm) wide, superficial, composed of septate hyphae, hyaline to sub-

hyaline when immature, latter becoming branched and melanized, sporulated after 4 weeks. Sexual morph: Undetermined. Asexual morph: *Conidiophores* 100–250 × 2–4 μm ($\overline{x}$ = 136 × 3 μm, n = 20), hyaline to sub hyaline, macronematous, mononematous, solitary, septate, unbranched, percurrently 2–5 times proliferating, with monophialidic aperture at the apex, with 2–5 intercalary percurrent phialides. *Conidiogenous cells* phialidic, cylindrical to lageniform, each with multiple enteroblastic conidiogenous loci producing conidia. *Conidia* 2.4–3.5 × 2.3–3.2 μm ($\overline{x}$ = 3× 2.8 μm, n = 20), globose to subglobose, aseptate, hyaline, with minutely rough surface.

Material examined – Thailand, Krabi Province, Khao Phanom District, Na Khao 8.3811N, 98.9286 E, on tropical forest soil, 28 April 2019, E. Yasanthika, B103 (MFLU 21-0142), living culture (MFLUCC 21-0110).

Notes – As examined morphological characteristics largely overlap with *C. gonytrichii* isolates (SMH3785, HKAS 93031, and HKAS 93053), we accordingly report our collection (MFLUCC 21-0110) as a new record of *C. gonytrichii* from soil-based habitats in Thailand. Our isolate (MFLUCC 21-0110) resembles *C. gonytrichii* in having macronematous, mononematous, solitary, multi-septate, unbranched, percurrently proliferating conidiophores, phialidic, cylindrical to lageniform conidiogenous cells, and globose to sub-globose and aseptate conidia (Luo et al., 2019). Multi-locus phylogeny (LSU and ITS) also indicates that our collection grouped with *C. gonytrichii* isolates in a strongly supported clade (100% ML, 0.99 BYPP). *C. gonytrichii* was initially introduced by Réblová et al. (2016), which was previously known as *Melanopsammella gonytrichii* (Fernández & Huhndorf, 2005). *C. gonytrichii* seems to have cosmopolitan distribution since it has been reported from both terrestrial and freshwater habitats (Fernández & Huhndorf, 2005; Wei et al., 2018; Luo et al., 2019). Interestingly, this is the first soil-inhabiting *C. gonytrichii* (MFLUCC 21-0110) record in *Chaetosphaeriaceae*.

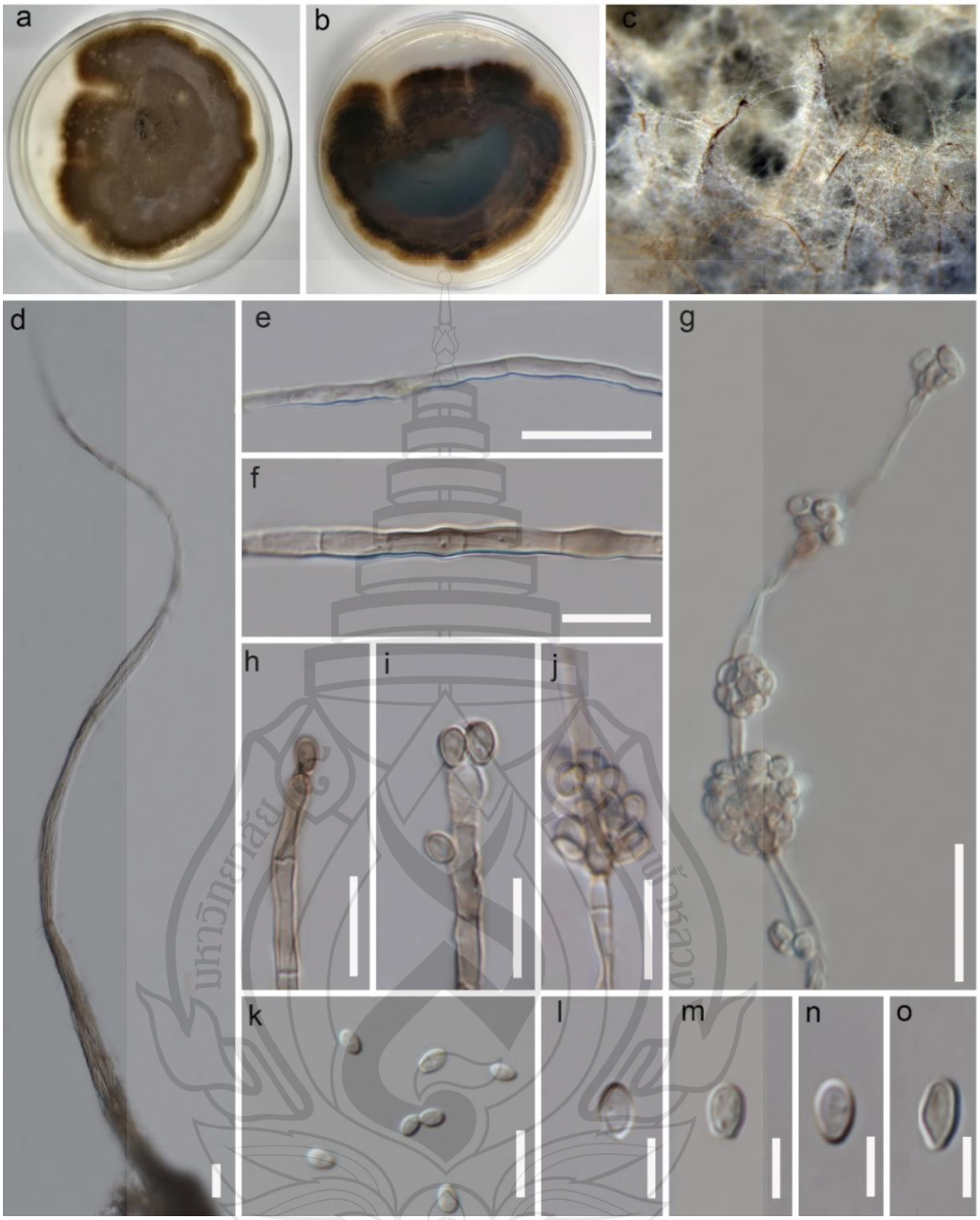


Figure 4.172 *Chloridium gonytrichii* (MFLUCC 21-0110)

Figure 4.172, a Colony from above (on PDA). b Colony from below (on PDA). c Sporulated colony with conidial attachments on the mycelium. d Erect young immature synnema. e Immature aseptate hyphae. f Mature septate melanized hyphae. g Macronematous conidiogenesis on the conidiophore. h–j Conidiogenesis on the conidiophore. k–o Conidia. Scale bars: d = 25 μm, e, g = 20 μm, f, h–k = 10 μm, l–o = 5 μm

Dinemasporium Lév., Annls Sci. Nat., Bot., sér. 3 5: 274 (1846)

Index Fungorum number: IF8040; Facesoffungi number: FoF01763

Le´veille´ (1846) introduced *Dinemasporium* based on morphology and typified by *D. graminum.* Currently, 43 species are listed in the Species Fungorum (2025), and 27 of them are supported by the molecular data. Wu and Diao (2022) provided updated phylogeny (LSU and ITS) and morphological characterization for this genus while introducing new species. The asexual morph is coelomycetous with black, stromatic, cupulate conidomata that are initially closed later become erumpent and mostly covered with coidia masses, and hyaline, cylindrical to subcylindrical conidiophores are produced in the lining of the conidiomata cavity. Conidiogenous cells are hyaline and phialidic, producing hyaline, ellipsoid, allantoid to naviculate or fusiform, unicellular conidia with bipolar or lateral appendages. The sexual morph is characterized by immersed to semi-immersed, globose to elongated ascomata with 4–8-spored, unitunicate, cylindrical to subcylindrical, pedicellate asci and hyaline uniseriate, rarely sub-biseriate and biguttulate ascospores. Species have been recorded in dead woods, human sputum, soil and various plants in Argentina, Canada, China, Cuba, Czech Republic, France, Ghana, India, Italy, Japan and the Netherland (Hashimoto et al., 2015; Hyde et al., 2020c; Li et al., 2020b; Wu & Diao, 2022).

Table 4.212 *Dinemasporium* species isolated from soil

Species	Country	Habitat or soil type	References
Dinemasporium graminum	Australia	wheat field	Warcup (1957)
D. pseudoindicum	USA	tall grass soil	Réblová and Nekvindová (2023)

Kionochaeta P.M. Kirk & B. Sutton, Trans. Br. mycol. Soc. 85(4): 712 (1986) [1985]

Figure 4.173

Index Fungorum number: IF11111; Facesoffungi number: FoF13064

Kirk and Sutton (1985) introduced *Kionochaeta* and its type species, *K. ramifera*. Based on multi-gene phylogenetic analyses (LSU, SSU, *tef*1-α and *rpb2*), Maharachchikumbura et al. (2015) accepted this genus in *Chaetosphaeriaceae.* The genus accommodates 15 species (Species Fungorum, 2025), while have been supported by the molecular data. Lin et al. (2019) stated the polyphyletic nature of the

Kionochaeta within *Chaetosphaeriaceae*, based on combined SSU, ITS and LSU gene regions and the synopsis for asexual morphology of *Kionochaeta* species are illustrated. This genus is characterized by hyphomycetous asexual morph that has macronematous, mononematous, solitary conidiophores and ampulliform, lageniform or cylindrical conidiogenous cells with hyaline to pale yellow, monophialidic, ampulliform conidia (Hyde et al., 2020c; Kirk & Sutton, 1985). The species are discovered in freshwater and terrestrial habitats as saprobes living on decaying leaves, seeds, twigs and soils, that are collected from Australia, China, Ivory Coast, Kenya, Malaysia and Papua New Guinea (Hyde et al., 2020c; Lin et al., 2019; Yasanthika et al., 2022a). Pittayakhajonwut et al. (2002) investigated *K. pughii* for extracting 'pughiinin A' and 'pycnidione', which perform anti-plasmodium activity against *Plasmodium falciparum* and anti-cancer activity.

Table 4.213 *Kionochaeta* species isolated from soil

Species	Country	Habitat or soil type	References
Kionochaeta microspora	Thailand	Forest	Yasanthika et al. (2022a)

Kionochaeta microspora C.G. Lin & K.D. Hyde, Mycosphere 10: 678 (2019) Figure 4.174

Index Fungorum number: IF556708; Facesoffungi number: FoF 06289

Culture characteristics – *Colonies* on PDA at 25°C, become 2–3 cm diameter after 7 days, appearing in white become olive-green to dark green at the center, rind-like at the edge when mature, reverse yellowish-white at the center with olive-green to dark green rind at the edge, semi immersed to superficial, setae present and have a slimy raised surface with a filiform margin. *Mycelium* immersed to semi immersed, hyaline, producing immature aseptate, smooth-surfaced hyphae, becoming septate, less-branched, course-surfaced hyphae, sporulated after 4 weeks. Sexual morph: Undetermined. Asexual morph: *Conidiophores* 40–45.5 × 2–3 ($\overline{x}$ = 42 × 2.6) μm, macronematous, mononematous, caespitose, erect, straight or slightly curved, sometimes setiform, smooth, thick-walled, unbranched, septate, hyaline, cylindrical at the apex or middle fertile region when present 12–21 × 2–4.5 μm. *Conidiogenous cells* 3–4.5 × 2–3 ($\overline{x}$ = 3.9 × 2.2) μm, arising from the fertile region at the apex, hyaline monophialidic, discrete, determinate, terminal, narrowly ellipsoid, ampulliform.

Conidia 1.9–4.5 × 1.5–3.2 μm ($\bar{x}$ = 3.3 × 2.3 μm, n = 25), hyaline, smooth, spherical to ovate, and aseptate.

Material examined – Thailand, Krabi Province, Khao Phanom District, Na Khao, 8.3811N, 98.9286 E, on tropical forest soil, 28 April 2019, E. Yasanthika, ES1 (MFLU 21-0143, living culture (MFLUCC 21-0109).

Notes – The morphology of our collection (MFLUCC 21-0109) resembles *K. microspora* (MFLU 19-0206) in having monophialidic, discrete, determinate, terminal, rarely intercalary, narrowly ellipsoid conidiogenous cells and hyaline, smooth, spherical to ovate, aseptate slimy conidia (Luo et al., 2019). Multi-gene phylogeny (LSU and ITS) indicates that our isolate (MFLUCC 21-0109) nested with *K. microspora* isolates (GZCC 18-0036) in a well-supported clade (100% ML, 1.00 BYPP). Therefore, based on both morphology and phylogenetic evidence, we account our isolate (MFLUCC 21-0109) as *K. microspora*, collected from the forest soils in Thailand. *K. microspora* was initially introduced by Lin et al. (2019), which was isolated from decaying wood in China. Therefore, it is worthy to note that this is the first soil-inhabiting *K. microspora* (MFLUCC 21-0109) record in *Chaetosphaeriaceae*.

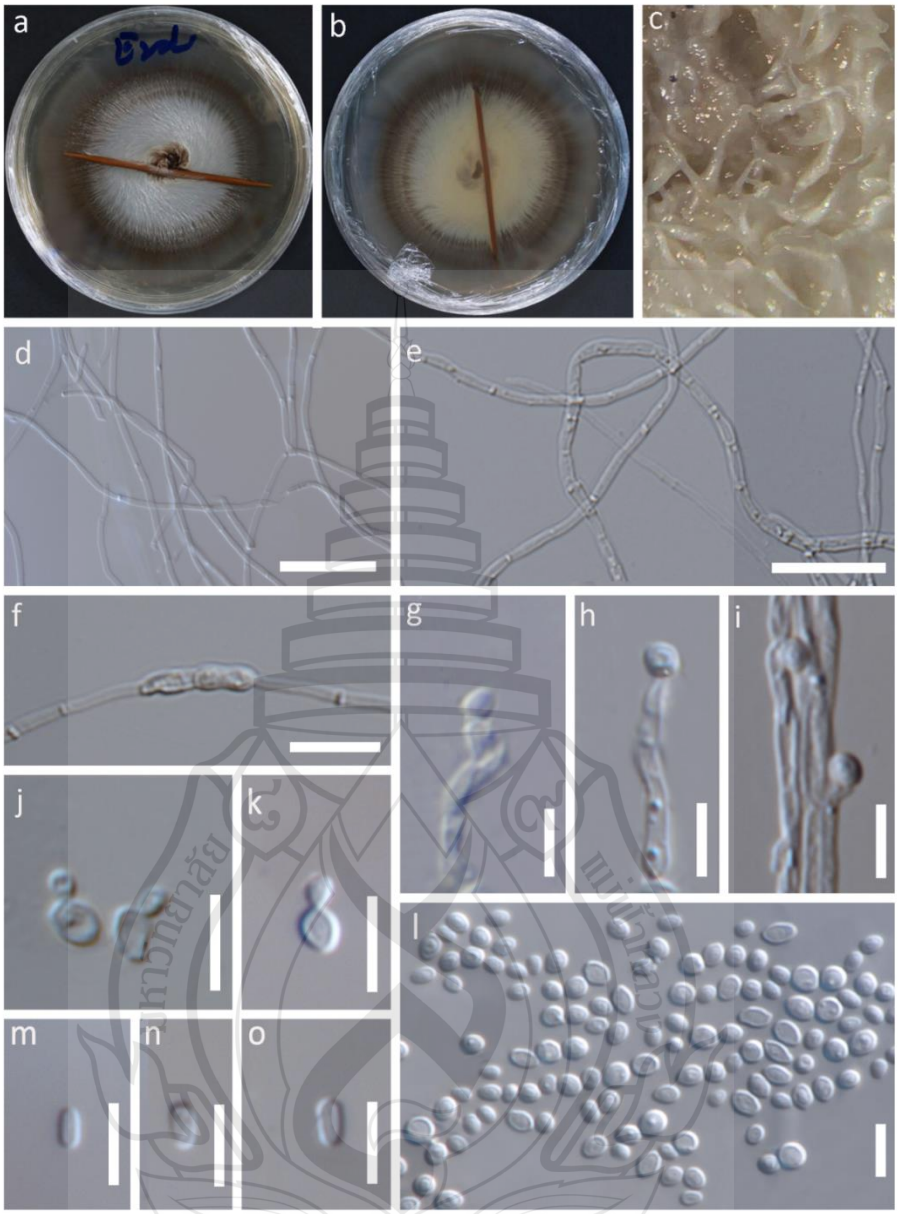


Figure 4.175 *Kionochaeta microspora* (MFLUCC 21-0109)

Figure 4.175, a Colony from above (on PDA). b Colony from below (on PDA). c Sporulated colony with conidial attachments on the mycelium. d Immature hyphae. e Mature septate course-surfaced hyphae. f Chlamydospores on the mycelium. g–i Conidiogenesis on the conidiophores. j, k Conidia attached to phialides. l–o Conidia Scale bars: d = 25 µm, e = 20 µm, f = 10 µm, g–o = 5 µm

Menispora Pers., Mycol. eur. (Erlanga) 1: 32 (1822)

Index Fungorum number: IF8902; Facesoffungi number: FoF13066

Menispora was introduced by (Persoon, 1822) and the type species is designated as *M. glauca.* The Species Fungorum (2025) lists 19 species in the genus, while nine are supported by the molecular data. The asexual morph is hyphomycetous, having macronematous, brown conidiophores with phialides in a lateral or terminal position that are tapering, strongly recurved apex and conidia are hyaline with inconspicous collarette and without or with polar setulae (Réblová & Seifert, 2008). The species have been isolated from decayed wood, bark or on decayed leaves and soil in Australia, China, Czech Republic, Germany and Ukraine (Hyde et al., 2020c).

Table 4.214 *Menispora* species isolated from soil

Species	Country	Habitat or soil type	References
Menispora sp.	Thailand	ND	Manoch (1998)

Thozetella Kuntze, Revis. gen. pl. (Leipzig) 2: 873 (1891)

Fig. 4.176

Index Fungorum number: IF10214; Facesoffungi number: FoF12974

Kuntze (1891) introduced *Thozetella* based on morphology and typified by *T. nivea*. Currently, 41 species are listed in the Species Fungorum (2025) and 29 of them have been supported with molecular data. Perera et al. (2016), Yan et al. (2023) and Réblová and Nekvindová (2023) illustrated the placement of *Thozetella* within *Chaetosphaeriaceae* based on different combinations of LSU,ITS, *tub2*, *tef*1-α and *rpb2* gene phylogeny. The asexual morph is hyphomycetous which is characterized by the sporodochial or synnematal conidiomata with phialidic conidiogenous cells and aseptate conidia with unbranched setula at each end and sterile microawns (Sutton & Cole, 1983; Jeewon et al., 2009). The genus has been reported in decaying plant parts and soil in freshwater and terrestrial habitats in Australia, China, France, India, Japan Panama and the USA (Hyde et al., 2020c; Perera et al., 2016).

Table 4.215 *Thozetella* species isolated from soil

Species	Country	Habitat or soil type	References
Thozetella tocklaiensis	India	Tea plantation soils	Agnihothrudu (1962)

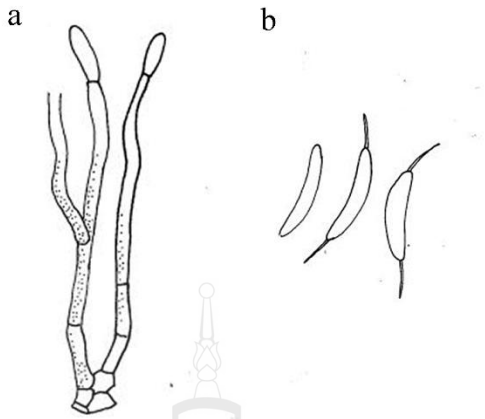


Figure 4.176 *Thozetella nivea*

Figure 4.176, a. Conidiophores and conidiogenesis. b Conidia Redrawn from redrawn from Seifert et al. (2011)

Verhulstia Hern.-Restr., in Crous et al., Persoonia 39: 449 (2017)

Index Fungorum number: IF823032; Facesoffungi number: FoF12972

Verhulstia was introduced by Crous et al. (2017a) to accommodate its type, *V. trisororum*; based on combined ITS and LSU phylogeny. Currently, two *Verhulstia* species are accepted, and Réblová and Nekvindová (2023) provided combined ITS,LSU, *tef1-α* and *rpb2* phylogeny for this genus. The asexual morph has sporodochial, superficial conidiomata and unbranched, cylindrical, hyaline to brown, dense layers of conidiophores that arise from the stroma. Conidiogenous cells are hyaline to pale brown, phialidic with a collarette and having hyaline, cylindrical to ellipsoidal, or obovoid aseptate and smooth conidia (Crous et al., 2017a; Hyde et al., 2020c). These species are found in China and the Netherlands from dead leaves and soil (Réblová & Nekvindová, 2023).

Table 4.216 *Verhulstia* species isolated from soil

Species	Country	Habitat or soil type	References
Verhulstia trisororum	Netherlands	ND	Crous et al. (2017a)

Subclass: *Coniochaetales* Huhndorf, A.N. Mill. & F.A. Fernández

Family: *Coniochaetaceae* Malloch & Cain

Coniochaeta (Sacc.) Cooke, Grevillea 16 (no. 77): 16 (1887)

Fig. 4.177

Index Fungorum number: IF1209; Facesofungi number: FoF01333

Cooke (1887) introduced *Coniochaeta* and the type species is accepted as *C. ligniaria*. It currently comprises 114 species (Species Fungorum 2025). Based on morphology (polyblastic conidiogenesis) and LSU phylogeny, García et al. (2006) transferred some *Coniochaeta* species to *Coniolariella* and *Coniocessia* (*Xylariales*) (Asgari & Zare, 2011). Subsequent, study of Kabtani et al. (2022), provided multigene phylogeny for *Coniochaeta* based on ITS, LSU, *tub2* and *tef1-α* gene regions. This genus is characterized by having pleomorphic yeasts. The asexual morph is characterized by the phialidic conidiogenous cells and the sexual morph has dark brown to black ascomata with setae (García et al., 2006; Si et al., 2021). Species are widely distributed and reported in butter, dung, plants, soil, uranium mines, wastewater and wood in saprobic or endophytic modes, while some have been found as human and animal pathogens in Argentina, Australia, China, Great Britain, Germany and Sweden (Harrington et al., 2019; Si et al., 2021).

Table 4.217 *Coniochaeta* species isolated from soil

Species	Country	Habitat or soil type	References
*Coniochaeta extramun*dana	USA	Arid chaparral soil	Romero et al. (1999)
C. tetraspora	Argentina	ND	
C. emodensis	Nepal	ND	García et al. (2006)
C. cruciate	Nigeria	ND	

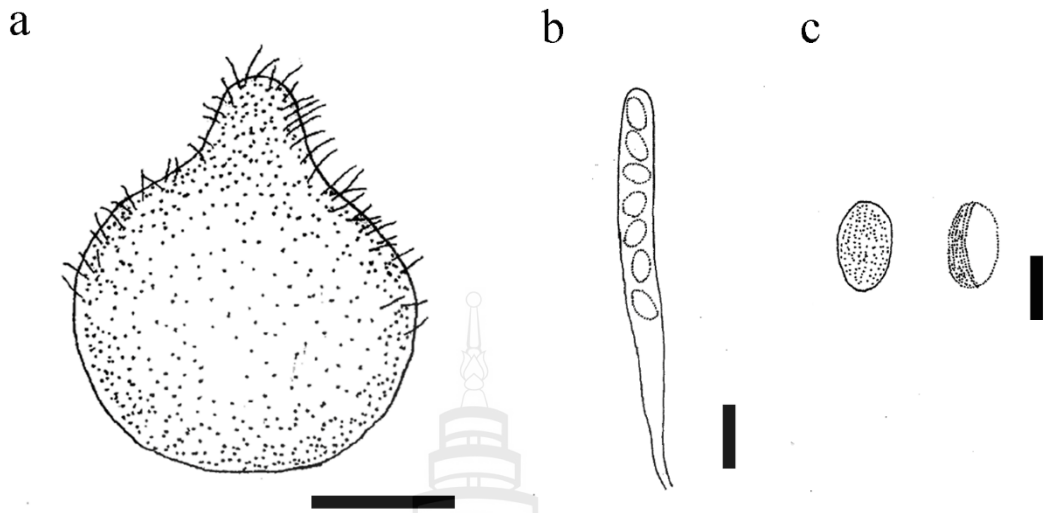


Figure 4.177 *Coniochaeta ligniaria* (HAH2883)

Figure 4.177, a Ascoma b Ascus. c Ascospore. Scale bars: a = 100 μm, b = 25 μm, c = 10 μm. Redrawn from Checa et al. (1988)

Family: *Cordanaceae* Nann.

Cordana Preuss, Linnaea 24: 129 (1851)

Index Fungorum number: IF7777; Facesofungi number: FoF01674

Cordana was introduced by Preuss (1851) by accommodating *C. polyseptata*, *C. pauciseptata* and *C. pedunculata* in the genus, however without a type species. Hernández-Restrepo et al. (2014)) designated an epitype (*C. pauciseptata*) and provide ITS phylogeny and a dichotomous key to the species. Currently, genus has 26 species (Species Fungorum 2025), while 14 are supported with the molecular data. This is a hyphomycetous genus and asexual morph is characterized by brown, septate conidiophores with swollen conidiogenous zones; terminal and intercalary conidiogenous cells and having pale brown to brown, 0–1-septate conidia (Hernandez Restrepo et al., 2015). Species are associated with living plants, plant debris and soil substrates as saprobes or pathogens. They are distributed in Africa, Central and South America, New Zealand, Southeast Asia and Spain (Hyde et al., 2020c).

Table 4.218 *Cordana* species isolated from soil

Species	Country	Habitat or soil type	References
Cordana terrestris	Thailand	Forest	Chethana et al. (2023)
C. yunnanensis	China	Rocky Soil	Yang et al. (2022)

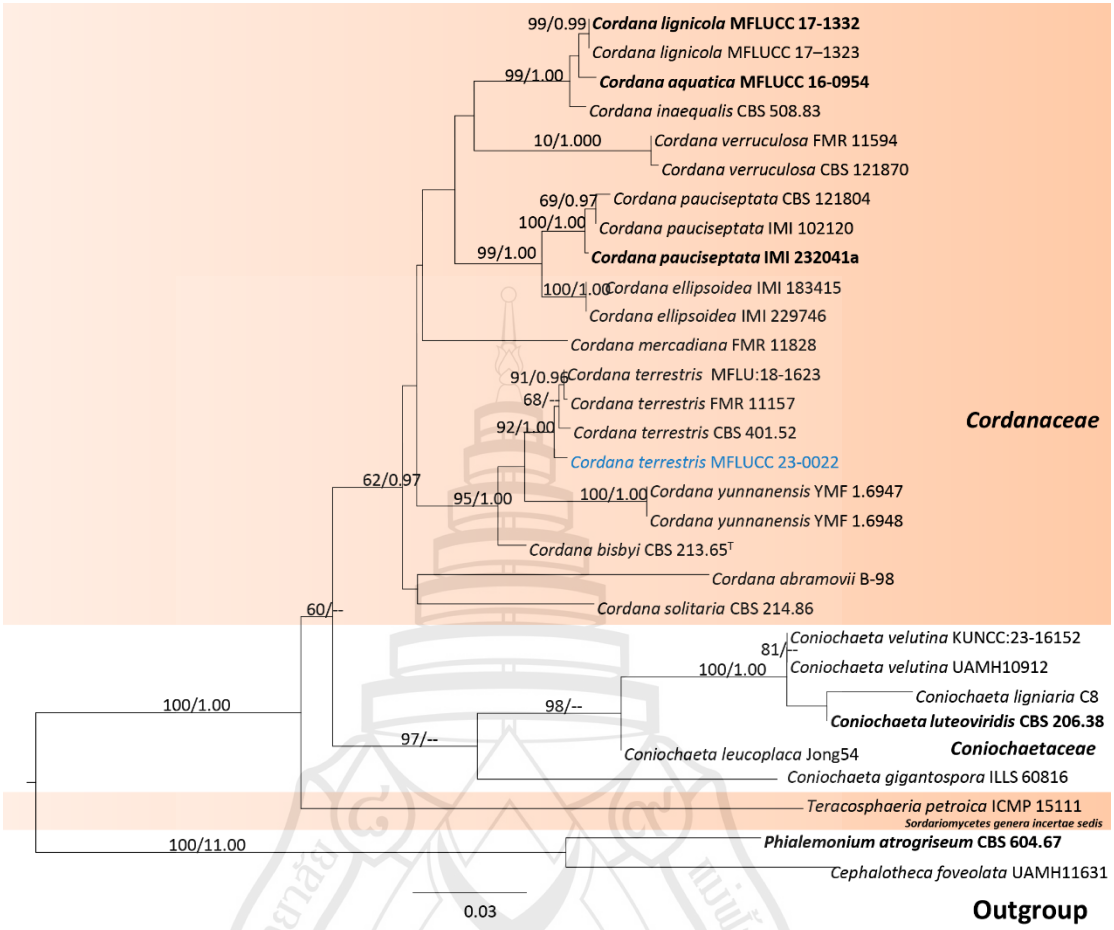


Figure 4.178 Phylogram generated from maximum likelihood analysis based on the combined ITS and LSU sequence data of *Cordanales and Coniochaetales* taxa

Figure 4.178, Twenty-nine strains are included in the combined analyses which comprised 1452 characters (595 characters for ITS and 857 characters for LSU) after aligned. Tree topology of the maximum likelihood analysis is similar to the Bayesian analysis. The best RAxML tree with a final likelihood value of -5536.915184 is presented. The matrix had 427 distinct alignment patterns, with 28.19% undetermined characters or gaps. Evolutionary models applied for ITS and LSU are SYM+I+G and GTR+I+G models, respectively. Bootstrap support values for ML greater than 60% and Bayesian posterior probabilities greater than 0.95 are given near nodes, respectively. The tree is rooted with *Cephalotheca foveolata* (UAMH11631), *Phialemonium atrogriseum* (CBS 604.67) and *Teracosphaeria petroica* (ICMP 15111). Ex-type strains are in bold. The newly generated sequences are indicated in yellow.

Cordana terrestris (Timonin) Hern.-Restr. et al.

Figure 4.179

Index Fungorum number IF807979; Facesoffungi number: FoF 05475,

Hyphae septate, branched, smooth, subhyaline to hyaline become rough, brown when mature. Asexual morph: Conidiophores 25–73 × 1.5–3.5 μm ($\bar{x}$ = 44 × 2 μm, n = 20), micronematous, mononematous, solitary, erect, unbranched or branched, septate, straight or flexuous, cylindrical, hyaline to sub-hyaline. Conidiogenous cells holoblastic, polyblastic, terminal, discrete, hyaline. Conidia 4–7 × 2.5–4.5 μm ($\bar{x}$ = 5 × 3.5 μm, n = 20), terminal, mostly oblong, sometimes ellipsoid or sub-sylindrical, guttulate, sometimes mid region slightly constricted, hyaline, smooth-walled. Sexual morph: Undetermined.

Culture characteristics— Colonies on PDA become 30mm diam. after 14 days at 25°C, flat, effuse, dark gary to black-brown, undulate margined. reverse grayish brown at the center become dark brown to brown at the rind.

Material examined—Thailand, Chiang Rai Province, May Yao, from forest soil, 20.0478N 99.7619 E, 863m, 23 September 2019, W.A. E. Yasanthika; living culture, MFLUCC 23-0022.

GenBank: (ITS: OQ690712, LSU: OQ690715)

Known hosts— Soil, Cecropia leaf, decaying wood submerged (Timonin, 1940; Fernández & S.M. Huhndorf, 2004; Luo et al., 2019)

Known distribution— China, Brazil, Canada, Cuba, Democratic Republic of Congo (Zaire), Jamaica, Japan, India, New Zealand, Panama, Poland, Puerto Rico, Thailand, USA (Georgia, Iowa) (Fernández & Huhndorf, 2004; Luo et al., 2019)

Notes— *Cordana terrestris* is wide spread and it has been identified from various aquatic and terrestrial habitats (Hyde et al., 2020). This species previously recorded from soils in Georgia (Timonin, 1940). *Spicularia terrestris* and *Pseudobotrytis fusca* were synonymized as *C. terrestris* by Herna´ndez-Restrepo et al. (2014). Our collection phylogenetically clustered with *C. terrestris*. Asexual morph of our isolate is similar to C. terrestris () in having, terminal, mostly oblong, ellipsoid or sub-sylindrical, guttulate conidia (Fernández & Huhndorf, 2004; Hernández-Restrepo et al., 2014; Luo et al., 2019). Conidial septation and macronematous conidiopores are absent in our isolate which contrast to C. terrestris described in Fernández and Huhndorf (2004) and Luo et al. (2019). This morphological differences can be resulted due to environmental adaptations (Francisco et al.,

2019). Based on biphasic approach we report our collection as *C. terrestris* which is the first record in Thailand soils.

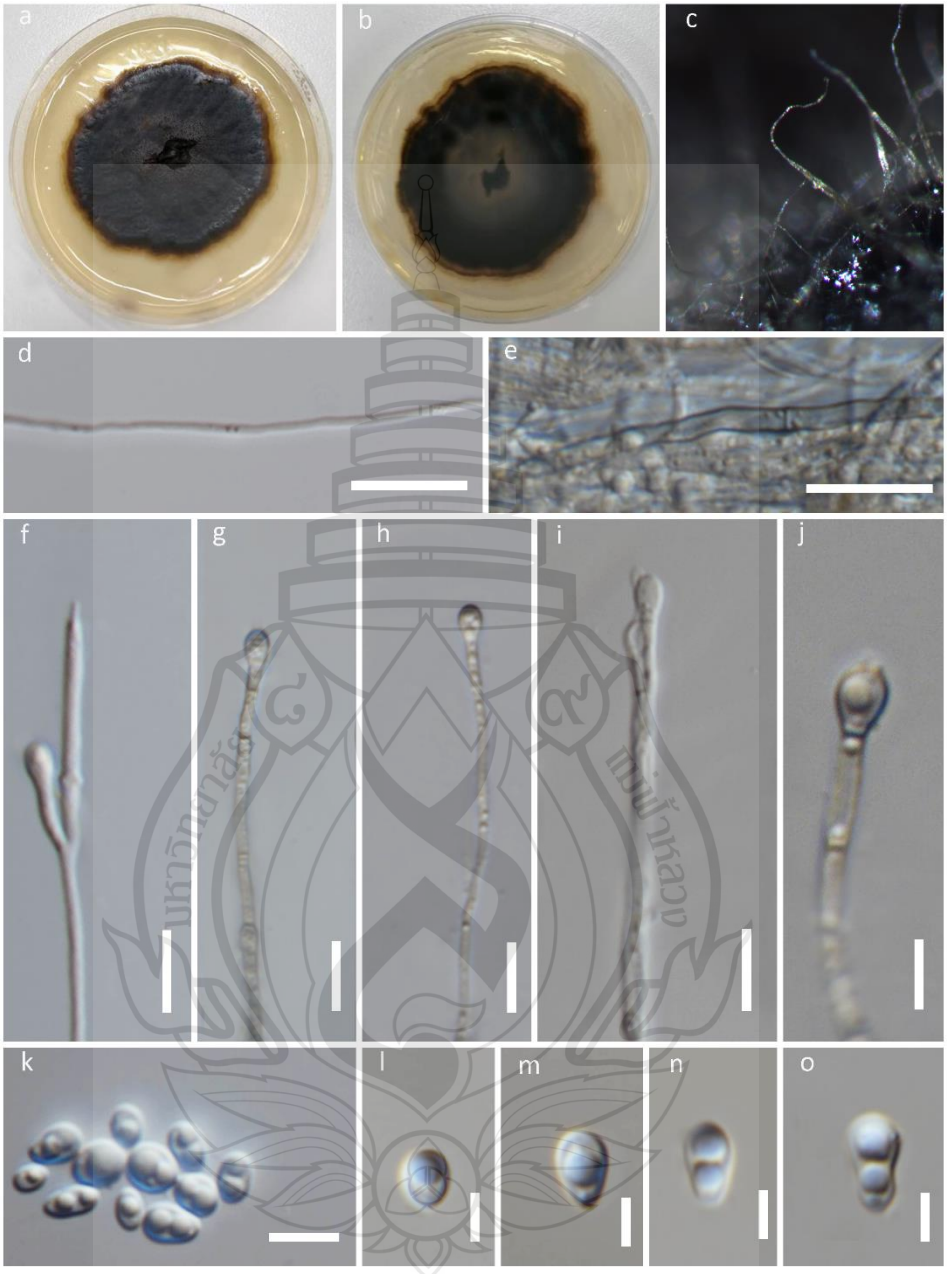


Figure 4.179 *Cordana terrestris* (MFLUCC 23-0022, new habitat record)

Figure 4.179, a Colony from above (on PDA) b Colony from below (on PDA). c Conidial attachments. d Immature hyphae. e Mature pigmented hyphae. f–j Conidiogenesis on the conidiophore. k–o Conidia. Scale bars: d = 20 µm, e = 15 µm, f – i = 10 µm, j, k – o = 5 µm.

Order: *Sordariales* Chad. ex D. Hawksw. & O.E. Erikss.

Family: *Chaetomiaceae* G. Winter

Achaetomium J.N. Rai, J.P. Tewari & Mukerji, Can. J. Bot. 42(6): 693 (1964)

Figure 4.180

Index Fungorum number: IF38; Facesoffungi: FoF06538

Achaetomium was established by Rai et al. (1964) and the type species is *A. globosum*. Subsequently, Mukerji (1978) and Cannon (1986) validated the genus. Based on LSU, SSU and *tef1-α* phylogeny, Maharachchikumbura et al. (2016) accommodated *Achaetomium* in *Chaetomiaceae*. The genus accommodates 16 species (Species Fungorum, 2025), and seven of them having molecular data. The asexual morph is described as *Lecythophora*-like structure that is present in *A. strumarium* (Abbott et al., 1995; Rodríguez et al., 2004). In some species, chlamydosphores can be present (von Arx, 1985; Mehrabi et al., 2020). The sexual morph is characterized by globose to pyriform, ostiolate ascomata covered with yellowish hypha-like hairs, with a relatively thick peridium consisting of cells of textura intricate, cylindrical asci and dark brown ascospores that are opaque with an apical germ pore (Rodríguez et al., 2004). *Achaetomium* is mostly found in soil, while some are associated with plant debris and human infections (Abbott et al., 1995; Rodríguez et al., 2004). They are distributed in Algeria, India, Israel, Pakistan, Spain and Thailand (Guarro et al., 2012).

Table 4.219 *Achaetomium* species isolated from soil

Species	Country	Habitat or soil type	References
Achaetomium globosum	India	Rhizosphere of Tamarindus indica	Rodríguez et al. (2004)
A. luteum	India	ND	
A. strumarium	India	Garden soil	
A. umbonatum	India	ND	
A. cristalliferum	Egypt	Arid soil	Locquin-Linard (1980)

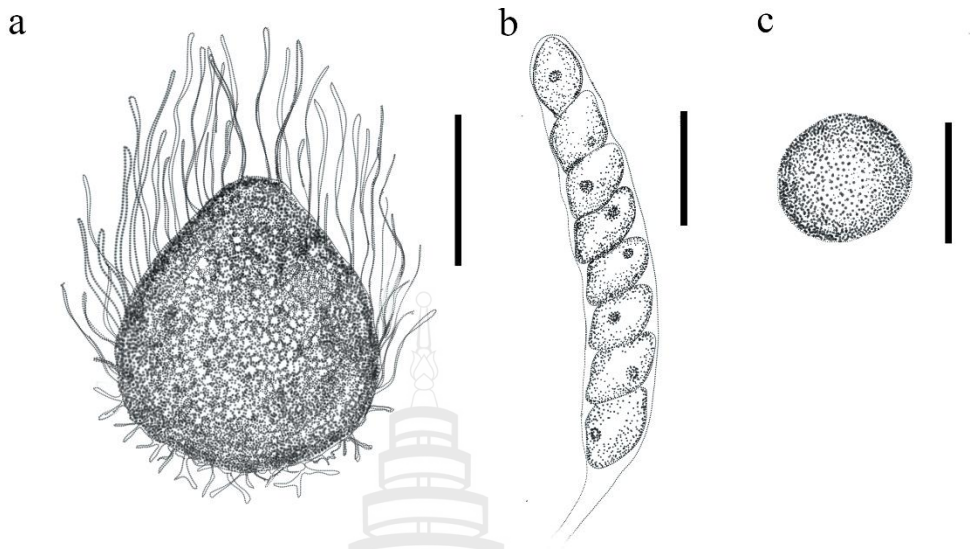


Figure 4.180 *Achaetomium sp.*

Figure 4.180 a Ascomata. b Ascus. *A. globosum* c Ascospore. Scale bars: a = 100 μm, b, c = 10 μm. Redrawn from redrawn from Guarro et al. (2012)

Arxotrichum A. Nováková & M. Kolařík, Persoonia 40: 259 (2018)

Figure 4.181

Index Fungorum number: IF824080; Facesoffungi: FoF13033

Crous et al. (2018a) introduced *Arxotrichum* based on morphology and LSU phylogeny, accommodating *A. wyomingense* as the type species. Wang et al. (2022a) provided *rpb2*, *tub2*, ITS and LSU multi gene phylogeny for *Chaetomiaceae* with eight accepted species in the genus. The asexual morph is hyphomycetous, conidiophores septate, stipe with basal part yellowish brown, upper part colourless, and hyaline conidiogenous cells producing solitary, aseptate, subglobose, rough-walled to rugose conidia. In sexual morph, ascomata can be absent or present in pale ochraceous to olivaceous gray, superficial, sphaerical to ovate, and the wall angular or irregular. Asci are obovate-clavate, short stalked, 8-spored evanescented and containing brown, ellipsoidal-fusoid, at both ends attenuated and rounded ascospores with distinct apical germ pores (Crous et al., 2018b). Species have been isolated from and Chile, China, Japan the USA from dung, soil and wood (Crous et al., 2018b; Hyde et al., 2020c).

Table 4.220 *Arxotrichum* species isolated from soil

Species	Country	Habitat or soil type	References
Arxotrichum piluliferoides	Japan	Grassland soil	Udagawa and& Horie (1975)
A. wyomingense	USA	NA	Crous et al. (2018b)
A. repens	Spain	NA	von Arx (1986)

Figure 4.182 *Arxotrichum wyomingense*

Figure 4.182, Conidiogenous cells and conidia. Scale bar = 10 μm. Redrawn from redrawn from Crous et al. (2018a).

Chaetomium Kunze, Mykologische Hefte (Leipzig) 1: 15 (1817)

Index Fungorum number: IF953; Facesoffungi: FoF01843;

Figure 4.183

Chaetomium was introduced by Kunze and Schmidt (1817) and typified by *C. globosum*. It is considered the largest genus in *Chaetomiaceae* (Wang et al., 2016a). The genus contains 211 morphological species, including 106 species with sequence data (Hyde et al., 2020c). Wang et al. (2022a), revised the genus and transferred some species in the other genera in *Chaetomiaceae* placing 42 species in the genus. The asexual morphs are acremonium-like (Wang et al., 2016a), and the sexual morph is characterized by globose, ellipsoid to ovate or obovate, sometimes ostiolate ascomata with hypha-like, flexuous ascomatal hairs, clavate or fusiform, evanescent asci, and limoniform to globose, bilaterally flattened ascospores. Species are widely distributed including, Austria, Brazil, China, Congo, Germany, Great Britain, India, Japan and the USA. Most of them are present on decaying twigs and soil, and indoor environments (Hyde et al., 2020c).

Table 4.221*Chaetomium* species isolated from soil

Species	Country	Habitat or soil type	References
Chaetomium angulare	China	ND	Zhang et al. (2017a)
C.erectum	China	ND	
C.murorum	Israel	Soil in Dead Sea	
C.nozdrenkoae	Russia	ND	

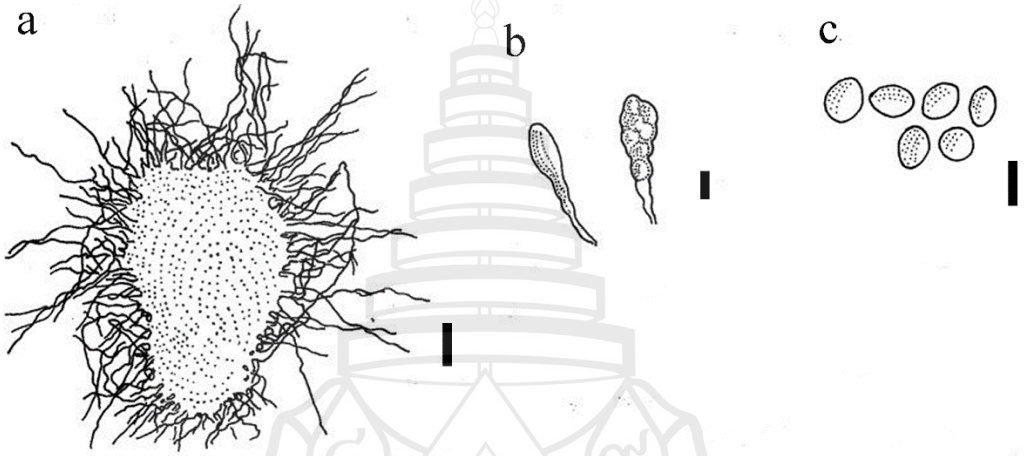


Figure 4.183 *Chaetomium globosum*

Figure 4.183 a Ascomata. b. Asci. c. Ascospore. Scale bar: a = 100μm, b, c = 10 μm. Redrawn from redrawn from Wang et al. (2016b)

Humicola Traaen, Nytt Mag. Natur. 52: 31 (1914)

Figure 4.184

Index Fungorum number: IF8566; Facesoffungi: FoF13038

Humicola was established by Traaen (1914) with *H. fuscoatra* (the type) and *H. grisea*. Presently, it comprises 66 species (Species Fungorum, 2025). Phylogenetic relationships of *Humicola* species in *Chaetomiaceae* were evaluated based on LSU, ITS, *tub2* and *rpb2* gene regions (Wang et al., 2019c, 2022a). While providing the phylogenetic revision for *Chaetomiaceae* Wang et al. (2022a), revised the genus placing 19 species. The asexual morph comprises aleurioconidia-like conidia, humicola-like, and acremonium-like characters. Humicola-like morph produces intercalary or lateral, monoblastic conidiogenous cells that reduced to a hyphal cell without conidiophores. Aleurioconidia-like conidia are 1-celled, solitary or rarely in chains of a few spores of brown, globose, subglobose or irregular-shaped.

Acremonium-like morph have lateral or terminal phialides with hyaline, aseptate, smooth, obovoid conidia in basipetal chains (Wang et al., 2022a). The sexual morph is characterized by superficial ascomata covered by aerial hyphae, ostiolate. Terminal hairs are flexuous and seta-like and ascospores are limoniform to quadrangular, bilaterally flattened, with an apical germ pore. Some *Humicola* species produce ascomata together with asexual morphs (Wang et al., 2019c). *Humicola* species produce thermostable enzymes such as cellulases, xylanases, feruloyl esterases, pectate lyases, and β-xylosidases with biotechnological and industrial importance (Ibrahim et al., 2021). Species are distributed in Brazil, China, Congo, Italy, Thaialnd and the USA, most of which are isolated from soil while some have been found on woody substrates (Bertoldi, 1976; Mel'nik, 2000; Wang et al., 2019c, 2022a).

Table 4.222 *Humicola* species isolated from soil

Species	Country	Habitat or soil type	References
Humicola lutea	Sardinia, Italy	woodland of Quercus	Bertoldi (1976)
H. repens	Sardinia, Italy	*Triticum aestivum* field	
H. rugose	Sardinia, Italy	Woodland soil	
H. sardiniae	Sardinia, Italy	Vineyard soil	
H. variabilis	Sardinia, Italy	Woodland soil	
H. interseminata	China	Mountain soil	Jiang and Zhang (2010)
H. macrospora	China	Mountain soil	
H. subminima	China	Rice field	

a

Figure 4.184 *Humicola fuscoatra* (CBS 516.67)

Figure 4.184, a Formation of aleurioconidia. Redrawn from Domsch et al. (1980)

Staphylotrichum J. Mey. & Nicot, Bull. trimest. Soc. mycol. Fr. 72: 322 (1957) [1956]

Figure 4.185

Index Fungorum number: IF10065; Facesoffungi: FoF13045

Staphylotrichum was established by (Nicot & Meyer, 1956) with the type *S. coccosporum*. There are 11 epithets listed in Species Fungorum (2025), while nine of them are supported with molecular data. Phylogenetic revisions for *Staphylotrichum* were inferred based on concatenated LSU, ITS, *tub2*, and *rpb2* (Qiao et al., 2021; Wang et al., 2022a), while transferring *Humicola* species in the genus. The asexual morph consists of two types, macronematous and micronematous. The macronematous type has thick-walled, apically branched conidiophores and cylindrical or denticle-like, monoblastic or sympodial polyblastic conidiogenous cells. The micronematous type has cylindrical or denticle-like, monoblastic, rarely sympodial polyblastic conidiogenous cells and single-celled, smooth or slightly verrucose, hyaline to pale brown, globose, subglobose or obovoid conidia rhexolytic when seceding (Wang et al., 2022a). The sexual morph consists of two types: *Ascomata* of type I with conspicuous neck, superficial or covered by aerial hyphae, ostiolate, elongated obpyriform ascomata and *Ascomata* of type II, with superficial, ostiolate, ovate to subglobose ascomata with terminal hairs, clavate to fusiform asci and broad limoniform to globose, bilaterally flattened ascospores with an apical germ pore (Wang et al., 2022a). Species of this genus were reported from different substances, including air, hare dung, plant litter and soils in China, Poland, South Africa and the USA (Qiao et al., 2021).

Table 4.223 *Staphylotrichum* species isolated from soil

Species	Country	Habitat or soil type	References
Staphylotrichum boninense	Japan	Soil under *Elaeagnus rotundata*	Qiao et al. (2021)
S. sinense	China	ND	

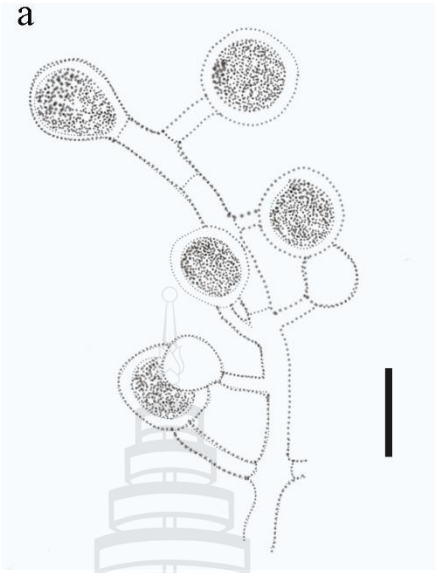


Figure 4.185 *Staphylotrichum coccosporum*

Figure 4.185, a Conidiophores and conidia. Redrawn from Domsch et al. (1980).

Stellatospora Tad. Ito & Nakagiri, Mycoscience 35(4): 413 (1994)

Figure 4.186

Index Fungorum number: IF27456; Facesoffungi: FoF13568.

Stellatospora was introduced by Ito and Nakagiri (1994) and the type species is *S. terricola*. *Stellatospora* is monospecific, and previously Wijayawardene et al. (2017) and Hyde et al. (2020) listed this genus in *Sordariaceae*. However, the combined phylogeny (LSU, SSU, *rpb2* and *tef*1-α) treated in *Sordariomycetes* by the Huang et al. (2021), placed the genus in *Chaetomiaceae*. The asexual morph is not determined. The sexual morph is characterized by cleistothecial, solitary or gregarious, globose to subglobose, dark brown to black, ascomata, 3–8-spored, unitunicate, obpyriform to oval, evanescento bpyriform asci and multiseriate, pale greenish brown to brown, stellate ascospores (Ito & Nakagiri, 1994).

Table 224 *Stellatospora* species isolated from soil

Species	Country	Habitat or soil type	References
Stellatospora terricola	Japan	Rice field	Ito and Nakagiri (1994)

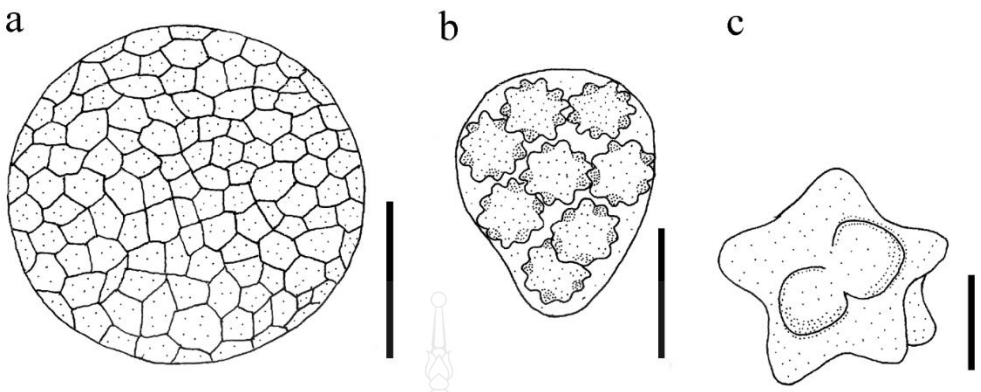


Figure 4.186 *Stellatospora terricola*

Figure 4.186, a Ascoma. b Ascus. c Ascospore. Scale bar: a = 50 μm, b = 25 μm, c = 5 μm. Redrawn from Guarro et al. (2012).

Thielavia Zopf, Verh. bot. Ver. Prov. Brandenb. 18: 105 (1876)

Index Fungorum number: IF5450; Facesoffungi: FoF13048

Thielavia is typified with *T. basicola* Zopf (1876). There are 80 species listed in the Species Fungorum (2025). Phylogeny of *Thielavia* species was resolved based on combined *rpb2*, *tub2*, ITS and LSU (Wang et al., 2019b) gene regions. The sexual morph is characterized by non-ostiolate ascomata with a thin peridium and single-celled, smooth, ellipsoidal with attenuated ends, or fusiform, pigmented ascospores with one germ pore. The majority of species identified from soil (Wang et al., 2019b) including desert, grassland, or alkaline soils and seeds, animals, dung, and decaying plant materials (Ibrahim et al., 2022). Some *Thielavia* species can be endophytes, lichenicolous, coprophilous, and even marine-derived (Ibrahim et al., 2022). *Thielavia* species are important source of enzymes with industrial potential as laccases, cutinases, glucuronoyl esterases, feruloyl esterases, 1,4-b-endoglucanase, and lytic polysaccharide monooxygenases (Ibrahim et al., 2022). In addition, secondary metabolites such as depsides (e.g. thielocins and thielavins), azaphilones (spiro-, bis-spiro-, and nor-spiro-azaphilone), pyrazines, naphthodianthrones, and anthraquinones derivatives have been identified in phytochemical studies (Ibrahim et al., 2022).

Table 4.225 *Thielavia* species isolated from soil

Species	Country	Habitat or soil type	References
Thielavia achromatica	India	ND	Subrahmanyam (1981)
T. ampullata	India	Farm soil	Rai and Wadhwani (1977)
T. aurantiaca	Japan	Field soil	Ito et al. (1998)

Trichocladium Harz, Bull. Soc. Imp. nat. Moscou 44(1): 125 (1871)

Figure 4.187

Index Fungorum number: IF10278; Facesoffungi: FoF13049

Trichocladium was introduced by (Harz, 1871) with the type *T. asperum*. There are 60 species listed in Species Fungorum (2025), and 23 species are supported with moecular data. Phylogenetic relationships of *Trichocladium* were inferred based on combined ITS, *tub2*, and *rpb2* (Belosokhov et al., 2022), and LSU, ITS, *tub2*, and *rpb2* (Wang et al., 2022a) gene regions. The asexual morph is characterized by simple or branched conidiophores arising laterally or terminally from hyphae, monoblastic or polyblastic conidiogenous cells, 1-celled, didymo-, phragmo- or muriform, globose, subglobose, oblate, ellipsoid, obovoid, pyriform, hyaline, brown conidia. Some species have Acremonium-like phialides and hyaline, aseptate, obovoid, smooth Acremonium-like conidia in basipetal chains or in a false slimy head (Wang et al., 2022a). The sexual morph is characterized by superficial or immersed, ostiolate or non-ostiolate ascomata, cylindrical or clavate to fusiform 8-spored asci and broadly ovate, bilaterally flattened, or ellipsoidal ascospores with an apical germ pore (Wang et al., 2022a). *Trichocladium* species are commonly identified from dung, estuarine sediment, grass, leaf, and soil, from Brazil, China, Germany, India, Italy, Malaysia and the USA (Tagele et al., 2019) and a few members are known as thermophilic (Belosokhov et al., 2022).

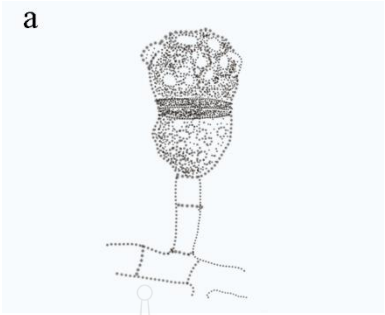


Figure 4.187 *Trichocladium asperum*

Figure 4.187, a Conidiogenesis and conidum. Redrawn from Domsch et al. (1980)

Table 4.226 *Trichocladium* species isolated from soil

Species	Country	Habitat or soil type	References
Trichocladium pyriforme	Ireland	ND	Dixon (1968)
Trichocladium griseum	South Korea	paddy field	Tagele et al. (2019)

Family: *Diplogelasinosporaceae* Y. Marin & Stchigel

Diplogelasinospora Cain, Can. J. Bot. 39: 1669 (1961)

Figure 4.188

Index Fungorum number: IF1609; Facesoffungi: FoF14636;

Diplogelasinospora was introduced by Cain (1961) and typified by *D. princeps*. This genus was previously considered a member of *Neurosporaceae*. Based on ITS, LSU *rpb2*, and *tub2* phylogeny, Marin-Felix et al. (2020) introduced *Diplogelasinosporaceae* and accommodated *Diplogelasinospora* as the type genus. Marin-Felix et al. (2020) have accepted four species in this genus and all of them are supported with the molecular data. The asexual morph has conidiophores that are lacking or not distinctly differentiated from vegetative hyphae, and blastic, arthric, terminal or intercalary, hyaline, oblong to cylindrical conidia. Sexual morph of this genus has non-ostiolate, immersed or superficial ascomata with membranaceous to slightly coriaceous and textura angularis ascomatal wall. Asci are unitunicate, 8-spored, cylindrical to cylindrical-clavate that contain initially hiyaline, aseptate, ellipsoidal, becoming transversely septate and two-celled ascospores with one hyaline cell and black and opaque cell. (Cain, 1961; Marin-Felix et al., 2020b). Species have been

isolated from seeds and soil collected from Brazil, China, India, Thailand and the USA (Marin-Felix et al., 2020b).

Table 4.227 *Diplogelasinospora* species isolated from soil

Species	Country	Habitat or soil type	References
Diplogelasinospora moalensis	Spain	ND	Marin-Felix et al. (2020b)
D. princeps	USA	ND	

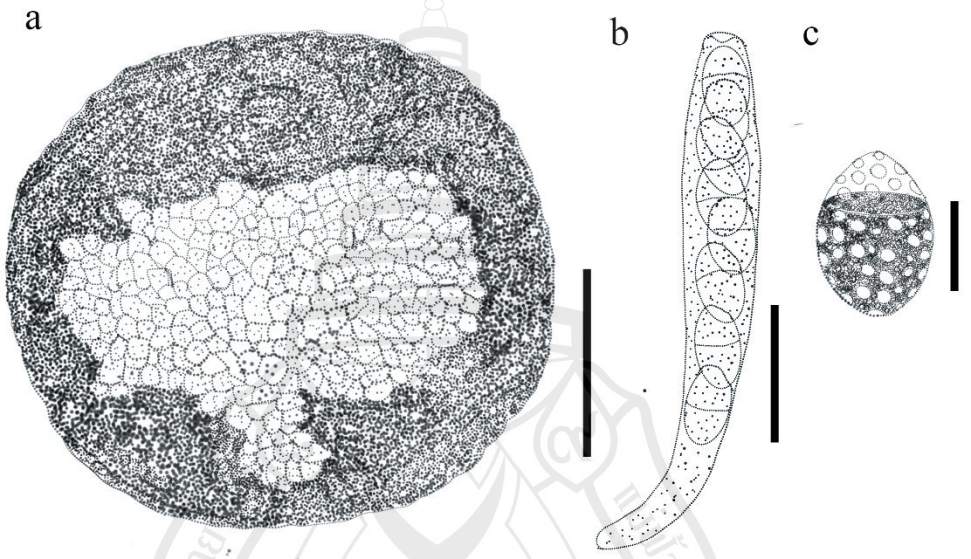


Figure 4.188 *Diplogelasinospora* sp.

Figure 4.188, a Ascomata. b Ascus. *D. princeps* c Ascospore Scale bars: a = 100 µm, b = 25 µm, c = 10 µm. Redrawn from redrawn from Guarro et al. (2012)

Family: ***Naviculisporaceae*** Y. Marin & Stchigel

Naviculispora Stchigel, Y. Marín, Cano & Guarro, Microorganisms 8(9, no. 1430): 14 (2020)

Figure 4.189

Index Fungorum number: IF812135; Facesoffungi: FoF14640

Marin-Felix et al. (2020) introduced *Naviculispora* with its type *N. terrestris,* while accommodating the genus in *Naviculisporaceae* based on LSU, ITS, *rpb2* and *tub2* multigene phylogeny and the morphological characterization. It is a monospecific genus (Species Fungorum, 2025). Asexual morph has conidiophores that are reduced to conidiogenous cells or sympodially proliferating. Conidiogenous cells are phialidic,

producing holoblastic, sometimes sessile, hyaline to subhyaline, ellipsoidal to subspherical, obovoid or clavate conidia (Marin-Felix et al., 2020b). The sexual morph is characterized by scattered or aggregated, immersed or superficial, ostiolate or rarely non-ostiolate, brown to dark brown or black, globose to subglobose, pyriform or ovate, ascomata that are glabrous or with flexous or stiff hairs and the ascomatal wall is composed of textura angularis or irregularly-shaped cells. Asci are unitunicate, cylindrical or clavate, evanescent, long- or short-stipitate with two types of ascospores. Mostly, 2-celled ascospores are present; 1-celled ascospores initially hyaline, becoming ochraceous to brown or blackish brown when mature and two-celled ascospores are initially one-celled and hyaline, clavate, cylindrical or spatuliform becoming two-celled with transversely septate, olivaceous or brown to dark brown navicular (Marin-Felix et al., 2020b).

Table 4.228 *Naviculispora* species isolated from soil

Species	Country	Habitat or soil type	References
Naviculispora terrestris	Argentina	valley	Marin-Felix et al. (2020b)

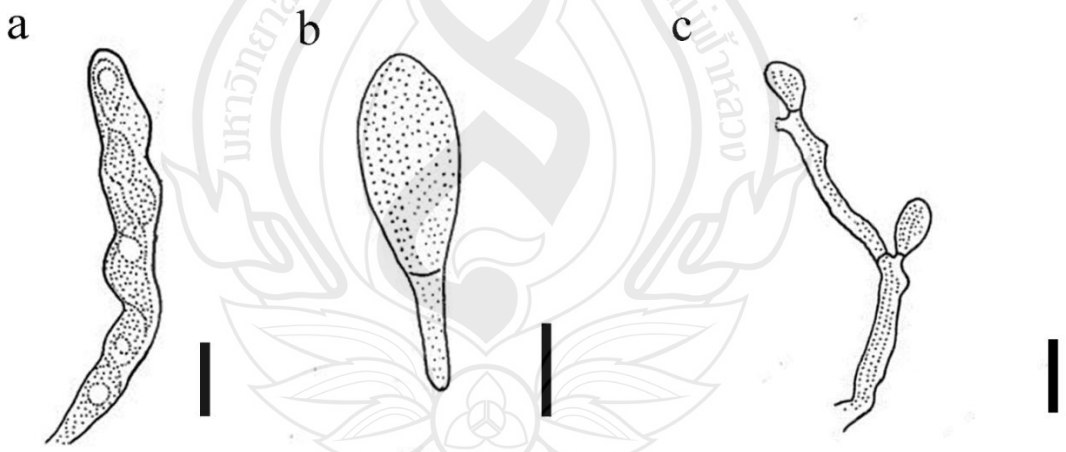


Figure 4.189 *Naviculispora terrestris*

Figure 4.189, a Ascus. b Ascospore. c Sessile conidia. Scale bars: a = 20 μm, b = 15μm, c = 5μm. Redrawn from Marin-Felix et al. (2020).

Family: *Podosporaceae* X. Wei Wang & Houbraken

Cladorrhinum Sacc. & Marchal, Bull. Soc. Roy. Bot. Belgique 24: 64. (1885)

Figure 4.190

Index Fungorum number: IF7678; Facesoffungi: FoF13545

Cladorrhinum was introduced by Saccardo and Marchal in 1885 accomodating the type speceis *C. foecundissimum* (Marchal, 1885). The genus accommodates 16 species (Species Fungorum 2025), and 13 of them have molecular data. Carmarán et al. (2015) and Wang et al. (2019) described *Cladorrhinum* as polyphyletic genus, however Marin-Felix et al. (2020) treated this as a monophyletic group based on ITS, LSU, *rpb2* and *tub2* phylogeny. Asexual morph is hyphomycetous, conidiophores can be absent or present as micronematous conidiophores and reduced to intercalary, occasionally terminal, conidiogenous cells with enteroblastic conidiogenesis producing one-celled, hyaline, broad obovoid, ellipsoidal or subglobose conidia. *C. tomentosum* and *C. coprophilum* are introduced as new combinations by Marin-Felix et al. (2020) and the genus description was amended with new sexual characteristics. The sexual morph is characterized by ostiolate or non-ostiolate, superficial to immersed, solitary or aggregated, globose to subglobose ascomata with membranaceous wall, and unitunicate, eight-spored, cylindrical, evanescent asci. There are two type of ascospores: 1-celled ochraceous or olivaceous brown to dark brown, ellipsoidal to broadly fusiform, ovoid or obovoid ascospores or two-celled, biseriate or triseriate, initially hyaline, upper cell brown, ellipsoidal and lower cell cylindrical ascospores (Marin-Felix et al., 2020b). Species are saprobes living in dung, plant parts and soil, while some of them can be root endophytes. Species have been discovered from China, France, India, Italy and the USA (Carmarán et al., 2015; Hyde et al., 2020c). *Cladorrhinum foecundissimum* found to be reducing the damping-off caused by *Rhizoctonia solani* and *Pythium ultimum* (Carmarán et al., 2015; Marin-Felix et al., 2020b) .

Table 4.229 *Cladorrhinum* species isolated from soil

Species	Country	Habitat or soil type	References
Cladorrhinum globisporum	China	Acidic soil	Marin-Felix et al. (2020b
C. terricola	Japan	River sediment	Ueda (1994)

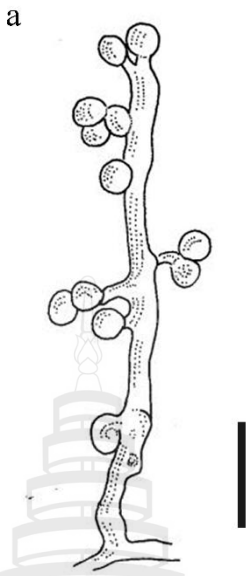


Figure 4.190 *Cladorrhinum foecundissimum* (CBS180.66)

Figure 4.190, a. Conidiogenous cells and conidia. Scale bars: a = 10μm. Redrawn from Wang et al. (2019).

Podospora Ces., Hedwigia 1(15): 103 (1856)

Index Fungorum number: IF4284; Facesoffungi: FoF13546

Cesati (1856) introduced *Podospora*, which was considered one of the largest genera in *Lasiosphaeriaceae* (Hyde et al., 2020c; Wang et al., 2019b). However, according to the phylogeny of Wang et al. (2019) *Podospora* was suggested as a monophyletic genus, placing it in *Podosporaceae,* while many species were synonymized to other genra. Based on the ITS, LSU *rpb2*, and *tub2* phylogeny of Marin-Felix et al. (2020), five species have been accepted in the *Podospora* as *sensu-stricto* and several *Podospora* species that are not corresponding to the type species have been provided as unsupported clade and suggested belong in *Lasiosphaeriaceae*. The asexual morph has conidiophores that are micronematous, reduced to conidiogenous cells and intercalary conidiogenous cells that are originating from a lateral peg-like structure with a flaring collarette. Conidia are blastic, single-celled, hyaline, smooth-walled, globose or ellipsoidal to elongate. Sexual morph of *Podospora* characterized by superficial, solitary, ostiolate and pyriform, or less frequently non-ostiolate and globose, covered by erect or flexuous ascomata with unitunicate, eight-

spored, clavate or cylindrical asci and uniseriate or biseriate, two-celled, upper cell olivaceous brown to brown or dark brown, ellipsoidal to ovoid or obovoid ascospores (Marin-Felix et al., 2020b). The species have been recorded from dung, plant roots and soil (Marin-Felix et al., 2020b; Wang et al., 2019b).

Table 4.230 *Podospora* species isolated from soil

Species	Country	Habitat or soil type	References
Podospora australis	Australia	Sand and loamy soils	Lundqvist (1972)
P. striatispora	Thailand	ND	Marin-Felix et al. (2020b)
P. bulbillosa	Egypt	Desert soil	Wang et al. (2019b)
P. granulostriata	Southeast Asia	Fire-affected soils	Richardson (1998)

Triangularia Boedijn, Ann. Mycol. 32: 302 (1934)

Figure 4.191

Index Fungorum number: IF5534; Facesoffungi: FoF13547

Triangularia was introduced by Boedijn (1934) and typified by *T. bambusae*. Currently, 29 species are listed in the Species Fungorum (2025), while nine species have molecular data. Marin-Felix et al. (2020) provided recent phylogeny (ITS, LSU, *rpb2* and *tub2*) of *Triangularia* accepting it as a monophyletic clade and the generic description has been re-arranged. The asexual morph is a cladorrhinum-like and have micronematous conidiophore reduced to conidiogenous cells. Conidiogenous cells are intercalary or occasionally terminal, sometimes phialidic, and have 1-celled, hyaline, globose to subglobose or pyriform conidia. The sexual morph is characterized by ostiolate or non-ostiolate, often superficial, sometimes semi-immersed to immersed, globose to subglobose, ovoid, or obpyriform to ampulliform, glabrous ascomata. The asci are unitunicate, four to eight or multi-spored, cylindrical to elongated clavate or fusiform and short or long stipitate, containing 1-celled ascospores that are uniseriate and hyaline becoming yellowish, olivaceous to brown-black, ellipsoidal with an apical germ pore; and two-celled ascospores are uniseriate, biseriate, triseriate with an apical or subapical pore (Hyde et al., 2020c; Marin-Felix et al., 2020b). Species prefer warm environmental conditions and occur in aquatic sediments, plant debris and soil (Hyde et al., 2020c). They have been reported from Brazil, Canada, Central Africa, India, Japan, Panama, Spain, Ukraine and the USA (Marin-Felix et al., 2020b).

Table 4.231 *Triangularia* species isolated from soil

Species	Country	Habitat or soil type	References
Triangularia angulispora	Panama	Tropical forest soil	Domsch et al. (1993)
T. verruculosa	USA	Soil, associated with *Avena sativa*	Guarro and Cano (1988)
T. matsushimae	Japan	Forest soil	Huang (1976)
T. backusii	USA	Garden soil	
T. batistae	Brazil	ND	Marin-Felix et al. (2020b)
T. longicaudata	Spain	Sandy soil	Arx (1975)

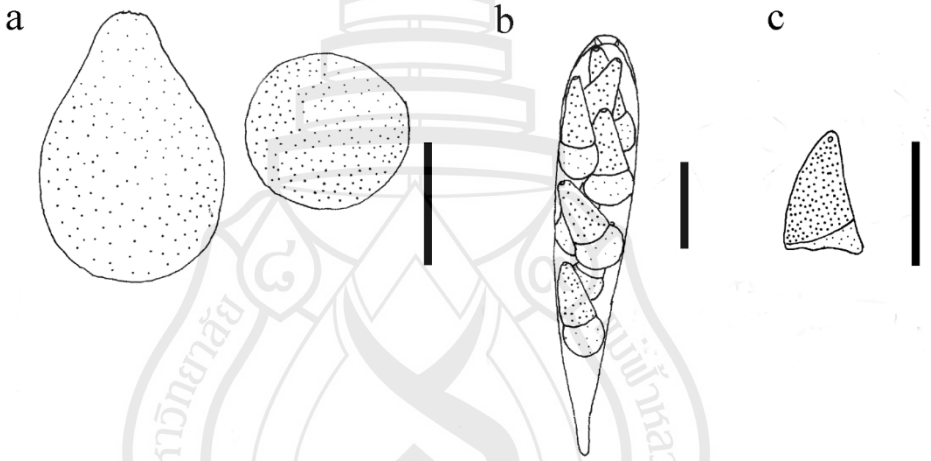


Figure 4.191 *Triangularia sp.*

Figure 4.191, a Ascomata b Ascus. *T. bambusae* c Ascospore. Scale bars: a = 100 μm, b, c = 25μm. Redrawn from Guarro et al. (2012).

Family: *Schizotheciaceae* Y. Marin & Stchigel

Jugulospora N. Lundq., Symb. bot. upsal. 20(no. 1): 256 (1972)

Figure 4.192

Index Fungorum number: IF2538; Facesoffungi: FoF13304

Lundqvist (1972) introduced *Jugulospora* and accommodated *J. rotula* as the type species. The genus currently accommodates five species (Species Fungorum, 2025), and all are with molecular data. The asexual morph can be present or absent, and conidia are characterized by the hyaline to pale brown, smooth-walled, ovate to elongate and they are produced laterally or terminally on undifferentiated hyphae. The

sexual morph is characterized by the ostiolate ascomata covered with pale brown, flexuous, septate, thick-walled hairs and the ascomata wall is membranaceous and semi-transparent. The asci are unitunicate, 8-spored, cylindrical, with a thin apical ring that contain initially 1-celled, hyaline, clavate ascospores become septate upper cell brown, navicular, globose, or obovoid, warted, finely granulated, or pitted with an apical germ pore and hyaline, thin gelatinous sheath rarely present. The species are associated with soil substrates in Antarctica, Great Britain, Spain and the USA (Marin-Felix et al., 2020b).

Table 4.232 *Jugulospora* species isolated from soil

Species	Country	Habitat or soil type	References
Jugulospora antarctica	Antarctica	Island	Stchigel et al. (2003)
J. vestita	Nepal	Fire-affected soils	Udagawa and Horie (1982)
J. carbonaria	Great Britain	Burnt soil:	Marin-Felix et al. (2020b)
J. minor	Sweden	Burnt soil	
J. rotula	Great Britain	Burnt soil:	

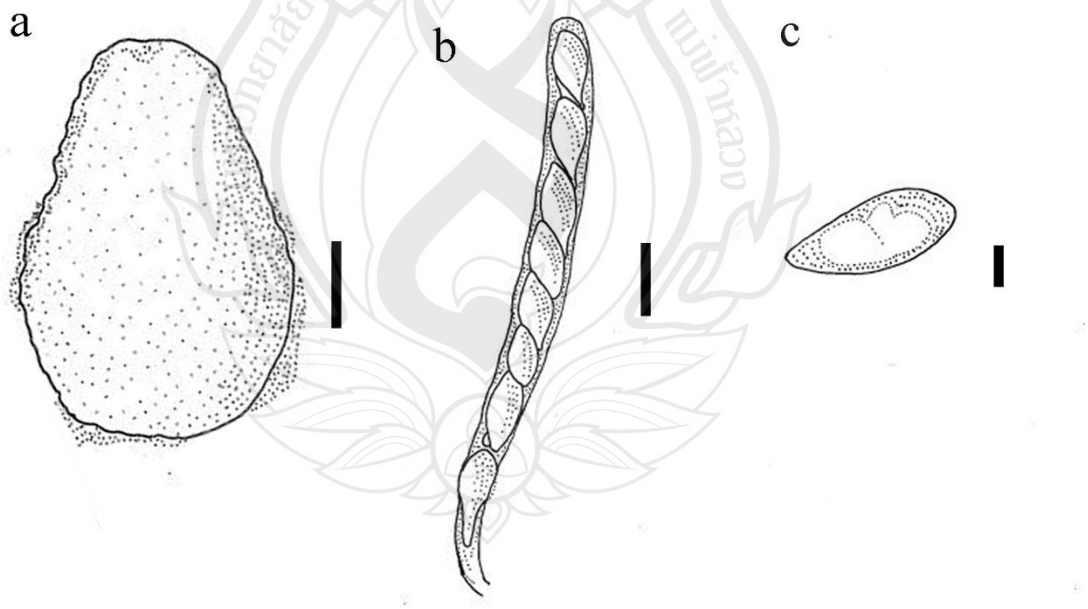


Figure 4.192 *Jugulospora rotula* (FMR12428)

Figure 4.192, a Ascoma. b Ascus. c Ascospore. Scale bars: a = 100 μm, b = 15 μm, c = 5μm. Redrawn from Marin-Felix et al. (2020b)

Lundqvistomyces Y. Marin & Stchigel, Microorganisms 8(9, no. 1430): 29 (2020)

Index Fungorum number: IF835508; Facesoffungi: FoF14649

Marin-Felix et al.(2020) introduced *Lundqvistomyces* based on morphology and phylogeny (LSU, ITS, rpb2 and *tub2*), with its type species, *L. karachiensis*. There are two *Lundqvistomyces* species listed in the Species Fungorum (2025). The asexual morph can be absent or present with conidia delimited from peg-like non-proliferating structures on undifferentiated hyphae. The sexual morph is characterized by the ostiolate, immersed to almost superficial, scattered or aggregated, brown to nearly black, pyriform ascomata, and unitunicate, eight-spored, clavate or cylindrical-clavate, thin-walled, short stipitate asci with biseriate, at first one-celled, ellipsoidal, becoming transversely uniseptate and two-celled ascospores (Marin-Felix et al., 2020b). Species have been isolated from animal dung, plant material and soil that are reported from several countries including Brazil, China, Egypt, Germany, India, Russia, Sweden and the USA (Marin-Felix et al., 2020b).

Table 4.233 *Lundqvistomyces* species isolated from soil

Species	Country	Habitat or soil type	References
Lundqvistomyces karachiensis	Egypt	Arid soil in desert	Marin-Felix et al. (2020b)

Family: *Sordariaceae* G. Winter

Boothiella Lodhi & Mirza, Mycologia 54(2): 217 (1962)

Figure 4.193

Index Fungorum number: IF 627; Facesoffungi: FoF4655

Boothiella was established by Lodhi and Mirza (1962). It includes only the type, *B. tetraspora* that has been supported with the molecular data (Hyde et al., 2020c, 2024a). Kirk et al. (2009) transferred *Boothiella* to *Sordariaceae* and (Maharachchikumbura et al., 2015) placed this genus in *Chaetomiaceae*. Phylogenetic analyses of LSU, ITS, *tub2* and *rpb2* by Wang et al. (2019b) and Huang et al. (2021b) confirmed the placement of *Boothiella* in *Sordariaceae*. The sexual morph is characterized by superficial to immersed, solitary or gregarious, cleistothecial ascomata, membranaceous peridium composed of cells of textura angularis,

unitunicate, clavate to cylindrical, 4-spored asci and oval to citriform, 1–2-apiculate, hyaline to brown ascospores with a germ pore at one or each end (Huang et al., 2021b; Lodhi & Mirza, 1962; Wang et al., 2019c). Species has been reported from soil and frogs in China, India and Pakistan (Kirk et al., 2009; Yang et al., 2023).

Table 4.234 *Boothiella* species isolated from soil

Species	Country	Habitat or soil type	References
Boothiella tetraspora	India	ND	Wang et al. (2019b)
B. tetraspora	Pakistan	Barley field soil	

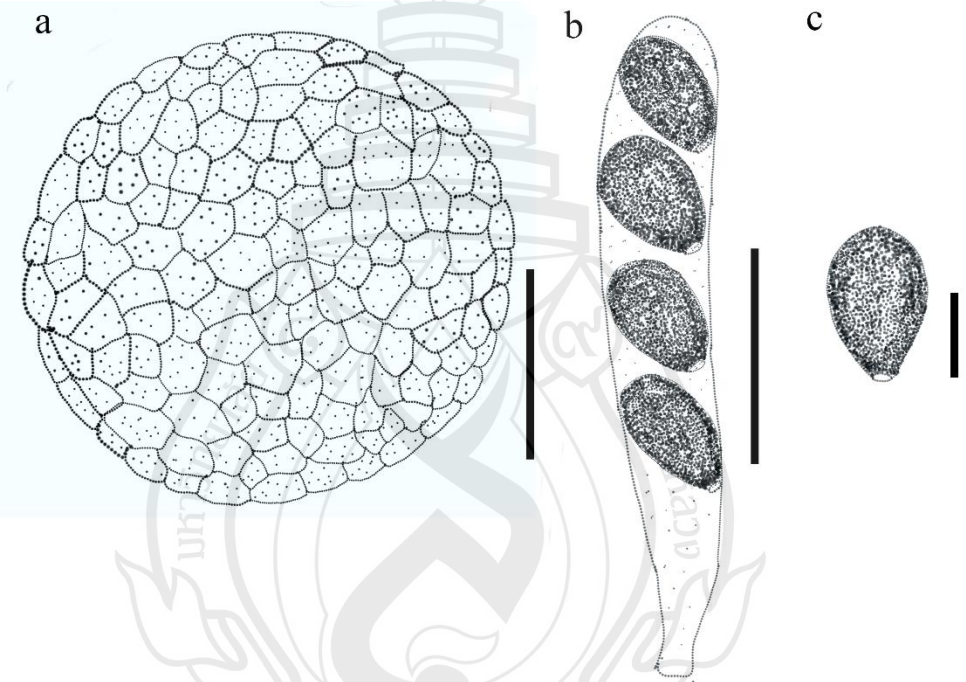


Figure 4.193 *Boothiella tetraspora*

Figure 4.193, a Ascomata. b Ascus. c Ascospore. Scale bars: a = 100 μm, b = 25 μm, c = 10 μm. Redrawn from Guarro et al. (2012)

Neurospora Shear & B.O. Dodge, J. Agric. Res., Washington 34: 1025 (1927)

Index Fungorum number: IF3502; Facesoffungi: FoF13566

Shear and Dodge (1927) introduced *Neurospora* to accommodate dark ascospores, with a grooved surface and longitudinal ribs, with four accepted species including the type speceis, *N. sitophila*. There are 57 species listed in the Species Fungorum (2025), and 36 have molecular data. The phylogenetic relationships between

Neurospora and *Gelasinospora* were investigated by Dettman et al. (2001), based on ITS, *gapdh*, mating-type A-1, and mating-type a-1. *Gelasinospora* is another genus in *Sordariaceae* that has similar ascospore morphology to *Neurospora*. The main difference between *Neurospora* and *Gelasinospora* is the ornamentation of the surface of their ascospore wall (García et al. 2004). However, García et al. (2004) analyzed phylogenetic relationships between *Neurospora* and *Gelasinospora* based on the 28S rDNA gene and showed *Gelasinospora* did not form a distinct group from *Neurospora*. Therefore, they treated *Gelasinospora* as a synonym of *Neurospora. Neurospora* species were recorded from dung, root, stem, soil, and wood from various geographical regions including Brazil, China, Kenya, Thailand and the USA (García et al., 2004).

