

TAXONOMY AND PHYLOGENY OF PATHOGENIC ASCOMYCETE GENERA ASSOCIATED WITH MANGROVES

CHADA NORPHANPHOUN

DOCTOR OF PHILOSOPHY
IN
BIOSCIENCES

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

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Chada Norphanphoun

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Author	Chada Norphanphoun
Degree	Doctor of Philosophy (Biosciences)
Advisor	Assoc. Prof. Kevin David Hyde, Ph. D.

ABSTRACT

In this study, the taxonomy of mangrove and other fungi are investigated using a dual taxonomic approach including morphological and molecular analyses. Fungal specimens associated with various hosts in terrestrial habitats were collected from Italy, Russia, Taiwan, and Thailand. The collections were morphologically examined and their DNA sequence data from rDNA loci and protein coding genes (ITS, LSU, SSU, *ef1-α*, *β-tubulin*, *act*, *endoPG*, *gapdh*, *rpb2*, *Alta1*, OPA10-2) were analysed to verify their identities and phylogenetic affinities to better assess their natural placement. The backbone tree reflects a more natural classification for all the fungal groups considered in this study. Descriptions, illustrations, and rationales for these novelties are provided for each taxon. Morphological differences and analysis of datasets of single genes and combined sequences support the validity of the species in this study and their placement. Forty-one species are accommodated in ten genera (*Alternaria*, *Cytospora*, *Hercospora*, *Lamproconium*, *Melomastia*, *Neopestalotiopsis*, *Pestalotiopsis*, *Phyllosticta*, *Pseudopestalotiopsis*, *Seimatosporium*), six families (Botryosphaeriaceae, Cytosporaceae, Lamproconiaceae, Pleosporaceae, Pleurotremaceae, Sporocadaceae). Novel fungal taxa that described include one new family (Lamproconiaceae), 32 new species (*Cytospora ampulliformis*, *C. curvata*, *C. donetzica*, *C. erumpens*, *C. longiostiolata*, *C. lumnitzericola*, *C. melnikii*, *C. parakantschavelii*, *C. paratranslucens*, *C. rusanovii*, *C. salicacearum*, *C. salicina*, *C. sorbi*, *C. sorbicola*, *C. thailandica*, *C. ulmi*, *C. xylocarpi*, *Melomastia italica*, *Neopestalotiopsis acrostichi*, *N. brachiate*, *N. petila*, *N. rhizophorae*,

N. sonneratae, *N. thailandica*, *Pestalotiopsis rhizophorae*, *P. thailandica*, *Pseudopestalotiopsis avucenniae*, *Ps. curvatispora*, *Ps. rhizophorae*, *Ps. thailandica*, *Phyllosticta rhizophorae*, *Seimatosporium physocarpi*), one designed epitype (*Seimatosporium rosae*), two reference specimens (*Lamproconium desmazieresi*, *S. lichenicola*), a recombined species (*Melomastia maolanensis*), new host records for four species (*Alternaria gaisen*, *C. nivea*, *C. parasitica*, *C. salicicola*), and a studied herbarium specimens (*Hercospora tiliae*).

Two complex genera, *Diaporthe* and *Phyllosticta* are revisited with morphological evidence coupled with support from multi-gene phylogeny of single gene trees and combined sequence data. Herein, we assembled a comprehensive dataset and for *Diaporthe* with ITS, *ef1 α*, *β-tubulin*, *cal* and *his3* sequence data. Thirteen workable species complexes for *Diaporthe* were introduced, including the *D. arecae*, *D. biconispora*, *D. carpini*, *D. decedens*, *D. eres*, *D. oncostoma*, *D. pustulata*, *D. rudis*, *D. scobina*, *D. sojae*, *D. toxica*, *D. varians*, and *D. vawdreyi* species complexes. Nine species were kept as singletons (*D. acerina*, *D. acutispora*, *D. crataegi*, *D. multiguttulata*, *D. ocoteae*, *D. perjuncta*, *D. pseudoalnea*, *D. spartinicola*, *D. undulata*). Two genera of Diaporthaceae, are synonymized under genus *Diaporthe*, *D. cyatheae* (≡ *Ophiodiaporthe cyatheae*) and *D. pseudobauhiniae* (≡ *Chiangraiomyces bauhiniae*).

Six workable species complexes of *Phyllosticta* were introduced to assemble a comprehensive ITS, LSU, *ef1α*, *actin*, and *gapdh* dataset and reconstruct phylogenetic trees with combined sequence data. From this study, we synonymize two strains of *P. capitalensis* under the *P. rhizophorae*. Six strains are mentioned as unnamed species and probably represent new species. The phylogenetic relationships of *Phyllosticta* species will be revaluated and provide guidance for future work.

The phylogeny of *Diaporthe* (Diaporthaceae) and *Phyllosticta* (Phyllostic--taceae) received new assessments and suggestions for future work. All data presented herein are based on morphological examination of specimens, coupled with

phylogenetic sequence data to better integrate taxa into appropriate taxonomic ranks and infer their evolutionary relationships. The current study provided complete descriptions and illustrations for all the taxa introduced.

Keywords: Ascomycota, Dothideomycetes, Endophytic, Fungal Diversity, New species, Pathogenic, Phylogeny, Saprobic, Sordariomycetes, Taxonomy

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ABBREVIATIONS AND SYMBOLS

bp	base pair
cm	centimeter
com.	combination
dH_2O	distilled water
diam.	diameter
e.g.	for example
et al.	and others
g	gram
gen.	genus (singular) and genera (plural)
i.e.	that is
l	litre
ml	millilitre
mm	millimeter
mg	milligram
No.	number
nov.	novum (Latin for new thing)
sp.	species
spp.	species (plural)
viz.	number
$\bar{x}$	average
°C	degree centigrade
=	heterotypic (taxonomic, facultative) a synonym
≡	homotypic (nomenclatural, obligate) a synonym
µm	micrometer
µl	microliter
%	percent

ABBREVIATIONS AND SYMBOLS (continued)

α	alpha
β	beta

CHAPTER 1

INTRODUCTION

1.1 Selected Ascomycetes

Fungi are thought to be the second most diverse organism kingdom behind insects (Animalia Kingdom) on earth, with approximately 1.5 million species being the generally accepted figure. However, it is thought that only 15% of fungi are presently known. Ascomycota is a division of the kingdom Fungi. The members of Ascomycota are known as sac fungi, which are the largest phylum of fungi with more than 64,000 species. The ability to accurately identify fungi has advanced significantly with the use of molecular data. Previously, mycologists identified species based on morphology and naming of species was very much subjective and, in most cases, involved clumping species in morphological similar species, now known as species complexes. It is now possible to identify genera and species, including cryptic species, by DNA sequence analyses of single spore isolates of the taxa collected. Sequence data can also directly be obtained from the fungi, especially from basidiomycetes; with microfungi it is more difficult, but is possible if enough material is available. As long as one is aware that GenBank sequences are mostly wrongly named, and that analyses must therefore use DNA sequence data from type strains, it is relatively easy to identify species in the better studied and important genera. Dothideomycetes and Sordariomycetes are the most diversity of fungi that have been founded in the world.

Dothideomycetes and Sordariomycetes are an important class of ascomycetes, which were covered most fungi that have been reported. With some are phytopathogens causing leaf, stem, root and fruit diseases, while some are pathogenic to arthropod and mammals. Some members are endophytes and some are saprobes involved in decomposition and nutrient cycling. Some taxa are economically important as biocontrol agents and some species produce a important secondary metabolites

(Gostinčar et al., 2018; Harman et al., 2004; Hyde et al., 2019; Maharachchikumbura et al., 2014, 2016b; Norphanphoun et al., 2019; Sun et al., 2019; Zhang & Wang, 2015)

1.1.1 Dothideomycetes

Dothideomycetes is the largest class of Ascomycota, which was consisting more than 19,000 estimated species (Kirk et al., 2008). Dothideomycetes is the class that comprised of economically important fungi as they contain numerous plant pathogens and wood decomposers in harsh habitats, such as marine and dry environments. The class is mostly characterized by ascolocular ascomata and bitunicate, fissitunicate asci (Hongsanan et al., 2020a, b). Many fungi are pleomorphic, having more than one morphology in their life cycles. Phylogenetic studies of Dothideomycetes have been provided by several authors, and provide descriptions, notes and taxonomic placement (Nelsen et al., 2009, 2011; Hyde et al., 2013; Liu et al., 2017; Hongsanan et al., 2020a, b).

1.1.2 Sordariomycetes

Sordariomycetes is the second largest class of Ascomycota (Hyde et al., 2020), characterized by flask-shaped or less frequently cleistothecial ascomata, and unitunicate asci (Maharachchikumbura et al., 2016b; Hyde et al., 2020c), and can have a varied growth form and colonies diverse habitats (Hongsanan et al., 2017). Sordariomycetes has a worldwide distribution and can be found in almost all ecosystems (Pratibha et al., 2014; Jones et al., 2015). Previously, Hyde et al. (2020c) provided an updated class Sordariomycetes description, with represent the morphology and list of accepted genera, also provided economic and ecological significance of families. Sordariomycetes have a cosmopolitan distribution and can be found in almost all ecosystems (Pratibha et al., 2014; Jones et al., 2015). Some Sordariomycetes are phytopathogens causing leaf, stem, root and fruit diseases (e.g. *Colletotrichum*, *Coniella*, *Diaporthe*), while some are pathogenic to arthropod and mammals (eg. *Sporothrix*, *Fusarium*). Some members are endophytes (e.g. *Pestalotiopsis*) (Maharachchikumbura et al., 2014; Norphanphoun et al., 2019) and some are saprobes involved in decomposition and nutrient cycling (Chaetomium, Neurospora) (Zhang & Wang, 2015). Some taxa are fungicolous (Sun et al., 2019) and several are opportunistic pathogens of humans (Gostinčar et al., 2018). Some taxa of Sordariomycetes are

economically important as biocontrol agents (Harman et al., 2004; Hyde et al., 2019) and some species produce a wide range of important secondary metabolites (Maharachchikumbura et al., 2016b).

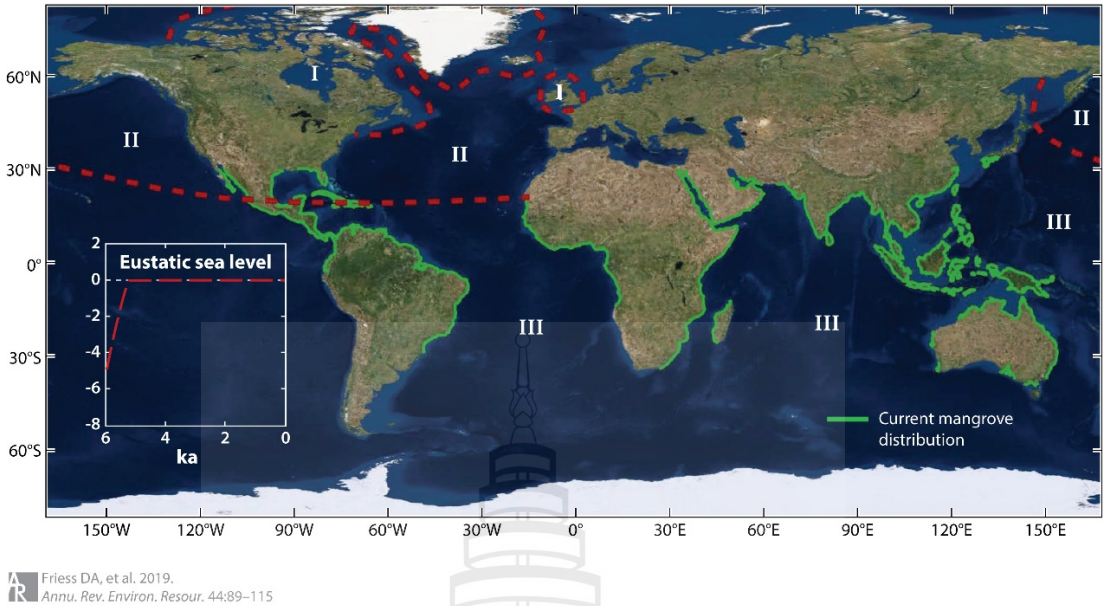
1.1.3 Selected Genera and Allied Species of Dothideomycetes and Sordariomycetes

The taxonomy of some genus in Dothideomycetes and Sordariomycetes class are challenging, which species member have overlapping morphological characters. This makes it difficult to identify characters related to taxonomic classification. Reliance on host associations for traditional identification is even more complicated. For example, *Botryosphaeria*, *Colletotrichum Cytospora*, *Diaporthe*, *Dipodia*, *Fusarium*, *Phyllosticta* etc. Collectively, these problems lead to taxonomic confusion, therefore, molecular phylogenetic greatly facilitate the identification and establishment of species complexes, a closely related organism group that are similar in appearance and the boundaries between them are often unclear (Al-Hatmi et al., 2016; Jayawardena et al., 2016; da Silva et al., 2020). For the same reason and for the sake of communication, the species complexes have been successfully introduced and resorve *viz*. *Colletotrichum*, *Fusarium* etc. (Jayawardena et al., 2016; da Silva et al., 2020), and *Fusarium* (Al-Hatmi et al., 2016).

1.2 Mangroves

1.2.1 Introduction of Mangroves

Mangrove forests are self-sufficient marine vegetation, which found along marshy tidal areas of estuaries and coastal at tropics and subtropics regions, between latitudes 25°N and 25°S (Giri et al., 2011; Hamilton & Casey, 2016; Friess et al., 2019). Mangroves are adapted to extreme, fluctuating conditions of salinity and temperature and to the swampy sediments with low oxygen conditions (Figures 1.1, 1.2, Giri et al., 2011). There are about 110 plant species that are considered mangroves, and the same number of “mangrove associated plants” that occur in mangroves forests, where the genus *Rhizophora* is common throughout the world (Giri et al., 2011; Mildred 2012; Hutchinson et al., 2014).



Note Current mangrove distribution

Source Hamilton and Casey (2016), Friess et al. (2019)

Figure 1.1 Current mangrove distribution

Mangroves have several interesting ecological adaptations (Figure 1.2). *Rhizophora* species feed themselves in marshy soil by producing prop roots and viviparous seedlings, which germination occurs while the seed is still attached the tree (Allen, 1998). *Avicennia* species have “breathing roots” called pneumatophores (Raghukumar, 2017). The enormous amount of decomposing litter produced by the dense vegetation of mangrove trees, the marshy sediments, and winding creeks of a mangrove forest are excellent habitats for fungi (Raghukumar, 2017). Moreover, mangroves are a treasure trove of marine mycologists, with mangrove trees and shrub are knowing as valuable resources for medicinal products in addition to their economic importance (Ananda & Sridhar, 2002; Arfi et al., 2012). The greatest biodiversity occurs in the mangroves of Indonesia, Malaysia and Thailand.