Table 4.235 *Neurospora* species isolated from soil

Species	Country	Habitat or soil type	References
Neurospora crassa	USA, India and Brazil	Post-fire soils and grasslands	Perkins and Turner (1988)
N. pseudocalospora	Papua New Guinea	Rainforest	Udagawa et al. (1973)

Pseudoneurospora Dania García, Stchigel & Guarro, Mycol. Res. 108(10): 1139 (2004)

Index Fungorum number: IF28887; Facesoffungi: FoF13567

Figure 4.194

Based on LSU phylogeny and morphology García et al. (2004) introduced *Pseudoneurospora* with the type species, *P. amorphoporcata*. Currently, the genus accommodates two species (Crous et al., 2014a), and both of which have molecular data. The asexual morph remains undetermined and the sexual morph is characterized by the pyriform, ostiolate, glabrous or gently hairy ascomata and the peridium textura angularis. Asci are cylindrical, 8-spored apical structure non-amyloid and ascospores are unicellular, ellipsoidal, reticulate with irregularly rounded crests (García et al., 2004). *Pseudoneurospora* species have been reported from plant debris and soil in Brazil, Japan and Thailand (Crous et al., 2014a; García et al., 2004).

Table 4.236 *Pseudoneurospora* species isolated from soil

Species	Country	Habitat or soil type	References
Pseudoneurospora amorphoporcata	Thailand	ND	García et al. (2004)
P. canariensis	Spain	Forest soil	Crous et al. (2014a)

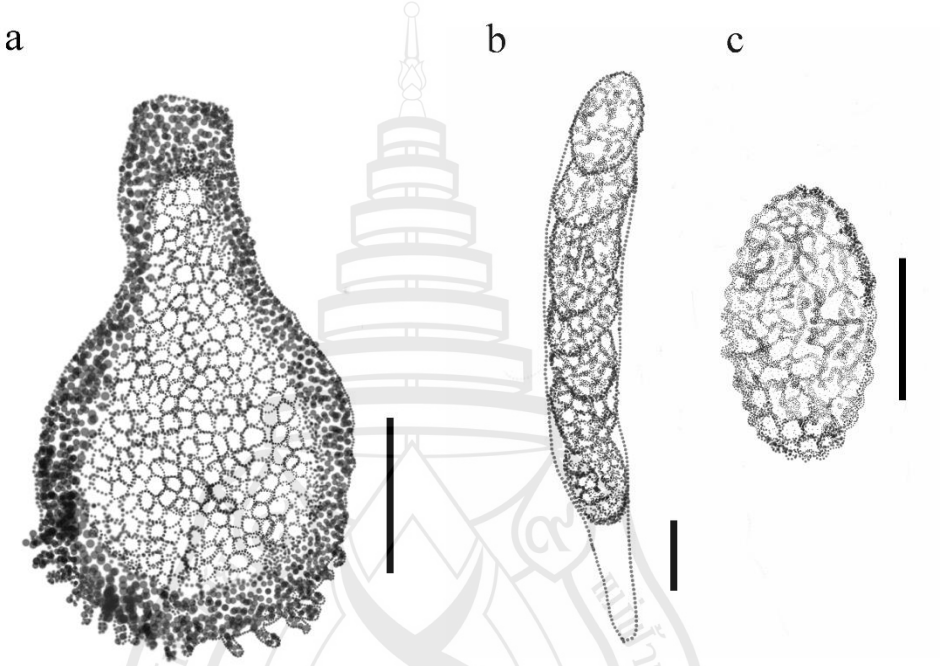


Figure 4.194 *Pseudoneurospora amorphoporcata*

Figure 4.194, a Ascomata. b Ascus. c Ascospore. Scale bars: a = 100 μm, b = 25 μm, c = 15 μm. Redrawn from Guarro et al. (2012)

Sordaria Ces. & De Not., Comm. Soc. crittog. Ital. 1(4): 225 (1863)

Index Fungorum number: IF5061; Facesoffungi: FoF01149;

Figure 4.195

Cesati and De Notaris (1863) introduced *Sordaria* and the type species is accepted as *S. fimicola*. The genus comprises around 50 species while 15 have molecular data (Hyde et al., 2020c, 2024a). The sexual morph is consist of superficial, obovate, pyriform, or ampulliform, with a conical or cylindrical ascomata with cylindrical, short stalked, unitunicate, at the truncate apex often ring-like thickenings, 8-spored asci and uniseriate, ellipsoidal, cylindrical, or fusiform with rounded ends, aseptate, brown or opaque when mature ascospores (Guarro & Von Arx, 1987). The

species are occurring on decaying plant materials, dung, herbaceous plants, seeds and soil and are globally reported including in Australia, Brazil, India, Japan and South Africa (Hyde et al., 2020a, 2024a)

Table 4.237 *Sordaria* species isolated from soil

Species	Country	Habitat or soil type	References
Sordaria fimicola	Japan and USA	ND	Kwon-Chung and Bennett (1992)
Sordaria macrospora	Japan, India and USA	ND	Mayr (1982)

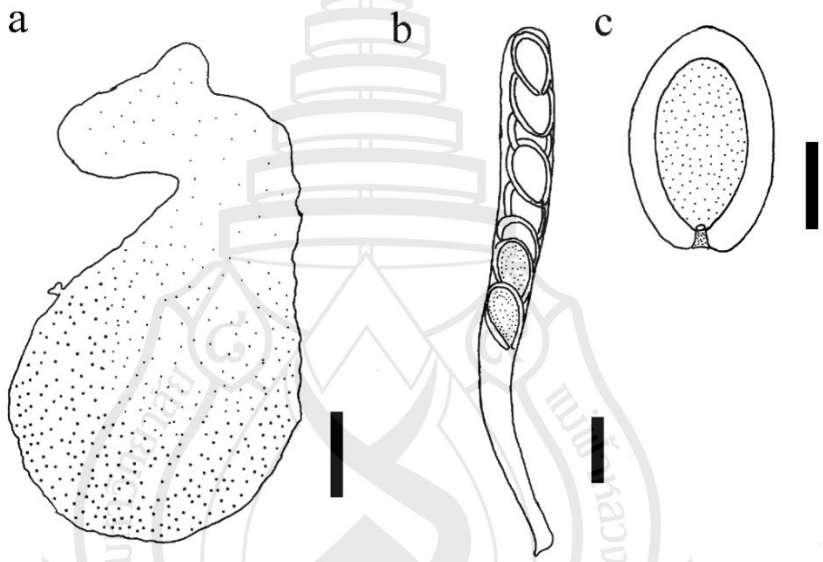


Figure 4.195 *Sordaria fimicola*

Figure 4.195, a Ascoma. c Ascospore. *Sordaria* sp. b Ascus. Scale bars: a = 100 μm, b = 25 μm, c = 10 μm. Redrawn from Guarro et al. (2012).

Sordariales* genera *incertae sedis

Eosphaeria Höhn., Annls mycol. 15(5): 362 (1917)

Index Fungorum number: IF1843; Facesoffungi: FoF13300

Eosphaeria was introduced by Höhnel (1917) and was typified by *E. uliginosa.* It is a monospecific genus, and sequence data is currently unavailable (Huang et al., 2021b, Index Fungorum, 2025). Previously, this was placed in *Lasiosphaeriaceae;* however, it is presently placed in *Sordariales* genera *incertae sedis* (Huang et al., 2021b; Wijayawardene et al., 2022). The asexual morph is hyphomycetous and phialophora-like and has small, oval to globose conidia. The sexual morph is

characterized by the perithecial, globose to subglobose, brown to black, carbonaceous, ostiolate ascomata with carbonaceous to membranaceous peridium, composed of black to pale brown to hyaline cells of *textura angularis* to *textura prismatica*. Asci are 8-spored, unitunicate, cylindrical, pedicellate, subapical globule and ascospores are biseriate, slightly curved, aseptate, multi-guttulate, hyaline and ellipsoidal when young becoming multi-septate, dark brown when mature, and bipolar short appendages are disappearing with age (Huang et al., 2021b). Species have been reported from plant debris and soil in Germany, India, UK and the USA (Nash & Pippin, 1981; Huang et al., 2021b).

Table 4.238*Eosphaeria* species isolated from soil

Species	Country	Habitat or soil type	References
Eosphaeria uliginosa	USA	Road and clay soils	Huang et al. (2021b)
E. uliginosa	Germany	Marshy lands	

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

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

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

Arthrinium Kunze, Mykologische Hefte (Leipzig) 1: 9 (1817)

Index Fungorum number: IF7214; Facesoffungi: FoF01781

Kunze and Schmidt (1817) initially introduced *Arthrinium* and the type species is designated as *A. caricicola*. Kwon et al. (2021) have used ITS, *tub2* and *tef-1α* combined phylogeny including 54 species while introducing eight new species in the genus. *Arthrinium* is accepted as anamorphic genus having basauxic conidiophores and the telemorph is linked to *Apiospora* (Hyde et al., 2020c). The genus has a wide host distribution where species associate with leaves, stems and roots of different plants in saprobic and endophytic modes, some have been reported as plant and human pathogens and have also been recorded from marine and soil habitats. It has a wide geographical distribution as well, including Brazil, China, India, Malaysia and the USA (Crous & Groenewald, 2013; Wang et al., 2018).

Table 4.239 *Arthrinium* species isolated from soil

Species	Country	Habitat or soil type	References
Arthrinium minutisporum	Korea	Mountain soil	Das et al. (2020c)
A. arundinis	China	Karst cave	Wang et al. (2018)
A. rasikravindrae	China	Karst cave	
A. xenocordella	Zimbabwe	Roadway	Crous and Groenewald (2013)

Nigrospora Zimm. Abt. II 8: 220 (1902)

Index Fungorum number: IF9124; Facesoffungi: FoF14273

Zimmerman (1902) introduced *Nigrospora* and was typified by *N. panici*. Currently, 35 species are present in the genus (Hyde et al., 2024c) and 33 of them are supported with the molecular data. The asexual morph is hyphomycetous with micronematons or semimacronematous conidiophores, monoblastic condiogenous cells, and black, shiny, aseptate condia. Sexual morph is characterized by perithecial ascomata, short-stalked asci with biseriated ascopsores Wang et al. (2017). *Nigrospora* has cosmopolitan distribution recorded from China, India, Indonesia, Germany, South Africa and the USA as endophytes, saprobes or pathogenes (human/plant) that occur on decaying and fresh plants, forest litter, human clinical samples and soil (Wang et al., 2017; Raza et al., 2019).

Table 4.240 *Nigrospora* species isolated from soil

Species	Country	Habitat or soil type	References
Nigrospora globose	China	Cave	Zhang et al. (2021c)
N. humicola	China	Garden soil	Zhang et al. (2024a)

Family: *Beltraniaceae* Nann.

Beltraniella Subram., Proc. Indian Acad. Sci., Sect. B 36: 227 (1952)

Index Fungorum number: IF7356; Facesoffungi: FoF05499

Subramanian (1952) introduced *Beltraniella* with the type speceis *B. odinae*. There are 30 species belong to this genus (Hyde et al., 2024c), while 11 are supported with the molecular data (ITS and LSU). The asexual morph possesses branched conidiophores having setiform apex and radially lobed basal cells. Conidiogenous cells are polyblastic and sympodial, producing acropleurogenous, turbinate or biconic conidia with a distinct hyaline transverse band (Subramanian, 1952). Species have been

isolated from fallen decomposing leaves, soil and submerged woods in freshwater and terrestrial habitats in tropical and subtropical regions of the world such as Australia, China, India, Peru, Puerto Rico, Thailand and the UK (Lin et al., 2017)

Table 4.241 *Beltraniella* species isolated from soil

Species	Country	Habitat or soil type	References
Beltraniella fertilis	Thailand	Forest soil	Yasanthika et al. (2020)

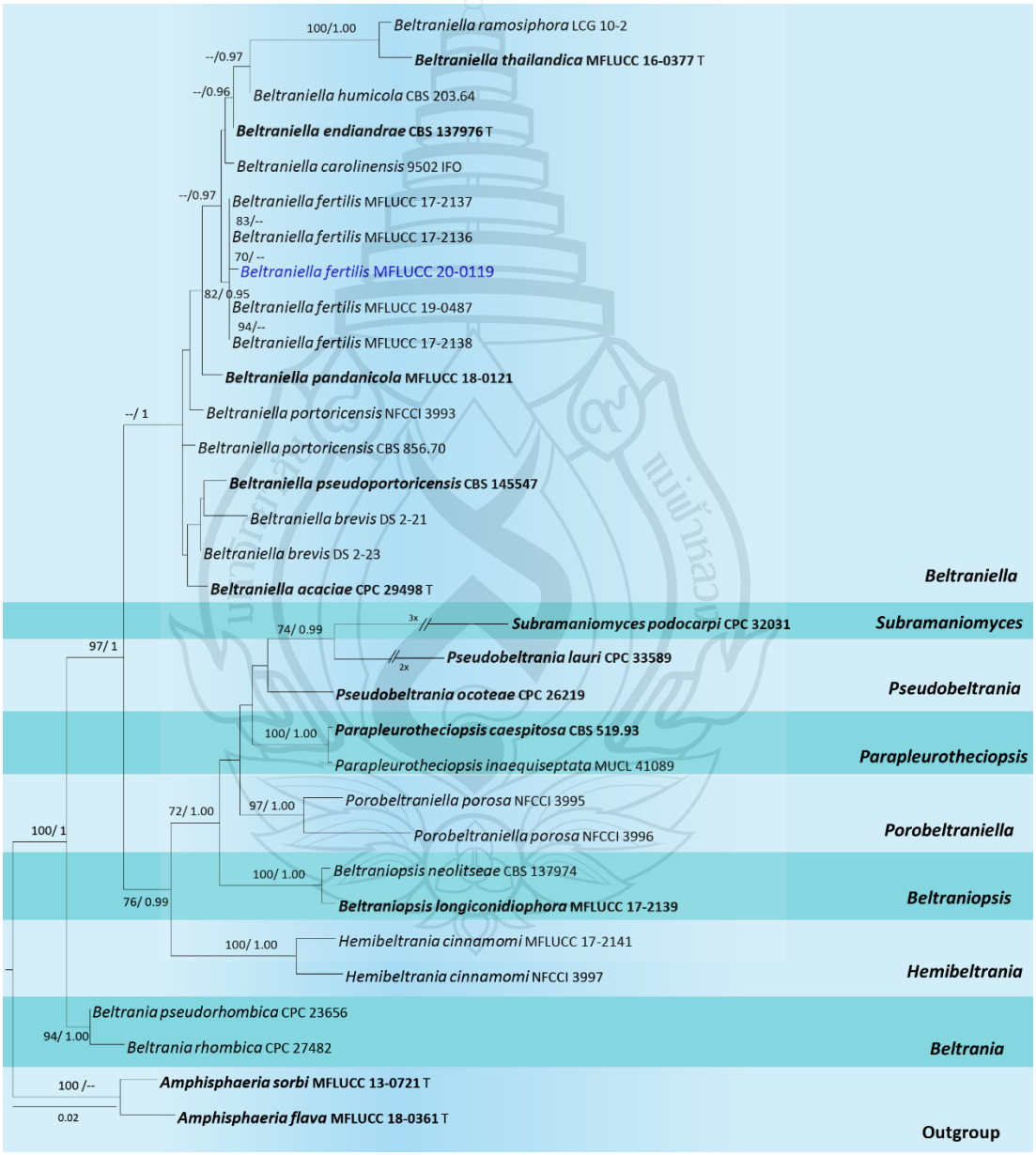


Figure 4.196 Maximum likelihood tree revealed by RAxML from an analysis of combined LSU-ITS matrix of *Beltraniella*

Figure 4.196, The tree showing the phylogenetic position of *Beltraniella fertilis* (MFLUCC 20-0119). ML bootstrap supports equal or greater than 60% and Bayesian posterior probabilities (PP) equal or greater than 0.95 are indicated above the nodes as (ML/ PP). The tree is rooted with *Amphisphaeria flava* (MFLUCC 18-0361) and *A. sorbi* (MFLUCC 13-0721). The ex-type strains are in bold and the new isolate of this study is in blue bold. The scale bar represents the expected number of nucleotide substitutions per site. The tree inferred from a RAxML analysis belonging to genera of Beltraniaceae (Fig. 4.196). The combined LSU and ITS alignment comprised 32 strains of Beltraniaceae, and the outgroup comprised two taxa; *Amphisphaeria flava* (MFLUCC 18-0361) and *A. sorbi* (MFLUCC 13-0721). The different alignments of each individual gene and a combined alignment of two genes were analyzed. A best scoring RAxML tree (Figure 4.196) has a final ML optimization likelihood value of –4404.133370. The matrix had 276 distinct alignment patterns, with 6.41 % of undetermined characters or gaps. Estimated base frequencies were as follows; A=0.252948, C=0.211572, G=0.267559, T=0.267921; substitution rates AC=1.018207, AG=2.648344, AT=1.489160, CG=0.752809, CT=6.303354, GT=1.000000; proportion of invariable sites I=0.672359; gamma distribution shape parameter α=0.612156. Both trees of ML and BYPP analyses were similar in topology at the generic relationships, which is in agreement with previous studies based on multi-gene phylogeny of Lin et al. (2017b) and Hyde et al. (2020). Our isolate *Beltraniella fertilis* (MFLUCC 20-0119) is cladded with *Beltraniella fertilis* (MFLUCC 17-2136, MFLUCC 17-2137, MFLUCC 17-2138, MFLUCC 19-0487) with 82%ML and 0.95 PP support.

Beltraniella fertilis Heredia, R.M. Arias, M. Reyes & R.F. Castañeda, Fungal Diversity 11: 100 (2002)

Figure 4.197

Index Fungorum number: IF489903

Faces of fungi number: FoF 03632

Culture characteristics — *Colonies* on PDA pale white, reaching a diam. of 2–3 cm in 4 days at 25°C, flat and circular-shaped, pale brown, smooth at surface and produce highly branched melanized hyphae with brownish exudates in old cultures,

after 16 weeks, with conidiophores forming on the mycelium; reverse light yellow to dark brown.

Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* mostly immersed in the substratum, composed of septate, branched subhyaline hyphae. *Setae* numerous, erect, arising from radially lobed, dark brown, swollen, basal cells, straight or flexuous, unbranched, single or in small groups, thick-walled, verrucose, dark brown at the base, paler at apex, 61.7–149.8 μm long, 2.5–7 μm wide ($\overline{x}$ = 113 × 4 μm, n = 30) at the base, tapering to a pointed apex, arising from a dark brown, swollen, radially lobed cell. *Conidiophores* macronematous, sometimes setiform; single, straight, septate, partly verrucose, thick-walled, smooth-walled, 6.4–91.5 μm long, 2.3–6.5 μm wide ($\overline{x}$ = 37 μm × 3.4, n =30), sometimes branched at the apical region, dark brown to sub hyaline at the swollen base, paler and slightly tapering towards a pointed apex. *Conidiogenous cells* holoblastic, monoblastic to polyblastic, integrated, terminal. *Conidia* solitary to aggregated, acrogenous, simple, dry, straight, smooth, thin-walled, biconic, turbinate to pyriform, rostrate to pointed at proximal end, truncate at distal end, hyaline to sub hyaline with a hyaline supra-equatorial transverse band, 5–15 μm long, 2–6.5 μm wide ($\overline{x}$ = 10.11 × 3.97 μm, n = 30) in the broadest part.

Distribution — Atlantic forests, Brazil, Mexico, Thailand

Known hosts — Dead leaves of *Mangifera indica* and *Parinari alvimii*

Material examined — THAILAND, Chiang Mai Province, Mae Tang district, Ban Pa Deng, Mushroom Research Center, in forest soil (dominated by Dipterocarpaceae), 20th March 2019, Erandi Yasanthika, Erscm11 (MFLU 20-0506), living culture MFLUCC 20-0119.

Notes — *Beltraniella fertilis* was introduced by Heredia et al. (2002) based on morphological characteristics. The sequence data for this species was provided by Lin et al. (2017b) including strains MFLUCC 17-2136, MFLUCC 17-2137 and MFLUCC 17-2138 isolated from decaying leaves collected in Thailand. Most of *Beltraniella* strains in GenBank have only ITS and LSU sequence data. In the combined phylogenetic tree (LSU-ITS) of Beltraniaceae (Figure 3.13), species delineation within *Beltraniella* have low bootstrap support. Resulting low bootstrap support can be due to a lack of protein coding gene sequences or else *B. fertilis* may be a species complex

(Jeewon & Hyde, 2016). *Beltraniella fertilis* strains in GenBank (MFLUCC 17-2136, MFLUCC 17-2137, MFLUCC 17-2138 and MFLUCC 19-0487) and our isolate (MFLUCC 20-0119) clustered with good support (ML=82%, PP=0.95) in the phylogenetic tree. Our strain (MFLU 20-0506) has similar characteristics to the holotype of *B. fertilis* (CB712XAL) in having numerous setae in the colony, setiform conidiophores and solitary to aggregated, acrogenous, simple, dry, straight, smooth, thin-walled, biconic, turbinate to pyriform, rostrate to pointed at proximal end, truncate at distal end, hyaline to sub-hyaline conidia. Hence, we report this collection as *B. fertilis* from forest soils in Thailand.

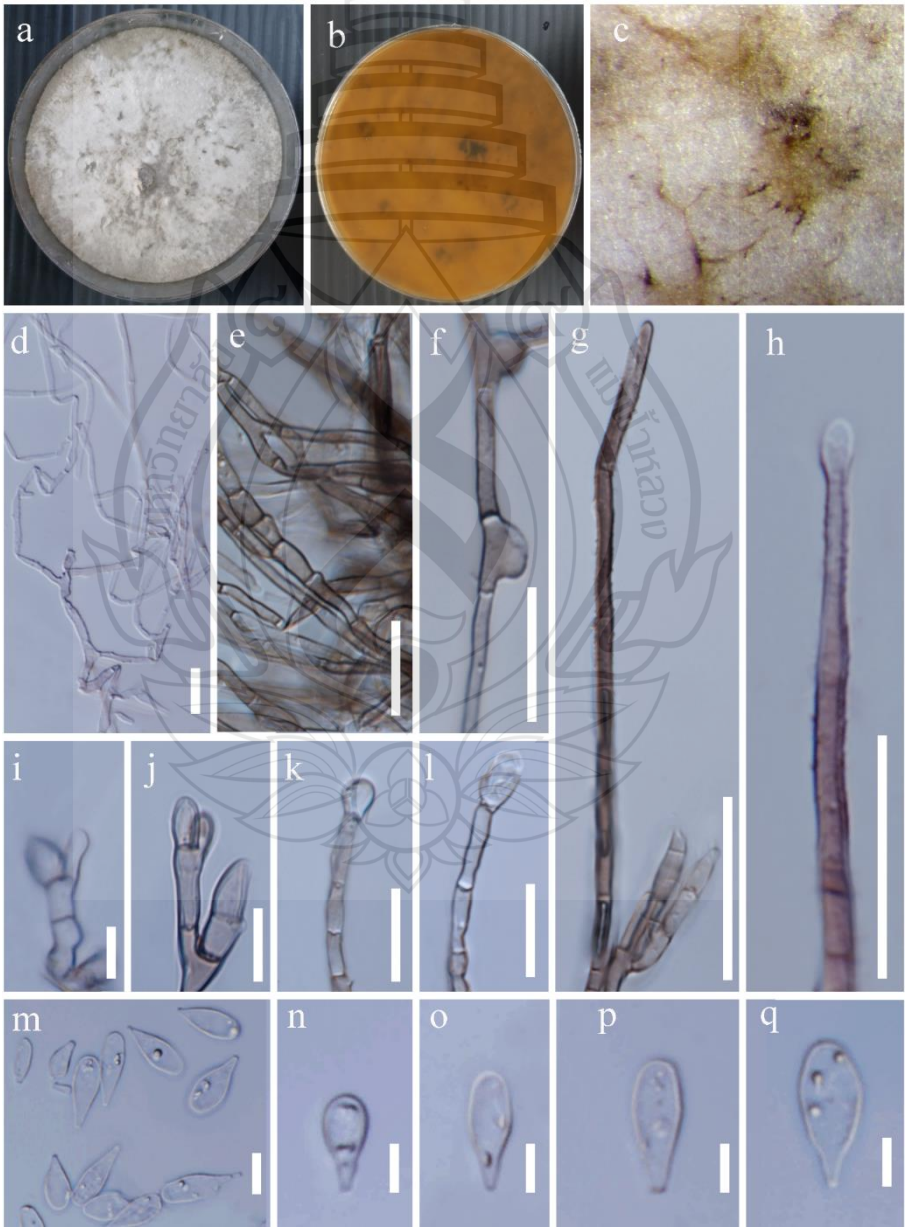


Figure 4.197 *Beltraniella fertilis* (MFLUCC 20-0119)

Figure 4.197, a Mature colony on PDA after 16 weeks with the sporulation b Reverse of the colonies on PDA after 16 weeks c Sporulation of the colony with conidial attachments on the mycelium. d Immature aseptate hyphae. e Mature pigmented, septate hyphae. f Chlamydospores on the mycelium. g Verrucose pigmented setae arising from the mycelium. h Conidiogenesis on the setae. i–l Conidiogenesis on the conidiophore. m–q Conidia. Scale bars: d, g, h, i = 20 μm, e, f, j, k, l, m = 10 μm, n–q = 5 μm

Family: *Sporocadaceae* Corda

Bartalinia Tassi, Bulletin Labor. Orto Bot. de R. Univ. Siena 3: 4 (1900)

Index Fungorum number: IF7327; Facesoffungi: FoF00659

Bartalinia was established by Tassi (1900) while designating *B. robillardoides* as the type species. Currently, 25 species are listed in the genus (Species Fungorum, 2025), and only 10 have molecular data. The asexual morph is characterized by the 3–4-septate conidia (Nag Raj, 1993). Species have wide distribution around the world where they have been found as saprobes and associated with leaf spots from various plants.

Table 4.242 *Bartalinia* species isolated from soil

Species	Country	Habitat or soil type	References
Bartalinia sp.	Thailand	ND	Manoch (1987)

Broomella Sacc., Syll. fung. (Abellini) 2: 557 (1883)

Index Fungorum number: IF658; Facesoffungi: FoF00626

Saccardo (1883) introduced *Broomella* with its type species *B. vitalbae*. It currently comprises 15 species (Species Fungorum, 2025), however only 3 have been supported with the molecular data. The asexual morph of the genus is pestalotia-like (Hyde et al., 2020c; Wanasinghe et al., 2018b) while the sexual morph has cylindric-elongate, unitunicate asci and J-, discoid apical ring, bearing 2-3-septate, ellipsoid to fusiform ascospores with brown, median and hyaline, terminal cells bearing centric appendages at each end (Liu et al., 2019a) *Broomella* has been explored as saprobes occurring on dead leaves, stems, wood and soil found from Australia, Ecuador, France, Great Britain, Italy, Pakistan and the Philippines (Hyde et al., 2020c).

Table 4.243 *Broomella* species isolated from soil

Species	Country	Habitat or soil type	References
Broomella sp.	Australia	Wheat-field	Walker (1984)

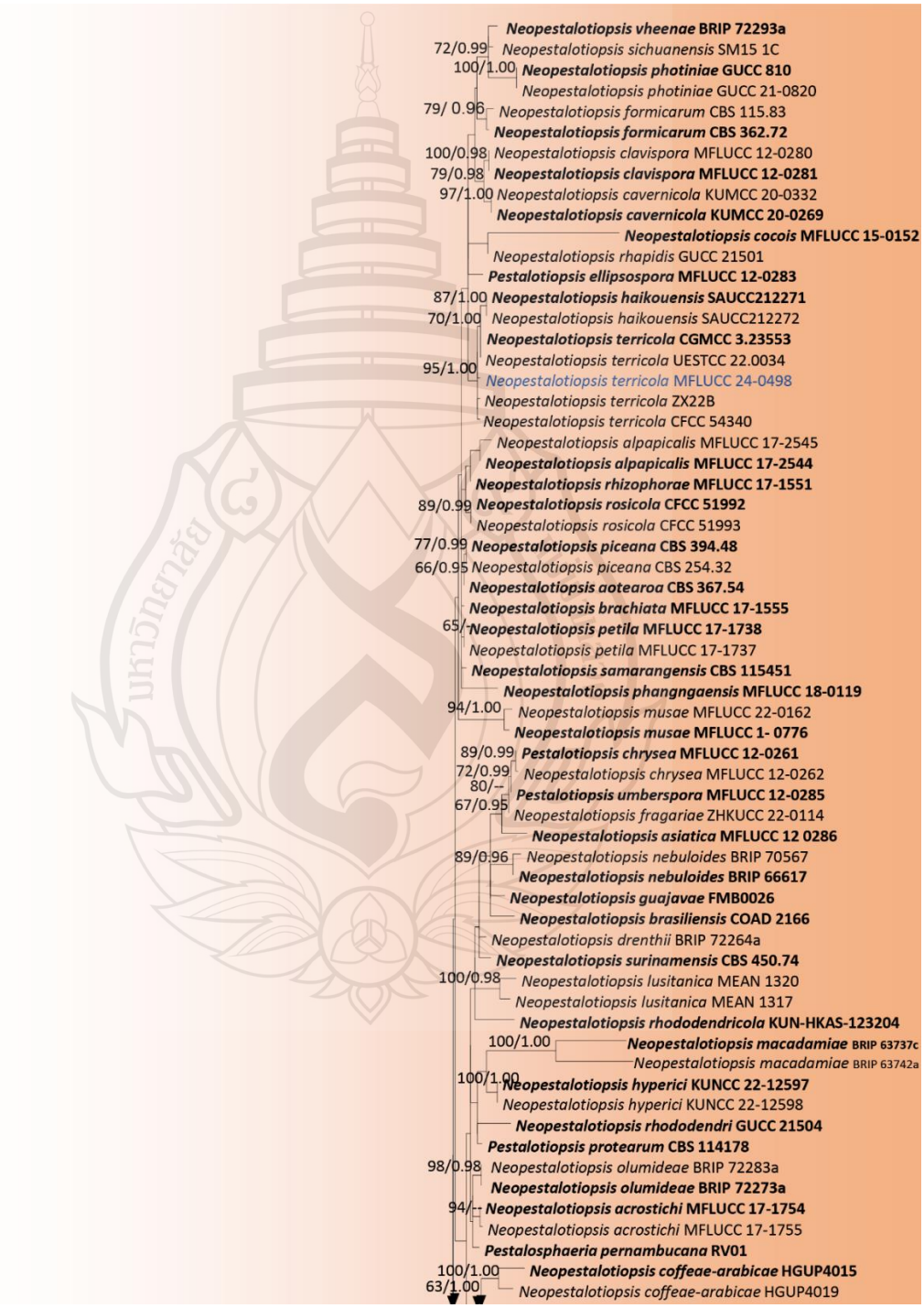


Figure 4.198 The best scoring maximum likelihood tree generated of the combined ITS, *tub2* and *tef1-α* sequence data for *Neopestalotiopsis*

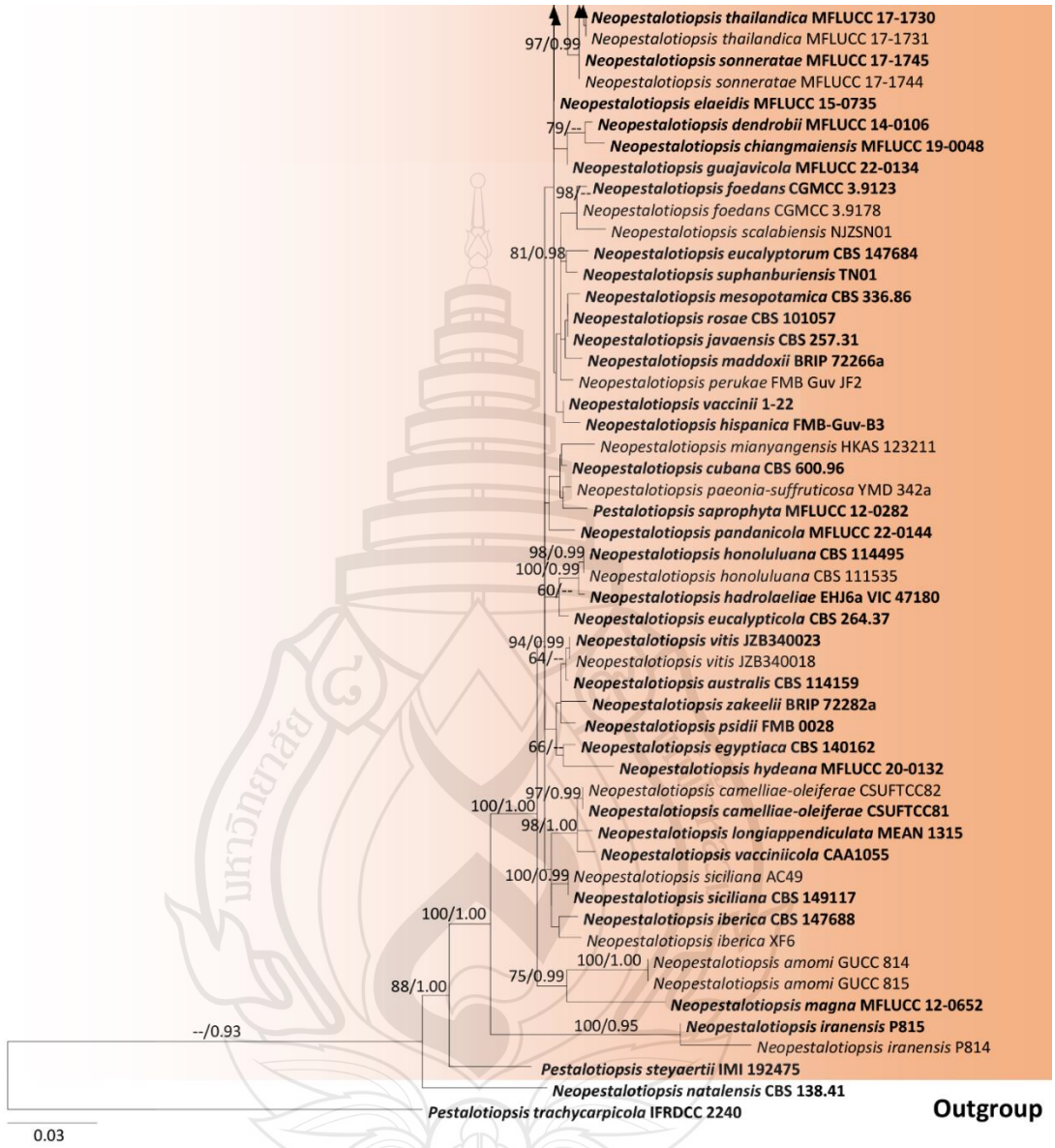


Figure 4.198 (continued)

Figure 4.198, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue and ex-type strains are in bold. The tree is rooted to *N. natalensis* (CBS138.41) and *P. trachicarpicola* (IFDRCC 2240). The topology and clade stability of the combined gene tree are compared with the single

gene analyses. The approximate length of the combined alignment is 1049 bp, and single gene alignments are ITS: 592 bp, tef1-α: 565bp and TUB: 445 bp.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous, Stud. Mycol. 79: 135 (2014) Index

Index Fungorum number: IF 809759, Facesoffungi number: FoF **.

Neopestalotiopsis was introduced by Maharachchikumbura et al. (2014) using ITS, *tub2* and *tef1-α* phylogeny and the morphology and *N. protearum* is designated as the type species. Razaghi et al. (2024) used LSU, ITS, *tef-1α*, *tub2*, and *rpb2* multigene phylogeny including 117 *Neopestalotiopsis* species while revising the genus and introducing 20 species. The asexual morph is chracaterized by acervular or pycnidial, subglobose, globose, clavate, solitary or aggregated, dark brown to black, immersed to erumpent, unilocular or irregularly plurilocular conidiomata; exuding dark brown to black conidia in a slimy, globose mass. Conidiophores are indistinct, often reduced to conidiogenous cells which are discrete, cylindrical, ampulliform to lageniform, hyaline, smooth, thin-walled with initially holoblastic conidiogenesis becoming percurrent. Conidia are fusoid, ellipsoid to subcylindrical, straight to slightly curved, 4-septate. Having conic to sub-cylindrical hyaline or pale brown to olivaceous, thin and rugose to smooth-walled basal cell that has truncate base, basal appendage single, tubular, unbranched, centric; three median cells doliiform, wall rugose to verruculose, versicoloured, septa darker than the rest of the cell; and hyaline, conic to cylindrical, thin- and smooth-walled apical cell with tubular apical appendages, one to many, filiform or attenuated, flexuous, branched or unbranched; (Maharachchikumbura et al., 2014). The species can be endophytes, saprobes, human and animal pathogens that have been recorded from air, dead and living plant parts (leaves and wood), fabrics and soil (Senanayake et al., 2020). The genus is distributed in Australia, China, Iraq, Iran, India, Pakistan, Portugal, Thailand and the USA (Maharachchikumbura et al., 2014; Razaghi et al., 2024).

Table 2.244 *Neopestalotiopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Neopestalotiopsis surinamensis	Suriname	Soil under *Elaeis guineensis*	Maharachchikumbura et al. (2014)

Neopestalotiopsis terricola W.L. Li & Jian K. Liu, Journal of Fungi 8 (11, no. 1175): 14 (2022)

Figure 4.199

Index Fungorum number: IF 833025

Sexual morph: Undetermined. Asexual morph: *Conidiomata* solitary, globose, semi-immersed, black. *Conidiophores* 2.5–6 × 1–4 µm ($\overline{x}$ = 4 × 2 µm, n=10) or sometimes reduced to conidiogenous cells. *Conidiogenous cells* 5.5–9 × 4.5–8 µm ($\overline{x}$ = 7 × 6 µm, n=10), hyaline, mostly integrated, ampulliform to lageniform, single, truncated apex, smooth-walled. *Conidia* 15–21 × 5–8 µm ($\overline{x}$ = 18 × 6 µm, n = 30), fusoid, ellipsoid, mostly straight, 4-septate; apical cell 2–3 µm ($\overline{x}$ = 2.5 µm) long, hyaline, cylindrical to sub-cylindrical, thin and smooth-walled with three apical tubular appendages, arising from the upper half of the apical cell just below the crest with different locus, unbranched, filiform, 7–19 µm ($\overline{x}$ = 11 µm) long; three medial cells hyaline to light brown to dark, thick walled, sometimes second cell from base paler than other medial cells; basal cell 2–4.5 µm ($\overline{x}$ = 3 µm) long, hyaline, conical to obconical, truncated base, thin walled, with basal appendix; single basal appendix, tubular, unbranched, centric, 2–3 µm ($\overline{x}$ = 2.5 µm).

Culture characteristics – *Colonies* on PDA at 25°C, become 2–3 cm diameter after 7 days, white and sparse mycelium densely grown when mature, conidial masses and conidiomata appear in black spots, reverse yellowish-white. raised, circular filiform margined. *Hyphae* superficial to semi-immersed hyaline septate, smooth-walled, 2.1–3.9 µm ($\overline{x}$ = 3 µm).

Material examined: Thailand, Chiang Mai, Mae Taeng District, Mushroom Research Centre, Forest, 19.2145N, 98.5953E, 1440m, 17, February 2019 W.A. Erandi Yasanthika (MFLU25-0125); living culture 122-CML4= MFLUCC 24-0498.

GenBank numbers – MFLUCC 24-0498: ITS: PQ570526, BTUB: PV611462

Notes– The multigene phylogeny of *Neopestalotiopsis* (Figure 4.198) shows that our strain (MFLUCC 24-0498) clusters with *N. terricola* with 95% ML, 1.00 BYPP statistical support. Our isolate resembles to *N. terricola* by having solitary, globose, semi-immersed, black conidiomata and hyaline, mostly integrated, ampulliform to lageniform,

single, truncated apex conidiogenous cells. Conidial morphology of our strain is similar to *N. terricola* by fusoid, ellipsoid, mostly straight, 4-septate conidia with three apical tubular appendages, and basal appendix (Li et al., 2022a). We confirm our species as *N. terricola* based on the morpho-molecular results. *Neopestalotiopsis terricola* was introduced by Li et al. (2022) from dead-diseased branch of *Paeonia suffruticosa* in China. This is the first record of *N. terricola* inhabiting in soil, that was collected in Thai forest.

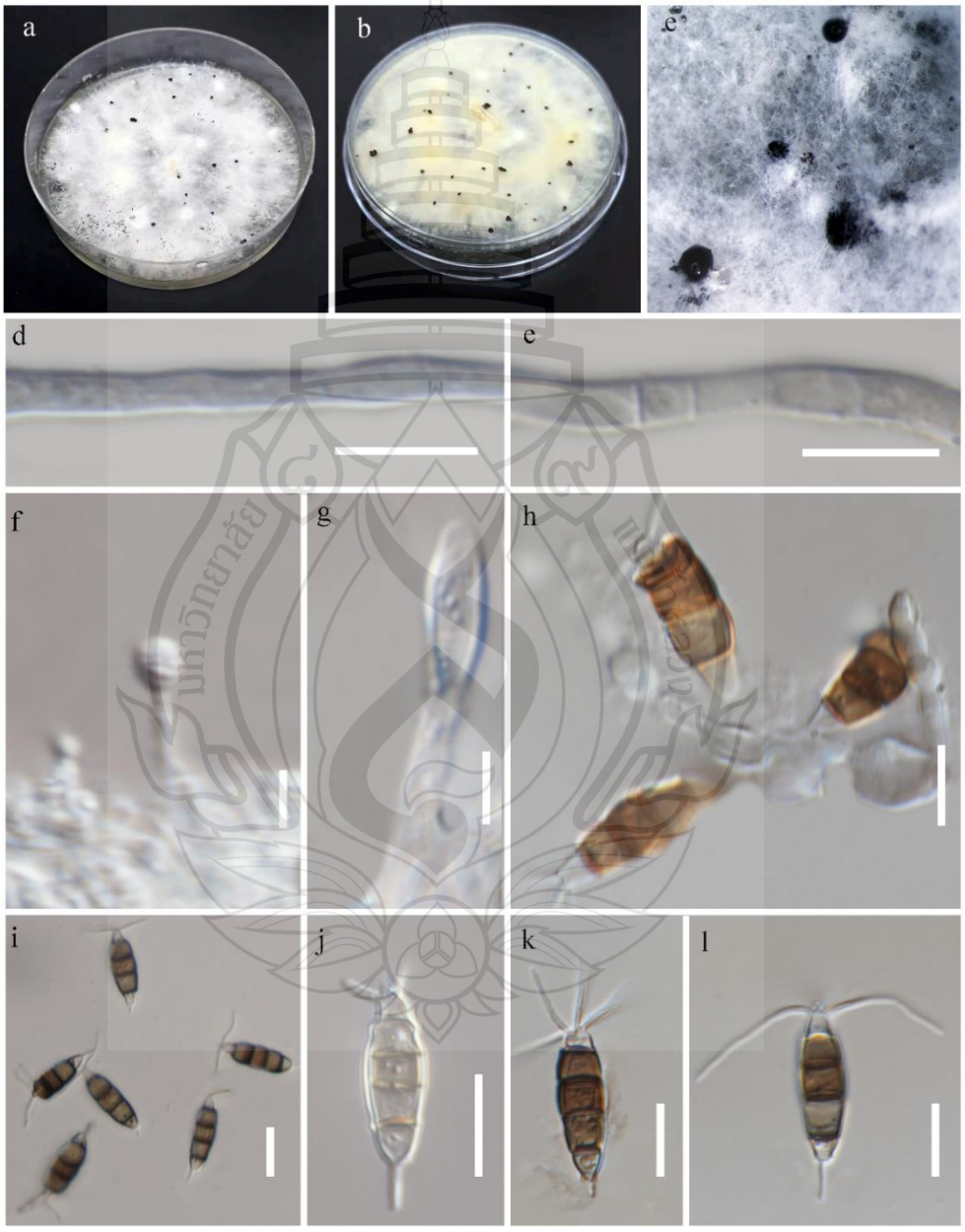


Figure 4.199 *Neopestalotiopsis terricola* (MFLU25-0125)

Figure 4.199, a, b Culture characters on the PDA (b = reverse). c Sporulated colony. d, e hyphae. f–h Conidiogenesis i–l Conidia. Scale bars: d, e, h–l = 10 μm, f, g = 5 μm

Robillarda Sacc., Michelia 2(no. 6): 8 (1880)

Index Fungorum number: IF22470; Facesoffungi: FoF01688

Saccardo (1880) erected *Robillarda* with the type species *R. sessilis*. *Robillarda* comprises 20 species while nine are supported with the molecular data. The asexual morph possesses solitary or gregarious, scattered, subglobose, unicellular, immersed, ostiolate, glabrous pycnidia and holoblastic conidiogenous cells that are sympodially or percurrently proliferating near the apex. Conidia are septate with flexuous, narrow and tubular polar appendages (Nattawut et al., 2012). Species occur on plant leaves, branches and stems from aquatic and terrestrial habitats and soils in China, France, Germany, India, Italy, Romania and Thailand (Dissanayake et al., 2024; Nattawut et al., 2012).

Table 4.245 *Robillarda* species isolated from soil

Species	Country	Habitat or soil type	References
Robillarda sp.	Thailand	ND	Manoch (1998)

Order: *Xylariales* Nannf.

Family: *Coniocessiaceae* Asgari & Zare

Coniocessia Dania García, Stchigel, D. Hawksw. & Guarro, Mycol. Res. 110(11): 1284 (2006)

Figure 4.200

Index Fungorum number: IF29049; Facesoffungi: FoF01297

Coniocessia was introduced by García et al. (2006) with the type species *C. nodulisporioides* by using morphology and LSU phylogeny. Based on ITS and LSU phylogeny, Asgari and Zare (2011) introduced *Coniocessiaceae* to accommodate *Coniocessia*. Currently, it comprises 5 species (Species Fungorum 2025), all of which have molecular data. The asexual morph is characterized by the hyaline, micronematous to macronematous, simple or branched, smooth-walled or verrucose conidiophores, and hyaline, sympodially elongating conidiogenous cells that produce hyaline, globose, subglobose to pyriform conidia. The sexual morph is characterized by the non-

stromatic, superficial, globose, subglobose to pyriform glabrous, ostiolate ascomata, and 4-spored, cylindrical to subcylindrical, non-amyloid asci with ellipsoidal or fusiform, dark brown to black ascospores (Asgari & Zare, 2011). Species have been recorded from Iran, Jordan and Spain from dung, wheat seeds, straw and soil (Asgari & Zare, 2011; García et al., 2006).

Table 4.246 *Coniocessia* species isolated from soil

Species	Country	Habitat or soil type	References
Coniocessia nodulisporioides	Jordan	ND	Asgari and Zare (2011)

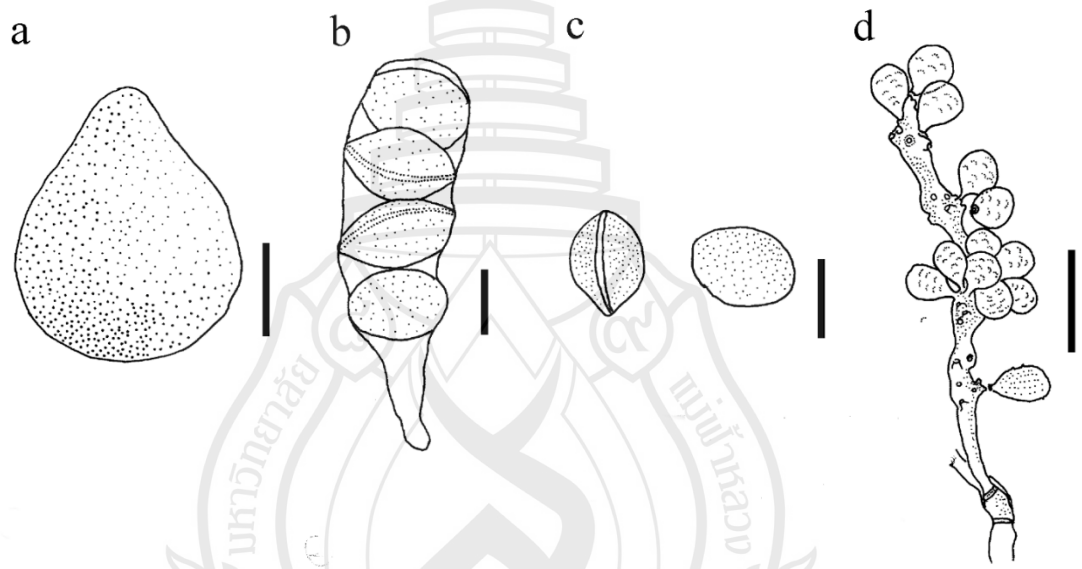


Figure 4.200 *Coniocessia nodulosporoides*

Figure 4.200, a Ascoma b Ascus c Ascospores d Conidiophore, conidiogenous cells, and conidia. Scale bars: a = 100 μm, b–d = 10 μm. Redrawn from Guarro et al. (2012).

Family: *Hansfordiaceae* Crous

Hansfordia S. Hughes, Mycol. Pap. 43: 15 (1951)

Index Fungorum number: IF8423

Hansfordia was introduced by Hughes (1951) accommodating *H. ovalispora* as the type species. Crous et al. (2019) introduced *Hansfordiaceae* to accommodate *Hansfordia* by using the LSU and ITS combined phylogeny. The genus presently accommodates 13 species (Species Fungorum, 2025), however, only two of them have

molecular data. The asexual morph is characterized by the superficial or setiform, solitary, erect, multi-septate with lateral branches, surface smooth, straight to flexuous, light brown conidiophores and hyaline, cylindrical or clavate, with subdenticulate apical loci conidiogenous cells that produce solitary, dry, aseptate, hyaline to pale brown, globose, ellipsoid to fusoid, smooth-walled or finely roughened conidia and the sexual morph is undetermined (Hyde et al., 2020c). Species have been isolated as saprobes, endophytes and lichenized fungi, from dead stems, leaves, litter and soils in Congo, China, Great Britain, Indonesia, Italy and the USA(Changtian et al., 2022; Crous et al., 2019). However, pathogenicity or toxicity has not been reported (Changtian et al., 2022).

Table 4.247 *Hansfordia* species isolated from soil

Species	Country	Habitat or soil type	References
Hansfordia rosea	China	Forest soil	Wu et al. (2015a)

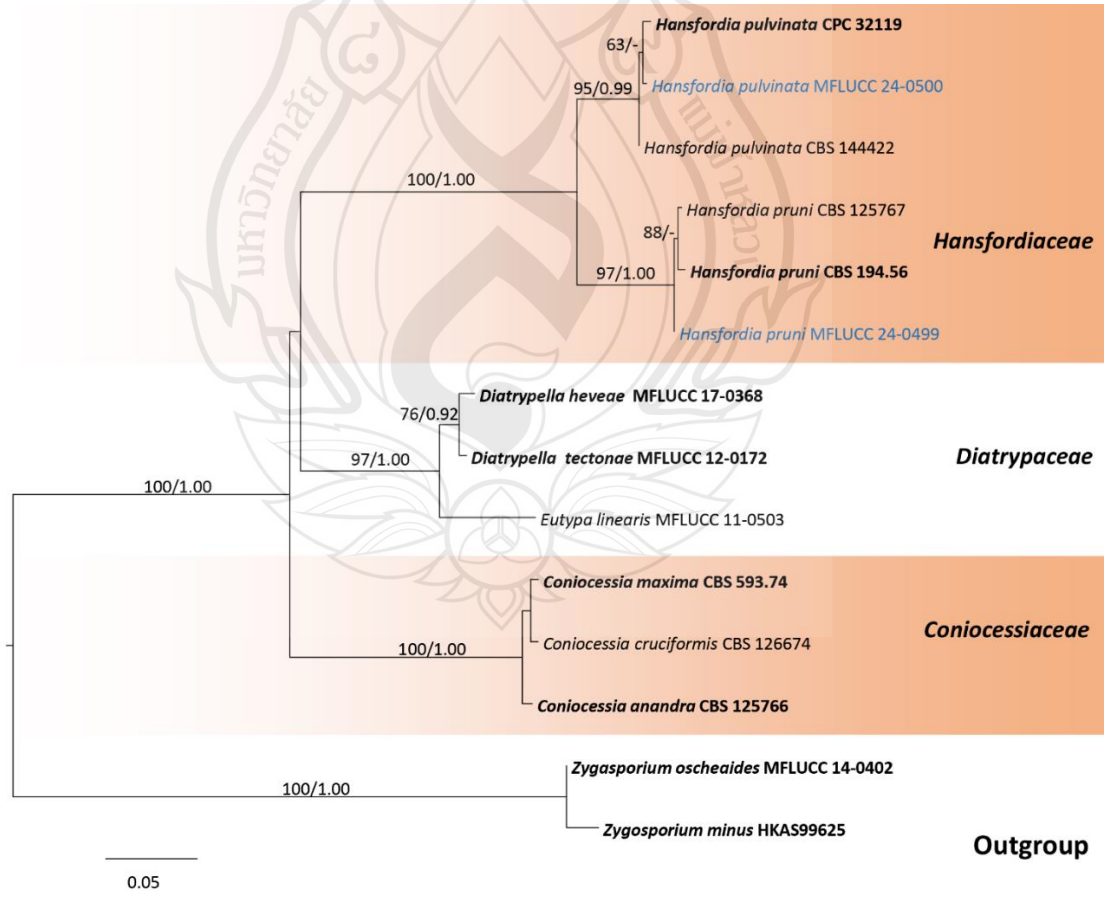


Figure 4.201 The best scoring maximum likelihood tree generated of the combined ITS sequence data for *Xylariales*

Figure 4.201, Bootstrap support values of maximum likelihood greater than 60% and Bayesian posterior probabilities (BYPP) greater than 0.90 are indicated above the nodes. Newly added strains are in blue and ex-type strains are in bold. The tree is rooted to *Zygasporium oscheaides* (MFLUCC 14-0402) and *Z. minus* (HKAS99625). The topology and clade stability of the combined gene tree are compared with the single gene analyses. The approximate length of the ITS alignment is 550 bp. The matrix had 209 distinct alignment patterns with 13.56% undetermined characters and gaps. Estimated base frequencies were as follows; A = 0.250, C = 0.250, G = 0.250, T = 0.250; substitution rates AC = 1.87336, AG = 2.59063, AT = 1.87336, CG = 1.00000, CT = 4.80167, GT = 1.00000; gamma distribution shape parameter α = 0.453.

Hansfordia pruni Crous, Fungal Systematics and Evolution 3: 84 (2019)

Figure 4.202

Index Fungorum number: IF 829306, Faces of Fungi number: FoF 16721

Sexual morph: Undetermined. Asexual morph: *Conidiophores* 36–44 × 1.5–2 µm ($\bar{x}$ = 39 × 2 µm, n=15), solitary, mostly erect, with lateral branches in upper half, hyaline, smooth to verucose, sometimes multi-septate. *Conidiogenous cells* 0.7 –1.5 × 0.9–2.5 µm, ($\bar{x}$ = 1 × 1.5 µm, n=10), holoblastic, hyaline, subcylindrical, tapering towards apices. *Conidia* 4.5–5.5 × 4.5–5.5 µm ($\bar{x}$ = 5 × 5 µm, n = 25), aseptate, solitary, dry, globose to subglobose, hyaline, smooth-walled.

Culture characteristics – *Colonies* on PDA at 25°C, become 3–4 cm diam. after seven days, white become yellowish white when mature, reverse brownish yellow in the center, bright yellow at the middle ring and whitish yellow at the periphery, flat, cottony surface, undulate margined. *Hyphae* superficial to semi -immersed, hyaline to pale brown, aseptate to septate, smooth-walled, 1.5–4 µm ($\bar{x}$ = 2 µm, n=30).

Material examined: Thailand, Chiang Rai, Buddha Cave (What Tham Phra), 99.788928N, 19.9175247E, 425m, 21 June 2021, W.A. Erandi Yasanthika (MFLU25-0173); living culture 42-cv5-606 =MFLUCC 24-0499.

GenBank numbers –MFLUCC 24-0499: ITS: PQ570527

Notes–As shown in Figure 4.184, our strain (MFLUCC 24-0499) clusters with *Hansfordia pruni* (CBS 125767, CBS27651) with 100% ML, 1.00 BYPP statistical support. Each gene region of our strain was compared with the type species, and resulted in having 100% similarity. *Hansfordia pruni* is morphologically comparable with our isolate in having solitary, mostly erect, smooth to verrucose, sometimes multi-septate conidiophores and conidiogenous cells that are subcylindrical and tapering towards apices. Our strain is similar in conidial morphology by aseptate, solitary, dry, globose to subglobose and smooth-walled conidia (Crous et al., 2019). Morphology and multi-gene phylogeny confirm that our strain is *H. pruni*. *Hansfordia pruni* was introduced from *Prunus persica* twigs in Italy (Crous et al., 2019). This study provides the first record of the species from soil which was isolated in disturbed-cave in Thailand.

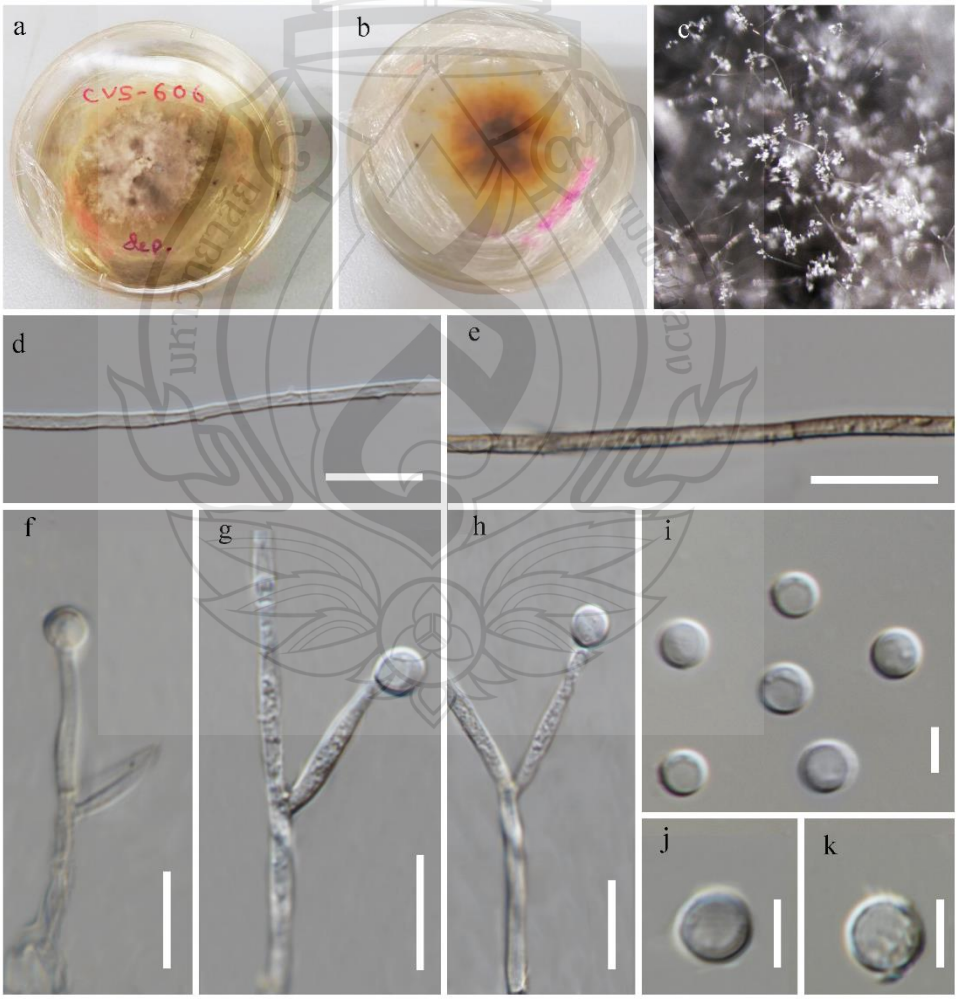


Figure 4.202 *Hansfordia pruni* (MFLU25-0173)

Figure 4.202, a, b Culture characters on PDA (b = reverse). c Sporulated colony with conidial attachments on the mycelium. d, e hyphae. f–h Conidiophores i–k Conidia. Scale bars: d, e = 20μm, f–h = 10 μm, i–k = 5μm.

Hansfordia pulvinata (Berk. & M.A. Curtis) S. Hughes, Canad. J. Bot. 36: 771. 1958.

Figure 4.203

Index Fungorum number: IF 298125, Facesoffungi number: FoF 16720

Sexual morph: Undetermined. Asexual morph: *Conidiophores* 37.3–47 × 2–3.5 μm. ($\overline{x}$ = 41.6 × 2.4 μm, n=15), solitary, erect to flexuous, unbranched or branched, hyaline, multi-septate, macronimatous, mononematous, smooth to verrucose, *Conidiogenous cells* 0.5–1.2 × 0.5–1.1 μm ($\overline{x}$ = 0.9 × 0.8 μm, n=10), subcylindrical, holoblastic, tapering towards the apices, hyaline. *Conidia* 5.3–4.6 μm × 51–4.1 μm ($\overline{x}$ = 4.8 × 4.6 μm, n = 25) hyaline, solitary, dry, globose, finely roughened, thick-walled.

Culture characteristics – *Colonies* on PDA at 25 °C, become 3–4 cm diam. after seven days, yellowish-white become brown when mature, reverse yellowish become dark brown to black when mature, flat, undulate filiform margined. *Hyphae* superficial to semi -immersed hyaline to pale brown, aseptate to septate, smooth-walled to verrucose, 1–2.2 μm ($\overline{x}$ = 1.6, n=20).

Material examined: Thailand, Chiang Rai, Buddha Cave (What Tham Phra), 99.788928N, 19.9175247E, 425m, 21 June 2021, W.A. Erandi Yasanthika (MFLU25-0174); living culture 40-cv5-602= MFLUCC 24-0500.

GenBank numbers – MFLUCC 24-0500: ITS: PQ570528

Notes–Based on phylogeny of *Xylariales* (Figure 4.184), our strain (MFLUCC 24-0500) grouped with *H. pulvinata* with 98% ML, 0.97 BYPP support. Comparing each gene region of our strain with *H. pulvinata* resulted in 100% similarity. Morphologically, *H. pulvinata* and our isolate has similar characteristics such as solitary, erect to flexuous, unbranched or branched conidiophores, subcylindrical conidiogenous cells tapering towards the apices and hyaline, solitary, dry, globose, finely roughened conidia (Huges, 1951). This species was introduced by Huges (1951) as fungicolus (Deighton, 1972), and has later been reported from *Macrozamia miquelii* in Australia (Crous et al., 2019). Based on morphology and multi-gene phylogeny we

confirm our species is *H. pulvinata* and it becomes the first strain to associate with soil habitats.

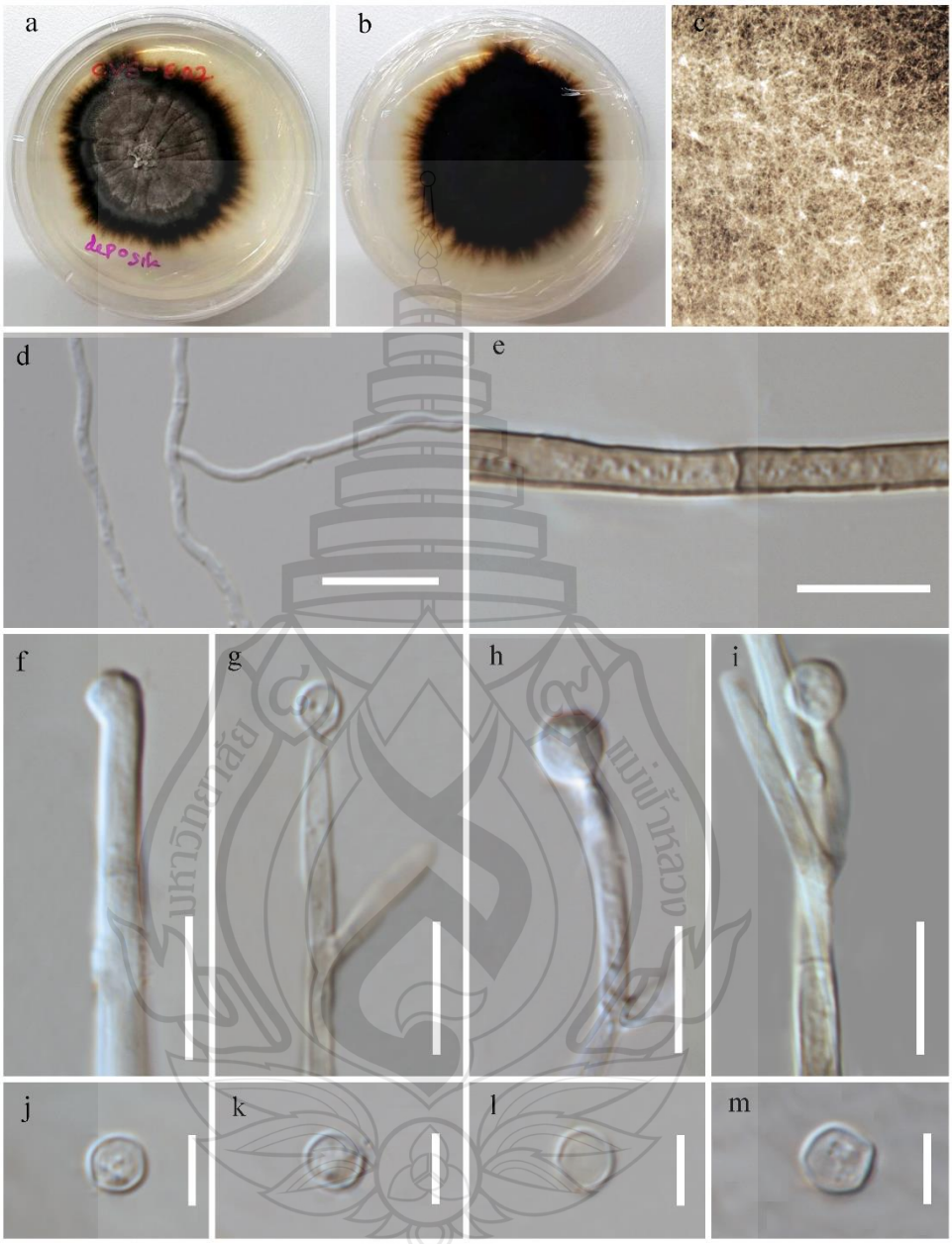


Figure 4.203 *Hansfordia pulvinata* (MFLU25-0174)

Figure 4.203, a, b Culture characters on PDA (b = reverse). c Sporulated colony with conidial attachments on the mycelium. d,e hyphae. f–i Conidiophores j–m Conidia. Scale bars: d–I = 10 μm, j–m = 5 μm.

Family: ***Microdochiaceae*** Hern.-Restr., Crous & J.Z. Groenew.

Idriella P.E. Nelson & S. Wilh., Mycologia 48: 550. (1956)

Figure 4.204

Index Fungorum number: IF8625; Facesoffungi: FoF06783

Nelson and Wilhelm (1956) introduced *Idriella* and *lunata* is accepted as the type species. Based on LSU, ITS, *tub2* and *rpb2* gene regions, Hernández-Restrepo et al. (2016a) provided phylogenetic re-evaluation for *Idriella*. Currently, there are 26 species listed in the Species Fungorum (2025), but only four have molecular data. The asexual morph is hyphomycetous and consists of brown, non-septate conidiophores with polyblastic, terminal, denticulate, lageniform to cylindrical conidiogenous cells, and dry, hyaline, unicellular, smooth, lunate, curved conidia. Sexual morph remains undetermined (Hernández-Restrepo et al., 2016a; Hyde et al., 2020c). The genus reported from Australia, Canada, China, Cuba, India, Japan, South Korea, Mexico, the Netherlands and the USA, that are inhabiting in dead leaves, roots and soil (Hyde et al., 2020c; Zhang et al., 2024b).

Table 4.248 *Idriella* species isolated from soil

Species	Country	Habitat or soil type	References
Idriella chlamydospora	China	A university land	Zhang et al. (2023e)
I. multiformispora	USA	A university land	
I. lunata	The Netherland	ND	Hernández-Restrepo et al. (2016a)
I. variabilis	China	Wildlife park	Zhang et al. (2024b)

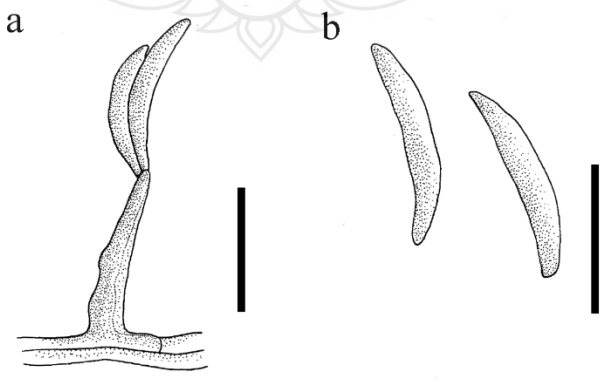


Figure 4.204 *Idriella lunata*

Figure 4.204, a Conidiogenesis on the conidiophore. b Conidia. Scale bars: a, b = 10μm. Redrawn from Hernández-Restrepo et al. (2016a).

Microdochium Syd. & P. Syd., Annls mycol. 22(3/6): 267 (1924)

Index Fungorum number: 8926; Facesoffungi: FoF02121

Microdochium was introduced by Sydow (1924), and it is typified by *M. phragmitis*. Based on LSU phylogeny, Hernández-Restrepo et al. (2016a) introduced *Microdochiaceae* and accommodated *Microdochium* as the type genus. Currently, 60 species are present in the genus (Species Fungorum 2025), and the molecualar data is available for 38 species. The asexual moprh of this genus is characterized by the hyphomycetes that are more or less verticillate, often slightly differentiated conidiophores reduced to conidiogenous cells that are hyaline, holoblastic, solitary or aggregated in small sporodochia, producing unicellular or multiseptate, hyaline, lunate, falcate, fusiform, filiform, obovoid or subpyriform conidia with dry or slimy mass. The sexual morph has perithecial, immersed, solitary or in groups, pale brown to black, globose, sub globose to oval, ostiolate ascomata. Asci are unitunicate, obolong to clavate, bi to multiseriate, and ascospoeres are hyaline to brown, clavate, fusoid or obolong and septate (Hernández-Restrepo et al., 2016a). They are economically important plant pathogens that cause microdochium patch, seedling blight, tar spot disease, scald disease, root and necrosis in cereals and grasses (Gao et al., 2022; Hyde et al., 2020c). They can be endophytes and saprobes from aquatic environments, cereals, leaves and soil, reported mostly in Europe and Asia. Bioactive compounds have been discovered from this genus that can be used against plant pathogenic fungi and human and animal diseases (Gao et al., 2022).

Table 4.249 *Microdochium* species isolated from soil

Species	Country	Habitat or soil type	References
Microdochium trichocladiopsis	ND	Rhizosphere of *Triticum aestivum*	Hernández-Restrepo et al. (2016a)
M. salmonicolor	Korea	Forest soil	Das et al. (2020b)

Family: ***Xylariaceae*** Tul. & C. Tul.

Ascotricha Berk., Ann. nat. Hist., Mag. Zool. Bot. Geol. 1: 257 (1838)

Index Fungorum number: IF384; Facesoffungi: FoF03021

Ascotricha was erected by Berkeley (1838) and typified with *A. chartarum*. Genus has 27 species in the Species Fungorum (2025), while only nine have the sequence data. Hyde et al. (2020c) suggested that this genus needs revision to infer its correct phylogenetic placement. The sexual morph has ascomata bearing long hairs with shorter hyaline branches and brown ellipsoidal ascospores with an equatorial germ slit. Species are distributed in France, the Philippines, Portugal that are associated with soil, paper, lignum or other cellulosic substrates and marine habitats (Cheng et al., 2015).

Table 4.250*Ascotricha* species isolated from soil

Species	Country	Habitat or soil type	References
Ascotricha distans	Japan	Cultivated soil	Udagawa et al. (1994)
A. hispanica.	Spain	Calcareous soil with the vegetation	Stchigel and Guarro (1998)
A. xylina	India	ND	Rai and Tewari (1961)

Coniolariella Dania García, Stchigel & Guarro, in García, Stchigel, Cano, Calduch, Hawksworth & Guarro, Mycol. Res. 110(11): 1285 (2006)

Index Fungorum number: IF29050; Facesoffungi: FoF03030

García et al. (2006) introduced *Coniolariella* based on morphology and LSU phylogeny and accommodated *C. gamsii* as the type species. It has four species listed in the Species Fungorum (2025), and all of them are supported with the molecular data. The asexual morph has branched, slightly pigmented conidiophores with sub-hyaline to pale olive–brown, sympodially elongating conidiogenous cells, and conidia are sub-hyaline to pale olivaceous, solitary or in small chains on ramoconidia. The sexual morph consists of globose, ostiolate, glabrous, ascomata surrounded at the base by brown, thick hyphae, pseudoparenchymatous to coriaceous, *textura intricata* to *textura angularis* peridium and paraphyses present. Asci are cylindrical, 8-spored, without apical structures, non-amyloid with one-celled, ellipsoidal, brown, dark brown to black

ascospores with longitudinal germ-slit (García et al., 2006). The species have been isolated from leaves, soil and twigs collected from Iran, Spain and the USA (Zare et al., 2010).

Table 4.251 *Coniolariella* species isolated from soil

Species	Country	Habitat or soil type	References
Coniolariella macrothecia	USA	Monument valley area	Zare et al. (2010)

Xylaria Hill ex Schrank, Baier. Fl. (München) 1: 200 (1786)

Index Fungorum number: IF5832; Facesoffungi: FoF000696

Xylaria was validated by Schrank (1786) and *X. hypoxylon* was designated as the type species. It is accepted as the type genus in *Xylariaceae*, with approximately 300 species included in the genus (Hyde et al., 2024c). Various combinations of ITS, *rpb2*, *tub2* and *actin* have been used for the phylogenetic analyses in *Xylaria* (Wangsawat et al., 2021; Ma et al., 2022). However, phylogenetic ambiguities are still remain in this genus, where some studies suggest that secondary metabolites can be a potential marker for species identification (Hyde et al., 2020c; Song et al., 2014). Around 188 secondary metabolites are found in *Xylaria* (Song et al., 2014). The asexual morph is a geniculosporium-like, and the sexual morph is characterized by cylindrical stromata, eight-spored asci with an amyloid apical apparatus and ascospores are brown unicellular with a germ slit (Wangsawat et al., 2021). The species have been globally reported from various habitats such as dung, fruits, leaves, seeds, soil, termite nests and wood (Li et al., 2024a; Wangsawat et al., 2021). Most of them are saprobes majourly contributing as wood decomposes in forest ecosystems. Some produce beneficial compounds with antibacterial, antioxidative and anticarcinogenic properties (Li et al., 2024b).

Table 4.252*Xylaria* species isolated from soil

Species	Country	Habitat or soil type	References
Xylaria chaiyaphumensis	Thailand	soil near termite nest	Wangsawat et al. (2021)
X. escharoidea	India	Inactive termite mounds in a forest	Karun and Sridhar
X. symploci	India	Soil under the standing dead tree in a forest	(2015)
X. curta	India	Mountain soil	Ramesh et al. (2012)
X. hirsuta	Congo	ND	Ju et al. (2023)

X. guepini	France	Humiferous sandy soil	Hsieh et al. (2022)

Sordariomycetes* orders *incertae sedis

Order: *Amplistromatales* M.J. D'souza, Maharachch. & K.D. Hyde

Family: *Amplistromataceae* Huhndorf, A.N. Mill., Greif & Samuels

Acidothrix Hujslová & M. Kolařík, Mycol. Progr. 13(3): 824 (2014)

Figure 4.205

Index Fungorum number: IF805194; Facesoffungi: FoF02965

Acidothrix was erected by Hujslová et al. (2014) based on LSU phylogeny and morphological analyses treated to *Amplistromataceae*. It is a monospecific genus and typified by *A. acidophila,* which was isolated from soil (Hujslová et al., 2014). Colonies are white to slightly salmon with abundant aerial mycelium. The asexual morph is hyphomycetous, having acrodontium–like conidiophores, producing single, globose, or ellipsoidal to lacrimose conidia. This species is morphologically similar to acrodontium-like asexual morphs of *Amplistroma* and *Wallrothiella* in *Amplistromataceae.* The sexual morph is undetermined (Hujslová et al., 2014).

Table 4.253*Acidothrix* species isolated from soil

Species	Country	Habitat or soil type	References
A. acidophila	Czech Republic	Highly acidic soil	Hujslová et al. (2014)

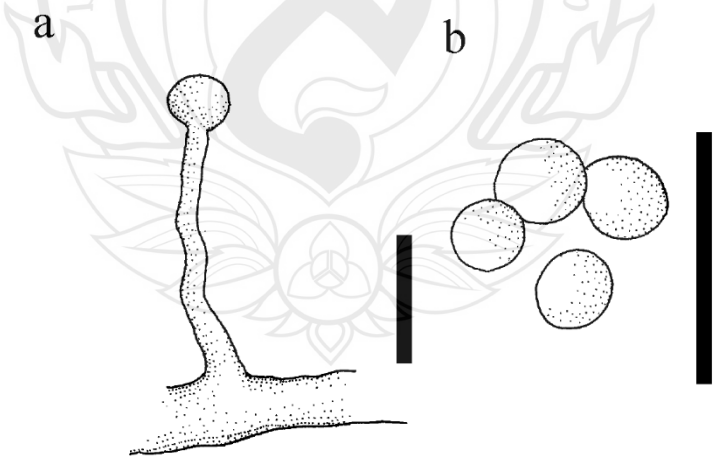


Figure 4.205 *Acidothrix acidophila*

Figure 4.205, a. Conidiophore b. Conidia. Scale bars: a, b = 10 μm. The drawings are redrawn from Hujslová et al. (2014)

Subphylum: ***Saccharomycotina*** O.E. Erikss. & Winka

Class: ***Dipodascomycetes*** M. Groenew., Hittinger, Opulente & A. Rokas

Order: ***Dipodascales*** M. Groenew., Hittinger, Opulente & A. Rokas

Family: ***Trichomonascaceae*** Kurtzman & Robnett

Trichomonascus H.S. Jacks., Mycologia 39(6): 712 (1948) [1947]

Index Fungorum number: IF 5562; Facesoffungi number: FoF16657

Trichomonascus was introduced by Jackson (1948), and the type species is designated as *T. mycophagus* (Smith et al., 2011). There are six species currently listed in the Species Fungorum (2025), and three of them have molecular data. In asexual reproduction, both pseudohyphae and true hyphae are formed, and multi-lateral budding occurs; these species produce blastoconidia in short chains. Heterothallic or homothallic occurs in sexual reproduction. Gametangia may form on hyphal tips or on hyphae after the fusion of two intercalary cells by lateral outgrowths. The asci are globose to ellipsoidal, with firm, thick walls, sometimes with a sterile apical cell and contain two to four ascospores. Ascospores are long-ellipsoidal to fusiform or hat- or helmet-shaped (Smith et al., 2011; Groenewald et al., 2018). Species are distributed in Canada, Hungary, South Africa and the Netherlands and are associated with fungicolous, fungi, human clinical samples, marine aquatic environments and pollen stored in honeycomb and soil (Smith et al., 2011; Groenewald et al., 2018).

Table 4.254 *Trichomonascus* species isolated from soil

Species	Country	Habitat or soil type	References
Trichomonascus vanleenenius	the Netherlands	A garden	Groenewald et al. (2018)
T. ciferrii	South Africa	ND	Cosio et al. (2024)

Zygoascus M.T. Sm., Antonie van Leeuwenhoek 52: 27 (1986)

Index Fungorum number: IF 25781; Facesoffungi number: FoF16658

Zygoascus was established by Smith (1986), and *Z. hellenicus* is designated as the type species. There are nine species listed in the Species Fungorum (2025), and only six have molecular data (LSU, ITS and *rpb2*). The asexual reproduction is characterized by multi-lateral budding and pseudohyphae, and septate hyphae are present where blastoconidia are formed. Hyphal septa have micropores. Species can be homo- or

heterothallic. Asci are obovate to spherical and contain one to four hemispherical to galeate ascospores (Smith, 1986). Species have been isolated from fermenting grapes, decaying wood, emulsion of white oil and polysorbate, soil and tar in Canada, China, France, Japan, South Africa and the Netherlands (Chai et al., 2022).

Table 4.255 *Zygoascus* species isolated from soil

Species	Country	Habitat or soil type	References
Zygoascus flipseniorum	the Netherlands	A garden	Groenewald et al. (2018)

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

Order: *Pichiales* M. Groenew., Hittinger, Opulente & A. Rokas

Family: *Pichiaceae* Zender

Ogataea Y. Yamada, K. Maeda & Mikata, Biosc., Biotechn., Biochem. 58(7): 1253 (1994)

Index Fungorum number: IF 27299; Facesoffungi number: FoF16654

Ogataea was introduced by Yamada et al. (1994) and typified with *O. minuta* (Kurtzman, 2011a). Currently, there are 38 species listed in the Species Fungorum (2025), and all of them have molecular data. The asexual reproduction is a process with multi-lateral budding on a narrow base, and cells are spherical to ellipsoidal. Pseudohyphae can occur with a few elongated cells. True hyphae are not formed. The sexual morph has asci that are deliquescent and may be unconjugated or show conjugation between a cell and its bud or between independent cells, one to four, or sometimes more asci are produced, with hat-shaped, allantoid, or spherical ascospores. Species are characterized by homothallic or infrequently heterothallic nature (Kurtzman, 2011a). They have been found in Australia, Brazil, Canada, China, Colombia, Hungary, Italy, South Africa, Thailand and the USA in association with dung, grapefruits, leaves and soil (Garcia-Acero et al., 2024; Kurtzman, 2011a).

Table 4.256 *Ogataea* species isolated from soil

Species	Country	Habitat or soil type	References
Ogataea Polymorpha	Brazil, the USA	ND	Kurtzman (2011a)
O. thermomethanolica	Thailand	ND	
O. degrootiae	the Netherlands	A garden	Groenewald et al. (2018)
Ogataea chonburiensis	Thailand	ND	Limtong et al. (2008)

Pichia E.C. Hansen, Centbl. Bakt. ParasitKde, Abt. I 12(19): 538 (1904)

Index Fungorum number: IF 4095; Facesoffungi number: FoF16655

Pichia was introduced by Hansen (1904) (Kurtzman, 2011b) and typified with *P. membranifacien.* The genus accommodates 61 species (Species Fungorum, 2025), and most of them are supported by the molecular data (ITS and LSU). Species have spheroidal, ellipsoidal, or elongated, occasionally tapered cells. In the sexual morph, the asci are deliquescent but occasionally persistent, containing one to four ascospores that are hat-shaped (galeate), hemispheroidal, or spheroidal with a ledge. Hyphal or pseudo-hyphal cells may serve as asci (Kurtzman, 1998). It has been isolated from decaying plant tissues and soil in Mexico, India and Indonesia (Groenewald et al., 2018).

Table 4.257 *Pichia* species isolated from soil

Species	Country	Habitat or soil type	References
Pichia gijzeniarum	the Netherlands	ND	Groenewald et al. (2018)
Pichia chibodasensis	Indonesia	ND	Kobayashi et al. (2017)

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

Order: *Ascoideales* J.H. Schaffner

Family: *Saccharomycopsidaceae* Arx & Van der Walt

Saccharomycopsis Schiønning, C. r. Trav. Laboratoire d. Carlsberg 6(2): 124 (1903)

Index Fungorum number: IF 4816; Facesofungi number: FoF16656

Schiönning (1903) introduced *Saccharomycopsis* and designated *S. capsularis* as its type. The genus currently comprises 15 species (Species Fungorum, 2025), and all of them have molecular data (LSU). The asexual morph has multipolar budding, and the sexual morph shows significant variations in the ascospore shapes (Hajihosseinali et al., 2020). Species have been isolated from alcoholic drinks, dairy products, fallen fruits and soil that are distributed in Australia, Chile, India, Japan, Iran and the Soviet Union (Groenewald et al., 2018; Hostinová et al., 2010; Kohlwein & Paltauf, 1984).

Table 4.258 *Saccharomycopsis* species isolated from soil

Species	Country	Habitat or soil type	References
Saccharomycopsis oosterbeekiorum	the Netherlands	A garden	Groenewald et al. (2018)
S. praedatoria	Brazil	Amazonian rainforest	Santos et al. (2023)

Order: ***Saccharomycodales*** *M. Groenew., Hittinger, Opulente & A. Rokas*

Family: ***Saccharomycodaceae*** Kudryavtsev

Hanseniaspora Zikes, Centbl. Bakt. ParasitKde, Abt. II 30: 148 (1911)

Index Fungorum number: IF 2218; Facesofungi number: FoF16653

Hanseniaspora was introduced by Zikes in 1911 (Cadez & Smith, 2011), and *H. valbyensis* is accepted as the type species. Currently, the genus has 16 accepted species (Groenewald et al., 2018; Species Fungorum, 2025), and all are having molecular data. In the asexual morph, bipolar budding can be seen, and blastoconidia are produced in basipetal succession on a broad base. Cells appear in apiculate and ovoid to long-ovoid or elongate. Pseudohyphae can be present. The sexual morph possesses persistent or deliquescent asci and forms one to four ascospores that are smooth, hat- or helmet-shaped, spherical, and with an equatorial ledge or spherical and warty with an equatorial ledge (Cadez & Smith, 2011). These species have been identified from various substrates such as insect frass, lichen, soil and wood that are distributed in China, France, Georgia, South Africa and the Netherlands (Jindamorakot et al., 2009).

Table 4.259 *Hanseniaspora* species isolated from soil

Species	Country	Habitat or soil type	References
Hanseniaspora vineae	South Africa	vineyard soil	Cadez and Smith (2011)
H. occidentalis	West Indies and Java		
H. mollemarum	The Netherlands	A garden	Groenewald et al. (2018)
H. valbyensis	Denmark		Limongelli et al. (2023)
H. terricola	China		Liu et al. (2019c)
H.occidentalis	France		

Ascomycota* genera *incertae sedis

Effetia Bartoli, Maggi & Persiani, Mycotaxon 19: 517 (1984)

Figure 4.205

Index Fungorum number: IF25588; Facesoffungi: FoF13564

Effetia was introduced by Bartoli et al. (1984), accommodating *E. craspedoconidica* as the type species. The genus has one species in the Species Fungorum (2025), however, no molecular data is provided and it needs to be further studied (Bartoli et al., 1984; Huang et al., 2021b). Previously, *Effetia* was placed in *Sordariaceae* based on its sexual morph, subsequently, Huang et al. (2021b) suggested transferring this genus to *Ascomycota* genera *incertae sedis*. The asexual morph is hyphomycetous with brown, unbranched, straight or flexuous, septate conidiophores and polyblastic, terminal conidiogenous cells, producing acropleurogenous, oval to ellipsoidal, aseptate, light brown to dark brown conidia. The sexual morph is characterized by the perithecial, solitary, brown to dark brown, globose to subglobose, ostiolate ascomata, 8-spored, unitunicate, cylindrical, apex rounded asci, and hyaline to brown, ellipsoidal, aseptate ascospores. Species have been isolated from litter and soil in Ivory Coast (Bartoli et al., 1984; Huang et al., 2021b).

Table 4.260 *Effetia* species isolated from soil

Species	Country	Habitat or soil type	References
Efetia craspedoconidica	Ivory Coast	Woodland soil	Bartoli et al. (1984)

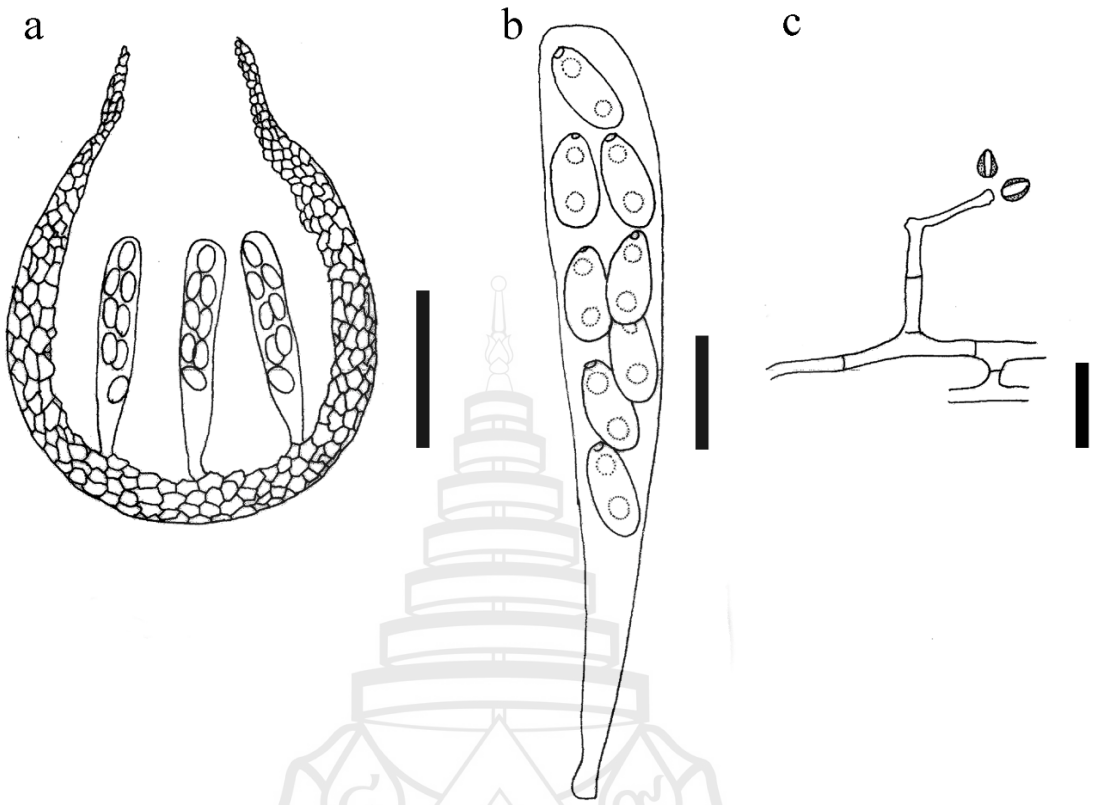


Figure 4.205 *Effetia craspedoconidica*

Figure 4.205, a Ascoma with asci b Ascus with ascospores. c. Conidiophores and conidia. Scale bars: a = 50 μm, c = 20 μm, b =10 μm. Redrawn from Huang et al. (2021b).

Heterocephalum Thaxt., Bot. Gaz. 35: 157 (1903)

Index Fungorum number: IF8521; Facesoffungi number: FoF16642

The type species is *Heterocephalum aurantiacum*, currently the genus is comprised of two species (Hyde et al., 2024c), and only one species has molecular data. They have been isolated from dung, lesion on turtle and soil found in Jamaica, Ivory Coast and the Philippines (Yaguchi et al., 1996).

Table 4.261*Heterocephalum* species isolated from soil

Species	Country	Habitat or soil type	References
Heterocephalum taiense	Ivory Coast	Forest soil	Persiani and Maggi (1986)
H. taiense	Japan	volcanic island	Yaguchi et al. (1996)
H. aurantiacum	India	ND	Sharma et al. (2004)

Gilmaniella G.L. Barron, Mycologia 56(4): 514 (1964)

Index Fungorum number: IF8334; Facesoffungi: FoF16643

Barron (1964) introduced *Gilmaniella* and the type species is accomodated as *G. humicola*. There are eight species present in the genus (Species Fungorum, 2025), and only two are have molecular data. The asexual morph is characterized by conidiophores that are single, short, septate, simple or branched and the branches and stalk are frequently inflated, while conidia are born singly or in clusters appearing in dark brown with an apical germ pore (Barron, 1964). The species are recorded from Australia, China, Egypt, India, Kuwait and Pakistan, that are associated with dung, leaves, stems and soil (Mouchacca, 2007).

Table 4.262 *Gilmaniella* species isolated from soil

Species	Country	Habitat or soil type	References
Gilmaniella humicola	Canada	ND	Barron (1964)
Gilmaniella humicola	Thailand	ND	Manoch (1987)
Gilmaniella macrospora	Kuwait	Salt marsh soil	Moustafa (1975)
Gilmaniella subornata	China	ND	Morinaga and Udagawa (1978)
Gilmaniella multiporosa	Egypt	Salt marsh soil	Mouchacca (2007)

Phaeotrichoconis Subram., Proc. Indian Acad. Sci., Sect. B 44: 2 (1956)

Index Fungorum number: IF9325; Facesoffungi number: FoF16644

Subramanian (1956a) accommodated *Phaeotrichoconis* with the type species, *P. crotalariae*. The genus comprises seven species (Hyde et al., 2024c), and no molecular data is provided for any of them. The asexual morph has conidiophores that are micronematous, erect, septate, with swollen apex and producing acrogenous, brown, elongate, fusiform conidia with a long appendage at the apex (Subramanian, 1956a). Species are reported as animal pathogens, plant endophytes or saprobes. They have been isolated from both aquatic and terrestrial habitats, that are associated with branches, clinical samples, leaves, pods, and soil in Brazil, India, Ivory Coast and Puerto Rico (Lima et al., 2012; Shukla et al., 1989; Subramanian, 1956a).

Table 4.263 *Phaeotrichoconis* species isolated from soil

Species	Country	Habitat or soil type	References
Phaeotrichoconis crotalariae	Thailand	ND	Manoch (1998)
Phaeotrichoconis crotalariae	India	Rhizosphere of *Ocimum sanctum*	Lima et al. (2012)

Solosympodiella Matsush., Microfungi of the Solomon Islands and Papua-New Guinea (Osaka): 55 (1971)

Index Fungorum number: IF9954; Facesoffungi number: FoF16645

Solosympodiella was erected by Matsushima (1971) accommodating *S. clavata* as the type species. There are eight species in the genus (Hyde et al., 2024c), but molecualr data is unavailable. The asexual morph is characterized by macronematous, mononematous hyaline or pigmented erect, solitary, conidiophores sometimes branched with polyblastic, integrated, terminal, sympodial, denticulate conidiogenous cells. Conidia are acropleurogenous, ellipsoidal to clavate, truncate at the base, sometimes septate and clear brown (Matsushima, 1971). Species are discovered from dead leaves, stems and soil in Australia, China, Japan, Papua New Guinea and Peru (Rambelli, 2011).

Table 4.264 *Solosympodiella* species isolated from soil

Species	Country	Habitat or soil type	References
Solosympodiella sp.	Thailand	ND	Manoch (1998)
Solosympodiella clavata	Papua New Guinea	Forest soil	Matsushima (1971)
Solosympodiella queenslandic	Australia	ND	Matsushima (1989)

4.3 Discussion

Soil is one of the most diverse habitats on Earth (Thies & Grossman, 2023). The soil-inhabiting fungal groups are documented in the Global Soil Mycobiome Consortium (Tedersoo et al., 2021), GlobalFungi (Větrovský et al., 2020), and UNITE (Nilsson et al., 2019). The Global Soil Mycobiome Consortium (GSMc) reported that soil fungi represent 722,682 OTUs (Operational Taxonomic Units), and 62.4% of those OTUs were accommodated in *Ascomycota*. Although *Ascomycota* is considered the most abundant fungal group in many soils, the HTS data is often limited to higher taxonomic ranks (Egidi et al., 2019).

Moreover, by incorporating morpho-molecular studies, species and genera of *Ascomycota* have been extensively studied and revised over the past two decades. However, information on soil-inhabiting taxa remains scattered across different sources. We have compiled those dispersed data by developing a comprehensive outline of genera of soil *Ascomycota*.

This provides an overview of the genera recorded from soils globally. Moreover, we have provided 270 *Ascomycota* genera notes that include information on updated phylogeny, morphology, and ecological status. The genera are mainly comprised of *Dothideomycetes, Eurotiomycetes* and *Sordariomycetes* classes (Figure 4.190), while several other *Ascomycota* classes have also been included. Previously, Domsch et al. (1993, 2007) have provided around 170 genera notes of *Ascomycota* and some lower fungal groups in soil. However, most of these taxa had been subjected to phylogenetic and morphological reappraisal over time, and our study provides the most recent updates on their generic information. These compiled data will be useful for the taxonomists, researchers or students who are working on soil-inhabiting *Ascomycota*.

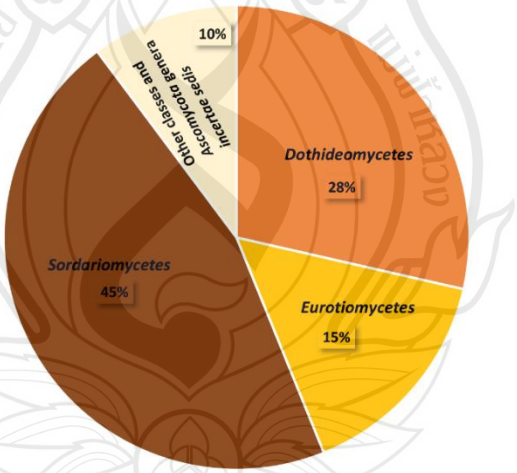


Figure 4.206 The percentage of *Dothideomycetes*, *Eurotiomycetes* and *Sordariomycetes* genera that are compiled in this study

Ascomycota groups are highly diverse, and are variably distributed across the globe (Tedersoo et al., 2014; Wu et al., 2019; Baldrian et al., 2022b). There are different soil types and soil-associated habitats present on the earth, and the fungal communities residing in each of them can be varied (Tedersoo et al., 2022). The habitats and soil types of the compiled generic data in our study are graphically illustrated in Figure

4.191, showing that the genera of *Dothideomycetes*, *Eurotiomycetes* and *Sordariomycetes* are mostly reported from forests, cultivated lands, and urban areas. This suggests that the soils of these habitats have been relatively well-studied as compared to others.

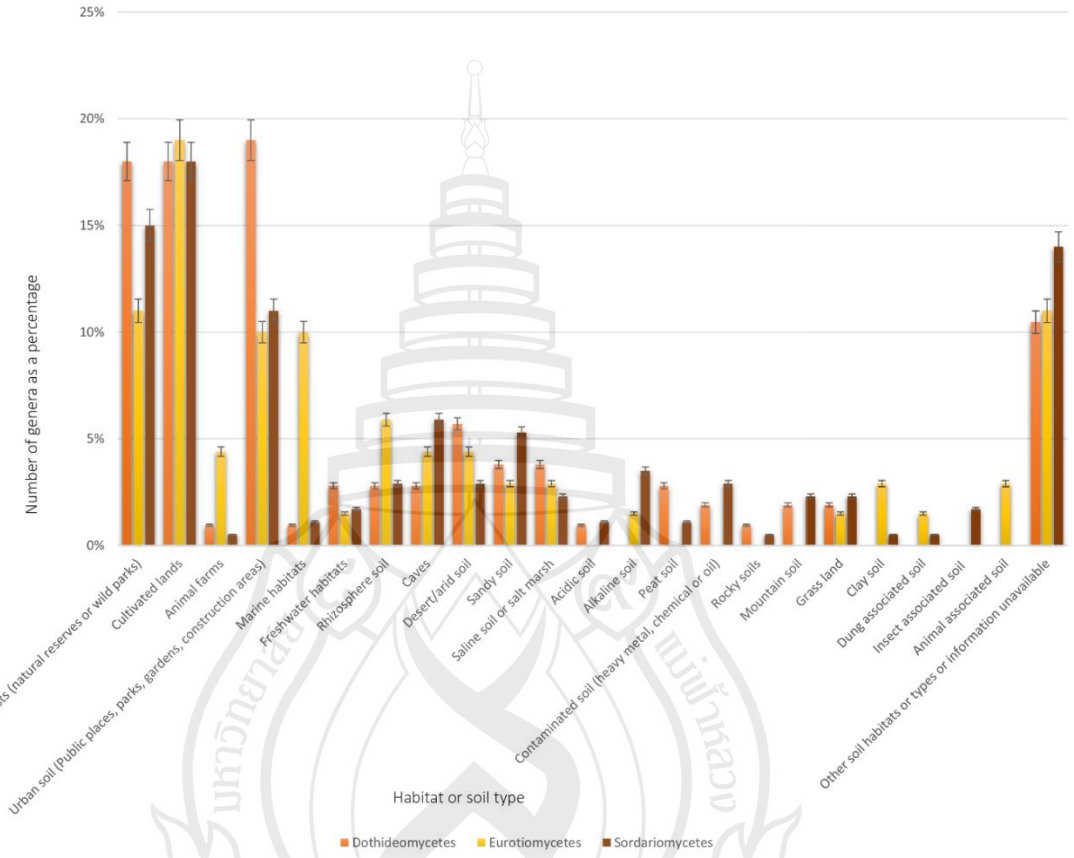


Figure 4.207 The genera of *Dothideomycetes*, *Eurotiomycetes* and *Sordariomycetes* that have been compiled in this study are shown as a percentage. The total number of the genera belonging to these three classes are 243, and they vary based on the habitat or soil type that they have been reported

Ascomycota species are ubiquitous and abundant; others are rare in soil. Based on the GlobalFungi database, Baldrian et al. (2022) have conducted a combine analysis of the HTS results from worldwide studies to estimate global fungal number, resulted in 6.3 million species, with *Ascomycota* representing 57% (Baldrian et al., 2022), and the study further explained that soil as one of the habitats with the highest alpha diversity of fungi. Moreover, Baldrian et al. (2022) explained, most of the worldwide HTS studies are conducted from the soil substrates, especially from forest habitats that

also can be a limitation in estimating true diversity. Therefore, they have suggested the importance of studying various habitats and environmental conditions to recover total diversity estimations. The soil genera compilation of my study, enable to determine that culture-based studies have similar pattern that they are also majourly focused on the forests and agricultural lands (Figure 4.207). Thus, it is important to extend the studies on unexplored soil habitats. However, deteails of several species that I have isolated from Thai soils were not available in GlobalFungi website, such as *Cumuliphoma indica*, *Beltraniela fertilis*, *Remotididymella ageratinae* and *Epicoccum catenisporum*.

Considering the *Ascomycota* classes, *Sordariomycetes* is the most dominant, and we compiled 123 genera, which is 45% of the total compiled genera (Figure 4.191). Reportedly, *Podospora*, *Chaetomium*, *Fusarium*, and *Trichoderma* are common soil inhabitants. Further, *Aspergillus, Exophiala*, *Knufia*, *Penicillium*, *Cadophora and Leohumicola* are some of the *Leotiomycetes* and *Eurotiomycetes* that are relatively common in edaphic habitats (Egidi et al., 2019; Do Nascimento Barbosa et al., 2016; Tedersoo et al., 2020). Of the total, 28% are *Dothideomycetes* genera (Figure 4.206), with *Alternaria*, *Aureobasidium*, *Cladosporium*, and *Curvularia* (Egidi et al., 2019) being the most common soil-inhabiting *Dothideomycetes*. The dominance of certain species over others can result from their dispersal abilities, life styles and functional attributes. Many of these genera, including *Alternaria*, *Aureobasidium*, *Cladosporium*, *Penicillium*, *Fusarium*, *Chaetomium*, *Acremonium*, and *Curvularia* are wind-dispersed, which may partially explain their abundance in soil. Another common character among these genera is their flexible trophic nature, which allows them to colonize in multiple niches. For example, some species can shift from a plant or human pathogenic state to a saprobic state (*i.e.*, *Fusarium*, *Alternaria*, *Chaetomium*, *Cladophialophora*, *Knufia* and *Exophiala*) (Egidi et al., 2019; Janowski & Leski, 2022). This adaptability enhances their ability to utilize resources, compete, and tolerate environmental stress. Additionally, their fast growth and high adaptability make them easier to isolate (Bridge & Spooner, 2001; Mueller et al., 2004; Tedersoo et al., 2014; Taylor & Sinsabaugh, 2015).

However, in most mycobiomes, including soils, fungal diversity is primarily represented by rare taxa. These rare sub-communities are more sensitive to host selection and play a crucial role in fungal co-occurrence networks and ecosystem

functions, such as crop yield and soil enzyme activities (Xiong et al., 2021). Moreover, approximately 80% of fungal species are considered rare and may be prone to extinction (Banerjee et al., 2024). Anderson (2009) identified several factors contributing to the rarity of certain fauna species in soil, which could also be applied to rare fungal species. These include seasonal population occurrences, adaptations to above-ground environments, intrinsically rare nutritional or niche requirements, distribution limitations, and the lack of standardized sampling and detection methods. Even when rare taxa are detected through HTS, isolating them *in-vitro* can still be a challenge. Many are slow growing, lack necessary nutrients in growth media, lose mutual relationships, or are highly sensitive to micro-climatic changes in the soil. (Bridge & Spooner, 2001; Tedersoo et al., 2014, 2020; Wu et al., 2019; Yasanthika et al., 2022b). Therefore, isolating uncommon soil ascomycetes could lead to the discovery of novel taxa, unveil hidden biodiversity, and open new approaches for biotechnological applications.

Due to its high biodiversity, we selected Thailand to uncover the soil-dwelling *Ascomycota* species. Finlay (2007) estimated that approximately 75,000 belowground fungal species had been globally reported at the time of their study. However, in Thailand, only 89 genera and 95 species had been discovered by 1998 (Manoch, 2004). From 2000 to 2024, soil fungal research in the country has been conducted using both morpho-molecular methods. In Table 267, we have listed the soil-associated *Dothideomycetes*, *Eurotiomycetes* and *Sordariomycetes* genera published in Thailand over the past two decades. The data show that studies have mostly focused on agriculture sites, including cultivated lands (rice, rubber and palm, pineapple plantations), livestock farms, and forest ecosystems (Manoch, 1993, 1998; Kosol, 1999; Manoch et al., 2000; Dethoup et al., 2007; Puangsombat et al., 2010). Meanwhile, some have used the HTS methods. Amma et al. (2018) reported *Sordariomycetes* as the most abundant class, particularly from the *Hypocreales* and *Xylariales* orders, with *Fusarium* as dominant genus. They also identified *Eurotiomycetes*, *Orbiliomycetes* and *Leotiomycetes* in Dipterocarpaceae-dominated forests. Another HTS study discovered *Aspergillus*, *Penicillium*, *Cladosporium*, *Talaromyces*, *Xylaria*, and *Trichoderma* as the most common genera in caves of Satun Geopark, Thailand (Suetrong et al., 2023).

Among the culture-dependent studies, around 185 species belonging to 79 *Ascomycota* genera have been reported over the last two decades. In these studies, frequently isolated genera include *Aspergillus*, *Chaetomium*, *Fusarium*, *Trichoderma, Cladosporium, Penicillium, Talaromyces, Curvularia, Paecilomyces Scopulariopsis, Ophiocordyceps* and *Scedosporium.* Some of the reported genera have moderate distribution in the soil, such as *Purpureocillium*, *Paecilomyces, Ophiocordyceps, Ephelis, Cladosporium, Scedosporium, Cephalosporium, Chaetomella, Chloridium, Geotrichum, Gliocladium, Heterocephalum, Humicola, Leptographium, Mariannaea, Monocillium, Penicillium, Hamigera, Eupenicillium, Nectria, Thielavia, Cephalosporium, Chaetomella, Pestalotiopsis, Phialophora, Scopulariopsis, Scytalidium, Cylindrocladium, Cylindrocarpon, Diheterospora, Drechslera, Emericella, Neurospora, Gilmaniella, Idriella* and *Mariannaea.* Uncommon soil species like *Nigrospora*, *Monilia*, *Drechslera*, *Arthrinium*, *Leptographium* and *Byssochlamys* have also been found (Eamvijarn et al., 2013; Kladwang et al., 2003; Liamthong et al., 2017; Luplertlop et al., 2016, 2019; Maneeboon et al., 2023; Manoch, 2004; Pornsuriya et al., 2008, 2011; Puangsombat et al., 2010; Seephueak et al., 2019; Wingfield et al., 2021). Compared to the rest of the world, there is a significant gap in soil *Ascomycota* discoveries in Thailand (Puangsombat et al., 2010; Farias et al., 2023). In contrast, the neighbouring countries like China, which share similar climatic regions with Thailand, have conducted extensive fungal studies across a wide range of habitats, revealing many new species (Man et al., 2015, 2018; Zhang et al., 2019a, 2021c, 2023e; Zheng & Song, 2022). Moreover, most of the fungal studies in Thailand conducted before 2010 relied solely on the morphological identification. Gradually, over time, studies have adopted morpho-molecular approaches for more accurate taxonomic identification. For fungal isolations, the dilution plate method has frequently been used, while several studies have also used soil plate method, baiting method and heat treatment methods (Table 4.267) (Manoch, 1998, 2004; Puangsombat et al., 2010; Seephueak et al., 2019; Yasanthika et al., 2022a).

Table 4.266 The genera isolated from different soil habitats in Thailand from 2000 to 2024

Genera	Soil habitat or soil type	Isolation method	References
Acremonium	Limestone areas, rhizosphere soil	Modified soil plate method	Ito et al. (2001), Kladwang et al. (2003)
Alternaria	Rice field	Soil dilution series method	Seephueak et al. (2019, Wingfield et al. (2021)
Aspergillus	Pig farm, coastal forest soil, pineapple and sugar cane fields, fertile soil, mangrove areas, rice field, poultry farms, man-made solar saltern, mountain forests, chicken-feather dumping soil, rhizosphere soil	Soil dilution series method, modified soil plate method, alcohol treatment, modified heat treatment method, moist chamber and baiting technique	Ali et al. (2013), Dethoup and Manoch (2010), Reanprayoon and Pathomsiriwong (2012) Seephueak et al. (2019)
Bipolaris	Rice field, agricultural lands	Soil dilution series method	Reanprayoon and Pathomsiriwong (2012), Seephueak et al. (2019)
Byssochlamys	Mountain forests, agricultural lands	Soil plate method, soil dilution series method	Dethoup and Manoch (2010), Luangsa-ard et al. (2004)
Cephalosporium	Forest	Soil dilution series method	Puangsombat et al. (2010)
Chaetomella	Forest	Soil dilution series method	Puangsombat et al. (2010)
Chloridium	Forest	Soil dilution series method	Puangsombat et al. (2010)
Chaetomium	Pineapple plantations, forest reserve, rice field, poultry farms, chicken-feather dumping soil	Soil plate method, soil dilution series method, baiting technique (sterilized straws, filter paper, tissue paper and pineapple leaves) and moist chamber method	Pornsuriya et al. (2008, 2011), Seephueak et al. (2019), Reanprayoon and Pathomsiriwong (2012)

Table 4.266 (continued)

Genera	Soil habitat or soil type	Isolation method	References
Cladosporium	Pig farm, rice field, chicken-feather dumping soil, rhizosphere soil	Modified soil plate method, soil dilution series method, moist chamber and baiting technique	Kitisin et al. (2021), Seephueak et al. (2019), Wingfield et al. (2021), Penkhrue et al. (2015)
Colletotrichum	Rice field	Soil dilution series method, moist chamber and baiting technique	Seephueak et al. (2019)
Curvularia	Pig farm, rice field	Modified soil plate method, soil dilution series method, moist chamber and baiting technique	Seephueak et al. (2019), Wingfield et al. (2021)
Emericella	Agricultural lands	Heat treatments, soil plate method, alcholo treatment	Dethoup and Manoch (2010)
Eurotium	Agricultural lands	Alcohol treatment	Dethoup and Manoch (2010)
Eupenicillium	Agricultural lands	Heat treatments	Dethoup and Manoch (2010)
Fusarium	Pig farm, chicken-feather dumping soil, rhizosphere soil	Modified soil plate method, Soil dilution series method	Dalee et al. (2018), Ito et al. (2001), Kitisin et al. (2021)
Heterocephalum	Forests	Soil dilution series method	Puangsombat et al. (2010)
Humicola	Forests	Soil dilution series method	Puangsombat et al. (2010)
Hypoxylon	Caves	Soil dilution series method	Preedanon et al. (2023)
Gleocladium	Chicken-feather dumping soil	Soil dilution series method	Dalee et al. (2018)
Geotrichum	Pig farm, forests	Modified soil plate method, Soil dilution series method	Puangsombat et al. (2010), Kitisin et al. (2021)

Table 4.266 (continued)

Genera	Soil habitat or soil type	Isolation method	References
Gliomastrix	Limestone areas	Soil plate method	Kladwang et al. (2003)
Leptographium	Forests	Soil dilution series method	Puangsombat et al. (2010)
Leptobacillium	Caves	Soil dilution series method	(Preedanon et al. 2023)
Malbranchea	Caves, agricultural lands	Soil plate, Soil dilution series method	Dethoup and Manoch (2010), (Preedanon et al. (2023)
Myceliophthora	Agricultural lands	Alcohol treatment	Ito et al. (2001), Dethoup and Manoch (2010)
Myrothecium	Rhizosphere soil	Soil dilution series method	Ito et al. (2001)
Neosartoya	Agricultural lands	Alcohol treatment	Dethoup and Manoch (2010)
Neurospora	Rhizosphere soil	Soil dilution series method	Ito et al. (2001)
Nigrospora	Rhizosphere soil, rice field	Soil dilution series method, moist chamber and baiting technique	Ito et al. (2001)
Penicillium	Pig farm, pineapple and sugar cane fields, forests, mangrove areas, rice feld, chicken-feather dumping soil, rhizosphere soil	Modified soil plate method, modified heat treatment method, soil dilution series method, moist chamber and baiting technique	Ito et al. (2001), Kitisin et al. (2021), Maneeboon et al. (2023), Puangsombat et al. (2010), Liamthong et al. (2017), Seephueak et al. (2019)
Pithomyces	Rhizosphere soil	Soil dilution series method	Kitisin et al. (2021)
Pestalotiopsis	Forests	Soil dilution series method	Puangsombat et al. (2010)

Table 4.266 (continued)

Genera	Soil habitat or soil type	Isolation method	References
Talaromyces	Pig farm, forests, pineapple and sugar cane fields, longan field soil non-agricultural soil, agricultural lands, caves	Modified soil plate method, modified heat treatment method, soil dilution series method, soil plate, heat treatment, alcohol treatment methods	Nuankaew et al. (2022), Dethoup et al. (2007), Luangsa-ard et al. (2004), Dethoup and Manoch (2010), Kitisin et al. (2021), Maneeboon et al. (2023), Puangsombat et al. (2010)
Thielavia	Agricultural lands	Alcohol treatment, soil plate	Dethoup and Manoch (2010)
Phialophora	Forests	Soil dilution series method	Puangsombat et al. (2010)
Purpureocillium	ND	Soil dilution series method	Penkhrue et al. (2015)
Paecilomyces	Rice fields, forests, poultry farms, pineapple and sugar cane fields	Soil dilution series method and heat treatments	Dethoup and Manoch (2010), Maneeboon et al. (2023), Wingfield et al. (2021)
Ophiocordyceps	ND	ND	Maneeboon et al. (2023)
Microsporum	Chicken-feather dumping soil, poultry farm	Soil dilution series method	Wingfield et al. (2021), (Dalee et al. (2018)
Trichoderma	Forests, mangrove areas, poultry farms, rice fields, pig farm	Modified soil plate method, Soil dilution series method	Puangsombat et al. (2010), Kitisin et al. (2021), Liamthong et al. (2017), Wingfield et al. (2021), Dethoup and Manoch (2010)
Scedosporium	Caves, Public parks	Modified soil plate method, soil dilution series method	Luplertlop et al. (2019), Preedanon et al. (2023)
Scolecobasidium	Rhizosphere soil	Soil dilution series method	Ito et al. (2001)

Table 4.266 (continued)

Genera	Soil habitat or soil type	Isolation method	References
Scopulariopsis	Poultry farms, forests	Soil dilution series method	Puangsombat et al. (2010), Wingfield et al. (2021)
Staphylotrichum	Chicken-feather dumping soil	Soil dilution series method	(Dalee et al. (2018)
Hamigera	Pineapple and sugar cane fields	Modified heat treatment method	Maneeboon et al. (2023)
Nectria	Forests	Soil dilution series method	Puangsombat et al. (2010)
Verticillium	Forests, limestone areas	Soil dilution series method, modified soil plate method	Puangsombat et al. (2010), Kladwang et al. (2003)
Xylaria	On soil near termite nest	Stromata of *Xylaria* species were collected	Wangsawat et al. (2021)

In Thailand, the land use patterns have been changing rapidly, with highlands being converted for farming and tourism, while lowland plains are increasingly occupied by urbanization, affecting soil biodiversity (Pansak et al., 2024). As a result, fungal communities in these soils may become restricted to certain locations or adapt to different ecosystems in response to these changes (Farias et al., 2023; Tedersoo et al., 2022). To obtain a diverse collection of *Ascomycota* species, we selected three different soil-based habitats: forests, caves, and urban areas, including both disturbed and undisturbed locations. Notably, caves and urban areas remain understudied habitats in Thailand (Table 4.266).

In this study, 30 species are discovered, including nine new species and 21 new records, belonging to three classes (*Dothideomycetes*, *Eurotiomycetes* and *Sordariomycetes*), isolated from forests, caves and urban areas in Thailand. In addition, under the same project two new species and seven new records (*Dothideomycetes* and *Sordariomycetes*) were mentioned in the previous chapter (Chapter 3): *Neptunomyces soli*, *Curvularia dactylocteniicola* (Yasanthika et al., 2024), *Verruconis soli* and *Verruconis thailandica* (Yasanthika et al., 2023), *Chloridium gonytrichii* and *Kionochaeta microspora* (Yasanthika et al., 2022a), *Beltraniella fertilis* (Yasanthika et

al. 2020), and *Pochonia chlamydosporia* and *Cordana terrestris* (Chethana et al., 2023). These species were isolated from Thai forests soils. Thereby, bringing the total number of soil-inhabiting species identified in our research to 39, across three different habitats. As shown in Figure 4.192 (a), our collection consists of 26 *Dothideomycetes* species, 15 *Sordariomycetes* species and one *Eurotiomycetes*. They belong to 21 families and 35 genera, as illustrated in Figure 4.192 (b).

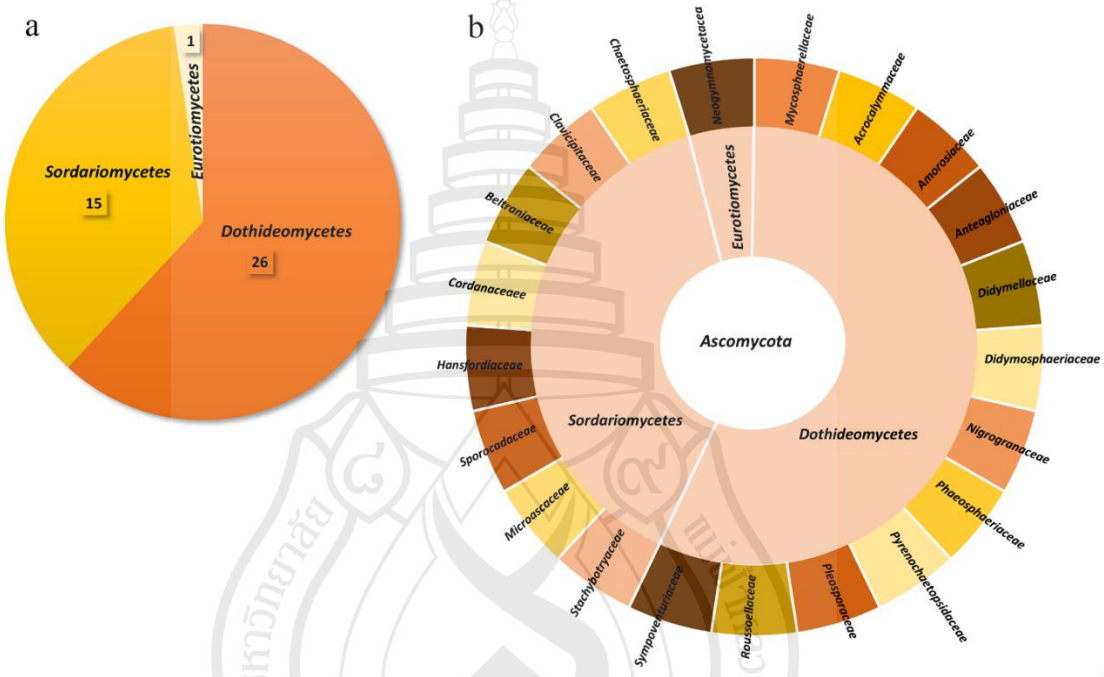


Figure 4.208 a The number of soil-inhabiting species collected in our research (total 39 species). b The species are distributed in 21 families in *Dothediomycetes*, *Eurotiomycetes* and *Sordariomycetes*

In the current study, we isolated *Curvularia*, *Paraconiothyrium*, *Pyrenochaetopsis*, *Stachybotrys*, and *Microascus* common to various soil habitats. In contrast, we obtained *Anteaglonium*, *Diaporthosporella*, *Neoceratosperma*, *Paraleptospora* and *Pararoussoella* genera that have not been recovered from the soils before. Additionally, *Beltraniella fertilis*, *Chloridium gonytrichii Kionochaeta microspora*, and *Neptunomyces soli* are some uncommon species that we have published previously (Yasanthika et al., 2020; Yasanthika et al., 2022a; Yasanthika et al., 2024).

Figure 4.193 shows the distribution of the 39 species isolated from three habitats (Forests, caves and urban areas). Forests are undisturbed habitats, comprising of 34.06% of the country's area. However, due to the ongoing deforestation, this area is continuously decreasing (Pansak et al., 2024). *Talaromyces thailandensis*, *Wickerhamomyces anomalus*, *Cyberlindnera subsufficiens*, *Aspergillus restrictus* and *Paecilomyces variotii*, have previously been reported from Thai forest soils (Manoch, 1998, 2004; Puangsombat et al., 2010). However, this study recovers eight additional genera from forest soils: *Neopestalotiopsis terricola*, *Neoroussoella entadae*, *Paraconiothyrium cyclothyrioides*, *Paraleptospora thailandica*, *Pararoussoella lincangensis*, *Pseudopithomyces chartarum*, *Pyrenochaetopsis tropicalis* and *Roussoella terrestris*. Additionally, our previous publications revealed nine species from forest soils (*Neptunomyces soli*, *Curvularia dactylocteniicola*, *Kionochaeta microspora* and *Beltraniella fertilis*, *Chloridium gonytrichii*, *Pochonia chlamydosporia* and *Cordana terrestris*, accounting to a total of 17 species from forest soils in our study (Figure 4.193).

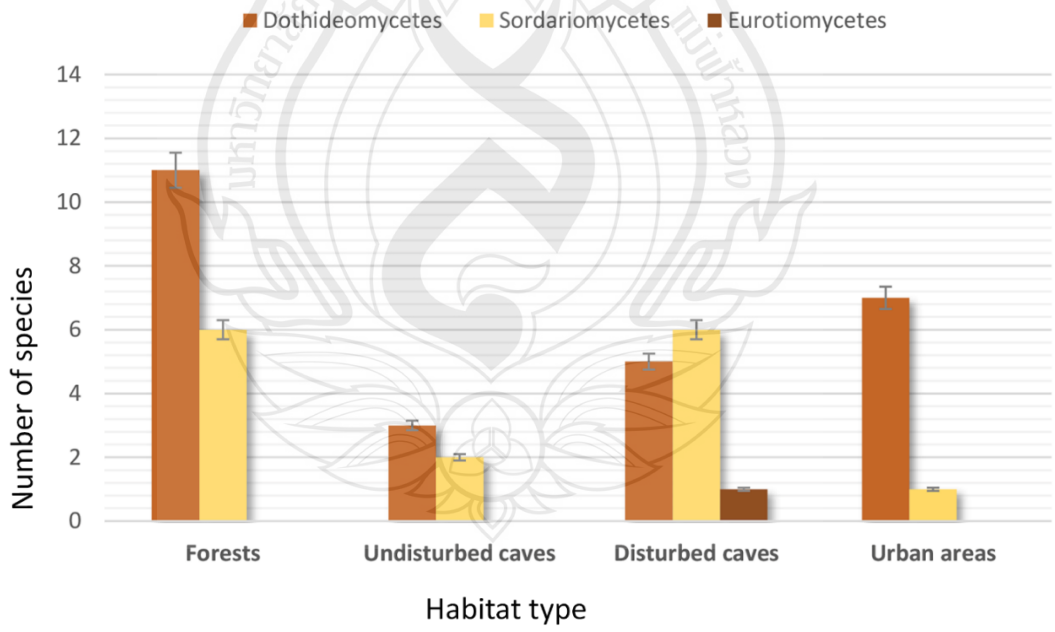


Figure 4.209 The number of species collected from each soil habitat (Forests, undisturbed caves, disturbed caves and urban areas) in our study

As cave inhabitants, we discovered 12 species from disturbed caves, namely *Anteaglonium soli*, *Acrocalymma medicaginis*, *Currahmyces indicus*, *Diaporthosporella soli*, *Hansfordia pruni*, *H. pulvinata*, *Microascus croci*, *Neoceratosperma soli*, *Neopyrenochaeta telephoni*, *Remotididymella ageratinae*, *Wardomycopsis fusca* and *Yunnania penicillata*(, and five species from undisturbed caves, including *Amorocoelophoma soli*, *Cumuliphoma indica*, *Nigrograna speluncae*, *Microascus croci* and *Wardomycopsis fusca*, totaling 15 species across 14 genera (Figure 4.193). We have isolated *Microascus croci* and *Wardomycopsis fusca* from both disturbed and undisturbed cave soils (Figure 4.210). Interestingly, these two species have previously been reported from cave air and soil as well (Jurado et al., 2021; Zhang et al., 2021c). In addition, Zhang et al. (2021) reported *Microascus levis*, *M. trigonus* and *Wardomycopsis dolichi* from cave soils, suggesting that these genera may be well-adapted to cave ecosystems. Furthermore, *Yunnania* was also isolated in Thai caves in this study, while *Pseudoscopulariopsis* and *Scopulariopsis* have been previously reported from Chinese caves (Zhang et al., 2017b, 2021c). These studies highlight the preference of *Microascaceae* members for cave habitats. Previously, *Hypoxylon phuphaphetense*, *Leptobacillium latisporum*, *Malbranchea phuphaphetensis*, *Scedosporium satunense*, *Talaromyces phuphaphetensis*, *T. satunensis* have been isolated from Thai caves (Nuankaew et al., 2022; Preedanon et al., 2023). Most of these reported species are *Eurotiomycetes* and *Sordariomycetes*, whereas we were able to recover *Dothideomycetes* species as well. As shown in Table 4.266, the studies on soil fungi in Thai caves are relatively few compared to other habitats. Based on our results, we suggest that further study of Thai caves could provide valuable insights into the country's fungal diversity.

Urbanization is rapidly increasing in Thailand, which considerably impacts the natural properties of soils (Kachenchart et al., 2020; Pansak et al., 2024). We isolated eight species (Figure 4.192), namely *Curvularia suttoniae*, *Ectophoma multirostrata*, *Epicoccum catenisporum*, *Paraconiothyrium zingiberacearum*, *Pyrenochaetopsis thailandensis*, *Remotididymella ageratinae*, *Setophoma thailandica* and *Stachybotrys phaeophialis* from urban soils, representing eight genera. *Scedosporium* species have previously been investigated in city soils in Thailand, where they are associated as human pathogens (Luplertlop et al., 2016, 2019). We isolated *Curvularia* and

Stachybotrys, both of which are known to cause respiratory diseases in humans (Iturrieta-González et al., 2020; Lombard et al., 2016). *Stachybotrys* has also been reported from building materials, indicating its potential to thrive in indoor environments (Lombard et al., 2016). We isolated two *Pyrenochaetopsis* species from both forests and urban areas. This genus has been formerly recorded in urban soils associated with parks in Finland and lawns in China (Hui et al., 2017; Xun et al., 2020). Similarly, we have obtained *Curvularia* from both urban environments (this study) and forest habitats (Yasanthika et al., 2024). That indicates their ability to survive in diverse environments. This adaptability of *Curvularia* and *Pyrenochaetopsis* highlights their ecological plasticity and their potential to be found in a wide range of habitats. In our study, *Remotididymella ageratinae* was recovered from both urban areas and disturbed caves (Figure 4.194), environments impacted by anthropogenic activities, showing its adaptability to stressful environments. Fungi in urban soils, such as *Remotididymella ageratinae*, may possess mechanisms for stress tolerance, including the production of secondary metabolites, which could be useful in extracting bioactive compounds (Shi et al., 2021). While several recent studies have focused on urban soil fungi, there is still a need to further explore these communities in urban areas of Thailand. Many of these fungi can be beneficial to maintain ecological balance and soil nutrition levels in urban environments. However, due to their high tolerance to harsh and artificial environments, some of these fungi can adversely affect humans. Thus, having a deeper understanding of the fungal communities in these environments is crucial to mitigate health concerns and manage potential risks.

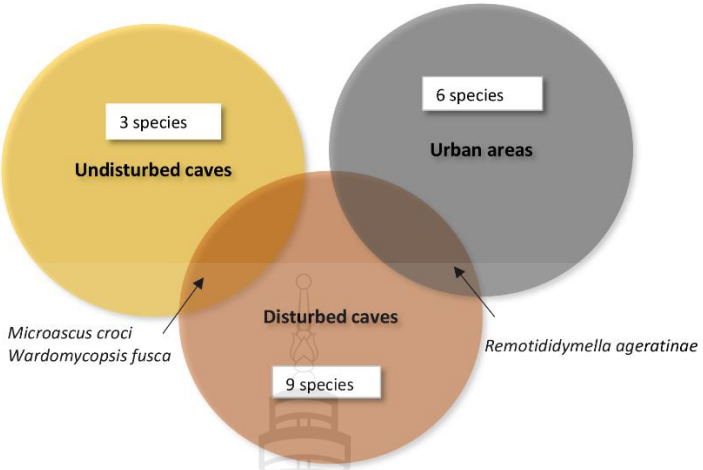


Figure 4.210 *Microascus croci* and *Wardomycopsis fusca* are collected from both disturbed and undisturbed caves and *Remotididymella ageratinae* was collected from disturbed caves and urban areas

Many of the previously recorded species from Thailand were identified as hyphomycetous asexual morphs (Manoch, 1998, 2004; Seephueak et al., 2019), whereas our study recovered ten *Dothediomycetes* (*Anteaglonium soli*, *Cumuliphoma indica*, *Ectophoma multirostrata*, *Nigrograna speluncae*, *Paraconiothyrium cyclothyrioides*, *P. zingiberacearum*, *Pararoussoella lincangensis*, *Pyrenochaetopsis orizicola*, *P. tropicalis*, and *Roussoella terrestris*), which produced coelomycetes asexual morphs. Additionally, we also isolated one *Sordariomycetes* (*Diaporthosporella soli*), which also exhibited a coelomycetes asexual morph. Numerous studies have revealed the high diversity of *Dothideomycetes* genera in Thailand soils, including *Ascochyta*, *Calophoma*, *Didymocyrtis*, *Paraboeremia*, and *Parathyridaria* (Pem et al., 2021). Members of this class are known to resist extreme environmental conditions, such as high temperatures, severe droughts, and high levels of solar radiation (Hou et al., 2020a). Similarly, we explored *Dothideomycetes* from cave and urban environments. Additionally, we encountered *Epicoccum catenisporum*, *Paraleptospora thailandica*, *Setophoma thailandica* and *Neopyrenochaeta telephoni*, all of which did not produce asexual or sexual morphs, but some of these produced chlamydospores. Chlamydospores are characterized by solitary, intercalary, and relatively thick-walled asexual spores, produced from swellings in young, aseptate mycelia. They function as survival structures under unfavorable conditions (Krug et al.,

2004). We employed the soil dilution plate method and baiting method to isolate colonies of *Ascomycota* species from the soil, which is recognized as an effective method to recover soil fungi. In order to obtain slow-growing and rare taxa, relatively high dilution levels, ranging from 10^{-3} to 10^{-6} have been used. It was found that low dilution levels can result in more fast-growing fungal colonies (Yasanthika et al., 2022b). I have used PDA as the growth media for fungal colony isolations, however there are several other growth media that can be used to successfully isolate and sporulate fungal colonies from soil such as Czapek-Dox agar medium, corn meal agar, Oat meal agar, potato carrot agar, diluted Sabouraud dextrose agar with salts, Malt extract agar, Czapek yeast extract agar, Phytone yeast extract agar, Malt yeast 4.% Sucrose agar, Yeast powder-soluble starch agar and water agar (Yasanthika et al., 2022). *Arthroderma* species can be sporulated using Phytone yeast extract agar and Yeast powder-soluble starch agar is used for sporulaing *Gymnoascus* species (Guarro et al., 2010).

Ascomycota, being one of the most abundant and diverse groups, is found across a wide range of genera in different ecosystems, suggesting that they are more adapted to environmental changes and stress (Tedersoo et al., 2022; Farias et al., 2023). This study has contributed to uncovering some of the uncommon taxa in soil, which is an important step toward revealing the true diversity of below-ground Ascomycota in Thailand. When compared to neighboring countries such as China, fungal investigations in Thailand, especially in diverse habitats such as caves, urban cities and hot springs, are still limited (Table 4.266). Thus, we suggest to focus on investigating different types of habitats in Thailand to gain a more comprehensive understanding of the diversity of below-ground *Ascomycota*. Thereby, we can discover the full extent of soil-dwelling *Ascomycota* species and their ecological roles, which is crucial for biodiversity conservation and understanding soil ecosystems.

CHAPTER 5

WEBSITE TO SERVE AS THE ONLINE DATABASE FOR SOIL *ASCOMYCOTA*

5.1 Introduction

Soil is a remarkably complex substrate that provides various niches for microbial communities. In this environment, fungi are the main biotic component and mediate many belowground functions. However, their distribution is variable due to inconsistencies in resource levels (nutrition, soil, water, and air) (Coleine et al., 2022). Besides, most fungi spend at least one stage of their life in the soil, showing different trophic modes such as pathogenic, saprobic, or mutualistic (Senanayake et al., 2022; Wilkes et al., 2021). Studies have shown that *Ascomycota*, *Basidiomycota*, *Chytridiomycota*, *Glomeromycota*, *Mortierellomycota* and *Rozellomycota* are widely distributed in edaphic habitats (Tedersoo et al., 2014; Tedersoo et al., 2020, 2021).

Culturing and high-throughput sequencing (HTS) methods are currently applied for detecting belowground *Ascomycota* groups (Baldrian et al., 2022; Tedersoo et al., 2014; Tedersoo et al., 2021; Wu et al., 2019). *Ascomycota* is represented by dominant classes in soil, including *Arthoniomycetes*, *Dothideomycetes*, *Eurotiomycetes*, *Leotiomycetes*, and *Sordariomycetes* (Blackwell, 2011; Tedersoo et al., 2014, 2020, 2021; Zhou et al., 2016). Of them, some genera, such as *Fusarium*, *Penicillium*, and *Phoma*, are prevalent (Crous et al., 2021; Tedersoo et al., 2021), while others, such as *Ambrosiella*, *Arcopilus*, *Didymocyrtis*, *Kionochaeta*, and *Parathyridaria* have rarely been isolated (Das et al., 2021; Lee et al., 2019; Park et al., 2017). This is because exclusive adaptations to belowground environments and a lack of isolation techniques make it difficult to recover *Ascomycota* species. Most soil ascomycetes are identified at higher taxonomic ranks through HTS, which has led to many recent publications and databases showing the taxonomy and distribution patterns of belowground fungi at the class or family levels (Yasanthika et al., 2022).

High-throughput sequencing has impacted the estimation of the number of fungi and the endemicity of soil taxa in different parts of the world (Tedersoo et al., 2022; Větrovský et al., 2020; Wu et al., 2019). Some databases have attempted to gather information on soil fungal diversity based on HTS. For example, the GlobalFungi (https://globalfungi.com/) provides information on taxonomy, ecology, and reference sequences of taxa from different habitats, including soil (Větrovský et al., 2020). The Global Soil Mycobiome consortium dataset, a global soil study, recovered 722,682 fungal Operational Taxonomic Units (OTUs), representing 62.4% of the total OTUs (Tedersoo et al., 2021). Among them, 330,054 OTUs were assigned to *Ascomycota*. The total number of fungi is estimated as 6.28 million species (Baldrian et al., 2022), and the highest diversity was found in soil and litter samples, revealing that soil fungal sequences have 75% overlap with previously known species. In addition, some studies have recovered unculturable fractions representing several new lineages at the phylum level (Blackwell, 2011; Senanayake et al., 2022; Tedersoo et al., 2014; Tedersoo et al., 2017, 2020).

Few studies compare the taxa recovered by HTS and culturing methods from the same sample or location. For example, Stefani et al. (Stefani et al., 2015) compared the fungal diversity from petrochemical-contaminated soils in Canada. They found that the number of OTUs ranged from 153 to 235, depending on the level of contamination (slightly to highly contaminated), and culturing methods yielded 8 to 43, respectively. Based on these results, we can roughly estimate that only around 5–65% of the soil fungal community can be cultured in any environment, and we need to develop methods to approach the rest of the 35–95%. A study on Antarctic crypto-endolithic fungal communities identified several black fungal species that were only detectable through cultivation and found a 12% overlap of species from both culture-dependent and -independent approaches, which resulted in 4,618 colonies and 1,439,748 sequences (Selbmann et al., 2021). The successful isolation of these species highlights the importance of using both complementary techniques (Selbmann et al., 2021). Compared to overall HTS results, the cultured fraction is smaller, and have vast differences between the two approaches. However, HTS results can excel in culturing the soil taxa, for example, to plan on isolating targeted taxa or selecting suitable fungal isolating methods in a particular area (Wu et al., 2019; Yasanthika et al., 2022).

Culturing is essential to obtain molecular and morphological data of species and to recover the undetectable ones from HTS.

Using an updated database to understand the total number of soil *Ascomycota* genera recovered from the culturing method

Around 80% of all soil-inhabiting taxa are not assigned to species level, and 20% to known orders (Hawksworth, 2001; Tedersoo et al., 2014; Tedersoo et al., 2017). Thus, the soil can potentially reveal many undiscovered species in the future (Baldrian et al., 2022; Wu et al., 2019). Contemporary studies have described and resolved soil-associated *Ascomycota* species from *Dothideomycete*s, *Eurotiomycetes*, *Leotiomycetes*, and *Sordariomycetes* with morpho-molecular support (Groenewald et al., 2018; Hou et al., 2020; Kandemir et al., 2022; Sun et al., 2020; Valenzuela-Lopez et al., 2018; Zhang et al., 2021). However, no recently updated study or database shows the total number of species isolated from the soil (Yasanthika et al., 2022).

Over the last few decades, several books were published based on morphology, such as Compendium of soil fungi (Domsch et al., 1980, 1993, 2007), Manual of soil fungi (Gilman, 1968), The Genera of Hyphomycetes from soil (GW, 1968), and Soil fungi: diversity and detection (Bridge & Spooner, 2001), which provided the diversities of worldwide soil species with comprehensive morphological illustrations. The Atlas of soil ascomycetes (Guarro et al., 2012) illustrated anamorphic and teleomorphic (fruit body and hyphomycetes form on cultures) structures, culture characteristics, and keys to the species. Currently, many taxonomists have adopted DNA sequences to determine species boundaries. However, species delineation criteria can differ among groups, such as cryptic species, pathogenic genera, and species complexes that need solid phylogenetic resolution (Bhunjun et al., 2022; Chethana et al., 2021; Jayawardena et al., 2021; Manawasinghe et al., 2021). Considering this scenario in soil-associated fungal groups, there are cryptic species, pathogenic genera, and species complexes of *Ascomycota* that the taxonomists have been using the polyphasic approach, combining morphological, physiological, ecological, and molecular methods to determine them (Chethana et al., 2021; Jayawardena et al., 2021; Jeewon & Hyde, 2016; Maharachchikumbura et al., 2021). Precise identification of fungal species/genera is integral for further use in taxonomy and biotechnology research (Ac & Thomas, 2021; Hyde et al., 2019; Wei et al., 2022; Wu et al., 2019; Yasanthika et al., 2022). For

example, pathogens are important in disease management, while soil-borne extremophilic genera (e.g., Verruconis) are sources of bioactive compounds (Chambergo & Valencia, 2016; Gutleben et al., 2018; Hyde et al., 2019). As a result of phylogenetic advancement over the recent years, the taxonomic data is being amended and updated, including the soil-residing *Ascomycota*. Similarly, the taxonomy and diversity studies have been conducted on a wide range of species in edaphic habitats worldwide. Thus, it consumes lots of time and effort to refer and retrieve mostly updated information of them present in various sources.

Therefore, rather than having scattered information on various resources, a database integrating taxonomy, ecological, and economic information of soil fungi helps to identify these organisms by end-users. The Soil Fungi website aims to collect and provide accurately identified soil fungi and continuously update checklists and notes on genera. Thus, it will be able to help to understand the total number of species/genera of *Ascomycota* isolated from soil worldwide. Further, this will increase the availability of information in the field and provide a valuable resource for researchers and students studying soil fungi. The website will be a central database of soil-associated fungal species, including their taxonomic descriptions and other relevant information. Users will be able to easily access and retrieve information from the website, such as the distribution of certain fungal species and their ecological roles. The website will also provide a platform for collaboration between researchers and interested parties, allowing them to share information and ideas. Furthermore, the Soil Fungi website will help estimate the number of soil genera discovered over time. This information will be useful for understanding the diversity and distribution of soil fungi and for developing conservation strategies for these important organisms.

5.2 Why is it Important to have a Database for Soil Fungi Recovered from Culturing Methods

The current information on soil fungal taxonomy is available as HTS and culture-dependent data (Alshuwaili et al., 2021; Aritonang et al., 2022; Gautam et al., 2022; Iliushin et al., 2022; Senanayake et al., 2022; Tedersoo et al., 2020; Wu et al.,

2019). These two forms of data can cause contradictions in species identifications and seem unstable, and affect studies. Moreover, the number of fungal species in the soil has been estimated from HTS methods, but there is no updated account for recently identified or recorded species from the soil. In addition, morpho-molecular identifications also face shortfalls as some genera are well-studied, while some have phylogenetic ambiguities (Dai et al., 2022; Hongsanan et al., 2020; Hyde et al., 2020). For example, specious genera, such as *Aspergillus*, *Cladosporium*, *Fusarium*, *Mucor*, *Penicillium*, and *Trichoderma*, are common in soil. Due to the similar morphologies resulting from hybridization, cryptic speciation, and convergent evolution, their species delineation is difficult (Montoya-Castrillón et al., 2021). Therefore, compiling updated phylogenetic and morphological data of the genera/species present in the soil is essential. It is also important to gather data on the type of soil ecosystem, locality, identification method, and economic impact of the species or genera. Since most of the information is scattered among various publications and databases, compiling them into a single database is beneficial for mycologists, ecologists, clinical studies, and the general public.

Even though information about soil fungi is available in online databases, e.g., Fungal Genera (Monkai, 2019), GlobalFungi (Větrovský et al., 2020), UNITE (Nilsson et al., 2019), and Global Soil Mycobiome consortium (GSMc) (Tedersoo et al., 2021), they lack specific information on fungal species and relevant morpho-molecular data. Further, in other databases like “Faces of Fungi” (http://www.facesoffungi.org) (Jayasiri et al., 2015), “Dothideomycetes” (https://www.dothideomycetes.org/) (Pem, 2019), “Sordariomycetes” (https://sordariomycetes.org/) (Bundhun, 2020), GMS microfungi (https://www.gmsmicrofungi.org/) (Chaiwan et al., 2021), and “Coelomycetes” (https://coelomycetes.org/) (Naruemon Huanraluek et al., 2021) information about Ascomycota studies are commonly found. However, a website compiling morpho-molecular data of soil fungi had not been developed. Therefore, I developed and implemented a web-based platform as the information hub for soil fungi research. The website provides a checklist of all the soil-associated *Ascomycota* genera. These generic notes include taxonomic descriptions, phylogenetic data, and other hosts/-substrates for each species, accompanied by photographic plates or drawings and detection methods. It also provides a list of novel or existing species of

soil fungi for each genus, which will be updated over time. The data from previous studies will be periodically included to disseminate information in a holistic approach, enhancing the in-depth understanding of the soil-inhabiting fungi and resource for retrieving multiple data.

5.3 Soil Fungi Website

The website provides a comprehensive checklist of all the soil-associated genera in *Ascomycota* essential for identifying and classifying soil fungi. The generic notes contain morphological descriptions, information on phylogenetic analyses such as gene regions, a summary of the latest phylogenetic revisions, ecological and economic impacts and the distribution. For each genus, a list of novel or existing soil-inhabiting species is provided, which will be uploaded and updated over time. Each species is accompanied by taxonomic descriptions, photographic plates or drawings, and detection methods. Each species/genus description is linked to the original publication/(s), thus, users have real-time access to further details (Figure 5.4). The website ensures that researchers can access the latest information about soil fungal taxonomy and keep up with the latest research developments. The data from previous studies are rearranged, and future studies will be periodically included to disseminate information in a holistic approach. Therefore, the website remains an up-to-date resource for researchers, providing them access to the latest research on soil fungi. These data will enhance an in-depth understanding of the soil-inhabiting fungi and will be important for future research. All the taxonomists and interested parties who work on soil fungi are encouraged to contribute their published data to this website, which will enhance the information availability and ensure that the website becomes an invaluable resource for retrieving multiple data, providing researchers a platform to share their research and collaborate with others in the field.

5.4 Construction

On the website, taxa are arranged according to the latest classification (Dai et al., 2022). The history of soil taxonomy is briefly described, and links to related literature are provided. All taxonomic entries are checked by the curators prior to uploading and are published in a consistent format. The list of curators and their contact details are displayed in Table 5.1.

Table 5.1 List of curators for the https://soilfun.org/ website

Position	Name	Contact details
Head curator	Dr. K. W. Thilini Chethana	kandawatte.thi@mfu.ac.th
Expert curator	Prof. Dr. Rasoul Zare	simplicillium@yahoo.com
Managing curator	Ms. W. A. Erandi Yasanthika	eyasanthika@gmail.com
Curators	Prof. Dr. Kevin D. Hyde	kdhyde3@gmail.com
	Prof. Dr. Lei Cai	cail@im.ac.cn
	Prof. Dr. Sajeewa Maharachchikumbura	sajeewa83@yahoo.com
	Dr. Dhanushka Wanasinghe	dnadeeshan@gmail.com/ wanasinghe@mail.kib.ac.cn
	Dr. Danushka Sandaruwan Tennakoon	danushkasandaruwanatm@gmail.com
	Dr. Rekhani Hansika Perera	hansi.rekha2@gmail.com

5.5 Interface and Visualization of the Database

The website is available at https://soilfun.org/ and provides a user-friendly interface to retrieve updated information on the classification of soil-inhabiting

Ascomycota. It is easy to access and navigate. The homepage comprises a navigation bar and a search tool to retrieve information.

5.5.1 Homepage

The Home page displays the summary of the project (Figure 5.1). A navigation bar is displayed at the top of the page. Below the navigation bar, the main objectives of the webpage are displayed in the left column, while the right column displays the search tool and the recently updated entries. The bottom of the page shows the publisher details, copyright information, and contact details. The navigation bar comprises eight menu items (Home, Outline, Archives, Reference, Curators, History, Reference, Notes, and Contact). These menu items facilitate easy navigation throughout the website, allowing users to access the information they need quickly and efficiently.

5.5.2 Outline

Under this navigation menu item, the website presents the latest taxonomic representation of genera that are recorded from soil obtained from peer-reviewed publications (Figure 5.2). The user can scroll down to find any taxa, or the search bar is optional, where the user can type preferred taxa and be directed to the exact location. Each taxon is linked to its corresponding taxonomic description, which can be accessed by clicking on the relevant name.

5.5.3 Archives

The orders to which different fungi isolated from soil belong are listed alphabetically under this menu item (Figure 5.3). When the user clicks on a preferred order, a dropdown list containing its families and a “Read more about…” link to the description of each hierarchical taxonomic level is displayed. Similarly, when the user clicks on a family, it shows the related genera and a “Read more about…” link to the family description. When the user selects a preferred genus, a “Read more about…” link to the description of the genus and a list of soil-associated species linked to their taxonomic descriptions and illustrations are shown (Figure 5.4). Each taxonomic description includes a web source link, enabling the reader to access the original publication directly. This information is continuously updated according to the latest publications, ensuring user access to the most up-to-date and accurate information on soil-inhabiting Ascomycota.

5.5.4 Curators

Curators and contact details are provided under this menu item (Fig. 5.5). These curators are expert fungal taxonomists who continuously monitor the webpage and suggest improvements.

5.5.5 History

Under this menu item, the evolution of soil fungal taxonomy is briefly discussed, together with the available culture-dependent and independent approaches (Figure 5.6).

5.5.6 References

References used in the entries are provided under this menu.

5.5.7 Notes

Important events, information, and the latest trends in soil fungal taxonomy are provided here.

References used in the entries are provided under this menu.

5.5.8 Contact

Under this menu item, a dialogue box is provided for the users to exchange information directly or share their suggestions and/or comments. Furthermore, the email and the address of the publisher are also given.

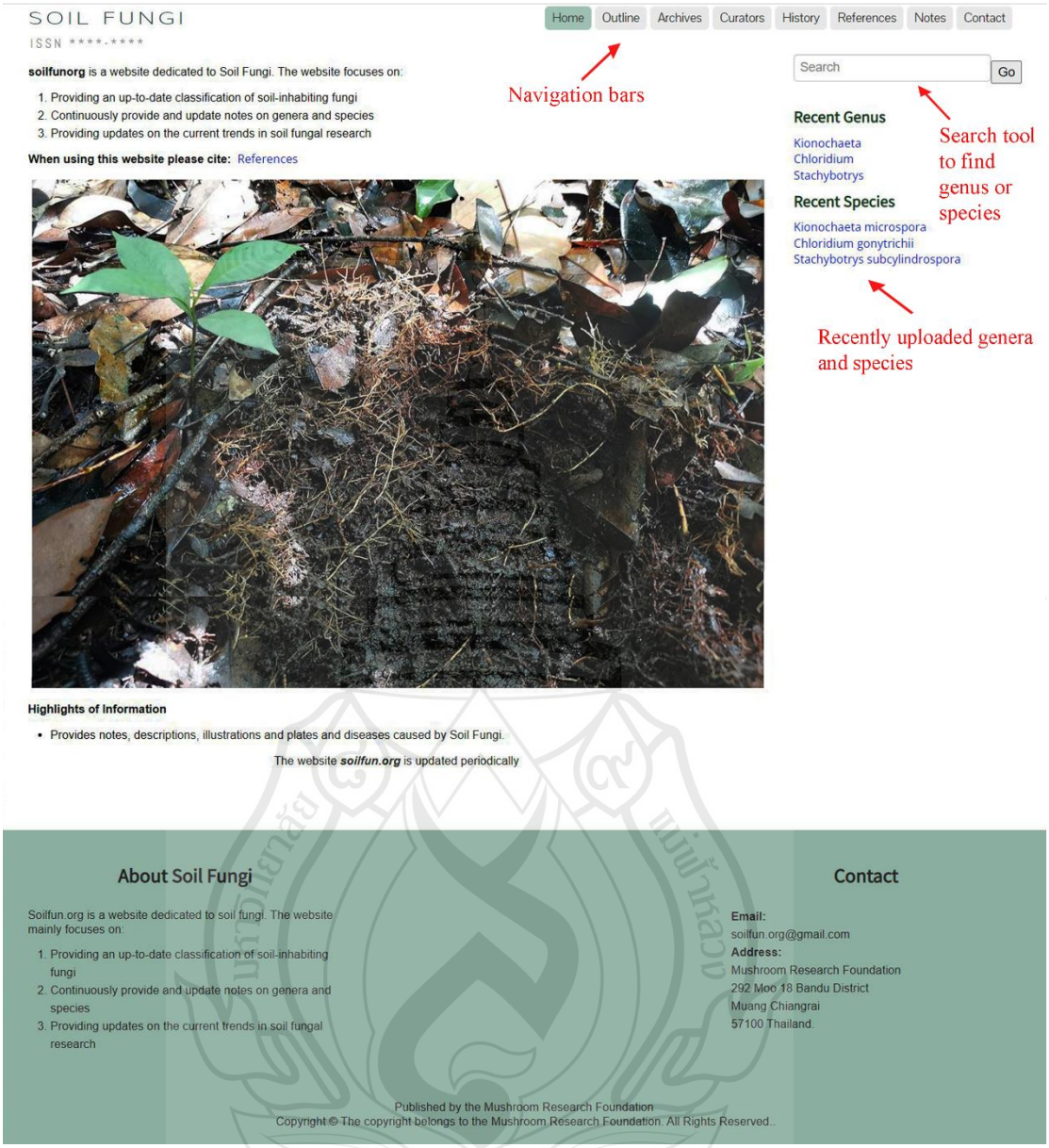


Figure 5.1 Home page of the Soil Fungi webpage

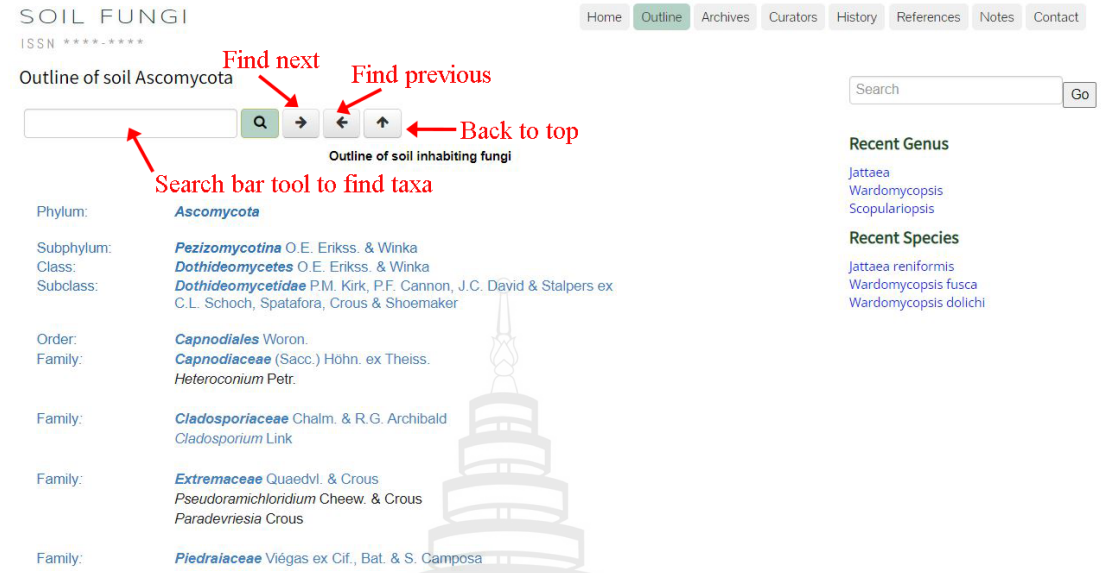


Figure 5.2 Heading "Outline" contains soil-inhabiting *Ascomycota* taxa according to the latest classification

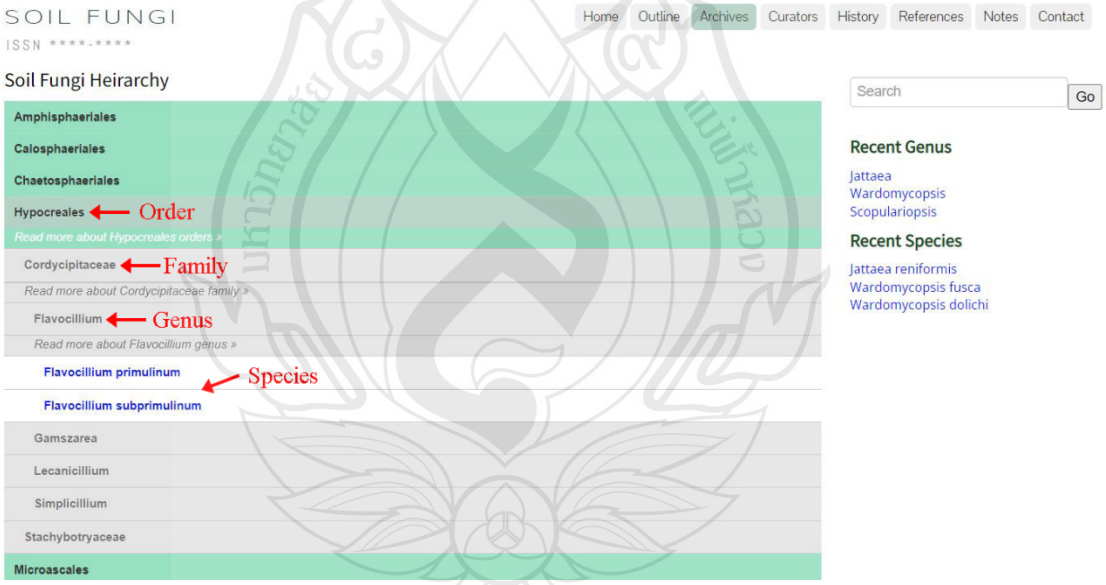


Figure 5.3 Heading "Archives" configured with a dropdown list of taxonomic hierarchy with links to order, family, genera, and species descriptions

SOIL FUNGI

ISSN ****-****

Home | Outline | Archives | Curators | History | References | Notes | Contact

Amphisphaeriales » Beltraniaceae » Beltraniella

Beltraniella fertilis

Species name

Beltraniella fertilis Heredia, R.M. Arias, M. Reyes & R.F. Castañeda, Fungal Diversity 11: 100 (2002) Fig. X

Index Fungorum number: IF489903; Faces of fungi number: FoF 03632 — IF and FOF numbers

Colonies on PDA pale white, reaching a diam. of 2–3 cm in 4 days at 25°C, flat and circular-shaped, pale brown, smooth at surface and produce highly branched melanized hyphae with brownish exudates in old cultures, after 16 weeks, with conidiophores forming on the mycelium; reverse light yellow to dark brown. Sexual morph: Undetermined. Asexual morph: Hyphomycetous. *Mycelium* mostly immersed in the substratum, composed of septate, branched subhyaline hyphae. *Setae* numerous, erect, straight or flexuous, unbranched, single or in small groups, thick-walled, verrucose, dark brown at the base, paler at apex, 61.7–149.8 µm long, 2.5–7 µm wide ($\bar{x}$ = 113 × 4 µm, n = 30) at the base, tapering to a pointed apex. *Conidiophores* macronematous, sometimes setiform; single, straight, septate, partly verrucose, thick-walled to smooth-walled, 6.4–91.5 µm long, 2.3–6.5 µm wide ($\bar{x}$ = 37 µm × 3.4, n = 30), sometimes branched at the apical region, dark brown to sub hyaline at the swollen base, paler and slightly tapering towards a pointed apex. *Conidiogenous cells* holoblastic, monoblastic to polyblastic, integrated, terminal. *Conidia* solitary to aggregated, acrogenous, simple, dry, straight, smooth, thin-walled, biconic, turbinate to pyriform, rostrate to pointed at proximal end, rounded at distal end, hyaline to sub hyaline, 5–15 µm long, 2–6.5 µm wide ($\bar{x}$ = 10.11 × 3.97 µm, n = 30) in the broadest part.

Morphological description

Distribution – Atlantic forests, Brazil, Mexico, Thailand — Host-substrate and distribution

Known hosts – Dead leaves of *Mangifera indica* and *Parinari alvimii*

Material examined – Thailand, Chiang Mai Province, Mae Tang district, Ban Pa Deng, Mushroom Research Center, N 19° 07' 13.7", E 98° 43' 52,9", 905 m, in forest soil (dominated by Dipterocarpaceae), 20th March 2019, Erandi Yasanthika, Erscm11 (MFLU 20-0506), living culture MFLUCC 20-0119.

Notes:

Beltraniella fertilis was introduced by Heredia et al. (2002) based on morphological characteristics. The sequence data for this species was provided by Lin et al. (2017) from strains which was isolated from decaying leaves collected in Thailand.

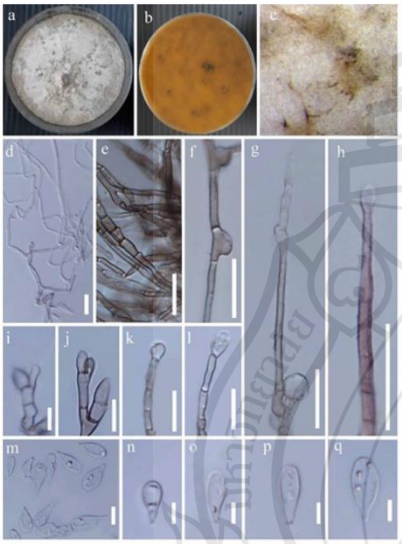


Figure legend

Figure X – ***Beltraniella fertilis*** (MFLUCC 20-0119) a Mature colony on PDA after 16 weeks with the sporulation. b Reverse of the colonies on PDA after 16 weeks. c Sporulation of the colony with conidial attachments on the mycelium. d Immature aseptate hyphae. e Mature pigmented, septate hyphae. f Chlamydospores on the mycelium. g Verrucose pigmented setae arising from the mycelium. h Conidiogenesis on the setae. I–l Conidiogenesis on the conidiophore. m–q Conidia. Scale bars: g = 25 µm d, h, i = 20 µm, e, f, j, k, l, m = 10 µm, n–q = 5 µm.

References:

Heredia G, Arias RM, Reyes M, Castañeda–Ruíz R. 2002 – New anamorph fungi with rhombic conidia from Mexican tropical forest litter. Fungal Diversity 11, 99–107.

Lin CG, Hyde KD, Lumyong S, Mckenzie EHC. 2017b – *Beltrania*–like taxa from Thailand. Cryptogamie, Mycologie 38, 301–319

Source:

Data and figures were reprinted with permission from:

Yasanthika WAE, Wanasinghe DN, Karunarathna SC, Bhat DJ, Samarakoon SMBC, Ren GC, Monkai J, Mortimer PE, Hyde KD 2020 – Two new Sordariomycetes records from forest soils in Thailand. Asian Journal of Mycology 3(1), 456–472, Doi 10.5943/ajom/3/1/16 -in AJOM

Web link

Recent Genus

Pseudopithomyces
Yunnania
Eosphaeria

Recent Species

Eosphaeria uliginosa
Stellatospora terricola
Pseudoneurospora amorphoporcata

Figure 5.4 Information provided for the soil-inhabiting species with taxonomic description

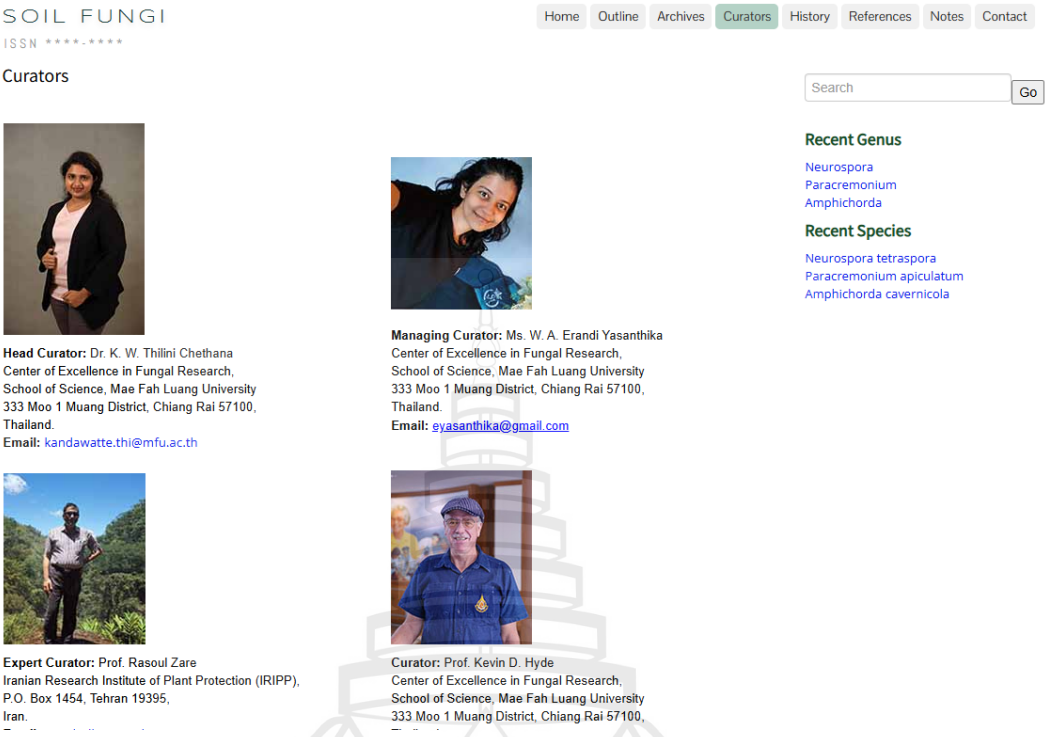


Figure 5.5 Heading "Curators" provides the list of curators with their contact details

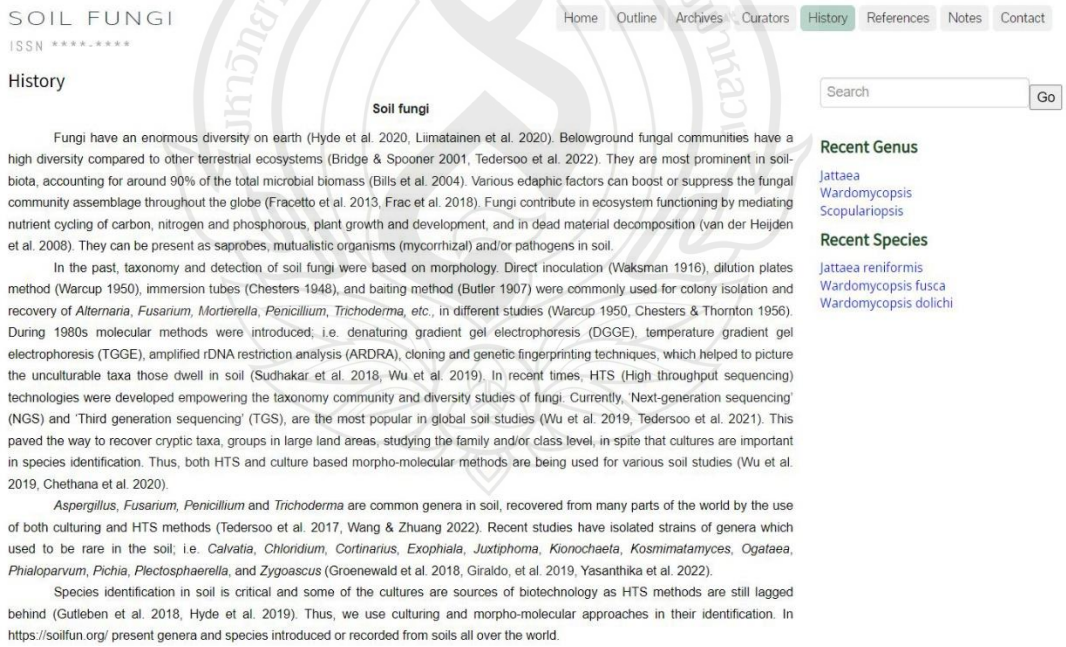


Figure 5.6 Heading "History" provides the history and development of studies on soil fungal taxonomy

CHAPTER 6

CONCLUSION

6.1 Overall Conclusion

This study primarily focused on four key areas: soil fungal isolation methods, global and Thai soil ascomycetes, and data digitization for soil *Ascomycota*. It provides a comprehensive review highlighting the value of culturing soil fungi in modern taxonomy. The study outlines twelve fungal isolation methods, compiles soil-associated *Ascomycota* genera recovered through culture-based methods worldwide with accompanying generic notes and the latest taxonomic outline, and offers a detailed taxonomic account of soil *Ascomycota* isolated from both disturbed and undisturbed habitats in Thailand, with special emphasis on uncommon species. Furthermore, it establishes a web-based platform that serves as the first dedicated database for globally recorded soil *Ascomycota* isolated through culture-dependent methods.