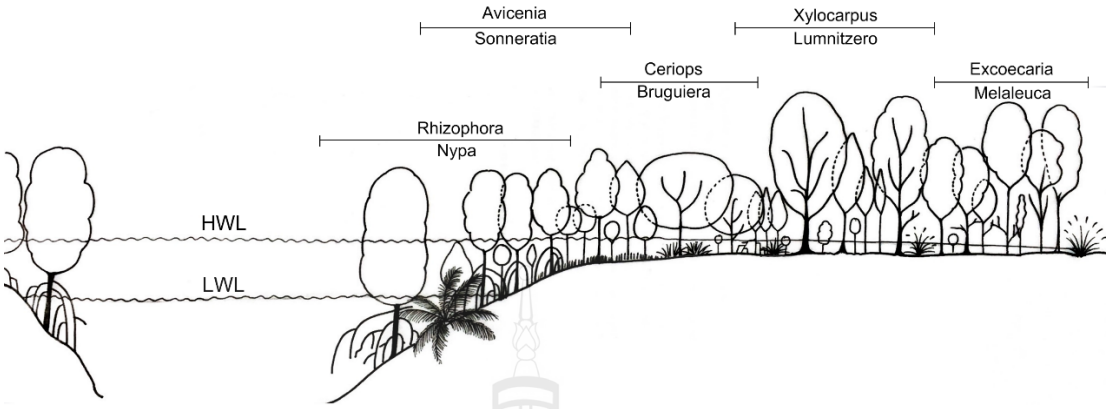


Figure 1.2 Mangrove species zones

1.2.2 Fungi on Mangroves

Most of mangrove fungi belong to the division Pezizomycotina of Phylum Ascomycota, especially in classes Dothideomycetes and Sordariomycetes, as well as marine lignicolous fungi in general (Raghukumar, 2017). Alias and Jones (2009) listed 339 fungi known from mangroves with the majority of ascomycetes. Later, Jones et al. (2015) reported 807 species within 353 genera from marine fungi. Currently, fifty-five mangrove trees and their associates are reported to support 191 higher marine fungi (Alias, 1996). Most studies on fungi of mangrove trees, have listed and identified the fungi taxon (Jones & Kuthubutheen, 1989; Alias & Jones, 2000a, b) and even recent research has discovered new species of fungi of mangrove trees (Pang et al., 2010). As special host plants, mangrove forests are a rich resource for endophytic fungi. More than 200 endophytic fungal species have been isolated and classified from mangrove forests and is the second largest community of marine fungi studied (Gilbert & Sousa, 2002; Thatoi et al., 2013). However, saprobic fungi on mangrove woods, leaves and roots are well-documented (Alias & Jones, 2009; Jones et al., 2009; Pang et al., 2010; Sarma & Hyde, 2001), while endophytic and pathogenic fungi have received much less attention (Alias & Jones, 2009; Hyde & Cannon, 1992; Jones & Pang, 2012).

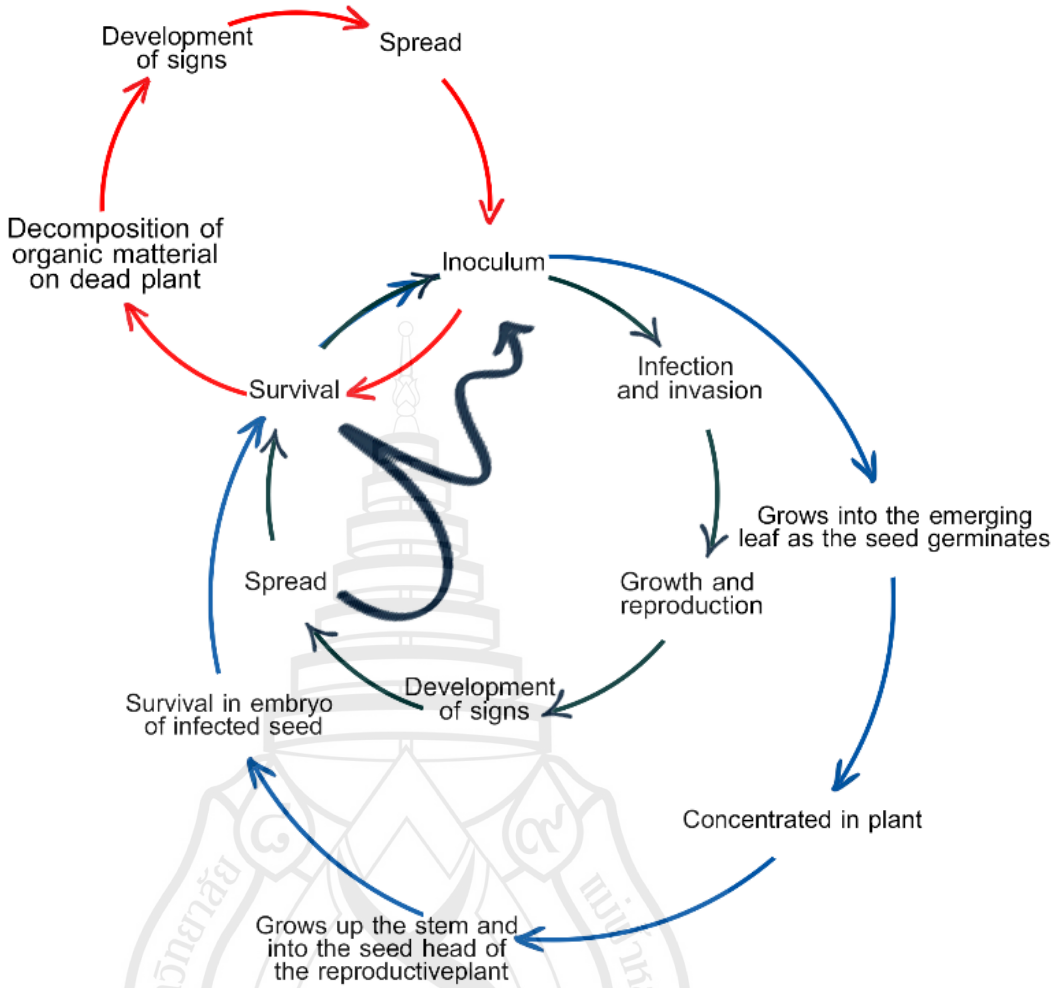


Figure 1.3 A major role of mangrove fungi

Dieback of mangrove trees has been reported to occur throughout Queensland. In Moreton Bay, areas of mangroves dieback have been noted for at least the last 20 years. A soil fungus, *Phytophthora cinnamomi*, caused large areas of dieback around Gladstone, central Queensland. There are also several basidiomycetes that cause disease in mangroves ecosystems, for example heart and butt rots have been identified as serious cause of disease of many tree species (Vollbrecht et al., 1995; Barnard, 2000; Kinge & Mih, 2011). The causal fungi for heart and butt rots are mainly basidiomycetes e.g. *Heterobasidionannosum, Ganoderma, Phellinus, Inonotus* (Ryvarden, 2000; Fox, 2001), as indicated by developing fruiting bodies at or near the base of declining trees (Fox, 2001). In mangroves ecosystems, heart or butt rot has been reported for many

trees and isthe result of fungal infection (Chalermpongse, 1991; Mwangi, 2001; Gilbert et al., 2008). The genus *Phellinus* has been reported as the causative pathogen of mangrove trees in many countries e.g. Brazil, Panama, Kenya, Micronesia and Thailand (Chalermpongse, 1991; Campos & Cavalcanti, 2000; Mwangi, 2001; Gilbert & Sousa, 2002; Campos et al., 2005; Gilbert et al., 2008; Baltazar et al., 2009a, b). In Brazil, *Phellinus mangrovicus* is associated with *Rhizophora* tree mortality (Campos & Cavalcanti, 2000; Campos et al., 2005; Baltazar et al., 2009a), and in Kenya *P. pachyphloeus* and *P. rimosus*, the cause heart and butt rot in old growth stands of *R. apiculata* (Mwangi, 2001). *Phellinus swieteniae* was commonly found associated with live, hollowed out *Avicennia germinans* trees (Gilbert et al., 2008), with *P. mangrovicus* and *P. fastuosus* collected on *Bruguiera gymnorhiza*, *Sonneratia alba*, *Lumnitzera littorea* and *X. granatum* on the islands Kosrae and Pohnpei, Micronesia (Gilbert et al., 2008), while in Thailand several basidiomycetes caused Butt rot of *Xylocarpus granatum* (Sakayaroj et al., 2012).

Avicennia marina, commonly known as grey mangrove or white mangrove, is a species of mangrove tree classified in the plant family Acanthaceae (formerly in the *Verbenaceae* or *Avicenniaceae*). *Avicennia marina* is the most widespread species of the Old World, extending from East Africa to Fiji in Polynesia and the North Island of New Zealand, and occurring at the coldest localities in New Zealand, subtropical China (26 degrees north latitude), and southeastern Australia (Mildred, 2012). *Phellinus swieteniae* was commonly found associated with live, hollowed out *Avicennia germinans* trees (Gilbert et al., 2008), with *P. mangrovicus* and *P. fastuosus* collected on *Bruguiera gymnorhiza, Sonneratia alba, Lumnitzera littorea* and *X. granatum* on the Kosrae and Pohnpei islands, Micronesia (Gilbert et al., 2008). However, the fungi causing apical wilt of *Avicennia marina* trees have been rarely reported. According to E.B.G. Jones (unpublished data), apical wilt of *Avicennia marina* trees has been reported from Morib mangrove, while *Rhizophora* seedlings frequently fail to grow at Kuala Selangor mangrove. The apical wilt of *A. marina* has been attributed to insect attack followed by colonization by the marine ascomycetes *Julella avicenniae* and*Eutypella naqsii*. With changes in climate and movements of pathogens between continents it is expected that new diseases of forest including mangroves will occur. This is already apparent in American and European forests, where introductions of

pathogens resulted in decline of the American chestnut (Elliott & Swank, 2008), and the European Elm (Gibbs et al., 1994). Some pathogens have also been shown to jump hosts and this may also be an important concern for forest tress (Slippers et al., 2005; Pérez et al., 2008). Endophytes or weak pathogens have also been shown to change their lifestyle and become virulent for unknown reasons and this has resulted in entire losses of populations of tree species (Kowalski, 2006; Kowlaski & Holdenrieder, 2009). For example, the Ash trees of Europe are now likely to disappear from forests as a previous Japanese endophytic *Chalara* sp., has become a virulent pathogen, killing trees throughout Europe including recently in the UK (Loos et al., 2009; Kraj et al., 2012).

As long as one is aware that GenBank sequences are mostly wrongly named (e.g. 86% wrongly named *Colletotrichum gloeosporioides*, Cai et al., 2009a, b), and that analyses must therefore use sequence data from type strains, it is relatively easy to identify species in the better studied and important genera (Cai et al., 2011). Genera and or groups (*Bipolaris*, *Botryosphaeria*, *Colletotrichum*, *Curvularia*, *Diaporthe*, *Fusarium*, *Pestalotiopsis*, and Xylariaceae) that would be common in the mangrove hosts are now relatively well-studied at the molecular level (Liu et al., 2012; Manamgoda et al., 2012; Udayanga et al., 2012). The mangrove hosts should therefore contain cryptic species if fungal estimates are correct. Based on molecular data, important pathogenic genera have been shown to comprise several species complexes that comprise cryptic species (Damm et al., 2012; Weir et al., 2012).

1.3 Phylogeny of Fungi

The ability to accurately identify fungi has advanced significantly in recent years with molecular data (Jeewon et al., 2009; Ko Ko et al., 2011). Previously, mycologists identified species based on morphology and naming of species was subjective and, in most cases, involved clumping species into morphologically similar species (Udayanga et al., 2011, 2012, 2014a, b), which now known as species complexes with possible to identify genera and species, including cryptic species, by sequencing single spore isolates of the taxa collected (Boonmee et al., 2012;

Maharachchikumbura et al., 2012). There are considerable progress has been made towards resolving the phylogenetic position of fungi. Fungi are highly diverse eukaryotes which can be correctly classified by carefully choosing appropriate characters at different levels, adequate taxon sampling, and application of proper methods of analysis. Furthermore, sexual/asexual relationships are interesting to highlight in order to apply recent taxonomic rule of one fungus = one name (Rossman, 2014). The scale of fungal species diversity is an open examination with approximately 6 to 1 ratio of fungal and host species (Hawksworth, 1991, 2001).

As molecular sequence data has become more readily available, it is commonly used to classify the fungi in order to develop a natural classification system (Chomnunti et al., 2011, 2012). Sequence data can directly be obtained from the fungi, especially from basidiomycetes (mushrooms), although with microfungi it is more difficult, but is possible if enough material is available. This has resulted in a better understanding of fungal classification at the higher taxonomic levels and has also shown that morphologically similar fungi (species complexes) comprise many cryptic species. Endophytes that were previously almost impossible to name to species or genera can now be named by blasting DNA sequence data in GenBank. However, many researchers have made the mistake of believing the names of fungi in GenBank although there is absolutely no control on what is place in this public database. Therefore, many of the papers published today are highly erroneous. Ko Ko et al. (2011) explained that researchers must use sequences from type strains in their analyses if they want to identify the fungi accurately.

1.4 Research Objectives

1.4.1 To identify the species associated with Mangroves based on morphology and multi-gene phylogeny.

1.4.2 To conduct in-depth genus and family rank revisions for selected taxa and their allied species.

1.4.3 To update the multi-gene phylogeny of complex genera, including *Diaporthe*, and *Phyllosticta.*

1.4.4 To contribute to the fungal taxonomy and phylogeny by studying fungi in Sordariomycetes and Dothideomycetes.

1.5 Research Outlines

This thesis is divided into eleven chapters. Chapter 1 is introduction to research background of this study; Chapters 2–5 are research part of genus and family rank revisions for selected taxa and their allied species; Chapter 6–10 are research part of fungi that founded from mangroves; Chapter 10 is overall conclusion in this study.

Chapter 1 – An introduction to the importance of the study of taxonomy, phylogeny, comprises of general introduction to research background of selected fungi, emphasis on mangroves selected fungi. An overview of some selected genera.

Chapter 2 – A study of novel *Cytospora* species (Cytosporaceae, Diaporthales), *C. lumnitzericola*, *C. thailandica*, and *C. xylocarpi*, species associated with mangroves in Thailand.

Chapter 3 – A study of novel species of Pestalotioid species associated with mangroves in Thailand. The study provides novel species and an updated phylogenetic placement of *Neopestalotiopsis*, *Pestalotiopsis* and *Pseudopestalotiopsis* (Sporocadaceae, Amphisphaeriales).

Chapter 4 – A study of a new host record of *Alternaria gaisen* (Pleosporaceae, Pleosporales), associated with *Ficus microcarpa* (Moraceae), and *Kandelia candel* (Rhizophoraceae), mangrove plants in Taiwan.

Chapter 5 – A study of a new species, *Phyllosticta rhizophorae* (Phyllostictaceae, Botryosphaeriales) from mangroves in Taiwan with two published strains of *P. capitalensis* were synonymized, six strains of *P. capitalensis* are treated as unnamed species, and seventeen strains are excluded from *Phyllosticta*. Six workable species complexes were introduced, with assembled a comprehensive dataset.

Chapter 6 – A study of formalizing species-group of *Diaporthe* (Diaporthaceae, Diaporthales), with 13 workable species complexes were introduced.

Chapter 7 – The study of the species *Seimatosporium* from Russia. A novel species that isolated from dead branches of *Physocarpus opulifolius* was introduced as

S. physocarpi sp. nov. A specimen from *Rosa kalmiussica* is designated as epitype for *S. rosae* and provide a detailed description for *S. lichenicola*, ann asexual morph of *Discostroma fuscellum*.

Chapter 8 – In the course of a study on the genus *Lamproconium*, specimens from Russia. The species *Melanconis desmazieri* is synonymized under *Lamproconium desmazieri* and the novel family Lamproconiaceae (Diaporthales) was introduced.

Chapter 9 – The study of *Cytoapora* species, collections from Russia. There are 14 new species are described and illustrated, and three known species were identified.

Chapter 10 – A study about the phylogenetic investigations also revealed some interesting taxonomic insights pertaining to the intergeneric relationships of genus *Dyfrolomyces* and *Melomastia* with an additional new species, *Melomastia italica*, a collection from Italy, while *Dyfrolomyces maolanensis* is transferred to the genus *Melomastia*. The phylogenetic relationships and intergeneric taxonomy within the family Pleurotremaceae in the class Dothideomycetes are revisited.

Chapter 11 – Provides overall conclusions and perspectives on this study.