The study reviewed both culture-dependent and culture-independent methods that are used to isolate belowground *Ascomycota*. It discussed the evolution of the taxonomic approaches used in detecting soil-dwelling *Ascomycota* over time. While emphasizing the value of the culture-dependent methods in modern taxonomy, twelve soil fungal isolation methods are briefly discussed with the steps, their uses, and their importance. Mostly used isolation methods are the dilution plate method and the baiting method. The HTS method is widely applied in large-scale studies, and it has a high impact on estimating total fungal numbers in the global soil habitats. Therefore, it provides a broad understanding of fungal groups that are present in a given ecosystem. Therefore, the metadata generated in HTS can be useful in isolating fungi from soil. Thus, combining the fungal isolation methods with the HTS methods can be an important step in investigating new species from soil habitats.

The study provided the outline of *Ascomycota* recorded from worldwide edaphic habitats. We have compiled 270 genera notes, each note accompanied by comprehensive phylogenetic information, the sexual and asexual characteristics, the

ecological information with their host and geographical distribution, and the economic impact. The generic notes are updated with the recently updated molecular data, as many of the genera are revised by the various publications, and the data are scattered, thus, we have compiled the most updated phylogenetic information under each genus. Under each genus, the species recorded from soils are listed with the type of ecosystem and the country in which they have been reported. From the compiled genera, 45% are *Sordariomycetes* and 28% are *Dothideomycetes*. Among these genera, most of the species are reported from forest and agricultural areas, and some studies have focused on urban areas. However, caves and other extreme environments are poorly studied.

In Thailand, soil fungal studies are mainly focused on agricultural and forest soils, with around 185 species belonging to 79 genera reported over the past two decades. Therefore, we investigated *Ascomycota* species from three different soil ecosystems in Thailand. Samples were collected from caves, forests, and urban areas to capture a variety of genera present. The collection sites were further categorized as undisturbed and disturbed localities, which include undisturbed forests and caves and disturbed caves and urban areas. Species isolations were conducted using the soil dilution and soil baiting methods, and the species identification was carried out by morphological characterization and phylogenetic analyses using maximum likelihood and Bayesian methods. Different combinations of ITS, LSU, *rpb2*, *gapdh*, *tef1-α*, and *tub2* sequences were used in the species identification. Our study reveals 39 *Ascomycota* species, including eleven new species and 28 hosts and geographical records. Commonly recovered genera include *Curvularia*, *Paraconiothyrium*, *Pyrenochaetopsis*, *Stachybotrys*, and *Microascus*. We reported uncommon genera and species from the soil, namely *Anteaglonium*, *Diaporthosporella*, *Neoceratosperma*, *Paraleptospora*, *Pararoussoella*, *Kionochaeta*, and *Beltraniella* are genera that are newly reported in soil. *Anteaglonium*, *Diaporthosporella*, *Neoceratosperma* are isolated from cave habitats. *Paraleptospora* and *Pararoussoella*, *Kionochaeta*, and *Beltraniella* have been isolated from forest soils. Further, *Diaporthosporella soli*, *Paraleptospora thailandica*, *Pararoussoella lincangensis*, *Anteaglonium soli*, *Neoceratosperma soli*, *Roussoella terrestris*, *Acrocalymma medicaginis*, *Hansfordia pruni*, *H. pulvinata*, *Neoroussoella entadae*, *Paraconiothyrium cyclothyrioides*, *Curvularia dactylocteniicola* are newly reported from soil habitats. From the total

collection, 37 species were isolated using the dilution series method from the soil samples collected from all three habitat types. To obtain slow-growing and rare taxa, relatively high dilution levels, ranging from 10^{-3} to 10^{-6}, have been used. Two species were obtained from the baiting method using the forest soil samples. We introduced *Neptunomyces soli* (*Didymosphaeriaceae*) as a lignocellulophillic species isolated using wooden baits, and reported *Curvularia dactylocteniicola* as the keratinophilic species isolated using hair baits.

The https://soilfun.org/ website was established during this study, which serves as an online platform to compile the soil-associated *Ascomycota* species with comprehensive taxonomic descriptions and molecular data that are continuously being updated, following the most recent classifications. Because much information on *Ascomycota* in edaphic habitats is scattered in numerous publications, and continuously revised by various research groups, the information from those publications are/will be extracted and conglomerated on the website, where users have quick and user-friendly access. Therefore, users will be able to easily access and retrieve information from the website. As a step toward to the future, the Soil Fungi website will be an essential tool for researchers, students, and other interested parties in the field of soil mycology.

6.2 Research Advantages

This research provided an account of 270 genera reported from worldwide soils that serves as the most recent compilation and the taxonomic outline of the worldwide belowground *Ascomycota* genera. This comprehensive study expanded the taxonomic knowledge on *Ascomycota* inhabiting soils, including the taxonomic and phylogenetic information, ecological distribution, nutritional mode and biotechnological uses of each genus. Further, it listed the species recorded from soil with the country and habitat type, under each genus. This provides the preferences of these genera in various soil types and soil-associated habitats. This compilation further elucidates the frequently studied and poorly studied soil habitats. Soil fungi have mainly been isolated from forests and agricultural lands, which shows the need for focusing rest of the soil-associated habitats in the world. These notes summarize their nutritional modes while giving information

on the pathogenic (human/ animal/ plant), saprobic and mutual relationships that they have. Some of the human and animal pathogens are transferred from the soil; thus, understanding those genera and their distribution is helpful to minimize the risk and enhance the medical research. The study further provided the first up-to-date taxonomic outline dedicated to soil-associated *Ascomycota* genera.

Even though Thailand is a tropical country that has a high fungal diversity in the aboveground, there are lack of studies of Thai soil fungi, we investigated 39 species with morpho-molecular identifications. Most of the previously identified species are solely based on morphology, and we have provided DNA sequence data while introducing our species with more accurate identifications. Most of the research on Thai soils are conducted on agricultural lands and forests, however, we obtained a diverse range of *Dothideomycetes, Eurotiomycetes* and *Sordariomycetes* from forest, urban and cave habitats. Caves and urban habitats are poorly studied localities in Thailand. Our *Ascomycota* species collection from Thai soils provides better insights into which caves and urban habitats in Thailand hold a wide range of fungal species and the genera that have not been previously recorded from soils. Thus, fungal diversity in the caves and urban areas in Thailand is high. Previously, most of the species investigated in Thai soils were *Sordariomycetes*, whereas we investigated 24 *Dothideomycetes* species belonging to 12 families, 13 *Sordariomycetes* species belonging to 8 families and one *Eurotiomycetes* species. Thus, we obtained a diverse collection of *Ascomycota* with rare species and genera that are reported for the first time in edaphic habitats. Further, we have listed the soil-inhabiting ascomycete genera recorded from Thai soils during the past two decades. The list includes the habitat and the isolation method of the recorded genera, which becomes the first compilation of fungal genera recorded from Thai soils. It further provides an overview of Thai soil fungal studies and understands that Thai soil fungal studies need more molecular-based identification, as most of the reported genera were based on morphological identification. Our study revealed two *Dothideomycetes* species from the baiting method, which have lignocellulophillic and keratinophilic characteristics that potentially impact lingocellulose and keratin degradation in the soil ecosystem.

This study established the first web-based platform dedicated to *Ascomycota* species and genera isolated from soil habitats worldwide. It stands out among other

web-based fungal taxonomy platforms by providing a summary of soil *Ascomycota* species and genera, with information extracted from a wide range of scattered sources. While many global HTS-based soil studies are supported by online databases, taxa identified through culture-based morpho-molecular methods have, until now, lack a centralized database. This platform addresses that gap, offering a valuable resource for researchers working with soil-associated *Ascomycota*. Thus, it is an essential tool for researchers, students, and other interested parties in the field of soil mycology.

6.3 Future Directions

Ascomycota is the most abundant fungal phylum in soil ecosystems. While many recent global research have focused on HTS studies to recover soil fungi, this study emphasizes morpho-molecular studies for identifying belowground *Ascomycota*. HTS methods, although powerful in providing broad overviews of fungal communities at the class, family, or genus level, lack physical specimens necessary for detailed taxonomic study and long-term preservation. In contrast, isolation and culturing techniques are essential for obtaining living specimens that can be examined morphologically, sequenced, deposited in collections, and tested for biochemical properties. HTS results can guide the design and implementation of isolation-based studies by indicating which fungal taxa are abundant in a given location. However, HTS may fail to detect fungi present in low abundance, which can sometimes be successfully recovered through culturing. Among isolation methods, the dilution plate technique is widely applied to increase theyield of fungal colonies, facilitating the discovery of new species and capturing greater fungal diversity. The baiting method is particularly effective for revealing substrate preferences of soil fungal species. Isolates obtained through baiting can also be tested for their biochemical activities, such as their role in organic matter degradation. Therefore, isolation and culturing methods remain indispensable in soil fungal taxonomy. They not only provide physical specimens for taxonomic verification and future reference but also enable functional studies, including the screening of bioactive compounds.Focusing on studying soil *Ascomycota* is important as it is one of the largest fungal phyla in soil, providing opportunity to

study new fungal species and lineages present in the soil. HTS studies have identified several potentially new higher lineages in edaphic habitats; thus, it further confirms the opportunity to isolate new fungal species from below-ground habitats. *Alternaria*, *Aureobasidium*, *Cladosporium*, *Penicillium*, *Fusarium*, *Chaetomium*, *Acremonium*, and *Curvularia*, *Aspergillus*, *Exophiala*, *Knufia*, *Penicillium*, *Cladosporium*, *Talaromyces*, *Xylaria*, and *Trichoderma*, *Podospora*, *Chaetomium*, *Fusarium*, *Cadophora* and *Leohumicola* are some of the commonly found genera in soil that have high tolerance and adaptations to various niches. Thus, they are easily isolated, however, it needs to focus more on the uncommon species in below-ground habitats, which will help recover new species. These rare species are highly impacted in increasing the fungal diversity in a given ecosystem, which is indirectly beneficial in recovering the true fungal diversity in soils. To isolate the uncommon fungal species, the dilution series will be a successful method with high dilution rates, which facilitates to isolate slow slow-growing and uncommon fungal species. In addition, using effective media and various isolation methods will be helpful in isolating uncommon species residing in the soil.

The *Ascomycota* species are well studied in forests, agricultural lands and some of the urban areas globally. However, there are many poorly studied edaphic habitats that can potentially hold high fungal diversity. As previous studies explained, the forests hold high fungal diversity, however, it requires thorough studies on poorly studied habitats as well, in order to understand the actual distribution of fungi in global soils. Thus, focusing on the soil ecosystems, including caves, deserts, grasslands and extreme environments, will be important in understanding the accurate soil fungal diversity. Further, focusing on identifying the ascomycete species in the agricultural areas is important to identify the existence of potential plant pathogens in these environments. Similarly, identifying and understanding potential human pathogens living in the urban soils will be helpful in mitigating the risks. Fungi residing in the caves, extreme environments, urban soils, and deserts can have exclusive adaptation, which can possibly produce various bioactive compounds. Thus, focusing on isolating the fungi in harsh environments can be a source for biotechnology.

Thailand is a tropical country with high fungal diversity in the above-ground habitats. It needs more studies to focus on identifying the fungal species in the below-

ground environments. Agricultural soils and forests are relatively well studied in the country; thus, it needs to focus on unusual habitats as well. It is important to compile the fungal species isolated from edaphic habitats in Thailand, which will eventually help in understanding the total number of soil fungal species isolated from Thai soils. As most of the species from Thai soils are identified based on morphology, it is necessary to incorporate DNA sequences in the fungal identifications.

Taxonomy of the *Ascomycota* species is continuously updating field; however, compiling the genera and the species recorded from the soil habitats is important to understand the number of species recorded from worldwide soils. Therefore, updating https://soilfun.org/ website as a global online database will be helpful in obtaining the total fungal number isolated from soils worldwide. It will also facilitate as a medium for research to share the information, and it needs to further develop as a medium to engage in research discussions related to soil fungal studies.

6.4 Publications

Nine papers as the first author have been published as a result of this study in international journals, and 14 were published as co-author.

6.4.1 First Author Publications

Yasanthika, E., Dissanayake, L. S., Wanasinghe, D. N., Karunarathna, S. C., Mortimer, P. E., Samarakoon, B. C., . . . Hyde, K. D. (2020). *Lonicericola fuyuanensis* (Parabambusicolaceae): A new terrestrial pleosporalean ascomycete from Yunnan Province, China. *Phytotaxa, 446*(2), 103–113.

Yasanthika, W. A. E., Wanasinghe, D. N., Karunarathna, S. C., Bhat, D. J., Samarakoon, S. M. B. C., Ren, G. C., Monkai, J., Mortimer, P. E., & Hyde, K. D. (2020). Two new Sordariomycetes records from forest soils in Thailand. *Asian Journal of Mycology, 3*, 456–472.

Yasanthika, W. A. E., Wanasinghe, D. N., Ren, G. C., Karunarathna, S. C., Tennakoon, D. S., Monkai, J., Gui, H., Mortimer, P. E., Lumyong, S., & Hyde, K. D. (2021). Taxonomic and phylogenetic insights into novel Ascomycota from contaminated soils in Yunnan, China. *Phytotaxa, 513*, 203–225.

Yasanthika, W. A. E., Tennakoon, D. S., Farias, A. R. G., Bhat, D. J., & Wanasinghe, D. N. (2022). New soil-inhabiting Chaetosphaeriaceous records from Thailand. *Asian Journal of Mycology, 5*, 16–30.

Yasanthika, W. A. E., Wanasinghe, D. N., Mortimer, P. E., Monkai, J., & Farias, A. R. G. (2022). The importance of culture-based techniques in the genomic era for assessing the taxonomy and diversity of soil fungi. *Mycosphere, 13*, 724–751.

Yasanthika, W. A. E., Tennakoon, D. S., Gomes de Farias, A. R., Chethana, K. W. T., Bhat, J., & Wanasinghe, D. N. (2023). Isolation and characterization of novel Dothideomycetes species from forest soils in Chiang Rai and Krabi (Thailand): Additions to the diversity of *Curvularia* and *Verruconis*. *Phytotaxa, 609*, 17–44.

Yasanthika, W. A. E., Gomes de Farias, A. R., Wanasinghe, D. N., Chethana, K. W. T., Zare, R., Cai, L., Maharachchikumbura, S. S. N., Tennakoon, D. S., Perera, R. H., Luangharn, T., & Chomnunti, P. (2023). https://soilfun.org/, a web-based platform for soil-inhabiting *Ascomycota* species. *Studies in Fungi, 8*.

Yasanthika, W. A. E., Chethana, K. W. T., Wanasinghe, D. N., Tennakoon, D. S., Al-Otibi, F., & Hyde, K. D. (2024). Taxonomic novelties of soil-inhabiting pleosporalean fungi in Thailand using baiting method. *Phytotaxa, 676*, 1–24.

Yasanthika, W. A. E., Chethana, K. W. T., Fatimah Al-Otibi, Wanasinghe, D. N., Tennakoon, D. S., Samarakoon, M. C., Bhat, D. J., Ren, G. C., de Silva, N. I., Ekanayaka, A. H., Thakshila, S. A. D., Farias, A. R. G., & Hyde, K. D. (2025). Genera of soil *Ascomycota* and an account of soil-inhabiting species isolated from Thailand. *Manuscript submitted for publication.*

6.4.2 Co-author Publications

Chethana, K. W. T., Rathnayaka, A. R., Samarakoon, B. C., Wu, N., Wijesinghe, S. N., Yasanthika, W. A. E., . . . Hyde, K. D. (2023). AJOM new records and collections of fungi: 151–200. *Asian Journal of Mycology, 6*(2), 89–243.

Gomes de Farias, A. R., Yasanthika, W. A. E., & Monkai, J. (2023). Insights into the profile of soil fungal diversity in Thailand. *Asian Journal of Mycology, 6*(2), 305–317.

Htet, Y. M., Yasanthika, W. A. E., Hurdeal, V. G., & de Farias, A. R. G. (2024). *Absidia thailandica* sp. nov., an addition to the diversity of soil fungi from Thailand. *Phytotaxa, 646*(2), 157–168.

Hyde, K. D., Abdel-Wahab, M. A., Abdollahzadeh, J., Abeywickrama, P. D., Absalan, S., Afshari, N., . . . Ertz, D. (2023). Global consortium for the classification of fungi and fungus-like taxa. *Mycosphere, 14*(1), 1960–2012.

Hyde, K. D., Amuhenage, T. B., Apurillo, C. C. S., Asghari, R., Aumentado, H. D., Bahkali, A. H., . . . Dai, D. Q. (2023). *Fungalpedia*, an illustrated compendium of the fungi and fungus-like taxa. *Mycosphere, 14*(1), 1835–1959.

Hyde, K. D., Tennakoon, D. S., Jeewon, R., Bhat, D. J., Maharachchikumbura, S. S., Rossi, W., . . . Doilom, M. (2019). Fungal diversity notes 1036–1150: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 96*, 1–242.

Hyde, K. D., Xu, J., Rapior, S., Jeewon, R., Lumyong, S., Niego, A. G. T., . . . Stadler, M. (2019). The amazing potential of fungi: 50 ways we can exploit fungi industrially. *Fungal Diversity, 97*, 1–136.

Mikryukov, V., Dulya, O., Zizka, A., Bahram, M., Hagh-Doust, N., Anslan, S., . . . Tedersoo, L. (2023). Connecting the multiple dimensions of global soil fungal diversity. *Science Advances, 9*(48), eadj8016.

Ren, G., Wanasinghe, D. N., de Farias, A. R. G., Hyde, K. D., Yasanthika, E., Xu, J., . . . Gui, H. (2022). Taxonomic novelties of woody litter fungi (Didymosphaeriaceae, Pleosporales) from the Greater Mekong Subregion. *Biology, 11*(11), 1660.

Ren, G. C., Wanasinghe, D. N., Wei, D. P., Monkai, J., Yasanthika, E., Gui, H., . . . Hyde, K. D. (2020). *Loculosulcatispora thailandica* gen. et sp. nov. (Sulcatisporaceae), saprobic on woody litter in Thailand. *Phytotaxa, 475*, 67–78.

Tedersoo, L., Mikryukov, V., Anslan, S., Bahram, M., Khalid, A. N., Corrales, A., . . . Abarenkov, K. (2021). The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. *Fungal Diversity, 111*, 573–588.

Tedersoo, L., Mikryukov, V., Zizka, A., Bahram, M., Hagh-Doust, N., Anslan, S., . . . Abarenkov, K. (2022). Global patterns in endemicity and vulnerability of soil fungi. *Global Change Biology, 28*(22), 6696–6710.

Orders of *Ascomycota* paper (In prep)

Families of *Sordariomycetes* paper (Working)

REFERENCES

Ababaikeli, G., Abbas, A., Guo, S. Y., Tumier, A., & Mamuti, R. (2016). *Diploschistes tianshanensis* sp. nov., a corticolous species from Northwestern China. *Mycotaxon, 131*, 565–574. https://doi.org/10.5248/131.565

Abbott, E. V. (1927). *Scolecobasidium*, a new genus of soil fungi. *Mycologia, 19*, 29–31.

Abbott, S. P., Sigler, L., McAleer, R., McGough, D. A., Rinaldi, M. G., & Mizell, G. (1995). Fatal cerebral mycoses caused by the ascomycete *Chaetomium strumarium*. *Journal of Clinical Microbiology, 33*, 2692–2698. https://doi.org/10.1128/jcm.33.10.2692-2698.1995

Abdullah, S. K., & Saadullah, A. A. (2013). Soil myco-biota at grapevine plantations in Duhok, North Iraq. *Mesopotamia Journal of Agriculture, 41*, 402–412.

Abrantes, R. A., Refojo, N., Hevia, A. I., Fernandez, J., Isla, G., Cordoba, S., . . . Stchigel, A. M. (2021). *Scedosporium* spp. from clinical setting in Argentina, with the proposal of the new pathogenic species *Scedosporium americanum*. *Journal of Fungi, 7*, 160. https://doi.org/10.3390/jof7030160

Abreu, L. M., Moreira, G. M., Ferreira, D., Rodrigues-Filho, E., & Pfenning, L. H. (2014). Diversity of *Clonostachys* species assessed by molecular phylogenetics and MALDI-TOF mass spectrometry. *Fungal Biology, 118*, 1004–1012. https://doi.org/10.1016/j.funbio.2014.10.001

Absalan, S., Armand, A., Jayawardena, R. S., & McKenzie, E. H. C. (2024). Diversity of Pleosporalean fungi isolated from rice (*Oryza sativa* L.) in Northern Thailand and descriptions of five new species. *Journal of Fungi, 10*, 763. https://doi.org/10.3390/jof10110763

Abu-Mejdad, N. M. J. A. (2013). Biochemical study for three keratins baiting and using it to isolation and identification some fungi from soil in Basrah, Iraq. *International Journal of Engineering and Innovative Technology, 3*, 216–224.

Acharius, E. (1852). *Conatum Praem. Gen. Lich.: 20*. Diploschistes.

Adams, P. B., & Ayers, W. A. (1979). Ecology of *Sclerotinia* species. *Phytopathology, 69*, 896–899.

Adikaram, N. K. B., & Yakandawala, D. M. D. (2020). A checklist of plant pathogenic fungi and Oomycota in Sri Lanka. *Ceylon Journal of Science*, *49*, 93–123. https://doi.org/10.4038/cjs.v49i1.7709

Adhikari, M., Kim, S. W., Gwon, B. H., Ju, H. J., Lee, H. B., & Lee, Y. S. (2019). *Westerdykella reniformis*: A new record from field soils in Korea. *Korean Journal of Mycology, 47*, 47–53. https://doi.org/10.4489/KJM.20200005

Adhikari, M., Yadav, D. R., Kim, S., Um, Y. H., Kim, H. S., Lee, H. B., . . . Lee, Y. S. (2015). Discovery of two new *Talaromyces* species from crop field soil in Korea. *Mycobiology, 43*, 402–407. https://doi.org/10.5941/MYCO.2015.43.4.402

Aghamirian, M. R., & Ghiasian, S. A. (2013). The prevalence of fungi in soil of Qazvin, Iran. *Jundishapur Journal of Microbiology, 6*, 76–79. https://doi.org/10.5812/jjm.4591

Agnihothrudu, V. (1962). A comparison of some techniques for the isolation of fungi from tea soils. *Mycopathologia*, *16*, 235–242. https://doi.org/10.1007/BF02145735

Ahebwa, A., Mongkol, R., Sawangsri, P., & Kanjanamaneesathian, M. (2020). Vapour-phase efficacy of selected essential oils individually and in combination against Aspergillus flavus, A. niger, Fusarium proliferatum, and Curvularia lunata. *New Zealand Plant Protection, 73*, 40–48. https://doi.org/10.30843/nzpp.2020.73.11713

Aime, M. C., Miller, A. N., Aoki, T., Bensch, K., Cai, L., Crous, P. W., . . . Schoch, C. L. (2021). How to publish a new fungal species, or name, version 3.0. *IMA Fungus*, *12*, 1–15. https://doi.org/10.1186/s43008-021-00063-1

Al-Bedak, O. (2019). *Paracremonium moubasheri*, a new species from an alkaline sediment of lake Hamra in Wadi-El-Natron, Egypt with a key to the accepted species. *Studies in Fungi*, *4*, 216–222. https://doi.org/10.5943/sif/4/1/23

Albarracín Orio, A. G., Brücher, E., & Ducasse, D. A. (2016). A strain of *Bacillus subtilis* subsp. *subtilis* shows a specific antagonistic activity against the soil-borne pathogen of onion *Setophoma terrestris*. *European Journal of Plant Pathology*, *144*, 217–223. https://doi.org/10.1007/s10658-015-0762-0

Alcorn, J. L., & Irwin, J. A. G. (1987). *Acrocalymma medicaginis* gen. et sp.nov. causing root and crown rot of *Medicago sativa* in Australia. *Transactions of the British Mycological Society, 88*, 163–167. https://doi.org/10.1016/S0007-1536(87)80211-5

Ali, I., Kanhayuwa, L., Rachdawong, S., & Rakshit, S. K. (2013). Identification, phylogenetic analysis and characterization of obligate halophilic fungi isolated from a man-made solar saltern in Phetchaburi province, Thailand. *Annals of Microbiology, 63*, 887–895. https://doi.org/10.1007/s13213-012-0540-6

Ali, A. M., Moghazy, S., Shaban, G., & El-Sababty, Z. (2009). Heat-resistant fungi isolated from soil in minia governorate, Egypt. *Assiut University Journal of Botany, Assiut University, 38*, 93–106. https://doi.org/10.25130/tjps.23.2018.147

Alidadi, A., Vala, S. A., & Jouzani, G. S. (2020). *Botryotrichum iranicum* sp. nov. and *Trematosphaeria magenta* sp. nov. as two new species from Iran. *Mycological Progress, 19*, 1575–1586. https://doi.org/10.1007/s11557-020-01648-7

Almaguer, M., Rojas, T. I., Dobal, V., Batista, A., & Aira, M. J. (2013). Effect of temperature on growth and germination of conidia in Curvularia and Bipolaris species isolated from the air. *Aerobiologia, 29*, 13–20. https://doi.org/10.1007/s10453-012-9257-z

Alotaibi, M. O., Sonbol, H. S., Alwakeel, S. S., Suliman, R. S., Fodah, R. A., Jaffal, A. S. A., . . . Mohammed, A. E. (2020). Microbial Diversity of Some Sabkha and Desert Sites in Saudi Arabia. *Saudi Journal of Biological Sciences, 27*, 2778–2789. https://doi.org/10.1016/j.sjbs.2020.06.038

Altayyar, I. A., Osman, N. A., Elbreki, M. F., Ibrahim, H., Aboalasad, A., Barkah, A., & Almahdi, N. (2016). Isolation and identification of soil keratinophilic fungi from different area in south of Libya. *International Journal of Applied Medical and Biological Research, 1*, 27–32.

Amin, I., Nazir, R., & Rather, M. A. (2024). Evaluation of multi-heavy metal tolerance traits of soil-borne fungi for simultaneous removal of hazardous metals. *World Journal of Microbiology and Biotechnology, 40*, 175. https://doi.org/10.1007/s11274-024-03987-z

Amma, S., Toju, H., Wachrinrat, C., Sato, H., Tanabe, A. S., Artchawakom, T., & Kanzaki, M. (2018). Composition and diversity of soil fungi in *Dipterocarpaceae*-dominated seasonal tropical forests in Thailand. *Microbes and Environments, 33*, 135–143. https://doi.org/10.1264/jsme2.ME17168

Anandaraj, M., & Sarma, Y. R. (1990). A simple baiting technique to detect and isolate Phytophthora capsici ("P. palmivora" MF4) from soil. *Mycological Research, 94*, 1003–1004. https://doi.org/10.1016/S0953-7562(09)81321-X

Anderson, J. M. (2009). Why should we care about soil fauna?. *Pesquisa Agropecuária Brasileira, 44*, 835–842.

An, Z.-Q., Hendrix, J. W., Hershman, D. E., & Henson, G. T. (1990). Evaluation of the "Most Probable Number" (Mpn) and Wet-Sieving Methods for Determining Soil-Borne Populations of Endogonaceous Mycorrhizal Fungi. *Mycologia, 82*, 576–581. https://doi.org/10.1080/00275514.1990.12025932

Anandaraj, M., & Sarma, Y. R. (1990). A simple baiting technique to detect and isolate Phytophthora capsici ('P. Palmivora' MF4) from soil. *Mycological Research, 94*, 1003–1004. https://doi.org/10.1016/S0953-7562(09)81321-X

Anderson, I. C., & Cairney, J. W. (2004). Diversity and ecology of soil fungal communities: Increased understanding through the application of molecular techniques. *Environmental Microbiology, 6*, 769–779.

Apinis, A. E. (1967). *Dactylomyces* and *Thermoascus*. *Transactions of the British Mycological Society, 50*, 573–582.

Apinis, A. E. (1968). Relationships of certain keratinophilic *Plectascales*. *Mycopathologia et Mycologia Applicata, 35*, 97–104. https://doi.org/10.1007/BF02049572

Aptroot, A. (1995). A monograph of *Didymosphaeria*. *Studies in Mycology, 37*, 1–160.

Aragona, M., Haegi, A., Valente, M. T., Riccioni, L., Orzali, L., Vitale, S., . . . Infantino, A. (2022). New-generation sequencing technology in diagnosis of fungal plant pathogens: A dream comes true?. *Journal of Fungi, 8*, 737. https://doi.org/10.3390/jof8070737

Ariyawansa, H., Kang, J., Chukeatirote, E., & Hyde, K. (2014a). *Pyrenophora*. *Mycosphere, 5*, 351–362. https://doi.org/10.5943/mycosphere/5/2/9

Ariyawansa, H. A., Hyde, K. D., Jayasiri, S. C., Buyck, B., Chethana, K. T., Dai, D. Q., . . . Hernawati. (2015a). Fungal diversity notes 111–252—taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity, 75,* 27–274. https://doi.org/10.1007/s13225-015-0346-5

Ariyawansa, H. A., Phukhamsakda, C., Thambugala, K. M., Bulgakov, T. S., Wanasinghe, D. N., Perera, R. H., . . . Bhat, J. D. (2015b). Revision and phylogeny of *Leptosphaeriaceae*. *Fungal Diversity, 74*, 19–51. https://doi.org/10.1007/s13225-015-0349-2

Ariyawansa, H. A., Tanaka, K., Thambugala, K. M., Phookamsak, R., Tian, Q., Camporesi, E., . . . Hyde, K. D. (2014b). A molecular phylogenetic reappraisal of the *Didymosphaeriaceae* (= *Montagnulaceae*). *Fungal Diversity, 68,* 69–104. https://doi.org/10.1007/s13225-014-0305-6

Ariyawansa, H. A., Tsai, I., Thambugala, K. M., Chuang, W. Y., Lin, S. R., Hozzein, W. N., . . . Cheewangkoon, R. (2020). Species diversity of Pleosporalean taxa associated with *Camellia sinensis* (L. Kuntze in Taiwan). *Scientific Reports, 10,* 1–20. https://doi.org/10.1038/s41598-020-69718-0

Arnaud, G. (1952). Mycologie concrète: Ggenera. *Bulletin Trimestriel de la Société Mycologique de France, 68,* 181–223.

von Arx, J. (1971). With plates – *Gymnoascaceae* opinion especially *Apinis* clarify identity variety fungi *Gymnoascaceae* YpSs- species developing species descriptions following disposition proposed: Mycologia Tieghem – YpSs-agar velvety furrowed, yellow, gametangia coiling.

von Arx, J. A. (1975). The ascomycete genus *Triangularia* in Europe. *Persoonia, 8,* 391–398.

von Arx, J. A. (1985). On *Achaetomium* and a new genus *Subramaniula* (*Ascomycota*). *Proceedings of the Indian Academy of Sciences, 94*, 341−345.

Arzanlou, M. (2012). *Aureobasidium iranianum*, a new species on bamboo from Iran. *Mycosphere, 3*, 404–408. https://doi.org/10.5943/mycosphere/3/4/2

Arzanlou, M., Groenewald, J. Z., Gams, W., Braun, U., Shin, H. D., . . . Crous, P. W. (2007). Phylogenetic and morphotaxonomic revision of *Ramichloridium* and allied genera. *Studies in Mycology, 58,* 57–93. https://doi.org/10.3114/sim.2007.58.03

Asemaninejad, A., Thorn, R. G., Branfireun, B., & Lindo, Z. (2018). Climate change favours specific fungal communities in boreal peatlands. *Soil Biology and Biochemistry, 120*, 28–36. https://doi.org/10.1016/j.soilbio.2018.01.029

Asgari, B., & Zare, R. (2010). Two new species of *Preussia* from Iran. *Nova Hedwigia, 90*, 533.

Asgari, B., & Zare, R. (2011). A contribution to the taxonomy of the genus *Coniocessia* (*Xylariales*). *Mycol Prog, 10*, 189–206.

Austin, C. P., Brady, L. S., Insel, T. R., & Collins, F. S. (2004). NIH Molecular libraries initiative. *Science, 306*, 1138–1139. https://doi.org/10.1126/science.1105511

Aveskamp, M. M., de Gruyter, J., Woudenberg, J. H. C., Verkley, G. J. M., & Crous, P. W. (2010). Highlights of the *Didymellaceae*: A polyphasic approach to characterise *Phoma* and related pleosporalean genera. *Studies in Mycology, 65*, 1–60. https://doi.org/10.3114/sim.2010.65.01

Averill, C., Werbin, Z. R., Atherton, K. F., Bhatnagar, J. M., & Dietze, M. C. (2021). Soil microbiome predictability increases with spatial and taxonomic scale. *Nature Ecology & Evolution*, *5*, 747–756. https://doi.org/10.1038/s41559-021-01445-9

Ayim, B. Y., Das, K., Cho, Y. J., Lee, S. Y., & Jung, H. Y. (2020). A New Record of *Epicoccum draconis* isolated from the soil in Korea. *The Korean Journal of Mycology*, *48*, 39–45. https://doi.org/10.4489/KJM.20200004

Ayvar-Serna, S., Díaz-Nájera, J. F., Vargas-Hernández, M., Mena-Bahena, A., Mora-Romero, G. A., Leyva-Madrigal, K. Y., . . . Tovar-Pedraza, J. M. (2022). Curvularia brachyspora causing leaf spot on Cucurbita argyrosperma in Mexico. *Journal of General Plant Pathology, 88*, 331–335. https://doi.org/10.1007/s10327-022-01078-1

Azaz, A. D. (2003). Isolation and identification of soil borne fungi in fields irrigated by GAP in Harran Plain using two isolation methods. *Turkish Journal of Botany, 27*, 83–92.

Aziz, N., & Zainol, N. (2018). Isolation and identification of soil fungi isolates from forest soil for flooded soil recovery. *IOP Conference Series: Materials Science and Engineering, 342*. https://doi.org/012028.10.1088/1757-899X/342/1/012028

Giridhar Babu, A., Kim, S. W., Yadhav, D. R., Adhikari, M., Kim, C., Lee, H. B., ... & Lee, Y. S. (2014). A new record of *Pseudallescheria boydii* isolated from crop field soil in Korea. *Mycobiology, 42*, 397–400. https://doi.org/10.5941/MYCO.2014.42.4.397

Bagga, R., & Chattu, V. K. (2018). *Triadelphia pulvinata*: A rare invasive fungal infection in a diabetic patient. *Medical Mycology Case Reports, 22*, 8–10. https://doi.org/10.1016/j.mmcr.2018.07.001

Baimai, V. (2010). Biodiversity in Thailand. *The Journal of the Royal Institute of Thailand, 2*, 107–118.

Bailey, F., & Gray, N. F. (1989). The comparison of isolation techniques for nematophagous fungi from soil. *Annals of Applied Biology, 114*, 125–132. https://doi.org/10.1111/j.1744-7348.1989.tb06792.x

Bainier, G. (1907a). Mycothe`que de l'e´cole de Pharmacie. XI *Paecilomyces*, genre nouveau de Muce´dine´es. *Bull Soc Mycol Fr., 23*, 26–27.

Bainier, G. (1907b). Mycothèque de l'École de Pharmacie, XIV. *Scopulariopsis* (*Penicillium* pro parte – genre nouveau de mucédinées). *Bulletin Trimestriel de la Société Mycologique de France, 23*, 98–105.

Baldrian, P., Větrovský, T., Lepinay, C., & Kohout, P. (2021). High-throughput sequencing view on the magnitude of global fungal diversity. *Fungal Diversity, 114*(1), 539–547. https://doi.org/10.1007/s13225-021-00472-y

Baldrian, P., Bell-Dereske, L., Lepinay, C., Větrovský, T., & Kohout, P. (2022a). Fungal communities in soils under global change. *Studies in Mycology, 103*, 1–24. https://doi.org/10.3114/sim.2022.103.01

Baldrian, P., Větrovský, T., Lepinay, C., & Kohout, P. (2022b). High-throughput sequencing view on the magnitude of global fungal diversity. *Fungal Diversity, 114*, 539–547. https://doi.org/10.1007/s13225-021-00472-y

Ballhausen, M., Veen, J., Hundscheid, M., & de Boer, W. (2015). Methods for baiting and enriching fungus-feeding (mycophagous) rhizosphere bacteria. *Frontiers in Microbiology, 6,* 1416. https://doi.org/10.3389/fmicb.2015.01416

Banerjee, S., Zhao, C., Garland, G., Edlinger, A., García-Palacios, P., Romdhane, S., . . . van der Heijden, M. G. (2024). Biotic homogenization, lower soil fungal diversity and fewer rare taxa in arable soils across Europe. *Nature Communications, 15,* 327. https://doi.org/10.1038/s41467-023-44073-6

Bao, D. F., Hyde, K. D., Maharachchikumbura, S. S., Perera, R. H., Thiyagaraja, V., Hongsanan, S., . . . Luo, Z. L. (2023). *Taxonomy, phylogeny and evolution of freshwater Hypocreomycetidae (Sordariomycetes)*. Springer Netherlands.

Baranetzky, J. (1872). Entwickelungsgeschichte des *Gymnoascus* Reessii. *Bot. Zeitung, 30,* 145.

Barbosa, M. A., Araújo, M. A., Oliveira, M. S., Costa, P. M., Malosso, E., & Castañeda-Ruiz, R. F. (2015). Two new records of microfungi from the Brazilian Atlantic forest. *Mycotaxon, 130,* 967–970. https://doi.org/10.5248/130.967

Bahram, M., & Netherway, T. (2022). Fungi as mediators linking organisms and ecosystems. *FEMS Microbiology Reviews, 46*(2), fuab058. https://doi.org/10.1093/femsre/fuab058

Barr, M. E. (1987a). New taxa and combinations in the *Loculoascomycetes*. *Mycotaxon, 29,* 501–505.

Barr, M. E. (1987b). *Prodromus to class Loculoascomycetes*. University of Massachusetts Press.

Barr, M. E. (2000). *Teichosporaceae,* another family in the *Pleosporales*. *Mycotaxon, 82,* 373–389.

Barron, G. L. (1964). A new genus of the Hyphomycetes from soil. *Mycologia, 56,* 514–518.

Barron, G. L., Cain, R. F., & Gilman, J. C. (1961). A revision of the genus *Petriella*. *Canadian Journal of Botany, 39,* 837–845. https://doi.org/10.1139/b61-071

Barseghyan, G. S., & Solomon, P. (2011). The genus *Peziza* Dill. ex Fr. (*Pezizales, Ascomycota* – in Israel. *Ascomycete Org, 2,* 39–50.

Basha, S., & Ulaganathan, K. (2002). Antagonism of Bacillus species (strain BC121) towards Curvularia lunata. *Current Science, 82*, 1457–1463.

Basu, S., Bose, C., Ojha, N., Das, N., Das, J., Pal, M., . . . Khurana, S. (2015). Evolution of bacterial and fungal growth media. *Bioinformation, 11*, 182. https://doi.org/10.6026/97320630011182

Bartoli, A., Maggi, O., & Persiani, A. M. (1984). Effetia, a new genus of ascomycetes from tropical forest soils. *Mycotaxon, 19*, 515–522.

Bates, S. T., Garcia-Pichel, F., Thomas, H., & Nash, I. I. I. (2010). Fungal components of biological soil crusts: Insights from culture-dependent and culture-independent studies. *Bibliotheca Lichenologica, 105*, 197–210

Batista, A. C., Maia, H., & da S. (1959). Uma nova doença fungica de peixe ornamental. *Anais da Sociedade de Biologia de Pernambuco, 16*, 153–159.

Batista, A. C., & Fonseca, O. M. (1965). *Pochonia humicolan*. gen. en. sp., uma curiosa entidade fungica dos solos do Nordeste do Brasil. *Publicacões do Instituto de Micologia, Universidade do Recife, 462*, 1–11.

Belosokhov, A., Yarmeeva, M., Kokaeva, L., Chudinova, E., Mislavskiy, S., & Elansky, S. (2022). *Trichocladium solani* sp. nov.—A new pathogen on potato tubers causing yellow rot. *Journal of Fungi, 8*, 1160. https://doi.org/10.3390/jof8111160

Benjamin, C. (1955). Ascocarps of Aspergillus and Penicillium. *Mycologia, 47*, 669–687.

Bennett, S. E. B. J. W. (2007). *An overview of the genus Aspergillus*. The Aspergilli.

Bensch, K., Braun, U., Groenewald, J. Z., & Crous, P. W. (2012). The genus Cladosporium. *Studies in Mycology, 72*, 1–401. https://doi.org/10.3114/sim0003

Berbee, M. L., & Taylor, J. W. (1992). 18S Ribosomal RNA gene sequence characters place the human pathogen Sporothrix schenckii in the genus Ophiostoma. *Experimental Mycology, 16*, 87–91. https://doi.org/10.1016/0147-5975(92)90044-R.

Berbee, M. L., Pirseyedi, M., & Hubbard, S. (1999). Cochliobolus phylogenetics and the origin of known, highly virulent pathogens, inferred from ITS and glyceraldehyde-3-phosphate dehydrogenase gene sequences. *Mycologia, 91*, 964–977. https://doi.org/10.1080/00275514.1999.12061106

Berkeley, M. J., & Broome, C. E. (1873). Enumeration of the fungi of ceylon. part II., containing the remainder of the Hymenomycetes, with the remaining established tribes of fungi. *Botanical Journal of the Linnean Society, 14*, 29–64.

Berkeley, M. J., & Broome, C. (1850). Notices of british fungi (438-501). *The Annals and Magazine of Natural History, 5*, 455–466.

Berkeley, M. J. (1838). Notices of british fungi. *Ann Mag Nat Hist Ser, 11*, 257–264.

Berkeley, M. J. (1860). *Outlines of british fungology: Containing characters of above a thousand species of fungi, and a complete list of all that have been described as natives of the British Isles*. L. Reeve.

Berlese, A. N. (1900). *Icones fungorum ad usum sylloges Saccardianae adcommodatae. 3. Sphaeriaceae allantosporae*. Cramer.

Bertoldi, M. de. (1976). New species of Humicola: An approach to genetic and biochemical classification. *Canadian Journal of Botany, 54*, 2755–2768. https://doi.org/10.1139/b76-296

Beuchat, L. R., & Pitt, J. I. (1992). Detection and enumeration of heat-resistant molds. In C. Vanderzant & D. F. Splittstoesser (eds.), *Compendium of methods for the microbiological examination of foods* (pp. 251–263). American Public Health Association.

Beyma, F. H. V. (1940). Beschreibung einiger neuer Pilzarten aus dem Centraalbureau voor Schimmelcultures, Baarn (Nederland), VI. Mitteilung. *Antonie van Leeuwenhoek, 6*, 263– 290.

Bhanot, V., Mamta, Gupta, S., & Panwar, J. (2024). Phylloplane fungus Curvularia dactyloctenicola VJP08 effectively degrades commercially available PS product. *Journal of Environmental Management, 351*, 119920. https://doi.org/10.1016/j.jenvman.2023.119920

Bhatnagar, A., & Bhatnagar, M. (2005). Microbial diversity in desert ecosystems. *Current Science, 89*(1), 91–100.

Bhunjun, C. S., Dong, Y., Jayawardena, R. S., Jeewon, R., Phukhamsakda, C., Bundhun, D., . . . Sheng, J. (2020). A polyphasic approach to delineate species in Bipolaris. *Fungal Diversity, 102*, 225–256. https://doi.org/10.1007/s13225-020-00446-6

Bhunjun, C. S., Niskanen, T., Suwannarach, N., Wannathes, N., Chen, Y. J., McKenzie, E. H., . . . Lumyong, S. (2022). The numbers of fungi: Are the most speciose genera truly diverse?. *Fungal Diversity, 114*, 387-462. https://doi.org/10.1007/s13225-022-00501-4

Bills, G. F., Christensen, M., Powell, M., & Thorn, G. (2004). Saprobic soil fungi. In G. M. Mueller, G. F. Bills & M. S. Foster (eds.), *Biodiversity of fungi, inventory and monitoring methods* (pp. 271–302). Elsevier Academic Press.

Bills, G. F., Arias, R. M., Reyes, M., & Heredia, G. (2001). *Merimbla humicoloides* sp. nov. from conifer forest soil of Veracruz state. Mexico. *Mycological Research, 105*, 1273–1279. https://doi.org/10.1016/S0953-7562(08)62000-6

Biswas, R., & Sarkar, A. (2018). 'Omics' Tools in Soil Microbiology: The state of the art. In T. Adhya, B. Lal, B. Mohapatra, D. Paul & S. Das (eds.), *Advances in soil microbiology: Recent trends and future prospects* (pp 35–64). Springer. https://doi.org/10.1007/978-981-10-6178-3_3

Bisby, G. (1945). Stachybotrys and memnoniella. *Transactions of the British Mycological Society, 28*, 11–12.

Blackwell, M. (2011). The fungi: 1, 2, 3 … 5.1 million species?. *American Journal of Botany, 98*, 426–438. https://doi.org/10.3732/ajb.100029

Boedijn, K. B. (1933). Über einige phragmosporen Dematiazen. *Bulletin du Jardin Botanique de Buitenzorg, 13*, 120–134.

Boedijn, K. B. (1934). Ueber di neue gattung trigonia van beyma thoe kingma. *Ann. Mycol. Notitiam Sci. Mycol. Universal, 32*, 302.

Boehm, E. W. A., Mugambi, G. K., Miller, A. N., Huhndorf, S. M., Marincowitz, S., Spatafora, J. W., . . . Schoch, C. L. (2009). A molecular phylogenetic reappraisal of the hysteriaceae, mytilinidiaceae and gloniaceae (pleosporomycetidae, dothideomycetes – with keys to world species). *Studies in Mycology, 64*, 49–83. https://doi.org/10.3114/sim.2009.64.03

Boerema, G. H., & Bollen, G. J. (1975). Conidiogenesis and conidial septation as differentiating criteria between Phoma and Ascochyta. *Persoonia, 8,* 111–144.

Boerema, G. H., de Gruyter, J., Noordeloos, M. E., & Hamers, M. E. C. (2004). *Phoma identification manual differentiation of specific and infra-specific taxa in culture*. CABI Publishing.

Boesewinkel, H. J. (1982). Cylindrocladiella, a new genus to accommodate Cylindrocladium parvum and other small-spored species of Cylindrocladium. *Can J Bot, 60,* 2288–2294.

Bohacz, J., & Korniłłowicz-Kowalska, T. (2019). Fungal diversity and keratinolytic activity of fungi from lignocellulosic composts with chicken feathers. *Process Biochemistry, 80,* 119–128. https://doi.org/10.1016/j.procbio.2019.02.012

Bojanich, M. V., Sarmiento, M. M., Giusiano, G., Mangiaterra, M., & Basualdo, J. Á. (2015). Huevos de Toxocara canis como anzuelo para hongos geófilos en una ciudad subtropical. *Revista Iberoamericana de Micología, 32,* 273–276. https://doi.org/10.1016/j.riam.2014.09.004

Bolger, T., & Ellis, M. (2015). An overview of caves & caving in Thailand. In *Asian Transkarst Conference* (pp. 203–207). https://www.researchgate.net/publication/316596220_An_overview_of_caves_caving_in_Thailand

Bonito, G., Benucci, G. M. N., Hameed, K., Weighill, D., Jones, P., Chen, K. H., . . . Vilgalys, R. (2019). Fungal-bacterial networks in the populus rhizobiome are impacted by soil properties and host genotype. *Frontiers in Microbiology, 10,* 481. https://doi.org/10.3389/fmicb.2019.00481

Bonorden, H. F. (1864). *Abhandlungen aus dem gebiete der mykologie*. Abhandlungen der Naturforschenden Gesellschaft zu Halle.

Boonmee, S., Wanasinghe, D. N., Calabon, M. S., Huanraluek, N., Chandrasiri, S. K., Jones, G. E., . . . Hyde, K. D. (2021). Fungal diversity notes 1387–1511: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 111,* 1–335. https://doi.org/10.1007/s13225-021-00489-3

Borelli, R. (1980). Revision of the genus Cladophialophora. *Mycologia, 72,* 720–728.

Borut, S. Y., & Johnson, T. W. (1962). Some biological observations on fungi in estuarine sediments. *Mycologia, 54*, 181–193. https://doi.org/10.1080/00275514.1962.12024990

Brauna-Morževska, E., Stoddard, F. L., Bankina, B., Kaņeps, J., Bimšteine, G., Petrova, I., . . . Fridmanis, D. (2023). Evaluation of pathogenicity of Botrytis species isolated from different legumes. *Frontiers in Plant Science, 14*. https://doi.org/10.3389/fpls.2023.1069126

Brierley, W. B., Jewson, S. T., & Brierley, M. (1928). The quantitative study of soil fungi. *International Congress of Soil Science, 3*, 48–71.

Bridge, P., & Spooner, B. (2001). Soil fungi: Diversity and detection. *Plant and Soil 232*, 147–154. https://doi.org/10.1023/A:1010346305799

Bisby, G. (1943). Stachybotrys. *Transactions of the British Mycological Society, 26*, 133–143.

Bisby, G. (1945). Stachybotrys and Memnoniella. *Transactions of the British Mycological Society, 28*, 11–12.

Brooks, F. T., & Hansford, C. G. (1923). Mould growths upon cold-storage meat. *Trans. Brit. Mycol. Soc., 8,* 113–141.

Bucher, V. V. C., Pointing, S. B., Hyde, K. D., & Reddy, C. A. (2004). Production of wood decay enzymes, loss of mass, and lignin solubilization in wood by diverse tropical freshwater fungi. *Microbial Ecology, 48*, 331–337. https://doi.org/10.1007/s00248-003-0132-x

Bundhun, D., Wanasinghe, D. N., Maharachchikumbura, S. S., Bhat, D. J., Huang, S. K., Lumyong, S., . . . Hyde, K. D. (2021). *Yuxiensis granularis* gen. et sp. nov., a novel quellkörper-bearing fungal taxon added to Scortechiniaceae and inclusion of Parasympodiellaceae in Coronophorales based on phylogenetic evidence. *Life, 11*, 1011. https://doi.org/10.3390/life11101011

Butler, E. J. (1907). An account of the genus Pythium and some Chytridiaceae. *Memoirs of the Department of Agriculture in India, 1*, 1–162

Cadez, N., & Smith, M. T. (2011). Hanseniaspora Zikes (1912). In C. P. Kurtzman, J. W. Fell & T. Boekhout (eds.), *The yeasts* (pp. 421-434). Elsevier.

Cai, L., Jeewon, R., & Hyde, K. D. (2006). Molecular systematics of Zopfella and allied genera: Evidence from multigene sequence analyses. *Mycological Research, 110*, 359–368. https://doi.org/10.1016/j.mycres.2006.01.007

Cain, R. F. (1956). Studies of coprophilous ascomycetes: II Phaeotrichum, a new cleistocarpous genus in a new family, and its relationships. *Canadian Journal of Botany, 34*, 675–687.

Cain, R. F. (1961). Anixiella and diplogelasinospora, two genera with cleistothecia and pitted ascospores. *Canadian Journal of Botany, 39*, 1667–1677. https://doi.org/10.1139/b61-145

Calabon, M. S., Jones, E. G., Pang, K. L., Abdel-Wahab, M. A., Jin, J., Devadatha, B., ... & Hyde, K. D. (2023). Updates on the classification and numbers of marine fungi. *Botanica Marina, 66*, 213–238. https://doi.org/10.1515/bot-2023-0032

Calduch, M., Gené, J., Stchigel, A. M., Cano, J. F., & Guarro, J. (2004). Ramophialophora, a new anamorphic genus of Sordariales. *Studies in Mycology, 50*, 83–88.

Calvillo-Medina, R. P., Ponce-Angulo, D. G., Raymundo, T., Müller-Morales, C. A., Escudero-Leyva, E., Campos Guillén, J., . . . Bautista-de Lucio, V. M. (2021). *Purpureocillium roseum* sp. nov. a new ocular pathogen for humans and mice resistant to antifungals. *Mycoses, 64*, 162–173. https://doi.org/10.1111/myc.13198

Calduch, M., Gené, J., Stchigel, A. M., Cano, J. F., & Guarro, J. (2004). Ramophialophora, a new anamorphic genus of Sordariales. *Studies in Mycology, 50*, 83–88.

Călin, M., Răut, I., Constantinescu-Aruxandei, D., Doni, M. B., Arsene, M. L., Corneli, N. O., . . . Lazăr, V. (2017). Influence of culture conditions on growth of keratinophilic fungal strains. Scientific Bulletin. Series F. *Biotechnologies, 21*, 173–178.

Cameron, E. K., Martins, I. S., Lavelle, P., Mathieu, J., Tedersoo, L., Gottschall, F., . . . Eisenhauer, N. (2018). Global gaps in soil biodiversity data. *Nature Ecology & Evolution, 2*, 1042–1043. https://doi.org/10.1038/s41559-018-0573-8

Cannon, P., Buddie, A., Bridge, P., de Neergaard, E., Lübeck, M., & Askar, M. (2012a). Lectera, a new genus of the Plectosphaerellaceae for the legume pathogen Volutella colletotrichoides. *MycoKeys, 3*, 23–36. https://doi.org/10.3897/mycokeys.3.3065

Cannon, P. F., Damm, U., Johnston, P. R., & Weir, B. S. (2012b). Colletotrichum: Current status and future directions. *Studies in Mycology, 73*, 181–213.

Cannon, P. F. (1986). A revision of achaetomium, achaetomiella and subramaniula, and some similar species of chaetomium. *Transactions of the British Mycological Society, 87*, 45–76.

Cano, J., Solé, M., & Guarro, J. (2002). Pseudoamauroascus, a new genus of the family Amauroascaceae. *Studies in Mycology, 47*, 175–180.

Cano, J., & Guarro, J. (1990). The genus aphanoascus. *Mycological Research, 94*, 355–377. https://doi.org/10.1016/S0953-7562(09)80361-4

Carbone, I., & Kohn, L. M. (1999). A method for designing primer sets for speciation studies in filamentous ascomycetes. *Mycologia, 91*, 553. https://doi.org/10.2307/3761358

Caretta, G., & Piontelli, E. (1997). Preserved ascomatal and other fungal structures on the remains of a ninth century Longobard abbess exhumed from a Monastery in Pavia, Italy. *Mycopathologia, 140*, 77-83. https://doi.org/10.1023/A:1006805226954

Carter, E., & Boudreaux, C. (2004). Fatal cerebral phaeohyphomycosis due to Curvularia lunata in an immunocompetent patient. Journal of Clinical *Microbiology, 42*, 5419–5423. https://doi.org/10.1128/JCM.42.11.5419-5423.2004

Carmaran, C. C., Berretta, M., Martínez, S., Barrera, V., Munaut, F., & Gasoni, L. (2015). Species diversity of Cladorrhinum in Argentina and description of a new species, Cladorrhinum australe. *Mycological Progress, 14*, 94. https://doi.org/10.1007/s11557-015-1106-3

Carmichael, J. W. (1966). Cerebral mycetoma of trout due to a phialophora-like fungus. *Subouraudia, 5*, 120–123.

Carneiro de Almeida, D. A., Pascholati Gusmão, L. F., & Miller, A. N. (2014). A new genus and three new species of hysteriaceous ascomycetes from the semiarid region of Brazil. *Phytotaxa, 176*, 298–308.

Carreiro, M. M., & Koske, R. E. (1992). Room temperature isolations can bias against selection of low temperature microfungi in temperate forest soils. *Mycologia, 84*(6), 886-900. https://doi.org/10.1080/00275514.1992.12026221

Carvalhais, L. C., Dennis, P. G., Tyson, G. W., & Schenk, P. M. (2012). Application of meta transcriptomics to soil environments. *Journal of Microbiological Methods, 91*, 246–251. https://doi.org/10.1016/j.mimet.2012.08.011

Castañeda–Ruiz, R. F., Cano, J., & Guarro, J. (1996). Notes on conidial fungi. VII. Two new species of Beltraniella from Cuba. *Mycotaxon, 58*, 243−251.

Castellani, A., & Chalmers, A. J. (1919). *Manual of tropical medicine*. Baillière, Tindal & Cox.

Castrillón, A. L., Moraes, M. A. P. D., & Furtado, M. D. S. S. (1976). Isolamento de Microsporum amazonicum do solo do estado do Amazonas, Brasil. *Acta Amazônica, 6*, 487–490.

Cesati, V. (1856). *Botanische zeitung*. Leipzig.

Cesati, V., de Notaris, G. (1863). Schema di classificazione degle sferiacei italici aschigeri piu' o meno appartenenti al genere Sphaeria nell'antico significato attribuitoglide Persono. *Commentario della Società Crittogamologica Italiana, 1*, 177–420.

Chai, C. Y., Gao, W. L., Yan, Z. L., & Hui, F. L. (2022). Four new species of Trichomonascaceae (Saccharomycetales, Saccharomycetes) – from Central China. *MycoKeys, 90*, 1–18. https://doi.org/10.3897/mycokeys.90.83829

Chaiwan, N., Gomdola, D., Wang, S., Monkai, J., Tibpromma, S., Doilom, M., . . . Hyde, K. D. (2021). https://gmsmicrofungi. org: an online database providing updated information of microfungi in the Greater Mekong Subregion. *Mycosphere, 12*, 1409–1422. https://doi.org/10.5943/mycosphere/12/1/19

Chambergo, F. S., & Valencia, E. Y. (2016). Fungal biodiversity to biotechnology. *Applied Microbiology and Biotechnology, 100*, 2567–2577. https://doi.org/10.1007/s00253-016-7305-2

Chang, R., Wang, Y., Liu, Y., Wang, Y., Li, S., Zhao, G., . . . Si, H. (2023). Nine new species of black lichenicolous fungi from the genus Cladophialophora (Chaetothyriales – from two different climatic zones of China). *Frontiers in Microbiology, 14*. https://doi.org/10.3389/fmicb.2023.1191818

Changtian, L., Fenghua, T., Jae-Seoun, H. U. R., Yu, L. I., & Ahmadi, H. (2022). Studies on endolichenic fungi in Myelochroa (Lichenized fungi, Ascomycota – in Jeju Island, Korea. *Journal of Clinical and Medical Images, 6*, 1–9.

Chaudhary, P., Campbell, J., Hawksworth, D. L., & Sastry, K. N. (2006). Vittatispora, a new melanosporaceous genus from Indian soil. *Mycologia, 98*, 460–467.

Checa, J., Barassa, J., Moreno, G., Fort, F., & Guarro, J. (1988). The genus Coniochaeta (Sacc.) Cooke (Coniochaetaceae, Ascomycotina) in Spain. *Cryptogamie. Mycologie, 9*, 1–34.

Cheewangkoon, R., Groenewald, J. Z., Summerell, B. A., Hyde, K. D., To-Anun, C., & Crous, P. W. (2009). Myrtaceae, a cache of fungal biodiversity. *Persoonia: Molecular Phylogeny and Evolution of Fungi, 23*, 55–85. https://doi.org/10.3767/003158509X474752.

Chen, J., Xu, L. L., Liu, B., & Liu, X. Z. (2007). Taxonomy of Dactylella complex and Vermispora. I. Generic concepts based on morphology and ITS sequences data. *Fungal Divers, 26*, 73–83.

Chen, Q., Hou, L. W., Duan, W. J., Crous, P. W., & Cai, L. (2017). Didymellaceae revisited. *Studies in Mycology, 87*, 105–159. https://doi.org/10.1016/j.simyco.2017.06.002

Chen, Q., Jiang, J. R., Zhang, G. Z., Cai, L., & Crous, P. W. (2015). Resolving the Phoma enigma. *Studies in Mycology, 82*, 137–217. https://doi.org/10.1016/j.simyco.2015.10.003

Chen, T., Wang, S., Jiang, X., Huang, Y., Mo, M., & Yu, Z. (2023). New species of Didymellaceae within aquatic plants from Southwestern China. *Journal of Fungi, 9*, 761. https://doi.org/10.3390/jof9070761

Chen, W. H., Li, D., Liang, J. D., Ren, X. X., Zhao, J. H., & Han, Y. F. (2024). Two new Cordyceps-like species, *Perennicordyceps zongqii* sp. nov. (Polycephalomycetaceae – and *Purpureocillium zongqii* sp. nov. (Ophiocordycipitaceae), in Hypocreales from karst region of China. *MycoKeys, 110*, 141–158. https://doi.org/10.3897/mycokeys.110.135724

Chen, Y., Ran, S. F., Dai, D. Q., Wang, Y., Hyde, K. D., Wu, Y. M., . . . Jiang, Y. L. (2016). Mycosphere essays 2. myrothecium. *Mycosphere, 7*, 64–80.

Cheng, X., Li, W., & Cai, L. (2015). Molecular phylogeny of Ascotricha, including two new marine algae-associated species. *Mycologia, 107*, 490–504. https://doi.org/10.3852/14-210

Chernomor, O., von Haeseler, A., & Minh, B. Q. (2016). Terrace aware data structure for phylogenomic inference from supermatrices. *Systematic Biology, 65*, 997–1008. https://doi.org/10.1093/sysbio/syw037

Chesters, C. G. C. (1940). A method for isolating soil fungi. *Transaction of the British Mycological Society, 2*, 352–355.

Chesters, C. G. C. (1948). A contribution to the study of fungi in the soil. *Transactions of the British Mycological Society, 30*, 100–113. https://doi.org/10.1016/S0007-1536(48)80038-0

Chesters, C. G. C., & Thornton, R. H. (1956). A comparison of techniques for isolating soil fungi. *Transactions of the British Mycological Society, 39*, 301–313. https://doi.org/10.1016/S0007-1536(56)80015-6

Chethana, K. W. T., Jayawardena, R. S., & Hyde, K. D. (2020). Hurdles in fungal taxonomy: Effectiveness of recent methods in discriminating taxa. *Megataxa, 1*, 114–122. https://doi.org/10.11646/megataxa.1.2.2

Chethana, K. W. T., Manawasinghe, I. S., Hurdeal, V. G., Bhunjun, C. S., Appadoo, M. A., Gentekaki, E., . . . Hyde, K. D. (2021). What are fungal species and how to delineate them?. *Fungal Diversity, 109*, 1–25. https://doi.org/10.1007/s13225-021-00483-9

Chethana, K. W. T., Rathnayaka, A. R., Samarakoon, B. C., Wu, N., Wijesinghe, S. N., Yasanthika, W. A. E., . . . Hyde, K. D. (2023). AJOM new records and collections of fungi: 151–200. *Asian Journal of Mycology, 6*, 89–243. https://doi.org/10.5943/ajom/6/2/7

Chiriví-Salomón, J. S., Danies, G., Restrepo, S., & Sanjuan, T. (2015). *Lecanicillium sabanense* sp. nov. (Cordycipitaceae – a new fungal entomopathogen of coccids). *Phytotaxa, 234*, 63–74.

Chuaseeharonnachai, C., Suetrong, S., Nuankaew, S., Somrithipol, S., Hongsanan, S., Srikitikulchai, P., . . . Boonyuen, N. (2020). *Synnematotriadelphia* gen. nov. (S. stilboidea comb. nov. and S. synnematofera comb. nov. – and *Triadelphia hexaformispora* sp. nov. in the family Triadelphiaceae. *Mycological Progress, 19*, 127–137. https://doi.org/10.1007/s11557-019-01547-6

Ciferri, R., Batista, A. C., & Campos, C. A. (1956). Taxonomy of Piedraia hortai and systematic position of the Piedraiaceae family. *Publicações do Instituto de Micologia da Universidade do Recife, 45*, 1–9.

Ciferri, R. (1958). *Manuale di micologia medica*. Pavia.

Clements, F. E., & Shear, C. L. (1931). *The genera of fungi*. H.W. Wilson.

Clendenin, I. (1896). Lasiodiplodia Ellis & Everh. n. gen. Bot. gaz. *Crawfordsville, 21*, 92–93.

Čmoková, A., Rezaei-Matehkolaei, A., Kuklová, I., Kolařík, M., Shamsizadeh, F., Ansari, S., . . . Hubka, V. (2021). Discovery of new *trichophyton* members, *T. persicum* and *T. spiraliforme* spp. nov., as a cause of highly inflammatory Tinea Cases in Iran and Czechia. *Microbiology Spectrum, 9*(2). https://doi.org/10.1128/Spectrum.00284-21

Cochet, G. (1939). Sur un nouveau champignon arthrosporé (*Arthrographis langeroni* ng, n. sp. – agent pathogène d'une onychomycose humaine. *Annales de Parasitologie Humaine et Comparée, 17*, 98–101.

Cooke, M. (1887). Synopsis Pyrenomycetum. *Grevillea, 16*, 16–19.

Coleine, C., Zucconi, L., Onofri, S., Pombubpa, N., Stajich, J. E., & Selbmann, L. (2018). Sun exposure shapes functional grouping of fungi in crypto-endolithic Antarctic communities. *Life, 8*, 19.

Coleine, C., Stajich, J. E., & Selbmann, L. (2022). Fungi are key players in extreme ecosystems. *Trends in Ecology & Evolution, 37*, 517–528. https://doi.org/10.1016/j.tree.2022.02.002

Collado, J., Platas, G., Paulus, B., & Bills, G. F. (2007). High-throughput culturing of fungi from plant litter by a dilution-to-extinction technique. *FEMS Microbiology Ecology, 60*, 521–533. https://doi.org/10.1111/j.1574-6941.2007.00294.x

Corda, A. C. I. (1831). *Die pilze deutschlands. abt., tab. 21-32*. Sturm.

Corda, A. C. J. (1837). *Icones fungorum hucusque cognitorum* (vol. 1). R. and J.E. Taylor.

Corda, A. C. J. (1838). *Icones fungorum hucusque cognitorum* (vol. 2). R. and J.E. Taylor.

Corda, A. C. J. (1839a). *Icones fungorum hucusque cognitorum*. Prague.

Corda, A. K. J. (1840). *Icones fungorum hucusque cognitorum*. Prague.

Corda, A. K. J. (1839b). *Pracht-flora europaeischer schimmelbildungen*. Leipzig.

Corlett, R. T. (2014). *The ecology of tropical East Asia* (2nd ed.). Oxford University Press.

Corrêa-Moreira, D., de Lima Neto, R. G., da Costa, G. L., de Moraes Borba, C., & Oliveira, M. M. E. (2022). Purpureocillium lilacinum an emergent pathogen: Antifungal susceptibility of environmental and clinical strains. *Letters in Applied Microbiology, 75*, 45–50. https://doi.org/10.1111/lam.13707

Cosio, T., Pica, F., Fontana, C., Pistoia, E. S., Favaro, M., Valsecchi, I., . . . Gaziano, R. (2024). Stephanoascus ciferrii complex: The current state of infections and drug resistance in humans. *Journal of Fungi, 10*, 294. https://doi.org/10.3390/jof10040294

Crane, J. L., & Miller, A. N. (2016). Studies in genera similar to Torula: *Bahusaganda, Bahusandhika, Pseudotorula*, and *Simmonsiella* gen. nov. *IMA Fungus, 7*, 29–45. https://doi.org/10.5598/imafungus.2016.07.01.03

Crous, P. W., & Groenewald, J. Z. (2013). A phylogenetic re-evaluation of Arthrinium. *IMA Fungus, 4*, 133–154. https://doi.org/10.5598/imafungus.2013.04.01.13

Crous, P. W., Wingfield, M. J., Burgess, T. I., Hardy, G. E. St.J., Gené, J., Guarro, J., . . . Groenewald, J. Z. (2018b). Fungal planet description sheets: 716–784. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 40*, 239–392. https://doi.org/10.3767/persoonia.2018.40.10

Crous, P. W., Wingfield, M. J., Carnegie, A. J., Hernández-Restrepo, M., Lombard, L., Roux, J., . . . Groenewald, J. Z. (2018c). Fungal planet description sheets: 785–867. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 41*, 238–417. https://doi.org/10.3767/persoonia.2018.41.12

Crous, P. W., Wingfield, M. J., Schumacher, R. K., Summerell, B. A., Giraldo, A., Gené, J., . . . Groenewald, J. Z. (2014b). Fungal planet description sheets: 281–319. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 33*, 212–289. https://doi.org/10.3767/003158514X685680

Crous, P. W., Shivasr, G., Quaedvliegw, Van Derbank, M., Zhangy, Summerellb, A., . . . Groenewald, J. Z. (2014). Fungal planet description sheets: 214–280. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 32*, 184 –306. https://doi.org/10.3767/003158514X682395

Crous, P. W., Boers, J., Holdom, D., Steinrucken, T. V., Tan, Y. P., Vitelli, J. S., . . . Groenewald, J. Z. (2022). Fungal planet description sheets: 1383–1435. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 48*, 261–371. https://doi.org/10.3767/persoonia.2022.48.08

Crous, P. W., Carris, L. M., Giraldo, A., Groenewald, J. Z., Hawksworth, D. L., Hemández-Restrepo, M., . . . Wood, A. R. (2015a). The genera of fungi - fixing the application of the type species of generic names - G 2: Allantophomopsis, Latorua, Macrodiplodiopsis, Macrohilum, Milospium, Protostegia, Pyricularia, Robillarda, Rotula, Septoriella, Torula, and Wojnowicia. *IMA Fungus*, *6*, 163–198. https://doi.org/10.5598/imafungus.2015.06.01.11

Crous, P. W., Hernández-Restrepo, M., Schumacher, R. K., Cowan, D. A., Maggs-Kölling, G., Marais, E., . . . Groenewald, J. Z. (2021a). New and interesting fungi. 4. *Fungal Systematics and Evolution, 7*, 255–343. https://doi.org/10.3114/fuse.2021.07.13

Crous, P. W., Osieck, E. R., Jurjević, Ž., Boers, J., Van Iperen, A. L., Starink-Willemse, M., . . . Maggs-Kölling, G. (2021b). Fungal planet description sheets: 1284–1382. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 47*, 178–374. https://doi.org/10.3767/persoonia.2021.47.06

Crous, P. W., Schoch, C. L., Hyde, K. D., Wood, A. R., Gueidan, C., De Hoog, G. S., & Groenewald, J. Z. (2009). Phylogenetic lineages in the Capnodiales. *Studies in Mycology*, *64*, 17–47. https://doi.org/10.3114/sim.2009.64.02

Crous, P. W., Schubert, K., Braun, U., De Hoog, G. S., Hocking, A. D., Shin, H. D., & Groenewald, J. Z. (2007). Opportunistic, human-pathogenic species in the Herpotrichiellaceae are phenotypically similar to saprobic or phytopathogenic species in the Venturiaceae. *Studies in Mycology*, *58*, 185–217. https://doi.org/10.3114/sim.2007.58.07

Crous, P. W., Schumacher, R. K., Akulov, A., Thangavel, R., Hernández-Restrepo, M., Carnegie, A. J., . . . Groenewald, J. Z. (2019). New and interesting fungi. 2. *Fungal Systematics and Evolution*, *3*, 57–134. https://doi.org/10.3114/fuse.2019.03.06

Crous, P. W., Schumacher, R. K., Wingfield, M. J., Akulov, A., Denman, S., Roux, J., ... & Groenewald, J. Z. (2018a). New and interesting fungi. 1. *Fungal Systematics and Evolution*, *1*, 169–215. https://doi.org/10.3114/fuse.2018.01.08

Crous, P. W., Wingfield, M. J., Burgess, T. I., Carnegie, A. J., Hardy, G., Smith, D., . . . Rodríguez-Andrade, E. (2017a). Fungal planet description sheets: 625 – 715. *Persoonia - Molecular Phylogeny and Evolution of Fungi*, *39*, 270–467. https://doi.org/10.3767/persoonia.2017.39.11

Crous, P. W., Wingfield, M. J., Burgess, T. I., Hardy, G., Barber, P. A., Alvarado, P., . . . Vabeikhokhei, J. M. C. (2017b). Fungal planet description sheets: 558 – 624. *Persoonia - Molecular Phylogeny and Evolution of Fungi*, *38*, 240–384. https://doi.org/10.3767/003158517X698941

Crous, P. W., Wingfield, M. J., Burgess, T. I., Hardy, G., Crane, C., Barrett, S., . . . Sutton, D. A. (2016). Fungal planet description sheets : 469 – 557. *Persoonia - Molecular Phylogeny and Evolution of Fungi*, *37*, 218–403. https://doi.org/10.3767/003158516X694499

Crous, P. W., Wingfield, M. J., Guarro, J., Hernández-Restrepo, M., Sutton, D. A., Acharya, K., . . . Groenewald, J. Z. (2015c). Fungal planet description sheets 371-399. *Persoonia - Molecular Phylogeny and Evolution of Fungi*, *34*, 167–266. https://doi.org/10.3767/003158515X690269

Crous, P. W., Wingfield, M. J., Schumacher, R. K., Akulov, A., Bulgakov, T. S., Carnegie, A. J., . . . Groenewald, J. Z. (2020). New and interesting fungi. 3. *Fungal Systematics and Evolution, 6*, 157–231. https://doi.org/10.3114/fuse.2020.06.09

Crous, P. W., Jurjević, Ž., Balashov, S., De la Peña-Lastra, S., Mateos, A., Pinruan, U., . . . Groenewald, J. Z. (2024). Fungal planet description sheets: 1614–1696. *Fungal Systematics and Evolution, 13*, 183–440. https://doi.org/10.3114/fuse.2024.13.11

Crous, P. W., Mohammed, C., Glen, M., Verkley, G. J. M., & Groenewald, J. Z. (2007). Eucalyptus microfungi known from culture. 3. *Eucasphaeria* and *Sympoventuria genera* nova, and new species of Furcaspora, Harknessia, Heteroconium and Phacidiella. *Fungal Diversity, 25*, 19–36.

Crous, P. W., Schoch, C. L., Hyde, K. D., Wood, A. R., Gueidan, C., de Hoog, G. S., & Groenewald, J. Z. (2009). Phylogenetic lineages in the Capnodiales. *Studies in Mycology, 64*, 17–47. https://doi.org/10.3114/sim.2009.64.02

da Cunha, K. C., Sutton, D. A., Fothergill, A. W., Gené, J., Cano, J., Madrid, H., . . . Guarro, J. (2013). In vitro antifungal susceptibility and molecular identity of 99 clinical isolates of the opportunistic fungal genus Curvularia. *Diagnostic Microbiology and Infectious Disease, 76*, 168–174. https://doi.org/10.1016/j.diagmicrobio.2013.02.034

Cunha, A. O., Bezerra, J. D., Oliveira, T. G., Barbier, E., Bernard, E., Machado, A. R., . . . Souza-Motta, C. M. (2020). Living in the dark: Bat caves as hotspots of fungal diversity. *Plos ONE, 15*, e0243494. https://doi.org/10.1371/journal.pone.0243494

Currah, R. S. (1985). Taxonomy of the onygenales: Arthrodermataceae, Gymnoascaceae, Myxotrichaceae and Onygenaceae. *Mycotaxon, 24*, 1–216.

Currah, R. S. (1988). An annotated key to the genera of the Onygenales. *Syst Ascomycetum, 7*, 1–12.

Curzi, C. (1930). Petriella, una nuova generica dei Trypanosomatidi. *Bollettino della Reale Stazione di Patologia Vegetale di Roma, 10*, 384.

Dai, D. Q., Phookamsak, R., Wijayawardene, N. N., Li, W. J., Bhat, D. J., Xu, J. C., . . . Chukeatirote, E. (2017). Bambusicolous fungi. *Fungal Diversity, 82*, 1–105. https://doi.org/10.1007/s13225-016-0367-8

Das, K., Lee, S. Y., & Jung, H. Y. (2021). Morphology and phylogeny of two novel species within the class Dothideomycetes collected from Soil in Korea. *Mycobiology, 49*, 15–23. https://doi.org/10.1080/12298093.2020.1838114

Das, K., Lee, S. Y., & Jung, H. Y. (2019). *Cladophialophora lanosa* sp. nov., a new Species isolated from soil. *Mycobiology, 47*, 173–179. https://doi.org/10.1080/12298093.2019.1611242

Das, K., Lee, S. Y., Choi, H. W., Eom, A. H., Cho, Y. J., & Jung, H. Y. (2020). Taxonomy of *Arthrinium minutisporum* sp. nov., Pezicula neosporulosa, and Acrocalymma pterocarpi: New Records from Soil in Korea. *Mycobiology, 48*, 450–463. https://doi.org/10.1080/12298093.2020.183074

de Beer, Z. W., Seifert, K. A., & Wingfield, M. J. (2013). The ophiostomatoid fungi: Their dual position in the *Sordariomycetes*. *CBS Biodiversity Series, 12*, 1–9.

de Beer, Z. W., & Wingfield, M. (2013). Emerging lineages in the *Ophiostomatales*. In K. A. Seifert, Z. W. De Beer & M. J. Wingfield (eds.), *The ophiostomatoid fungi: Expanding frontiers* (pp. 12, 21–46). Centraalbureau voor Schimmelcultures (CBS).

de Beer, Z. W., Duong, T. A., Barnes, I., Wingfield, B. D., & Wingfield, M. J. (2014). Redefining *Ceratocystis* and allied genera. *Studies in Mycology, 79*, 187–219. https://doi.org/10.1016/j.simyco.2014.10.001

de Beer, Z. W., Duong, T. A., & Wingfield, M. J. (2016). The divorce of *Sporothrix* and *Ophiostoma*: Solution to a problematic relationship. *Studies in Mycology, 83*, 165–191. https://doi.org/10.1016/j.simyco.2016.07.001

de Beer, Z. W., Procter, M., Wingfield, M. J., Marincowitz, S., & Duong, T, A. (2022). Generic boundaries in the *Ophiostomatales* reconsidered and revised. *Studies in Mycology, 101*, 57–120. https://doi.org/10.3114/sim.2022.101.02

de Hoog, G. S., Guarro, J., Gené, J., & Figueras, M. J. (2011). *Atlas of clinical fungi*. CBS-KNAW Fungal Biodiversity Centre.

Delgado-Baquerizo, M., Reich, P. B., Trivedi, C., Eldridge, D. J., Abades, S., Alfaro, F. D., . . . Singh, B. K. (2020). Multiple elements of soil biodiversity drive ecosystem functions across biomes. *Nature Ecology & Evolution, 4*, 210–220. https://doi.org/10.1038/s41559-019-1084-y

Delgado, E. F., Valdez, A. T., Covarrubias, S. A., Tosi, S., & Nicola, L. (2021). Soil fungal diversity of the aguarongo andean forest (Ecuador). *Biology, 10*, 1289. https://doi.org/10.3390/biology10121289

Dentinger, B. T., Gaya, E., O'Brien, H., Suz, L. M., Lachlan, R., Díaz-Valderrama, J. R., . . . Aime, M. C. (2016). Tales from the crypt: Genome mining from fungarium specimens improves resolution of the mushroom tree of life. *Biological Journal of the Linnean Society, 117*, 11–32. https://doi.org/10.1111/bij.12553

Dissanayake, A. J., Purahong, W., Wubet, T., Hyde, K. D., Zhang, W., Xu, H., . . . Yan, J. (2018). Direct comparison of culture-dependent and culture-independent molecular approachesreveal the diversity of fungal endophytic communities in stems of grapevine (Vitis vinifera). *Fungal Diversity, 90*, 85–107. https://doi.org/10.1007/s13225-018-0399-3

Dai, D. Q., Wijayawardene, N. N., Dayarathne, M. C., Kumla, J., Han, L. S., Zhang, G. Q., . . . Chen, H. H. (2022). Taxonomic and phylogenetic characterizations reveal four new species, two new asexual morph reports, and six new country records of *Bambusicolous Roussoella* from China. *Journal of Fungi, 8*. https://doi.org/10.3390/jof8050532

Dalee, A. D., Chehama, M., Sali, K., Hayeeyusoh, N., & Hayeewangoh, Z. (2018). Keratinase-producing fungi from local environmental samples of Far South Thailand and their efficiency in hydrolyzing keratinous wastes. *Journal of Physics: Conference Series, 1097*, 012036. https://doi.org/10.1088/1742-6596/1097/1/012036

Das, A. C. (1962). New species of *Thielavia* and *Sordaria*. *Transactions of the British Mycological Society, 45*, 545–548.

Das, K., Lee, S. Y., Choi, H. W., Eom, A. H., Cho, Y. J., & Jung, H. Y. (2020a). Taxonomy of *Arthrinium minutisporum* sp. nov., *Pezicula neosporulosa*, and *Acrocalymma pterocarpi*: New Records from soil in Korea. *Mycobiology, 48*, 450–463. https://doi.org/10.1080/12298093.2020.1830741

Das, K., Lee, S. Y., & Jung, H. Y. (2019). *Cladophialophora lanosa* sp. nov., a New species isolated from soil. *Mycobiology, 47*, 173–179. https://doi.org/10.1080/12298093.2019.1611242

Das, K., Lee, S. Y., & Jung, H. Y. (2020b). Molecular and morphological characterization of two novel species collected from soil in Korea. *Mycobiology, 48*, 9–19. https://doi.org/10.1080/12298093.2019.1695717

Das, K., Lee, S. Y., Choi, H. W., Eom, A. H., Cho, Y. J., & Jung, H. Y. (2020c). Taxonomy of *Arthrinium minutisporum* sp. nov., *Pezicula neosporulosa*, and *Acrocalymma pterocarpi*: New records from soil in Korea. *Mycobiology, 48*, 450–463. https://doi.org/10.1080/12298093.2020.1830741

Davidson, D. E., & Christensen, M. (1971). *Emericellopsis stolkiae* sp. nov. from saline soils in Wyoming. *Transactions of the British Mycological Society, 57*, 85-IN3.

Davolos, D., Pietrangeli, B., Persiani, A. M., & Maggi, O. (2019). *Victoriomyces antarcticus* gen. Nov., sp. nov., a distinct evolutionary lineage of the *Cephalothecaceae* (*Ascomycota* – based on sequence-based phylogeny and morphology). *International Journal of Systematic and Evolutionary Microbiology, 69*, 1099–1110. https://doi.org/10.1099/ijsem.0.003275

Dayarathne, M. (2020). Morpho-molecular characterization of microfungi associated with marine based habitats. *Mycosphere, 11*, 1–188. https://doi.org/10.5943/mycosphere/11/1/1

Deharveng, L., Ellis, M., Bedos, A., & Jantarit, S. (2023). Tham Chiang Dao: A hotspot of subterranean biodiversity in Northern Thailand. *Diversity, 15*, 1076. https://doi.org/10.3390/d15101076

Deighton, F. C. (1972). Synonymy of *Hansfordia pulvinata* (Berk. & Curt.) Hughes. *Transactions of the British Mycological Society, 59*, 531–536. https://doi.org/10.1016/s0007-1536(72)80140-2

Deshmukh, S. K., Verekar, S. A., & Chavan, Y. G. (2018). Keratinophilic fungi from the vicinity of salt pan soils of sambhar lake Rajasthan (India). *Journal de Mycologie Médicale, 28*, 457–461. https://doi.org/10.1016/j.mycmed.2018.06.002

Desmazières, J. B. H. J. (1827). Observations sur le Sporendonema casei, nouveau genre des Mucédinées. *Ann Sci Nat Bot*, *11*, 246–249.

Dethoup, T., Manoch, L., Visarathanonth, N., Chamswarng, C., & Kijjoa, A. (2007). Morphology and distribution of *Talaromyces flavus* from soil and potential use as a biological control agent against plant pathogenic fungi. *Thai J Agric Sci.*, *40*, 37–50.

Dethoup, T., & Manoch, L. (2010). *Study of thermophilic and thermotolerant fungi from soils and agricultural wastes*. Department of Plant Pathology, Faculty of Agriculture, Kasetsart University.

Dettman, J. R., Harbinski, F. M., & Taylor, J. W. (2001). Ascospore morphology is a poor predictor of the phylogenetic relationships of *Neurospora* and *Gelasinospora*. *Fungal Genetics and Biology*, *34*, 49–61.

Dick, M. W. (1992). Patterns of phenology in populations of zoosporic fungi. In J. Dighton & J. F. White (eds.), *The fungal community, its organization and role in the ecosystem* (2nd ed., pp. 355–382). CRC Press.

Diedicke, H. (1912). Die abteilung hyalodidymae der sphaerioideen. *Annales Mycologici*, *10*, 135–152.

Dissanayake, L. S., Samarakoon, M. C., Maharachchikumbura, S. S., Hyde, K. D., Tang, X., Li, Q. R., . . . Wanasinghe, D. N. (2024). Exploring the taxonomy and phylogeny of *Sordariomycetes* taxa emphasizing *Xylariomycetidae* in Southwestern China. *Mycosphere*, *15*, 1675–1793. https://doi.org/10.5943/mycosphere/15/1/15

Dissanayake, A. J., Bhunjun, C. S., Maharachchikumbura, S. S. N., & Liu, J. K. (2020). Applied aspects of methods to infer phylogenetic relationships amongst fungi. *Mycosphere, 11*, 2652–2676. https://doi.org/10.5943/mycosphere/11/1/-18

Dixon, L. J., Schlub, R. L., Pernezny, K., & Datnoff, L. E. (2009). Host specialization and phylogenetic diversity of *Corynespora cassiicola*. *Phytopathology, 99*, 1015–1027. https://doi.org/10.1094/PHYTO-99-9-1015

Dixon, M. (1968). *Trichocladium pyriformis* sp. nov. *Transactions of the British Mycological Society, 51*, 160-IN17. https://doi.org/10.1016/S0007-1536(68)80139-1

Dög˘en, A., Kaplan, E., Oksüz, Z., & Serin, M. S. (2013). Dishwashers are a major source of human opportunistic yeast-like fungi in indoor environments in Mersin, Turkey. *Medical Mycology, 51*, 493–498.

Domsch, K. H., Gams, W., & Anderson, T. H. (1980). *Compendium of soil fungi* (volume 1). Academic Press.

Domsch, K. H., Gams, W., & Anderson, T. H. (1993). *Compendium of soil fungi*. IHWVerlag Press.

Domsch, K. H., Gams, W., & Anderson, T. H. (2007). Compendium of soil fungi. *European Journal of Soil Science, 59*(5), 1007. https://doi.org/10.1111/j.1365-2389.2008.01052_1.x

Domsch, K. H., Garrett, S. D., & Gams, W. (1973). Fungi in agricultural soils. *The Journal of Applied Ecology, 10*, 897. https://doi.org/10.2307/2401880

Dong, Q. Y., Wang, Y., Wang, Z. Q., Tang, D. X., Zhao, Z. Y., Wu, H. J., . . . Yu, H. (2022). Morphology and phylogeny reveal five novel species in the genus *Cordyceps* (*Cordycipitaceae, Hypocreales* – from Yunnan, China). *Frontiers in Microbiology*, *13*. https://doi.org/10.3389/fmicb.2022.846909

Dong, Q., Wang, H., Xing, X., & Ji, S. (2012). Identification and characterization of a special species of *Paecilomyces*. *Annals of Microbiology, 62*, 1587–1592. https://doi.org/10.1007/s13213-011-0414-3

Dong, W., Hyde, K. D., Jeewon, R., Liao, C. F., Zhao, H. J., Kularathnage, N. D., . . . Doilom, M. (2023). Mycosphere notes 449–468: Saprobic and endophytic fungi in China, Thailand, and Uzbekistan. *Mycosphere, 14*, 2208–2262. https://doi.org/10.5943/mycosphere/14/1/26

Dong, W., Wang, B., Hyde, K. D., McKenzie, E. H., Raja, H. A., Tanaka, K., . . . Zhang, H. (2020). *Freshwater Dothideomycetes*. Springer Netherlands.

Dorhout, D. L., Sappington, T. W., Lewis, L. C., & Rice, M. E. (2011). Flight behaviour of European corn borer infected with Nosema pyrausta. *Journal of Applied Entomology, 135*, 25–37. https://doi.org/10.1111/j.1439-0418.2010.01523

Dos Santos, M. V. O., Barbosa, F. R., Magalhães, D. M. A., Luz, E. D. M. N., & Bezerra, J. L. (2014). Beltraniella species associated with leaf litter of the Atlantic Forest in southern Bahia, Brazil. *Mycotaxon, 129*, 1–6.

Doweld, A. (2013). *Spiromastigoides*, a new genus of the family *Amauroascaceae*. *Index Fungorum, 30*, 1–2.

Dowsett, J. A., Reid, J., & Kalkat, R. S. (1984). A New species of arthrobotrys from soil. *Mycologia, 76*, 559–562. https://doi.org/10.1080/00275514.1984.12023880

Dugan, F. M., Braun, U., Groenewald, J. Z., & Crous, P. W. (2008). Morphological plasticity in *Cladosporium sphaerospermum*. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 21*, 9–16. https://doi.org/10.3767/003158508X334389

Dukik, K., De Hoog, G. S., Stielow, J. B., Freeke, J., van Den Ende, B. G., Vicente, V. A., . . . Ahmed, S. A. (2020). Molecular and phenotypic characterization of *Nannizzia* (*Arthrodermataceae*). *Mycopathologia, 185*, 9–35. https://doi.org/10.1007/s11046-019-00336-9

Dukik, K., Muñoz, J. F., Jiang, Y., Feng, P., Sigler, L., Stielow, J. B., . . . de Hoog, S. (2017). Novel taxa of thermally dimorphic systemic pathogens in the *Ajellomycetaceae* (*Onygenales*). *Mycoses, 60*, 296–309. https://doi.org/10.1111/myc.12601

Duong, L. M., Mckenzie, E. H. C., Lumyong, S., & Hyde, K. D. (2008). Fungal succession on senescent leaves of Castanopsis diversifolia in Doi Suthep–Pui National Park, Thailand. *Fungal Diversity, 30*, 23– 36.

Durán, P., Barra, P. J., Jorquera, M. A., & Viscardi, S. (2019). Occurrence of soil fungi in Antarctic pristine environments. *Frontiers in Bioengineering and Biotechnology, 7*, 28. https://doi.org/10.3389/fbioe.2019.00028

Durie, E. B., & Frey, D. (1957). A new species of *Trichophyton* from New South Wales. *Mycologia, 49*, 401–411. https://doi.org/10.1080/00275514.1957.12024654

Dutra, Y. L. G., Rosado, A. W. C., Condé, T. O., Leão, A. F., Neves, S. D. C., Fraga, L. M. S., . . . Pereira, O. L. (2023). Two new *Cladosporium* species from a quartzite cave in Brazil. *Brazilian Journal of Microbiology, 54*, 3021–3031. https://doi.org/10.1007/s42770-023-01156-2

Van Dyke, M. C. C., Thompson, G. R., Galgiani, J. N., & Barker, B. M. (2019). The rise of *Coccidioides*: Forces against the dust devil unleashed. *Frontiers in Immunology, 10*. https://doi.org/10.3389/fimmu.2019.02188

Eamvijarn, A., Manoch, L., Chamswarng, C., Piasai, O., Visarathanonth, N., Luangsa-ard, J. J., . . . Kijjoa, A. (2013). *Aspergillus siamensis* sp. nov. from soil in Thailand. *Mycoscience, 54*, 401–405. https://doi.org/10.1016/j.myc.2013.01.005

Egidi, E., Delgado-Baquerizo, M., Plett, J. M., Wang, J., Eldridge, D. J., Bardgett, R. D., . . . Singh, B. K. (2019). A few *Ascomycota* taxa dominate soil fungal communities worldwide. *Nature Communications, 10*. https://doi.org/10.1038/s41467-019-10373-z

Eidam, E. (1880). Beitrag zur Kenntnis der Gymnoasceen. *Beiträge zur Biologie der Pflanzen, 3*, 267–305.

Elad, Y., Chet, I., & Henis, Y. (1981). A selective medium for improving quantitative isolation of *Trichoderma* spp. from soil. *Phytoparasitica, 91*, 59–67.

El-Ganainy, S. M., Ismail, A. M., Iqbal, Z., Elshewy, E. S., Alhudaib, K. A., Almaghasla, M. I., . . . Magistà, D. (2022). Diversity among *Lasiodiplodia* species causing dieback, root rot and leaf spot on fruit trees in Egypt, and a description of *Lasiodiplodia newvalleyensis* sp. nov. *Journal of Fungi, 8*, 1203. https://doi.org/10.3390/jof8111203

Ellis, J. B., & Everhart, B. M. (1894). New species of fungi from various localities. *The Journal of Mycology, 4*(4/5), 44-46. https://doi.org/10.2307/3753026

Ellis, M. B., & Ellis, J. P. (1985). *Microfungi on land plants–An identification handbook*. Macmillan Publishing.

Ellis, M. B. (1949). *Tetraploa*. *Transactions of the British Mycological Society, 32*, 246–251.

Ellis, M. B. (1971). *Dematiaceous hyphomycetes*. Commonwealth Mycological Institute.

Ellis, M. B. (1976). *More dematiaceous hyphomycetes*. Commonwealth Mycological Institute.

Elnaiem, M. H., Taniguchi, T., & El Siddig, M. (2021). *Taxonomic and functional composition of soil mycobiome of two agricultural sites in Khartoum State, Sudan*. Research Square. https://doi.org/10.21203/rs.3.rs-765136/v1

English, M. P. (1963). *The saprophytic growth of keratinophilic fungi on keratin*. Mikologia lekarska.

English, M. P. (1965). The saprophytic growth of non keratinophilic fungi on keratinized substrata, and a comparison with keratinophilic fungi. *Trans. Br. Mycol. Soc., 48*, 219. https://doi.org/10.1016/S0007-1536(65)80088-2

Fadnes, P., Fedosova, A. G., & Kučera, V. (2021). *Hemileucoglossum pusillum*, an earth tongue new to Norway. *Agarica, 42*, 65–73. https://doi.org/10.5617/agarica.11157

Farias, A. R. G., Yasanthika, W. A. E., & Monkai, J. (2023). Insights into the profile of soil fungal diversity in Thailand. *Asian Journal of Mycology, 6*(2), 305–317. https://doi.org/10.5943/ajom/6/2/11

Farley, J. D. (1972). A selective medium for assay of *Colletotrichum coccodes* in soil. *Phytopathology, 62*, 1288-1293.

Fei, G. X., Guan, J. Q., Tian, H. L., & Zhou, Y. M. (2024). A new entomopathogenic fungus, *Ophiocordyceps xifengensis* sp. nov., from Liaoning, China. *Phytotaxa, 642*, 211–224. https://doi.org/10.11646/phytotaxa.642.3.1

Ferna´ndez, F. A., & Huhndorf, S. M. (2005). New species of *Chaetosphaeria, Melanopsammella* and *Tainosphaeria* gen. nov. from the Americas. *Fungal Diversity, 18*, 15–57.

Ferdinandez, H. S., Manamgoda, D. S., & Udayanga, D. (2024). First report of Curvularia dactylocteniicola causing leaf spots on Zea mays and Sorghum in Sri Lanka. *Ceylon Journal of Science, 53*, 39–43. https://doi.org/10.4038/cjs.v53i1.8315

Ferdinandez, H. S., Manamgoda, D. S., Udayanga, D., Munasinghe, M. S., & Castlebury, L. A. (2023). Molecular phylogeny and morphology reveal two new graminicolous species, *Curvularia aurantia* sp. nov. and *C. vidyodayana* sp. nov. with new records of *Curvularia* sp. from Sri Lanka. *Fungal Systematics and Evolution, 12*, 219–246. https://doi.org/10.3114/fuse.2023.12.11

Ferdinandez, H. S., Manamgoda, D. S., Udayanga, D., Deshappriya, N., Munasinghe, M. S., & Castlebury, L. A. (2021). Molecular phylogeny and morphology reveal three novel species of Curvularia (Pleosporales, Pleosporaceae) associated with cereal crops and weedy grass hosts. *Mycological Progress, 20*, 431–451. https://doi.org/10.1007/s11557-021-01681-0

Fernández-Brime, S., Llimona, X., Lutzoni, F., & Gaya, E. (2013). Phylogenetic study of *Diploschistes* (lichen–forming *Ascomycota*: *Ostropales*: *Graphidaceae*), based on morphological, chemical, and molecular data. *Taxon, 62*, 267–280.

Fernandes, É. K., Keyser, C. A., Rangel, D. E., Foster, R. N., & Roberts, D. W. (2010). CTC medium: A novel dodine-free selective medium for isolating entomopathogenic fungi, especially Metarhizium acridum, from soil. *Biological Control, 54*, 197–205. https://doi.org/10.1016/j.biocontrol.2010.05.009

Finlay, R. D. (2007). The fungi in soil. In J. D. van Elsas, J. T. Trevors, A. S. Rosado & P. Nannipieri (eds.), *Modern soil microbiology* (pp. 107–146). CRC Press.

Finlay, R. D., & Thorn, R. G. (2019). The fungi in soil. In J. D. van Elsas, J. T. Trevors, A. S. Rosado & P. Nannipieri (eds.), *Modern soil microbiology* (3rd ed., pp. 65-90). CRC Press.

Fonseca, O., & Areakio, A. (1928). *Sobre os cogumelos da piedra brasileira*. Fecha del número.

Foster, M. S., Mueller, G. M., & Bills, G. F. (2011). *Biodiversity of fungi: Inventory and monitoring methods*. Elsevier.

Frąc, M., Hannula, S. E., Bełka, M., & Jędryczka, M. (2018). Fungal biodiversity and their role in soil health. *Frontiers in Microbiology, 9*. https://doi.org/10.3389/fmicb.2018.00707

Frąc, M., Jędryczka, M., & Hannula, E. S. (2019). *Soil fungal biodiversity for plant and soil health*. Frontiers Media SA.

Fracetto, G. G., Azevedo, L. C., Fracetto, F. J., Andreote, F. D., Lambais, M. R., & Pfenning, L. H. (2013). Impact of Amazon land use on the community of soil fungi. *Scientia Agricola, 70*, 59–67. https://doi.org/10.1590/S0103-90162013000200001

Francisco, C. S., Ma, X., Zwyssig, M. M., McDonald, B. A., & Palma-Guerrero, J. (2019). Morphological changes in response to environmental stresses in the fungal plant pathogen Zymoseptoria tritici. *Scientific Reports, 9*, 9642. https://doi.org/10.1038/s41598-019-45994-3

Franzosa, E. A., Hsu, T., Sirota-Madi, A., Shafquat, A., Abu-Ali, G., Morgan, X. C., . . . Huttenhower, C. (2015). Sequencing and beyond: Integrating molecular 'omics' for microbial community profiling. *Nature Reviews Microbiology, 13*, 360–372. https://doi.org/10.1038/nrmicro3451

von Freiesleben, P., Moroz, O. V., Blagova, E., Wiemann, M., Spodsberg, N., Agger, J. W., . . . Krogh, K. B. (2019). Crystal structure and substrate interactions of an unusual fungal non-CBM carrying GH26 endo-β-mannanase from *Yunnania penicillata*. *Scientific Reports*, *9*, 2266. https://doi.org/10.1038/s41598-019-38602-x

Frey, D., & Griffin, D. M. (1961). *Ctenomyces serratus* Eidam. *Transactions of the British Mycological Society*, *44*, 449-452.

Fries, E. M. (1818). *Observationes mycologiae* (vol. 2 Cancellansissue). G. Bonnieri.

Fries, E. M. (1822). *Peziza*. *Systema Mycologicum*, *2*, 40.

Fries, E. M. (1825). *Systema orbis vegetabilis: Plantæ homonemeæ*. Typographia academica.

Fries, E. M. (1849). *Summa vegetabilium Scandinaviae*., Sectio Posterior.

Frisvad, J. C., Samson, R. A. (2004). Polyphasic taxonomy of *Penicillium* subgenus *Penicillium*. A guide to identification of food and air-borne terverticillate Penicillia and their mycotoxins. *Studies in Mycology, 49*, 1–174.

Fuckel, K. W. G. L. (1870). Sclerotinia. *Jahrbücher des Nassauischen Vereins für Naturkunde, 330*, 23–24.

Fuckel, L. (1866). Fungi Rhenani exsiccati Cent. 12-17 (2), no 1450-1632. *Hedwigia, 5*, 23-30.

Furst, H. M., Kraepelin, G., & Görisch, H. (1998). Detection of *Amorphotheca resinae* in German soil by an improved selective isolation method. *Mycological Research, 102*, 323–326. https://doi.org/10.1017/S0953756297005066

Furuya, K., & Naito, A. (1979). An effective method for isolation of Ascodesmis from soil. *Transactions of the Mycological Society of Japan, 20*, 171–175

Furuya, K., & Naito, A. (1980). Stimulation of ascospore germination by phenolic compounds in numbers of the Sordariaceae. *Transactions of the Mycological Society of Japan, 21*, 77–85.

Gams, W. (2017). An annotated checklist of epithets published in *Verticillium* and *Acrostalagmus*, some similar genera, and teleomorphs associated with verticillium-like anamorphs. *Nova Hedwigia, 104*, 381–450.

Gams, W. (1971). *Tolypocladium*, eine Hyphomycetengattung mit geschwollenen Phialiden. *Persoonia-Molecular Phylogeny and Evolution of Fungi, 6*, 185–191.

Gams, W. (1978). Connected and disconnected chains of Phialoconidia and *Sagenomella* gen. nov. segregated from *Acremonium*. *Persoonia-Molecular Phylogeny and Evolution of Fungi, 10*, 97–112.

Gams, W. (1980). *Chaunopycnis alba*, gen. et sp. nov., a soil fungus intermediate between *Moniliales* and *Sphaeropsidales*. *Persoonia-Molecular Phylogeny and Evolution of Fungi, 11*, 75–79.

Gams, W. (2000). *Phialophora* and some similar morphologically little-differentiated anamorphs of divergent ascomycetes. *Studies in Mycology, 45*, 187–200.

Gams, W., Zare, R., & Summerbell, R. C. (2005). (1654) Proposal to conserve the generic name *Verticillium* (anamorphic Ascomycetes) with a conserved type. *Taxon, 54*, 179–179. https://doi.org/10.2307/25065318

Gao, Y., Ren, G. C., Wanasinghe, D. N., Xu, J. C., Gomes de Farias, A. R., & Gui, H. (2022). Two new species and a new record of *Microdochium* from grasses in Yunnan province, South-West China. *Journal of Fungi, 8*, 1297. https://doi.org/10.3390/jof8121297

Garcia-Acero, A. M., Morais, C. G., Souza, G. F., Santos, A. R. O., Lachance, M. A., Velásquez-Lozano, M. E., . . . Rosa, C. A. (2024). *Ogataea nonmethanolica* f.a, sp. nov., a novel yeast species isolated from rotting wood in Brazil and Colombia. *International Journal of Systematic and Evolutionary Microbiology*, *74*(2). https://doi.org/10.1099/ijsem.0.006273

García, D., Stchigel, A. M., Cano, J., Calduch, M., Hawksworth, D. L., & Guarro, J. (2006). Molecular phylogeny of *Coniochaetales*. *Mycological Research, 110*, 1271–1289.

García, D., Stchigel, A. M., José, C., Guarro, J., & Hawksworth, D. L. (2004). A synopsis and re-circumscription of *Neurospora* (syn. *Gelasinospora*) – based on ultrastructural and 28S rDNA sequence data. *Mycological Research, 108*, 1119–1142. https://doi.org/10.1017/S0953756204000218

Garfinkel, A. R. (2021). The history of botrytis taxonomy, the rise of phylogenetics, and implications for species recognition. *Phytopathology*, *111*, 437–454. https://doi.org/10.1094/phyto-06-20-0211-ia

Garrett, S. D. (1981). *Soil fungi and soil fertility* (2nd ed.). Pergamon Press.

Garrett, S. D. (2016). *Soil fungi and soil fertility: An introduction to soil mycology*. Elsevier.

Gerdemann, J. W., & Nicolson, T. H. (1963). Spores of mycorrhizalendogone species extracted from soil by wet-sieving and decanting. *Transactions of the British Mycological Society, 46*, 235–244.

Geltner, C., Sorschag, S., Willinger, B., Jaritz, T., Saric, Z., & Lass-Flörl, C. (2015). Necrotizing mycosis due to Verruconis gallopava in an immunocompetent patient. *Infection*, *43*, 743–746. https://doi.org/10.1007/s15010-015-0757-y

Ghodsalavi, B., Svenningsen, N. B., Hao, X., Olsson, S., Nicolaisen, M. H., Al-Soud, W. A., . . . Nybroe, O. (2017). A novel baiting microcosm approach used to identify the bacterial community associated with Penicillium bilaii hyphae in soil. *PloS one, 12*, e0187116. https://doi.org/10.1371/journal.pone.0187116

Gilchrist, T. C., & Stokes, W. R. (1898). A case of pseudo-lupus vulgaris caused by a blastomyces *Blastomyces*. *J Exp Med., 3*(1), 53–78. https://doi.org/10.1084/jem.3.1.53

Giraldo, A., & Crous, P. W. (2019). Inside *Plectosphaerellaceae*. *Studies in Mycology, 92*, 227–286. https://doi.org/10.1016/j.simyco.2018.10.005

Giraldo, A., Gené, J., Cano, J., de Hoog, S., & Guarro, J. (2012). Two new species of *Acremonium* from Spanish soils. *Mycologia, 104*, 1456–1465. https://doi.org/10.3852/11-402

Giraldo, A., Gené, J., Sutton, D. A., Madrid, H., Cano, J., Crous, P. W., & Guarro, J. (2014a). Phylogenetic circumscription of *Arthrographis* (*Eremomycetaceae*, *Dothideomycetes*). *Persoonia: Molecular Phylogeny and Evolution of Fungi 32*, 102–114. https://doi.org/10.3767/003158514X680207

Giraldo, A., Gené, J., Sutton, D. A., Wiederhold, N., & Guarro, J. (2017). New acremonium-like species in the *Bionectriaceae* and *Plectosphaerellaceae*. *Mycological Progress, 16*, 349–368. https://doi.org/10.1007/s11557-017-1271-7

Giraldo, A., Hernández-Restrepo, M., & Crous, P. W. (2019). New *plectosphaerellaceous* species from Dutch garden soil. *Mycological Progress, 18*, 1135–1154. https://doi.org/10.1007/s11557-019-01511-4

Giraldo, A., Sutton, D. A., Samerpitak, K., De Hoog, G. S., Wiederhold, N. P., Guarro, J., . . . Gené, J. (2014b). Occurrence of *Ochroconis* and *Verruconis* Species in Clinical Specimens from the United States. *Journal of Clinical Microbiology, 52*, 4189–4201. https://doi.org/10.1128/JCM.02027-14

Giri, B., Giang, P. H., Kumari, R., Prasad, R., & Varma, A. (2005). Microbial diversity in soils. In A. Varma & F. Buscot (eds.), *Microorganisms in soils: Roles in genesis and functions* (pp. 19–55). Springer.

Giudice, M. C., Reis-Menezes, A. A., Rittner, G. M. G., Mota, A. J., & Gambale, W. (2012). Isolation of Microsporum gypseum in soil samples from different geographical regions of Brazil, evaluation of the extracellular proteolytic enzymes activities (keratinase and elastase) and molecular sequencing of selected strains. *Brazilian Journal of Microbiology, 43*, 895–902. https://doi.org/10.1590/S1517-83822012000300007

Glass, N. L., & Donaldson, G. C. (1995). Development of primer sets designed for use with the PCR to amplify conserved genes from filamentous ascomycetes. *Applied and Environmental Microbiology, 61*, 1323–1330. https://doi.org/10.1128/aem.61.4.1323-1330.1995

Gochenaur, S. E. (1964). A modification of the immersion tube method for isolating soil fungi. *Mycologia, 56*, 921–923. https://doi.org/10.2307/3756658

Goh, Y. K., Goh, T. K., Marzuki, N. F., & Tung, H. J. (2015). *Scytalidium parasiticum* sp. nov., a New Species Parasitizing on *Ganoderma boninense* Isolated from Oil Palm in Peninsular Malaysia. *Mycobiology, 43*, 107–117. https://doi.org/10.5941/MYCO.2015.43.2.107

Goh, T. K., & Hyde, K. D. (1998). A synopsis of and a key to Diplococcium species, based on the literature, with a description of a new species. *Fungal Diversity, 1*, 65–83.

Goh, T. K., & Hyde, K. D. (1996). *Spadicoides cordanoides* sp. nov., a new dematiaceous hyphomycete from submerged wood in Australia, with a taxonomic review of the genus. *Mycologia, 88*, 1022–1031.

Goh, T. K., & Hyde, K. D. (1997). The generic distinction between Chaetopsina and Kionochaeta, with descriptions of two new species. *Mycological Research, 101*, 1517–1523.

Gohel, V., Singh, A., Vimal, M., Ashwini, P., & Chhatpar, H. S. (2006). Bioprospecting and antifungal potential of chitinolytic microorganisms. *African Journal of Biotechnology, 5*, 54–72.

Gomzhina, M., & Gasich, E. (2024). *Ascochyta erotica* sp. nov. Pathogenic on *Convolvulus arvensis*. *Diversity, 16*, 246. https://doi.org/10.3390/d16040246

Gonçalves, M. F. M., Aleixo, A., Vicente, T. F. L., Esteves, A. C., & Alves, A. (2019a). Three new species of *Neocamarosporium* isolated from saline environments: *N. aestuarinum* sp. nov., *N. endophyticum* sp. nov. and *N. halimiones* sp. nov. *Mycosphere, 10*, 608–621. https://doi.org/10.5943/mycosphere/10/1/11

Gonçalves, M. F. M., Esteves, A. C., & Alves, A. (2020). Revealing the hidden diversity of marine fungi in Portugal with the description of two novel species, *neoascochyta fuci* sp. Nov. and *paraconiothyrium salinum* sp. nov. *International Journal of Systematic and Evolutionary Microbiology, 70*, 5337–5354. https://doi.org/10.1099/ijsem.0.004410

Gonçalves, M. F. M., Vicente, T. F. L., Esteves, A. C., & Alves, A. (2019b). *Neptunomyces aureus* gen. et sp. nov. (*Didymosphaeriaceae, Pleosporales*) – isolated from algae in Ria de Aveiro, Portugal. *MycoKeys, 60*, 31–44. https://doi.org/10.3897/mycokeys.60.37931

González, M., del, C., Hanlin, R.T., Herrera, T., & Ulloa, M. (2000). Fungi colonizing hair-baits from three coastal beaches of Mexico. *Mycoscience, 41*, 259–262. https://doi.org/10.1007/BF02489680

Gonzalez-Menendez, V., Martin, J., Siles, J. A., Gonzalez-Tejero, M. R., Reyes, F., Platas, G., . . . Genilloud, O. (2017). Biodiversity and chemotaxonomy of *Preussia* isolates from the Iberian Peninsula. *Mycological Progress, 16*, 713–728. https://doi.org/10.1007/s11557-017-1305-1

Goos, R. D. (1964). A new record of *Cephaliophora Irregularis*. *Mycologia, 56*, 133. https://doi.org/10.2307/3756407

Gordon, M. A. (1953). The occurrence of the dermatophyte, *Microsporum gypseum*, as a saprophyte in soil. *Journal of Investigative Dermatology, 20*(3), 201-206. https://doi.org/10.1038/jid.1953.23

Greco, G., Cutroneo, L., Piazza, S. D., Capello, M., & Zotti, M. (2020). Trapping of marine-derived fungi on wooden baits to select species potentially usable in mycoremediation. *Italian Journal of Mycology, 49*, 101–115. https://doi.org/10.6092/issn.2531-7342/10769

Grifon, E., & Maublanc, A. (1909). Sur une maladie du cacaoyer. *Bull Trimest Soc Mycol Fr., 25*, 51–58.

Griffiths, B. S., & Philippot, L. (2013). Insights into the resistance and resilience of the soil microbial community. *FEMS Microbiology Reviews, 37*, 112–129. https://doi.org/10.1111/j.1574-6976.2012.00343.x

Groenewald, M., Lombard, L., de Vries, M., Lopez, A. G., Smith, M., & Crous, P. W. (2018). Diversity of yeast species from Dutch garden soil and the description of six novel Ascomycetes. *FEMS Yeast Research, 18*, 1–14. https://doi.org/10.1093/femsyr/foy076

Groenewald, M., Groenewald, J. Z., & Crous, P. W. (2005). Distinct species exist within the Cercospora apii morphotype. *Phytopathology, 95*, 951–959.

Grossbard, E. (1952). Antibiotic production by fungi on organic manures and in soil. *Microbiology, 6*, 295–310. https://doi.org/10.1099/00221287-6-3-4-295

Gruby, M. (1843). Mémoire sur les teignes. *Archives Générales de Médecine, 1*, 129–188.

Grum-Grzhimaylo, A. A., Georgieva, M. L., Bondarenko, S. A., Debets, A. J. M., & Bilanenko, E. N. (2016). On the diversity of fungi from soda soils. *Fungal Diversity, 76*, 27–74. https://doi.org/10.1007/s13225-015-0320-2

De Gruyter, J., Woudenberg, J. H. C., Aveskamp, M. M., Verkley, G. J. M., Groenewald, J. Z., & Crous, P. W. (2013). Redisposition of phoma-like anamorphs in *Pleosporales*. *Studies in Mycology, 75*, 1–36. https://doi.org/10.3114/sim0004

de Gruyter, J., Woudenberg, J. H., Aveskamp, M. M., Verkley, G. J., Groenewald, J. Z., & Crous, P. W. (2010). Systematic reappraisal of species in *Phoma* section *Paraphoma*, *Pyrenochaeta* and *Pleurophoma*. *Mycologia, 102*, 1066–1081. https://doi.org/10.3852/09-240

Guarro, J., Gené, J., & De Vroey, C. H. (1993). A new species of *Spiromastix* from Africa. *Mycotaxon, 46*, 307–313.

Guarro, J., & Von Arx, J. A. (1987). The ascomycete genus *Sordaria*. *Persoonia, 13*, 301–313.

Guarro, J., Gene, J., Stchigel, A. M., & Figueras, M. J. (2012). *Atlas of soil ascomycetes*. CBS-KNAW Fungal Biodiversity Centre.

Guarro, J., Punsola, L., & Figueras, M. J. (1987). *Brunneospora reticulata*, gen. et spec. nov. A keratinophilic ascomycete from Spain. *Persoonia-Molecular Phylogeny and Evolution of Fungi*, *13*, 387–390.

Guarro, J., & Cano, J. (1988). The genus *Triangularia*. *Transactions of the British Mycological Society, 91*, 587–591. https://doi.org/10.1016/S0007-1536(88)80031-7

Guarro, J., Kantarcioglu, A. S., Horré, R., Luis Rodriguez-Tudela, J., Cuenca Estrella, M., Berenguer, J., . . . Sybren De Hoog, G. (2006). *Scedosporium apiospermum*: Changing clinical spectrum of a therapy-refractory opportunist. *Medical Mycology, 44*, 295–327. https://doi.org/10.1080/13693780600752507

Guatimosim, E., Schwartsburd, P. B., Barreto, R. W., & Crous, P. W. (2016). Novel fungi from an ancient niche: Cercosporoid and related sexual morphs on ferns. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 37*, 106–141. https://doi.org/10.3767/003158516X690934

Guého, E., & de Hoog, G. S. (1991). Taxonomy of the medical species of Pseudallescheria and Scedosporium. *Journal de Mycologie Médicale, 1*, 3–9.

Guerra-Mateo, D., Gené, J., Baulin, V., & Cano-Lira, J. F. (2023). Phylogeny and taxonomy of the genus *Amphichorda* (Bionectriaceae): An update on *Beauveria*-like strains and description of a novel species from marine sediments. *Diversity, 15*(7), 795. https://doi.org/10.3390/d15070795

Guerra, C. A., Heintz-Buschart, A., Sikorski, J., Chatzinotas, A., Guerrero-Ramírez, N., Cesarz, S., . . . Eisenhauer, N. (2020). Blind spots in global soil biodiversity and ecosystem function research. *Nature Communications, 11*, 1–13. https://doi.org/10.1038/s41467-020-17688-2

Guimarães, L. H. S., Peixoto-Nogueira, S. C., Michelin, M., Rizzatti, A. C. S., Sandrim, V. C., Zanoelo, F. F., . . . Polizeli, M. L. T. M. (2006). Screening of filamentous fungi for production of enzymes of biotechnological interest. *Brazilian Journal of Microbiology, 37*, 474–480. https://doi.org/10.1590/S1517-83822006000400001

Guiraud, P., Steiman, R., Seigle-Murandi, F., & Sage, L. (1995). Mycoflora of soil around the Dead Sea II - Deuteromycetes (except *Aspergillus* and *Penicillium*). *Systematic and Applied Microbiology, 18*, 318–322. https://doi.org/10.1016/S0723-2020(11)80403-0

Guo, J., Ling, N., Chen, Z., Xue, C., Li, L., Liu, L., . . . Shen, Q. (2020). Soil fungal assemblage complexity is dependent on soil fertility and dominated by deterministic processes. *New Phytologist, 226*, 232–243. https://doi.org/10.1111/nph.16345

Gurusinghe, S., Brooks, T. L., Barrow, R. A., Zhu, X., Thotagamuwa, A., Dennis, P. G., . . . Weston, L. A. (2019). Technologies for the selection, culture and metabolic profiling of unique rhizosphere microorganisms for natural product discovery. *Molecules, 24*, 1955. https://doi.org/10.3390/molecules24101955

Gusmão, L. F., Grandi, R. A., & Milanez, A. I. (2000). A new species of *Beltraniopsis* from Brazil, with a key to the known species. *Mycological Research, 104*, 251–253.

Güssow, P. (1906). *Corynespora*. *Zeitschrift für Pflanzenkrankheiten und Pflanzenschutz, 16*, 10.

Guevara-Suarez, M., García, D., Cano-Lira, J. F., & Guarro, J. (2020). Species diversity in *Penicillium* and *Talaromyces* from herbivore dung, and the proposal of two new genera of penicillium-like fungi in *Aspergillaceae*. *Fungal Systematics and Evolution, 5*, 39. https://doi.org/10.3114/fuse.2020.05.03

Gutleben, J., Chaib De Mares, M., Van Elsas, J. D., Smidt, H., Overmann, J., & Sipkema, D. (2018). The multi-omics promise in context: From sequence to microbial isolate. *Critical Reviews in Microbiology, 44*, 212–229. https://doi.org/10.1080/1040841X.2017.1332003

Hainsworth, S., Kučerová, I., Sharma, R., & Cañete-Gibas, C. F., & Hubka, V. (2021). Three-gene phylogeny of the genus *Arthroderma*: Basis for future taxonomic studies. *Medical Mycology, 59*, 355–365. https://doi.org/10.1093/mmy/myaa057

Hajihosseinali, M., Nasr, S., Amoozegar, M. A., & Yurkov, A. (2020). *Saccharomycopsis oxydans* sp. nov., a new non-fermentative member in the genus *Saccharomycopsis* isolated from a traditional dairy product of Iran. *International Journal of Systematic and Evolutionary Microbiology, 70*, 1059–1063. https://doi.org/10.1099/ijsem.0.003874

Hall, T. (1999). BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series, 41*, 95–98.

Halsted, B. D. (1890). Some fungous diseases of the sweet potato. The black rot. *New Jersey Agriculture Experiment Station Bulletin, 76*, 7–14.

Halsted, B. D., & Fairchild, D. G. (1891). Sweet-potato black rot (*Ceratocystis fimbriata*, Ell. & Hals.). *The Journal of Mycology, 7*, 1–11.

Hambleton, S., Egger, K. N., & Currah, R. S. (1998). The genus *Oidiodendron*: Species delimitation and phylogenetic relationships based on nuclear ribosomal DNA analysis. *Mycologia, 90*, 854–868.

Hamada, N., Baba, T., & Sakuma, D. (2024). Culturable keratinophilic fungi isolated from house dust by hair-baiting technique. *International Biodeterioration & Biodegradation, 186*, 105702. https://doi.org/10.1016/j.ibiod.2023.105702

Hamm, P. S., Mueller, R. C., Kuske, C. R., & Porras-Alfaro, A. (2020). Keratinophilic fungi: Specialized fungal communities in a desert ecosystem identified using culture-based and Illumina sequencing approaches. *Microbiological Research, 239*, 126530. https://doi.org/10.1016/j.micres.2020.126530

Hansen, K., Læssøe, T., & Pfister, D. H. (2002). Phylogenetic diversity in the core group of *Peziza* inferred from ITS sequences and morphology. *Mycological Research, 106*, 879–902. https://doi.org/10.1017/S0953756202006287

Hansen, M. C., Potapov, P. V., Moore, R., Hancher, M., Turubanova, S. A., Tyukavina, A., . . . Townshend, J. R. G. (2013). High-resolution global maps of 21st-century forest cover change. *Science, 342*, 850–853.

HaoQin, P., Haibo, X., & Tianyu, Z. (2012). Three newly recorded species of Veronaea and Wardomyces from China. *Mycosystema, 31*, 133–135.

Haridas, S., Albert, R., Binder, M., Bloem, J., LaButti, K., Salamov, A., . . . Grigoriev, I. V. (2020). 101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. *Studies in Mycology, 96*, 141–153. https://doi.org/10.1016/j.simyco.2020.01.003

Harrington, A. H., del Olmo-Ruiz, M., U'Ren, J. M., Garcia, K., Pignatta, D., Wespe, N., . . . Arnold, A. E. (2019). *Coniochaeta endophytica* sp. nov., a foliar endophyte associated with healthy photosynthetic tissue of Platycladus orientalis (Cupressaceae). *Plant and Fungal Systematics, 64*, 65–79. https://doi.org/10.2478/pfs-2019-0008

Harrington, T. C. (1981). Cycloheximide sensitivity as a taxonomic character in Ceratocystis. *Mycologia, 73*, 1123–1129.

Harrington, T. C. (2013). Ceratocystis diseases. In *Infectious forest diseases* (pp. 230–255). CABI.

Harz, C. O. (1871). Einige neue Hyphomyceten Berlins und Wiens nebst Beiträgen zur Systematik derselben. *Bulletin de la Société Impériale des Naturalistes de Moscou, 44*, 88–146.

Hashimoto, A., Sato, G., Matsuda, T., Hirayama, K., Hatakeyama, S., Harada, Y., . . . Tanaka, K. (2015). Molecular taxonomy of Dinemasporium and its allied genera. *Mycoscience, 56*, 86–101. https://doi.org/10.1016/j.myc.2014.04.001

Hawksworth, D. L. (2001). The magnitude of fungal diversity: The 1.5 million. *Mycological Research, 105*, 1422–1432.

Hawksworth, D. L., & Rossman, A. Y. (1997). Where are all the undescribed fungi?. *Phytopathology, 87*, 888–891. https://doi.org/10.1094/PHYTO.1997.87.9.888

Hawksworth, D. L., & Lücking, R. (2017). Fungal diversity revisited: 2.2 to 3.8 million species. *Microbiology Spectrum, 5*(4). https://doi.org/10.1128/microbiolspec.FUNK-0052-2016

Hawksworth, D. L., Yen, C. C., & Sheridan, J. E. (1979). Bimuria novae-zelandiae gen. et sp. nov., a remarkable ascomycete isolated from a New Zealand barley field. *New Zealand Journal of Botany, 17*, 267–273. https://doi.org/10.1080/0028825X.1979.10426900

He, J., Kang, J., Lei, B., & Wen, T. (2011). Paecilomyces wawuensis, a new species isolated from soil in China. *Mycotaxon, 115*, 303–310. https://doi.org/10.5248/115.303

Hektoen, L., & Perkins, C. F. (1900). Refractory subcutaneous abscesses caused by *Sporothrix schenckii*. A new pathogenic fungus. *Journal of Experimental Medicine, 5*, 77–89. https://doi.org/10.1084/jem.5.1.77

Hennebert, G. L. (1962). Wardomyces and asteromyces. *Canadian Journal of Botany 40*, 1203–1216. https://doi.org/10.1139/b62-111

Hennebert, G. L., & Desai, B. (1974). *Lomentospora prolificans*, a new hyphomycete from greenhouse soil. *Mycotaxon, 1*, 45–50.

Hennings, P. (1902). Fungi javanici novi a cl. Prof. Dr. Zimmermann collecti. *Hedwigia, 41*, 140–144.

Heredia, G., Ulloa, M., & Sosa, V. J. (1988). Comparative study of fungal communities of soil and rhizosphere of spinach plants cultivated in chinampas. *Revista Latinoamericana de Microbiología, 30*, 155–161.

Heredia, G., Arias, R. M., Reyes, M., & Castañeda–Ruíz, R. (2002). New anamorph fungi with rhombic conidia from Mexican tropical forest litter. *Fungal Diversity, 11*, 99–107.

Herrmann, L., Lesueur, D., Bräu, L., Davison, J., Jairus, T., Robain, H., . . . Öpik, M. (2016). Diversity of root-associated arbuscular mycorrhizal fungal communities in a rubber tree plantation chronosequence in Northeast Thailand. *Mycorrhiza, 26*, 863–877.

Hernández-Restrepo, M., Gené, J., Mena-Portales, J., Cano, J., Madrid, H., Castaneda-Ruiz, R. F., . . . Guarro, J. (2014). New species of *Cordana* and *epitypification* of the genus. *Mycologia, 106*, 723–734.

Hernández-Restrepo, M., Madrid, H., Tan, Y. P., Da Cunha, K. C., Gené, J., Guarro, J., . . . Crous, P.W. (2018). Multi-locus phylogeny and taxonomy of Exserohilum. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 41*, 71–108. https://doi.org/10.3767/persoonia.2018.41.05

Hernãndez-Restrepo, M., Bezerra, J. D. P., Tan, Y. P., Wiederhold, N., Crous, P. W., Guarro, J., . . . Gené, J. (2019). Re-evaluation of *Mycoleptodiscus* species and morphologically similar fungi. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 42*, 205–227. https://doi.org/10.3767/persoonia.2019.42.08

Hernández-Restrepo, M., Giraldo, A., Van Doorn, R., Wingfield, M. J., Groenewald, J. Z., Barreto, R. W., . . . Crous, P. W. (2020). The genera of fungi – G6: *Arthrographis, Kramasamuha, Melnikomyces*, *Thysanorea*, and *Verruconis*. *Fungal Systematics and Evolution, 6*, 1–24. https://doi.org/10.3114/fuse.2020.06.01

Hernández-Restrepo, M., Groenewald, J. Z., & Crous, P. W. (2016a). Taxonomic and phylogenetic re-evaluation of *Microdochium, Monographella* and *Idriella*. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 36*, 57–82. https://doi.org/10.3767/003158516X688676

Hernández-Restrepo, M., Groenewald, J. Z., Elliott, M. L., Canning, G., McMillan, V. E., & Crous, P. W. (2016b). Take-all or nothing. *Studies in Mycology, 83*, 19–48. https://doi.org/10.1016/j.simyco.2016.06.002

Hernandez Restrepo, M., Groenewald, J. Z., & Crous, P. W. (2015). *Neocordana* gen. nov., the causal organism of *Cordana* leaf spot on banana. *Phytotaxa, 205*, 229. https://doi.org/10.11646/phytotaxa.205.4.2

Hibbett, D. S., Ohman, A., Glotzer, D., Nuhn, M., Kirk, P., & Nilsson, R. H. (2011). Progress in molecular and morphological taxon discovery in Fungi and options for formal classification of environmental sequences. *Fungal Biology Reviews, 25*, 38–47. https://doi.org/10.1016/j.fbr.2011.01.001

Hidayat, I., & Ramadhani, I. (2019). Phylogenetic study of curvularia on sorghum from Indonesia based on ITS rDNA sequence. *Jurnal Mikologi Indonesia, 3*, 118. https://doi.org/10.46638/jmi.v3i2.64

Hirsch, J., Galidevara, S., Strohmeier, S., Devi, K. U., & Reineke, A. (2013). Effects on diversity of soil fungal community and fate of an artificially applied Beauveria bassiana strain assessed through 454 pyrosequencing. *Microbial Ecology, 66*, 608–620. https://doi.org/10.1007/s00248-013-0249-5

Hirooka, Y., Tanney, J. B., Nguyen, H. D. T., & Seifert, K. A. (2016). Xerotolerant fungi in house dust: Taxonomy of *Spiromastix*, *Pseudospiromastix* and *Sigleria* gen. nov. in *Spiromastigaceae* (*Onygenales*, *Eurotiomycetes*). *Mycologia, 108*, 135–156. https://doi.org/10.3852/15-065

Ho, W. H., Yanna, Hyde, K. D., & Hodgkiss, I. J. (2002). Seasonality and sequential occurrence of fungi on wood submerged in Tai Po Kau Forest Stream, Hong Kong. *Fungal Diversity, 10*, 21–43.

Hodge, K. T., Krasnoff, S. B., & Humber, R. A. (1996). *Tolypocladium inflatum* is the anamorph of 681 *Cordyceps subsessilis*. *Mycologia, 88*, 715–71.

Hodges, C. S., & Barr, M. E. (1971). A new species of pseudomassaria and its Beltraniella Conidial State. *Mycologia, 63*, 562–566.

Höhnel, F. V. (1917). Mycologische fragmente 174. uber *Sphaeria uliginosa* Fr. und die cephalothecaceen. *Annales Mycolologici, 15*, 360-363.

Hodkinson, I. D., & Wookey, P. A. (1999). Functional ecology of soil organisms in tundra ecosystems: Towards the future. *Applied Soil Ecology, 11*, 111–126. https://doi.org/10.1016/S0929-1393(98)00142-5

Holliday, P., & Mowat, W. P. (1963). *Foot rot of Piper nigrum L. (Phytophthora palmivora)*. Commonwealth Mycological Institute.

Hongsanan, S., Jeewon, R., Purahong, W., Xie, N., Liu, J. K., Jayawardena, R. S., ... & Peršoh, D. (2018). Can we use environmental DNA as holotypes?. *Fungal Diversity, 92*,1–30. https://doi.org/10.1007/s13225-018-0404-x

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C., Sarma, V. V., . . . Xie, N. (2020a). Refned families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. *Mycosphere, 11*, 1553–2107. https://doi.org/10.5943/MYCOSPHERE/11/1/13

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H., Sarma, V. V., . . . Xie, N. (2020b). Refined families of Dothideomycetes: Orders and families incertae sedis in Dothideomycetes. *Fungal Diversity, 105*, 17–318. https://doi.org/10.1007/s13225-020-00462-6

Von Höhnel, F. V. (1924). Studien über Hyphomyzeten. *Zentralblatt für Bakteriologie und Parasitenkunde Abteilung, 2, 60*, 1–26.

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H., Sarma, V. V., . . . Xie, N. (2020b). *Refined families of Dothideomycetes: orders and families incertae sedis in Dothideomycetes*. Springer Netherlands.

de Hoog, G. S., & de Hoog, C. M. (1974). *Cladophialophora*, a new genus of hyphomycetes. *Persoonia, 8*, 243–251.

de Hoog, G. S. (1974). *Cladophialophora carrionii* (type species of *Cladophialophora*). *Persoonia, 8*, 243-251.

de Hoog, G. S. (1977). *Rhinocladiella* and allied genera. *Studies in Mycology, 15*, 1–140.

de Hoog, G. S., Dukik, K., Monod, M., Packeu, A., Stubbe, D., Hendrickx, M., . . . Gräser, Y. (2017). Toward a novel multilocus phylogenetic taxonomy for the dermatophytes. *Mycopathologia, 182*, 5–31. https://doi.org/10.1007/s11046-016-0073-9

de Hoog, G. S., & Hermanides-Nijhof, E. J. (1977). The black yeasts and allied Hyphomycetes. *Studies in Mycology, 15*, 1–222.

Hostinová, E., Janeček, Š., & Gašperík, J. (2010). Gene sequence, bioinformatics and enzymatic characterization of α-amylase from *Saccharomycopsis fibuligera* KZ. *The Protein Journal, 29*, 355–364. https://doi.org/10.1007/s10930-010-9260-6

Hou, L., Hernández-Restrepo, M., Groenewald, J. Z., Cai, L., & Crous, P. W. (2020a). Citizen science project reveals high diversity in *Didymellaceae* (*Pleosporales, Dothideomycetes*). *MycoKeys, 65*, 49–99. https://doi.org/10.3897/mycokeys.65.47704

Hou, L., Hernández-Restrepo, M., Groenewald, J. Z., Cai, L., & Crous, P.W. (2020). Citizen science project reveals high diversity in Didymellaceae (Pleosporales, Dothideomycetes). *MycoKeys, 65,* 49–99. https://doi.org/10.3897/mycokeys.65.47704

Hou, L. W., Giraldo, A., Groenewald, J. Z., Rämä, T., Summerbell, R. C., Huang, G. Z., . . . Crous, P. W. (2023). Redisposition of acremonium-like fungi in *Hypocreales*. *Studies in Mycology, 105*, 23–203. https://doi.org/10.3114/sim.2023.105.02

Hou, L. W., Groenewald, J. Z., Pfenning, L. H., & Yarden, O. (2020b). The phoma-like dilemma. *Studies in Mycology, 96*, 309–396. https://doi.org/10.1016/j.simyco.2020.05.001

Houbraken, J., & Samson, R. A. (2011). Phylogeny of *Penicillium* and the segregation of *Trichocomaceae* into three families. *Studies in Mycology, 70*, 1–51. https://doi.org/10.3114/sim.2011.70.01

Hsieh, H. M., Ju, Y. M., Lechat, C., Fournier, J., & Huart, D. (2022). New ecological, morphological, cultural and molecular phylogenetic insights into *Xylaria guepini* (*Xylariaceae*). *Ascomycete, 14*, 177-184.

Hu, D. M., Wang, M., & Cai, L. (2017). Phylogenetic assessment and taxonomic revision of *Mariannaea*. *Mycological Progress, 16*, 271–283. https://doi.org/10.1007/s11557-016-1252-2

Huang, L. H. (1976). Cytology of *Triangularia backusii*. *Mycologia, 68*, 984. https://doi.org/10.2307/3758714

Huang, S. K., Hyde, K. D., Maharachchikumbura, S. S. N., McKenzie, E. H. C., & Wen, T. C. (2021a). Taxonomic studies of *Coronophorales* and *Niessliaceae* (*Hypocreomycetidae*). *Mycosphere, 12*, 875–992. https://doi.org/10.5943/mycosphere/12/1/9

Huang, S. K., Hyde, K. D., Mapook, A., Maharachchikumbura, S. S., Bhat, J. D., McKenzie, E. H., . . . Wen, T. C. (2021b). *Taxonomic studies of some often over-looked Diaporthomycetidae and Sordariomycetidae*. Springer Netherlands.

Huang, Y. T., Hung, T. C., Fan, Y. C., Chen, C. Y., & Sun, P. L. (2023). The high diversity of *Scedosporium* and *Lomentospora* species and their prevalence in human-disturbed areas in Taiwan. *Medical Mycology, 61*(4). https://doi.org/10.1093/mmy/myad041

Huanraluek, N., Phukhamsakda, C., Senwanna, C., & Hongsanan, S. (2019). *Verruconis heveae*, a novel species from *Hevea brasiliensis* in Thailand. *Phytotaxa, 403*, 47. https://doi.org/10.11646/phytotaxa.403.1.4

Huelsenbeck, J. P., & Ronqvist, F. (2001). MRBAYES: Bayesian inference of phylogenetic trees. *Bioinformatics, 17,* 754–755. https://doi.org/10.1093/bioinformatics/17.8.754

Huges, S. J. (1951). Studies on microfungi. IX. *Calcarisporium, Verticicladium* and *Hansfordia* (gen. nov.). *Mycological Papers, 43*. https://archive.org/details/hughes-1951

Hughes, S. J. (1951). *Stachylidium, Gonytrichum, Mesobotrys, Chaetopsis* and *Chaetopsella*. *Transactions of the British Mycological Society, 34*, 551–576.

Hughes, S. J. (1953). Conidiophores, conidia, and classification. *Canadian Journal of Botany, 31*, 577–659. https://doi.org/10.1139/b53-046

Hughes, S. J. (1958). Revisiones hyphomycetum aliquot cum appendice de nominibus rejiciendis. *Canadian Journal of Botany, 36*, 727–836. https://doi.org/10.1139/b58-06

Huhndorf, S. M., & Fernández, F. A. (2005). Teleomorph-anamorph connections: *Chaetosphaeria raciborskii* and related species, and their *Craspedodidymum*-like anamorphs. *Fungal Diversity, 19*, 23–49.

Hui, N., Jumpponen, A., Francini, G., & Kotze, D. J. (2017). Soil microbial communities are shaped by vegetation type and park age in cities under cold climate. *Environmental Microbiology, 19*, 1281–1295. https://doi.org/10.1111/1462-2920.13660

Huimei, L., & Tianyu, Z. (2004). A preliminary report of soil dematiaceous hyphomycetes from the Yellow River Delta I. *Mycosystema, 23*, 338–344.

Hujslová, M., Kubátová, A., Kostovčík, M., & Blanchette, R. A. (2014). Three new genera of fungi from extremely acidic soils. *Mycological Progress, 13*, 819–831. https://doi.org/10.1007/s11557-014-0965-3

Hujslová, M., Kubátová, A., Kostovčík, M., & Kolařík, M. (2013). *Acidiella bohemica* gen. et sp. nov. and *Acidomyces* spp. (*Teratosphaeriaceae*), the indigenous inhabitants of extremely acidic soils in Europe. *Fungal Diversity, 58*, 33–45. https://doi.org/10.1007/s13225-012-0176-7

Hunter, B. B., Hoyes, J. V., & Barnett, H. L. (1974). The additions of aureomycin and chloramphenicol to various fungal agar media to prevent bacterial contamination. In *Proceedings of the Pennsylvania Academy of Science* (pp. 88–92). Pennsylvania Academy of Science.

Hyde, K. D., Noorabadi, M. T., & Thiyagaraja, V. (2024a). The 2024 outline of fungi and fungus-like taxa. *Mycosphere, 15*, 5146–6239. https://doi.org/10.5943/mycosphere/15/1/25

Hyde, K. D., Baldrian, P., Chen, Y., Thilini Chethana, K. W., De Hoog, S., Doilom, M., . . . Walker, A. (2024b). Current trends, limitations and future research in the fungi?. *Fungal Diversity, 125*, 1–71. https://doi.org/10.1007/s13225-023-00532-5

Hyde, K. D., Dong, Y., Phookamsak, R., Jeewon, R., Bhat, D. J., Jones, E. G., . . . Sheng, J. (2020a). Fungal diversity notes 1151–1276: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 100*, 5–277. https://doi.org/10.1007/s13225-020-00439-5

Hyde, K. D., Fröhlich, J., & Taylor, J. E. (1998). Fungi from palms XXXVI Reflections on unitunicate ascomycetes with apiospores. *Sydowia, 50*, 21–80.

Hyde, K. D., Hongsanan, S., Jeewon, R., & Bhat, D. J. (2016). Fungal diversity notes 367–490: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity, 80*, 1–270. https://doi.org/10.1007/s13225-016-0373-x

Hyde, K. D., Jeewon, R., Chen, Y. J., Bhunjun, C. S., Calabon, M. S., Jiang, H. B., . . . Lumyong, S. (2020b). The numbers of fungi: Is the descriptive curve flattening?. *Fungal Diversity, 103*, 219–271. https://doi.org/10.1007/s13225-020-00458-2

Hyde, K. D., Jones, E. G., Liu, J. K., Ariyawansa, H., Boehm, E., Boonmee, S., . . . Zhang, M. (2013). Families of *Dothideomycetes*. *Fungal Diversity, 63*, 1–313. https://doi.org/10.1007/s13225-013-0263-4

Hyde, K. D., Norphanphoun, C., Chen, J., Dissanayake, A. J., Doilom, M., Hongsanan, S., . . . Stadler, M. (2018). Thailand's amazing diversity: Up to 96% of fungi in northern Thailand may be novel. *Fungal Diversity, 93*, 215–239. https://doi.org/10.1007/s13225-018-0415-7

Hyde, K. D., Norphanphoun, C., Maharachchikumbura, S. S. N., Bhat, D. J., Jones, E., Bundhun, D., . . . Xiang, M. M. (2020c). Refined families of *Sordariomycetes*. *Mycosphere, 11*, 305–1059. https://doi.org/10.5943/mycosphere/11/1/7

Hyde, K. D., Saleh, A., Aumentado, H. D. R., Boekhout, T., Bera, I., Khyaju, S., . . . Wanasinghe, D. N. (2024c). Fungal numbers: Global needs for a realistic assessment. *Fungal Diversity, 128*, 191–225. https://doi.org/10.1007/s13225-024-00545-8

Hyde, K. D., Dong, Y., Phookamsak, R., & Jeewon, R. (2020d). Fungal diversity notes 1151–1276: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 100*, 5–277. https://doi.org/10.1007/s13225-020-00439-5

Hyde, K. D., Baldrian, P., Chen, Y., Thilini Chethana, K.W., De Hoog, S., Doilom, M., . . . Walker, A. (2024a). Current trends, limitations and future research in the fungi?. *Fungal Diversity, 125*, 1–71. https://doi.org/10.1007/s13225-023-00532-5

Hyde, K. D., Jones, E. B. G., Liu, J.-K., Ariyawansa, H., Boehm, E., Boonmee, S., . . . Zhang, M. (2013). Families of Dothideomycetes. *Fungal Diversity, 63*, 1–313. https://doi.org/10.1007/s13225-013-0263-4

Hyde, K. D., Fryar, S., Tian, Q., Bahkali, A. H., & Xu, J. C. (2016). Lignicolous freshwater fungi along a north−south latitudinal gradient in the Asian/Australian region; can we predict the impact of global warming on biodiversity and function?. *Fungal Ecology, 19*, 190−200.

Hyde, K. D., Norphanphoun, C., Chen, J., Dissanayake, A. J., Doilom, M., Hongsanan, S., . . . Stadler, M. (2018). Thailand's amazing diversity - up to 96% of fungi in northern Thailand may be novel. *Fungal Diversity, 93*, 215–239.

Hyde, Y., & Hyde, K. D. (2002). New saprobic fungi on fronds of palms from northern Queensland, Australia. *Australian Systematic Botany, 15*, 755–764.

Hyde, K. D., Xu, J., Rapior, S., Jeewon, R., Lumyong, S., Niego, A. G. T., ... & Stadler, M. (2019). The amazing potential of fungi: 50 ways we can exploit fungi industrially. *Fungal Diversity, 97*, 1–136. https://doi.org/10.1007/s13225-019-00430-9

Hyde, K. D., Noorabadi, M. T., Thiyagaraja, V., Mq, H., Johnston, P. R., Wijesinghe, S. N., . . . Dianese, J. (2024b). The 2024 outline of fungi and fungus-like taxa. *Mycosphere, 15*(1), 5146–6239.

Hyde, K. D., Baldrian, P., Chen, Y., Thilini Chethana, K. W., De Hoog, S., Doilom, M., . . . Walker, A. (2024a). Current trends, limitations and future research in the fungi?. *Fungal Diversity, 125*, 1–71. https://doi.org/10.1007/s13225-023-00532-5

Ibrahim, S. R. M., Alzain, A. A., Elbadwi, F. A., Koshak, A. E., AlSaedi, A. H., Ashour, A., . . . Mohamed, G. A. (2024). Shedding light on *Paraconiothyrium brasiliense*: Secondary metabolites, biological activities, and computational studies. *Journal of Applied Pharmaceutical Science, 14*(10). https://doi.org/10.7324/JAPS.2024.184503

Ibrahim, S. R. M., Altyar, A. E., Mohamed, S. G. A., & Mohamed, G. A. (2022). Genus *Thielavia*: Phytochemicals, industrial importance and biological relevance. *Natural Product Research, 36*, 5108–5123. https://doi.org/10.1080/14786419.2021.1919105

Ibrahim, S. R. M., Mohamed, S. G. A., Altyar, A. E., & Mohamed, G. A. (2021). Natural products of the fungal genus *Humicola*: diversity, biological activity, and industrial importance. *Current Microbiology, 78,* 2488–2509. https://doi.org/10.1007/s00284-021-02533-6

Ide-Pérez, M. R., Sánchez-Reyes, A., Folch-Mallol, J. L., Sánchez-Carbente, M. del. R. (2024). *Exophiala chapopotensis* sp. nov., an extremotolerant black yeast from an oil-polluted soil in Mexico; phylophenetic approach to species hypothesis in the *Herpotrichiellaceae* family. *PLOS One, 19,* e0297232. https://doi.org/10.1371/journal.pone.0297232

Ikeda, K., Kuwabara, K., Urushibara, T., Soyai, P., Miki, S., & Shibata, S. (2012). Pink root rot of squash caused by *Setophoma terrestris* in Japan. *Journal of General Plant Pathology, 78,* 372–375. https://doi.org/10.1007/s10327-012-0398-2

Imoulan, A., Wu, H. J., Lu, W. L., & Li, Y. (2016). *Beauveria medogensis* sp. nov., a new fungus of the entomopathogenic genus from China. *Journal of Invertebrate Pathology*, *139*, 74–81. https://doi.org/10.1016/j.jip.2016.07.006

Index Fungorum. (2023). *Index Fungorum database*. Retrived January 21, 2023, from http://www.indexfungorum.org/Names/Names.asp

Index Fungorum. (2025). *Index Fungorum database*. Retrived February 12, 2025, from http://www.indexfungorum.org

IndexFungorum. (2024). *Index Fungorum database*. Retrived August 3, 2024, from http://www.indexfungorum.org/Names/ Names.asp

Index Fungorum. (2020). *Index Fungorum database*. Retrived August 6, 2020, from http://www.indexfungorum.org/names/names.asp

Ismail, M. A., Hussein, N. A., Abdel-Sater, M. A., & Sayed, R. M. (2020). Evaluation of physiological and biochemical characteristics of *Alternaria* species isolated from soil in Assiut governorate, Egypt, in addition to dichotomous key to the encountered species. *Assiut University Journal of Botany and Microbiology 49,* 34–59.

Ito, T., Nakagiri, A., Tanticharoen, M., & Manoch, L. (2001). Mycobiota of mangrove forest soil in Thailand. *IFO Research Communications, 20,* 50–60.

Ito, T., & Nakagiri, A. (1994). *Stellatospora*, a new genus of the *Sordariaceae*. *Mycoscience, 35*, 413–415. https://doi.org/10.1007/BF02268515

Ito, T., & Nakagiri, A. (1995). *Westerdykella globosa*, a proposal for a new combination. *Mycoscience, 36*, 361–363. https://doi.org/10.1007/BF02268614

Ito, T., Okane, I., & Nakagiri, A. (1998). *Thiolavia aurantiaca*, a new species from Japanese soil. *Mycoscience, 39*, 93–96. https://doi.org/10.1007/BF02461585

Ito, T., Okane, I., Nakagiri, A., & Gams, W. (2000). Two species of *Acremonium* section *Acremonium*: *A. borodinense* sp. nov. and *A. cavaraeanum* rediscovered. *Mycological Research, 104*, 77–80. https://doi.org/10.1017/S0953756299008977

Iturrieta-González, I., García, D., & Gené, J. (2021). Novel species of *Cladosporium* from environmental sources in Spain. *MycoKeys, 77*, 1–25. https://doi.org/10.3897/mycokeys.77.60862

Iturrieta-González, I., Gené, J., Guarro, J., Castañeda-Ruiz, R. F., & García, D. (2018). *Neodendryphiella*, a novel genus of the *Dictyosporiaceae* (*Pleosporales*). *MycoKeys*, *37*, 19–38. https://doi.org/10.3897/mycokeys.37.27275

Iturrieta-González, I., Gené, J., Wiederhold, N., & García, D. (2020). Three new *Curvularia* species from clinical and environmental sources. *MycoKeys*, *68*, 1–21. https://doi.org/10.3897/mycokeys.68.51667

Izuno, A., Kanzaki, M., Artchawakom, T., Wachrinrat, C., & Isagi, Y. (2016). Vertical structure of *Phyllosphere* fungal communities in a tropical forest in Thailand uncovered by high-throughput sequencing. *PLOS One, 11*, e0166669. https://doi.org/10.1371/journal.pone.0166669

Jackson, H. S. (1948). *Trichomonascus*. *Mycologia, 39*, 712.

Jacoby, R., Peukert, M., Succurro, A., & Koprivova, A. (2017). The role of soil microorganisms in plant mineral nutrition–current knowledge and future directions. *Frontiers in Plant Science, 8*, 1617. https://doi.org/10.3389/fpls.2017.01617

Jaklitsch, W. M., Fournier, J., & Voglmayr, H. (2018). Two unusual new species of Pleosporales: Anteaglonium rubescens and Atrocalyx asturiensis. *Sydowia, 4*, 129–140.

Jaklitsch, W. M., & Voglmayr, H. (2015). Biodiversity of *Trichoderma* (Hypocreaceae) in Southern Europe and Macaronesia. *Studies in Mycology, 80*, 1–87. https://doi.org/10.1016/j.simyco.2014.11.001

Jaklitsch, W. M., & Voglmayr, H. (2016). Hidden diversity in *Thyridaria* and a new circumscription of the Thyridariaceae. *Studies in Mycology, 85*, 35–64. https://doi.org/10.1016/j.simyco.2016.09.002

Janowski, D., & Leski, T. (2022). Factors in the distribution of mycorrhizal and soil fungi. *Diversity, 14*, 1122. https://doi.org/10.3390/d14121122

Jaklitsch, W. M., Checa, J., Blanco, M. N., Olariaga, I., Tello, S., & Voglmayr, H. (2018). A preliminary account of the Cucurbitariaceae. *Studies in Mycology, 90*, 71–118. https://doi.org/10.1016/j.simyco.2017.11.002

Jayasiri, S. C., Hyde, K. D., Jones, E. B. G., Jeewon, R., Ariyawansa, H. A., Bhat, J. D., . . . Kang, J. C. (2017). Taxonomy and multigene phylogenetic evaluation of novel species in *Boeremia* and *Epicoccum* with new records of *Ascochyta* and *Didymella* (Didymellaceae). *Mycosphere, 8*, 1080–1101. https://doi.org/10.5943/mycosphere/8/8/9

Jayasiri, S. C., Hyde, K. D., Jones, E. B. G., McKenzie, E. H. C., Jeewon, R., Phillips, A. J. L., . . . Karunarathna, S. C. (2019). Diversity, morphology and molecular phylogeny of Dothideomycetes on decaying wild seed pods and fruits. *Mycosphere, 10*, 1–186. https://doi.org/10.5943/mycosphere/10/1/1

Jayasiri, S. C., Jones, E. B. G., Kang, J. C., Promputtha, I., Bahkali, A. H., & Hyde, K. D. (2016). A new species of genus Anteaglonium (Anteagloniaceae, Pleosporales) with its asexual morph. *Phytotaxa, 263*, 233. https://doi.org/10.11646/phytotaxa.263.3.4

Jayasiri, S. C., Hyde, K. D., Ariyawansa, H. A., Bhat, J., Buyck, B., Cai, L., . . . Promputtha, I. (2015). The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. *Fungal Diversity, 74*, 3–18. https://doi.org/10.1007/s13225-015-0351-8

Jayawardena, R. S., Hyde, K. D., Chen, Y. J., Papp, V. (2020). One stop shop IV: Taxonomic update with molecular phylogeny for important phytopathogenic genera: 76–100 (2020). *Fungal Diversity, 103*, 87–218. https://doi.org/10.1007/s13225-020-00460-8

Jayawardena, R. S., Hyde, K. D., de Farias, A. R. G., & Bhunjun, C. S. (2021). What is a species in fungal plant pathogens? *Fungal Diversity, 109*, 239–266. https://doi.org/10.1007/s13225-021-00484-8

Jayawardena, R. S., Purahong, W., Zhang, W., Wubet, T., Li, X., Liu, M., . . . Yan, J. (2018). Biodiversity of fungi on *Vitis vinifera* L. revealed by traditional and high-resolution culture-independent approaches. *Fungal Diversity, 90*, 1–84. https://doi.org/10.1007/s13225-018-0398-4

Jayawardena, R. S., Hyde, K. D., Chen, Y. J., Papp, V., Palla, B., Papp, D., . . . Wang, Y. (2020). One stop shop IV: Taxonomic update with molecular phylogeny for important phytopathogenic genera: 76–100 (2020). *Fungal Diversity, 103*, 87–218. https://doi.org/10.1007/s13225-020-00460-8

Jeamjitt, O., Manoch, L., Visarathanonth, N., & Chamswarng, C. (2006). Diversity and distribution of hyphomycetes from dung in Thailand. *Agriculture and Natural Resources, 40*, 890–901.

Jeewon, R., & Hyde, K. D. (2016). Establishing species boundaries and new taxa among fungi: Recommendations to resolve taxonomic ambiguities. *Mycosphere, 7*, 1669–1677.

Jeewon, R., Yeung, S. Y. Q., & Hyde, K. D. (2009). A novel phylogenetic group within *Thozetella* (Chaetosphaeriaceae): A new taxon based on morphology and DNA sequence analyses. *Canadian Journal of Microbiology, 55*, 680–687.

Jeewon, R., & Hyde, K. D. (2007). Detection and diversity of fungi from environmental samples: Traditional versus molecular approaches. In A. Varma & R. Oelmüller (Eds.), *Advanced Techniques in Soil Microbiology* (Vol. 11, pp. 1–25). Springer. https://doi.org/10.1007/978-3-540-70865-01

Ji, Y., Ashton, L., Pedley, S. M., Edwards, D. P., Tang, Y., Nakamura, A., . . . Yu, D. W. (2013). Reliable, verifiable and efficient monitoring of biodiversity via metabarcoding. *Ecology Letters, 16*, 1245–1257. https://doi.org/10.1111/ele.12162

Jiang, X. Z., Yu, Z. D., Ruan, Y. M., & Wang, L. (2018a). Three new species of *Talaromyces* sect. *Talaromyces* discovered from soil in China. *Scientific Reports, 8*, 4932. https://doi.org/10.1038/s41598-018-23370-x

Jiang, Y. L., Wu, Y. M., Yang, B., & Xu, J. J. (2017a). New species of *Cephalotrichum*, *Leptographium*, and *Myrothecium* from soil in China. *Mycotaxon, 132*, 603–609. https://doi.org/10.5248/132.603

Jiang, Y. L., & Zhang, T. Y. (2010). Two new species of *Humicola* from soil. *Mycotaxon, 111*, 117–120. https://doi.org/10.5248/111.117

Jiang, Y., Dukik, K., Munoz, J. F., Sigler, L., Schwartz, I. S., Govender, N. P., . . . de Hoog, S. (2018b). Phylogeny, ecology and taxonomy of systemic pathogens and their relatives in *Ajellomycetaceae* (*Onygenales*): *Blastomyces*, *Emergomyces*, *Emmonsia*, *Emmonsiellopsis*. *Fungal Diversity, 90*, 245–291.

Jiang, Y., Tsui, C. K. M., Ahmed, S. A., & Hagen, F. (2020). Intraspecific diversity and taxonomy of *Emmonsia crescens*. *Mycopathologia, 185*, 613–627. https://doi.org/10.1007/s11046-020-00475-4

Jiang, Y. L., Wu, Y. M., Yang, B., Xu, J. J., Zhang, Z. G., Kong, J. H., . . . Zhang, T. Y. (2017b). *Cladosporium, Phialophora, Pseudoramichloridium* & *Ticogloea* spp. nov. from China. *Mycotaxon, 132*, 677–683.

Jiang, Y. L., & Zhang, T. Y. (2008). New species of *Bipolaris*, *Scolecobasidium* and *Torula* from soil. *Mycotaxon, 104*, 135–140.

Jie, C. Y., Geng, K., Jiang, Y. L., Xu, J. J., Hyde, K. D., McKenzie, E. H., . . . Wang, Y. (2013). *Stachybotrys* from soil in China, identified by morphology and molecular phylogeny. *Mycological Progress, 12*, 693–698.

Jiea, C. Y., Zhoua, Q. X., Zhao, W. S., Jiang, Y. L., Hyde, K. D., McKenzie, E. H., . . . Wang, Y. (2013). A new *Myrmecridium* species from Guizhou, China. *Mycotaxon, 124*, 1–8. https://doi.org/10.5248/124.1

Jindamorakot, S., Ninomiya, S., Limtong, S., & Yongmanitchai, W. (2009). Three new species of bipolar budding yeasts of the genus *Hanseniaspora* and its anamorph *Kloeckera* isolated in Thailand. *FEMS Yeast Research, 9*, 1327–1337. https://doi.org/10.1111/j.1567-1364.2009.00568.x

Jones, E. B. G., Pang, K. L., Abdel-Wahab, M. A., & Scholz, B. (2019). An online resource for marine fungi. *Fungal Diversity, 96*, 347–433. https://doi.org/10.1007/s13225-019-00426-5

Jong, S. C., & Davis, E. E. (1976). Contribution to the knowledge of *Stachybotrys* and *Memnoniella* in culture. *Mycotaxon, 3*, 409–485.

Jooste, W. J. (1978). *Leptographium reconditum* sp. nov. and observations on conidiogenesis in *Verticicladiella*. *Transactions of the British Mycological Society, 70*, 152–155. https://doi.org/10.1016/S0007-1536(78)80189-2

Ju, Y. M., Hsieh, H. M., & Suwannasai, N. (2023). *Xylaria furcata* reconsidered and nine resembling species. *Botanical Studies, 64*, 21. https://doi.org/10.1186/s40529-023-00392-x

Junier, P., Cailleau, G., Palmieri, I., Vallotton, C., Trautschold, O. C., Junier, T., . . . Chain, P. S. (2021). Democratization of fungal highway columns as a tool to investigate bacteria associated with soil fungi. *FEMS Microbiology Ecology, 97*, fiab003. https://doi.org/10.1093/femsec/fiab003

Jurburg, S. D., Keil, P., Singh, B. K., & Chase, J. M. (2021). All together now: Limitations and recommendations for the simultaneous analysis of all eukaryotic soil sequences. *Molecular Ecology Resources, 21*, 1759–1771. https://doi.org/10.1111/1755-0998.13401

Jurado, V., Del Rosal, Y., Liñán, C., Martin-Pozas, T., Gonzalez-Pimentel, J. L., & Saiz-Jimenez, C. (2021). Diversity and seasonal dynamics of airborne fungi in Nerja cave, Spain. *Applied Sciences, 11*, 6236. https://doi.org/10.3390/app11136236

Kabtani, J., Militello, M., & Ranque, S. (2022). *Coniochaeta massiliensis* sp. nov. isolated from a clinical sample. *Journal of Fungi, 8*, 999. https://doi.org/10.3390/jof8100999

Kachenchart, B., Kamlangkla, C., Puttanapong, N., & Limsakul, A. (2020). Urbanization effects on surface air temperature trends in Thailand during 1970–2019. *Environmental Engineering Research, 26*, 200378. https://doi.org/10.4491/eer.2020.378

Kadowaki, K., Sato, H., Yamamoto, S., Tanabe, A. S., Hidaka, A., & Toju, H. (2014). Detection of the horizontal spatial structure of soil fungal communities in a natural forest. *Population Ecology, 56*, 301–310. https://doi.org/10.1007/s10144-013-0424-z

Kaewchai, S., Soytong, K., & Hyde, K. D. (2009). Mycofungicides and fungal biofertilizers. *Fungal Diversity, 38*, 25–50.

Kaltseis, J., Rainer, J., & De Hoog, G. S. (2009). Ecology of *Pseudallescheria* and *Scedosporium* species in human-dominated and natural environments and their distribution in clinical samples. *Sabouraudia, 47*, 398–405.

Kamolmanit, B., Vityakon, P., Kaewpradit, W., Cadisch, G., & Rasche, F. (2013). Soil fungal communities and enzyme activities in a sandy, highly weathered tropical soil treated with biochemically contrasting organic inputs. *Biology and Fertility of Soils, 49*, 905–917. https://doi.org/10.1007/s00374-013-0785-7

Kandemir, H., Decock, C., Hernández-Restrepo, M., & Labuda, R. (2024). 200 years of taxonomic confusion: *Sporendonema* and allies. *Antonie van Leeuwenhoek, 117*, 53. https://doi.org/10.1007/s10482-024-01935-3

Kandemir, H., Dukik, K., de Melo Teixeira, M., & Stielow, J. B. (2022). Phylogenetic and ecological reevaluation of the order Onygenales. *Fungal Diversity, 115*, 1–72.

Kapeua-Ndacnou, M., de Abreu, L. M., de Macedo, D. M., da Nóbrega, T. F., Pereira, C. M., Evans, H. C., & Barreto, R. W. (2023). Assessing the biocontrol potential of *Clonostachys* species isolated as endophytes from *Coffea* species and as mycoparasites of hemileia rusts of coffee in Africa. *Journal of Fungi, 9*, 248. https://doi.org/10.3390/jof9020248

Karpinska-Kolaczek, M., Kolaczek, P., Heise, W., & Worobiec, G. (2010). *Tetraploa aristata* Berkeley and Broome (Fungi, Pleosporales), a new taxon to Poland. *Acta Societatis Botanicorum Poloniae, 3*, 79.

Katan, T. (1985). Heat activation of dormant ascospores of *Talaromyces flavus*. *Transactions of the British Mycological Society, 84*, 748–750. https://doi.org/10.1016/S0007-1536(85)80137-6

Karun, N. C., & Sridhar, K. R. (2015). *Xylaria* complex in the South Western India. *Plant Pathology & Quarantine, 5*, 83–96. https://doi.org/10.5943/ppq/5/2/7

Karunarathna, A., Phookamsak, R., Jayawardena, R. S., Cheewangkoon, R., Hyde, K. D., & Kuo, C. H. (2019). The holomorph of *Neoroussoella alishanense* sp. nov. (Roussoellaceae, Pleosporales) on *Pennisetum purpureum* (Poaceae). *Phytotaxa, 406*, 218–236. https://doi.org/10.11646/phytotaxa.406.4.1

Karunarathna, S. C., Samarakoon, M. C., & Senanayake, I. C. (2024). Recent advances in fungal taxonomy and phylogeny. *New Zealand Journal of Botany, 62*, 119–122. https://doi.org/10.1080/0028825X.2024.2369351

Kassam, R., Kamil, D., & Rao, U. (2021). *Caenorhabditis elegans* as bait for isolating promising biocontrol fungi against *Meloidogyne incognita* from soils across India. *Indian Phytopathology, 74*, 739–752. https://doi.org/10.1007/s42360-021-00354-y

Katoh, K., Rozewicki, J., & Yamada, K. D. (2019). MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics, 20*, 1160–1166.

Katoh, K., Misawa, K., Kuma, K., & Miyata, T. (2002). MAFFT: A novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research, 30*, 3059–3066.

Kaur, I., Gaur, V. K., Rishi, S., Anand, V., Mishra, S. K., Gaur, R., . . . Srivastava, P. K. (2023). Deciphering the kinetics and pathway of lindane biodegradation by novel soil ascomycete fungi for its implication in bioremediation. *Bioresource Technology*, *387*, 129581. https://doi.org/10.1016/j.biortech.2023.129581

Kayang, H. (2006). Soil microbial population numbers in sacred grove forest of Meghalaya, Northeast India. *Asian Journal of Microbiology, Biotechnology & Environmental Sciences, 8*, 521–526.

Kazemzadeh-Chakusary, M., Mohammadi, H., & Sohrabi, M. (2021). Occurrence and pathogenicity of *Jattaea algeriensis* (Calosphaeriales, Calosphaeriaceae) and *Biscogniauxia mediterranea* on forest trees in Guilan province (Iran). *Journal of Phytopathology, 169*, 129–138. https://doi.org/10.1111/jph.12967

Kazerooni, E. A., Maharachchikumbura, S. S., Rethinasamy, V., Al-Mahrouqi, H., & Al-Sadi, A. M. (2017). Fungal diversity in tomato rhizosphere soil under conventional and desert farming systems. *Frontiers in Microbiology, 8*, 1462. https://doi.org/10.3389/fmicb.2017.01462

Khuna, S., Suwannarach, N., Kumla, J., Meerak, J., Nuangmek, W., Kiatsiriroat, T., & Lumyong, S. (2019). *Apophysomyces thailandensis* (Mucorales, Mucoromycota), a new species isolated from soil in northern Thailand and its solubilization of non-soluble minerals. *MycoKeys*, *45*, 75–92.

Keller, S., Kessler, P., & Schweizer, C. (2003). Distribution of insect pathogenic soil fungi in Switzerland with special reference to *Beauveria brongniartii* and *Metharhizium anisopliae*. *BioControl*, *48*, 307–319.