CHAPTER 2

MORPHOLOGICAL AND PHYLOGENETIC CHARACTERISATION OF NOVEL *CYTOSPORA* SPECIES ASSOCIATED WITH MANGROVES[1]

Abstract

Mangroves are relatively unexplored habitats and have been shown to harbour a number of novel spe- cies of fungi. In this study, samples of microfungi were collected from symptomatic branches, stem and leaves of the mangrove species *Xylocarpus granatum*, *X. moluccensis* and *Lumnitzera racemosa* and examined morphologically. The phylogeny recovered supports our morphological data to introduce three new species, *Cytospora lumnitzericola*, *C. thailandica* and *C. xylocarpi*. In addition, a combined multi-gene DNA sequence dataset (ITS, LSU, *act* and *rpb2*) was analysed to investigate phylogenetic relationships of isolates and help in a more reliable species identification.

Keywords: 3 new species, Cytosporaceae, *Lumnitzera racemose*, Mangroves, Phylogeny, Taxonomy, *Xylocarpus granatum*, *Xylocarpus moluccensis*

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[1]This paper has been published in *MycoKeys*, 2018, *38*, 93–120. https://doi.org/10.3897/mycokeys.38.28011

2.1 Introduction

Mangroves are forests established in tropical and subtropical backwaters, estuaries, deltas, and lagoons. These forests play a major role in the ecology of coastal tropical/ subtropical waters, as they serve as hatchery and nursery habitats for marine organisms and protect coastlines from catastrophic events such as storms and tidal surges (Hyde & Jones, 1988; Fisher & Spalding, 1993; Hyde & Lee, 1995; Hyde et al., 1998). The greatest diversity of mangrove species occurs in the mangroves of Indonesia, Ma- laysia and Thailand (Alias & Jones, 2009; Alias et al., 2010).

Reports of fungi associated with mangroves are relatively few and data on diseases of mangroves are uncommon (Cribb & Cribb, 1955; Kohlmeyer & Kohlmeyer, 1979; Hyde & Jones, 1988). So far, a number of fungi collected from mangroves are either saprobes (e.g Swe et al., 2008a, b; Devadatha et al., 2018; Li et al., 2018) or endophytes (e.g Liu et al., 2012; Doilom et al., 2017). One early species documented from mangroves is that of Stevens (1920) who reported a species of *Anthostomella* that was found from a leaf spot in red mangroves (Rhizophora mangle) in Puerto Rico. Later, McMillan (1964) reported *Cercospora* which caused leaf spot on red mangroves in Florida and Kohlmeyer (1969) documented an undescribed *Cytospora* species on *R. mangle* in Hawaii. *Cytospora rhizophorae* has also been reported as a marine fungus from *Rhizophora mangle* in southwest Puerto Rico (Wier et al., 2000). Later, Shivas et al. (2009) reported a serious disease, caused by *Pseudocercospora avicenniae*, on leaves of *Avicennia marina* in Cape Tribulation, Queensland.

Cytospora was introduced by Ehrenberg (1818) and belongs to the family Cyto- sporaceae in Diaporthales (Wijayawardene et al., 2018). *Cytospora* species are phytopath- ogens or saprobes (Wehmeyer, 1975; Barr, 1978; Eriksson, 2001; Castlebury et al., 2002; Wijayawardene et al., 2018). *Cytospora* has a worldwide distribution and is an important pathogenic genus, causing canker and dieback disease on branches of a wide range of plants (Adams et al., 2005, 2006; Hyde et al., 2017; Norphanphoun et al., 2017). Currently, there are 614 epithets for *Cytospora* (Index Fungorum, 2018; 14 June 2018) with an estimated 110 species in Kirk et al. (2008). Recently, fourteen new species were introduced to this genus by Norphanphoun et al.

(2017). In this study, we report on three novel species of *Cytospora* associated with mangroves in Thailand. Detailed descriptions and illustrations of all the species identified are provided in this paper.

2.2 Materials and Methods

2.2.1 Sample Collection and Examination of Specimens

Samples collected were dead branches of *Xylocarpus granatum* K. D. Koenig, *X. moluccensis* (Lam.) M. Roem. and leaf spots of *Lumnitzera racemosa* Willd. from Phetchaburi and Ranong provinces, Thailand in 2016. Specimens were returned to the laboratory in paper bags, examined and described following Norphanphoun et al. (2017). Morphological characters of ascomata and conidiomata were examined using a Motic SMZ 168 dissecting microscope. Hand sections were mounted in water and examined for morphological details. Micro-morphology was studied using a Nikon Ni compound microscope and photographed with a Canon EOS 600D digital cam- era fitted to the microscope. Photo-plates were made using Adobe Photoshop CS6 Extended version 13.0 × 64 (Adobe Systems, USA), while Tarosoft (R) Image Frame Work programme v. 0.9.7 was used for measurements.

Cultures were obtained by single spore isolation method outlined in Chomnunti et al. (2014). Single germinating spores were observed and photographed using a Nikon Ni compound microscope fitted with Canon EOS 600D digital camera. Geminated spores were transferred aseptically to 2% malt extract agar (MEA, malt extract agar powder 32 g in 1000 ml water) and incubated at room temperature (18−25 °C). A tissue isolation method was used for isolation of taxa from leaf spots of *Lumnitzera racemosa*. Leaves with leaf spots were cut into small pieces (0.5 × 0.5 cm2) using a sterilised blade and surface was sterilised using 70% ethanol for 1 minute, followed by three rinses with sterile dis- tilled water, 1 minute in 3% sodium hypochlorite (NaOCl) and rinsed with sterile water for 1–2 minutes and dried by blotting on sterile filter paper. Four to five segments including the edge of the leaf spot were placed on water agar (WA) plates, supplemented with 100 mg/ml streptomycin. The dishes were incubated at 27 °C ± 2 °C for 7–10 days. Fun- gal colonies were transferred using single hyphal tips on to

potato dextrose agar (PDA) plates throughout a 2-week period. Pure cultures were maintained for further studies on PDA (Bharathidasan & Panneerselvam, 2011). The specimens/dried cultures and living cultures are deposited in the Herbarium Mae Fah Luang University (MFLU) and culture collection Mae Fah Luang University (MFLUCC), Chiang Rai, Thailand and duplicated in the International Collection of Micro-organisms from Plants (ICMP). Facesoffungi numbers were registered as in Jayasiri et al. (2015). New taxa are established based on recommendations as outlined by Jeewon and Hyde (2016).

2.2.2 DNA Extraction, PCR Amplification and Sequencing

Genomic DNA was extracted from fresh fungal mycelia growing on MEA at room tem- perature (18−25 °C) for three weeks using a E.Z.N.A.TM Fungal DNA MiniKit (Omega Biotech, CA, USA) following the manufacturer's protocols. Polymerase chain reactions (PCR) were carried out using primer pairs of ITS1 (5'-TCCGTAGGTGAACCT- GCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') to amplify the ITS region (White et al., 1990), primer pairs of NL1 (5'-GCATATCA ATAAGCGGAGGAAAAG-3') and NL4 (5'-GGTCCGTGTTTCAAGACGG-3') to amplify part of the large subunit rDNA (28S, LSU) (O'Donnell, 1993), the partial *act* region was amplified using primers ACT512F (5'-ATGTGCAAGGCCGGTTTCGC-3') and ACT783R (5'-TAC-GAGTCCTTCTGGCCCAT-3') (Carbone & Kohn, 1999) and the partial *rpb2* region was amplified using primers bRPB2-6F (5'-TGGGGYATG GTNTGYCCYGC-3') and bRPB2-7.1R (5'-CCCATRGCYTGYTTMCCCATDGC-3') (Matheny, 2005).

The amplification reactions were carried out with the following protocol: 50 µl reaction volume containing 2 µl of DNA template, 2 µl of each forward and reverse primers, 25 µl of 2 × Bench TopTMTaq Master Mix (mixture of Taq DNA Polymerase (recombinant): 0.05 units/µl, MgCl2: 4 mM and dNTPs (dATP, dCTP, dGTP, dTTP): 0.4 mM) and 19 µl of double-distilled water (ddH2O) (sterilised water) using the thermal cycle programme in Norphanphoun et al. (2017). Purification and sequencing of PCR products with the same primers mentioned above were carried out at Life Biotechnology Co., Shanghai, China.

2.2.3 Phylogenetic Analysis

The sequences were assembled by GENEIOUS Pro v. 11.0.5 (Biomatters) and BLAST searches were made to retrieve the closest matches in GenBank and multiple alignment also included recently published sequences (Norphanphoun et al., 2017; Hyde et al., 2017, 2018). Combined analyses of ITS1, 5.8S, ITS2, LSU, *rpb2* and *act* sequence data of 86 taxa were performed under different optimality criteria (MP, ML, BI). *Diaporthe eres* (AFTOL-ID 935) was used as the outgroup taxon. In order to obtain a better picture of the phylogenetic relationships amongst our strains and closely related strains, a separate ITS1+ITS2 phylogeny was inferred, because only ITS sequences were available for many strains in that group and because less ambiguously aligned (and excluded) positions are expected in a dataset with narrower taxonomic coverage. Nineteen strains were selected for this analysis based on preliminary analyses and results from the multigene phylogeny. All sequences were aligned separately using the MAFFT v.7.110 online programme (http://mafft.cbrc. jp/alignment/server/; Katoh & Standley, 2013) and Gblocks v. 0.91b was used to exclude ambiguously aligned positions in the ITS and *act* alignments (Castresana, 2000; Talavera & Castresana, 2007). A partition homogeneity test (PHT) was performed with PAUP 4.0b10* (Swofford, 2002) to determine whether the individual datasets were congruent and could be combined. The combined sequence alignments were obtained from MEGA7 version 7.0.14 (Kumar et al., 2015), missing data were coded as question marks (?) and further manual adjustments were made wherever necessary in BioEdit 7.2.3 (Hall, 1999). The combined sequence alignment was con- verted to NEXUS file for maximum parsimony analysis using ClustalX v. 2 (Larkin et al., 2007). The NEXUS file was prepared for MrModeltest v. 2.2 (Nylander, 2004) in PAUP v.4.0b10 (Swofford, 2002).

Maximum Parsimony (MP) analysis was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10* (Swofford, 2002) with 1000 bootstrap replicates using a heuristic search with random stepwise addition and tree-bisection reconnection (TBR), as detailed by Jeewon et al. (2002) and Cai et al. (2005). Maxtrees was set to 1000, branches of zero length were collapsed. The following descriptive tree statistics were calculated: parsimony tree length [TL], consistency index [CI], retention index [RI], rescaled consistency index [RC] and homoplasy index [HI].

For both Maximum Likelihood and Bayesian analyses, a partitioned analysis was performed with the following six partitions: ITS1+ITS2, 5.8S, LSU, ACT-exons, ACT-introns and *rpb2*. Maximum-likelihood (ML) analysis was performed with RAxML (Stamatakis, 2006) implemented in the CIPRES Science Gateway web server (RAxML- HPC2 on XSEDE; Miller et al., 2010), 25 categories, 1000 rapid bootstrap replicates were run with the GTRGAMMA model of nucleotide evolution. Maximum likelihood bootstrap values (MLBS) equal or greater than 50% are given above each node.

Bayesian Inference (BI) analysis was performed using the Markov Chain Monte Carlo (MCMC) method with MrBayes 3.2.2 (Ronquist et al., 2012). The best-fit nucleotide substitution model for each dataset was separately determined using MrModeltest version 2.2 (Nylander, 2004). GTR+I+G was selected as the best-fit model for the ITS1+ITS2, LSU, *act* (*act*-exons and *act*-introns) and *rpb2* datasets and K80 for 5.8S. The MCMC analyses, with four chains starting from random tree topology, were run for 5,000,000 or 10,000,000 generations for the combined dataset or the ITS1+ITS2 dataset. Trees were sampled every 100 generations. Tracer v. 1.5.0 was used to check the effective sampling sizes (ESS) that should be above 200, the stable likelihood plateaus and burn-in value (Rambaut et al., 2013). The first 5000 samples were excluded as burn-in.

The phylogram was visualised in FigTree v1.4.0 (http://tree.bio.ed.ac.uk/ software/ figtree/; Rambaut, 2014) and edited in Adobe Illustrator CC and Adobe Photoshop CS6 Extended version 13.1.2 × 64. Newly generated sequences in this study are deposited in GenBank. The finalised alignment and tree were deposited in TreeBASE, submis- sion ID: 22942 (combined sequence alignment).

Table 2.1 GenBank accession numbers of the sequences used in phylogenetic analyses

No	Taxon	Strain[a]	Host	Origin	GenBank accession numbers				References
					ITS	LSU	*rpb2*	*act*	
1	*Cytospora abyssinica*	CMW 10181[T]	*Eucalyptus globulus*	Wondo Genet, Ethiopia	AY347353	–	–	–	Adams et al. (2005)
2	*C. acaciae*	CBS 468.69	*Ceratonia siliqua*	Spain, Mallorca	DQ243804	–	–	–	Adams et al. (2006)
3	*C. ampulliformis*	MFLUCC 16-0583[T]	*Sorbus intermedia*	Russia	KY417726	KY417760	KY417794	KY417692	Norphanphoun et al. (2017)
4	*C. atrocirrhata*	HMBF156			KF225610	KF225624	–	KF498673	Fan et al. (2015a)
5	*C. austromontana*	CMW 6735[T]	*Eucalyptus pauciflora*	Australia	AY347361	–	–	–	Adams et al. (2005)
6	*C. berberidis*	CFCC 89927[T]	*Berberis dasystachya*	China	KR045620	KR045702	KU710948	KU710990	Liu et al. (2015)
7	*C. berkeleyi*	StanfordT3[T]	*Eucalyptus globulus*	California, USA	AY347350	–	–	–	Adams et al. (2005)
8	*C. brevispora*	CBS 116829	*Eucalyptus grandis*	Venezuela	AF192321	–	–	–	Adams et al. (2005)
9	*C. carbonacea*	CFCC 89947	*Ulmus pumila*	Qinghai, China	KR045622	KP310812	KU710950	KP310842	Yang et al. (2015)
10	*C. centravillosa*	MFLUCC 16-1206[T]	*Sorbus domestica*	Italy	MF190122	MF190068	MF377600	–	Senanayake et al. (2017)
11	*C. ceratosperma*	MFLUCC 16-0625	*Acer platanoides*	Russia	KY563246	KY563248	KY563244	KY563242	Tibpromma et al. (2017)
12	*C. chrysosperma*	HMBF151			KF225605	KF225619	–	KF498668	Fan et al. (2015a)
13	*C. cinereostroma*	CMW 5700[T]	*Eucalyptus globulus*	Chile	AY347377	–	–	–	Adams et al. (2005)
14	*C. cotini*	MFLUCC 14-1050[T]	*Cotinus coggygria*	Russia	KX430142	KX430143	KX430144	–	Norphanphoun et al. (2017)
15	*C. curvata*	MFLUCC 15-0865 [T]	*Salix alba*	Russia	KY417728	–	–	KY417694	Norphanphoun et al. (2017)
16	*C. cypri*	CBS 201.42[T]	*Syringa* sp.	Switzerland	DQ243801	–	–	–	Adams et al. (2006)
17	*C. diatrypelloidea*	CMW 8549[T]	*Eucalyptus globulus*	Orbost, Australia	AY347368	–	–	–	Adams et al. (2005)
18	*C. disciformis*	CMW6509			AY347374	–	–	–	Adams et al. (2005)
19	*C. donetzica*	MFLUCC 16-0574[T]	*Rosa* sp.	Russia	KY417731	KY417765	KY417799	KY417697	Norphanphoun et al. (2017)
20	*C. elaeagni*	CFCC 89632	*Elaeagnus angustifolia*	Ningxia, China	KR045626	KR045706	KU710955	KU710995	Fan et al. (2015b)
21	*C. erumpens*	MFLUCC 16-0580[T]	*Salix* × *fragilis*	Russia	KY417733	KY417767	KY417801	KY417699	Norphanphoun et al. (2017)

Table 2.1 (continued)

No	Taxon	Strain[a]	Host	Origin	GenBank accession numbers				References
					ITS	LSU	*rpb2*	*act*	
22	*C. eriobotryae*	IMI136523[T]	*Eriobotrya japonica*	India	AY347327	–	–	–	Adams et al. (2005)
23	*C. eucalypti*	LSEQ	*Sequoia sempervirens*	California, USA	AY347340	–	–	–	Adams et al. (2005)
24	*C. eucalyptina*	CMW 5882	*Eucalyptus grandis*	Cali, Columbia	AY347375	–	–	–	Adams et al. (2005)
25	*C. fabianae*	Dunnii	*Eucalyptus*		AY347360	–	–	–	Adams et al. (2005)
26	*C. friesii*	CBS 113.81	*Picea abies*	Norway	AY347318	–	–	–	Adams et al. (2005)
27	*C. gelida*	MFLUCC 16-0634 [T]	*Cotinus coggygria*	Russia	KY563245	KY563247	KY563243	KY563241	Tibpromma et al. (2017)
28	*C. germanica*	CXY1322	*Elaeagnus oxycarpa*	China	JQ086563	JX524617	–	–	Zhang et al. (2013)
29	*C. gigalocus*	HMBF154			KF225608	KF225622	–	KF498671	Fan et al. (2015a)
30	*C. gigaspora*	CFCC 89634[T]	*Salix psammophila*	China	KF765671	KF765687	KU710960	KU711000	Fan et al. (2015b)
31	*C. hippophaes*	CFCC 89636			KF765678	KF765694	KF765710	–	Fan et al. (2015b)
32	*C. japonica*	CBS375.29	*Prunus persica*	Japan	AF191185	–	–	–	Adams et al. (2002)
33	*C. junipericola*	MFLUCC 17-0882[T]	*Juniperus communis*	Italy	MF190125	MF190072	–	–	Senanayake et al. (2017)
34	*C. kantschavelii*	287-2	*Populus deltoides*	Iran	EF447367	–	–	–	Fotouhifar et al. (2010)
35	*C. kunzei*	CBS 118556	*Pinus radiata*	Eastern Cape, SA	DQ243791	–	–	–	Adams et al. (2006)
36	*C. leucostoma*	CFCC 50015	*Sorbus pohuashanensis*	China	KR045634	KR045714	–	KU711002	Yang et al. (2015)
37	*C. longiostiolata*	MFLUCC 16-0628[T]	*Salix × fragilis*	Russia	KY417734	KY417768	KY417802	KY417700	Norphanphoun et al. (2017)
38	*C. lumnitzericola*	MFLUCC 17-0508	*Lumnitzera racernosa*	Phetchaburi, Thailand	MG975778	MH253461	MH253453	MH253457	In this study
39	*C. mali*	CFCC 50044	*Malus baccata*	Haidong, Qinghai	KR045637	KR045717	KU710966	KU711005	Yang et al. (2015)
40	*C. malicola*	167			EF447414	–	–	–	Adams et al. (2002)
41	*C. mali-sylvestris*	MFLUCC 16-0638 [T]	*Malus sylvestris*	Russia	KY885017	KY885018	KY885020	KY885019	Hyde et al. (2017)
42	*C. melnikii*	MFLUCC 15-0851[T]	*Malus domestica*	Russia	KY417735	KY417769	KY417803	KY417701	Norphanphoun et al. (2017)

Table 2.1 (continued)

No	Taxon	Strain[a]	Host	Origin	GenBank accession numbers				References
					ITS	LSU	*rpb2*	*act*	
43	*C. multicollis*	CBS 105.89[T]	*Quercus ilex* subsp. *rotundifolia*	Spain	DQ243803	–	–	–	Adams et al. (2006)
44	*C. myrtagena*	HiloTib1[T]	*Tibouchiina urvilleana*	Hilo, Hawaii	AY347363	–	–	–	Adams et al. (2005)
45	*C. nitschkii*	CMW10180[T]	*Eucalyptus globulus*	Wondo Genet, Ethiopia	AY347356	–	–	–	Adams et al. (2005)
46	*C. nivea*	MFLUCC 15-0860	*Salix acutifolia*	Russia	KY417737	KY417771	KY417805	KY417703	Norphanphoun et al. (2017)
47	*C. palmae*	CXY1280[T]	*Cotinus coggygria*	Beijing, China	JN411939	–	–	–	Zhang et al. (2014)
48	*C. parakantschavelii*	MFLUCC 15-0857[T]	*Populus* × *sibirica*	Russia	KY417738	KY417772	KY417806	KY417704	Norphanphoun et al. (2017)
49	*C. parapersoonii*	T28.1[T]	*Prunus persicae*	Michigan, USA	AF191181	–	–	–	Adams et al. (2002)
50	*C. paratranslucens*	MFLUCC 16-0506[T]	*Populus alba* var. *bolleana*	Russia	KY417741	KY417775	KY417809	KY417707	Norphanphoun et al. (2017)
51	*C. parasitica*	MFLUCC 16-0507	*Malus domestica*	Russia	KY417740	KY417774	KY417808	KY417706	Norphanphoun et al. (2017)
52	*C. pini*	CBS224.52[T]	*Pinus strobus*	New York	AY347316	–	–	–	Adams (2005)
53	*C. populina*	CFCC 89644	*Salix psammophila*	Shaanxi, China	KF765686	KF765702	KF765718	–	Fan et al. (2015b)
54	*C. predappioensis*	MFLU 17-0327	*Platanus hybrida*	Italy	MH253451	MH253452	MH253450	MH253449	Hyde et al. (2018)
55	*C. prunicola*	MFLU 17-0995 [T]	*Prunus* sp.	Italy	MG742350	MG742351	MG742352	MG742353	Hyde et al. (2018)
56	*C. pruinopsis*	CFCC 50034[T]	*Ulmus pumila*	Shaanxi, China	KP281259	KP310806	KU710970	KP310836	Yang et al. (2015)
57	*C. pruinosa*	CFCC 50036	*Syzygium aromaticum*	Qinghai, China	KP310800	KP310802	–	KP310832	Yang et al. (2015)
58	*C. quercicola*	MFLUCC 14-0867[T]	*Quercus* sp.	Italy	MF190129	MF190073	–	–	Senanayake et al. (2017)
59	*C. rhizophorae*	ATCC38475	*Rhizophora mangle*	LA, USA	DQ996040	–	–	–	He et al. (2003)
60	*C. rhizophorae*	ATCC66924	*Haliclona caerulea*	HI, USA	DQ092502	–	–	–	Unpublished

Table 2.1 (continued)

No	Taxon	Strain[a]	Host	Origin	GenBank accession numbers				References
					ITS	LSU	*rpb2*	*act*	
61	*C. ribis*	CFCC 50026	*Ulmus pumila*	Qinghai, China	KP281267	KP310813	KU710972	KP310843	Yang et al. (2015)
62	*C. rosae*	MFLUCC 14-0845[T]	*Rosa canina*	Italy	MF190131	MF190075	–	–	Senanayake et al. (2017)
63	*C. rosarum*	218			EF447387	–	–	–	Fotouhifar et al. (2010)
64	*C. rostrata*	CFCC 89909[T]	*Salix cupularis*	Gansu, China	KR045643	KR045722	KU710974	KU711009	Unpublished
65	*C. rusanovii*	MFLUCC 15-0854[T]	*Salix babylonica*	Russia	KY417744	KY417778	KY417812	KY417710	Norphanphoun et al. (2017)
66	*C. sacculus*	HMBF281			KF225615	KF225629	–	KF498678	Fan et al. (2015a)
67	*C. salicacearum*	MFLUCC 16-0509[T]	*Salix alba*	Russia	KY417746	KY417780	KY417814	KY417712	Norphanphoun et al. (2017)
68	*C. salicicola*	MFLUCC 14-1052[T]	*Salix alba*	Russia	KU982636	KU982635	–	KU982637	Li et al. (2016)
69	*C. salicina*	MFLUCC 15-0862[T]	*Salix alba*	Russia	KY417750	KY417784	KY417818	KY417716	Norphanphoun et al. (2017)
70	*C. schulzeri*	CFCC 50040	*Malus domestica*	Ningxia, China	KR045649	KR045728	KU710980	KU711013	Unpublished
71	*C. sibiraeae*	CFCC 50045[T]	*Sibiraea angustata*	Gansu, China	KR045651	KR045730	KU710982	KU711015	Liu et al. (2015)
72	*C. sorbi*	MFLUCC 16-0631[T]	*Sorbus aucuparia*	Russia	KY417752	KY417786	KY417820	KY417718	Norphanphoun et al. (2017)
73	*C. sorbicola*	MFLUCC 16-0584[T]	*Acer pseudoplatanus*	Russia	KY417755	KY417789	KY417823	KY417721	Norphanphoun et al. (2017)
74	*C. sordida*	HMBF159			KF225613	KF225627	–	KF498676	Fan et al. (2015a)
75	*C. sophorae*	CFCC 50047	*Styphnolobium japonicum*	Shanxi, China	KR045653	KR045732	KU710984	KU711017	Fan et al. (2014)
76	*C. sophoricola*	CFCC 89596	*Styphnolobium japonicum*	Gansu, China	KR045656	KR045735	KU710987	KU711020	Unpublished
77	*C. tanaitica*	MFLUCC 14-1057[T]	*Betula pubescens*	Russia	KT459411	KT459412	–	KT459413	Ariyawansa et al. (2015)
78	*C. thailandica*	MFLUCC 17-0262	*Xylocarpus moluccensis*	Ranong, Thailand	MG975776	MH253463	MH253455	MH253459	In this study

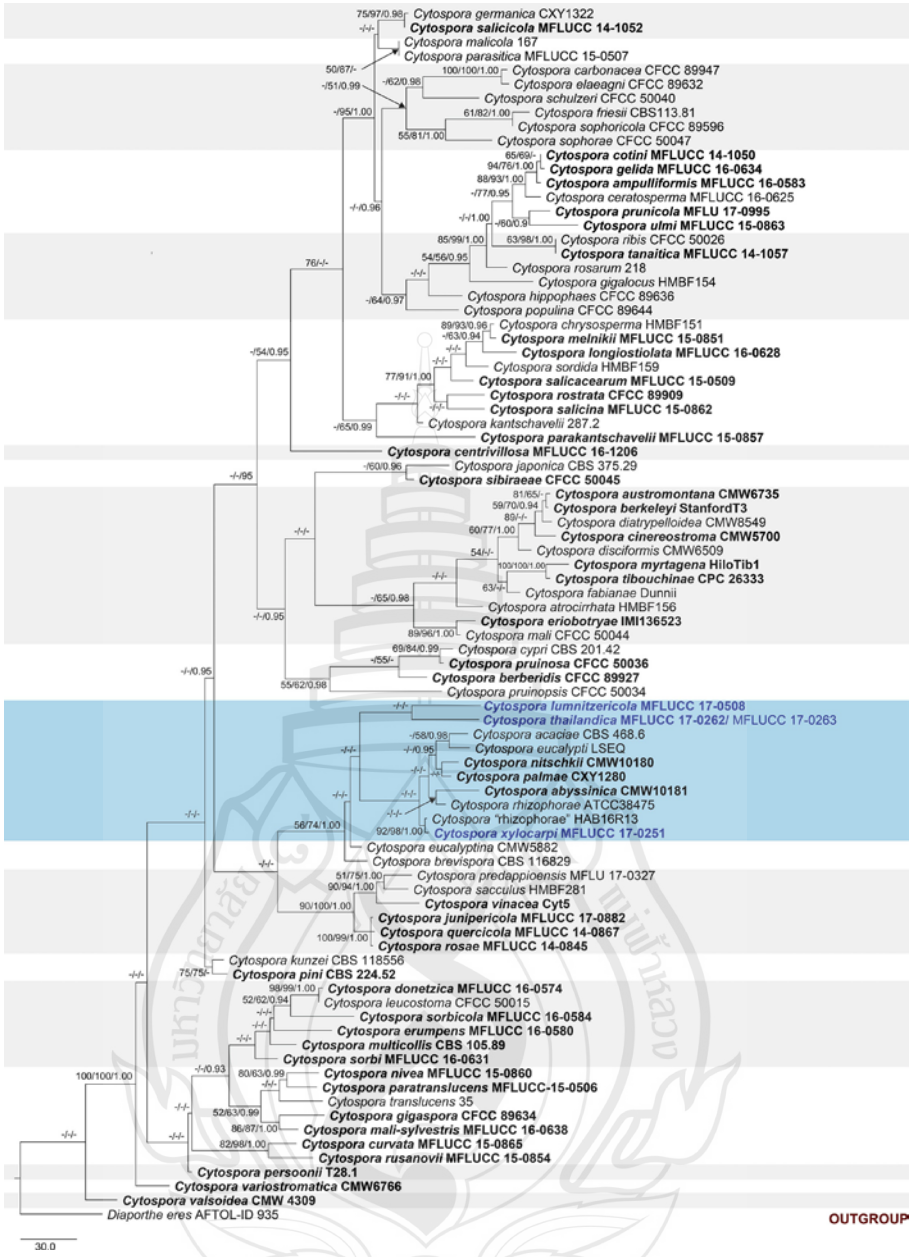
Table 2.1 (continued)

No	Taxon	Strain[a]	Host	Origin	GenBank accession numbers				References
					ITS	LSU	*rpb2*	*act*	
79	*C. thailandica*	MFLUCC 17-0263	*Xylocarpus moluccensis*	Ranong, Thailand	MG975777	MH253464	MH253456	MH253460	In this study
80	*C. tibouchinae*	CPC 26333[T]	*Tibouchina semidecandra*	La Reunion, France	KX228284	KX228335	–	–	Unpublished
81	*C. translucens*	35			EF447403	–	–	–	Fotouhifar et al. (2010)
82	*C. ulmi*	MFLUCC 15-0863[T]	*Ulmus minor*	Russia	KY417759	KY417793	KY417827	KY417725	Norphanphoun et al. (2017)
83	*C. valsoidea*	CMW 4309[T]	*Eucalyptus grandis*	Sibisa, North Sumatra	AF192312	–	–	–	Adams et al. (2005)
84	*C. variostromatica*	CMW 6766[T]	*Eucalyptus globulus*	Australia	AY347366	–	–	–	Adams et al. (2005)
85	*C. vinacea*	CBS 141585[T]	*Vitis* sp.	New Hampshire, USA	KX256256	–	–	–	Lawrence et al. (2017)
86	*C. xylocarpi*	MFLUCC 17-0251	*Xylocarpus granatum*	Ranong, Thailand	MG975775	MH253462	MH253454	MH253458	In this study
87	*Diaporthe eres*	AFTOL-ID 935			DQ491514	–	DQ470919	–	Spatafora et al. (2006)
88	*C.* "rhizophorae"	A761	*Morinda officinalis*	China	KU529867	–	–	–	Unpublished
89	*C.* "rhizophorae"	HAB16R13	*Cinnamomum porrectum*	Malaysia	HQ336045	–	–	–	Harun et al. (2011)
90	*C.* "rhizophorae"	M225	*Rhizophora mucronata*	Philippines	KR056292	–	–	–	Unpublished
91	*C.* "rhizophorae"	MUCC302	*Eucalyptus grandis*	Australia	EU301057	–	–	–	Unpublished