Kepler, R. M., Humber, R. A., Bischoff, J. F., & Rehner, S. A. (2014). Clarification of generic and species boundaries for *Metarhizium* and related fungi through multigene phylogenetics. *Mycologia*, *106*, 811–829. https://doi.org/10.3852/13–319

Kepler, R. M., Luangsa-Ard, J. J., Hywel-Jones, N. L., Quandt, C. A., Sung, G. H., Rehner, S. A., . . . Shrestha, B. (2017). A phylogenetically-based nomenclature for Cordycipitaceae (Hypocreales). *IMA Fungus*, *8*, 335–353. https://doi.org/10.5598/imafungus.2017.08.02.08

Kim, D. G., Bae, S. G., & Shin, Y. S. (2001). Distribution of nematophagous fungi under different habitats. *Korean Journal of Mycology*, *29*, 123–126.

Kirichuk, N. N., Pivkin, M. V., & Matveeva, T. V. (2017). Three new *Penicillium* species from marine subaqueous soils. *Mycological Progress*, *16*, 15–26. https://doi.org/10.1007/s11557-016-1247-z

Kirk, P., Cannon, P., Minter, D., & Stalpers, J. (2009). *Ainsworth and Bisby's dictionary of the fungi* (10th ed.). CABI.

Kirk, P. M., Stalpers, J. A., Braun, U., Crous, P. W., Hansen, K., Hawksworth, D. L., . . . Stadler, M. (2013). A without-prejudice list of generic names of fungi for protection under the International Code of Nomenclature for algae, fungi, and plants. *IMA Fungus*, *4*, 381–443. https://doi.org/10.5598/imafungus.2013.04.02.17

Kirk, P. M. (1981). New or interesting microfungi. III, A preliminary account of micro fungi colonizing *Laurus nobilis* leaf litter. *Transactions of the British Mycological Society*, *77*, 457–473.

Kirk, P. M., & Sutton, B. C. (1985). A reassessment of the anamorph genus *Chaetopsina* (Hyphomycetes). *Transactions of the British Mycological Society, 85*, 709–717.

Kitisin, T., Muangkaew, W., Ampawong, S., Chutoam, P., Thanomsridetchai, N., Tangwattanachuleeporn, M., . . . Sukphopetch, P. (2021). Isolation of fungal communities and identification of *Scedosporium* species complex with pathogenic potentials from a pigsty in Phra Nakhon Si Ayutthaya, Thailand. *New Microbiologica, 44*, 33–41.

Kladwang, W., Bhumirattana, A., & Hywel-Jones, N. (2003). Alkaline-tolerant fungi from Thailand. *Fungal Diversity, 13*, 69–83.

Klebahn, H. (1929). Vergilbende junge Treibgurken, ein darauf gefundenes *Cephalosporium* und dessen Schlauchfrüchte. *Phytopathologische Zeitschrift, 1*, 31–44.

Klein, B. S., Vergeront, J. M., Weeks, R. J., Kumar, U. N., Mathai, G., & Varkey, B. (1986). Isolation of *Blastomyces dermatitidis* in soil associated with a large outbreak of blastomycosis in Wisconsin. *New England Journal of Medicine, 314*, 529–534. https://doi.org/10.1056/NEJM198602273140901

Klotzsch, C. W. F. von. (1830). *Plantae Cryptogamae quas in Arduenna collegit* (Fasc. 1, p. 8).

Kobayashi, R., Kanti, A., & Kawasaki, H. (2017). *Pichia chibodasensis* sp. nov., isolated in Indonesia. *International Journal of Systematic and Evolutionary Microbiology, 67*, 1024–1027. https://doi.org/10.1099/ijsem.0.001735

Kobayasi, Y. (1941). The genus *Cordyceps* and its allies. *Scientific Reports of the Tokyo Bunrika Daigaku, Series B, 84*, 53–260.

Kohlwein, S. D., & Paltauf, F. (1984). Uptake of fatty acids by the yeasts, *Saccharomyces uvarum* and *Saccharomycopsis lipolytica*. *Biochimica et Biophysica Acta (BBA) - Lipids and Lipid Metabolism, 792*, 310–317. https://doi.org/10.1016/0005-2760(84)90198-X

Kohlmeyer, J., & Kohlmeyer, E. (1972). Permanent microscopic mounts. *Mycologia, 64*(3), 666–669.

Kolařík, M. (2018). New taxonomic combinations in endophytic representatives of the genus *Nigrograna*. *Czech Mycology, 70*, 123–126.

Kolařík, M., Spakowicz, D. J., Gazis, R., Shaw, J., Kubátová, A., Nováková, A., . . . Narváez-Trujillo, A. (2017). *Biatriospora* (Ascomycota: Pleosporales) is an ecologically diverse genus including facultative marine fungi and endophytes with biotechnological potential. *Plant Systematics and Evolution, 303,* 35–50. https://doi.org/10.1007/s00606-016-1350-2

Kolařík, M., Stępniewska, H., & Jankowiak, R. (2021). Taxonomic revision of the acidophilic genus *Acidiella* (Dothideomycetes, Capnodiales) with a description of new species from Poland. *Plant Systematics and Evolution, 307,* 38. https://doi.org/10.1007/s00606-021-01753-4

Kondo, N., Tokiwa, T., Sato, K., Ōmura, S., & Nonaka, K. (2020). *Metapochonia hahajimaensis* (Clavicipitaceae, Hypocreales), a new species from soil in Hahajima Island, Tokyo, Japan. *Mycoscience, 61,* 337–341. https://doi.org/10.1016/j.myc.2020.06.001

Kong, H. (1998). *Yunnania* gen. nov. of Hyphomycetes. *Mycotaxon, 69,* 319–325.

Kong, J. H. K. J., Zhang, T. Y. Z. T., & Zhang, W. Z. W. (2007). Notes on soil dematiaceous hyphomycetes from Hexi Corridor, Gansu province. *Mycosystema, 26,* 196–201.

Konta, S., Tibpromma, S., Karunarathna, S. C., Samarakoon, M. C., Steven, L. S., Mapook, A., . . . Hyde, K. D. (2023). Morphology and multigene phylogeny reveal ten novel taxa in Ascomycota from terrestrial palm substrates (Arecaceae) in Thailand. *Mycosphere, 14,* 107–152. https://doi.org/10.5943/mycosphere/14/1/2

Kowalski, D. T. (1965). The development and cytology of *Didymocrea sadasavanii*. *Mycologia, 57,* 404–416.

Knudsen, G. R., & Dandurand, L. M. C. (2014). Ecological complexity and the success of fungal biological control agents. *Advances in Agriculture, 2014,* Article 542703. https://doi.org/10.1155/2014/542703

Kritzman, G., & Netzer, D. (1978). A selective medium for isolation and identification of *Botrytis* spp. from soil and onion seed. *Phytoparasitica, 6,* 3–7.

Krohn, K., Sohrab, M. H., van Ree, T., Draeger, S., Schulz, B., Antus, S., & Kurtan, T. (2008). Dinemasones A, B and C – new bioactive metabolites from the endophytic fungus *Dinemasporium strigosum*. *European Journal of Organic Chemistry, 2008*(33), 5638–5646.

Kruasilp, J., Pattanakiat, S., Lawawirojwong, S., Phutthai, T., Vardhanabindu, P., Evans, W. K., . . . Jacquine, A. (2024). Unveiling long-term impacts of forest cover changes and carbon storage assessment in Nan province, Thailand. *Applied Environmental Research, 46*.

Krug, J. C., Benny, G. L., & Keller, H. W. (2004). Coprophilous fungi. In *Biodiversity of Fungi* (pp. 467–499). Elsevier.

Kruys, A., & Wedin, M. (2009). Phylogenetic relationships and an assessment of traditionally used taxonomic characters in the Sporormiaceae (Pleosporales, Dothideomycetes, Ascomycota), utilising multi-gene phylogenies. *Systematics and Biodiversity, 7*, 465–478.

Kučera, V., & Fedosova, A. G. (2017). First record of *Hemileucoglossum littorale* in Slovakia. *Catathelasma, 18*, 33–38.

Kuehn, H. H., & Orr, G. (1964). *Arachniotus ruber*. *Transactions of the British Mycological Society, 47*, 553–558.

Kuehn, H. H. (1957). Observations on Gymnoascaceae. V. Developmental morphology of two species representing a new genus of the Gymnoascaceae. *Mycologia, 49*, 694–706. https://doi.org/10.1080/00275514.1957.12024681

Kuehn, H. H., & Orr, G. F. (1959). Observations on Gymnoascaceae. VI. A new species of *Arachniotus*. *Mycologia, 51*, 864–870. https://doi.org/10.1080/00275514.1959.12024867

Kuehn, H. H., & Orr, G. F. (1962a). A new genus of Gymnoascaceae. *Mycologia, 54*, 160–167. https://doi.org/10.1080/00275514.1962.12024988

Kuehn, H. H., & Orr, G. F. (1962b). Tolerance of certain fungi to actidione and its use in isolation of Gymnoascaceae. *Sabouraudia, 1*, 220–229. https://doi.org/10.1080/00362176285190421

Kueh, T. K., & Khew, K. L. (1982). Survival of *Phytophthora palmivora* in soil and after passing through alimentary canals of snails. *Plant Disease, 66*, 897–899.

Kusai, N. A., Azmi, M. M. Z., Zulkifly, S., Yusof, M. T., & Zainudin, N. A. I. M. (2016). Morphological and molecular characterization of *Curvularia* and related species associated with leaf spot disease of rice in Peninsular Malaysia. *Rendiconti Lincei, 27*, 205–214. https://doi.org/10.1007/s12210-015-0458-6

Kuhad, R. C., Gupta, R., & Singh, A. (2011). Microbial cellulases and their industrial applications. *Enzyme Research, 2011*, Article 280696. https://doi.org/10.4061/2011/280696

Kularathnage, N. D., Senanayake, I. C., Wanasinghe, D. N., Doilom, M., Stephenson, S. L., Song, J., . . . Xu, B. (2023). Plant-associated novel Didymellaceous taxa in the South China Botanical Garden (Guangzhou, China). *Journal of Fungi, 9*, 182. https://doi.org/10.3390/jof9020182

Kumar, M., Thomas, P., Nair, S. S., Bagra, J. K., Chaturvedi, V. K., Kumar, B., . . . Rudramurthy, S. M. (2023). Molecular epidemiology of *Trichophyton* infections among canines from Northern India. *Journal of Medical Mycology, 33*, 101352. https://doi.org/10.1016/j.mycmed.2022.101352

Kumar, P. R., Hemanth, G., Niharika, P. S., & Kolli, S. K. (2015). Isolation and identification of soil mycoflora in agricultural fields at Tekkali Mandal in Srikakulam District. *International Journal of Advances in Pharmacy, Biology and Chemistry*, *4*(2), 484–490.

Kuntze, O. (1891). *Revisio generum plantarum* (Vol. 2, pp. 375–1011).

Kunze, G., & Schmidt, J. (1817). *Mykologische Hefte* (Vol. 1). Leipzig, Germany.

Kunze, T. F. L., & Schmidt, J. F. (1823). *Mykologische Hefte* (Vol. 2, p. 108). Leipzig, Germany.

Kurtzman, C. P. (1998). *Pichia* E. C. Hansen emend. Kurtzman. In *The Yeasts* (pp. 273–352). Elsevier.

Kurtzman, C. P. (2011a). *Ogataea* Y. Yamada, K. Maeda & Mikata (1994). In *The Yeasts* (pp. 645–671). Elsevier.

Kurtzman, C. P. (2011b). *Pichia* E. C. In *The Yeasts* (pp. 685–707). Elsevier.

Kuthubutheen, A. J., & Nawawi, A. (1988). Two new species of *Kionochaeta* (Hyphomycetes) and *K. ramifera* from Malaysia. *Transactions of the British Mycological Society, 90*, 437–444.

Kuvarina, A. E., Gavryushina, I. A., Sykonnikov, M. A., Efimenko, T. A., Markelova, N. N., Bilanenko, E. N., . . . Sadykova, V. S. (2022). Exploring peptaibol's profile, antifungal, and antitumor activity of Emericellipsin A of *Emericellopsis* species from soda and saline soils. *Molecules, 27*(5), 1736.

Kutateladze, L. Y., Zakariashvili, N. G., Jobava, M. D., Burduli, T. A., & Sadunishvili, T. A. (2016). Microscopic fungi spread in different types of soils in Western Georgia. *Annals of Agrarian Science, 14*, 227–232. https://doi.org/10.1016/j.aasci.2016.08.007

Kwon-Chung, K. J., & Bennett, J. W. (1992). *Medical Mycology*. University of Pennsylvania Press.

Kwon, S. L., Park, M. S., Jang, S., Lee, Y. M., Heo, Y. M., Hong, J. H., . . . Kim, J. J. (2021). The genus *Arthrinium* (Ascomycota, Sordariomycetes, Apiosporaceae) from marine habitats from Korea, with eight new species. *IMA Fungus, 12*, 13. https://doi.org/10.1186/s43008-021-00065-z

Labuda, R., Bernreiter, A., Hochenauer, D., Kubátová, A., Kandemir, H., & Schüller, C. (2021). Molecular systematics of *Keratinophyton*: The inclusion of species formerly referred to *Chrysosporium* and description of four new species. *IMA Fungus, 12*, Article 70. https://doi.org/10.1186/s43008-021-00070-2

Labuda, R., Bernreiter, A., Schüller, C., Kubátová, A., Hellinger, R., & Strauss, J. (2018). *Metapochonia lutea*, a new species isolated from the Danube River in Austria. *Nova Hedwigia, 107*, 487–500. https://doi.org/10.1127/nova_hedwigia/2018/0487

Labuda, R., Scheffenacker, V., Schüller, A., Voleková, B., Kubátová, A., Kandemir, H., . . . Strauss, J. (2024). Two novel members of Onygenales, *Keratinophyton kautmanovae* and *K. keniense* spp. nov. from soil. *Scientific Reports, 14*, 16525. https://doi.org/10.1038/s41598-024-67475-y

Lackner, M., & de Hoog, G. S. (2011). *Parascedosporium* and its relatives: Phylogeny and ecological trends. *IMA Fungus, 2*, 39–48. https://doi.org/10.5598/imafungus.2011.02.01.07

Lackner, M., de Hoog, G. S., Yang, L., Ferreira Moreno, L., Ahmed, S. A., Andreas, F., . . . Liporagi Lopes, L. C. (2014). Proposed nomenclature for *Pseudallescheria*, *Scedosporium* and related genera. *Fungal Diversity, 67*, 1–10. https://doi.org/10.1007/s13225-014-0295-4

Lagerberg, T., Lundberg, G., & Melin, E. (1927). Biological and practical researches into blueing in pine and spruce. *Svenska Skogsvårdsföreningens Tidskrift, 2*, 145–272.

Larki, R., Mehrabi-Koushki, M., & Farokhinejad, R. (2019). *Ectophoma iranica* sp. nov. and new hosts and records of *Allophoma* spp. in Iran. *Journal of Phytopathology, 167*, 538–545. https://doi.org/10.1111/jph.12840

Laundon, G. F. (1971). *Curvularia trifolii* f. sp. *gladioli* [Descriptions of Fungi and Bacteria]. *Descriptions of Fungi and Bacteria, 31*, Sheet 307. https://doi.org/10.1079/DFB/20056400307

Lawrence, D. P., Rotondo, F., & Gannibal, P. B. (2016). Biodiversity and taxonomy of the pleomorphic genus *Alternaria*. *Mycological Progress, 15*, Article 3. https://doi.org/10.1007/s11557-015-1144-x

Léveillé, J. H. (1846). Description des champignons de l'herbier du Muséum de Paris. *Annales des Sciences Naturelles Botanique*, *Série 3*, 249–305.

Leão-Ferreira, S. M., & Gusmão, L. F. P. (2010). Conidial fungi from the semi-arid Caatinga biome of Brazil. New species of *Endophragmiella* and *Spegazzinia* with new records for Brazil, South America, and Neotropica. *Mycotaxon, 111*, 1–10. https://doi.org/10.5248/111.1

Lechat, C., Hairaud, M., & Lesage-Meessen, L. (2013). *Stachybotrys oleronensis* Lechat, Hairaud & Lesage–Messen, sp. nov., Fungal Planet 208. *Persoonia, 31*, 282–283.

Lee, D. H., Cho, S. E., Oh, J. Y., Cho, E. J., & Kwon, S. (2021). A novel species of *Aureobasidium* (Dothioraceae) recovered from *Acer pseudosieboldianum* in Korea. *Journal of Asia-Pacific Biodiversity, 14*, 657–661. https://doi.org/10.1016/j.japb.2021.08.005

Lee, S. H., Park, H. S., Nguyen, T. T. T., & Lee, H. B. (2019). Characterization of three species of *Sordariomycetes* isolated from freshwater and soil samples in Korea. *Mycobiology, 47*, 20–30.

Lee, J. H., Ten, L. N., Lim, S. K., Ryu, J. J., Avalos-Ruiz, D., Lee, S. Y., . . . Jung, H. Y. (2022). Molecular and morphological characteristics of a new species collected from an insect (*Cicindela transbaicalica*) in Korea. *Mycobiology, 50*, 181–187. https://doi.org/10.1080/12298093.2022.2080333

Leewijit, T., Pongnak, W., Soytong, K., & Poeaim, S. (2016). Isolation of soil and endophytic fungi from rice (*Oryza sativa* L.). *International Journal of Agricultural Technology, 12*, 2191–2202.

Lewis, E. R. G., Bowers, J. R., & Barker, B. M. (2015). Dust devil: The life and times of the fungus that causes valley fever. *PLoS Pathogens, 11*, Article e1004762. https://doi.org/10.1371/journal.ppat.1004762

Li, J. F., Phookamsak, R., Jeewon, R., Bhat, D. J., Mapook, A., Camporesi, E., . . . Hyde, K. D. (2017). Molecular taxonomy and morphological characterization reveal new species and new host records of *Torula* species (Torulaceae, Pleosporales). *Mycological Progress, 16*(4), 447–461. https://doi.org/10.1007/s11557-017-1292-2

Li, Q. R., Habib, K., Long, S. H., Wu, Y. P., Zhang, X., Hu, H. M., . . . Kang, J. C. (2024a). Unveiling fungal diversity in China: New species and records within the Xylariaceae. *Mycosphere, 15*(1), 275–364. https://doi.org/10.5943/mycosphere/15/1/2

Li, Q. R., Habib, K., Wu, Y. P., Long, S. H., Zhang, X., Hu, H. M., . . . Kang, J. C. (2024b). Revisiting *Xylaria* diversity in Southern China: Descriptions of 40 new species. *Journal of Systematics and Evolution, 62*(6), 1255–1330. https://doi.org/10.1111/jse.13058

Li, Q. R., & Jiang, Y. L. (2011). *Stachybotrys subreniformis*, new from soil in China. *Mycotaxon, 115*, 171–173.

Li, W. J., McKenzie, E. H., Liu, J. K., Bhat, D. J., Dai, D. Q., Camporesi, E., . . . Hyde, K. D. (2020a). Taxonomy and phylogeny of hyaline-spored coelomycetes. *Fungal Diversity, 100*, 279–801. https://doi.org/10.1007/s13225-020-00440-y

Li, W., Liang, R., Dissanayake, A., & Liu, J. (2023). Mycosphere Notes 413–448: Dothideomycetes associated with woody oil plants in China. *Mycosphere, 14*(1), 1436–1529. https://doi.org/10.5943/mycosphere/14/1/16

Li, W. J., McKenzie, E. H., Liu, J. K., Bhat, D. J., Dai, D. Q., Camporesi, E., . . . Hyde, K. D. (2020b). Taxonomy and phylogeny of hyaline-spored coelomycetes. *Fungal Diversity, 100*, 279–801. https://doi.org/10.1007/s13225-020-00440-y

Li, W. L., Dissanayake, A. J., Zhang, T., Maharachchikumbura, S. S. N., & Liu, J. K. (2022a). Identification and pathogenicity of pestalotiod fungi associated with woody oil plants in Sichuan province, China. *Journal of Fungi, 8*(11), 1175. https://doi.org/10.3390/jof8111175

Li, X. Q., Xu, K., Liu, X. M., & Zhang, P. (2020c). A systematic review on secondary metabolites of *Paecilomyces* species: Chemical diversity and biological activity. *Planta Medica, 86*(11), 805–821. https://doi.org/10.1055/a-1196-1906

Li, X., Zhang, Z. Y., Ren, Y. L., Chen, W. H., Liang, J. D., Pan, J. M., . . . Han, Y. F. (2022b). Morphological characteristics and phylogenetic evidence reveal two new species of *Acremonium* (Hypocreales, Sordariomycetes). *MycoKeys, 91*, 85–96. https://doi.org/10.3897/mycokeys.91.86257

Li, X., Zhang, Z. Y., Chen, W. H., Liang, J. D., Huang, J. Z., Han, Y. F., . . . Liang, Z. Q. (2022c). A new species of *Arthrographis* (Eremomycetaceae, Dothideomycetes), from the soil in Guizhou, China. *Phytotaxa, 538*(3), 175–181. https://doi.org/10.11646/phytotaxa.538.3.1

Liamthong, S., Wongthong, S., Arlee, A., Sittiphajirasakool, P., Aumoodee, S., & Yago, M. (2017). Isolation and identification of soil fungi from mangrove in Nakhon Si Thammarat province. *Wichcha Journal Nakhon Si Thammarat Rajabhat University, 36*(2), 80-91.

Liang, J., Liu, B., Li, Z., Meng, W., Wang, Q., & Xu, L. (2019). *Myxotrichum albicans*, a new slowly-growing species isolated from forest litters in China. *Mycoscience, 60*(4), 232–236. https://doi.org/10.1016/j.myc.2019.03.002

Liang, Z. Q. (1990). Studies on classification of the genus *Hirsutella* Pat. I. Advances and the characteristics of taxonomy. *Journal of Guizhou Agricultural College, 9*, 58–68.

Libor, B., Harms, H., Kehraus, S., Egereva, E., Crüsemann, M., & König, G. M. (2019). Isolation of fungi using the diffusion chamber device FIND technology. *Beilstein Journal of Organic Chemistry*, *15*, 2191–2203. https://doi.org/10.3762/bjoc.15.216

Liimatainen, K., Niskanen, T., Dima, B., Ammirati, J. F., Kirk, P. M., & Kytövuori, I. (2020). Mission impossible completed: Unlocking the nomenclature of the largest and most complicated subgenus of *Cortinarius*, *Telamonia*. *Fungal Diversity*, *104*(1), 291–331. https://doi.org/10.1007/s13225-020-00459-1

Lima, T. E. F. de, Bezerra, J. L., & Cavalcanti, M. A. de Q. (2012). *Phaeotrichoconis crotalariae*, endophytic on *Vitis labrusca* in Brazil. *Mycotaxon*, *120*(1), 291–294. https://doi.org/10.5248/120.291

Limongelli, R., Minervini, F., & Calasso, M. (2023). Fermentation of pomegranate matrices with *Hanseniaspora valbyensis* to produce a novel food ingredient. *LWT*, *180*, 114687. https://doi.org/10.1016/j.lwt.2023.114687

Limsakul, A., Kammuang, A., Paengkaew, W., Sooktawee, S., & Aroonchan, N. (2023). Changes in slow-onset climate events in Thailand. *Environmental Engineering Research*, *29*, 220784. https://doi.org/10.4491/eer.2022.784

Limtong, S., Srisuk, N., Yongmanitchai, W., Yurimoto, H., & Nakase, T. (2008). *Ogataea chonburiensis* sp. nov. and *Ogataea nakhonphanomensis* sp. nov., thermotolerant, methylotrophic yeast species isolated in Thailand, and transfer of *Pichia siamensis* and *Pichia thermomethanolica* to the genus *Ogataea*. *International Journal of Systematic and Evolutionary Microbiology*, *58*(2), 302–307. https://doi.org/10.1099/ijs.0.65380-0

Lin, C. G., McKenzie, E. H. C., Liu, J. K., Jones, E. B. G., & Hyde, K. D. (2019). Hyaline-spored chaetosphaeriaceous hyphomycetes from Thailand and China, with a review of the family Chaetosphaeriaceae. *Mycosphere*, *10*(1), 655–700. https://doi.org/10.5943/mycosphere/10/1/14

Lin, C. G., Hyde, K. D., Lumyong, S., & McKenzie, E. H. C. (2017). Beltrania-like taxa from Thailand. *Cryptogamie, Mycologie*, *38*(3), 301–319. https://doi.org/10.7872/crym/v38.iss3.2017.301

Lin, C. G., Dai, D. Q., Bhat, D. J., Hyde, K. D., Tang, L. Z., & To-Anun, C. (2017a). *Subsessila turbinata* gen. et sp. nov. (Beltraniaceae), a *Beltrania*-like fungus from Thailand. *Mycological Progress, 16*, 393–401.

Lin, C. G., Hyde, K. D., Lumyong, S., & McKenzie, E. H. C. (2017b). Beltrania-like taxa from Thailand. *Cryptogamie, Mycologie, 38*, 301–319.

Lin, C. G., McKenzie, E., Bhat, D. J., Ran, S. F., Chen, N. Y., Hyde, K. D., . . . Wang, Y. (2016). *Stachybotrys*-like taxa from karst areas and a checklist of *Stachybotrys*-like species from Thailand. *Mycosphere, 7*, 1273–1291.

Lindahl, B. D., Nilsson, R. H., Tedersoo, L., Abarenkov, K., Carlsen, T., Kjøller, R., . . . Kauserud, H. (2013). Fungal community analysis by high-throughput sequencing of amplified markers: A user's guide. *New Phytologist, 199*(1), 288–299. https://doi.org/10.1111/nph.12243

Link, H. (1815). *Magazin der neuesten Entdeckungen in der gesammten Naturkunde der Gesellschaft Naturforschender Freunde zu Berlin, 7*, 32.

Link, H. F. (1809). Observationes in ordines plantarum naturales. Dissertatio I. *Magazin der Gesellschaft Naturforschenden Freunde zu Berlin, 3*, 3–42.

Link, J. H. F. (1816). Enumeratio fungorum in Germaniae superiore crescentium. *Magazin der Gesellschaft Naturforschender Freunde zu Berlin, 7*, 37.

Liu, J. K., Hyde, K. D., Jeewon, R., Phillips, A. J. L., Maharachchikumbura, S. S. N., Ryberg, M., . . . Zhao, Q. (2017). Ranking higher taxa using divergence times: A case study in Dothideomycetes. *Fungal Diversity, 84*, 75–99. https://doi.org/10.1007/s13225-017-0385-1

Liu, J. K., Yang, J., Maharachchikumbura, S. S. N., McKenzie, E. H. C., Jones, E. B. G., Hyde, K. D., . . . Liu, Z. Y. (2016). Novel chaetosphaeriaceous hyphomycetes from aquatic habitats. *Mycological Progress, 15*, 1157–1167.

Liu, F., Bonthond, G., Groenewald, J. Z., Cai, L., & Crous, P. W. (2019a). Sporocadaceae, a family of coelomycetous fungi with appendage-bearing conidia. *Studies in Mycology, 92*, 287–415.

Liu, F., Ma, Z. Y., Hou, L. W., Diao, Y. Z., Wu, W. P., Damm, U., . . . Cai, L. (2022). Updating species diversity of *Colletotrichum*, with a phylogenomic overview. *Studies in Mycology, 101*, 1–56. https://doi.org/10.3114/sim.2022.101.01

Liu, F., Wang, J., Li, H., Wang, W., & Cai, L. (2019b). *Setophoma* spp. on *Camellia sinensis*. *Fungal Systematics and Evolution, 4*, 43–57. https://doi.org/10.3114/fuse.2019.04.05

Liu, H. L. H., & Zhang, T. Z. T. (2007). Species of *Pithomyces* (Hyphomycetes) from soil in the warm temperate zone of eastern China. *Mycosystema, 26*, 484–489.

Liu, J. K., Phookamsak, R., Dai, D. Q., Tanaka, K., Jones, E. B. G., Xu, J. C., . . . Hyde, K. D. (2014). Roussoellaceae, a new pleosporalean family to accommodate the genera *Neoroussoella* gen. nov., *Roussoella* and *Roussoellopsis*. *Phytotaxa, 181*(1), 1–45. https://doi.org/10.11646/phytotaxa.181.1.1

Liu, J., Hu, Y., Luo, X., Castañeda-Ruíz, R. F., Xia, J., Xu, Z., . . . Ma, J. (2023a). Molecular phylogeny and morphology reveal four novel species of *Corynespora* and *Kirschsteiniothelia* (Dothideomycetes, Ascomycota) from China: A checklist for *Corynespora* reported worldwide. *Journal of Fungi, 9*(1), 107. https://doi.org/10.3390/jof9010107

Liu, M., Mommer, L., van Ruijven, J., van der Werf, W., Xu, Z., Zhang, F., . . . Maciá-Vicente, J. G. (2024). Unraveling the prevalence of soil-borne fungal pathogens in the North China Plain: A global analysis approach. *European Journal of Plant Pathology, 168*, 649–664. https://doi.org/10.1007/s10658-023-02790-0

Liu, N. G., Lin, C. G., Liu, J. K., Samarakoon, M. C., Hongsanan, S., Bhat, D. J., . . . Jumpathong, J. (2018). Lentimurisporaceae, a new pleosporalean family with divergence time estimates. *Cryptogamie, Mycologie, 39*(2), 259–282. https://doi.org/10.7872/crym/v39.iss2.2018.259

Liu, X., Tibpromma, S., Hughes, A., Chethana, K., Wijayawardene, N., Dai, D., . . . Mortimer, P. (2023b). Culturable mycota on bats in central and southern Yunnan Province, China. *Mycosphere, 14*(1), 497–662. https://doi.org/10.5943/mycosphere/14/1/7

Liu, Y., & Chen, S. (2023). Diversity and distribution of *Calonectria* species in soils from *Eucalyptus urophylla* × *E. grandis*, *Pinus massoniana*, and *Cunninghamia lanceolata* plantations in four provinces in Southern China. *Journal of Fungi, 9*(2), 198. https://doi.org/10.3390/jof9020198

Liu, Y., & Chen, S. F. (2024). *Cylindrocladiella* species from *Cunninghamia lanceolata* plantation soils in southwestern China. *Fungal Systematics and Evolution, 13*, 143–152. https://doi.org/10.3114/fuse.2024.13.08

Liu, Y. W., & Zeng, X. Y. (2022). *Acrocalymma chuxiongense* sp. nov., a new species of Acrocalymmaceae (Pleosporales) on leaves of *Quercus*. *Biodiversity Data Journal, 10*, e89635. https://doi.org/10.3897/BDJ.10.e89635

Liu, Z., Wang, M. M., Wang, G. S., Li, A. H., Wangmu, & Wang, Q. M. (2019c). *Hanseniaspora terricola* sp. nov., an ascomycetous yeast isolated from Tibet. *International Journal of Systematic and Evolutionary Microbiology, 71*, 004741. https://doi.org/10.1099/ijsem.0.004741

Locquin, M. (1984). *Mycologie générale et structurale* (p. 551). Masson.

Lodhi, S. A., & Mirza, F. (1962). A new genus of the Eurotiales. *Mycologia, 54*(2), 217–219.

Lombard, L., Crous, P. W., Wingfield, B. D., & Wingfield, M. J. (2010). Phylogeny and systematics of the genus *Calonectria*. *Studies in Mycology*, *66*, 31–69. https://doi.org/10.3114/sim.2010.66.03

Lombard, N., Prestat, E., van Elsas, J. D., & Simonet, P. (2011). Soil-specific limitations for access and analysis of soil microbial communities by metagenomics. *FEMS Microbiology Ecology*, *78*(1), 31–49. https://doi.org/10.1111/j.1574-6941.2011.01140.x

Lombard, L., Houbraken, J., Decock, C., Samson, R. A., Meijer, M., Réblová, M., . . . Crous, P. W. (2016). Generic hyper-diversity in *Stachybotriaceae*. *Persoonia, 36*, 156–246. https://doi.org/10.3767/003158516X691582

Lombard, L., van der Merwe, N. A., Groenewald, J. Z., & Crous, P. W. (2015). Generic concepts in *Nectriaceae*. *Studies in Mycology*, *80*, 189–245. https://doi.org/10.1016/j.simyco.2014.12.002

Lombard, L., Shivas, R. G., To-Anun, C., & Crous, P. W. (2012). Phylogeny and taxonomy of the genus *Cylindrocladiella*. *Mycological Progress, 11*, 835–868. https://doi.org/10.1007/s11557-011-0799-1

López-López, M., Léon-Félix, J., Allende-Molar, R., Lima, N. B., Tovar-Pedraza, J. M., & García-Estrada, R. S. (2020). First report of *Setophoma terrestris* causing corky and pink root of tomato in Sinaloa, Mexico. *Plant Disease, 104*(6), 1553. https://doi.org/10.1094/pdis-10-19-2226-pdn

Luo, Z. L., Hyde, K. D., Liu, J. K., Maharachchikumbura, S. S. N., Jeewon, R., Bao, D. F., . . . Su, H. Y. (2019). Freshwater *Sordariomycetes*. *Fungal Diversity, 99*, 451–660.

Lu, L., Karunarathna, S. C., Dai, D. Q., Jayawardena, R. S., Suwannarach, N., & Tibpromma, S. (2022). Three new species of *Nigrograna* (Dothideomycetes, Pleosporales) associated with Arabica coffee from Yunnan province, China. *MycoKeys, 94*, 51–71. https://doi.org/10.3897/mycokeys.94.95751

Luangsa-Ard, J., Houbraken, J., van Doorn, T., Hong, S. B., Borman, A. M., Hywel-Jones, N. L., . . . Samson, R. A. (2011). *Purpureocillium*, a new genus for the medically important *Paecilomyces lilacinus*. *FEMS Microbiology Letters, 321*, 141–149. https://doi.org/10.1111/j.1574-6968.2011.02322.x

Luangsa-Ard, J., Tasanathai, K., Thanakitpipattana, D., Khonsanit, A., & Stadler, M. (2018). Novel and interesting *Ophiocordyceps* spp. (Ophiocordycipitaceae, Hypocreales) with superficial perithecia from Thailand. *Studies in Mycology, 89*, 125–142. https://doi.org/10.1016/j.simyco.2018.02.001

Luangsa-Ard, J. J., Manoch, L., Hywel-Jones, N., Artjariyasripong, S., & Samson, R. A. (2004). Thermotolerant and thermoresistant *Paecilomyces* and its teleomorphic states isolated from Thai forest and mountain soils. *Agriculture and Natural Resources, 38*, 94–101.

Lücking, R., Sipman, H. J. M., Umaña, L., Chaves, J. L., & Lumbsch, H. T. (2007). *Aptrootia* (Dothideomycetes: Trypetheliaceae), a new genus of pyrenocarpous lichens for *Thelenella terricola*. *Lichenologist, 39*(3), 187–193. https://doi.org/10.1017/S0024282907006445

Lumbsch, H. T., & Mangold, A. (2007). *Diploschistes elixii* (Ostropales: Thelotremataceae), an overlooked terricolous species from Western Australia. *The Lichenologist, 39*(5), 459–462. https://doi.org/10.1017/S0024282907007049

Lumbsch, H. T., & Huhndorf, S. M. (2007). Outline of Ascomycota – 2007. *Myconet, 13*, 1–58.

Lumbsch, H. T., & Huhndorf, S. M. (2010). *Myconet Volume 14*. Part one: Outline of Ascomycota 2009. Part two: Notes on ascomycete systematics (Nos. 4751–5113). *Fieldiana Life and Earth Sciences, 1*, 1–64. https://doi.org/10.3158/1557.1

Lumini, E., Orgiazzi, A., Borriello, R., Bonfante, P., & Bianciotto, V. (2010). Disclosing arbuscular mycorrhizal fungal biodiversity in soil through a land-use gradient using a pyrosequencing approach. *Environmental Microbiology, 12*(8), 2165–2179. https://doi.org/10.1111/j.1462-2920.2009.02099.x

Lundqvist, N. (1972). *Nordic Sordariaceae s. lat. Symbolae Botanicae Upsalienses, 20*, 1–374.

Luplertlop, N., Muangkaew, W., Pumeesat, P., Suwanmanee, S., & Singkum, P. (2019). Distribution of *Scedosporium* species in soil from areas with high human population density and tourist popularity in six geographic regions in Thailand. *PLOS One, 14*, e0210942. https://doi.org/10.1371/journal.pone.0210942

Luplertlop, N., Pumeesat, P., Muangkaew, W., Wongsuk, T., & Alastruey-Izquierdo, A. (2016). Environmental screening for the *Scedosporium apiospermum* species complex in public parks in Bangkok, Thailand. *PLOS One, 11*, e0159869. https://doi.org/10.1371/journal.pone.0159869

Luttrell, E. S. (1955). The ascostromatic Ascomycetes. *Mycologia, 47*(4), 511–532. https://doi.org/10.1080/00275514.1955.12024473

Luttrell, E. S., & Rogerson, C. T. (1959). Homothallism in an undescribed species of *Cochliobolus* and in *Cochliobolus kusanoi*. *Mycologia, 51*(2), 195–202. https://doi.org/10.2307/3756212

Ma, H., Song, Z., Pan, X., Qu, Z., Yang, Z., Li, Y., . . . Zhu, A. (2022). Four new pale-spored species of *Xylaria* (Xylariaceae, Xylariales) with a key to worldwide species on fallen fruits and seeds. *Biology, 11*(6), 885. https://doi.org/10.3390/biology11060885

Ma, R., Chen, Q., Fan, Y., Wang, Q., Chen, S., Liu, X., . . . Yao, B. (2017). Six new soil-inhabiting *Cladosporium* species from plateaus in China. *Mycologia, 109*(2), 244–260. https://doi.org/10.1080/00275514.2017.1302254

McGuire, K. L., D'Angelo, H., Brearley, F. Q., Gedallovich, S. M., Babar, N., Yang, N., . . . Fierer, N. (2015). Responses of soil fungi to logging and oil palm agriculture in Southeast Asian tropical forests. *Microbial Ecology, 69*(4), 733–747.

Machouart, M., Menir, P., Helenon, R., Quist, D., & Desbois, N. (2013). *Scytalidium* and scytalidiosis: What's new in 2012? *Journal de Mycologie Médicale, 23*(1), 40–46. https://doi.org/10.1016/j.mycmed.2013.01.002

Madrid, H., Gené, J., Quijada, L., Cantillo, T., Gacitúa, R., Valdés, J., . . . Godoy, P. (2023). *Exophiala atacamensis* sp. nov. and *E. crusticola* from the Atacama Desert, Northern Chile. *Sydowia, 75*, 181–192.

Madrid, H., Gené, J., Cano, J., & Guarro, J. (2012). A new species of *Leptodiscella* from Spanish soil. *Mycological Progress, 11*(2), 535–541. https://doi.org/10.1007/s11557-011-0768-8

Madrid, H., da Cunha, K. C., Gené, J., Dijksterhuis, J., Cano, J., Sutton, D. A., . . . Crous, P. W. (2014). Novel *Curvularia* species from clinical specimens. *Persoonia, 33*, 48–60. https://doi.org/10.3767/003158514X683538

Mafune, K. K., Godfrey, B. J., Vogt, D. J., & Vogt, K. A. (2019). A rapid approach to profiling diverse fungal communities using the MinION nanopore sequencer. *BioTechniques, 68*(2), 72–78. https://doi.org/10.2144/btn-2019-0072

Magaña-Dueñas, V., Stchigel, A. M., & Cano-Lira, J. F. (2021). New coelomycetous fungi from freshwater in Spain. *Journal of Fungi, 7*(5), 368. https://doi.org/10.3390/jof7050368

Magalhães, D. M. A., Luz, E. D. M. N., Magalhães, A. F., dos Santos Filho, L. P., Loguercio, L. L., & Bezerra, J. L. (2011). Riqueza de fungos anamorfos na serapilheira de *Manilkara maxima*, *Parinari alvimii* e *Harleyodendron unifoliolatum* na Mata Atlântica do Sul da Bahia. *Acta Botânica Brasílica, 25*(4), 899–907.

Maharachchikumbura, S. S. N., Hyde, K. D., Groenewald, J. Z., Xu, J., & Crous, P. W. (2014). *Pestalotiopsis* revisited. *Studies in Mycology, 79*, 121–186. https://doi.org/10.1016/j.simyco.2014.09.005

Maharachchikumbura, S. S. N., Hyde, K. D., Jones, E. G., McKenzie, E. H. C., Bhat, J. D., Dayarathne, M. C., . . . Wijayawardene, N. N. (2016). Families of *Sordariomycetes*. *Fungal Diversity, 79*, 1–317. https://doi.org/10.1007/s13225-016-0369-6

Maharachchikumbura, S. S. N., Hyde, K. D., Jones, E. G., McKenzie, E. H. C., Huang, S. K., Abdel-Wahab, M. A., . . . Xu, J. (2015). Towards a natural classification and backbone tree for *Sordariomycetes*. *Fungal Diversity, 72*, 199–301. https://doi.org/10.1007/s13225-015-0331-z

Maharachchikumbura, S. S. N., Chen, Y., Ariyawansa, H. A., Hyde, K. D., Haelewaters, D., Perera, R. H., . . . Stadler, M. (2021). Integrative approaches for species delimitation in *Ascomycota*. *Fungal Diversity, 109*, 155–179. https://doi.org/10.1007/s13225-021-00486-6

Maharachchikumbura, S. S. N., Wanasinghe, D. N., Cheewangkoon, R., & Al-Sadi, A. M. (2021). Uncovering the hidden taxonomic diversity of fungi in Oman. *Fungal Diversity, 106*, 229–268.

Malewski, T., Borowik, P., Olejarski, I., Rutkiewicz, A., Okorski, A., & Oszako, T. (2023). Addition of organic matter to pine plantations on agricultural land positively alters the mycobiome of agricultural soils. *Applied Sciences, 13*, 5800. https://doi.org/10.3390/app13095800

Malloch, D., & Salkin, I. F. (1984). A new species of *Scedosporium* associated with osteomyelitis in humans. *Mycotaxon, 21*, 247–255.

Malmsten, E. (1848). *Trichophyton. Archives d'anatomie, de physiologie et de médecine (Arch. Anat. Physiol. Wiss. Med.), 14*, 1–14.

Mamut, R., Fang, J., & Payzulla, T. (2022). A new species of the lichen genus *Diploschistes* from China. *Mycosystema, 41*(11), 1932–1940.

Man, B., Wang, H., Xiang, X., Wang, R., Yun, Y., & Gong, L. (2015). Phylogenetic diversity of culturable fungi in the Heshang Cave, Central China. *Frontiers in Microbiology, 6*, 1138. https://doi.org/10.3389/fmicb.2015.01158

Man, B., Wang, H., Yun, Y., Xiang, X., Wang, R., Duan, Y., . . . Cheng, X. (2018). Diversity of fungal communities in Heshang cave of Central China revealed by mycobiome-sequencing. *Frontiers in Microbiology, 9,* Article 1400. https://doi.org/10.3389/fmicb.2018.01400

Manamgoda, D. S., Rossman, A. Y., Castlebury, L. A., Chukeatirote, E., & Hyde, K. D. (2015). A taxonomic and phylogenetic re-appraisal of the genus *Curvularia* (Pleosporaceae): Human and plant pathogens. *Phytotaxa, 212*(3), 175. https://doi.org/10.11646/phytotaxa.212.3.1

Manamgoda, D. S., Cai, L., Bahkali, A. H., Chukeatirote, E., & Hyde, K. D. (2011). *Cochliobolus*: An overview and current status of species. *Fungal Diversity, 51*, 3–42. https://doi.org/10.1007/s13225-011-0139-4

Manamgoda, D. S., Rossman, A. Y., Castlebury, L. A., Crous, P. W., Madrid, H., Chukeatirote, E., . . . Hyde, K. D. (2014). The genus *Bipolaris*. *Studies in Mycology, 79*, 221–288. https://doi.org/10.1016/j.simyco.2014.10.002

Mandeel, Q. A. (2006). Biodiversity of the genus *Fusarium* in saline soil habitats. *Journal of Basic Microbiology, 46*(6), 480–494. https://doi.org/10.1002/jobm.200510128

Maneeboon, T., Sangchote, S., Hongprayoon, R., Chuaysrinule, C., & Mahakarnchanakul, W. (2023). Occurrence of heat-resistant mold ascospores in pineapple and sugarcane field soils in Thailand. In D. Muleta (Ed.), *International Journal of Microbiology, 2023*, 1–13. https://doi.org/10.1155/2023/8347560

Mankau, R. (1975). A semi-quantitative method for enumerating and observing parasites and predators of soil nematodes. *Journal of Nematology, 7*(2), 119–122.

Manoch, L. (1987). *Comparative studies on fungi isolated from agricultural and non-agricultural soils in Thailand* [Unpublished doctoral dissertation]. University of Tsukuba.

Manoch, L. (1998). Biodiversity of soil fungi in Thailand. In *Proceedings of the Asia-Pacific Mycological Conference on Biodiversity and Biotechnology* (pp. 126–140). Hua Hin, Thailand.

Manoch, L. (2004). Soil fungi. In E. B. G. Jones, M. Tantichareon, & K. D. Hyde (Eds.), *Thai fungal diversity* (pp. 141–154). BIOTECH, Thailand.

Manoch, L., Dethoup, T., Yilmaz, N., Houbraken, J., & Samson, R. A. (2013). Two new *Talaromyces* species from soil in Thailand. *Mycoscience, 54*(5), 335–342. https://doi.org/10.1016/j.myc.2012.12.002

Mapook, A., Hyde, K. D., McKenzie, E. H. C., Jones, E. B. G., Bhat, D. J., Jeewon, R., . . . Purahong, W. (2020). Taxonomic and phylogenetic contributions to fungi associated with the invasive weed *Chromolaena odorata* (Siam weed). *Fungal Diversity, 101*, 1–175. https://doi.org/10.1007/s13225-020-00444-8

Mar Htun, Z., Laikul, A., Pathomsakulwong, W., Yurayart, C., Lohnoo, T., Yingyong, W., . . . Krajaejun, T. (2021). Identification and biotyping of *Pythium insidiosum* isolated from urban and rural areas of Thailand by multiplex PCR, DNA barcode, and proteomic analyses. *Journal of Fungi, 7*(4), Article 242. https://doi.org/10.3390/jof7040242

Marano, A. V., Gleason, F. H., Bärlocher, F., Pires-Zottarelli, C. L. A., Lilje, O., Schmidt, S. K., . . . Edwards, J. E. (2012). Quantitative methods for the analysis of zoosporic fungi. *Journal of Microbiological Methods, 89*(1), 22–32. https://doi.org/10.1016/j.mimet.2012.02.003

Marasas, W. F. O., Burgess, L. W., Anelich, R. Y., Lamprecht, S. C., & van Schalkwyk, D. J. (1988). Survey of *Fusarium* species associated with plant debris in South African soils. *South African Journal of Botany, 5*(2), 63–71. https://doi.org/10.1016/S0254-6299(16)31363-1

Marchal, E. (1885). Champignons coprophiles de la Belgique. *Bulletin de la Société Royale de Botanique de Belgique, 24*, 57–77.

Marchisio, V. F. (2000). Keratinophilic fungi: Their role in nature and degradation of keratinic substrates. *Revista Iberoamericana de Micología, 17*(2), 86–92.

Marcus, L., Vismer, H. F., Van der Hoven, H. J., Gove, E., & Meewes, P. (1992). Mycotic keratitis caused by *Curvularia brachyspora* (Boedijn). *Mycopathologia, 119*(1), 29–33. https://doi.org/10.1007/BF00492227

Marin-Felix, Y., Groenewald, J. Z., Cai, L., Chen, Q., Marincowitz, S., Barnes, I., . . . Crous, P. W. (2017a). Genera of phytopathogenic fungi: GOPHY 1. *Studies in Mycology, 86*, 99–216. https://doi.org/10.1016/j.simyco.2017.04.002

Marin-Felix, Y., Hernández-Restrepo, M., Iturrieta-González, I., & García, D. (2019). Genera of phytopathogenic fungi: GOPHY 3. *Studies in Mycology, 94*, 1–124. https://doi.org/10.1016/j.simyco.2019.05.001

Marin-Felix, Y., Guarro, J., García, D., & Stchigel, A. M. (2018). *Melanospora* (Sordariomycetes, Ascomycota) and its relatives. *MycoKeys, 44*, 81–122. https://doi.org/10.3897/mycokeys.44.29742

Marin-Felix, Y., Hernández-Restrepo, M., & Crous, P. W. (2020a). Multi-locus phylogeny of the genus *Curvularia* and description of ten new species. *Mycological Progress, 19*, 559–588. https://doi.org/10.1007/s11557-020-01576-6

Marin-Felix, Y., Miller, A. N., Cano-Lira, J. F., Guarro, J., García, D., Stadler, M., . . . Stchigel, A. M. (2020b). Re-evaluation of the order Sordariales: Delimitation of *Lasiosphaeriaceae* s. str., and introduction of the new families *Diplogelasinosporaceae*, *Naviculisporaceae*, and *Schizotheciaceae*. *Microorganisms, 8*(9), Article 1430. https://doi.org/10.3390/microorganisms8091430

Marin-Felix, Y., Senwanna, C., Cheewangkoon, R., & Crous, P. W. (2017b). New species and records of *Bipolaris* and *Curvularia* from Thailand. *Mycosphere, 8*(9). https://doi.org/10.5943/mycosphere/8/9/11

Marin-Felix, Y., Miller, A. N., Cano-Lira, J. F., Guarro, J., García, D., Stadler, M., . . . Stchigel, A. M. (2015). *Emmonsiellopsis*, a new genus related to the thermally dimorphic fungi of the family *Ajellomycetaceae*. *Mycoses, 58*(8), 451–460. https://doi.org/10.1111/myc.12336

Marin-Felix, Y., Groenewald, J. Z., Cai, L., Chen, Q., Marincowitz, S., Barnes, I., Bensch, K., . . . Crous, P. W. (2017a). Genera of phytopathogenic fungi: GOPHY 1. *Studies in Mycology, 86*, 99–216. https://doi.org/10.1016/j.simyco.2017.04.002

Marin-Felix, Y., Hernández-Restrepo, M., & Crous, P. W. (2020a). Multi-locus phylogeny of the genus *Curvularia* and description of ten new species. *Mycological Progress, 19*, 559–588. https://doi.org/10.1007/s11557-020-01576-6

Markovskaja, S. (2007). New data on some rare species of hyphomycetes from Lithuania. *Acta Mycologica, 42*. https://doi.org/10.5586/am.2007.022 *(If DOI not available, omit the link)*

Marques, M. F. O., Barbosa, F. R., Gusmão, L. F. P., Castañeda-Ruiz, R. F., & Maia, L. C. (2007). Conidial fungi from the semi-arid Caatinga biome of Brazil: *Cubasina microspora* sp. nov., a note on *C. albofusca*, and some new records for South America. *Mycotaxon, 102*, 17–23.

Martin, S. A., & Ritchie, R. J. (2020). Sourcing Thai geography literature for ASEAN and international education. *Singapore Journal of Tropical Geography, 41*, 61–85. https://doi.org/10.1111/sjtg.12296

Masoudi, A., Wang, M., Zhang, X., Wang, C., Qiu, Z., Wang, W., . . . Liu, J. (2020). Meta-analysis and evaluation by insect-mediated baiting reveal different patterns of Hypocrealean entomopathogenic fungi in the soils from two regions of China. *Frontiers in Microbiology, 11*, Article 1133. https://doi.org/10.3389/fmicb.2020.01133

Matar, N., Macadre, C., Ammar, G. A., Peres, A., Collet, B., Boustany, N. E., . . . Ratet, P. (2022). Identification of beneficial Lebanese *Trichoderma* spp. wheat endophytes. *Frontiers in Plant Science, 13*, Article 1017890. https://doi.org/10.3389/fpls.2022.1017890

Matos, T., De Hoog, G. S., De Boer, A. G., De Crom, I., & Haase, G. (2002). High prevalence of the neurotrope *Exophiala dermatitidis* and related oligotrophic black yeasts in sauna facilities. *Mycoses, 45*, 373–377.

Matsushima, T. (1971). *Microfungi of the Solomon Islands and Papua New Guinea*. Kobe, Japan.

Matsushima, T. (1975). *Icones microfungorum a Matsushima lectorum*. Japan.

Matsushima, T. (1989). *Matsush. Mycol. Mem., 6*, 39.

Mayr, F. (1982). *Sordaria macrospora* in soil habitats. *Transactions of the Mycological Society of Japan, 23*, 237–245.

McPartland, J. M. (1994). Cannabis pathogens X: *Phoma*, *Ascochyta* and *Didymella* species. *Mycologia, 86*, 870–887. https://doi.org/10.2307/3760723 *(If DOI is not correct, remove it)*

McCarthy, P. M., & Kantvilas, G. (1993). *Laurera robusta* (Trypetheliaceae), a new alpine lichen from Tasmania. *Lichenologist, 25*, 51–55.

McKemy, J. M. (1997). *Phialophora and related dematiaceous genera: A molecular phylogenetic and taxonomic study* (Master's thesis). State University of New York College of Environmental Science and Forestry.

Medlar, E. M. (1915). A new fungus, *Phialophora verrucosa*, pathogenic for man. *Mycologia, 7*, 200–203.

Meenakshi, Kumar, J., & Yadav, R. (2022). Optimization of cultural conditions for keratinase production by *Curvularia lunata* (JK17) using response surface methodology. *Journal of Scientific Research, 14*(1), 363–374. https://doi.org/10.3329/jsr.v14i1.53950

Mehrabi, M., Asgari, B., & Zare, R. (2020). Description of *Allocanariomyces* and *Parachaetomium*, two new genera, and *Achaetomium aegilopis* sp. nov. in the Chaetomiaceae. *Mycological Progress, 19*, 1415–1427. https://doi.org/10.1007/s11557-020-01636-x

Mel'nik, V. A. (2000). *Key to the fungi of the genus Ascochyta Lib. (Coelomycetes).* Biologischen Bundesanstalt für Land- und Forstwirtschaft, Berlin und Braunschweig. Berlin: Parey.

Melin, E., & Nannfeldt, J. A. (1934). Researches into the blueing of ground wood-pulp. *Svenska Skogsvårdsföreningens Tidskrift, 32*, 397–616.

Mena-Portales, J., Cantillo-Pérez, T., & Minter, D. W. (2017). A new species of the conidial fungal genus *Spegazzinia* (Pleosporales, Didymosphaeriaceae) collected on sugarcane in Cuba. *Phytotaxa, 331*(2), 295. https://doi.org/10.11646/phytotaxa.331.2.14

de Meyer, E. M., de Beer, Z. W., Summerbell, R. C., Moharram, A. M., de Hoog, G. S., Vismer, H. F., . . . Wingfield, M. J. (2008). Taxonomy and phylogeny of new wood- and soil-inhabiting *Sporothrix* species in the *Ophiostoma stenoceras–Sporothrix schenckii* complex. *Mycologia, 100*, 647–661. https://doi.org/10.3852/07-157R

Meyling, N. V. (2007). *Methods for isolation of entomopathogenic fungi from the soil environment*. Laboratory manual, Department of Ecology, Faculty of Life Sciences, University of Copenhagen.

Micheli, P. (1794). *A. Nova Plantarum Genera*. *Neues Magazin für die Botanik, 1,* 120.

Miehe, H. (1907). *Die Selbsterhitzung des Heues*. Jena: G. Fischer.

Miller, M. A., Pfeiffer, W., & Schwartz, T. (2010). Creating the CIPRES science gateway for inference of large phylogenetic trees. In *Proceedings of the Gateway Computing Environments Workshop 2010 (GCE)* (pp. 1–8). New Orleans, LA.

Ming, D. Q., Luo, L. Y., He, X. X., Wang, M. S., Fang, W. X., Chen, S. F., . . . Liang, Z. Q. (2021). *Paracremonium lepidopterorum*, a new insect-associated fungus. *Fungal Biology, 524,* 85–91. *(Add journal name if not Fungal Biology – the volume number suggests an issue)*

Mitra, S., Kambar, S., & Shanbhag, S. S. (2024). *Pseudopithomyces maydicus* and *Phialophora chinensis* rare fungal keratitis: Case series, DNA sequencing, antifungal susceptibility patterns. *Ocular Immunology and Inflammation, 32,* 2238–2242. https://doi.org/10.1080/09273948.2024.2303352

Mohamed Zubi, W. S., Mohd, M. H., Mohamed Nor, N. M. I., & Zakaria, L. (2021). *Fusarium* species in mangrove soil in Northern Peninsular Malaysia and the soil physico-chemical properties. *Microorganisms, 9,* 497. https://doi.org/10.3390/microorganisms9030497

Mohammadi, A. (2015). Molecular characterization and identification of *Acrostalagmus luteoalbus* from saffron in Iran. *Agriculture Science Developments*, 16–18.

Mongkolsamrit, S., Khonsanit, A., Thanakitpipattana, D., Tasanathai, K., Noisripoom, W., Lamlertthon, S., . . . Luangsa-Ard, J. (2020). Revisiting *Metarhizium* and the description of new species from Thailand. *Studies in Mycology, 95,* 171–251. https://doi.org/10.1016/j.simyco.2020.04.001

Monpierre, L., Aït-Ammar, N., Valsecchi, I., & Normand, A.-C. (2022). Species identification and in vitro antifungal susceptibility of *Paecilomyces/Purpureocillium* species isolated from clinical respiratory samples: A multicenter study. *Journal of Fungi, 8,* 684. https://doi.org/10.3390/jof8070684

Moore, M. K. (1992). The infection of human skin and nail by *Scytalidium* species (pp. 1–42). *(Missing publication source or publisher — please confirm)*

Morelet, M. (1968). De aliquibus in Mycologia novitatibus. *Bulletin de la Société des Sciences naturelles et d'Archéologie de Toulon et du Var, 175*, 5–6.

Morelet, M. (1969). Micromycètes du Var et d'ailleurs (2me Note). *Annales de la Société des Sciences Naturelles et d'Archéologie de Toulon et du Var, 21*, 104–106.

Morinaga, M., & Udagawa. (1978). *Gilmaniella subornata*. *Transactions of the Mycological Society of Japan, 19*, 147.

Mota, R. M. A., Abarca, G. H., Ruíz, R. F. C., & Hernández, C. I. B. (2008). Two new species of *Polyschema* and *Vanakripa* and other microfungi recorded from mangrove in Veracruz, Mexico. *Mycotaxon, 106*, 29–40.

Mouchacca, J. (2007). Heat-tolerant fungi and applied research: More data on pseudothermophilic taxa. *Cryptogamie Mycologie, 28*, 91.

Moulíková, Š., Kolářik, M., Lorch, J. M., Kolarczyková, D., Hubka, V., & Moková, A. (2023). Wild rodents harbour high diversity of *Arthroderma*. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 50*, 27–47. https://doi.org/10.3767/persoonia.2023.50.02

Moustafa, A. F. (1975). A new species of *Gilmaniella* from the soil of Kuwait. *Persoonia, 8*, 332–333.

Mueller, G. M., Bills, G. F., & Foster, M. S. (2004). *Biodiversity of fungi: Inventory and monitoring methods*. Elsevier Academic Press.

Müller, E. E. L., Glaab, E., May, P., & Vlassis, N. (2013). Condensing the omics fog of microbial communities. *Trends in Microbiology, 21*(7), 325–333. https://doi.org/10.1016/j.tim.2013.04.009

Mueller, K. E., & Durrell, L. (1957). Sampling tubes for soil fungi. *Phytopathology, 47*, 243.

Mugambi, G. K., & Huhndorf, S. M. (2009). Parallel evolution of hysterothecial ascomata in ascolocularous fungi (Ascomycota, Fungi). *Systematics and Biodiversity, 7*(4), 453–464.

Muggia, L., Hafellner, J., Wirtz, N., Hawksworth, D. L., & Grube, M. (2008). The sterile microfilamentous lichenized fungi *Cystocoleus ebeneus* and *Racodium rupestre* are relatives of plant pathogens and clinically important dothidealean fungi. *Mycological Research, 112*(1), 50–56. https://doi.org/10.1016/j.mycres.2007.08.025

Mukerji, K. G. (1978). Taxonomy of the Chaetomiales in relation to its morphology and cytology. In C. V. Subramanian (Ed.), *Taxonomy of fungi* (Vol. 1, pp. 258–262).

Mukerji, K. G. (2002). Soil microbes. In *Techniques in Mycorrhizal Studies* (pp. 7–13). https://doi.org/10.1007/978-94-017-3209-3_2

Munk, A. (1957). Danish pyrenomycetes: A preliminary flora. *Dansk Botanisk Arkiv, 17*, 1–491.

Nag Raj, T. R. (1993). *Coelomycetous anamorphs with appendage bearing conidia*. Mycologue Publications.

Nagler, M., Insam, H., Pietramellara, G., & Ascher-Jenull, J. (2018). Extracellular DNA in natural environments: Features, relevance and applications. *Applied Microbiology and Biotechnology, 102*, 6343–6356. https://doi.org/10.1007/s00253-018-9120-4

Nagler, M., Podmirseg, S. M., Mayr, M., Ascher-Jenull, J., & Insam, H. (2021). The masking effect of extracellular DNA and robustness of intracellular DNA in anaerobic digester NGS studies: A discriminatory study of the total DNA pool. *Molecular Ecology, 30*, 438–450. https://doi.org/10.1111/mec.15740

Nguyen, L.-T., Schmidt, H. A., von Haeseler, A., & Minh, B. Q. (2015). IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution, 32*, 268–274. https://doi.org/10.1093/molbev/msu300

Naranjo-Ortiz, M. A., & Gabaldón, T. (2019). Fungal evolution: Diversity, taxonomy and phylogeny of the Fungi. *Biological Reviews, 94*, 2101–2137.

do Nascimento Barbosa, R., Pereira Bezerra, J. D., Oller Costa, P. M., & Correia de Lima-Júnior, N. (2016). *Aspergillus* and *Penicillium* (Eurotiales: Trichocomaceae) in soils of the Brazilian tropical dry forest: Diversity in an area of environmental preservation. *Revista de Biología Tropical, 64*(1), 45. https://doi.org/10.15517/rbt.v64i1.18223

Naseem, M., Verma, P. C., Raghuwanshi, R., Gaur, V. K., Singh, M., Seth, S., . . . Srivastava, P. K. (2024). Soil microbiome and its functional attributes under the gradient of arsenic contamination in paddy soils. *Water, Air, & Soil Pollution, 235*, 597. https://doi.org/10.1007/s11270-024-07412-x

Nash, T. H., & Pippin, D. R. (1981). The fungal genus *Sphaeria* in aquatic habitats. *Canadian Journal of Botany, 59*, 1922–1933.

Nattawut, R., Jariya, S., Sayanh, S., Narumol, P., & Gareth, E. B. (2012). Phylogeny of the appendaged coelomycete genera: *Pseudorobillarda*, *Robillarda*, and *Xepiculopsis* based on nuclear ribosomal DNA sequences. *Cryptogamie, Mycologie, 33*, 319–332. https://doi.org/10.7872/crym.v33.iss3.2012.319

Nees von Esenbeck, C. G. (1816). *Das System der Pilze und Schwämme*. Würzburg, Germany.

Negroni, P., & Fischer, I. (1944). *Pseudallescheria sheari* n. gen., n. sp. aislada de un paramicetoma de la rodilla. *Revista del Instituto Bacteriológico "Dr. Carlos G. Malbrán"*.

Nelson, P. E., & Wilhelm, S. (1956). An undescribed fungus causing a root rot of strawberry. *Mycologia, 48*, 547–551.

Nelson, R. R. (1964). The perfect stage of *Curvularia geniculata*. *Mycologia*, *56*, 777–779.

Newbury, S., Moriello, K., Coyner, K., Trimmer, A., & Kunder, D. (2015). Management of endemic *Microsporum canis* dermatophytosis in an open admission shelter: A field study. *Journal of Feline Medicine and Surgery, 17*, 342–347. https://doi.org/10.1177/1098612X14543854

Nguyen, T. T., Pangging, M., & Lee, H. B. (2017). Three unrecorded fungal species from fecal and freshwater samples in Korea. *The Korean Journal of Mycology, 45*, 304–318.

Nicot, J., & Meyer, J. (1956). Un hyphomycète nouveau des sols tropicaux: *Staphylotrichum coccosporum* nov. gen., nov. sp. *Bulletin de la Société Mycologique de France, 72*, 318–323.

Niego, A. G. T., Lambert, C., Mortimer, P., & Thongklang, N. (2023a). The contribution of fungi to the global economy. *Fungal Diversity, 121*, 95–137. https://doi.org/10.1007/s13225-023-00520-9

Niego, A. G. T., Rapior, S., Thongklang, N., Raspé, O., Hyde, K. D., & Mortimer, P. (2023b). Reviewing the contributions of macrofungi to forest ecosystem processes and services. *Fungal Biology Reviews, 44*, 100294. https://doi.org/10.1016/j.fbr.2022.11.002

Nierman, W. C., Pain, A., Anderson, M. J., Wortman, J. R., Kim, H. S., Arroyo, J., . . . Denning, D. W. (2005). Genomic sequence of the pathogenic and allergenic filamentous fungus *Aspergillus fumigatus*. *Nature, 438,* 1151–1156. https://doi.org/10.1038/nature04332

Niessl, G. von. (1875). Notizen über neue und kritische Pyrenomyceten. *Verhandlungen des Naturforschenden Vereines in Brünn, 14*, 165–217.

Nikitin, D. A., Ivanova, E. A., Semenov, M. V., Zhelezova, A. D., Ksenofontova, N. A., Tkhakakhova, A. K., . . . Kholodov, V. A. (2023). Diversity, ecological characteristics and identification of some problematic phytopathogenic *Fusarium* in soil: A review. *Diversity, 15*, 49. https://doi.org/10.3390/d15010049

Nilsson, R. H., Anslan, S., Bahram, M., Wurzbacher, C., Baldrian, P., & Tedersoo, L. (2019). Mycobiome diversity: High-throughput sequencing and identification of fungi. *Nature Reviews Microbiology, 17*, 95–109. https://doi.org/10.1038/s41579-018-0116-y

Noman, E. A., Al-Gheethi, A. A., Talip, B. A., Mohamed, R. M. S. R., Almoheer, R., Al-Wrafy, F. A., . . . El Enshasy, H. A. (2023). New fungal strains from peat soil in Malaysia: Morphological and molecular characteristics. *Sustainability, 15*, 5902. https://doi.org/10.3390/su15075902

Nonaka, K., Kaneta, T., Ōmura, S., & Masuma, R. (2015). *Mariannaea macrochlamydospora*, a new hyphomycete (Nectriaceae) from soil in the Bonin Islands, Japan. *Mycoscience, 56*, 29–33. https://doi.org/10.1016/j.myc.2014.02.001

Nonaka, K., Ōmura, S., Masuma, R., Kaifuchi, S., & Masuma, R. (2013). Three new *Pochonia* taxa (Clavicipitaceae) from soils in Japan. *Mycologia, 105*, 1202–1218. https://doi.org/10.3852/12-132

Norphanphoun, C., Hongsanan, S., Bhat, J., Kuo, C.-H., & Hyde, K. D. (2021). *Ficus microcarpa* (Moraceae) and *Kandelia candel* (Rhizophoraceae), two new host records for *Alternaria gaisen* from Taiwan. *Chiang Mai Journal of Science, 48*, 1478–1499.

Nuankaew, S., Chuaseeharonnachai, C., Preedanon, S., Somrithipol, S., Saengkaewsuk, S., Kwantong, P., … Boonyuen, N. (2022). Two novel species of *Talaromyces* discovered in a karst cave in the Satun UNESCO Global Geopark of Southern Thailand. *Journal of Fungi*, *8*, 825. https://doi.org/10.3390/jof8080825

Nundaeng, S., Suwannarach, N., Limtong, S., Khuna, S., Kumla, J., & Lumyong, S. (2021). An updated global species diversity and phylogeny in the genus *Wickerhamomyces* with addition of two new species from Thailand. *Journal of Fungi*, *7*, 957. https://doi.org/10.3390/jof7110957

Nwokeoma, C. I. (2017). Keratinophilic fungi associated with soils from selected villages in Ugwunye and Ojebogene towns, Enugu state, Nigeria and their disease implications. *The Bioscientist Journal, 5*(1), 20–31.

Nylander, J. A. A. (2004). MrModeltest (Version 2.2) [Computer software]. http://www.abc.se/~nylander/

O'Brien, H. E., Parrent, J. L., Jackson, J. A., Moncalvo, J. M., & Vilgalys, R. (2005). Fungal community analysis by large-scale sequencing of environmental samples. *Applied and Environmental Microbiology, 71*(9), 5544–5550. https://doi.org/10.1128/AEM.71.9.5544-5550.2005

O'Donnell, K., Al-Hatmi, A. M., Aoki, T., Brankovics, B., Cano-Lira, J. F., Coleman, J. J., … Zhang, S. X. (2020). No to *Neocosmospora*: Phylogenomic and practical reasons for continued inclusion of the *Fusarium solani* species complex in the genus *Fusarium*. *Mycosphere, 5*. https://doi.org/10.1128/msphere.00810-20

O'Donnell, K., Kistler, H. C., Cigelnik, E., & Ploetz, R. C. (1998). Multiple evolutionary origins of the fungus causing Panama disease of banana: Concordant evidence from nuclear and mitochondrial gene genealogies. *Proceedings of the National Academy of Sciences, 95*(5), 2044–2049. https://doi.org/10.1073/pnas.95.5.2044

Oh, J. J., Kim, Y. J., Kim, J. Y., Kwon, S. L., Lee, C., Lee, M. E., … Kim, G. H. (2021). Genomic analysis and assessment of melanin synthesis in *Amorphotheca resinae* KUC3009. *Journal of Fungi, 7*(4), 289. https://doi.org/10.3390/jof7040289

Olivas-Peraza, D. D., Leyva-Madrigal, K. Y., Maldonado-Mendoza, I. E., & Félix-Gastélum, R. (2022). *Curvularia muehlenbeckiae* causing leaf spot on Johnson grass in Mexico. *Mycological Progress, 21*, 50. https://doi.org/10.1007/s11557-022-01805-0

Oliveira, L. G., Cavalcanti, M. A. Q., Fernandes, M. J. S., & Lima, D. M. M. (2013). Diversity of filamentous fungi isolated from the soil in the semiarid area, Pernambuco, Brazil. *Journal of Arid Environments, 95*, 49–54. https://doi.org/10.1016/j.jaridenv.2013.03.007

Orgiazzi, A., Bardgett, R. D., & Barrios, E. (2016). *Global soil biodiversity atlas*. European Commission.

Orr, G. F., & Kuehn, H. H. (1971). Notes on Gymnoascaceae. I. A review of eight species. *Mycologia, 63*, 191–203.

Orr, G. F., Kuehn, H. H., & Plunkett, O. A. (1963). A new genus of the Gymnoascaceae with swollen peridial septa. *Canadian Journal of Botany, 41*, 1439–1456.

Orr, G. F., Ghosh, G. R., & Roy, K. (1977). The genera *Gymnascella*, *Arachniotus,* and *Pseudoarachniotus*. *Mycologia, 69,* 126–163. https://doi.org/10.1080/00275514.1977.12020039

Orr, G. F., & Kuehn, H. H. (1972). Notes on Gymnoascaceae. II. Some Gymnoascaceae and keratinophilic fungi from Utah. *Mycologia, 64*, 55–72. https://doi.org/10.1080/00275514.1972.12019235

Orwa, P., Mugambi, G., Wekesa, V., & Mwirichia, R. (2020). Isolation of haloalkaliphilic fungi from Lake Magadi in Kenya. *Heliyon, 6*, e02823. https://doi.org/10.1016/j.heliyon.2019.e02823

Osono, T., Ishii, Y., Takeda, H., Seramethakun, T., Khamyong, S., To-Anun, C., . . . Kakishima, M. (2009). Fungal succession and lignin decomposition on *Shorea obtusa* leaves in a tropical seasonal forest in northern Thailand. *Fungal Diversity*, *36*, 101–119.

Ostafińska, A., Jankowiak, R., Bilański, P., Solheim, H., & Wingfield, M. J. (2021). Six new species of *Sporothrix* from hardwood trees in Poland. *MycoKeys, 82*, 1–32. https://doi.org/10.3897/mycokeys.82.66603

Overy, D., Rämä, T., Oosterhuis, R., Walker, A., & Pang, K.-L. (2019). The neglected marine fungi, sensu stricto, and their isolation for natural products' discovery. *Marine Drugs, 17*, 42. https://doi.org/10.3390/md17010042

Özkaya, S., Soylu, S., Kara, M., Gümüş, Y., Soylu, E. M., Teke, İ., … Lavkor, I. (2024). Disease prevalence, incidence, morphological and molecular characterisation of *Lasiodiplodia pseudotheobromae* causing collar rot disease on peanut plants in Turkey. *Journal of Plant Diseases and Protection, 131*, 1639–1651. https://doi.org/10.1007/s41348-024-00933-x

Pacioni, G. (1991). Wet-sieving and decanting technique for spore extraction. *Methods in Microbiology*, *23*, 317–322.

Palmer, M. A., Covich, A. P., Finlay, B., Gibert, J., Hyde, K. D., Johnson, R. K., . . . Strayer, D. L. (1997). Biodiversity and ecosystem function in freshwater sediments. *Ambio, 26*(8), 571–577.

Pan, H., Yu, J., Wu, Y., Zhang, T., & Wang, H. (2008). Diversity analysis of soil dematiaceous hyphomycetes from the Yellow River source area: I. *Journal of Zhejiang University Science B, 9*(9), 829–834. https://doi.org/10.1631/jzus.B0860002

Pandey, A., Agrawal, G. P., & Singh, S. M. (1990). Pathogenic fungi in soils of Jabalpur, India. *Mycoses, 33*(3), 116–125. https://doi.org/10.1111/myc.1990.33.3.116

Pandeya, J. P. N., & Saksena, S. B. (1978). A new species of *Polyschema* from Indian soil. *Mycologia, 70*(5), 876–879. https://doi.org/10.1080/00275514.1978.12020298

Pangging, M., Nguyen, T. T. T., & Lee, H. B. (2019). New records of four species belonging to Eurotiales from soil and freshwater in Korea. *Mycobiology, 47*(2), 154–164.

Pansak, W., Takrattanasaran, N., Nongharnpitak, N., & Khongdee, N. (2024). Soil-related laws in Thailand. In *[Book or Proceedings Title]* (pp. 243–262).

Papendorf, M. C. (1967). Two new genera of soil fungi from South Africa. *Transactions of the British Mycological Society, 50*(1), 69–75.

Papendorf, M. (1969a). *Leptodiscella africana* gen. et comb. nov. *Transactions of the British Mycological Society*, *53*(1), 145–147. https://doi.org/10.1016/S0007-1536(69)80021-5

Papendorf, M. C. (1969b). New South African soil fungi. *Transactions of the British Mycological Society*, *52*(3), 483-IN20. https://doi.org/10.1016/S0007-1536(69)80132-4

Papizadeh, M., Soud, M. R., Amini, L., Wijayawardene, N. N., & Hyde, K. D. (2017). *Pyrenochaetopsis tabarestanensis* (Cucurbitariaceae, Pleosporales), a new species isolated from rice farms in north Iran. *Phytotaxa, 297*(1), 15–28. https://doi.org/10.11646/phytotaxa.297.1.2

Papizadeh, M., Wijayawardene, N. N., Amoozegar, M. A., Saba, F., Fazeli, S. A. S., & Hyde, K. D. (2018). *Neocamarosporium jorjanensis*, *N. persepolisi*, and *N. solicola* spp. nov. (Neocamarosporiaceae, Pleosporales) isolated from saline lakes of Iran indicate the possible halotolerant nature for the genus. *Mycological Progress, 17*(4), 661–679. https://doi.org/10.1007/s11557-017-1341-x

Pakshir, K., Ghiasi, M. R., Zomorodian, K., & Gharavi, A. R. (2013). Isolation and molecular identification of keratinophilic fungi from public parks soil in Shiraz, Iran. *BioMed Research International, 2013*, Article ID 619576. https://doi.org/10.1155/2013/619576

Parbery, D. (1969). *Amorphotheca resinae*, gen. nov., sp. nov.: The perfect state of *Cladosporium resinae*. *Australian Journal of Botany, 17*(3), 331. https://doi.org/10.1071/BT9690331

Park, M. S., Lee, J. W., Kim, S. H., & Park, J.-H. (2020). *Penicillium* from rhizosphere soil in terrestrial and coastal environments in South Korea. *Mycobiology, 48*(4), 431–442. https://doi.org/10.1080/12298093.2020.1823611

Park, M. S., Romanoski, C. E., & Pryor, B. M. (2008). A re-examination of the phylogenetic relationship between the causal agents of carrot black rot, *Alternaria radicina* and *A. carotiincultae*. *Mycologia, 100*(3), 511–527. https://doi.org/10.3852/07-186R1

Park, S. W., Nguyen, T. T. T., & Lee, H. B. (2017). Characterization of two species of *Acremonium* (unrecorded in Korea) from soil samples: *A. variecolor* and *A. persicinum*. *Mycobiology, 45*(4), 353–361. https://doi.org/10.5941/MYCO.2017.45.4.353

Parkinson, D., & Kendrick, W. B. (1960). Investigations of soil microhabitats. In *Ecology of Soil Fungi* (pp. 22–28). Liverpool University Press.

Parkinson, D., & Williams, S. T. (1960). A method for isolating fungi from soil microhabitats. *Plant and Soil, 13*(3), 347–355. https://doi.org/10.1007/BF01394646

Parkinson, D., & Thomas, A. (1965). A comparison of methods for the isolation of fungi from rhizospheres. *Canadian Journal of Microbiology, 11*(10), 1001–1007. https://doi.org/10.1139/m65-133

Pchelin, I. M., Zlatogursky, V. V., Rudneva, M. V., Chilina, G. A., Rezaei-Matehkolaei, A., Lavnikevich, D. M., … Taraskina, A. E. (2016). Reconstruction of phylogenetic relationships in dermatomycete genus *Trichophyton* Malmsten 1848 based on ribosomal internal transcribed spacer region, partial 28S rRNA and beta-tubulin genes sequences. *Mycoses, 59*(6), 566–575. https://doi.org/10.1111/myc.12505

Peck, C. H. (1884). Report of the botanist, 1882. *Annual Report on the New York State Museum of Natural History, 35*, 125–164.

Peintner, U., Knapp, M., Fleischer, V., Walch, G., & Dresch, P. (2016). *Myrmecridium hiemale* sp. nov. from snow-covered alpine soil is the first eurypsychrophile in this genus of anamorphic fungi. *International Journal of Systematic and Evolutionary Microbiology, 66*(6), 2592–2598. https://doi.org/10.1099/ijsem.0.001090

Pem, D., Jeewon, R., Bhat, D. J., Doilom, M., Boonmee, S., Hongsanan, S., … Hyde, K. D. (2019). Mycosphere notes 275–324: A morpho-taxonomic revision and typification of obscure Dothideomycetes genera (Incertae sedis). *Mycosphere, 10*(1), 1115–1246. https://doi.org/10.5943/mycosphere/10/1/22

Pem, D., Jeewon, R., Chethana, K. W. T., & Hongsanan, S. (2021). Species concepts of Dothideomycetes: Classification, phylogenetic inconsistencies and taxonomic standardization. *Fungal Diversity, 109*(1), 283–319. https://doi.org/10.1007/s13225-021-00485-7

Pem, D., Hyde, K. D., McKenzie, E. H. C., Hongsanan, S., Wanasinghe, D. N., Boonmee, S., … Dong, W. (2024). A comprehensive overview of genera in Dothideomycetes. *Mycosphere, 15*, 2175–4568. https://doi.org/10.5943/mycosphere/15/1/18

Peng, Q., Zhong, X., Lei, W., Zhang, G., & Liu, X. (2013). Detection of *Ophiocordyceps sinensis* in soil by quantitative real-time PCR. *Canadian Journal of Microbiology, 59*(3), 204–209. https://doi.org/10.1139/cjm-2012-0490

Peng, W., He, X., Wang, Y., Zhang, Y., Ye, X., Jia, D., … Sun, Q. (2014). A new species of *Scytalidium* causing slippery scar on cultivated *Auricularia polytricha* in China. *FEMS Microbiology Letters, 359*(1), 72–80. https://doi.org/10.1111/1574-6968.12564

Penkhrue, W., Khanongnuch, C., Masaki, K., Pathom-Aree, W., Punyodom, W., & Lumyong, S. (2015). Isolation and screening of biopolymer-degrading microorganisms from northern Thailand. *World Journal of Microbiology and Biotechnology, 31*(9), 1431–1442. https://doi.org/10.1007/s11274-015-1895-1

Perdomo, H., Cano, J., Gené, J., García, D., Hernández, M., & Guarro, J. (2013). Polyphasic analysis of *Purpureocillium lilacinum* isolates from different origins and proposal of the new species *Purpureocillium lavendulum*. *Mycologia, 105*(1), 151–161. https://doi.org/10.3852/11-190

Perera, R. H., Hyde, K. D., Maharachchikumbura, S. S. N., Jones, E. B. G., McKenzie, E. H. C., Stadler, M., … Liu, Z. Y. (2020). Fungi on wild seeds and fruits. *Mycosphere, 11*(1), 2108–2480. https://doi.org/10.5943/MYCOSPHERE/11/1/14

Perera, R. H., Maharachchikumbura, S. S. N., Bhat, J. D., Al-Sadi, A. M., Liu, J. K., Hyde, K. D., . . . Liu, Z. Y. (2016). New species of *Thozetella* and *Chaetosphaeria* and new records of *Chaetosphaeria* and *Tainosphaeria* from Thailand. *Mycosphere, 7*(9), 1301–1321. https://doi.org/10.5943/mycosphere/7/9/5

Perkins, D. D., & Turner, B. C. (1988). *Neurospora* from natural populations: Towards the population biology of a haploid eukaryote. *Experimental Mycology, 12*(1), 91–131.

Persiani, A. M., & Maggi, O. (1986). A new species of *Heterocephalum* from Ivory Coast soil. *Transactions of the British Mycological Society, 87*(4), 631–635.

Peršoh, D., Stolle, N., Brachmann, A., Begerow, D., & Rambold, G. (2018). Fungal guilds are evenly distributed along a vertical spruce forest soil profile while individual fungi show pronounced niche partitioning. *Mycological Progress, 17*(8), 925–939. https://doi.org/10.1007/s11557-018-1405-6

Persoon, C. (1974). Neuer Versuch einer systematischen Eintheilung der Schwämme. *Neues Magazin für die Botanik, 1,* 63–80.

Persoon, C. H. (1795). Torula. *Annales Botanici (Usteri), 15*, 25.

Persoon, C. H. (1801). *Synopsis Methodica Fungorum*. Neues Magazin für die Botanik, 1, 120.

Persoon, C. H. (1822). *Mycologia Europaea* (Vol. 1). Palm.

Pesante, A. (1957). Osservazione su una carie del plantano. *Annali di Sperimentazione Agraria Nuova Serie, 11*, CCXLXI–CCLXVI.