2.3 Results

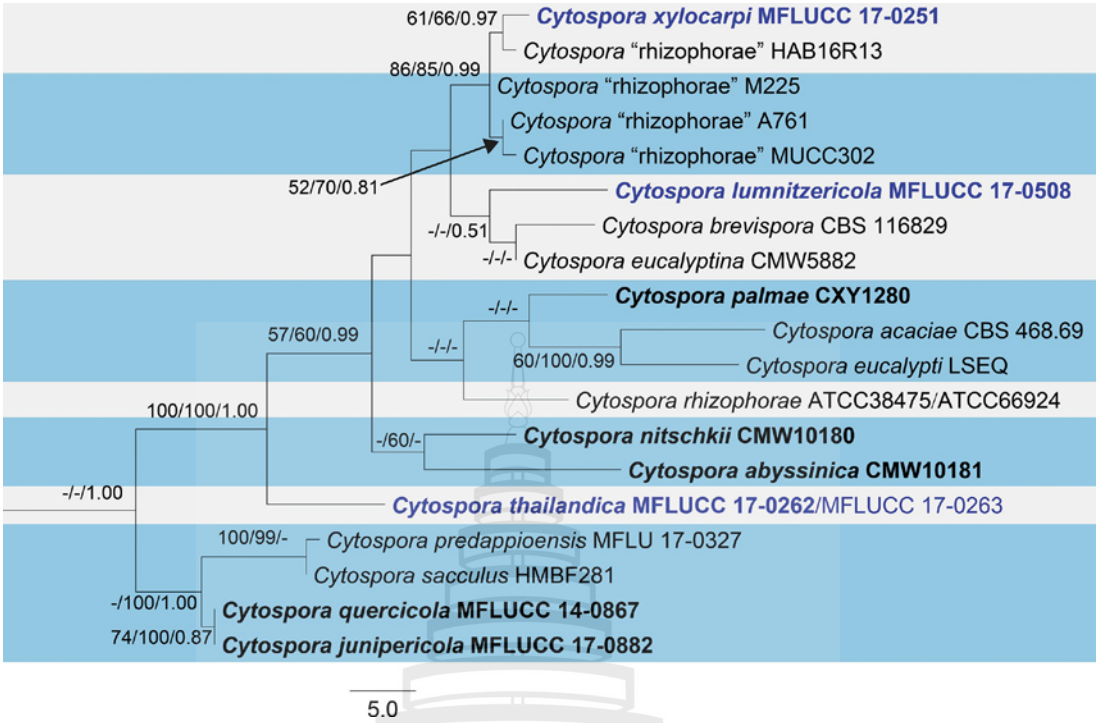
2.3.1 Phylogenetic Analysis

The combined alignment of ITS, LSU, *act* and *rpb2* sequences comprised 86 taxa, including our strains, with *Diaporthe eres* (CBS 183.5) as the outgroup taxon. The total length of the dataset was 2037 characters including alignment gaps (1–199, 200–357, 358–518, 519–1056, 1057–1296 and 1297–2037 corresponding to ITS1, 5.8S, ITS2, LSU, *act* and *rpb2*, respectively). The combined dataset contained 1426 constant, 144 parsimony uninformative and 467 parsimony informative characters. The result from the partition homogeneity test (PHT) was not significant (level 95%), indicating that the individual datasets were congruent and could be combined. The combined dataset was analysed using MP, ML and Bayesian analyses. The trees generated under different optimality criteria were essentially similar in topology and did not differ significantly (data not shown). The descriptive statistics of the phylogram generated from MP analysis based on the combined dataset of ITS, LSU, *act* and *rpb2* (Figure 2.1) were TL = 2418, CI = 0.375, RI = 0.650, RC = 0.244, HI = 0.625. The best scoring likelihood tree selected with a final value for the combined dataset = -14466.797686. The aligned sequence matrix of the ITS1+ITS2 dataset comprising 19 taxa had 279 constant, 23 parsimony uninformative and 57 parsimony informative characters. The descriptive statistics of the most parsimonious tree (Figure 2.2) were TL = 2418, CI = 0.375, RI = 0.650, RC = 0.244, HI = 0.625. The best scoring likelihood tree obtained for the ITS1+ITS2 dataset had a log-likelihood of= -1276.782916.



Note Phylogram generated from maximum parsimony analyses based on analysis of combined ITS, LSU, *act* and *rpb2* sequence data. The tree is rooted to *Diaporthe eres* (AFTOL-ID 935). Maximum parsimony and maximum likelihood bootstrap values ≥50%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/PP) are given at the nodes. The species obtained in this study are in blue font. Ex-type taxa from other studies are in black bold.

Figure 2.1 Phylogenetic analysis of *Cytospora*, generated from Maximum parsimony analyses based on combined analysis



Note Maximum parsimony phylogenetic tree inferred from ITS1 and ITS2 sequence data. Maximum parsimony and maximum likelihood bootstrap values ≥50%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/BIPP) are given at the nodes. The species obtained in this study are in blue font. Ex-type taxa from other studies are in black bold.

Figure 2.2 Phylogenetic analysis of *Cytospora*, generated from Maximum parsimony analyses based on ITS1 and ITS2 sequence data

2.3.2 Taxonomy

Cytospora lumnitzericola Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 2.3

Index Fungorum number: IF554778

Facesoffungi number: FoF 04603

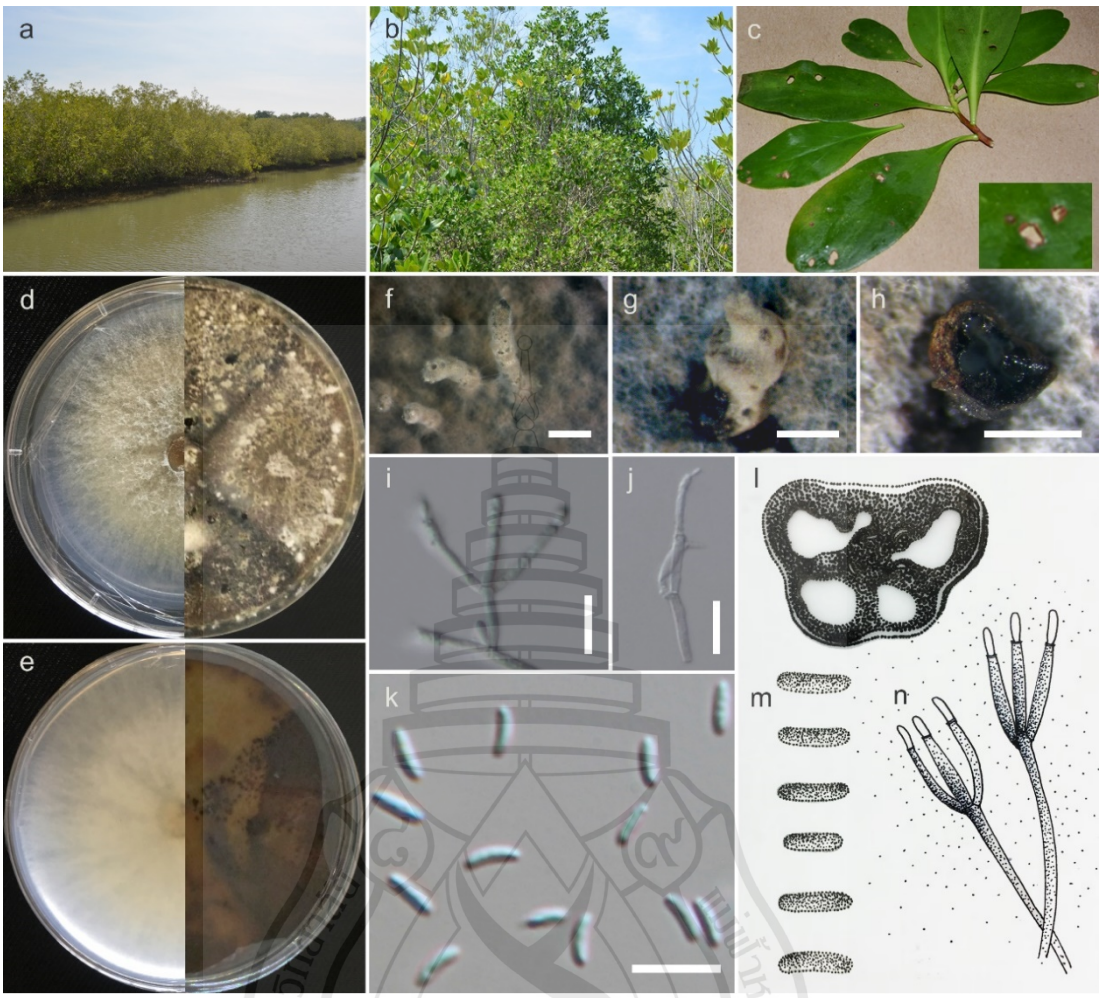
Etymology: refers to the host where the fungus was isolated.

Holotype: MFLU 18-1227

Isolated from leaf spot of *Lumnitzera racemosa*. Culture characteristic: *Colonies* on MEA reaching 5–6 cm diameter after 2 days at room temperature, colonies circular to irregular, medium dense, flat or effuse, slightly raised, with edge fimbriate, fluffy to fairly fluffy, white to grey from above, light yellow to green from below; not producing pigments in agar. Asexual morph: *Conidiogenous* cells (8–)8.5–14 × 0.6–1.4(–1.6) μm ($\bar{x}$ = 8.4 × 1.4, n = 15), blastic, enteroblastic, flask-shaped, phialidic, hyaline and smooth-walled. *Conidia* (3.7–)4–4.5 × 1–1.3(–1.5) μm ($\bar{x}$ = 4 × 1.2 μm, n = 30), uni- cellular, subcylindrical, hyaline, smooth-walled.

Material examined: THAILAND, Phetchaburi Province, the Sirindhorn International Environmental Park, on leaf spot of *Lumnitzera racemosa*, 30 November 2016, Chada Norphanphoun NNS23-2a (MFLU 18-1227 dried culture, holotype; PDD, isotype); ex-type-living culture, MFLUCC 17-0508, ICMP.

Notes: Based on the multigene phylogeny, *Cytospora lumnitzericola* is closely related to *Cytospora thailandica* (Figure 2.1). Although conidial sizes of both species are similar, they have significant differences in nucleotides: ITS (26 nt), *act* (22 nt), and *rpb2* (53 nt) (Table 2.5). The phylogeny derived from the ITS regions depicts *C. lumnitzericola* as an independent lineage close to *C. brevispora* CBS 116829 and *C. eucalyptina* CMW5882 (Figure 2.2). In future, more collections are needed to confirm whether *C. lumnitzericola* can exist as a saprobe or endophyte as well as performing tests to confirm its pathogenicity.



Note *Cytospora lumnitzericola* (MFLUCC 17-0508, from culture). a Mangrove collecting site. b, c *Lumnitzera racemosa* in mangroves forest. d, e Colonies on MEA after 6 days (left) and 30 days (right) (d-from above, e-from below). f, g Conidiomata produced on MEA. h, l Transverse sections of conidioma. i, j, n Conidiogenous cells with attached conidia. k, m Conidia. Scale bars: f = 1000 µm, g, h = 500 µm, i, j = 10 µm, k = 5 µm.

Figure 2.3 Morphological characters of *Cytospora lumnitzericola* (MFLUCC 17-0508, from culture)

Cytospora thailandica Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 2.4

Index Fungorum number: IF554779

Facesoffungi number: FoF 04605

Etymology: refers to the country where the fungus was collected.

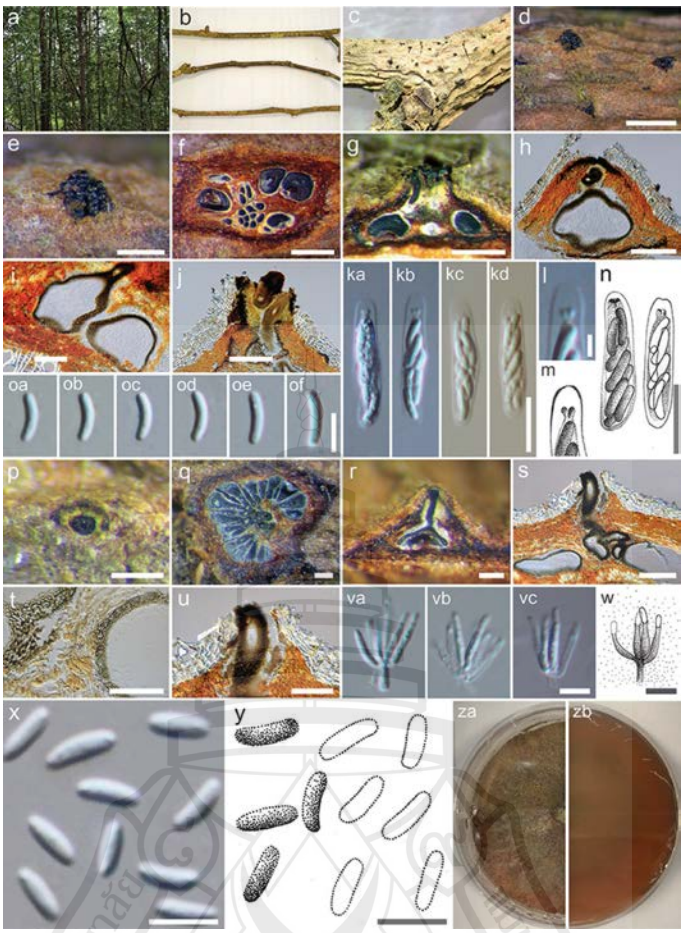
Holotype: MFLU 17-0709

Associated with twigs and branches of *Xylocarpus moluccensis*. Sexual morph: *Stromata* immersed in bark. *Ascostromata* 400–1000 × 70–250 μm diameter, semi-immersed in host tissue, scattered, erumpent, uni- or multi-loculate, with ostiolar neck. Ostiole 70–150 μm diameter, numerous, dark brown to black, at the same level as the disc, occasionally area below disc a lighter entostroma. *Peridium* comprising several layers of cell of *textura angularis*, with innermost layer thick, brown, outer layer dark brown. Hamathecium comprising long cylindrical, cellular, anastomosed paraphyses. *Asci* (21–)23–25 × 4.1–4.7(–5) μm ($\bar{x}$ = 22 × 4.3 μm, n = 15), 6–8-spored, unitunicate, clavate to elongate obovoid, with a J-, refractive apical ring. *Ascospores* (5.6–)6–6.8 × 1.3–1.5(–2) μm ($\bar{x}$ = 6.6 × 1.5 μm, n = 20), biseriate, elongate-allantoid, unicellular, hyaline, smooth-walled. Asexual morph: *Conidiomata* 400–1200 × 180–380 μm diameter, semi-immersed in host tissue, solitary, erumpent, scattered, discoid, circular to ovoid, with multi-loculate, pycnidial, embedded in stromatic tissue, with ostiole. *Ostioles* 230–300 μm long, with an ostiolar neck. Peridium comprising few layers of cells of *textura angularis*, with innermost layer thin, pale brown, outer layer brown to dark brown. *Conidiophores* unbranched or occasionally branched at the bases, formed from the innermost layer of pycnidial wall, with conidiogenous cells. *Conidiogenous cells* (3.3–)6–9.1 × 1–1.3(–1.7) μm ($\bar{x}$ = 6 × 1.3 μm, n = 15), blastic, enteroblastic, flask-shaped, phialidic, hyaline and smooth-walled. *Conidia* (3.3–)3.8–4 × 1–1.3(–1.5) μm ($\bar{x}$ = 3.8 × 1.3 μm, n = 30), unicellular, subcylindrical, hyaline, smooth-walled.

Material examined: THAILAND, Ranong Province, Ngao Mangrove Forest, on branches of *Xylocarpus moluccensis*, 6 December 2016, Chada Norphanphoun NG02a (MFLU 17-0709, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-0262, MFLUCC 17-0263, ICMP.

Notes: *Cytospora thailandica* was collected from branches of *Xylocarpus moluccensis*. The new species resembles some other *Cytospora* species, but is

characterised by uni- or multi-loculate ascomata/conidiomata with unicellular, subcylindrical and hyaline spores in both morphs. *Cytospora* species associated with *Xylocarpus granatum* is also reported in this study as *C. xylocarpi* (MFLUCC 17-0251, Figure 2.5). *Cytospora xylocarpi* is similar to *C. thailandica* in its conidiomata being multi-loculate and in the length of conidia in the asexual morph (*C. xylocarpi*: conidia 3 × 1.1 μm versus 3.8 × 1.3 μm in *C. thailandica*). However, *C. thailandica* differs from *C. xylocarpi* in having shorter ostiolar necks and larger asci and ascospores (Table 2.2). Phylogenetic analysis of our combined gene also reveals *C. thailandica* is closely related to *C. lumnitzericola* (Figure 2.1), but there are nucleotide differences as mentioned in notes of *C. lumnitzericola*. The individual ITS1+ITS2 phylogenetic tree also indicates that *C. thailandica* is distinct with good support (Figure 2.2).



Note *Cytospora thailandica* (MFLU 17-0709, holotype). a *Xylocarpus moluccensis*. b Branch of *Xylocarpus moluccensis*. c Ascostromata on host substrate. d, e Surface of ascomata. f Transverse sections through ascostroma to show distribution of locules. g–h Longitudinal sections through ascostroma to show distribution of locules. i Peridium. j Ostiolar neck. ka–kd, n Asci. l, m Apical ring. oa–of Ascospores. p Surface of conidioma. q Transverse sections through conidioma to show distribution of locules. r, s Longitudinal sections through conidioma to show distribution of locules. t Peridium. u Ostiolar neck. va–vc, w Conidiogenous cells with attached conidia. x, y Conidia. za, zb Colonies. on MEA (za-from above, zb-from below). Scale bars: d = 1000 μm, e–g = 400 μm, h, j, p–s = 200 μm, i, u = 100 μm, ka–kd, n = 10 μm, l, m = 2 μm, oa–of, va–vc, w = 5 μm, t = 50 μm, x, y = 4 μm.

Figure 2.4 Morphological characters of *Cytospora thailandica* (MFLU 17-0709, holotype)

Cytospora xylocarpi Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 2.5

Index Fungorum number: IF554810

Facesoffungi number: FoF 04604

Etymology: refers to the host genus that fungus was collected.

Holotype: MFLU 17-0708

Associated with *Xylocarpus granatum* branches. Sexual morph: Stromata immersed in bark. *Ascostromata* 230–600 × 90–250 μm diameter, semi-immersed in host tissue, scattered, erumpent, multi-loculate, with ostiolar neck. *Ostiole* 160–200 μm diameter, numerous, dark brown to black, at the same level as the disc, occasion- ally area surrounded with white hyphae. *Peridium* comprising several layers of cells of *textura angularis*, with innermost layer thick, pale brown, outer layer dark brown to black. *Hamathecium* comprising long cylindrical, cellular, anastomosed paraphyses. *Asci* (22–)24–28.8 × 3.6–4.8(–5.1) μm ($\bar{x}$ = 26 × 4 μm, n = 15), 6–8-spored, unitunicate, clavate to elongate obovoid, with a refractive, J-, apical ring. *Ascospores* (5.5–)6–6.5 × 1.7–1.8(–2) μm ($\bar{x}$ = 5.7 × 1.8 μm, n = 20), biseriate, elongate-allantoid, unicellular hyaline, smooth-walled. Asexual morph: *Conidiomata* 700–1200 × 400–480 μm diameter, semi-immersed in host tissue, solitary, erumpent, scattered, multi-loculate, with ostiole. *Ostioles* 200–250 μm long, with 1–2 ostiolar necks. *Peridium* comprising several layers of cells of *textura angularis*, with innermost layer brown, outer layer dark brown to black. *Conidiophores* unbranched or occasionally branched at the bases, formed from the innermost layer of pycnidial wall, with conidiogenous cells. *Conidiogenous cells* (6.3–)7.9–10 × 0.9–1.4(–1.6) μm ($\bar{x}$ = 8.5 × 1.4 μm, n = 15), blastic, enteroblastic, flask-shaped, phialidic, hyaline and smooth- walled. *Conidia* (2.4–)3–3.1 × 0.8–1(–1.2) μm ($\bar{x}$ = 3 × 1 μm, n = 30), unicellular, subcylindrical, hyaline, smooth-walled.

Material examined: THAILAND, Ranong Province, Ngao Mangrove Forest, on branches of *Xylocarpus granatum*, 6 December 2016, Chada Norphanphoun NG09b (MFLU 17-0708, holotype; PDD); ex-type-living cultures, MFLUCC 17-0251, ICMP.

Notes: The asexual morph of *C. xylocarpi*, studied here, is most similar to *C. rhizophorae* from dead roots of *Rhizophora mangle* L. in Guatemala, in having multi-loculate conidiomata and allantoid, slightly curved, hyaline and 3–6 × 1.1–1.5 μm

conidia (Kohlmeyer & Kohlmeyer, 1971). However, the phylogenies, generated herein, show that *C. xylocarpi* is distinct from *C. rhizophorae* (ATCC 38475), a strain from Rhizophora mangle that was identified by Kohlmeyer, the author of the species (Figure 2.2). The two species also differ by 25 substitutions in ITS1+ITS2 and were collected from different hosts. Therefore, the collection in the present study is designated as a new species.

Our phylogeny also indicates a close relationship to unpublished sequences from GenBank (Figures 2.1, 2.2). Given that no morphological descriptions are available for these, the similarity in the ITS1 and ITS2 sequence between our strain and the sequences from GenBank (HAB16R13, M225, A761, MUCC302) are presented in Table 2.3. Those strains were collected from different hosts (Table 2.3) and, together with our strain, show substantial variation in ITS1 and ITS2 (Table 2.4). More collections are needed to further study morphological and genetic variation in this group.



Note *Cytospora xylocarpi* (MFLU 17-0708, holotype). a *Xylocarpus granatum*. b Branch of *Xylocarpus granatum*. c Ascostromata on host substrate. d Surface of ascomata. e Transverse sections through ascos- troma to show distribution of locules. f, g Longitudinal sections through ascostroma to show distribution of locules. h Peridium. i–l, n Asci. m, o Ascospores. p Germinating spore. q, r Colonies on MEA (q-from above, r-below). s Transverse sections through conidioma to show distribution of locules. t Longitudinal sections through conidioma to show distribution of locules. u, v Conidiogenous cells with attached conidia. w Mature conidia. Scale bars: c = 2000 μm, d–f = 500 μm, g = 200 μm, h = 20 μm, i, p = 10 μm, j–o, u–w = 5 μm, s, t = 400 μm.

Figure 2.5 Morphological characters of *Cytospora xylocarpi* (MFLU 17-0708, holotype)

Table 2.2 Synopsis of species of *Cytospora* discussed in the paper

Taxon	Sexual morph				Asexual morph				References
	Ascostoma	Ostiolar neck	Asci	Ascospores	Conidiomata	Ostiolar neck	Conidiogenous cell	Conidia	
C. lumnitzericola	–	–	–	–	–	–	8.4 × 1.4	4 × 1.2	In this study
C. rhizophorae	–	–	–	–	370–500 × 100–310	30 × 10–25	13–20 × 1–1.8	3–6 × 1.1–1.5	Kohlm. and Kohlm. (1971)
C. thailandica	400–1000 × 70–250	70–150	22 × 4.3	6.6 × 1.5	400–1200 × 180–380	230–300	6 × 1.3	3.8 × 1.3	In this study
C. xylocarpi	230–600 × 90–250	160–200	26 × 4	5.7 × 1.8	700–1200 × 400–480	200–250	8.5× 1.4	3 × 1	In this study

Table 2.3 GenBank BLAST search from ITS1 and ITS2 of *Cytospora xylocarpi* (MFLUCC 17-0251) with sequence from GenBank identified as *C. rhizophorae*

Toxon	Strain	Host	Country	Accessions	ITS1	ITS2	ITS1+ITS2	Identities (I), Query cover (QC)	References
C. "rhizophorae"	HAB16R13	*Cinnamomum porrectum*	Malaysia	HQ336045	213/215	167/169	380/384	I=98.9%, QC=99%	Harun et al. (2011)
C. "rhizophorae"	M225	*Rhizophora mucronata*	Philippines	KR056292	213/217	167/169	380/386	I=98.4%, QC=100%	Unpublished
C. "rhizophorae"	A761	*Morinda officinalis*	China	KU529867	213/217	166/169	379/386	I=98.2%, QC=100%	Unpublished
C. "rhizophorae"	MUCC302	*Eucalyptus grandis*	Australia	EU301057	213/217	164/169	377/386	I=97.7%, QC=100%	Unpublished
C. rhizophorae	ATCC38475	*Rhizophora mangle*	LA, USA	DQ996040	187/202	156/166	343/368	I=93.2%, QC=100%	He et al. (2003)

Table 2.4 Nucleotide differences in the ITS1+ITS2 of *Cytospora xylocarpi* (MFLUCC 17-0251) with sequence from GenBank identified as *C. rhizophorae*

Taxon	Strain	ITS1																	
		14	**16**	**18**	**30**	**92**	**93**	**96**	**99**	**102**	**103**	**104**	**105**	**113**	**115**	**118**	**119**	**135**	**154**
C. xylocarpi	MFLUCC 17-0251	-	G	A	C	C	C	C	G	G	G	C	G	C	T	T	C	A	G
C. rhizophorae	ATCC38475	G	A	C	T	G	A	T	A	T	T	T	A	T	-	C	T	-	T
C. "*rhizophorae*"	HAB16R13	?	G	A	C	C	C	C	G	G	G	C	G	C	T	T	C	A	T
C. "*rhizophorae*"	M225	?	G	A	T	C	C	C	G	G	G	C	G	C	T	T	C	A	T
C. "*rhizophorae*"	A761	?	G	A	T	C	C	C	G	G	G	C	G	C	T	T	C	A	T
C. "*rhizophorae*"	MUCC302	?	G	A	T	C	C	C	G	G	G	C	G	C	-	T	C	A	T
Taxon	**Strain**	**ITS2**																	
		13	**24**	**40**	**46**	**47**	**50**	**51**	**75**	**111**	**112**	**115**	**123**						
C. xylocarpi	MFLUCC 17-0251	C	C	A	T	-	T	T	C	A	A	C	T						
C. rhizophorae	ATCC38475	T	T	-	T	-	-	T	C	G	T	A	T						
C. "*rhizophorae*"	HAB16R13	C	T	A	T	-	T	T	C	A	A	C	C						
C. "*rhizophorae*"	M225	C	T	A	T	-	T	T	C	A	A	C	T						
C. "*rhizophorae*"	A761	C	T	A	T	T	-	T	C	A	A	C	T						
C. "*rhizophorae*"	MUCC302	C	T	A	-	-	-	-	T	A	A	C	T						

Table 2.5 Nucleotides differences in the ITS, *act* and *rpb2* sequences of *Cytospora lumnitzericola*, *C. thailandica* and *C. xylocarpi*

Taxon	**Strain**	**ITS**																	
		29	88	91	92	93	94	96	97	99	101	102	103	104	105	106	107	108	111
C. lumnitzericola	MFLUCC 17-0508	T	C	T	T	T	T	C	T	C	G	G	A	C	T	A	T	A	G
C. thailandica	MFLUCC 17-0262	T	-	T	-	-	-	T	C	T	C	A	G	-	-	A	C	G	C
C. thailandica	MFLUCC 17-0263	T	-	T	-	-	-	T	C	T	C	A	G	-	-	A	C	G	C
C. xylocarpi	MFLUCC 17-0251	C	C	C	-	-	C	C	C	C	G	G	G	-	-	G	C	G	G
Taxon	**Strain**	**ITS**																	
		119	120	121	122	123	124	125	134	157	389	396	404	405	412	413	414	415	420
C. lumnitzericola	MFLUCC 17-0508	T	T	C	-	-	-	-	-	T	T	A	A	-	-	-	-	T	G
C. thailandica	MFLUCC 17-0262	C	T	T	C	-	G	G	-	T	T	G	T	T	-	-	-	-	A
C. thailandica	MFLUCC 17-0263	C	T	T	C	-	G	G	-	T	T	G	T	T	-	-	-	-	A
C. xylocarpi	MFLUCC 17-0251	T	C	T	C	C	G	G	A	G	C	A	A	A	C	T	T	T	G
Taxon	**Strain**	**ITS**					***act***												
		439	468	485	487	488	74	78	80	92	95	96	97	107	122	125	129	136	137
C. lumnitzericola	MFLUCC 17-0508	T	T	C	T	A	G	C	A	T	T	-	-	C	T	A	G	A	A
C. thailandica	MFLUCC 17-0262	T	T	T	C	T	T	G	A	A	T	-	-	T	C	T	G	A	G
C. thailandica	MFLUCC 17-0263	T	T	T	C	T	T	G	A	A	T	-	-	T	C	T	G	A	G
C. xylocarpi	MFLUCC 17-0251	C	C	C	T	T	G	C	T	A	C	C	C	T	C	A	A	G	A

Table 2.5 (continued)

Taxon	Strain	*act*																	
		139	146	147	148	149	150	152	159	165	198	209	210	212	215	216	217	218	223
C. lumnitzericola	MFLUCC 17-0508	A	A	G	C	T	C	C	G	T	C	T	C	G	A	A	A	C	A
C. thailandica	MFLUCC 17-0262	A	G	-	-	T	T	T	T	T	T	T	C	A	A	A	-	C	A
C. thailandica	MFLUCC 17-0263	A	G	-	-	T	T	T	T	T	T	T	C	A	A	A	-	C	A
C. xylocarpi	MFLUCC 17-0251	G	G	-	-	A	A	C	T	C	C	A	T	A	T	G	-	A	-
Taxon	**Strain**	***act***							***rpb2***										
		224	225	231	234	242	245	246	4	18	33	42	57	84	85	96	102	108	120
C. lumnitzericola	MFLUCC 17-0508	C	G	C	-	-	A	A	T	T	C	T	C	C	T	T	C	G	A
C. thailandica	MFLUCC 17-0262	T	T	C	T	G	T	G	T	C	A	T	C	T	C	T	C	A	G
C. thailandica	MFLUCC 17-0263	T	T	C	T	G	T	G	T	C	A	T	C	T	C	T	C	A	G
C. xylocarpi	MFLUCC 17-0251	T	T	A	C	G	T	A	C	T	C	C	T	T	C	C	A	A	G
Taxon	**Strain**	***rpb2***																	
		123	126	129	144	153	171	174	177	204	210	213	216	222	231	237	243	246	279
C. lumnitzericola	MFLUCC 17-0508	C	G	C	G	T	G	C	C	G	C	T	C	T	T	C	T	C	T
C. thailandica	MFLUCC 17-0262	T	A	T	A	C	G	T	C	G	T	C	C	C	T	T	T	T	C
C. thailandica	MFLUCC 17-0263	T	A	T	A	C	G	T	C	G	T	C	C	C	T	T	T	T	C
C. xylocarpi	MFLUCC 17-0251	C	A	C	A	T	A	T	T	C	C	C	T	C	G	C	C	C	T

Table 2.5 (continued)

Taxon	Strain	*rpb2*																	
		282	294	306	309	336	339	342	351	352	357	378	390	393	396	402	405	435	441
C. lumnitzericola	MFLUCC 17-0508	C	A	T	C	T	C	G	T	C	G	A	C	C	G	T	T	C	T
C. thailandica	MFLUCC 17-0262	T	G	C	T	C	A	A	C	T	C	G	C	T	A	T	C	C	T
C. thailandica	MFLUCC 17-0263	T	G	C	T	C	A	A	C	T	C	G	C	T	A	T	C	C	T
C. xylocarpi	MFLUCC 17-0251	T	A	C	C	T	C	G	T	C	C	A	T	T	A	C	T	T	G
Taxon	**Strain**	***rpb2***																	
		456	465	468	492	498	510	516	517	543	561	570	576	603	612	613	615	627	633
C. lumnitzericola	MFLUCC 17-0508	C	T	C	G	T	T	A	T	T	A	A	G	T	T	C	C	C	G
C. thailandica	MFLUCC 17-0262	C	C	G	C	C	C	A	T	C	A	G	A	C	C	T	G	C	G
C. thailandica	MFLUCC 17-0263	C	C	G	C	C	C	A	T	C	A	G	A	C	C	T	G	C	G
C. xylocarpi	MFLUCC 17-0251	T	T	T	G	T	C	G	C	C	G	G	G	T	C	T	G	G	A
Taxon	**Strain**	***rpb2***																	
		651	663	675	678	690	693	699	702	711	732								
C. lumnitzericola	MFLUCC 17-0508	T	A	C	T	T	G	T	C	C	T								
C. thailandica	MFLUCC 17-0262	C	G	T	C	G	A	C	T	C	C								
C. thailandica	MFLUCC 17-0263	C	G	T	C	G	A	C	T	C	C								
C. xylocarpi	MFLUCC 17-0251	C	A	T	C	T	A	C	C	T	T								

Note All isolates are new taxa in this study; "-" gap (insertion/deletion); "?" missing data

CHAPTER 3

MORPHOLOGICAL AND PHYLOGENETIC CHARACTERIZATION OF NOVEL PESTALOTIOID SPECIES ASSOCIATED WITH MANGROVES IN THAILAND[2]

Abstract

Pestalotioid fungi are associated with a wide variety of plants worldwide and are endophytes, pathogens and saprobes. The present study provides an updated phylogenetic placement of *Neopestalotiopsis*, *Pestalotiopsis* and *Pseudopestalotiopsis* using fresh collections from mangrove plants in Thailand. Twelve novel species are characterized based on combined sequence data analyses of internal transcribed spacer (ITS), beta tubulin (*β-tubulin*) and translation elongation factor 1-alpha (*ef1α*) coupled with morphological characters. The taxonomy and phylogenetic relationships of pestalotioid-fungi are reappraised with suggestions for future work.