Petch, T. (1931). Notes on entomogenous fungi. *Transactions of the British Mycological Society, 16*(1), 55–75. https://doi.org/10.1016/S0007-1536(31)80006-3

Petersen, P. M. (1967). Studies on ecology of some species of Pezizales. *Botanisk Tidsskrift, 62*, 312–322.

Petersen, P. M. (1985). The ecology of Danish soil inhabiting Pezizales with emphasis on edaphic conditions. *Opera Botanica, 77*, 1–38.

Peterson, S. W., Jurjevic, Z., Bills, G. F., Stchigel, A. M., Guarro, J., & Vega, F. E. (2010). Genus *Hamigera*, six new species and multilocus DNA sequence based phylogeny. *Mycologia*, *102*(4), 847–864. https://doi.org/10.3852/09-268

Pfister, D. H., & Healy, R. (2021). Pezizomycetes. In *Encyclopedia of Mycology* (pp. 295–309). Elsevier.

Pham, N. Q., Barnes, I., Chen, S., Pham, T. Q., Lombard, L., Crous, P. W., & Wingfield, M. J. (2018). New species of *Cylindrocladiella* from plantation soils in South-East Asia. *MycoKeys, 32*, 1–24. https://doi.org/10.3897/mycokeys.32.23754

Pham, N. Q., Barnes, I., Chen, S., Liu, F., Dang, Q. N., Pham, T. Q., . . . Wingfield, M. J. (2019). Ten new species of *Calonectria* from Indonesia and Vietnam. *Mycologia, 111*(1), 78–102. https://doi.org/10.1080/00275514.2018.1522179

Phookamsak, R., Hyde, K. D., Jeewon, R., Bhat, D. J., Jones, E. G., Maharachchikumbura, S. S., . . . Xu, J. (2019). Fungal diversity notes 929–1035: Taxonomic and phylogenetic contributions on genera and species of fungi. *Fungal Diversity, 95*, 1–273. https://doi.org/10.1007/s13225-019-00421-w

Phookamsak, R., Jiang, H., Suwannarach, N., Lumyong, S., Xu, J., Xu, S., . . . Chomnunti, P. (2022). Bambusicolous fungi in Pleosporales: Introducing four novel taxa and a new habitat record for *Anastomitrabeculia didymospora*. *Journal of Fungi, 8*(6), 630. https://doi.org/10.3390/jof8060630

Phukhamsakda, C., McKenzie, E. H., Phillips, A. J., Gareth Jones, E. B., Jayarama Bhat, D., Stadler, M., … Hyde, K. D. (2020). Microfungi associated with *Clematis* (Ranunculaceae) with an integrated approach to delimiting species boundaries. *Fungal Diversity, 120*, 1–203.

Pinruan, U., McKenzie, E. H., Jones, E. G., & Hyde, K. D. (2004). Two new species of *Stachybotrys*, and a key to the genus. *Fungal Diversity, 17*, 145–157.

Pirozynski, K. A. (1963). Beltrania and related genera. *Mycological Papers, 90*, 1–37.

Pittayakhajonwut, P., Theerasilp, M., Kongsaeree, P., Rungrod, A., Tanticharoen, M., & Thebtaranonth, Y. (2002). Pughiinin A, a sesquiterpene from the fungus *Kionochaeta pughii* (BCC). *Planta Medica*, *68*(11), 1017–1019.

Poli, A., Bovio, E., Ranieri, L., Varese, G. C., & Prigione, V. (2020). News from the sea: A new genus and seven new species in the pleosporalean families Roussoellaceae and Thyridariaceae. *Diversity*, *12*(4), 144. https://doi.org/10.3390/d12040144

Pomoim, N., Trisurat, Y., Hughes, A. C., & Corlett, R. T. (2022). Can Thailand protect 30% of its land area for biodiversity, and will this be enough? *Diversity, 14*(5), 344. https://doi.org/10.3390/d14050344

Pordel, A., Ahmadpour, A., Behnia, M., & Javan-Nikkhah, M. (2015). New records of Hyphomycetes fungi in Iran. *Mycologia Iranica, 2*, 69–74. https://doi.org/10.22043/mi.2015.14227

Pornsuriya, C., Lin, F. C., Kanokmedhakul, S., & Soytong, K. (2008). New record of *Chaetomium* species isolated from soil under pineapple plantation in Thailand. *Journal of Agricultural Technology*, *4*(1), 91–103.

Pornsuriya, C., Soytong, K., Poeaim, S., Kanokmedhakul, S., Khumkomkhet, P., Lin, F. C., . . . Hyde, K. D. (2011). *Chaetomium siamense* sp. nov., a soil isolate from Thailand, produces a new chaetoviridin, G. *Mycotaxon, 115*, 19–27. https://doi.org/10.5248/115.19

Pornsuriya, C., Ito, S. I., & Sunpapao, A. (2018). First report of leaf spot on lettuce caused by *Curvularia aeria*. *Journal of General Plant Pathology*, *84*(4), 296–299. https://doi.org/10.1007/s10327-018-0782-7

Porras-Alfaro, A., Herrera, J., Natvig, D. O., Lipinski, K., & Sinsabaugh, R. L. (2011). Diversity and distribution of soil fungal communities in a semiarid grassland. *Mycologia*, *103*(1), 10–21. https://doi.org/10.3852/09-297

Pratibha, J., Prabhugaonkar, A., Hyde, K. D., & Bhat, D. J. (2014). Phylogenetic placement of *Bahusandhika*, *Cancellidium* and *Pseudoepicoccum* (asexual Ascomycota). *Phytotaxa*, *176*(1), 68–80. https://doi.org/10.11646/phytotaxa.176.1.9

Preedanon, S., Suetrong, S., Srihom, C., Somrithipol, S., Kobmoo, N., Saengkaewsuk, S., . . . Boonyuen, N. (2023). Eight novel cave fungi in Thailand's Satun Geopark. *Fungal Systematics and Evolution*, *12*, 1–30. https://doi.org/10.3114/fuse.2023.12.01

Preuss, C. G. T. (1851). Übersicht untersuchter Pilze, besonders aus der Umgegend von Hoyerswerda. *Linnaea*, *24*, 99–153.

Promputtha, I., Hyde, K. D., McKenzie, E. H. C., Peberdy, J. F., & Lumyong, S. (2010). Can leaf degrading enzymes provide evidence that endophytic fungi becoming saprobes? *Fungal Diversity*, *41*, 89–99.

Prosser, J. I. (2015). Dispersing misconceptions and identifying opportunities for the use of 'omics' in soil microbial ecology. *Nature Reviews Microbiology*, *13*(7), 439–446. https://doi.org/10.1038/nrmicro3468

Pryor, B. M., Davis, R. M., & Gilbertson, R. L. (1998). Detection of soilborne *Alternaria radicina* and its occurrence in California carrot fields. *Plant Disease*, *82*(8), 891–895. https://doi.org/10.1094/PDIS.1998.82.8.891

Puangsombat, P., Sangwanit, U., & Marod, D. (2010). Diversity of soil fungi in different land use types in Tha Kum-Huai Raeng forest reserve, Trat province. *Kasetsart Journal (Natural Science)*, *44*(5), 1162–1175.

Qiao, M., Zhang, Z., Yang, L., & Yu, Z. (2021). *Staphylotrichum sinense* sp. nov., a new hyphomycete (Chaetomiaceae) from China. *International Journal of Systematic and Evolutionary Microbiology*, *71*, e004747.

Qiao, M., Tian, W., Castañeda-Ruiz, R. F., Xu, J., & Yu, Z. (2019). Two new species of *Verruconis* from Hainan, China. *MycoKeys, 48*, 41–60. https://doi.org/10.3897/mycokeys.48.32147

Qiu, M., Zhang, R., Xue, C., Zhang, S., Li, S., Zhang, N., . . . Shen, Q. (2012). Application of bio-organic fertilizer can control Fusarium wilt of cucumber plants by regulating microbial community of rhizosphere soil. *Biology and Fertility of Soils, 48*(8), 807–816. https://doi.org/10.1007/s00374-012-0675-4

Quaedvlieg, W., Binder, M., Groenewald, J. Z., Summerell, B. A., Carnegie, A. J., Burgess, T. I., . . . Crous, P. W. (2014). Introducing the consolidated species concept to resolve species in the Teratosphaeriaceae. *Persoonia, 33*, 1–40.

Rai, J. N., & Tewari, J. P. (1961). Additions to our knowledge of Indian soil fungi. *Proceedings of the Indian Academy of Sciences, 54,* 209–217.

Rai, J. N., & Wadhwani, K. (1977). New species of *Thielavia* (*Thielavia ampullata*) from Indian soils. *Sydowia*, [volume and page numbers not provided].

Rai, J. N., Tewari, J. P., & Mukerji, K. G. (1964). *Achaetomium*, a new genus of ascomycetes. *Canadian Journal of Botany, 42*(4), 693–697.

Rainer, J., & De Hoog, G. S. (2006). Molecular taxonomy and ecology of *Pseudallescheria, Petriella* and *Scedosporium prolificans* (Microascaceae) containing opportunistic agents on humans. *Mycological Research, 110*(2), 151–160. https://doi.org/10.1016/j.mycres.2005.08.003

Raj, T. R. N., Morgan-Jones, G., & Kendrick, B. (1972). Genera coelomycetarum IV. *Pseudorobillarda* gen. nov., a generic segregate of *Robillarda* Sacc. *Canadian Journal of Botany, 50*(4), 861–867. https://doi.org/10.1139/b72-103

Raja, H. A., Miller, A. N., Pearce, C. J., & Oberlies, N. H. (2017). Fungal identification using molecular tools: A primer for the natural products research community. *Journal of Natural Products, 80*(3), 756–770. https://doi.org/10.1021/acs.jnatprod.6b01085

Rambelli, A. (2011). Some dematiaceous hyphomycetes from Mediterranean maquis litters. *Flora Mediterranea, 21*, 5–204.

Rambaut, A. (2010). FigTree: Tree figure drawing tool version 1.3.1. Institute of Evolutionary Biology, University of Edinburgh. http://tree.bio.ed.ac.uk/software/figtree/

Rambaut, A. (2012). FigTree version 1.4.0. http://tree.bio.ed.ac.uk/software/figtree/

Ramdass, A. C., & Rampersad, S. N. (2021). Diversity and oil degradation potential of culturable microbes isolated from chronically contaminated soils in Trinidad. *Microorganisms, 9*(6), 1167. https://doi.org/10.3390/microorganisms9061167

Ramachandran, N., Sarma, Y. R., & Nambiar, K. N. (1986). Spatial distribution of *Phytophthora palmivora*–MF4 in the root zones of *Piper nigrum*. *Indian Phytopathology, 39*(3), 414–417.

Ramadan, N. A., & Ismael, H. M. (2011). Isolation of fungi seasonally from soil, air and water in villages in "Binary Safeen". In *The 4th International Scientific Conference of Salahaddin University-Erbil* (Vol. 1, pp. 612–666).

Ramakrishnan, K. (1955). Some aspects of soil fungal ecology. *Proceedings: Plant Sciences, 41*(1), 110–116. https://doi.org/10.1007/BF03050034

Ramesh, V., Thalavaipandian, A., Karunakaran, C., & Rajendran, A. (2012). Identification and comparison of *Xylaria curta* and *Xylaria* sp. from Western Ghats - Courtallum Hills, India. *Mycosphere, 3*(4), 607–615.

Ramesh, R., Thamilvanan, D., Ramkumar, A., Balakumar, B. S., & Kumaresan, S. (2019). Bio-activity of secondary metabolites extracted from soil fungi. *International Journal of Scientific Research and Reviews, 8*(6), 887–901.

Ramirez-Garcia, A., Pellon, A., Rementeria, A., & Buldain, I. (2018). *Scedosporium* and *Lomentospora*: An updated overview of underrated opportunists. *Medical Mycology, 56*(suppl_1), S102–S125. https://doi.org/10.1093/mmy/myx113

Rao, S., Hyde, K. D., & Pointing, S. B. (2013). Comparison of DNA and RNA, and cultivation approaches for the recovery of terrestrial and aquatic fungi from environmental samples. *Current Microbiology, 66*(2), 185–191. https://doi.org/10.1007/s00284-012-0256-7

Ran, H., Zhang, J., Gao, Q., Lin, Z., & Bao, J. (2014). Analysis of biodegradation performance of furfural and 5-hydroxymethylfurfural by *Amorphotheca resinae* ZN1. *Biotechnology for Biofuels, 7*, 1–12.

Rannala, B., & Yang, Z. (1996). Probability distribution of molecular evolutionary trees: A new method of phylogenetic inference. *Journal of Molecular Evolution, 43*(3), 304–311. https://doi.org/10.1007/BF02338839

Randhawa, H. S., & Sandhu, R. S. (1963). On the occurrence of two new species of *Trichophyton* in Indian soils. *Mycopathologia et Mycologia Applicata, 20*(3), 225–238. https://doi.org/10.1007/BF02089211

Randhawa, H. S., & Sandhu, R. S. (1964). *Keratinophyton terreum* gen. nov., sp. nov., a keratinophilic fungus from soil in India. *Medical Mycology, 3*(4), 251–256. https://doi.org/10.1080/00362176485190421

Raper, K. B. (1965). *The genus Aspergillus*. The Williams and Wilkins Co.

Rashmi, M., Kushveer, J. S., & Sarma, V. V. (2019). A worldwide list of endophytic fungi with notes on ecology and diversity. *Mycosphere, 10*(1), 798–1079.

Raza, M., Zhang, Z.-F., Hyde, K. D., Diao, Y.-Z., & Cai, L. (2019). Culturable plant pathogenic fungi associated with sugarcane in southern China. *Fungal Diversity, 99*(1), 1–104. https://doi.org/10.1007/s13225-019-00434-5

Razaghi, P., Raza, M., Han, S. L., Ma, Z. Y., Cai, L., Zhao, P., . . . Liu, F. (2024). Sporocadaceae revisited. *Studies in Mycology, 109*, 155–272. https://doi.org/10.3114/sim.2024.109.03

Reanprayoon, P., & Pathomsiriwong, W. (2012). Tropical soil fungi producing cellulase and related enzymes in biodegradation. *Journal of Applied Sciences (Faisalabad), 12*(10), 1909–1916.

Rebentisch, J. F. (1804). *Prodromus flora neomarchicae*. Schüppel.

Réblová, M., & Seifert, K. A. (2008). A new species of *Chaetosphaeria* with *Menispora ciliata* and phialophora-like anamorphs. *Fungal Diversity, 29*, 99–105.

Réblová, M., Hernandez-Restrepo, M., Sklenář, F., Nekvindová, J., Réblová, K., & Kolařík, M. (2022). Consolidation of *Chloridium*: New classification into eight sections with 37 species and reinstatement of the genera *Gongromeriza* and *Psilobotrys*. *Studies in Mycology, 103*, 86–211. https://doi.org/10.3114/sim.2022.103.04

Réblová, M., Jaklitsch, W. M., Réblová, K., & Štěpánek, V. (2015). Phylogenetic reconstruction of the Calosphaeriales and Togniniales using five genes and predicted RNA secondary structures of ITS, and *Flabellascus tenuirostris* gen. et sp. nov. *PLoS ONE, 10*(11), e0144616. https://doi.org/10.1371/journal.pone.0144616

Réblová, M., & Nekvindová, J. (2023). New genera and species with chloridium-like morphotype in the Chaetosphaeriales and Vermiculariopsiellales. *Studies in Mycology, 106*, 199–258. https://doi.org/10.3114/sim.2023.106.04

Réblová, M., Nekvindová, J., & Hernández-Restrepo, M. (2021a). Reflections on *Menisporopsis*, *Multiguttulispora* and *Tainosphaeria* using molecular and morphological data. *Journal of Fungi, 7*(6), 438. https://doi.org/10.3390/jof7060438

Réblová, M., Nekvindová, J., & Miller, A. N. (2021b). Phylogeny and taxonomy of *Catenularia* and similar fungi with catenate conidia. *MycoKeys, 81*, 1–44. https://doi.org/10.3897/mycokeys.81.67785

Réblová, M., Barr, M. E., & Samuels, G. J. (1999). Chaetosphaeriaceae, a new family for *Chaetosphaeria* and its relatives. *Sydowia, 51*, 49–70.

Réblová, M., Kolařík, M., Nekvindová, J., Miller, A. N., & Hernández-Restrepo, M. (2021). Phylogeny, global biogeography and pleomorphism of *Zanclospora*. *Microorganisms, 9*(4), 706.

Réblová, M., Miller, A. N., Rossman, A. Y., Seifert, K. A., Crous, P. W., Hawksworth, D. L., . . . Wijayawardene, N. N. (2016). Recommendations for competing sexual-asexually typified generic names in Sordariomycetes (except Diaporthales, Hypocreales, and Magnaporthales). *IMA Fungus, 7*(1), 131–153.

Rehner, S. A., Minnis, A. M., Sung, G. H., Luangsa-ard, J. J., Devotto, L., & Humber, R. A. (2011). Phylogeny and systematics of the anamorphic, entomopathogenic genus *Beauveria*. *Mycologia, 103*(5), 1055–1073. https://doi.org/10.3852/10-302

Rehner, S. A., & Buckley, E. (2005). A *Beauveria* phylogeny inferred from nuclear ITS and EF1-α sequences: Evidence for cryptic diversification and links to *Cordyceps* teleomorphs. *Mycologia, 97*(1), 84–98. https://doi.org/10.3852/mycologia.97.1.84

Reisinger, O., & Kiffer, E. (1974). Contribution to the fungal microflora of the Congo IV. *Polyschema congolensis* sp. nov. taxonomy and ultrastructure. *Transactions of the British Mycological Society, 62*(2), 289–294.

Ren, G. C., Jayasiri, S. C., Tibpromma, S., De Farias, A. R. G., Chethana, K. W. T., Faraj, K. H., . . . Gui, H. (2024). Saprobic ascomycetes associated with woody litter from the Greater Mekong Subregion (Southwestern China and Northern Thailand). *Mycosphere, 15*(1), 954–1082. https://doi.org/10.5943/mycosphere/15/1/8

Ren, H., Wang, F., Ye, W., & Zhang, Q. (2021). Bryophyte diversity is related to vascular plant diversity and microhabitat under disturbance in karst caves. *Ecological Indicators, 120*, 106947. https://doi.org/10.1016/j.ecolind.2020.106947

Révay, A. (1993). Some new or interesting hyphomycetes from Hungary. *Nova Hedwigia, 56*(1-2), 73–82.

Reyes, I., Bernier, L., Simard, R. R., Tanguay, P., & Antoun, H. (1999). Characteristics of phosphate solubilization by an isolate of a tropical *Penicillium rugulosum* and two UV induced mutants. *FEMS Microbiology Ecology*, *28*(3), 291–295.

Rezaei-Matehkolaei, A., Jahangiri, A., Mahmoudabadi, A. Z., Najafzadeh, M. J., Nouripour-Sisakht, S., & Makimura, K. (2017). Morpho-molecular characterization of soil inhabitant dermatophytes from Ahvaz, Southwest of Iran, a high occurrence of *Microsporum fulvum*. *Mycopathologia*, *182*(7-8), 691–699. https://doi.org/10.1007/s11046-017-0116-x

Richards, J. K., Xiao, C.-L., & Jurick, W. M. (2021). *Botrytis* spp.: A contemporary perspective and synthesis of recent scientific developments of a widespread genus that threatens global food security. *Phytopathology*, *111*(3), 432–436. https://doi.org/10.1094/phyto-10-20-0475-IA

Richardson, M. J. (1998). Coprophilous fungi from Indonesia. *Tropical Mycology, 2*, 197–203.

Richer, L., Sigalet, D., Kneteman, N., Shapiro, J., Jones, A., Scott, R. B., . . . Smith, L. (1997). Fulminant hepatic failure following ingestion of moldy homemade rhubarb wine. *Gastroenterology, 112*(4), A1366.

Rifai, M. A., Zainuddin, H., & Cholil, A. (2014). The Javanese species of *Tetraploa*. *Reinwardtia, 10*, 419–423.

Rincon-Florez, V. A., Carvalhais, L. C., & Schenk, P. M. (2013). Culture-independent molecular tools for soil and rhizosphere microbiology. *Diversity, 5*(3), 581–612. https://doi.org/10.3390/d5030581

Ritz, K., & Young, I. M. (2004). Interactions between soil structure and fungi. *Mycologist, 18*(2), 52–59.

Rixford, E., & Gilchrist, T. C. (1896). Two cases of protozoan (coccidioidal) infection of the skin and other organs. *Johns Hopkins Hospital Reports, 1*, 209–268.

Rizki, M. A. A. H., & Ilmi, M. (2021). The potential of oleaginous filamentous fungi isolated from soil of Baturraden Botanical Garden, Central Java, Indonesia. *IOP Conference Series: Earth and Environmental Science, 736*, 012060. https://doi.org/10.1088/1755-1315/736/1/012060

Rizzo, L., Sutton, D. A., Wiederhold, N. P., Thompson, E. H., Friedman, R., Wickes, B. L., . . . Guarro, J. (2014). Isolation and characterization of the fungus *Spiromastix asexualis* sp. nov. from discospondylitis in a German Shepherd dog, and review of *Spiromastix* with the proposal of the new order Spiromastixales (Ascomycota). *Mycoses, 57*(7), 419–428. https://doi.org/10.1111/myc.12178

Robak, H. (1932). Investigations regarding fungi on Norwegian ground wood pulp and fungal infections at woodpulp mills. *Saertr. Nyt Mag. Naturvidensk, 71*, 185–330.

del Rocío Reyes-Montes, M., Pérez-Huitrón, M. A., Ocaña-Monroy, J. L., Frías-De-León, M. G., Martínez-Herrera, E., Arenas, R., . . . Duarte-Escalante, E. (2016). The habitat of *Coccidioides* spp. and the role of animals as reservoirs and disseminators in nature. *BMC Infectious Diseases, 16*, 1–8. https://doi.org/10.1186/s12879-016-1902-7

Rodriguez, R. J., & Redman, R. S. (1997). Fungal lifestyles and ecosystem dynamics: Biological aspects of plant pathogens, plant endophytes and saprophytes. *Advances in Botanical Research, 24*, 169–193.

Rodríguez-Andrade, E., Cano-Lira, J. F., Wiederhold, N., Pérez-Cantero, A., Guarro, J., & Stchigel, A. M. (2021a). A revision of malbranchea-like fungi from clinical specimens in the United States of America reveals unexpected novelty. *IMA Fungus, 12*, 25. https://doi.org/10.1186/s43008-021-00075-x

Rodríguez-Andrade, E., Stchigel, A. M., & Cano-Lira, J. F. (2021b). New xerophilic species of *Penicillium* from soil. *Journal of Fungi, 7*(2), 126. https://doi.org/10.3390/jof7020126

Rodríguez, K., Stchigel, A. M., Cano, J. F., & Guarro, J. (2004). A new species of *Achaetomium* from Indian soil. *Studies in Mycology, 50*, 77–82. https://doi.org/10.1139/b62-079

Roeun, V., Esther Das, K., Lee, S.-Y., & Jung, H.-Y. (2022). Molecular and morphological characterization of two novel species from soil and beetles (*Dorcus titanus castanicolor*) in Korea. *Mycobiology, 50*(4), 429–438. https://doi.org/10.1080/12298093.2022.2149927

Rombach, M. C., Humber, R. A., & Evans, H. C. (1987). *Metarhizium album*, a fungal pathogen of leaf- and plant-hoppers of rice. *Transactions of the British Mycological Society, 88*(3), 451–459.

Romero, A. I., Carmaran, C. C., & Lorenzo, L. E. (1999). A new species of *Coniochaeta* with a key to the species known in Argentina. *Mycological Research, 103*(6), 689–695. https://doi.org/10.1017/S0953756298007564

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D. L., Darling, A., Höhna, S., . . . Huelsenbeck, J. P. (2012). MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology, 61*(3), 539–542.

Rosas-Medina, M., Maciá-Vicente, J. G., & Piepenbring, M. (2019). Diversity of fungi in soils with different degrees of degradation in Germany and Panama. *Mycobiology, 47*(2), 1–9. https://doi.org/10.1080/12298093.2019.1700658

Rosling, A., Cox, F., Cruz-Martinez, K., Ihrmark, K., Grelet, G. A., Lindahl, B. D., . . . James, T. Y. (2011). Archaeorhizomycetes: Unearthing an ancient class of ubiquitous soil fungi. *Science, 333*(6044), 876–879. https://doi.org/10.1126/science.1206958

Rossman, A. Y., Samuels, G. J., Rogerson, C. T., & Lowen, R. (1999). Genera of Bionectriaceae, Hypocreaceae and Nectriaceae (Hypocreales, Ascomycetes). *Studies in Mycology, 42*, 1–248.

Rossman, A. Y. (1979). *Calonectria* and its type species, *C. daldiniana*, a later synonym of *C. pyrochroa*. *Mycotaxon, 8*(2), 321–328.

Rubio, C., & Lázaro, R. (2023). Patterns in biocrust recovery over time in semiarid southeast Spain. *Frontiers in Microbiology, 14*, 1184065. https://doi.org/10.3389/fmicb.2023.1184065

Ruma, K., Sunil, K., Kini, K. R., & Prakash, H. S. (2015). Genetic diversity and antimicrobial activity of endophytic *Myrothecium* spp. isolated from *Calophyllum apetalum* and *Garcinia morella*. *Molecular Biology Reports, 42*(6), 1533–1543. https://doi.org/10.1007/s11033-015-3884-8

Rusterholz, H., & Baur, B. (2023). Changes in soil fungal diversity and composition along a rural–urban gradient. *Forests, 14*(11), 2226.

Saccardo, P. A. (1880). Fungi Gallici lecti a cl. viris P. Brunaud, Abb. Letendre, A. Malbranche, J. Therry vel editi in *Mycotheca Gallica* C. Roumeguèri (pp. 39–135).

Saccardo, P. A., & Paoletti, G. (1885). Mycetes Malacenses. Funghi della penisola di Malacca raccolti nel 1885 dell'Ab. Benedetto Scortechini. *Atti Accademia delle Scienze Veneto-Trentino-Istriana, 6*, 387–428.

Saccardo, P. A. (1879). Fungi Gallici lecti a cl. viris P. Brunaud, C. C. Gillet et Abb. Letendre. *Michelia, 1*, 500–538.

Saccardo, P. A. (1882). Fungi Gallici lecti a Cl viris Brunaud P, Gillet CC, Letendre Abb, Malbranche A, Therry J. *Libert d Series IV Michelia, 2*, 583–648.

Saccardo, P. A. (1883). *Sylloge Pyrenomycetum, Vol. II*. Sylloge Fungorum (Vol. 2).

Saccardo, P. A. (1911). Notae mycologicae. Series XIII. *Annales Mycologici, 9*, 249–257.

Sakayaroj, J., Phongpaichit, S., & Jones, E. B. G. (2005). Viability and biodiversity of freshwater hyphomycetes in foam at Ton Nga Chang Wildlife Sanctuary, Songkhla, southern Thailand. *Fungal Diversity, 18*, 135–145.

Salar, R. K., & Aneja, K. R. (2007). Thermophilic fungi: Taxonomy and biogeography. *Journal of Agricultural Technology, 3*, 77–107.

Salvatore, M. M., Andolfi, A., & Nicoletti, R. (2020). The thin line between pathogenicity and endophytism: The case of *Lasiodiplodia theobromae*. *Agriculture, 10*(10), 488. https://doi.org/10.3390/agriculture10100488

Salvatore, M. M., Dellagreca, M., Andolfi, A., & Nicoletti, R. (2022). New insights into chemical and biological properties of Funicone-like compounds. *Toxins, 14*(7). https://doi.org/10.3390/toxins14070466

Salvioli, A., & Bonfante, P. (2013). Systems biology and "omics" tools: A cooperation for next-generation mycorrhizal studies. *Plant Science, 203*, 107–114. https://doi.org/10.1016/j.plantsci.2013.01.001

Samerpitak, K., Alfjorden, A., Seyedmousavi, S., Rijs, A. J., Gerrits van den Ende, A. H. G., & de Hoog, G. S. (2019). *Ochroconis globalis* infecting Atlantic salmon (*Salmo salar*), with a review of *Ochroconis* species in cold-blooded animals. *Journal of Fish Diseases, 42*(7), 947–957. https://doi.org/10.1111/jfd.12999

Samerpitak, K., Duarte, A. P. M., Attili-Angelis, D., Pagnocca, F. C., Heinrichs, G., Rijs, A. J., . . . Hoog, G. S. (2015). A new species of the oligotrophic genus *Ochroconis* (Sympoventuriaceae). *Mycological Progress, 14*(1), 1–10. https://doi.org/10.1007/s11557-015-1023-5

Samerpitak, K., Gerrits van den Ende, B. H. G., Stielow, J. B., Menken, S. B. J., & de Hoog, G. S. (2016). Barcoding and species recognition of opportunistic pathogens in *Ochroconis* and *Verruconis*. *Fungal Biology, 120*(3), 219–230. https://doi.org/10.1016/j.funbio.2015.08.010

Samerpitak, K., Van der Linde, E., Choi, H. J., Gerrits Van Den Ende, A. H. G., Machouart, M., Gueidan, C., . . . De Hoog, G. S. (2014). Taxonomy of *Ochroconis*, genus including opportunistic pathogens on humans and animals. *Fungal Diversity, 65*, 89–126. https://doi.org/10.1007/s13225-013-0253-6

Samiksha, & Sanjeev, K. (2021). Molecular taxonomy, diversity, and potential applications of genus *Fusarium*. In A. M. Abdel-Azeem, A. N. Yadav, N. Yadav, & Z. Usmani (Eds.), *Industrially Important Fungi for Sustainable Development* (pp. 278–290). Springer International Publishing.

Samson, R. A. (1974). *Paecilomyces* and some allied hyphomycetes. *Studies in Mycology, 6*, 1–119.

Samson, R. A., & Luiten, B. (1975). *Eleutherascus tuberculatus*, a new heat resistant ascomycete. *Transactions of the British Mycological Society, 64*(2), 338–340.

Samson, R. A., Houbraken, J., & Thrane, U. (2010). *Food and indoor fungi*. CBS KNAW Biodiversity Center.

Samson, R. A., & Mouchacca, J. (1975). Two new soil-borne cleistothecial ascomycetes. *Canadian Journal of Botany, 53*(15), 1634–1639. https://doi.org/10.1139/b75-194

Sánchez, C. (2009). Lignocellulosic residues: Biodegradation and bioconversion by fungi. *Biotechnology Advances, 27*(2), 185–194. https://doi.org/10.1016/j.biotechadv.2008.11.001

Sandoval-Denis, M., Gené, J., Sutton, D. A., Cano-Lira, J. F., De Hoog, G. S., Decock, C. A., . . . Guarro, J. (2016a). Redefining *Microascus, Scopulariopsis* and allied genera. *Persoonia: Molecular Phylogeny and Evolution of Fungi, 36*, 1–36. https://doi.org/10.3767/003158516X688027

Sandoval-Denis, M., Guarro, J., Cano-Lira, J. F., Sutton, D. A., Wiederhold, N. P., De Hoog, G. S., . . . Gené, J. (2016b). Phylogeny and taxonomic revision of Microascaceae with emphasis on synnematous fungi. *Studies in Mycology, 83*, 193–233. https://doi.org/10.1016/j.simyco.2016.07.002

Sandoval-Denis, M., Lombard, L., & Crous, P. W. (2019). Back to the roots: A reappraisal of *Neocosmospora*. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 43*, 90–185.

Sandoval-Denis, M., Sutton, D. A., Cano-Lira, J. F., Gené, J., Fothergill, A. W., Wiederhold, N. P., . . . Guarro, J. (2014). Phylogeny of the clinically relevant species of the emerging fungus *Trichoderma* and their antifungal susceptibilities. In D. W. Warnock (Ed.), *Journal of Clinical Microbiology, 52*(6), 2112–2125. https://doi.org/10.1128/JCM.00429-14

Sanjuan, T., Tabima, J., Restrepo, S., Læssøe, T., Spatafora, J. W., & Franco-Molano, A. E. (2014). Entomopathogens of Amazonian stick insects and locusts are members of the *Beauveria* species complex (Cordyceps sensu stricto). *Mycologia, 106*(2), 260–275.

Santos, A. R. O., Barros, K. O., Batista, T. M., Souza, G. F., Alvarenga, F. B., Abegg, M. A., . . . Rosa, C. A. (2023). *Saccharomycopsis praedatoria* sp. nov., a predacious yeast isolated from soil and rotten wood in an Amazonian rainforest biome. *International Journal of Systematic and Evolutionary Microbiology, 73*(1), 006125. https://doi.org/10.1099/ijsem.0.006125

Sato, H., Tanabe, A. S., & Toju, H. (2015). Contrasting diversity and host association of ectomycorrhizal basidiomycetes versus root-associated ascomycetes in a dipterocarp rainforest. *PLoS ONE*, *10*(4), e0125550.

Santos, J. A. D., Meyer, E., & Sette, L. D. (2020). Fungal community in Antarctic soil along the retreating Collins Glacier (Fildes Peninsula, King George Island). *Microorganisms, 8*(8), 1145. https://doi.org/10.3390/microorganisms8081145

Sarrocco, S., Diquattro, S., Baroncelli, R., Cimmino, A., Evidente, A., Vannacci, G., . . . Doveri, F. (2015). A polyphasic contribution to the knowledge of *Auxarthron* (Onygenaceae). *Mycological Progress*, *14*, 1–20. https://doi.org/10.1007/s11557-015-1128-x

Sastry, M. M. L., & Hedge, R. K. (1988). Survival of *Phytophthora palmivora*. *Indian Phytopathology, 41*, 118–121.

Satyanarayana, T., Deshmukh, S. K., & Deshpande, M. V. (Eds.). (2019). *Advancing frontiers in mycology and mycotechnology: Basic and applied aspects of fungi*. Springer Nature. https://doi.org/10.1007/978-981-13-9349-5_3

Scattolin, L., & Montecchio, L. (2007). First report of damping-off of common oak plantlets caused by *Cylindrocladiella parva* in Italy. *Plant Disease, 91*, 771.

Schiönning, H. (1903). Nouveau genre de la famille des Saccharomycetès. *Comptes Rendus des Travaux du Laboratoire Carlsberg, 6*, 101–125.

Schlatter, D. C., Kahl, K., Carlson, B., Huggins, D. R., & Paulitz, T. (2018). Fungal community composition and diversity vary with soil depth and landscape position in a no-till wheat-based cropping system. *FEMS Microbiology Ecology, 94*, fiy098. https://doi.org/10.1093/femsec/fiy098

Schmidt, P. A., Bálint, M., Greshake, B., Bandow, C., Römbke, J., & Schmitt, I. (2013). Illumina metabarcoding of a soil fungal community. *Soil Biology and Biochemistry, 65*, 128–132. https://doi.org/10.1016/j.soilbio.2013.05.014

Schneider, R., & Gerlach, W. (1973). *Pyrenochaeta lycopersici*. Commonwealth Mycological Institute Description of Pathogenic Fungi and Bacteria, 398.

Schoch, C. L., Crous, P. W., Groenewald, J. Z., Boehm, E. W. A., Burgess, T. I., De Gruyter, J., . . . Spatafora, J. W. (2009). A class-wide phylogenetic assessment of Dothideomycetes. *Studies in Mycology, 64*, 1–15. https://doi.org/10.3114/sim.2009.64.01

Schoch, C. L., Seifert, K. A., Huhndorf, S., Robert, V., Spouge, J. L., Levesque, C. A., . . . White, M. M. (2012). Fungal Barcoding Consortium. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *Proceedings of the National Academy of Sciences, 109*, 6241–6246. https://doi.org/10.1073/pnas.1117018109

Schrank, F. P. (1786). *Baierische Flora* (Vol. 1). München: Joseph Lentner.

Schroers, H.-J. (2001). A monograph of *Bionectria* (Ascomycota, Hypocreales, Bionectriaceae) and its *Clonostachys* anamorphs. *Studies in Mycology, 46*, 1–214.

Schroers, H.-J., Samuels, G. J., Seifert, K. A., & Gams, W. (1999). Classification of the mycoparasite *Gliocladium roseum* in *Clonostachys* as *C. rosea*, its relationship to *Bionectria ochroleuca*, and notes on other *Gliocladium*-like fungi. *Mycologia, 91*, 365–385. https://doi.org/10.1080/00275514.1999.12061028

Schroeter, J. (1893). Die Pilze Schlesiens. *Cohn Kryptogamenflora Schlesiens, 3*, 210–213.

Schubert, K., & Braun, U. (2005). Taxonomic revision of the genus *Cladosporium* s.l. 4. Species reallocated to *Asperisporium*, *Dischloridium*, *Fusicladium*, *Passalora*, *Pseudoasperisporium* and *Stenella*. *Fungal Diversity, 20*, 187–208.

Schubert, K., Ritschel, A., & Braun, U. (2003). A monograph of *Fusicladium* s. lat. (Hyphomycetes). *Schlechtendalia, 9*, 1–132.

Seephueak, P., Preecha, C., & Seephueak, W. (2019). The diversity of fungi associated with rice (*Oryza sativa* L.) from Nakhon Si Thammarat, Thailand. *International Journal of Agricultural Technology, 15*, 485–500.

Seifert, K. A. (1985). A monograph of *Stilbella* and some allied Hyphomycetes. *Studies in Mycology, 27*, 1–235.

Seifert, K. A., Morgan–Jones, G., Gams, W., & Kendrick, B. (2011). *The genera of hyphomycetes*. CBS–KNAW Fungal Biodiversity Centre.

Seifert, K. A., Nickerson, N. L., Corlett, M., Jackson, E. D., Louis-Seize, G., & Davies, R. J. (2004). *Devriesia*, a new hyphomycete genus to accommodate heat-resistant, cladosporium-like fungi. *Canadian Journal of Botany, 82*, 914–926. https://doi.org/10.1139/B04-070

Selbmann, L., Stoppiello, G. A., Onofri, S., & Stajich, J. E. (2021). Culture-dependent and amplicon sequencing approaches reveal diversity and distribution of black fungi in Antarctic cryptoendolithic communities. *Journal of Fungi, 7*, 213.

Semenov, M. V. (2021). Metabarcoding and metagenomics in soil ecology research: Achievements, challenges, and opportunities. *Biology Bulletin Reviews, 11*, 40–53. https://doi.org/10.1134/S2079086421010084

Sena, H. H., Sanches, M. A., Rocha, D. F. S., & Segundo, F. (2018). Production of bio-surfactants by soil fungi isolated from the Amazon forest. *International Journal of Microbiology, 2018*. https://doi.org/10.1155/2018/5684261

Senanayake, I. (2020). New geographical records of *Neopestalotiopsis* and *Pestalotiopsis* species in Guangdong province, China. *Asian Journal of Mycology, 3*, 512–533. https://doi.org/10.5943/ajom/3/1/19

Senanayake, I. C., Rathnayaka, A. R., Marasinghe, D. S., Calabon, M. S., Gentekaki, E., Lee, H. B., . . . Xiang, M. M. (2020). Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. *Mycosphere, 11*, 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Senanayake, I. C., Rossi, W., Leonardi, M., Weir, A., McHugh, M., Rajeshkumar, K. C., . . . Song, J. (2023). Fungal diversity notes 1611–1716: Taxonomic and phylogenetic contributions on fungal genera and species emphasis in south China. *Fungal Diversity, 122*, 161–403.

Senanayake, I. C., Pem, D., Rathnayaka, A. R., Wijesinghe, S. N., Tibpromma, S., Wanasinghe, D. N., . . . Xie, N. (2022). Predicting global numbers of teleomorphic ascomycetes. *Fungal Diversity*, 1–42. https://doi.org/10.1007/s13225-022-00504-1

Shao, Q.-Y., Qi, Y.-H., Wang, J., & Yang, Y.-M. (2022a). *Acrocalymma guizhouense* sp. nov. (Acrocalymmaceae, Dothideomycetes) from soil in China. *Phytotaxa, 558*, 229–236. https://doi.org/10.11646/phytotaxa.558.2.6

Shao, Q.-Y., Ren, Y.-L., Chen, W.-H., & Liang, J.-D. (2022b). *Verruconis guizhouensis* sp. nov. (Sympoventuriaceae, Venturiales) from soil in China. *Phytotaxa, 572*, 259–267. https://doi.org/10.11646/phytotaxa.572.3.4

Sharma, R., Gräser, Y., & Singh, S. K. (2013). *Auxarthronopsis*, a new genus of Onygenales isolated from the vicinity of Bandhavgarh National Park, India. *IMA Fungus, 4*, 89–102. https://doi.org/10.5598/imafungus.2013.04.01.09

Sharma, R., Sharma, R., & Crous, P. W. (2015). *Matsushimamyces*, a new genus of keratinophilic fungi from soil in central India. *IMA Fungus, 6*, 337–343. https://doi.org/10.5598/imafungus.2015.06.02.05

Sharma, R., & Shouche, Y. S. (2020). Diversity of Onygenalean fungi in keratin-rich habitats of Maharashtra (India) and description of three novel taxa. *Mycopathologia, 185*, 67–85. https://doi.org/10.1007/s11046-019-00346-7

Sharma, R., & Singh, S. K. (2013). A new species of *Gymnoascus* with verruculose ascospores. *IMA Fungus, 4*, 177–186. https://doi.org/10.5598/imafungus.2013.04.02.03

Sharma, R. R. S., Rajak, R. C., & Pandey, A. K. (2004). *Heterocephalum aurantiacum*: Isolation and distribution in Indian soils. *Journal of Mycology and Plant Pathology, 34*, 69–72.

Sharma, L., Oliveira, I., Torres, L., & Marques, G. (2018). Entomopathogenic fungi in Portuguese vineyards soils: Suggesting a 'Galleria-Tenebrio-bait method' as bait-insects *Galleria* and *Tenebrio* significantly underestimate the respective recoveries of *Metarhizium* (robertsii) and *Beauveria* (bassiana). *MycoKeys, 38*, 1. https://doi.org/10.3897/mycokeys.38.26790

Sharma, B., Nawange, S., Pandey, A., & Singh, S. M. (1997). Examination of soils from residential garbage in Betul, India, for fungi by the keratin baiting technique. *Zentralblatt für Bakteriologie*, 286, 139–145.

Shear, C. L., & Dodge, B. O. (1927). Life histories and heterothallism of the red breadmold fungi of the *Monilia sitophila* group. *Journal of Agricultural Research, 34*, 1019–1042.

Shearer, C. A., & Crane, J. L. (1971). Fungi of the Chesapeake Bay and its tributaries. I. Patuxent River. *Mycologia, 63*, 237–260.

Shearer, C. A., Crane, J. L., & Reddy, K. R. (1990). Studies in *Leptosphaeria*. Lectotypification of *Sphaeria doliolum*. *Mycologia, 82*, 496–500. https://doi.org/10.1080/00275514.1990.12025913

Shen, M., Zhang, J. Q., Zhao, L. L., & Groenewald, J. Z. (2020). Venturiales. *Studies in Mycology, 96*, 185–308. https://doi.org/10.1016/j.simyco.2020.03.001

Shen, M., Zhang, J. Q., Zhao, L. L., Groenewald, J. Z., Crous, P. W., & Zhang, Y. (2020). Venturiales. *Studies in Mycology, 96*, 185–308. https://doi.org/10.1016/j.simyco.2020.03.001

Shukia, P., Shukla, C. B., Kango, N., & Shukla, A. (2003). Isolation and characterization of a dermatophyte, *Microsporium gypseum* from poultry farm soils of Rewa (Madhya Pradesh), India. *Pakistan Journal of Biological Sciences, 6*, 622–625.

Shi, C., Chen, J., Ge, Q., & Sun, J. (2021). Draft genomes and comparative analysis of seven mangrove rhizosphere-associated fungi isolated from *Kandelia obovata* and *Acanthus ilicifolius*. *Frontiers in Fungal Biology, 2*, 626904. https://doi.org/10.3389/ffunb.2021.626904

Shi, L., Dossa, G. G., Paudel, E., Zang, H., Xu, J., & Harrison, R. D. (2019). Changes in fungal communities across a forest disturbance gradient. *Applied and Environmental Microbiology, 85*, e00080-19. https://doi.org/10.1128/AEM.00080-19

Shi, T., Wang, H., Li, Y. J., Wang, Y. F., Pan, Q., Wang, B., & Shang, E. L. (2023). Genus *Acrostalagmus*: A prolific producer of natural products. *Biomolecules, 13*, 1191. https://doi.org/10.3390/biom13081191

Shi, Y., Pan, Y., Xiang, L., Zhu, Z., Fu, W., Hao, G., . . . Han, D. (2022). Assembly of rhizosphere microbial communities in *Artemisia annua*: Recruitment of plant growth-promoting microorganisms and inter-kingdom interactions between bacteria and fungi. *Plant and Soil, 470*, 127–139. https://doi.org/10.1007/s11104-021-04829-9

Shirouzu, T., Hirose, D., Tokumasu, S., To-anun, C., & Maekawa, N. (2010). Host affinity and phylogenetic position of a new anamorphic fungus *Beltraniella botryospora* from living and fallen leaves of evergreen oaks. *Fungal Diversity, 43*, 85–92.

Shoemaker, R. A. (1959). Nomenclature of *Drechslera* and *Bipolaris*, grass parasites segregated from "*Helminthosporium*." *Canadian Journal of Botany, 37*, 879–887. https://doi.org/10.1139/b59-073

Shoemaker, R. A., Babcock, C. E., & Irwin, J. A. G. (1991). *Massarina walkeri* n.sp., the teleomorph of *Acrocalymma medicaginis* from *Medicago sativa* contrasted with *Leptosphaeria pratensis, L. weimeri* n.sp., and *L. viridella*. *Canadian Journal of Botany, 69*, 569–573. https://doi.org/10.1139/b91-077

Shrestha, B., Sung, G. H., & Sung, J. M. (2017). Current nomenclatural changes in *Cordyceps* sensu lato and its multidisciplinary impacts. *Mycology, 8*, 293–302. https://doi.org/10.1080/21501203.2017.1386242

Shukla, P. K., Jain, M., Lal, B., Agrawal, P. K., & Srivastava, O. P. (1989). Mycotic keratitis caused by *Phaeotrichoconis crotalariae*. New Report. *Mycoses, 32*, 230–232. https://doi.org/10.1111/j.1439-0507.1989.tb02238.x

Si, H. L., Su, Y. M., Zheng, X. X., Ding, M. Y., Bose, T., & Chang, R. L. (2021). Phylogenetic and morphological analyses of *Coniochaeta* isolates recovered from Inner Mongolia and Yunnan revealed three new endolichenic fungal species. *MycoKeys, 83*, 105–121. https://doi.org/10.3897/mycokeys.83.71140

Sigler, L., & Carmichael, J. W. (1976). Taxonomy of *Malbranchea* and some other hyphomycetes with arthroconidia. *Mycotaxon, 4*, 349–488.

Sigler, L., Abbott, S. P., & Frisvad, J. (1996). Rubratoxin mycotoxicosis by *Penicillium crateriforme* following ingestion of home-made rhubarb wine. In *96th General Meeting of the American Society for Microbiology*, New Orleans.

Sigler, L., Gauer, P. K., Lichtwardt, R. W., & Carmichael, J. W. (1979). *Renispora favissima*, a new gymnoascaceous fungus with tuberculate conidia. *Mycotaxon, 10*, 133–141.

Sigler, L., Sutton, D. A., Gibas, C. F. C., Summerbell, R. C., Noel, R. K., & Iwen, P. C. (2010). *Phialosimplex*, a new anamorphic genus associated with infections in dogs and having phylogenetic affinity to the Trichocomaceae. *Medical Mycology, 48*, 335–345. https://doi.org/10.3109/13693780903225805

de Silva, N. I., Hyde, K. D., Lumyong, S., & Phillips, A. J. L. (2022). Morphology, phylogeny, host association and geography of fungi associated with plants of Annonaceae, Apocynaceae and Magnoliaceae. *Mycosphere, 13*, 955–1076. https://doi.org/10.5943/mycosphere/13/1/12

Silva, J., Freixo, R., Gibbs, P., & Teixeira, P. (2011). Spray-drying for the production of dried cultures. *International Journal of Dairy Technology, 64*, 321–335.

Silvera-Simón, C., Gené, J., Cano, J., & Guarro, J. (2008). *Wardomycopsis litoralis*, a new soil-borne hyphomycete from Spain. *Mycotaxon, 105*, 195–202.

Simon, A., Bindschedler, S., Job, D., Wick, L. Y., Filippidou, S., Kooli, W. M., . . . Junier, P. (2015). Exploiting the fungal highway: Development of a novel tool for the in situ isolation of bacteria migrating along fungal mycelium. *FEMS Microbiology Ecology, 91*, fiv116. https://doi.org/10.1093/femsec/fiv116

Simmons, R. W. (2004). Review of the current contamination status of potentially toxic elements (PTEs) in the Greater Mekong sub-region. *Mercury, 31*, 32.

Simpanya, M. F., & Baxter, M. (1996). Isolation of fungi from soil using the keratin-baiting technique. *Mycopathologia, 136*, 85–89. https://doi.org/10.1007/BF00437500

Sivanesan, A. (1987). Graminicolous species of *Bipolaris*, *Curvularia*, *Drechslera*, *Exserohilum* and their teleomorphs. *Mycological Research, 158*, 1–261.

Sivanesan, A. (1978). *The taxonomy and pathology of Venturia species*. Lubrecht & Cramer Ltd.

Sivasithamparam, K. (1974). *Spegazzinia parkeri* sp. nov. *Transactions of the British Mycological Society, 62*, 427–429. https://doi.org/10.1016/S0007-1536(74)80056-2

Smith, E. F. (1899). Wilt disease of cotton, watermelon and cowpea (*Neocosmospora* nov. gen.). *Bulletin, Division of Vegetable Physiology and Pathology, US Department of Agriculture, Washington, DC, 17*, 1–73.

Smith, M. T. (1986). *Zygoascus hellenicus* gen. nov., sp. nov., the teleomorph of *Candida hellenica* (=*C. inositophila = C. steatolytica*). *Antonie van Leeuwenhoek, 52*, 25–37.

Smith, M. T., de Hoog, G. S., Malloch, D., & Kurtzman, C. P. (2011). *Trichomonascus* H.S. Jackson emend. Kurtzman & Robnett (2007). In *The Yeasts* (pp. 875–881). Elsevier.

Smolińska, U., & Kowalska, B. (2018). Biological control of the soil-borne fungal pathogen *Sclerotinia sclerotiorum* – a review. *Journal of Plant Pathology, 100*, 1–12. https://doi.org/10.1007/s42161-018-0023-0

Solé, M., Cano, J., Pitarch, L. B., Stchigel, A. M., & Guarro, J. (2002). Molecular phylogeny of *Gymnoascus* and related genera. *Studies in Mycology, 47*, 141–152.

Song, F., Wu, S. H., Zhai, Y. Z., Xuan, Q. C., & Wang, T. (2014). Secondary metabolites from the genus *Xylaria* and their bioactivities. *Chemistry & Biodiversity, 11*, 673–694.

Song, J. Y., Tian, Q., & Liu, J. (2022). *Pseudorobillarda sichuanensis* sp. nov. associated with *Bambusa* sp. from Sichuan province, China. *Phytotaxa, 561*, 256–266. https://doi.org/10.11646/phytotaxa.561.3.3

Song, Y., Menezes da Silva, N., Vicente, V. A., Quan, Y., Teixeira, M., Gong, J., . . . Li, R. (2021). Comparative genomics of opportunistic *Phialophora* species involved in divergent disease types. *Mycoses, 64*, 555–568. https://doi.org/10.1111/myc.13244

Sopp, O. J. (1912). Monographie der Pilzgruppe *Penicillium* mit besonderer Berücksichtigung der in Norwegen gefundenen Arten. *Skrift Vidensk-Selsk Christiana, 11*, 1–208.

Sota, T., Kagata, H., Ando, Y., Utsumi, S., Osono, T., Sota, T., . . . Osono, T. (2014). Metagenomic approach yields insights into fungal diversity and functioning. In *Species diversity and community structure* (pp. 1–23). Springer, Tokyo. https://doi.org/10.1007/978-4-431-54261-2_1

Species Fungorum. (2023). *Species Fungorum database*. Retrived January 16, 2023, from https://wwwspeciesfungorumorg/Names/Namesasp

Species Fungorum. (2025). *Species Fungorum database*. Retrived February 14, 2025, from http://www.speciesfungorum.org

Species Fungorum. (2024). *Species Fungorum database.* Retrived March 4, 2024, from http://www.speciesfungorum.org.

Species Fungorum. (2021). *Species Fungorum database.* Retrived August 12, 2021, from https://wwwspeciesfungorumorg/Names/Namesasp

Spegazzini, C. L. (1919). Fungi Costaricenses nonnulli. *Bol. Acad. Nac. Cienc. Córdoba*.

Spychała, K., Kłosińska, K., Salwińska, W., & Ogórek, R. (2024). Diversity of soil-borne fungi isolated from places frequently visited by people in the city of Wrocław (Poland). *Applied Sciences, 14*, 2782. https://doi.org/10.3390/app14072782

Sreeja, P., Rani, R. O. P., & Chellappan, M. (2023). Characterization of insecticidal metabolite oosporein in *Lecanicillium saksenae* (Kushwaha) Kurihara and Sukarno, a geographically distinct isolate from Kerala, India. *Toxicon, 230*, 107176. https://doi.org/10.1016/j.toxicon.2023.107176

Srinath, J., Bagyaraj, D. J., & Satyanarayana, B. N. (2003). Enhanced growth and nutrition of micropropagated *Ficus benjamina* to *Glomus mosseae* co-inoculated with *Trichoderma harzianum* and *Bacillus coagulans*. *World Journal of Microbiology and Biotechnology, 19*, 69–72. https://doi.org/10.1023/a:1022569702845

Stamatakis, A. (2014). RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics, 30,* 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Stamatakis, A., Hoover, P., & Rougemont, J. (2008). A rapid bootstrap algorithm for the RAxML web servers. *Systematic Biology, 57*, 758–771.

Stefani, F. O., Bell, T. H., Marchand, C., De La Providencia, I. E., El Yassimi, A., St-Arnaud, M., . . . Hijri, M. (2015). Culture-dependent and -independent methods capture different microbial community fractions in hydrocarbon-contaminated soils. *PLoS One, 10,* e0128272. https://doi.org/10.1371/journal.pone.0128272

Stchigel, A. M., Guarro, J. (1998). A new species of *Ascotricha* from Spanish soil. *Mycological Research, 102*, 510–512. https://doi.org/10.1017/S0953756297005297

Stchigel, A. M., Guarro, J., & Mac Cormack, W. (2003). *Apiosordaria antarctica* and *Thielavia antarctica*, two new Ascomycetes from Antarctica. *Mycologia, 95,* 1218. https://doi.org/10.2307/3761922

Stchigel, A. M., Guarro, J., & Figueras, M. J. (1997). A new species of *Melanospora* from India. *Mycological Research, 101*, 446–448. https://doi.org/10.1017/S0953756296002948

Stchigel, A. M., Sutton, D. A., Cano-Lira, J. F., Wiederhold, N., & Guarro, J. (2017). New species *Spiromastigoides albida* from a lung biopsy. *Mycopathologia, 182*, 967–978. https://doi.org/10.1007/s11046-017-0179-8

Steenwyk, J. L., Balamurugan, C., Raja, H. A., Gonçalves, C., Li, N., Martin, F., … Rokas, A. (2024). Phylogenomics reveals extensive misidentification of fungal strains from the genus *Aspergillus*. In A. Alanio (Ed.), *Microbiology Spectrum, 12*. https://doi.org/10.1128/spectrum.03980-23

Steinrucken, T. V., Vitelli, J. S., Holdom, D. G., & Tan, Y. P. (2022). The diversity of microfungi associated with grasses in the *Sporobolus indicus* complex in Queensland, Australia. *Frontiers in Fungal Biology, 3*. https://doi.org/10.3389/ffunb.2022.956837

Stockdale, P. M. (1961). *Nannizzia incurvata* gen. nov., sp. nov., a perfect state of *Microsporum gypseum* (Bodin) Guiart et Grigorakis. *Sabouraudia, 1*, 41–48.

Stolk, A. C. (1955). *Emericellopsis minima* sp. nov. and *Westerdykella ornata* gen. nov., sp. nov. *Transactions of the British Mycological Society, 38*, 419-IN2.

Stolk, A. C., & Samson, R. A. (1971). Studies on *Talaromyces* and related genera I. *Hamigera* gen. nov. and *Byssochlamys*. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 6*(3), 341–357.

Su, L., Zhu, H., Niu, Y., Guo, Y., Du, X., Guo, J., … Qin, C. (2020). Phylogeny and taxonomic revision of *Kernia* and *Acaulium*. *Scientific Reports, 10*, 10302. https://doi.org/10.1038/s41598-020-67347-1

Su, P., Chen, Y., Syed, A., Bahkali, A. H., & Maharachchikumbura, S. S. N. (2023). Taxonomic novelty in Sichuan province, China: *Veronaea polyconidia* sp. nov. (Herpotrichiellaceae), a new addition to hyphomycetous fungi. *Phytotaxa, 632*, 118–130. https://doi.org/10.11646/phytotaxa.632.2.2

Subrahmanyam, A. (1981). *Thielavia achromatica* A. Subrahm. sp. nov. *Acta Mycologica, 17*.

Subramanian, C. V. (1956a). *Phaeotrichoconis*, a new genus of Dematiaceae. *Proceedings of the Indian Academy of Science, Section B, 44*, 1–2.

Subramanian, C. V. (1952). Fungi Imperfecti from Madras — iii. *Proceedings of The Indian Academy of Sciences – Section B, 36*, 223–228.

Subramanian, C. V. (1956b). Three new hyphomycetes. *Journal of Indian Botanical Society, 33*, 28–35.

Subramanian, C. V. (1962). A classification of the Hyphomycetes. *Current Science, 31*, 409–411.

Subramanian, C. V. (1971). *Hyphomycetes: An account of Indian species, except Cercospora*. Indian Council of Agricultural Research.

Subramanian, C. V. (1977). Revisions of Hyphomycetes I. *Kavaka, 5*, 93–98.

Subramanian, K. S. (1958). Bahusakala, a new genus of lichen. *Journal of the Indian Botanical Society, 37*.

Sudhakar, N., Shanmugam, H., Kumaran, S., Coelho, A., Nunes, R., & Carvalho, I. S. (2018). Omics approaches in fungal biotechnology: Industrial and medical point of view. In *Omics Technologies and Bio-engineering* (pp. 53–70). Academic Press. https://doi.org/10.1016/B978-0-12-815870-8.00004-8

Sue, P. K., Gurda, G. T., Lee, R., Watkins, T., Green, R., Memon, W., . . . Zhang, S. X. (2014). First report of *Westerdykella dispersa* as a cause of an angioinvasive fungal infection in a neutropenic host. In D. W. Warnock (Ed.), *Journal of Clinical Microbiology, 52*, 4407–4411. https://doi.org/10.1128/JCM.02012-14

Suetrong, S., Preedanon, S., Kobmoo, N., Srihom, C., Somrithipol, S., Saengkaewsuk, S., . . . Boonyuen, N. (2023). Unravelling the hidden diversity of cave mycobiota in Thailand's Satun Geopark. *Scientific Reports, 13*, 19162. https://doi.org/10.1038/s41598-023-43316-2

Summerbell, R. C., Gueidan, C., Guarro, J., Eskalen, A., Crous, P. W., Gupta, A. K., . . . Scott, J. A. (2018). The protean *Acremonium* A. sclerotigenum/egyptiacum: Revision, food contaminant, and human disease. *Microorganisms, 68*, 139–162.

Summerbell, R. C., Gueidan, C., Schroers, H. J., De Hoog, G. S., Starink, M., Rosete, Y. A., . . . Scott, J. A. (2011). Acremonium phylogenetic overview and revision of *Gliomastix*, *Sarocladium*, and *Trichothecium*. *Studies in Mycology, 68*, 139–162. https://doi.org/10.3114/sim.2011.68.06

Sun, J. Z., Liu, X. Z., McKenzie, E. H. C., Jeewon, R., Liu, J. K., Zhang, X. L., . . . Hyde, K. D. (2019). Fungicolous fungi: Terminology, diversity, distribution, evolution, and species checklist. *Fungal Diversity, 95*, 337–430.

Sun, B., Zhou, Y., & Chen, A. J. (2020). Two new *Microascus* species with spinous conidia isolated from pig farm soils in China. *Mycoscience, 61*, 190–196. https://doi.org/10.1016/j.myc.2020.03.003

Sundaram, B. M. (1977). Fungal flora of rice field soils. In *Proceedings of the Indian Academy of Sciences-Section B* (Vol. 85, pp. 90–99). Springer India. https://doi.org/10.1007/BF03050906

Sung, G. H., Hywel-Jones, N. L., Sung, J. M., Luangsa-Ard, J. J., Shrestha, B., & Spatafora, J. W. (2007). Phylogenetic classification of *Cordyceps* and the clavicipitaceous fungi. *Studies in Mycology, 57*, 5–59. https://doi.org/10.3114/sim.2007.57.01

Sur, B., & Ghosh, G. R. (1980). Keratinophilic fungi from Orissa, India I: Isolation from soils. *Medical Mycology, 18*, 269–274. https://doi.org/10.1080/00362178085380461

Sutton, B. C. (1980). *The Coelomycetes: Fungi imperfecti with pycnidia, acervuli and stromata*. Commonwealth Mycological Institute.

Sutton, B. C., & Cole, G. T. (1983). *Thozetella* (Hyphomycetes): An exercise in diversity. *Transactions of the British Mycological Society, 81*, 97–107.

Sutton, D. A., Rinaldi, M. G., & Sanche, S. E. (2009). "Dematiaceous fungi" in *Clinical Mycology* (2nd ed.). In E. J. Anaissie, M. R. McGinnis, & M. A. Pfaller (Eds.). Churchill Livingstone.

Sutton, D. A., Marín, Y., Thompson, E. H., Wickes, B. L., Fu, J., García, D., . . . Guarro, J. (2013). Isolation and characterization of a new fungal genus and species, *Aphanoascella galapagosensis*, from carapace keratitis of a Galapagos tortoise (*Chelonoidis nigra microphyes*). *Medical Mycology, 51*, 113–120. https://doi.org/10.3109/13693786.2012.701767

Sydow, H., & Sydow, P. (1904). *Phaeodothis*. *Annales Mycologici, 2*, 166.

Sydow, H. (1924). Sydow, Mycotheca Germanica. Fasc. XLII–XLV (No. 2051–2250). *Annales Mycologici, 22*, 257–268.

Taberlet, P., Coissac, E., Hajibabaei, M., & Rieseberg, L. H. (2012). Environmental DNA. *Molecular Ecology, 21*, 1789–1793. https://doi.org/10.1111/j.1365-294X.2012.05542.x

Tadych, M., Bergen, M., Johnson, J. C., Polashock, J., & Vorsa, N. (2012). Endophytic and pathogenic fungi of developing cranberry ovaries from flower to mature fruit: Diversity and succession. *Fungal Diversity, 54*, 101–116. https://doi.org/10.1007/s13225-012-0160-2

Tagele, S. B., Nguyen, T. T., Kim, S. W., Adhikari, M., Gurung, S. K., Lee, H. G., . . . Lee, Y. S. (2019). A new record of *Trichocladium griseum* in Korea: Morphological and molecular characterization. *The Korean Journal of Mycology, 47*, 105–112.

Takashio, M., & Vanbreuseghem, R. (1971). Production of ascospores by *Piedraia hortai* in vitro. *Mycologia, 63*, 612–618. https://doi.org/10.1080/00275514.1971.12019140

Tan, Y. P., & Steinrucken, T. V. (2024). *Index of Australian Fungi*. *Index of Australian Fungi*, *36*, 20.

Tan, Y. P., Crous, P. W., & Shivas, R. G. (2018). Cryptic species of *Curvularia* in the culture collection of the Queensland Plant Pathology Herbarium. *MycoKeys, 35*, 1–25. https://doi.org/10.3897/mycokeys.35.25665

Tan, Y. P., Bishop-Hurley, S. L., Shivas, R. G., Cowan, D. A., Maggs-Kölling, G., Maharachchikumbura, S. S., . . . Marqués-Gálvez, J. E. (2022). Fungal planet description sheets: 1436–1477. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 49*, 261–350. https://doi.org/10.3767/persoonia.2022.49.08

Tan, Y. P., Crous, P. W., & Shivas, R. G. (2016). Eight novel *Bipolaris* species identified from John L. Alcorn's collections at the Queensland Plant Pathology Herbarium (BRIP). *Mycological Progress, 15*, 1203–1214. https://doi.org/10.1007/s11557-016-1240-6

Tan, Y. P., Madrid, H., Crous, P. W., & Shivas, R. G. (2014). *Johnalcornia* gen. et comb. nov., and nine new combinations in *Curvularia* based on molecular phylogenetic analysis. *Australasian Plant Pathology, 43*, 589–603. https://doi.org/10.1007/s13313-014-0315-6

Tanaka, K., Hirayama, K., Yonezawa, H., Hatakeyama, S., Harada, Y., Sano, T., . . . Hosoya, T. (2009). Molecular taxonomy of bambusicolous fungi: Tetraplosphaeriaceae, a new pleosporalean family with Tetraploa-like anamorphs. *Studies in Mycology, 64*, 175–209. https://doi.org/10.3114/sim.2009.64.10

Tanaka, K., Hirayama, K., Yonezawa, H., Sato, G., Toriyabe, A., Kudo, H., . . . Hosoya, T. (2015). Revision of the Massarineae (Pleosporales, Dothideomycetes). *Studies in Mycology, 82*, 75–136. https://doi.org/10.1016/j.simyco.2015.10.002

Tang, J., Zhuang, K., Ran, X., Dai, Y., & Ran, Y. (2017). Chromoblastomycosis caused by *Cladophialophora carrionii*. *Indian Journal of Dermatology, Venereology and Leprology, 93*, 495–506.

Tangthirasunun, N., Silar, P., Bhat, D. J., Chukeatirote, E., Wijayawardene, D. N., Maharachchikumbura, S. S., . . . Hyde, K. D. (2014). Morphology and phylogeny of *Pseudorobillarda eucalypti* sp. nov., from Thailand. *Phytotaxa, 176*, 251–259. https://doi.org/10.11646/phytotaxa.176.1.24

Tassi, F. (1900). *Bartalinia Fl. Tassi*: Nuovo genere di Sphaeropsidaceae. *Bollettino del Laboratorio di Orto Botanico della Regia Università di Siena, 3*, 3–5.

Taylor, D. L., & Sinsabaugh, R. L. (2015). The soil fungi: Occurrence, phylogeny, and ecology. In *Soil Microbiology, Ecology, and Biochemistry* (4th ed., pp. 77–109).

Taylor, E. L. S., Resende-Stoianoff, M. A., & Ferreira, R. L. (2013). Mycological study for a management plan of a Neotropical show cave (Brazil). *International Journal of Speleology, 42*, 267–277.

Taylor, D. L., & Sinsabaugh, R. L. (2014). The soil fungi: Occurrence, phylogeny, and ecology. In E. A. Paul (Ed.), *Soil Microbiology, Ecology, and Biochemistry* (4th ed., p. 77). Academic Press.

Tedersoo, L., Anslan, S., Bahram, M., Kõljalg, U., & Abarenkov, K. (2020). Identifying the "unidentified" fungi: A global-scale long-read third-generation sequencing approach. *Fungal Diversity, 103*, 273–293. https://doi.org/10.1007/s13225-020-00456-4

Tedersoo, L., Bahram, M., Põlme, S., Kõljalg, U., Yorou, N. S., Wijesundera, R., . . . Abarenkov, K. (2014). Global diversity and geography of soil fungi. *Science, 346*. https://doi.org/10.1126/science.1256688

Tedersoo, L., Mikryukov, V., Zizka, A., & Bahram, M. (2022). Global patterns in endemicity and vulnerability of soil fungi. *Global Change Biology, 28*, 6696–6710. https://doi.org/10.1111/gcb.16398

Tedersoo, L., Bahram, M., Puusepp, R., Nilsson, R. H., & James, T. Y. (2017). Novel soil-inhabiting clades fill gaps in the fungal tree of life. *Microbiome, 5*, 42. https://doi.org/10.1186/s40168-017-0259-5

Tedersoo, L., Mikryukov, V., Zizka, A., Bahram, M., Hagh-Doust, N., Anslan, S., . . . Abarenkov, K. (2022). Towards understanding diversity, endemicity and global change vulnerability of soil fungi [Preprint]. *bioRxiv*. https://doi.org/10.1101/2022.03.17.484796

Tedersoo, L., Mikryukov, V., Anslan, S., Bahram, M., Khalid, A. N., Corrales, A., . . . Abarenkov, K. (2021). The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. *Fungal Diversity, 111*, 573–588. https://doi.org/10.1007/s13225-021-00493-7

Tennakoon, D. S., Kuo, C.-H., & Hyde, K. D. (2020). Multi-locus phylogeny reveals *Phaeodothis mori* sp. nov. (Didymosphaeriaceae, Pleosporales) from dead leaves of *Morus australis*. *Phytotaxa, 428*, 241–254. https://doi.org/10.11646/phytotaxa.428.3.5

Tennakoon, D. S., Kuo, C.-H., Maharachchikumbura, S. S., Thambugala, K. M., Gentekaki, E., Phillips, A. J., . . . Hyde, K. D. (2021). Taxonomic and phylogenetic contributions to *Celtis formosana*, *Ficus ampelas*, *Ficus septica*, *Macaranga tanarius* and *Morus australis* leaf litter inhabiting microfungi. *Fungal Diversity, 108*, 1–215. https://doi.org/10.1007/s13225-021-00474-w

Tennakoon, D. S., Thambugala, K. M., Silva, N. I. D., & Suwannarach, N. (2022). A taxonomic assessment of novel and remarkable fungal species in Didymosphaeriaceae (Pleosporales, Dothideomycetes) from plant litter. *Frontiers in Microbiology, 13*, 1016285. https://doi.org/10.3389/fmicb.2022.1016285

Thambugala, K. M., Ariyawansa, H. A., Li, Y.-M., & Boonmee, S. (2014). Dothideales. *Fungal Diversity, 68*, 105–158. https://doi.org/10.1007/s13225-014-0303-8

Thamsurakul, S. (1985). *Studies on soil fungi in the eastern part of Thailand*.

Thaxter, R. (1903). New or peculiar North American Hyphomycetes. III. *Botanical Gazette, 35*, 153–159.

Thies, J. E., & Grossman, J. M. (2023). The soil habitat and soil ecology. In *Biological Approaches to Regenerative Soil Systems* (pp. 69–84).

Thirumalachar, M. J., & Mathur, P. N. (1966). *Narasimhella*, a new genus of the Gymnoascaceae. *Sydowia, 19*, 184–186.

Thirumalachar, M. (1954). *Romanoa*, a new genus of soil fungi with antibiotic properties. *Rendiconti - Istituto Superiore di Sanità, 17*, 1323–1329.

Thiyagaraja, V., Piepenbring, M., Hyde, D. K., Wanasinghe, D. N., Davydov, E. A., Dai, D. Q., . . . Zhao, Q. (2024). Orders of Ascomycota. *Mycosphere*. In preparation.

Thompson, L. R., Sanders, J. G., McDonald, D., Amir, A., Ladau, J., Locey, K. J., . . . Knight, R. (2017). A communal catalogue reveals earth's multiscale microbial diversity. *Nature, 551*, 457–463. https://doi.org/10.1038/nature24621

Thongkantha, S., Lumyong, S., McKenzie, E. H. C., & Hyde, K. D. (2008). Fungal saprobes and pathogens occurring on tissues of *Dracaena lourieri* and *Pandanus* spp. in Thailand. *Fungal Diversity, 30*, 149–169.

Thornton, R. H. (1952). The screened immersion plate: A method of isolating soil microorganisms. *Research, 5*, 190–191.

Tibpromma, S., Hyde, K. D., Jeewon, R., & Maharachchikumbura, S. S. N. (2017). Fungal diversity notes 491–602: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity, 83*, 1–261. https://doi.org/10.1007/s13225-017-0378-0

Tivoli, B., & Banniza, S. (2007). Comparison of the epidemiology of Ascochyta blights on grain legumes. *European Journal of Plant Pathology, 119*, 59–76.

Tiwari, D. P. (1976). A new record of *Arxiella terrestris* for Indian soils. *Current Science, 45*, 150.

Tiwari, D. P., Agrawal, P. D., & Sutton, B. C. (1977). *Polyschema variabilis* sp. nov. from Indian soil. *Transactions of the British Mycological Society, 69*, 514–516. https://doi.org/10.1016/S0007-1536(77)80098-3

Tode, H. J. (1790). *Fungi Mecklenburgenses selecti. Fascicle 1. Nova Fungorum Genera Complectens* (pp. i–viii, 1–50).

Tomao, A., Antonio Bonet, J., Castaño, C., & de-Miguel, S. (2020). How does forest management affect fungal diversity and community composition? Current knowledge and future perspectives for the conservation of forest fungi. *Forest Ecology and Management, 457*. https://doi.org/10.1016/j.foreco.2019.117678

Torda, A. J., & Jones, P. D. (1997). Necrotizing cutaneous infection caused by *Curvularia brachyspora* in an immunocompetent host. *Australasian Journal of Dermatology, 38*, 85–87. https://doi.org/10.1111/j.1440-0960.1997.tb01114.x

Torres-Garcia, D., García, D., Cano-Lira, J. F., & Gené, J. (2022). Two novel genera, *Neostemphylium* and *Scleromyces* (Pleosporaceae) from freshwater sediments and their global biogeography. *Journal of Fungi, 8*, 868. https://doi.org/10.3390/jof8080868

Torres-Garcia, D., García, D., Réblová, M., Jurjević, Ž., Hubka, V., & Gené, J. (2023). Diversity and novel lineages of black yeasts in Chaetothyriales from freshwater sediments in Spain. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 51*, 194–228.

Traaen, A. E. (1914). Untersuchungen über Bodenpilze aus Norwegen. *Nytt Magazin for Naturvidenskapene, 52*, 1–121.

Trakunyingcharoen, T., Lombard, L., Groenewald, J. Z., Cheewangkoon, R., Toanun, C., Alfenas, A. C., . . . Crous, P. W. (2014). Mycoparasitic species of *Sphaerellopsis*, and allied lichenicolous and other genera. *IMA Fungus, 5*, 391–414. https://doi.org/10.5598/imafungus.2014.05.02.05

Tridico, S. R., Koch, S., Michaud, A., Thomson, G., Kirkbride, K. P., & Bunce, M. (2014). Interpreting biological degradative processes acting on mammalian hair in the living and the dead: Which ones are taphonomic? *Proceedings of the Royal Society B: Biological Sciences, 281*, 20141755. https://doi.org/10.1098/rspb.2014.1755

Triffitt, M. J. (1935). On cyst-like bodies, resembling cysts of *Heterodera schachtii* of common occurrence in British soils. *Helminthologia, 13*, 59–66.

Tsai, S. H., Selvam, A., & Yang, S. S. (2007). Microbial diversity of topographical gradient profiles in Fushan forest soils of Taiwan. *Ecological Research, 22*, 814–824.

Tsang, C. C., Chan, K. F., Chan, W., Chan, J. F., Au-Yeung, R. K., Ngan, A. H., . . . Woo, P. C. (2021). Hepatic phaeohyphomycosis due to a novel dematiaceous fungus, *Pleurostoma hongkongense* sp. nov., and importance of antifungal susceptibility testing. *Emerging Microbes & Infections, 10*, 81–96. https://doi.org/10.1080/22221751.2020.1866955

Tsao, P. H. (1970). Selective media for isolation of pathogenic fungi. *Annual Review of Phytopathology, 8*, 157–186. https://doi.org/10.1146/annurev.py.08.090170.001105

Tsao, P. H., & Ocana, G. (1969). Selective isolation of species of *Phytophthora* from natural soils on an improved antibiotic medium. *Nature, 223*, 636–638. https://doi.org/10.1038/223636a0

Tsudome, M., Deguchi, S., Tsujii, K., Ito, S., & Horikoshi, K. (2009). Versatile solidified nanofibrous cellulose-containing media for growth of extremophiles. *Applied and Environmental Microbiology, 75*, 4616–4619. https://doi.org/10.1128/AEM.00519-09

Tsuneda, A., Murakami, S., Nishimura, K., & Miyaji, M. (1986). Pleomorphism and conidiogenesis in *Rhinocladiella atrovirens* isolated from beetle galleries. *Canadian Journal of Botany, 64*, 1112–1119. https://doi.org/10.1139/b86-153

Tuininga, A. R., Miller, J. L., Morath, S. U., Daniels, T. J., Falco, R. C., Marchese, M., . . . Stafford, K. C. (2009). Isolation of entomopathogenic fungi from soils and *Ixodes scapularis* (Acari: Ixodidae) ticks: Prevalence and methods. *Journal of Medical Entomology, 46*, 557–565. https://doi.org/10.1603/033.046.0321

Tulasne, L. R., & Tulasne, C. (1863). *Selecta Fungorum Carpologia II*. Paris: Imperiali Typographeo Excudebatur.

Tulasne, E. L. R., & Tulasne, C. (1863). *Selecta Fungorum Carpologia, ea documenta et icones potissimum exhibens quae varia fructuum et seminum genera in eodem fungo simul aut vicissim adesse demonstrent; Xylariei, Valsei, Sphaeriei*. Imperiali Typograph; Saraswati Press.

Tulloch, M. (1972). The genus *Myrothecium* Tode ex Fr. *Mycological Papers, 130*, 1–42.

Uchiyama, S., Kamiya, S., & Udagawa, S. (1995). A new variety of *Myxotrichum ochraceum* from Japanese soil. *Mycoscience, 36*, 289–292. https://doi.org/10.1007/BF02268604

Udagawa, S., & Horie, Y. (1982). *Reports on the cryptogamic study in Nepal*. National Science Museum.

Udagawa, S., Furuya, K., & Horie, Y. (1973). *Gelasinospora pseudocalospora* sp. nov. and related fungi from soil in Papua New Guinea. *Bulletin of the National Science Museum, Tokyo, 16*, 517–523.

Udagawa, S., Uchiyama, S., & Kamiya, S. (1994). A new species of *Ascotricha* with non-ostiolate ascomata. *Mycotaxon, 50*, 73–80.

Udagawa, S., & Furuya, K. (1978). A new species of *Microascus* and its peculiar conidial state. *Mycotaxon, 7*, 91–96.

Udagawa, S., & Uchiyama, S. (1999a). Taxonomic studies on new or critical fungi of non-pathogenic Onygenales 1. *Mycoscience, 40*, 277–290. https://doi.org/10.1007/BF02463965

Udagawa, S., & Uchiyama, S. (2000). Taxonomic studies on new or critical fungi of non-pathogenic Onygenales 3. *Mycoscience, 41*, 303–311. https://doi.org/10.1007/BF02463943

Udagawa, S. I., & Horie, Y. (1975). Notes on some Japanese Ascomycetes XIV. *Transactions of the Mycological Society of Japan, 16*, 337–347.

Udagawa, S. I., & Uchiyama, S. (2001). Taxonomic studies on new or critical fungi of non-pathogenic Onygenales 4. *Mycoscience, 42*, 281–287. https://doi.org/10.1007/BF02463920

Ueda, S. (1994). A new *Cercophora* with a *Chrysosporium*-like anamorph. *Mycoscience, 35*, 287–290. https://doi.org/10.1007/BF02268451

Ülker, S., Özel, A., Çolak, A., & Karaoğlu, Ş. A. (2011). Isolation, production, and characterization of an extracellular lipase from *Trichoderma harzianum* isolated from soil. *Turkish Journal of Biology*. https://doi.org/10.3906/biy-1004-107

Upadhyay, H. P. (1966). Soil fungi from North-East Brazil, II. *Mycopathologia et Mycologia Applicata, 30*, 276–286. https://doi.org/10.1007/BF02053160

Urquhart, A. S., & Idnurm, A. (2023). A polyphasic approach including whole genome sequencing reveals *Paecilomyces paravariotii* sp. nov. as a cryptic sister species to *P. variotii*. *Journal of Fungi, 9*, 285. https://doi.org/10.3390/jof9030285

van Beyma thoe Kingma, F. H. (1944). Beschreibung einiger neuer pilzarten aus dem Centraalbureau voor Schimmelcultures, Baarn (Nederland). *Antonie van Leeuwenhoek, 10*, 41–56. https://doi.org/10.1007/BF02272784

Van Elsas, J. D., Trevors, J. T., Rosado, A. S., & Nannipieri, P. (Eds.). (2019). *Modern soil microbiology* (pp. 421–430). CRC Press.

Valenzuela-Lopez, N., Cano-Lira, J. F., Guarro, J., Sutton, D. A., Wiederhold, N., Crous, P. W., . . . Stchigel, A. M. (2018). Coelomycetous Dothideomycetes with emphasis on the families Cucurbitariaceae and Didymellaceae. *Studies in Mycology, 90*, 1–69. https://doi.org/10.1016/j.simyco.2017.11.003

Varsavsky, E., & Orr, G. F. (1971). A new genus of the Gymnoascaceae. *Mycopathologia et Mycologia Applicata, 43*, 229–234. https://doi.org/10.1007/BF02051726

Veen, K. H., & Ferron, P. (1966). A selective medium for the isolation of *Beauveria tenella* and of *Metarhizium anisopliae*. *Journal of Invertebrate Pathology, 8,* 268–269.

Verkley, G. J. M., Dukik, K., Renfurm, R., Göker, M., & Stielow, J. B. (2014). Novel genera and species of Coniothyrium-like fungi in Montagnulaceae (Ascomycota). *Persoonia: Molecular Phylogeny and Evolution of Fungi, 32,* 25–51. https://doi.org/10.3767/003158514X679191

Verkley, G. J. M., Da Silva, M., Wicklow, D. T., & Crous, P. W. (2004). *Paraconiothyrium*, a new genus to accommodate the mycoparasite *Coniothyrium minitans*, anamorphs of *Paraphaeosphaeria*, and four new species. *Studies in Mycology, 50*, 323–335.

Větrovský, T., Morais, D., Kohout, P., Lepinay, C., Algora, C., Awokunle Hollá, S., . . . Baldrian, P. (2020). Global Fungi, a global database of fungal occurrences from high-throughput-sequencing metabarcoding studies. *Scientific Data, 7*. https://doi.org/10.1038/s41597-020-0567-7

Viala, P., & Boyer, G. (1891). Sur un Basidiomycète inferieur, parasite des grains de raisins. *Comptes Rendus Hebdomadaires des Séances de l'Académie des Sciences, Paris, 112*, 1148–1150.