Keywords: 12 new species, Asymptomatic leaves, *Acrostichum aureum*, *Avicenia marina*, Leaf spots, Mangroves, *Neopestalotiopsis*, *Pestalotiopsis*, pestalotiopsis-like, Phylogeny, *Pseudopestalotiopsis*, *Rhizophora* sp., *Sonneronata alba*, Taxonomy

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3.1 Introduction

Mangrove forests are one of the most productive ecosystems which play a major role in the ecological communities in coastal tropical and subtropical waters (Hyde & Lee, 1995). They serve as hatcheries and nursery habitats for marine organisms and protect coastlines from catastrophic events such as storms and tidal surges (Hyde & Jones, 1988; Fisher & Spalding, 1993; Hyde & Lee, 1995; Hyde et al., 1998). The greatest diversity of mangrove species occurs in Indonesia, Malaysia and Thailand, which also harbour a great diversity of micro-organisms especially fungi (Alias & Jones, 2009; Alias et al., 2010). However, the phylogenetic and functional description of microbial diversity in mangrove ecosystems has not been addressed to the same extent as for other environments. Even though mangrove ecosystems are very rich in microbial diversity, less than 5%of species are believed to have been described (Thatoi et al., 2012). Recently developed technologies in molecular biology and genetics offer a great promise to explore the potential of microbial diversity. Hence, the present paper makes an effort to identify the species of fungi in mangrove ecosystems in Thailand (Guba, 1961; Barr, 1975a; Nag Raj, 1993; Norphanphoun et al., 2018; Kumar et al., 2019).

Several studies have focused on the diversity and the ecology of fungi in this special habitat and there are relatively few studies on disease-causing fungi of m angrove (Cribb & Cribb, 1955; Kohlmeyer & Kohlmeyer, 1979; Hyde & Jones, 1988). Most of the mangrove fungi are reported as saprobes and endophytes (e. g Hu et al., 2007; Jones et al., 2009; Pang et al., 2010; Doilom et al., 2017; Devadatha et al., 2018; Li et al., 2018; Kumar et al., 2019). Zhou et al. (2018) reported that the endophytic fungi *Diaporthe* sp., *Neopestalotiopsis protearum* and *Pestalotiopsis* sp. are predominant in mangrove trees in south China. Endophytic fungal genera such as *Cladosporium, Colletotrichum, Fusarium, Pestalotiopsis, Phomopsis, Phyllosticta* and *Xylaria* were also reported from Thailand mangroves (Chaeprasert et al., 2010; Doilom et al., 2017). Nevertheless, endophytic fungi are less well-studied and studies mainly identified taxa to the genus level (Chaeprasert et al., 2010; Abraham et al., 2015; Thomas et al., 2016). Pathogenic mangrove fungi have received much less attention

(e. g Hyde & Cannon, 1992; Jones & Pang, 2012; Jones et al., 2019). In the present study we focused on Pestalotioid taxa on *Acrostichum aureum*, *Avicennia marina*, *Rhizophora* (mainly *R. apiculata* and *R. mucronata*) and *Sonneronata alba*, which were abundant plants in Thailand mangroves. The most notable mangrove plant among Thailand mangroves is *Rhizophora*, a genus of tropical mangrove trees, which are collectively known as true mangroves (Hassan et al., 2018).

Pestalotioid fungi are characterized based on morphological features such as the median cell colour (Maharachchikumbura et al., 2011). They are common phytopathogens causing a variety of diseases or saprobes or endophytes, and are widely distributed in tropical and temperate regions (Guba, 1961; Barr, 1975a; Nag Raj, 1993; Maharachchikumbura et al., 2014). However, species identification in this genus remains a major challenge because of overlapping morphologies (Jeewon et al 2002; 2003; Maharachchikumbura et al., 2012, 2011). Maharachchikumbura et al. (2014) split *Pestalotiopsis* into three genera: *Neopestalotiopsis*, *Pseudopestalotiopsis* and *Pestalotiopsis*, based on conidia pigment colour, conidiophores and molecular phylogeny. *Neopestalotiopsis* can be easily distinguished from *Pseudopestalotiopsis* and *Pestalotiopsis* by its versicolourous median cells (Maharachchikumbura et al., 2014). *Pseudopestalotiopsis* differs from *Pestalotiopsis* by having darker three median cells and knobbed apical appendages (Maharachchikumbura et al., 2014). Many novel species were introduced into this group during recent years (Maharachchikumbura et al., 2016; Liu et al., 2017; Nozawa et al., 2017; Ariyawansa et al. 2018; Watanabe et al., 2018; Tsai et al., 2018; Tibpromma et al., 2018). This study aimed to identify the pestalotioid fungi associated with mangroves in Thailand based on both morphological characters and molecular phylogeny.

3.2 Materials and Methods

3.2.1 Sample Collection and Examination of Specimens

Fresh leaf samples (both diseased and healthy) were collected in 2016, from *Acrostichumaureum*, *Avicenia marina*, *Rhizophora apiculata*, *R. mucronata* and *Sonneronata alba* fromPhetchaburi, Ranong and Trat provinces, Thailand. Permission

for collecting specimens wereobtained where necessary. Fresh specimens were taken to the laboratory in paper bags, examinedand described following Norphanphoun et al. (2017). Morphological characters of conidiomatawere examined using a Motic SMZ 168 dissecting microscope (Motic Incorporation Ltd., HongKong). Hand sections were mounted in water and examined for morphological details. Micro-morphology was studied using a Nikon Ni compound microscope (Nikon Instruments Inc., NY,USA) fitted with a Canon EOS 600D digital camera (Canon Inc., Tokyo, Japan). Photo-plates weremade using Adobe Photoshop CS6 Extended version 13.0 × 64 (Adobe Systems, CA, USA), whileTarosoft (R) Image Frame Work program v. 0.9.7 (Tarosoft, Thailand) was used for measurements.Cultures were obtained by the tissue isolation method outlined in Norphanphoun et al. (2018). Single hyphal tips were transferred onto potato dextrose agar (PDA, Hardy Diagnostics, CA, USA) plates throughout a two-week period. Pure cultures were maintained for further studies on PDA. The specimens/dried cultures and living cultures are deposited in the Herbarium Mae Fah Luang University (MFLU) and culture collection Mae Fah Luang University (MFLUCC), Chiang Rai, Thailand and duplicated in the International Collection of Micro-organisms from Plants (ICMP). Facesoffungi numbers were obtained as in Jayasiri et al. (2015) and the new species were registered in Index Fungorum (Index Fungorum, 2019).

3.2.2 DNA Extraction, PCR Amplification and Sequencing

Genomic DNA was extracted from fresh fungal mycelia growing on PDA at room temperature (18−25 °C) for two weeks using a E.Z.N.A.TM Fungal DNA MiniKit (Omega Biotech, CA, USA) following the manufacturer's protocols. Polymerase chain reactions (PCR) were carried out using primer pairs of ITS1/ITS4 to amplify the ITS region (White et al., 1990), EF1-728f/EF2 to amplify *ef1α* (Carbone & Kohn, 1999; O'Donnell et al. 1998) and the partial *β-tubulin* region was amplified using primers T1/Bt2b (Glass & Donaldson, 1995; O'Donnell & Cigelnik, 1997).

The amplification reactions were carried out with the following protocol: 50 µl reaction volume containing 2 µl of DNA template, 2 µl of each forward and reverse primers, 25 µl of 2× Bench TopTMTaq Master Mix (mixture of Taq DNA Polymerase (recombinant): 0.05 units/µL, MgCl2: 4 mM, and dNTPs (dATP, dCTP, dGTP, dTTP):

0.4 mM) and 19 µl of double-distilled water (ddH2O) (sterilized water). The PCR thermal cycle program for each gene is described in Table 3.1. Purification and sequencing of PCR products with the same primers mentioned above were carried out at Life Biotechnology Co., Shanghai, China.

Table 3.1 Polymerase chain reactions (PCR) thermal cycle program for each gene

Gene	**Primers**	**PCR thermal cycle protocols**
ITS	ITS1/ITS4	initially 95 °C for 3 min, followed by 40 cycles of denaturation at 95 °C for 30s, annealing at 55 °C for 50s, elongation at 72 °C for 1min, final extension at 72 °C for 7 min
β-tubulin	T1/Bt2b	initially 95 °C for 3 min, followed by 40 cycles of denaturation at 94 °C for 30s, annealing at 55 °C for 50s, elongation at 72 °C for 1min, final extension at 72 °C for 7 min
ef1α	ef1-728f/ef2	initially 94 °C for 5 min, followed by 40 cycles of denaturation at94 °C for 30s, annealing at 52 °C for 30s, elongation at 72 °C for 30s, final extension at 72 °C for 7 min

3.2.3 Phylogenetic Analysis

The sequences were assembled by Geneious® 11.1.5 (http://www.geneious.com). Multiple alignments derived in this study were analysed with similar sequences, acquired from GenBank BLASTn queries and recently published articles (Maharachchikumbura et al., 2016; Liu et al., 2017; Nozawa et al., 2017; Tsai et al., 2018; Watanabe et al., 2018). ITSx 1.1 (a Perl-based software tool) was used to extract ITS1, 5.8S and ITS2 (Bengtsson-Palme et al. 2013). BioEdit 7.2.3 (Hall 1999) was used to extract the partition of *β-tubulin*, and *ef1α*, which follow the partition template based on nucleotide BLAST in GenBank. Combined analyses of ITS1+ITS2, 5.8S, *β-tubulin* and *ef1α* sequence data were performed using maximum parsimony (MP), maximum likelihood (ML) and Bayesian analysis (BI) for each genus separately. The dataset of *Neopestalotiopsis* consisted of 52 taxa (outgroup: *Pestalotiopsis diversiseta*, MFLUCC 12-0287); 70 taxa for *Pestalotiopsis* (outgroup: *Neopestalotiopsis saprophytica*, MFLUCC 12-0282) and 27 taxa for *Pseudopestalotiopsis* (outgroup: *Neopestalotiopsis natalensis*, CBS 138.41). All sequences were aligned for each gene separately using MAFFT v.7.110 online program (http://mafft.cbrc.jp/alignment/server/; Katoh & Standley, 2013) and Gblocks v. 0.91b was used to exclude ambiguously aligned positions in the ITS, *ef1α* and *β-tubulin* alignments (Castresana, 2000; Talavera & Castresana, 2007). A partition homogeneity test (PHT) was performed with PAUP* 4.0b10 to determine whether the individual datasets were congruent and could be combined(Swofford, 2002). The combined sequence alignments were obtained from MEGA7 version 7.0.14 (Kumar et al., 2015) and missing data were coded as gap (-) and further manual adjustments were made wherever necessary in BioEdit 7.2.3 (Hall, 1999). The combined sequence alignment was converted to NEXUS file for maximum parsimony analysis using ClustalX v. 2 (Larkin et al., 2007). The NEXUS file was prepared for MrModeltest v. 2.2 (Nylander, 2004) in PAUP* v.4.0b10 (Swofford, 2002).

Maximum parsimony (MP) analysis was performed using PAUP* v. 4.0b10 (Swofford, 2002) with 1000 bootstrap replicates using heuristic search with random stepwise addition and tree- bisection reconnection (TBR). Maxtrees were set to 1000 and branches of zero length were collapsed. The following descriptive tree statistics were calculated: parsimony tree length (TL), consistency index (CI), retention index

(RI), rescaled consistency index (RC) and homoplasy index (HI).

For both maximum likelihood and Bayesian analyses, a partitioned analysis was performed with the following six partitions: ITS1+ITS2, 5.8S, *β-tubulin* (exon), *β-tubulin* (intron), *ef1α* (exon), and *ef1α* (intron). Maximum-likelihood (ML) analysis was performed with RAxML (Stamatakis, 2006) implemented in the CIPRES Science Gateway web server (RAxML-HPC2on XSEDE; Miller et al., 2010), 1000 rapid bootstrap replicates were run with GTRGAMMA model of nucleotide evolution. Maximum likelihood bootstrap values (MLBS) equal or greater than 50% are presented above each node in the resulting phylogenetic trees.

Bayesian inference (BI) analysis was performed using the Markov Chain Monte Carlo (MCMC) method with MrBayes 3.2.2 (Ronquist et al., 2012). The best-fit nucleotide substitution model for each dataset was separately determined using MrModeltest version 2.2 (Nylander, 2004). GTR model was selected a best-fit model for the *β-tubulin*-exons (*Neopestalotiopsis*), GTR+Imodel was selected a best-fit model for the *β-tubulin*-exons (*Pseudopestalotiopsis*), ITS1+ITS2+5.8S (*Neopestalotiopsis*), GTR+I+G model for *β-tubulin*-exons (*Pestalotiopsis*), HKY model for ITS1+ITS2+5.8S (*Pseudopestalotiopsis*), HKY+G model for *ef1α*-introns (*Neopestalotiopsis*), *ef1α*-introns (*Pestalotiopsis*), and *β-tubulin*-introns (*Pseudopestalotiopsis*), HKY+I model for *ef1α*-introns (*Pseudopestalotiopsis*), HKY+I+G model for ITS1+ITS2+5.8S (*Pestalotiopsis*) and *β-tubulin*-introns (*Pestalotiopsis*), K80 model for *ef1α*-exons (*Pseudopestalotiopsis*), K80+G model for *β-tubulin*-introns (*Neopestalotiopsis*), SYM model for *ef1α*-exons (*Neopestalotiopsis*), SYM+I model was selected a best-fit model for the *ef1α*-exons (*Pestalotiopsis*). The MCMC analyses, with four chains starting from random tree topology, were run between 1,000,000-5,000,000 generations for each combined dataset. Trees were sampledevery 100 generations. Tracer v. 1.5.0 was used to check parameters including the effective sampling sizes (ESS) >200, the stable likelihood plateaus and burn-in value **(**Rambaut et al., 2013**)**. The first 5000 samples were excluded as burn-in.