Videira, S. I. R., Groenewald, J. Z., Nakashima, C., Braun, U., Barreto, R. W., de Wit, P. J., . . . Crous, P. W. (2017). Mycosphaerellaceae: Chaos or clarity? *Studies in Mycology, 87*, 257–421. https://doi.org/10.1016/j.simyco.2017.09.003

Vilgalys, R., & Hester, M. (1990). Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology, 172*, 4238–4246. https://doi.org/10.1128/JB.172.8.4238-4246.1990

Vilgalys, R., & Sun, B. L. (1994). Ancient and recent patterns of geographic speciation in the oyster mushroom *Pleurotus* revealed by phylogenetic analysis of ribosomal DNA sequences. *Proceedings of the National Academy of Sciences, 91,* 4599–4603. https://doi.org/10.1073/pnas.91.10.4599

Visagie, C. M., Cruywagen, E. M., & Duong, T. A. (2024a). A new *Paecilomyces* from wooden utility poles in South Africa. *Fungal Systematics and Evolution, 13*, 163–181. https://doi.org/10.3114/fuse.2024.13.10

Visagie, C. M., Houbraken, J., Frisvad, J. C., Hong, S. B., Klaassen, C. H. W., Perrone, G., . . . Samson, R. A. (2014). Identification and nomenclature of the genus *Penicillium*. *Studies in Mycology, 78*, 343–371. https://doi.org/10.1016/j.simyco.2014.09.001

Visagie, C. M., Yilmaz, N., Kocsubé, S., Frisvad, J. C., Hubka, V., Samson, R. A., . . . Houbraken, J. (2024b). A review of recently introduced *Aspergillus*, *Penicillium*, *Talaromyces* and other Eurotiales species. *Studies in Mycology, 107*, 1–66. https://doi.org/10.3114/sim.2024.107.01

Voglmayr, H., & Jaklitsch, W. M. (2017). *Corynespora*, *Exosporium* and *Helminthosporium* revisited - New species and generic reclassification. *Studies in Mycology, 87*, 43–76. https://doi.org/10.1016/j.simyco.2017.05.001

von Arx, J. A. (1971). On *Arachniotus* and related genera of the Gymnoascaceae. *Persoonia: Molecular Phylogeny and Evolution of Fungi, 6*, 371–380.

Vu, D., Groenewald, M., De Vries, M., Gehrmann, T., Stielow, B., Eberhardt, U., . . . Verkley, G. J. M. (2019). Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. *Studies in Mycology, 92*, 135–154. https://doi.org/10.1016/j.simyco.2018.05.001

Vuillemin, P. (1912). *Beauveria*, nouveau genre de Verticilliacées. *Bulletin de la Société Botanique de France, 59*, 34–40.

van Vuuren, N., Yilmaz, N., Wingfield, M. J., & Visagie, C. M. (2024). Five novel *Curvularia* species (*Pleosporaceae, Pleosporales*) isolated from fairy circles in the Namib desert. *Mycological Progress, 23*, 39. https://doi.org/10.1007/s11557-024-01977-x

Wagg, C., Schlaeppi, K., Banerjee, S., Kuramae, E. E., & van der Heijden, M. G. A. (2019a). Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. *Nature Communications, 10*, 4841. https://doi.org/10.1038/s41467-019-12798-y

Wagg, C., Schlaeppi, K., Banerjee, S., Kuramae, E. E., & van der Heijden, M. G. (2019b). Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. *Nature Communications, 10*, 1–10. https://doi.org/10.1038/s41467-019-12798-y

Wahdan, S. F. M., Hossen, S., Tanunchai, B., Sansupa, C., Schädler, M., Noll, M., . . . Purahong, W. (2022). Life in the wheat litter: Effects of future climate on microbiome and function during the early phase of decomposition. *Microbial Ecology, 84*, 90–105. https://doi.org/10.1007/s00248-021-01840-6

Waksman, S. A. (1922). A method for counting the number of fungi in the soil. *Journal of Bacteriology, 7*(3), 339.

Walker, G. E. (1984). Ecology of the mycophagous nematode *Aphelenchus avenae* in wheat-field and pine-forest soils. *Plant and Soil, 78*, 417–428. https://doi.org/10.1007/BF02450375

Wanasinghe, D. N., Hyde, K. D., Jeewon, R., Crous, P. W., Wijayawardene, N. N., Jones, E. G., . . . Karunarathna, S. C. (2017a). Phylogenetic revision of *Camarosporium* (Pleosporineae, Dothideomycetes) and allied genera. *Studies in Mycology, 87*, 207–256. https://doi.org/10.1016/j.simyco.2017.08.001

Wanasinghe, D. N., Jeewon, R., Gareth Jones, E. B., Boonmee, S., Kaewchai, S., Manawasinghe, I. S., . . . Hyde, K. D. (2018a). Novel palmicolous taxa within Pleosporales: Multigene phylogeny and taxonomic circumscription. *Mycological Progress, 17*, 571–590. https://doi.org/10.1007/s11557-018-1379-4

Wanasinghe, D. N., Jones, E. B., Camporesi, E., & Dissanayake, A. J. (2016). Taxonomy and phylogeny of *Laburnicola* gen. nov. and *Paramassariosphaeria* gen. nov. (Didymosphaeriaceae, Massarineae, Pleosporales). *Fungal Biology, 120*, 1354–1373. https://doi.org/10.1016/j.funbio.2016.06.006

Wanasinghe, D. N., Phookamsak, R., Jeewon, R., Li, W. J., Hyde, K. D., Jones, E. G., . . . Promputtha, I. (2017b). A family level rDNA based phylogeny of Cucurbitariaceae and Fenestellaceae with descriptions of new *Fenestella* species and *Neocucurbitaria* gen. nov. *Mycosphere, 8*, 397–414. https://doi.org/10.5943/mycosphere/8/4/2

Wanasinghe, D. N., Phukhamsakda, C., Hyde, K. D., & Jeewon, R. (2018b). Fungal diversity notes 709–839: Taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. *Fungal Diversity, 89*, 1–236. https://doi.org/10.1007/s13225-018-0395-7

Wanasinghe, D. N., Wijayawardene, N. N., Xu, J., Cheewangkoon, R., & Mortimer, P. E. (2020). Taxonomic novelties in Magnolia-associated pleosporalean fungi in the Kunming Botanical Gardens (Yunnan, China). *PLoS One, 15*, e0235855.

Wang, C. C., Wang, C. X., Jing, J., Dong, X. L., & Li, B. H. (2015a). Identification and pathogenicity of brown spot pathogen of bagged apples. *Mycosystema, 34*, 1036–1045.

Wang, J. T., Zheng, Y. M., Hu, H. W., Zhang, L. M., Li, J., & He, J. Z. (2015). Soil pH determines the alpha diversity but not beta diversity of soil fungal community along altitude in a typical Tibetan forest ecosystem. *Journal of Soils and Sediments, 15*, 1224–1232. https://doi.org/10.1007/s11368-015-1070-1

Wang, H., Yan, S., Ren, T., Yuan, Y., Kuang, G., Wang, B., . . . Liu, G. (2020). Novel environmental factors affecting microbial responses and physicochemical properties by sequentially applied biochar in black soil. *Environmental Science and Pollution Research, 27*, 37432–37443. https://doi.org/10.1007/s11356-020-10081-y

Wang, H. Y., Zhang, Z. Y., Ren, Y. L., Shao, Q. Y., Li, X., Chen, W. H., . . . Han, Y. F. (2023a). *Multiverruca sinensis* gen. nov., sp. nov., a thermotolerant fungus isolated from soil in China. *International Journal of Systematic and Evolutionary Microbiology, 73*, 0–9. https://doi.org/10.1099/ijsem.0.005734

Wang, J., Shao, S., Liu, C., & Song, Z. (2021). The genus *Paraconiothyrium*: Species concepts, biological functions, and secondary metabolites. *Critical Reviews in Microbiology, 47*, 781–810. https://doi.org/10.1080/1040841X.2021.1933898

Wang, K. Y., Wu, Y. M., Chen, Y., & Jiang, Y. L. (2019a). A new species of *Pyrenochaetopsis* and a key to the known species of the genus. *Mycosystema, 38*, 171–177. https://doi.org/10.13346/j.mycosystema.180261

Wang, M. M., Yang, S. Y., Li, Q., Zheng, Y., Ma, H. H., Tu, Y. H., . . . Cai, L. (2024a). Microascaceae from the marine environment, with descriptions of six new species. *Journal of Fungi, 10*, 45. https://doi.org/10.3390/jof10010045

Wang, M., Liu, F., Crous, P. W., & Cai, L. (2017). Phylogenetic reassessment of *Nigrospora*: Ubiquitous endophytes, plant and human pathogens. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 39*, 118–142. https://doi.org/10.3767/persoonia.2017.39.06

Wang, M., Tan, X. M., Liu, F., & Cai, L. (2018). Eight new *Arthrinium* species from China. *MycoKeys, 34*, 1–24. https://doi.org/10.3897/mycokeys.34.24221

Wang, W. P., Hyde, K. D., Bao, D. F., Wanasinghe, D. N., Lin, C. G., Shen, H. W., . . . Li, Y. X. (2024b). Lignicolous freshwater fungi from karst landscapes in Yunnan province, China. *Mycosphere, 15*, 6525–6640. https://doi.org/10.5943/mycosphere/15/1/29

Wang, X. W., Bai, F. Y., Bensch, K., & Meijer, M. (2019b). Phylogenetic re-evaluation of *Thielavia* with the introduction of a new family *Podosporaceae*. *Studies in Mycology, 93*, 155–252. https://doi.org/10.1016/j.simyco.2019.08.002

Wang, X. W., Han, P. J., Bai, F. Y., Luo, A., Bensch, K., Meijer, M., . . . Houbraken, J. (2022a). Taxonomy, phylogeny and identification of Chaetomiaceae with emphasis on thermophilic species. *Studies in Mycology, 101*, 121–243. https://doi.org/10.3114/sim.2022.101.03

Wang, X. W., Houbraken, J., Groenewald, J. Z., Meijer, M., Andersen, B., Nielsen, K. F., . . . Samson, R. A. (2016a). Diversity and taxonomy of *Chaetomium* and chaetomium-like fungi from indoor environments. *Studies in Mycology, 84*, 145–224. https://doi.org/10.1016/j.simyco.2016.11.005

Wang, X. W., Lombard, L., Groenewald, J. Z., Li, J., Videira, S. I. R., Samson, R. A., . . . Crous, P. W. (2016). Phylogenetic reassessment of the *Chaetomium globosum* species complex. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 36*, 83–133. https://doi.org/10.3767/003158516X689657

Wang, X. W., Yang, F. Y., Meijer, M., Kraak, B., Sun, B. D., Jiang, Y. L., . . . Houbraken, J. (2019). Redefining *Humicola* sensu stricto and related genera in the Chaetomiaceae. *Studies in Mycology, 93*, 65–153. https://doi.org/10.1016/j.simyco.2018.07.001

Wang, Y. B., Wang, Y., Fan, Q., Duan, D. E., Zhang, G. D., Dai, R. Q., . . . Yu, H. (2020). Multigene phylogeny of the family Cordycipitaceae (Hypocreales): New taxa and the new systematic position of the Chinese cordycipitoid fungus *Paecilomyces hepiali*. *Fungal Diversity, 103*, 1–46. https://doi.org/10.1007/s13225-020-00457-3

Wang, Y., Fan, Q., Wang, D., Zou, W. Q., Tang, D. X., Hongthong, P., . . . Yu, H. (2022). Species diversity and virulence potential of the *Beauveria bassiana* complex and *Beauveria scarabaeidicola* complex. *Frontiers in Microbiology, 13*. https://doi.org/10.3389/fmicb.2022.841604

Wang, Y., Hyde, K. D., McKenzie, E. H., Jiang, Y. L., Li, D. W., & Zhao, D. G. (2015). Overview of *Stachybotrys* (*Memnoniella*) and current species status. *Fungal Diversity*, *71*, 17–83. https://doi.org/10.1007/s13225-014-0319-0

Wang, Y., Liu, Y. F., Tang, D. X., Wang, Y. B., Adams, A. E., & Yu, H. (2021). *Tolypocladium reniformisporum* sp. nov. and *Tolypocladium cylindrosporum* (Ophiocordycipitaceae, Hypocreales) co-occurring on *Ophiocordyceps sinensis*. *Mycological Progress, 21*, 199–214. https://doi.org/10.1007/s11557-021-01675-y

Wang, Y., Tang, D. X., Luo, R., Wang, Y. B., Thanarut, C., Dao, V. M., . . . Yu, H. (2023). Phylogeny and systematics of the genus *Clonostachys*. *Frontiers in Microbiology, 14*. https://doi.org/10.3389/fmicb.2023.1117753

Wang, Y., Tu, Y., Chen, X., Jiang, H., Ren, H., Lu, Q., . . . Lv, W. (2024). Didymellaceae species associated with tea plant (*Camellia sinensis*) in China. *MycoKeys, 105*, 217–251. https://doi.org/10.3897/mycokeys.105.119536

Wang, Z. Q., Zhao, J., Dong, Q. Y., Wang, Y., Lu, Y. L., Luo, R., . . . Yu, H. (2024). Multi-locus molecular phylogenetic analysis reveals two new species of *Amphichorda* (Bionectriaceae, Hypocreales). *MycoKeys, 106*, 287–301. https://doi.org/10.3897/mycokeys.106.117205

Wang, Z., Liu, C., Song, X., Tie, Y., Wang, H., Liu, H., . . . Lu, Q. (2024). Ophiostomatalean fungi associated with *Polygraphus* bark beetles in the Qinghai-Tibet Plateau, China. *MycoKeys, 110*, 93–115. https://doi.org/10.3897/mycokeys.110.135538

Wang, Y., Hyde, K., McKenzie, E., Jiang, Y. L., Li, D. W., & Zhao, D. G. (2015). Overview of *Stachybotrys* (*Memnoniella*) and current species status. *Fungal Diversity, 71*, 17–83.

Wangsawat, N., Ju, Y. M., Phosri, C., Whalley, A. J. S., & Suwannasai, N. (2021). Twelve new taxa of *Xylaria* associated with termite nests and soil from northeast Thailand. *Biology, 10*(7), 575. https://doi.org/10.3390/biology10070575

Warcup, J. H. (1957). Studies on the occurrence and activity of fungi in a wheat-field soil. *Transactions of the British Mycological Society, 40*(3), 237–259, IN3. https://doi.org/10.1016/S0007-1536(57)80010-2

Warcup, J. H. (1950). The soil-plate method for isolation of fungi from soil. *Nature, 166*, 117. https://doi.org/10.1038/166117b0

Warcup, J. H. (1951). Soil-steaming: A selective method for the isolation of ascomycetes from soil. *Transactions of the British Mycological Society, 34*(4), 515–518. https://doi.org/10.1016/S0007-1536(51)80035-4

Warcup, J. H., & Baker, K. F. (1963). Occurrence of dormant ascospores in soil. *Nature, 197*, 1317. https://doi.org/10.1038/1971317a0

Warcup, J. H. (1955). Isolation of fungi from hyphae present in soil. *Nature, 175*, 953–954. https://doi.org/10.1038/175953b0

Watanabe, M., Yonezawa, T., Lee, K. I., Kumagai, S., Sugita-Konishi, Y., Goto, K., . . . Hara-Kudo, Y. (2011). Molecular phylogeny of the higher and lower taxonomy of the *Fusarium* genus and differences in the evolutionary histories of multiple genes. *BMC Evolutionary Biology, 11*, 322. https://doi.org/10.1186/1471-2148-11-322

Weber, G., Spaaij, F., & Wingfield, M. J. (1996). *Leptographium costaricense* sp. nov., a new species from roots of *Talauma sambuensis* from Costa Rica. *Mycological Research, 100*(6), 732–736. https://doi.org/10.1016/S0953-7562(96)80206-1

Wei, X., Wang, X., Cao, P., Gao, Z., Chen, A. J., & Han, J. (2020). Microbial community changes in the rhizosphere soil of healthy and rusty *Panax ginseng* and discovery of pivotal fungal genera associated with rusty roots. *BioMed Research International, 2020*, 1–13. https://doi.org/10.1155/2020/8018525

Wei, M. J., Zhang, H., Dong, W., Boonmee, S., & Zhang, D. (2018). Introducing *Dictyochaeta aquatica* sp. nov. and two new species of *Chloridium* (Chaetosphaeriaceae, Sordariomycetes) from aquatic habitats. *Phytotaxa, 362*(3), 187–199.

Wei, D. P., Wanasinghe, D. N., Hyde, K. D., Mortimer, P. E., Xu, J., Xiao, Y. P., . . . To-Anun, C. (2019). The genus *Simplicillium*. *MycoKeys, 60*, 69–92. https://doi.org/10.3897/mycokeys.60.38040

Wei, H., He, X., Riccardo, B., Yang, Y., & Yuan, Z. (2021). *Stagonosporopsis rhizophilae* sp. nov. (Didymellaceae, Pleosporales), a new rhizospheric soil fungus associated with *Populus deltoides* Marsh. *Phytotaxa, 491*(1), 23–34. https://doi.org/10.11646/phytotaxa.491.1.3

Wei, T. P., Wu, Y. M., Zhang, X., Zhang, H., Crous, P. W., & Jiang, Y. L. (2024). A comprehensive molecular phylogeny of *Cephalotrichum* and *Microascus* provides novel insights into their systematics and evolutionary history. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 52*, 119–160. https://doi.org/10.3767/persoonia.2024.52.05

Wei, T. P., Zhang, H., Zeng, X. Y., Crous, P. W., & Jiang, Y. L. (2022). Re-evaluation of Sympoventuriaceae. *Persoonia: Molecular Phylogeny and Evolution of Fungi, 48*, 219–260. https://doi.org/10.3767/persoonia.2022.48.07

Weiser, J., Matha, V., & Jegorov, A. (1991). *Tolypocladium terricola* sp. n., a new mosquito-killing species of the genus *Tolypocladium* Gams (Hyphomycetes). *Folia Parasitologica, 38*, 363–369.

White, T. J., Bruns, T. D., Lee, S. B., & Taylor, J. W. (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In M. A. Innis, D. H. Gelfand, J. J. Sninsky, & T. J. White (Eds.), *PCR protocols: A guide to methods and applications* (pp. 315–322). Academic Press.

Whitton, S. R., McKenzie, E. H. C., & Hyde, K. D. (2001). Microfungi on the Pandanaceae: *Stachybotrys*, with three new species. *New Zealand Journal of Botany*, *39*(3), 489–499.

Wijayawardene, N. N., Bahram, M., Sánchez-Castro, I., Dai, D. Q., Ariyawansa, K. G., Jayalal, U., . . . Tedersoo, L. (2021). Current insight into culture-dependent and culture-independent methods in discovering ascomycetous taxa. *Journal of Fungi*, *7*(9), 703. https://doi.org/10.3390/jof7090703

Wijayawardene, N. N., Hyde, K. D., Lumbsch, H. T., Liu, J. K., Maharachchikumbura, S. S., Ekanayaka, A. H., . . . Phookamsak, R. (2018). Outline of Ascomycota: 2017. *Fungal Diversity*, *88*(1), 167–263. https://doi.org/10.1007/s13225-018-0394-8

Wijayawardene, N. N., Hyde, K. D., Rajeshkumar, K. C., Hawksworth, D. L., Madrid, H., Kirk, P. M., . . . Karunarathna, S. C. (2017). *Notes for genera: Ascomycota* (pp. 1–594).

Wijayawardene, N. N., Phillips, A. J., Pereira, D. S., Dai, D. Q., Aptroot, A., Monteiro, J. S., . . . Thines, M. (2022). Forecasting the number of species of asexually reproducing fungi (Ascomycota and Basidiomycota). *Fungal Diversity*, 1–28. https://doi.org/10.1007/s13225-022-00500-5

Wijayawardene, N. N., Hyde, K. D., Dai, D., Sánchez-García, M., Goto, B., Saxena, R., . . . Thines, M. (2022). Outline of fungi and fungus-like taxa – 2021. *Mycosphere*, *13*(1), 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Wijayawardene, N. N., Hyde, K. D., Al-Ani, L. K. T., Tedersoo, L., Haelewaters, D., Rajeshkumar, K. C., . . . Thines, M. (2020). Outline of fungi and funguslike taxa. *Mycosphere*, *11*(1), 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

Wijesinghe, S. N., Wanasinghe, D. N., Maharachchikumbura, S. S. N., & Wang, Y. (2020). *Bimuria omanensis* sp. nov. (Didymosphaeriaceae, Pleosporales) from Oman. *Phytotaxa*, *449*(2), 97–108. https://doi.org/10.11646/phytotaxa.449.2.1

Wilhelmus, K. R., & Jones, D. B. (2001). Curvularia keratitis. *Transactions of the American Ophthalmological Society*, *99*, 111.

Wingfield, L. K., Phaichamnan, A., & Jumnongnit, T. (2021). Evaluation of biosecurity and fungal contaminants in the poultry farms in Songkhla province, Thailand. *ScienceAsia*, *47*(4), 486. https://doi.org/10.2306/scienceasia1513-1874.2021.058

Woo, P. C., Ngan, A. H., Tsang, C. C., Ling, I. W., Chan, J. F., Leung, S. Y., . . . Lau, S. K. (2013). Clinical spectrum of *Exophiala* infections and a novel *Exophiala* species, *E. hongkongensis*. *Journal of Clinical Microbiology*, *51*(1), 260–267.

Woudenberg, J. H. C., Groenewald, J. Z., Binder, M., & Crous, P. W. (2013). *Alternaria* redefined. *Studies in Mycology*, *75*, 171–212. https://doi.org/10.3114/sim0015

Woudenberg, J. H. C., Meijer, M., Houbraken, J., & Samson, R. A. (2017). Scopulariopsis and scopulariopsis-like species from indoor environments. *Studies in Mycology, 88*, 1–35. https://doi.org/10.1016/j.simyco.2017.03.001

Woudenberg, J. H. C., Sandoval-Denis, M., Houbraken, J., Seifert, K. A., & Samson, R. A. (2017). *Cephalotrichum* and related synnematous fungi with notes on species from the built environment. *Studies in Mycology*, *88*, 137–159. https://doi.org/10.1016/j.simyco.2017.09.001

Wu, B., Hussain, M., Zhang, W., Stadler, M., Liu, X., & Xiang, M. (2019). Current insights into fungal species diversity and perspective on naming the environmental DNA sequences of fungi. *Mycology, 10*(3), 127–140. https://doi.org/10.1080/21501203.2019.1614106

Wu, F., Feng, Z., Wang, M., & Wang, Q. (2023). Proposal of four new *Aureobasidium* species for exopolysaccharide production. *Journal of Fungi, 9*(4), 447. https://doi.org/10.3390/jof9040447

Wu, W., & Chen, S. (2021). Species diversity, mating strategy and pathogenicity of *Calonectria* species from diseased leaves and soils in the *Eucalyptus* plantation in Southern China. *Journal of Fungi, 7*(2), 73. https://doi.org/10.3390/jof7020073

Wu, W., & Diao, Y. (2022). *Anamorphic Chaetosphaeriaceous fungi from China* (pp. 1–546). Springer Netherlands.

Wu, Y. M., Wang, H. F., Xu, J. J., & Zhang, T. Y. (2015a). Two new species and a new record of *Hansfordia* from China. *Mycotaxon, 130*(3), 807–813. https://doi.org/10.5248/130.807

Wu, Y. M., Xu, J. J., Kong, J. H., & Zhang, T. Y. (2015b). New species of *Graphium* and *Periconia* from China. *Mycotaxon, 129*(2), 397–401. https://doi.org/10.5248/129.397

Wu, Y., Geng, Y., & Zhang, T. (2009). Three new species of *Monodictys* from soil. *Mycotaxon, 109*(1), 263–267.

Wu, Y. M., & Zhang, T. Y. (2010). Two new species of *Stachybotrys* from soil. *Mycotaxon, 114*(2), 459–462.

Wu, Y. T., Wubet, T., Trogisch, S., Both, S., Scholten, T., Bruelheide, H., . . . Buscot, F. (2013). Forest age and plant species composition determine the soil fungal community composition in a Chinese subtropical forest. *PLoS ONE, 8*(6), e66829. https://doi.org/10.1371/journal.pone.0066829

Wu, Y. M., & Zhang, T. Y. (2013). A new species and new record of *Chloridium* from the Qinghai-Tibet Plateau Area, China. *Mycotaxon, 123*(1), 277–280.

Xia, F., Liu, Y., Shen, G. R., Guo, L. X., & Zhou, X. W. (2015). Investigation and analysis of microbiological communities in natural *Ophiocordyceps sinensis*. *Canadian Journal of Microbiology, 61*(2), 104–111. https://doi.org/10.1139/cjm-2014-0610

Xiao, Y. P., Wen, T. C., Hongsanan, S., Jeewon, R., Luangsa-Ard, J. J., Brooks, S., . . . Hyde, K. D. (2018). Multigene phylogenetics of *Polycephalomyces* (Ophiocordycipitaceae, Hypocreales), with two new species from Thailand. *Scientific Reports, 8*, 18087. https://doi.org/10.1038/s41598-018-36792-4

Xiao, Y. P., Wang, Y. B., Hyde, K. D., Eleni, G., Sun, J. Z., Yang, Y., . . . Wen, T. C. (2023). *Polycephalomycetaceae*, a new family of clavicipitoid fungi segregates from Ophiocordycipitaceae. Springer Netherlands. https://doi.org/ (if available)

Xiong, C., He, J. Z., Singh, B. K., Zhu, Y. G., Wang, J. T., Li, P. P., . . . Zhang, L. M. (2021). Rare taxa maintain the stability of crop mycobiomes and ecosystem functions. *Environmental Microbiology, 23*(4), 1907–1924. https://doi.org/10.1111/1462-2920.15262

Xu, X., Zhang, X., Huang, Z., Xu, Y., Tang, D., Zhang, B., . . . Yu, H. (2022). Microbial community composition and soil metabolism in the coexisting *Cordyceps militaris* and *Ophiocordyceps highlandensis*. *Journal of Basic Microbiology*, *62*(11), 1254–1273. https://doi.org/10.1002/jobm.202200216

Xun, Z., Yang, W., Liu, J., Ren, B., & Bai, L. (2020). Fungi contribute more to N2O emissions than bacteria in nitrogen fertilized lawn soil. *Authorea*. https://doi.org/(if available)

Yadav, M. K., Ryu, J. J., Choi, J. S., & Jung, H. Y. (2023). Morphological and phylogenetic analysis of a new record of *Paraconiothyrium kelleni* from soil in Korea. *The Korean Journal of Mycology*, *51*(2), 101–109. https://doi.org/10.4489/KJM.20230011

Yaguchi, T., Someya, A., & Udagawa, S. (1995). Two interesting cleistothecial ascomycetes from soils. *Mycoscience*, *36*(2), 151–154. https://doi.org/10.1007/BF02268550

Yaguchi, T., Someya, A., & Udagawa, S. (1996). New and rare microfungi from the island of Hachijo-jima. *Mycoscience*, *37*(2), 157–162. https://doi.org/10.1007/BF02461340

Yamaguchi, Y., Masuma, R., Tomoda, H., & Omura, S. (2005). A new species of *Dinemasporium* from sugar cane on Irabujima island, Japan. *Mycoscience*, *46*(5), 367–369.

Yan, Q. H., Ni, Q. R., Gu, W. J., Liu, H. W., Yuan, X. Y., & Sun, J. Z. (2023a). *Simplicillium sinense* sp. nov., a novel potential pathogen of Tinea faciei. *Frontiers in Microbiology*, *14*, Article 1156027. https://doi.org/10.3389/fmicb.2023.1156027

Yan, X. Y., Huang, J. E., Song, H. Y., Gao, Y., Hu, H. J., Zhai, Z. J., . . . Hu, D. M. (2023b). A new species of *Dictyochaeta* (Sordariomycetes, Chaetosphaeriales, Chaetosphaeriaceae) from freshwater habitats in China. *Biodiversity Data Journal*, *11*, e97439. https://doi.org/10.3897/BDJ.11.E97439

Yang, A. L., Chen, L., Fang, K., Dong, X. F., Li, Y. X., Zhang, H. B., . . . Yu, Z. F. (2021a). *Remotididymella ageratinae* sp. nov. and *Remotididymella anemophila* sp. nov., two novel species isolated from the invasive weed *Ageratina adenophora* in PR China. *International Journal of Systematic and Evolutionary Microbiology, 71*(2), 1–13. https://doi.org/10.1099/ijsem.0.004572

Yang, C., Liu, N., & Zhang, Y. (2019). Soil aggregates regulate the impact of soil bacterial and fungal communities on soil respiration. *Geoderma, 337*, 444–452. https://doi.org/10.1016/j.geoderma.2018.10.002

Yang, C. L., Xu, X. L., Jeewon, R., Boonmee, S., Liu, Y. G., & Hyde, K. D. (2019). *Acremonium arthrinii* sp. nov., a mycopathogenic fungus on *Arthrinium yunnanum*. *Phytotaxa, 420*(4), 283–299. https://doi.org/10.11646/phytotaxa.420.4.4

Yang, E., Lu, W., Tibpromma, S., Dai, D., Gao, Y., Promputtha, I., . . . Karunarathna, S. C. (2023). Three interesting fungi from American bullfrog larvae (*Rana catesbeiana*) in Yunnan, China. *Phytotaxa, 587*(3), 251–268. https://doi.org/10.11646/phytotaxa.587.3.4

Yang, Q., Du, Z., Liang, Y. M., & Tian, C. M. (2018a). Molecular phylogeny of *Nectria* species associated with dieback and canker diseases in China, with a new species described. *Phytotaxa*, *356*(3), 199–214. https://doi.org/10.11646/phytotaxa.356.3.2

Yang, Q., Fan, X. L., Du, Z., & Tian, C. M. (2018b). Diaporthosporellaceae, a novel family of Diaporthales (Sordariomycetes, Ascomycota). *Mycoscience, 59*(3), 229–235. https://doi.org/10.1016/j.myc.2017.11.005

Yang, X., Lv, R., Yu, Z., Li, J., & Qiao, M. (2022). *Cordana yunnanensis* sp. nov., isolated from desertified rocky soil in Southwest China. *Current Microbiology, 79*, 183. https://doi.org/10.1007/s00284-022-02871-z

Yang, X. Q., Ma, S. Y., Peng, Z. X., Wang, Z. Q., Qiao, M., & Yu, Z. (2021b). Diversity of *Plectosphaerella* within aquatic plants from southwest China, with *P. endophytica* and *P. sichuanensis* spp. nov. *MycoKeys, 80*, 57–75. https://doi.org/10.3897/mycokeys.80.64624

Yang, J. C., & Insam, H. (1991). Microbial biomass and relative contributions of bacteria and fungi in soil beneath tropical rain forest, Hainan Island, China. *Journal of Tropical Ecology, 7*(3), 385–393.

Yasanthika, W. A. E., Tennakoon, D. S., Farias, A. R. G., Bhat, D. J., & Wanasinghe, D. N. (2022a). New soil-inhabiting Chaetosphaeriaceous records from Thailand. *Asian Journal of Mycology, 5*(1), 16–30.

Yasanthika, E., Wanasinghe, D. N., Ren, G. C., Karunarathna, S. C., Tennakoon, D. S., Monkai, J., . . . Hyde, K. D. (2021). Taxonomic and phylogenetic insights into novel Ascomycota from contaminated soils in Yunnan, China. *Phytotaxa, 513*(3), 203–225. https://doi.org/10.11646/phytotaxa.513.3.2

Yasanthika, W. A. E., Chethana, K. W. T., Wanasinghe, D. N., & Tennakoon, D. S. (2024). Taxonomic novelties of soil-inhabiting pleosporalean fungi in Thailand using baiting method. *Phytotaxa*, *676*(1), 1–24. https://doi.org/10.11646/phytotaxa.676.1.1

Yasanthika, W. A. E., de Farias, A. R. G., Wanasinghe, D. N., Chethana, K. W. T., Zare, R., Cai, L., . . . Chomnunti, P. (2023). https://soilfun.org/, a web-based platform for soil-inhabiting Ascomycota species. *Studies in Fungi*, *8*, Article SIF-2023-0016. https://doi.org/10.48130/SIF-2023-0016

Yasanthika, W. E., Tennakoon, D. S., de Farias, A. R. G., Chethana, K. T., Bhat, D. J., & Wanasinghe, D. N. (2023). Isolation and characterization of novel Dothideomycetes species from forest soils in Chiang Rai and Krabi (Thailand): Additions to the diversity of *Curvularia* and *Verruconis*. *Phytotaxa, 609*(1), 17–44. https://doi.org/10.11646/phytotaxa.609.1.3

Yasanthika, W. A. E., Wanasinghe, D. N., Mortimer, P. E., Monkai, J., & Farias, A. R. G. (2022b). The importance of culture-based techniques in the genomic era for assessing the taxonomy and diversity of soil fungi. *Mycosphere*, *13*(1), 724–751. https://doi.org/10.5943/mycosphere/13/1/8

Yasanthika, W. A. E., Wanasinghe, D. N., Karunarathna, S. C., Bhat, D. J., Samarakoon, S. M. B. C., Ren, G. C., . . . Hyde, K. D. (2020). Two new Sordariomycetes records from forest soils in Thailand. *Asian Journal of Mycology, 3*(2), 456–472. https://doi.org/10.5943/ajom/3/1/16

Yeh, Y. H., & Kirschner, R. (2019). A new species of *Alpestrisphaeria* (Dothideomycetes) with monodictys-like anamorph and revision of three *Monodictys* species. *Mycological Progress, 18*, 703–711. https://doi.org/10.1007/s11557-019-01482-6

Yeh, Y. W., Hsieh, C. M., Yeh, Y. H., Huang, Y. M., & Kirschner, R. (2023). A new species of *Memnoniella* (Hypocreales, Stachybotryaceae), *Memnoniella pseudodichroa*, from the ancient subtropical giant fern *Angiopteris lygodiifolia* (Marattiaceae) in Taiwan. *Plant Systematics and Evolution, 309*, 19. https://doi.org/10.1007/s00606-023-01855-1

Yilmaz, N., Visagie, C. M., Houbraken, J., Frisvad, J. C., & Samson, R. A. (2014). Polyphasic taxonomy of the genus *Talaromyces*. *Studies in Mycology, 78*, 175–341. https://doi.org/10.1016/j.simyco.2014.08.001

Yin, F., Song, Z., Liu, L., Xu, Q., Jiang, J., Xiao, Z., . . . Liu, M. (2024). Sclerotinia rot of *Zephyranthes candida* caused by *Sclerotinia sclerotiorum* and *Sclerotinia minor*. *Frontiers in Microbiology, 15*. https://doi.org/10.3389/fmicb.2024.1414141

Yoshida, N. (2022). Seasonal dynamics of the pink root fungus (*Setophoma terrestris*) in rhizosphere soil: Effect of crop species and rotation. *Plant Pathology, 71*, 361–372. https://doi.org/10.1111/ppa.13464

Youssef, K., Mustafa, Z. M. M., Kamel, M. A. M., & Mounir, G. A. (2020). Cigar end rot of banana caused by *Musicillium theobromae* and its control in Egypt. *Archives of Phytopathology and Plant Protection, 53*, 162–177. https://doi.org/10.1080/03235408.2020.1735139

Yuan, C., Wang, H. Y., Wu, C. S., Jiao, Y., Li, M., Wang, Y. Y., . . . Lou, H. X. (2013). Austdiol, fulvic acid and citromycetin derivatives from an endolichenic fungus, *Myxotrichum* sp. *Phytochemistry Letters, 6*, 662–666. https://doi.org/10.1016/j.phytol.2013.08.011

Yuan, Z. L., Lin, F. C., Zhang, C. L., & Kubicek, C. P. (2010). A new species of *Harpophora* (Magnaporthaceae) recovered from healthy wild rice (*Oryza granulata*) roots, representing a novel member of a beneficial dark septate endophyte. *FEMS Microbiology Letters, 307*, 94–101. https://doi.org/10.1111/j.1574-6968.2010.01963.x

Yuen, T. K., Hyde, K. D., & Hodgkiss, I. J. (1998). Physiological growth parameters and enzyme production in tropical freshwater fungi. *Material und Organismen, 32*, 2–16.

Zain, M. E., Awaad, A. S., Razak, A. A., Maitland, D. J., Khamis, N. E., & Sakhawy, M. A. (2009). Secondary metabolites of *Aureobasidium pullulans* isolated from Egyptian soil and their biological activity. *Journal of Applied Sciences Research, 5*, 1582–1591.

Zalar, P. D., De Hoog, G. S., Schroers, H. J., Crous, P. W., Groenewald, J. Z., & Gunde-Cimerman, N. (2007). Phylogeny and ecology of the ubiquitous saprobe *Cladosporium sphaerospermum*, with descriptions of seven new species from hypersaline environments. *Studies in Mycology, 58*, 157–183. https://doi.org/10.3114/sim.2007.58.06

Zare, R., Gams, W., Starink, M., & Summerbell, R. (2007). *Gibellulopsis*, a suitable genus for *Verticillium nigrescens*, and *Musicillium*, a new genus for *V. theobromae*. *Nova Hedwigia, 85*, 463–489. https://doi.org/10.1127/0029-5035/2007/0085-0463

Zare, R., & Gams, W. (2001). A revision of *Verticillium* section *Prostrata*. IV. The genera *Lecanicillium* and *Simplicillium* gen. nov. *Nova Hedwigia, 73*, 1–50.

Zare, R., Asgari, B., & Gams, W. (2010). The species of *Coniolariella*. *Mycologia, 102*, 1383–1388. https://doi.org/10.3852/10-035

Zare, R., Gams, W., & Evans, H. C. (2001). A revision of *Verticillium* section *Prostrata*. V. The genus *Pochonia*, with notes on *Rotiferophthora*. *Nova Hedwigia*, 51–86.

Zare, R., Gams, W., & Schroers, H. J. (2004). The type species of *Verticillium* is not congeneric with the plant-pathogenic species placed in *Verticillium* and it is not the anamorph of "*Nectria*" inventa. *Mycological Research, 108*, 576–582. https://doi.org/10.1017/S0953756204009839

Zhang, B., Li, X., Li, G., Wang, Q. M., & Wang, M. (2022a). *Cadophora* species from marine glaciers in the Qinghai-Tibet Plateau: An example of unsuspected hidden biodiversity. *IMA Fungus, 13*. https://doi.org/10.1186/s43008-022-00102-5

Zhang, F., Boonmee, S., Bhat, J. D., Xiao, W., & Yang, X. Y. (2022b). New *Arthrobotrys* nematode-trapping species (Orbiliaceae) from terrestrial soils and freshwater sediments in China. *Journal of Fungi, 8*, 671. https://doi.org/10.3390/jof8070671

Zhang, G., & Berbee, M. L. (2001). *Pyrenophora* phylogenetics inferred from ITS and glyceraldehyde-3-phosphate dehydrogenase gene sequences. *Mycologia, 93*, 1048–1063. https://doi.org/10.1080/00275514.2001.12063240

Zhang, J. F., Liu, J. K., Thambugala, K. M., Yang, J., Meng, Z. H., & Liu, Z. Y. (2020). Two new species and a new record of *Nigrograna* (Nigrograna ceae, Pleosporales) from China and Thailand. *Mycological Progress, 19*, 1365–1375. https://doi.org/10.1007/s11557-020-01633-0

Zhang, Y., Mo, M., Yang, L., Mi, F., Cao, Y., Liu, C., . . . Xu, J. (2021). Exploring the species diversity of edible mushrooms in Yunnan, Southwestern China, by DNA barcoding. *Journal of Fungi*, *7*, 310. https://doi.org/10.3390/jof7040310

Zhang, J. F., Liu, J. K., Hyde, K. D., Chen, Y. Y., Ran, H. Y., & Liu, Z. Y. (2023a). Ascomycetes from karst landscapes of Guizhou province, China. *Fungal Diversity*, *122*, 1–160. https://doi.org/10.1007/s13225-023-00524-5

Zhang, J. Y., Ma, J., Xiao, Y. P., Boonmee, S., Kang, J. C., & Lu, Y. Z. (2022c). Morphological and phylogenetic analyses reveal five new species in Chaetosphaeriaceae. *Journal of Fungi*, *8*, 643. https://doi.org/10.3390/jof8060643

Zhang, Y., Crous, P. W., Schoch, C. L., & Hyde, K. D. (2012). Pleosporales. *Fungal Diversity*, *53*, 1–221.

Zhang, J., Wang, X., Wu, J., & Kumari, D. (2019a). Fungal community composition analysis of 24 different urban parks in Shanghai, China. *Urban Ecosystems, 22*, 855–863. https://doi.org/10.1007/s11252-019-00867-5

Zhang, J., Wang, X., Wu, J., & Kumari, D. (2019b). Fungal community composition analysis of 24 different urban parks in Shanghai, China, 855–863.

Zhang, S., Zhang, C., Gao, Z. F., Qiu, C. W., Shi, S. H., Chen, Z. H., . . . Wu, F. (2023b). Integrated physiological and omics analyses reveal the mechanism of beneficial fungal *Trichoderma* sp. alleviating cadmium toxicity in tobacco (*Nicotiana tabacum* L.). *Ecotoxicology and Environmental Safety, 267*, 115631. https://doi.org/10.1016/j.ecoenv.2023.115631

Zhang, T. Y., Yu, Y., Zhang, M. Y., Cheng, J., Chen, Z. J., Zhang, J. Y., . . . Zhang, Y. X. (2018). *Verruconis panacis* sp. nov., an endophyte isolated from *Panax notoginseng*. *International Journal of Systematic and Evolutionary Microbiology, 68*, 2499–2503. https://doi.org/10.1099/ijsem.0.002862

Zhang, W., Groenewald, J. Z., Lombard, L., Schumacher, R. K., Phillips, A. J. L., & Crous, P. W. (2021a). Evaluating species in Botryosphaeriales. *Persoonia - Molecular Phylogeny and Evolution of Fungi*. https://doi.org/10.3767/persoonia.2021.46.03

Zhang, X. M., Tang, D. X., Li, Q. Q., Wang, Y. B., Xu, Z. H., Li, W. J., . . . Yu, H. (2021b). Complex microbial communities inhabiting natural *Cordyceps militaris* and the habitat soil and their predicted functions. *Antonie van Leeuwenhoek, 114*, 465–477. https://doi.org/10.1007/s10482-021-01534-6

Zhang, Y. Y., Zhang, T., Li, H. Y., Zheng, R., Ren, J., Yang, Q., . . . Jiang, N. (2024a). *Nigrospora humicola* (Apiosporaceae, Amphisphaeriales), a new fungus from soil in China. *Diversity, 16*, 118. https://doi.org/10.3390/d16020118

Zhang, Y., Chen, C., Chen, C., Chen, J., Xiang, M., Wanasinghe, D. N., . . . Manawasinghe, I. S. (2022d). Identification and characterization of *Calonectria* species associated with plant diseases in Southern China. *Journal of Fungi, 8*, 719. https://doi.org/10.3390/jof8070719

Zhang, Y., Wu, W., & Cai, L. (2017a). Polyphasic characterisation of *Chaetomium* species from soil and compost revealed high number of undescribed species. *Fungal Biology, 121*, 21–43. https://doi.org/10.1016/j.funbio.2016.08.012

Zhang, Z. Y., Feng, Y., Tong, S. Q., Ding, C. Y., Tao, G., & Han, Y. F. (2023c). Morphological and phylogenetic characterisation of two new soil-borne fungal taxa belonging to *Clavicipitaceae* (Hypocreales, Ascomycota). *MycoKeys, 98*, 113–132. https://doi.org/10.3897/mycokeys.98.106240

Zhang, Z. Y., Li, X., Chen, W. H., Liang, J. D., & Han, Y. F. (2023d). Culturable fungi from urban soils in China II, with the description of 18 novel species in Ascomycota (Dothideomycetes, Eurotiomycetes, Leotiomycetes and Sordariomycetes). *MycoKeys, 98*, 167–220. https://doi.org/10.3897/mycokeys.98.102816

Zhang, Z. Y., Li, X., Chen, W. H., Liang, J. D., & Han, Y. F. (2023e). Culturable fungi from urban soils in China II, with the description of 18 novel species in Ascomycota (Dothideomycetes, Eurotiomycetes, Leotiomycetes and Sordariomycetes). *MycoKeys, 98*, 167–220. https://doi.org/10.3897/mycokeys.98.102816

Zhang, Z., Liu, R., Liu, S., Mu, T., Zhang, X., & Xia, J. (2022e). Morphological and phylogenetic analyses reveal two new species of Sporocadaceae from Hainan, China. *MycoKeys, 88*, 171–192. https://doi.org/10.3897/mycokeys.88.82229

Zhang, Z. Y., Pan, H., Tao, G., Li, X., Han, Y. F., Feng, Y., . . . Ding, C. Y. (2024b). Culturable mycobiota from Guizhou wildlife park in China. *Mycosphere, 15*, 654–763. https://doi.org/10.5943/mycosphere/15/1/5

Zhang, Z. F., Liu, F., Zhou, X., Liu, X. Z., Liu, S. J., & Cai, L. (2017b). Culturable mycobiota from Karst caves in China, with descriptions of 20 new species. *Persoonia - Molecular Phylogeny and Evolution of Fungi, 39*, 1–31. https://doi.org/10.3767/persoonia.2017.39.01

Zhang, Z. F., Zhou, S. Y., Eurwilaichitr, L., Ingsriswang, S., Raza, M., Chen, Q., . . . Cai, L. (2021c). Culturable mycobiota from Karst caves in China II, with descriptions of 33 new species. *Springer Netherlands*, 29–136.

Zhang, Z. Y., Han, Y. F., Chen, W. H., & Liang, Z. Q. (2019c). Phylogeny and taxonomy of three new *Ctenomyces* (Arthrodermataceae, Onygenales) species from China. *MycoKeys, 47*, 1–16. https://doi.org/10.3897/mycokeys.47.30740

Zhang, Y., Crous, P. W., Schoch, C. L., Bahkali, A. H., Guo, L. D., & Hyde, K. D. (2011). A molecular, morphological and ecological reappraisal of *Venturiales*, new order of Dothideomycetes. *Fungal Diversity, 51*, 249–277. https://doi.org/10.1007/s13225-011-0141-x

Zhang, Y., Crous, P. W., Schoch, C. L., & Hyde, K. D. (2012). *Pleosporales*. *Fungal Diversity*, *53*, 1–221. https://doi.org/10.1007/s13225-011-0117-x

Zhang, T. Y., Yu, Y., Zhang, M. Y., Cheng, J., Chen, Z. J., Zhang, J. Y., . . . Zhang, Y. X. (2018). *Verruconis panacis* sp. nov., an endophyte isolated from *Panax notoginseng*. *International Journal of Systematic and Evolutionary Microbiology*, *68*, 2499–2503.

Zhao, H. J., Doilom, M., Mapook, A., Wang, G., Hyde, K. D., & Dong, W. (2024a). New insights into Tetraplosphaeriaceae based on taxonomic investigations of bambusicolous fungi and freshwater fungi. *Journal of Fungi*, *10*, 319. https://doi.org/10.3390/jof10050319

Zhao, R., Chen, K. Y., Mao, L. J., & Zhang, C. L. (2024b). Eleven new species of *Trichoderma* (Hypocreaceae, Hypocreales) from China. *Mycology*, 1–30. https://doi.org/10.1080/21501203.2024.2330400

Zhaxybayeva, O., & Gogarten, J. P. (2002). Bootstrap, Bayesian probability and maximum likelihood mapping: Exploring new tools for comparative genome analyses. *BMC Genomics*, *3*(1), 4. https://doi.org/10.1186/1471-2164-3-4

Zheng, L., & Song, W. (2022). Phosphorus limitation of trees influences forest soil fungal diversity in China. *Forests*, *13*(2), 223. https://doi.org/10.3390/f13020223

Zhou, J., Jiang, X., Zhou, B., Zhao, B., Ma, M., Guan, D., . . . Qin, J. (2016). Thirty-four years of nitrogen fertilization decreases fungal diversity and alters fungal community composition in black soil in northeast China. *Soil Biology and Biochemistry*, *95*, 135–143. https://doi.org/10.1016/j.soilbio.2015.12.012

Zhou, Y. M., Zhi, J. R., Qu, J. J., & Zou, X. (2022). Estimated divergence times of Lecanicillium in the family Cordycipitaceae provide insights into the attribution of Lecanicillium. *Frontiers in Microbiology*, *13*, 859886. https://doi.org/10.3389/fmicb.2022.859886

Zimmerman, A. (1902). Ueber einige an tropischen Kulturpflanzen beobachtete Pilze III. *Zentralblatt für Bakteriologie, Parasitenkunde*, *8*, 216–221.

Zopf, W. (1876). Thielavia basicola Zopf. Genus novum Perisporiacearum. *Verhandlungen des Botanischen Vereins für die Provinz Brandenburg*, *18*, 101–105.

Zukal, H. (1890). Ueber einige neue Pilzformen und über das Verhältniss der Gymnoascen zu den übrigen Ascomyceten. *Ber Dtsch Bot Ges, 8*, 295–296. https://doi.org/10.1111/j.1438-8677.1890.tb06010.x

Zukal, H. (1885). Ueber einige neue pilze, myxomyceten und bakterien. *Ver-handlungen der Zoologisch-Botanischen Gesellschaft Wien, 35*, 333–342.

Zweibel, S. M., & Wang, C. J. K. (1977). Reexamination of *Phialophora verrucosa*. *Pan American Health Organization, 356*, 91–100.

APPENDIX A

CHEMICAL REAGENTS AND MEDIA

1. Indian ink used for observing gelatinous appendages of ascospores in some species

2. Potato dextrose agar (PDA) used for fungal cultivation

Potato starch (from infusion) 4 g

Dextrose 20 g

Agar 15 g

Suspend 40 g of Potato dextrose agar in distilled water and mix thoroughly. Heat with frequent agitation and boil for 1 minute to completely dissolve the power and bring volume to 1000 ml. Autoclave at 121ºC for 15 minutes

APPENDIX B

PUBLICATIONS

Phytotaxa 446 (2): 103–113
https://www.mapress.com/j/pt/
Copyright © 2020 Magnolia Press

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.446.2.3

Lonicericola fuyuanensis (Parabambusicolaceae) a new terrestrial pleosporalean ascomycete from Yunnan Province, China

ERANDI YASANTHIKA[1,2,3,6], LAKMALI S. DISSANAYAKE[4,7], DHANUSHKA N. WANASINGHE[2,5,8], SAMANTHA C. KARUNARATHNA[2,5,9], PETER E. MORTIMER[2,10], BINU C. SAMARAKOON[3,11], JUTAMART MONKAI[3,12] & KEVIN D. HYDE[1,2,3,13]*

[1] *Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Haizhu District, Guangzhou 510225, People's Republic of China.*
[2] *Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People's Republic of China.*
[3] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand.*
[4] *Engineering Research Center of the Utilization for Characteristic Bio-Pharmaceutical Resources in Southwest, Ministry of Education, Guizhou University, Guiyang, Guizhou Province 550025, People's Republic of China.*
[5] *Center for Mountain Futures, Kunming Institute of Botany, Honghe County 654400, Yunnan, People's Republic of China.*
[6] eyasanthika@gmail.com; https://orcid.org/0000-0002-3757-3801
[7] dmlsdlakmali.ld@gmail.com; https://orcid.org/0000-0003-2933-3127
[8] dnadeesham@gmail.com; https://orcid.org/0000-0003-1759-3933
[9] samanthakarunarathna@gmail.com; https://orcid.org/0000-0001-7080-0781
[10] petermortimer@mac.com; https://orcid.org/0000-0003-3188-9327
[11] binusamarakoon2@gmail.com; https://orcid.org/0000-0002-6150-6190
[12] mjutamart@gmail.com; https://orcid.org/0000-0001-6043-0625
[13] kdhyde3@gmail.com; https://orcid.org/0000-0002-2191-0762
*Corresponding author: kdhyde3@gmail.com

Abstract

A new species of terrestrial ascomycetes belonging to the genus *Lonicericola* (Pleosporales, Dothideomycetes) found on dead branches of *Caprifolioideae* sp. in Yunnan Province, China is described and illustrated. A new classification is proposed to accommodate the new taxon based on the interpreted results from multigenic phylogenetic inference and micro morphological comparisons. The analysis of a combined SSU, LSU, ITS rDNA and *tef1* dataset significantly supports both the shared monophyletic origin of *Lonicericola* in Parabambusicolaceae as well as *L. fuyuanensis* as a distinct new species. Comparisons of the distinct morphology of the new species *L. fuyuanensis* with the type species of the genus, *L. hyalosepiispora*, and other genera of the family Parabambusicolaceae are made.

Keywords: 1 new species, hyaline spores, Massarineae, phylogeny, saprobic, taxonomy

Introduction

A study of the fungi of the Greater Mekong Subregion has been initiated by us and has resulted in discovery of high species novelty (Hyde *et al.* 2018). Yunnan Province, which is part of the Greater Mekong Subregion has 51.6 % of China's overall floristic diversity, containing over 18,000 plant species with high levels of endemism (Yang *et al.* 2004, Zhang *et al.* 2012). It is a unique region, with specific ecological conditions that encourage the growth and reproduction of higher fungi (Feng & Yang 2018). Out of the 4000 known fungal species in China, 40 % have been discovered in Yunnan Province, and about 500 type specimens have been collected from this region (Feng & Yang 2018). Nonetheless, most of these taxa are exclusively Basidiomycetes (Yu *et al.* 2018), and current understanding of the distribution and diversity of microfungi is still limited. To address this gap, there has been increasing interest in isolating microfungi from various plants across different counties of Yunnan Province (Su *et al.* 2016, 2018, Luo *et al.* 2017, Bao *et al.* 2018, Huang *et al.* 2018, Maharachchikumbura *et al.* 2018, Wanasinghe *et al.* 2018a, Jiang *et al.* 2019a, b, Phookamsak *et al.* 2019, Rathnayaka *et al.* 2019, Tibpromma *et al.* 2019). The genus *Lonicericola*

Accepted by Sajeewa Maharachchikumbura: 14 May 2020; published: 27 May 2020

Asian Journal of Mycology 3(1): 456–472 (2020) ISSN 2651-1339

www.asianjournalofmycology.org **Article**

Doi 10.5943/ajom/3/1/16

Two new Sordariomycetes records from forest soils in Thailand

Yasanthika WAE[1,2,6], Wanasinghe DN[3,4,5], Karunarathna SC[3,4,5], Bhat DJ[7], Samarakoon SMBC[1,2], Ren GC[1,3], Monkai J[1], Mortimer PE[3,5], Hyde KD[1,2,6*]

[1] Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand
[2] School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand
[3] CAS Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan, People's Republic of China
[4] World Agroforestry Centre, East and Central Asia, 132 Lanhei Road, Kunming 650201, Yunnan, People's Republic of China
[5] Centre for Mountain Futures (CMF), Kunming Institute of Botany, Kunming 650201, Yunnan, People's Republic of China
[6] Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Guang Dong Province, People's Republic of China
[7] Formerly, Department of Botany, Goa University, Goa, India; House No. 128/1-J, Azad Co-Op Housing Society, Curca, P.O. Goa Velha-403108, India

Yasanthika WAE, Wanasinghe DN, Karunarathna SC, Bhat DJ, Samarakoon SMBC, Ren GC, Monkai J, Mortimer PE, Hyde KD 2020 – Two new Sordariomycetes records from forest soils in Thailand. Asian Journal of Mycology 3(1), 456–472, Doi 10.5943/ajom/3/1/16

Abstract

Forest soils contain relatively high levels of fungal diversity compared to other soil types and are primarily comprised of pathogens, saprobes or mutualists. This study was conducted to investigate the fungal diversity of mixed deciduous forest soils in Thailand. Fungi were isolated using a dilution plate method and are illustrated, described and subjected to combined phylogenetic analyses (maximum likelihood and Bayesian analyses). We herewith report *Beltraniella fertilis* and *Stachybotrys subcylindrospora* for the first time from mixed deciduous forest soils of northern Thailand.

Key words – *Beltraniella fertilis* – dilution plate method – phylogeny – soil fungi – *Stachybotrys subcylindrospora*

Introduction

Soil is a highly diversified and unique habitat for various types of microorganisms (Bridge & Spooner 2001, Pangging et al. 2019, Wei et al. 2020). A large array of taxonomic and functional groups of fungi are found in soil ecosystems. These fungal groups have saprobic, pathogenic and mutualistic (mycorrhizal) nutritional modes, all of which play major roles in plant growth and nutrient cycling in forest ecosystems (Taylor & Sinsabaugh 2015, Shi et al. 2019). Besides Basidiomycetes, soil fungal taxa largely belong to Sordariomycetes, which are widely distributed across Thailand forest soils (Tedersoo et al. 2014, Amma et al. 2018). In our study, we report two species of Sordariomycetes, belonging to Beltraniaceae and Stachybotryaceae, from mixed deciduous forest (dominated by Dipterocarpaceae) soils in northern Thailand.

Submitted 2 September 2020, Accepted 9 October 2020, Published 26 October 2020

Asian Journal of Mycology 5(2): 16–30 (2022) ISSN 2651-1339

www.asianjournalofmycology.org **Article**

Doi 10.5943/ajom/5/2/2

New soil-inhabiting Chaetosphaeriaceous records from Thailand

Yasanthika E[1,2,3], Tennakoon DS[1,2], Farias ARG[1], Bhat DJ[4], Wanasinghe DN[5*]

[1]Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand
[2]School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand
[3]Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Guang Dong Province, People's Republic of China
[4]Formerly, Department of Botany, Goa University, Goa, India; House No. 128/1-J, Azad Co-Op Housing Society, Curca, P.O. Goa Velha-403108, India
[5]Center for Mountain Futures, Kunming Institute of Botany, Honghe County 654400, Yunnan, People's Republic of China

Yasanthika E, Tennakoon DS, Farias ARG, Bhat DJ, Wanasinghe DN. 2022 – New soil-inhabiting Chaetosphaeriaceous records from Thailand. Asian Journal of Mycology 5(1), 16–30, Doi 10.5943/ajom/5/1/2

Abstract

Soil fungi represent the most abundant and diverse taxonomic group on Earth. Tropical forest soil-based habitats contain both edaphic and climatic factors that boost fungal activities in soil. Despite having vital functions in terrestrial ecosystems, information on diversity, taxonomy, and ecological preferences of soil fungi on a global scale is lacking. This study focuses on fungal species inhabiting tropical forest soils in Krabi, Thailand. Fungal isolation was performed using the soil dilution plate method, and species delimitation was conducted via morphological characterization and phylogenetic analyses. *Chloridium gonytrichii* and *Kionochaeta microspora* are introduced herein as the soil-inhabiting records from Thailand. For each species, comprehensive descriptions and micrographs are provided.

Keywords – *Ascomycota* – *Chaetosphaeriaceae* – *Chloridium* – *Kionochaeta* – taxonomy

Introduction

Fungi are a heterogeneous group of organisms, representing a large and distinct component of microbial diversity (Naranjo-Ortiz & Gabaldon 2019, Maharachchikumbura et al. 2021). Most are cosmopolitan and feature wide geographical distribution across terrestrial and aquatic environments, including soil habitats (Coleine et al. 2018, Wu et al. 2019). They exhibit diverse lifestyles as biotrophs, endophytes, epiphytes, fungicolous, hemibiotrophs, and saprobes (Rodriguez & Redman 1997, Coleine et al. 2018, Wu et al. 2019). Global fungal diversity has been estimated to range between 2.8 to 3.8 million fungal species (Hawksworth & Lücking 2017). Recently, this has been updated by Baldrian et al. (2021), who, based on high-throughput sequencing, suggested that global fungal diversity could reach up to 6.28 million species. Nevertheless, only 1.08 million species are currently published, and it is clear that numerous species remain undescribed. One possible reason for the observed discrepancy is because fungi are cosmopolitan, featuring a wide geographical distribution across many countries on various substrates (Coleine et al. 2018, Tedersoo et al. 2020). For example, soil fungal diversity is not studied much in most Asian countries, such as Thailand (Amma et al. 2018).

Chaetosphaeriaceae (*Chaetosphaeriales*) is a genera-rich family in *Sordariomycetes*

Submitted 21 October 2021, Accepted 20 January 2022, Published 1 Febuary 2022
Corresponding Author: Dhanushka N. Wanasinghe – e-mail – dnadeeshan@gmail.com

Phytotaxa 513 (3): 203–225
https://www.mapress.com/j/pt/
Copyright © 2021 Magnolia Press

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.513.3.2

Taxonomic and phylogenetic insights into novel Ascomycota from contaminated soils in Yunnan, China

ERANDI YASANTHIKA[1,2,4,8], DHANUSHKA N. WANASINGHE[3,9], GUANG-CONG REN[1,2,10], SAMANTHA C. KARUNARATHNA[3,11], DANUSHKA S. TENNAKOON[1,2,12], JUTAMART MONKAI[1,13], HENG GUI[3,14], PETER E. MORTIMER[3,15], SAISAMORN LUMYONG [5,6,7,16] & KEVIN D. HYDE[1,2,4,5,17*]

[1] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[2] *School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[3] *Center for Mountain Futures, Kunming Institute of Botany, Honghe County 654400, Yunnan, People's Republic of China*
[4] *Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Guang Dong Province, People's Republic of China*
[5] *Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand*
[6] *Research Center of Microbial Diversity and Sustainable Utilization, Chiang Mai University, Chiang Mai 50200, Thailand*
[7] *Academy of Science, The Royal Society of Thailand, Bangkok 10300, Thailand*
[8] eyasanthika@gmail.com; https://orcid.org/0000-0002-3757-3801
[9] dnadeeshan@gmail.com; https://orcid.org/0000-0003-1759-3933
[10] guangcong.ren@gmail.com; https://orcid.org/0000-0001-9923-2626
[11] samakaru931@yahoo.com; https://orcid.org/0000-0001-7080-0781
[12] danushkasandaruwanatm@gmail.com; https://orcid.org/0000-0003-2306-1255
[13] mjutamart@gmail.com; https://orcid.org/0000-0001-6043-0625
[14] guiheng@mail.kib.ac.cn; https://orcid.org/0000-0002-0946-1589
[15] petermortimer@mac.com; https://orcid.org/0000-0003-3188-9327
[16] saisamorn.l@cmu.ac.th; https://orcid.org/0000-0002-6485-414X
[17] kdhyde3@gmail.com; https://orcid.org/0000-0002-2191-0762
* *Corresponding author:* kdhyde3@gmail.com

Abstract

Industrial soil contamination negatively affects flora and fauna in the soil. Nevertheless, some fungi have the ability to survive in such polluted soils. In this study, we isolated fungal strains from polluted soils in industrialized areas of Kunming City, Yunnan Province, China. Fungal strains underwent morphological observations, subjected to phylogenetic analyses and subsequently described using morphological characterizations and multigene phylogenetic inferences. The molecular data of partial nuclear ribosomal DNA (rDNA) (LSU, SSU and ITS) and protein-coding genes (*tef*1-α, *rpb*2 and *btub*) were used to resolve the phylogeny of newly generated sequences. Maximum likelihood and Bayesian inference analyses were constructed to clarify phylogenetic affinities. Based on the biphasic approach of incorporating morphology and molecular data, we introduce one new species, *Juxtiphoma yunnanensis sp. nov.* (Didymellaceae, Pleosporales), two new records *viz. Lecanicillium dimorphum* (J.D. Chen) Zare & W. Gams (Cordycipitaceae, Hypocreales) and *Scopulariopsis brevicaulis* (Sacc.) Bainier (Microascaceae, Microascales) inhabit polluted soils in China.

Keywords: 1 new species, Dothideomycetes, *Juxtiphoma*, *Lecanicillium*, *Scopulariopsis*, soil fungi, Sordariomycetes

Introduction

Due to the anthropogenic activities engaged in industry, farming and engineering, urban soils have been altered and contaminated worldwide (Fokaides *et al*. 2016, Yang *et al*. 2016, Guilland *et al*. 2018, Hu *et al*. 2018, Murata & Kawai 2018, Hyde *et al*. 2019, Lu *et al*. 2020, Renella 2020). Contaminated soils contain excessive quantities of heavy metals and metalloids (Cyanides, Zinc, Lead, Cadmium, and Arsenic) as well as organic and chemical pollutants (Newbound

Mycosphere 13(1): 724–751 (2022) www.mycosphere.org ISSN 2077 7019
Article
Doi 10.5943/mycosphere/13/1/8

The importance of culture-based techniques in the genomic era for assessing the taxonomy and diversity of soil fungi

Yasanthika WAE[1,2,3], Wanasinghe DN[4], Mortimer PE[4], Monkai J[5,6] and Farias ARG[1,*]

[1]Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand
[2]School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand
[3]Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Guangdong Province, People's Republic of China
[4]Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Sciences, Honghe County 654400, Yunnan, People's Republic of China
[5]Research Center of Microbial Diversity and Sustainable Utilization, Chiang Mai University, Chiang Mai 50200, Thailand
[6]Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand

Yasanthika WAE, Wanasinghe DN, Mortimer PE, Monkai J, Farias ARG 2022 – The importance of culture-based techniques in the genomic era for assessing the taxonomy and diversity of soil fungi. Mycosphere 13(1), 724–751, Doi 10.5943/mycosphere/13/1/8

Abstract

Fungi are a diverse and highly abundant group of organisms found in soils worldwide. Understanding fungi is essential as they are key drivers of below-ground ecosystem functions. Taxonomy is a fundamental discipline, acting as the initial step toward biodiversity, ecology, and biotechnology studies. Both culture-dependent and -independent methods are employed in the taxonomic investigations of soil-dwelling taxa. High-throughput sequencing (HTS) is a genomic-based method widely applied in global studies that has revealed numerous unculturable soil taxa. However, this method is limited by its inability to link physical specimens to species identification. Culturing methods result in specimens that can be used to obtain genetic sequences and morphological data in applied studies. Thus, combining both methods is an important trend in taxonomic studies. This review discusses how culturing is important for soil fungal discovery and describes the main culturing methods. It also briefly addresses the role of HTS in taxonomy and its drawbacks, and the potential to combine both culture-dependent and -independent methods to gain

Phytotaxa 609 (1): 017–044
https://www.mapress.com/pt/
Copyright © 2023 Magnolia Press

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.609.1.3

Isolation and characterization of novel *Dothideomycetes* species from forest soils in Chiang Rai and Krabi (Thailand): additions to the diversity of *Curvularia* and *Verruconis*

W. A. ERANDI YASANTHIKA[1,2,3,9], DANUSHKA S. TENNAKOON[4,5,10], ANTONIO R. GOMES DE FARIAS[2,11], K. W. THILINI CHETHANA[1,2,12*], D. JAYARAMA BHAT[6,7,13] & DHANUSHKA N. WANASINGHE[8,14*]

[1] *School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[2] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[3] *Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Guang Dong Province, People's Republic of China*
[4] *Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand*
[5] *Research Center of Microbial Diversity and Sustainable Utilization, Chiang Mai University, Chiang Mai 50200, Thailand*
[6] *Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 2455, Riyadh 11451, Saudi Arabia*
[7] *Formerly, Department of Botany, Goa University, Goa, India; House No. 128/1-J, Azad Co-Op Housing Society, Curca, P.O. Goa Velha-403108, India*
[8] *Center for Mountain Futures, Kunming Institute of Botany, Chinese Academy of Science, Honghe County 654400, Yunnan, People's Republic of China*
[9] ✉ *eyasanthika@gmail.com;* https://orcid.org/0000-0002-3757-3801
[10] ✉ *danushkasandaruwanatm@gmail.com;* https://orcid.org/0000-0003-2306-1255
[11] ✉ *rfariasagro@gmail.com;* https://orcid.org/0000-0003-4768-1547
[12] ✉ *kandawatte.thi@mfu.ac.th;* https://orcid.org/0000-0002-5816-9269
[13] ✉ *bhatdj@gmail.com;* https://orcid.org/0000-0002-3800-5910
[14] ✉ *dnadeeshan@gmail.com;* https://orcid.org/0000-0003-1759-3933
**Corresponding authors:* ✉ *dnadeeshan@gmail.com,* ✉ *kandawatte.thi@mfu.ac.th*

Abstract

Fungi are adapted to diverse environments, where the forest soils have complex fungal communities with a wide range of lifestyles. This study aims to explore and isolate *Dothideomycetes* from the forest soils in Thailand. Sampling sites were located in Chiang Rai and Krabi provinces. Cultures were obtained through soil dilution series, and the strains were subjected to morphological observations and multigene phylogenetic analyses for identification. Maximum likelihood and Bayesian inference analyses were conducted to clarify their phylogenetic affinities using partial nuclear ribosomal DNA (ITS, LSU, and SSU) and the protein-coding genes (*tef*1-α and *GADPH*). Herein, two new species (*Curvularia chiangraiensis sp. nov.* and *Verruconis soli sp. nov.*) and two new records (*C. chiangmaiensis* and *V. thailandica*) are described based on the morphological and phylogenetic evidence. *Curvularia chiangraiensis sp. nov.* is distinguished by its relatively smaller conidia and the presence of sympodial proliferation of conidiogenesis and *Verruconis soli sp. nov.* exhibits micronematous conidiophores and obovoid conidia that transform into sub-cylindrical or ellipsoidal shapes, and becoming 1-septate when mature. These unique characteristics set them apart from closely related taxa. The newly described taxa have been subjected to a thorough comparison with closely related species, enabling a comprehensive analysis. The study offers detailed descriptions and includes high-quality micrographs, with the aim of providing a comprehensive understanding of these newly identified taxa

Keywords: 2 new records, 2 new species, *Ascomycota*, *Pleosporales*, *Venturiales*

Introduction

Fungi are diverse microorganisms that play important functional roles in soil ecosystems (Tedersoo *et al.* 2017, 2021, Shi *et al.* 2022). In particular, they regulate nutrient cycling, disease suppression, and water dynamics, which promote

Studies in Fungi

ARTICLE

Open Access

https://doi.org/10.48130/SIF-2023-0016
Studies in Fungi **2023**, 8:16

https://soilfun.org/, a web-based platform for soil-inhabiting *Ascomycota* species

Weeragalle Arachchillage Erandi Yasanthika[1,2,3], Antonio Roberto Gomes de Farias[1*], Dhanushka N. Wanasinghe[4], Kandawatte Wedaralalage Thilini Chethana[1,2], Rasoul Zare[5], Lei Cai[6], Sajeewa S. N. Maharachchikumbura[7], Danushka S. Tennakoon[8,9], Rekhani Hansika Perera[10], Thatsanee Luangharn[1] and Putarak Chomnunti[2]

[1] *Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[2] *School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand*
[3] *Innovative Institute for Plant Health, Zhongkai University of Agriculture and Engineering, Guang Dong Province 510225, PR China*
[4] *Center for Mountain Futures, Kunming Institute of Botany, Honghe County 654400, Yunnan, PR China*
[5] *Iranian Research Institute of Plant Protection (IRIPP), Agricultural Research, Education and Extension Organization, PO Box 1454, Tehran 19395, Iran*
[6] *State Key Lab of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, PR China*
[7] *University of Electronic Science and Technology of China, Chengdu 611731, PR China*
[8] *Department of Biology, Faculty of Science, Chiang Mai University, Chiang Mai 50200, Thailand*
[9] *Research Center of Microbial Diversity and Sustainable Utilization, Chiang Mai University, Chiang Mai 50200, Thailand*
[10] *School of Biological Sciences and Institute of Microbiology, Seoul National University, Seoul 08826, Republic of Korea*
* Corresponding author, E-mail: antonio.gom@mfu.ac.th

Abstract

Soil covers a large area of the earth's crust and supports a high level of bio-diversity. This diversity is influenced by numerous geobiological variables, which impact soil fungal distribution worldwide. The taxonomy of soil-associated fungi has been investigated over the years using various approaches. To recover below-ground fungal species, researchers currently use culture-dependent and culture-independent approaches such as high-throughput techniques. As a result, a significant amount of taxonomic information is being generated and scattered throughout many publications. Most recent publications and databases of soil *Ascomycota* are derived from high-throughput techniques mainly focused on higher taxonomic ranks; however, information of the genera and species identified from soils are not conglomerated into a single database. Therefore, the Soil Fungi website aims to create an online platform to compile the soil-associated fungal species with comprehensive taxonomic descriptions and continuously update them following the most recent classifications. The scattered information will be obtained from publications and conglomerated on the website where users have quick and user-friendly access. This paper introduces the https://soilfun.org/ website with its objectives and functions and provides a guideline for accessing and retrieving information. The website will serve as a central database of soil-associated fungal species, including their taxonomic descriptions and other relevant information. Users will be able to access and retrieve information from the website easily. The Soil Fungi website will be an essential tool for researchers, students, and other interested parties in soil mycology.

Citation: Yasanthika WAE, Gomes de Farias AR, Wanasinghe DN, Chethana KWT, Zare R, et al. 2023. https://soilfun.org/, a web-based platform for soil-inhabiting *Ascomycota* species. *Studies in Fungi* 8:16 https://doi.org/10.48130/SIF-2023-0016

Introduction

Soil is a remarkably complex substrate that provides various niches for microbial communities. In this environment, fungi are the main biotic component and mediate many below-ground functions. However, their distribution is variable due to inconsistencies in resource levels (nutrition, soil, water, and air)[1,2]. Besides, most fungi spend at least one stage of their life in the soil, showing different trophic modes such as pathogenic, saprobic, or mutualistic[3,4]. Studies have shown that *tiomycetes*, *Leotiomycetes*, and *Sordariomycetes*[5–7,10,11]. Of them, some genera, such as *Fusarium*, *Penicillium*, and *Phoma*, are prevalent[7,12], while others, such as *Ambrosiella*, *Arcopilus*, *Didymocyrtis*, *Kionochaeta*, and *Parathyridaria* have rarely been isolated[13–15]. This is because exclusive adaptations to below-ground environments and a lack of isolation techniques make it difficult to recover *Ascomycota* species. Most soil ascomycetes are identified at higher taxonomic ranks through HTS, which led to many recent publications and databases showing the taxonomy and distribution patterns of belowground fungi only

Phytotaxa 676 (1): 001–024
https://www.mapress.com/pt/
Copyright © 2024 Magnolia Press

Article

ISSN 1179-3155 (print edition)
PHYTOTAXA
ISSN 1179-3163 (online edition)

https://doi.org/10.11646/phytotaxa.676.1.1

Taxonomic novelties of soil-inhabiting pleosporalean fungi in Thailand using baiting method

W.A.E. YASANTHIKA[1,2,3,8], K.W.T. CHETHANA[1,2,9*], D.N. WANASINGHE[4,5,10], D.S. TENNAKOON[6,11], F. AL-OTIBI[7,12] & K.D. HYDE[1,2,7,13*]

[1]*School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[2]*Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, 57100, Thailand*
[3]*Innovative Institute of Plant Health, Zhongkai University of Agriculture and Engineering, Guang Dong Province, People's Republic of China*
[4]*Department of Soil Science, College of Food and Agriculture Sciences, King Saud University, P.O. Box 145111, Riyadh 11362, Saudi Arabia*
[5]*Center for Mountain Futures, Kunming Institute of Botany, Honghe County 654400, Yunnan, People's Republic of China*
[6]*Shenzhen Key Laboratory of Microbial Genetic Engineering, College of Life Sciences and Oceanography, Shenzhen University, Shenzhen 518060, China*
[7]*Department of Botany and Microbiology, College of Science, King Saud University, P.O. Box 22452, Riyadh 11495, Saudi Arabia*
[8] *eyasanthika92@gmail.com; https://orcid.org/0000-0002-3757-3801*
[9] *kandawatte.thi@mfu.ac.th; https://orcid.org/0000-0002-5816-9269*
[10] *dnadeeshan@gmail.com; https://orcid.org/0000-0003-1759-3933*
[11] *danushkasandaruwanatm@gmail.com; https://orcid.org/0000-0003-2306-1255*
[12] *falotibi@ksu.edu.sa; https://orcid.org/0000-0003-3629-5755*
[13] *kdhyde3@gmail.com; https://orcid.org/0000-0002-2191-0762*
**Authors for correspondence*

Abstract

Ascomycota exhibit a cosmopolitan distribution across soil ecosystems, with notably higher diversity in tropical forests. The climatic and edaphic conditions in the natural forests of Thailand create a favorable niche for soil-dwelling *Ascomycota*. This study explores cellulophilic and keratinophilic pleosporalean taxa in tropical forest soils of Thailand. Species isolation was conducted using the soil baiting method, followed by a polyphasic approach for species identification. This included morphological characterization and phylogenetic analyses using maximum likelihood and Bayesian methods. The study identifies a new species, *Neptunomyces soli* (*Didymosphaeriaceae*) and a new habitat record for *Curvularia dactylocteniicola* (*Pleosporaceae*). The species are presented with comprehensive descriptions and micrographs, and their potential cellulophilic and keratinophilic characteristics are discussed.

Key words: 1 new species, *Ascomycota*, *Didymosphaeriaceae*, *Pleosporaceae*, soil fungi

Introduction

CURRICULUM VITAE

NAME Weeragalle Arachchillage Erandi Yasanthika

EDUCATIONAL BACKGROUND

2018 Bachelor of Science in Agricultural Technology & Management
Agricultural Extension
University of Peradeniya, Sri Lanka

SCHOLARSHIP

2019 Postgraduate Scholarship offered by the Center of Excellence in Fungal Research, Mae Fah Luang University, Thailand

PUBLICATION

First author Publications

Yasanthika, E., Dissanayake, L. S., Wanasinghe, D. N., Karunarathna, S. C., Mortimer, P. E., Samarakoon, B. C., . . . Hyde, K. D. (2020). *Lonicericola fuyuanensis* (Parabambusicolaceae): A new terrestrial pleosporalean ascomycete from Yunnan Province, China. *Phytotaxa, 446*(2), 103–113.

Yasanthika, W. A. E., Wanasinghe, D. N., Karunarathna, S. C., Bhat, D. J., Samarakoon, S. M. B. C., Ren, G. C., . . . Hyde, K. D. (2020). Two new Sordariomycetes records from forest soils in Thailand. *Asian Journal of Mycology, 3*, 456–472.

Yasanthika, W. A. E., Wanasinghe, D. N., Ren, G. C., Karunarathna, S. C., Tennakoon, D. S., Monkai, J., . . . Hyde, K. D. (2021). Taxonomic and phylogenetic insights into novel Ascomycota from contaminated soils in Yunnan, China. *Phytotaxa, 513*, 203–225.

Yasanthika, W. A. E., Tennakoon, D. S., Farias, A. R. G., Bhat, D. J., & Wanasinghe, D. N. (2022). New soil-inhabiting Chaetosphaeriaceous records from Thailand. *Asian Journal of Mycology, 5*, 16–30.

Yasanthika, W. A. E., Wanasinghe, D. N., Mortimer, P. E., Monkai, J., & Farias, A. R. G. (2022). The importance of culture-based techniques in the genomic era for assessing the taxonomy and diversity of soil fungi. *Mycosphere, 13*, 724–751.

Yasanthika, W. A. E., Tennakoon, D. S., Gomes de Farias, A. R., Chethana, K. W. T., Bhat, J., & Wanasinghe, D. N. (2023). Isolation and characterization of novel Dothideomycetes species from forest soils in Chiang Rai and Krabi (Thailand): Additions to the diversity of *Curvularia* and *Verruconis*. *Phytotaxa, 609*, 17–44.

Yasanthika, W. A. E., Gomes de Farias, A. R., Wanasinghe, D. N., Chethana, K. W. T., Zare, R., Cai, L., . . . Chomnunti, P. (2023). https://soilfun.org/, a web-based platform for soil-inhabiting *Ascomycota* species. *Studies in Fungi, 8*.

Yasanthika, W. A. E., Chethana, K. W. T., Wanasinghe, D. N., Tennakoon, D. S., Al-Otibi, F., & Hyde, K. D. (2024). Taxonomic novelties of soil-inhabiting pleosporalean fungi in Thailand using baiting method. *Phytotaxa, 676*, 1–24.

Yasanthika, W. A. E., Chethana, K. W. T., Fatimah Al-Otibi, Wanasinghe, D. N., Tennakoon, D. S., Samarakoon, M. C., . . . Hyde, K. D. (2025). Genera of soil *Ascomycota* and an account of soil-inhabiting species isolated from Thailand. *Manuscript submitted for publication*.

Co-author Publications

Chethana, K. W. T., Rathnayaka, A. R., Samarakoon, B. C., Wu, N., Wijesinghe, S. N., Yasanthika, W. A. E., . . . Hyde, K. D. (2023). AJOM new records and collections of fungi: 151–200. *Asian Journal of Mycology, 6*(2), 89–243.

Gomes de Farias, A. R., Yasanthika, W. A. E., & Monkai, J. (2023). Insights into the profile of soil fungal diversity in Thailand. *Asian Journal of Mycology, 6*(2), 305–317.

Htet, Y. M., Yasanthika, W. A. E., Hurdeal, V. G., & de Farias, A. R. G. (2024). *Absidia thailandica* sp. nov., an addition to the diversity of soil fungi from Thailand. *Phytotaxa, 646*(2), 157–168.

Hyde, K. D., Abdel-Wahab, M. A., Abdollahzadeh, J., Abeywickrama, P. D., Absalan, S., Afshari, N., . . . Ertz, D. (2023). Global consortium for the classification of fungi and fungus-like taxa. *Mycosphere, 14*(1), 1960–2012.

Hyde, K. D., Amuhenage, T. B., Apurillo, C. C. S., Asghari, R., Aumentado, H. D., Bahkali, A. H., . . . Dai, D. Q. (2023). *Fungalpedia*, an illustrated compendium of the fungi and fungus-like taxa. *Mycosphere, 14*(1), 1835–1959.

Hyde, K. D., Tennakoon, D. S., Jeewon, R., Bhat, D. J., Maharachchikumbura, S. S., Rossi, W., . . . Doilom, M. (2019). Fungal diversity notes 1036–1150: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity, 96*, 1–242.

Hyde, K. D., Xu, J., Rapior, S., Jeewon, R., Lumyong, S., Niego, A. G. T., . . . Stadler, M. (2019). The amazing potential of fungi: 50 ways we can exploit fungi industrially. *Fungal Diversity, 97*, 1–136.

Mikryukov, V., Dulya, O., Zizka, A., Bahram, M., Hagh-Doust, N., Anslan, S., . . . Tedersoo, L. (2023). Connecting the multiple dimensions of global soil fungal diversity. *Science Advances, 9*(48), eadj8016.

Ren, G., Wanasinghe, D. N., de Farias, A. R. G., Hyde, K. D., Yasanthika, E., Xu, J., . . . Gui, H. (2022). Taxonomic novelties of woody litter fungi (Didymosphaeriaceae, Pleosporales) from the Greater Mekong Subregion. *Biology, 11*(11), 1660.

Ren, G. C., Wanasinghe, D. N., Wei, D. P., Monkai, J., Yasanthika, E., Gui, H., . . . Hyde, K. D. (2020). *Loculosulcatispora thailandica* gen. et sp. nov. (Sulcatisporaceae), saprobic on woody litter in Thailand. *Phytotaxa, 475*, 67–78.

Tedersoo, L., Mikryukov, V., Anslan, S., Bahram, M., Khalid, A. N., Corrales, A., . . . Abarenkov, K. (2021). The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. *Fungal Diversity, 111*, 573–588.

Tedersoo, L., Mikryukov, V., Zizka, A., Bahram, M., Hagh-Doust, N., Anslan, S., . . . Abarenkov, K. (2022). Global patterns in endemicity and vulnerability of soil fungi. *Global Change Biology, 28*(22), 6696–6710.