The phylogram was visualized in FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/; Rambaut, 2014**)** and made in Adobe Illustrator CC (Adobe Systems, CA, U.S.A.) and Adobe Photoshop CS6 Extended version 13.1.2 × 64. Newly generated sequences in this study are deposited in GenBank (Table 3.2). The finalized

alignments and trees were deposited in TreeBASE. The phylogram was visualized in FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/; Rambaut, 2014**)** and made in Adobe Illustrator CC (Adobe Systems, CA, U.S.A.) and Adobe Photoshop CS6 Extended version 13.1.2 × 64. Newly generated sequences in this study are deposited in GenBank (Table 2). The finalized alignments and trees were deposited in TreeBASE, Figure 3.1: submission ID: 24243, Figure 3.8:submission ID: 24244, Figure 3.11: submission ID: 24245.

Table 3.2 GenBank accession numbers of the sequences used in phylogenetic analyses

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
Neopestalotiopsis acrostichi	**MFLUCC 17-1754** [T]	***Acrostichum aureum***	**Thailand**	**MK764272**	**MK764338**	**MK764316**
	MFLUCC 17-1755	***Acrostichum aureum***	**Thailand**	**MK764273**	**MK764339**	**MK764317**
N. brachiata	**MFLUCC 17-1555** [T]	***Rhizophora apiculata***	**Thailand**	**MK764274**	**MK764340**	**MK764318**
N. petila	**MFLUCC 17-1738** [T]	***Rhizophora mucronata***	**Thailand**	**MK764275**	**MK764341**	**MK764319**
	MFLUCC 17-1737	***Rhizophora mucronata***	**Thailand**	**MK764276**	**MK764342**	**MK764320**
N. rhizophorae	**MFLUCC 17-1550** [T]	***Rhizophora mucronata***	**Thailand**	**MK764277**	**MK764343**	**MK764321**
	MFLUCC 17-1551	***Rhizophora mucronata***	**Thailand**	**MK764278**	**MK764344**	**MK764322**
N. sonneratae	**MFLUCC 17-1745** [T]	***Sonneronata alba***	**Thailand**	**MK764279**	**MK764345**	**MK764323**
	MFLUCC 17-1744	***Sonneronata alba***	**Thailand**	**MK764280**	**MK764346**	**MK764324**
N. thailandica	**MFLUCC 17-1730** [T]	***Rhizophora mucronata***	**Thailand**	**MK764281**	**MK764347**	**MK764325**
	MFLUCC 17-1731	***Rhizophora mucronata***	**Thailand**	**MK764282**	**MK764348**	**MK764326**
N. alpapicalis	MFLUCC 17-2544 [T]	*Rhyzophora mucronata*	Thailand	MK357772	MK463545	MK463547
	MFLUCC 17-2545	symptomatic leaves *R. apiculate*	Thailand	MK357773	MK463546	MK463548

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
N. aotearoa	CBS 367.54 [T]	*Canvas*	New Zealand	KM199369	KM199454	KM199526
N. asiatica	MFLUCC 12-0286 [T]	unidentified tree	China	JX398983	JX399018	JX399049
N. australis	CBS 114159 [T]	*Telopea* sp.	Australia	KM199348	KM199432	KM199537
N. chrysea	MFLUCC 12-0261 [T]	dead leaves	China	JX398985	JX399020	JX399051
N. clavispora	MFLUCC 12-0281 [T]	*Magnolia* sp.	China	JX398979	JX399014	JX399045
N. cocoes	MFLUCC 15-0152 [T]	*Cocos nucifera*	Thailand	NR_156312	-	KX789689
N. coffea-arabicae	HGUP4015 [T]	*Coffea arabica*	China	KF412647	KF412641	KF412644
N. cubana	CBS 600.96 [T]	leaf litter	Cuba	KM199347	KM199438	KM199521
N. ellipsospora	MFLUCC 12-0283 [T]	dead plant material	China	JX398980	JX399016	JX399047
N. egyptiaca	CBS 140162 [T]	*Mangifera indica*	Egypt	KP943747	KP943746	KP943748
N. eucalypticola	CBS 264.37 [T]	*Eucalyptus globulus*	-	KM199376	KM199431	KM199551
N. foedans	CGMCC 3.9123 [T]	unidentified mangrove plant	China	JX398987	JX399022	JX399053
N. formicarum	CBS 362.72 [T]	dead ant	Ghana	KM199358	KM199455	KM199517
N. honoluluana	CBS 114495 [T]	*Telopea* sp.	USA	KM199364	KM199457	KM199548
N. iraniensis	CBS 137768 [T]	*Fragaria* × *ananassa*	Iran	KM074048	KM074057	KM074051

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
N. javaensis	CBS 257.31 [T]	*Cocos nucifera*	Indonesia	KM199357	KM199457	KM199548
N. keteleeria	MFLUCC 13-0915 [T]	living leaves of *Keteleeria pubescens*	China	KJ503820	KJ503821	KJ503822
N. magna	MFLUCC 12-0652 [T]	*Pteridium* sp.	France	KF582795	KF582793	KF582791
N. mesopotamica	CBS 336.86 [T]	*Pinus brutia*	Iraq	KM199362	KM199441	KM199555
N. musae	MFLUCC 15-0776 [T]	*Musa* sp.	Thailand	NR_156311	KX789686	KX789685
N. natalensis	CBS 138.41 [T]	*Acacia mollissima*	South Africa	NR_156288	KM199466	KM199552
N. pernambucana	GS-2014 RV01 [T]	*Vismia guianensis*	Brazil	KJ792466	-	-
N. piceana	CBS 394.48 [T]	*Picea* sp.	UK	KM199368	KM199453	KM199527
	CBS 254.32	*Cocos nucifera*	Indonesia	KM199372	KM199452	KM199529
	CBS 225.3	*Mangifera indica*	-	KM199371	KM199451	KM199535
N. protearum	CBS 114178 [T]	*Leucospermum cuneiforme* cv. "Sunbird"	Zimbabwe	JN712498	KM199463	KM199542
	CMM1357	-	-	KY549597	KY549632	KY549594

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
N. rosae	CBS 101057 [T]	*Rosa* sp.	New Zealand	KM199359	KM199429	KM199523
N. rosicola	CFCC 51992 [T]	*Rosa chinensis*	China	KY885239	KY885245	KY885243
	CFCC 51993	*Rosa chinensis*	China	KY885240	KY885246	KY885244
N. samarangensis	MFLUCC 12-0233 [T]	*Syzygium samarangense*	Thailand	JQ968609	JQ968610	JQ968611
N. saprophytica	MFLUCC 12-0282 [T]	*Magnolia* sp.	China	KM199345	KM199433	KM199538
N. steyaertii	IMI 192475 [T]	*Eucalyptus viminalis*	Australia	KF582796	KF582794	KF582792
N. surinamensis	CBS 450.74 [T]	soil under *Elaeis guineensis*	Suriname	KM199351	KM199465	KM199518
	CBS 111494	*Protea eximia*	Zimbabwe	-	KM199462	KM199530
N. umbrinospora	MFLUCC 12-0285 [T]	unidentified plant	China	JX398984	JX399019	JX399050
N. vitis	MFLUCC 15-1265 [T]	*Vitis vinifera* cv. “Summer black"	China	KU140694	KU140685	KU140676
N. zimbabwana	CBS 111495 [T]	*Leucospermum cunciforme* cv. “Sunbird”	Zimbabwe	JX556231	KM199456	KM199545
Pestalotiopsis rhizophorae	**MFLUCC 17-0416 [T]**	***Rhizophora apiculata***	**Thailand**	**MK764283**	**MK764349**	**MK764327**

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
	MFLUCC 17-0417	***Rhizophora apiculata***	**Thailand**	**MK764284**	**MK764350**	**MK764328**
P. thailandica	**MFLUCC 17-1616** [T]	***Rhizophora apiculata***	**Thailand**	**MK764285**	**MK764351**	**MK764329**
	MFLUCC 17-1617	***Rhizophora apiculata***	**Thailand**	**MK764286**	**MK764352**	**MK764330**
P. adusta	ICMP 6088 [T]	on refrigerator door PVC gasket	Fiji	JX399006	JX399037	JX399070
P. aggestorum	LC6301 [T]	*Camellia sinensis*	China	KX895015	KX895348	KX895234
P. anacardiacearum	IFRDCC 2397 [T]	*Mangifera indica*	China	KC247154	KC247155	KC247156
P. arceuthobii	CBS 434.65 [T]	*Arceuthobium campylopodum*	USA	KM199341	KM199427	KM199516
P. arengae	CBS 331.92 [T]	*Arenga undulatifolia*	Singapore	KM199340	KM199426	KM199515
P. australasiae	CBS 114126 [T]	*Knightia* sp.	New Zealand	KM199297	KM199409	KM199499
P. australis	CBS 114193 [T]	*Grevillea* sp.	Australia	KM199332	KM199383	KM199475
P. biciliata	CBS 124463 [T]	*Platanus* × *hispanica*	Slovakia	KM199308	KM199399	KM199505
P. brachiata	LC2988 [T]	*Camellia* sp.	China	KX894933	KX895265	KX895150

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
P. brassicae	CBS 170.26 [T]	*Brassica napus*	New Zealand	KM199379	-	KM199558
P. camelliae	MFLUCC 12-0277 [T]	*Camellia japonica*	China	JX399010	JX399041	JX399074
P. chamaeropis	CBS 186.71 [T]	*Chamaerops humilis*	Italy	KM199326	KM199391	KM199473
P. clavata	MFLUCC 12-0268 [T]	*Buxus* sp.	China	JX398990	JX399025	JX399056
P. colombiensis	CBS 118553 [T]	*Eucalyptus eurograndis*	Colombia	KM199307	KM199421	KM199488
P. digitalis	ICMP 5434 [T]	*Digitalis purpurea*	New Zealand	KP781879	KP781883	-
P. diploclisiae	CBS 115587 [T]	*Diploclisia glaucescens*	Hong Kong	KM199320	KM199419	KM199486
P. distincta	LC3232 [T]	*Camellia sinensis*	China	KX894961	KX895293	KX895178
P. diversiseta	MFLUCC 12-0287 [T]	dead plant material	China	NR_120187	JX399040	JX399073
P. dracontomelon	MFUCC 10-0149 [T]	*Dracontomelon dao*	Thailand	KP781877	-	KP781880
P. ericacearum	IFRDCC 2439 [T]	*Rhododendron delavayi*	China	KC537807	KC537821	KC537814
P. formosana	NTUCC 17-009 [T]	on dead grass	Taiwan	MH809381	MH809385	MH809389
	NTUCC 17-010	on dead grass	Taiwan	MH809382	MH809386	MH809390
P. furcata	MFLUCC 12-0054 [T]	*Camellia sinensis*	Thailand	JQ683724	JQ683708	JQ683740

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
P. gaultheria	IFRD 411-014 [T]	*Gaultheria forrestii*	China	KC537805	KC537819	KC537812
P. gibbosa	NOF 3175 [T]	*Gaultheria shallon*	Canada	LC311589	LC311590	LC311591
P. grevilleae	CBS 114127 [T]	*Grevillea* sp.	Australia	KM199300	KM199407	KM199504
P. hawaiiensis	CBS 114491 [T]	*Leucospermum* sp.	USA	KM199339	KM199428	KM199514
P. hollandica	CBS 265.33 [T]	*Sciadopitys verticillata*	The Netherlands	KM199328	KM199388	KM199481
P. humus	CBS 336.97 [T]	soil	Papua New Guinea	KM199317	KM199420	KM199484
P. inflexa	MFLUCC 12-0270 [T]	dead plant material	China	JX399008	JX399039	JX399072
P. intermedia	MFLUCC 12-0259 [T]	dead plant material	China	JX398993	JX399028	JX399059
P. italiana	MFLUCC 12-0657 [T]	*Cupressus glabra*	Italy	KP781878	KP781882	KP781881
P. jester	CBS 109350 [T]	*Fagraea bodenii*	Papua New Guinea	KM199380	KM199468	KM199554
P. jiangxiensis	LC4399 [T]	*Camellia* sp.	China	KX895009	KX895341	KX895227
P. jinchanghensis	LC6636 [T]	*Camellia sinensis*	China	KX895028	KX895361	KX895247
P. kenyana	CBS 442.67 [T]	*Coffea* sp.	Kenya	KM199302	KM199395	KM199502
P. knightiae	CBS 114138 [T]	*Knightia* sp.	New Zealand	KM199310	KM199408	KM199497

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
P. licualacola	HGUP4057 T	*Licuala grandis*	China	KC492509	KC481683	KC481684
P. linearis	MFLUCC 12-0271 T	*dead plant material*	China	JX398992	JX399027	JX399058
P. longiappendiculata	LC3013 T	*Camellia sinensis*	China	KX894939	KX895271	KX895156
P. lushanensis	LC4344 T	*Camellia sp.*	China	KX895005	KX895337	KX895223
P. macadamiae	BRIP 63738B T	*Macadamia sp.*	Australia	KX186588	KX186680	KX186621
P. malayana	CBS 102220 T	*Macaranga triloba*	Malaysia	KM199306	KM199411	KM199482
P. monochaeta	CBS 144.97 T	*Quercus robur*	Netherlands	KM199327	KM199386	KM199479
P. montellica	MFLUCC 12-0279 T	*dead plant material*	China	JX399012	JX399043	JX399076
P. neglecta	TAP1100 T	*Quercus myrsinaefolia*	Japan	AB482220	LC311599	LC311600
P. neolitseae	NTUCC 17-011 T	*on leaf of Neolitsea villosa*	Taiwan	MH809383	MH809387	MH809391
P. novae-hollandiae	CBS 130973 T	*Banksia grandis*	Australia	KM199337	KM199425	KM199511
P. oryzae	CBS 353.69 T	*Oryza sativa*	Denmark	KM199299	KM199398	KM199496
P. papuana	CBS 331.96 T	*coastal soil*	Papua New Guinea	KM199321	KM199413	KM199491
P. parva	CBS 265.37 T	*Delonix regia*	-	KM199312	KM199404	KM199508

Table 3.2 (continued)

Taxa	Strain number a	Host	Country	ITS	*β-tubulin*	*ef1α*
	CBS 278.35	*Leucothoe fontanesiana*	-	KM199313	KM199405	KM199509
P. pallidotheae	MAFF 240993 T	*Pieris japonica*	Japan	NR111022	LC311584	LC311585
P. portugalica	CBS 393.48 T	-	Portugal	KM199335	KM199422	KM199510
P. rhododendri	IFRDCC 2399 T	*Rhododendron sinogrande*	China	KC537804	KC537818	KC537811
P. rhodomyrtus	HGUP4230 T	*Rhodomyrtus tomentosa*	China	KF412648	KC537818	KF412645
P. rosea	MFLUCC 12-0258 T	*dead plant material*	China	JX399005	JX399036	JX399069
P. scoparia	CBS 176.25 T	*Chamaecyparis sp.*	-	KM199330	KM199393	KM199478
P. shorea	MFLUCC 12-0314 T	*dead seed wing of Shorea obtusa*	Thailand	KJ503811	KJ503814	KJ503817
Pestalotiopsis sp.	LC3637 T	*Camellia sp.*	China	KX894993	KX895324	KX895210
P. spathulata	CBS 356.86 T	*Gevuina avellana*	Chile	KM199338	KM199423	KM199513
P. telopeae	CBS 114161 T	*Telopea sp.*	Australia	KM199296	KM199403	KM199500
P. trachicarpicola	IFRDCC 2240 T	*Trachycarpus fortunei*	China	NR_120109	-	-
P. unicolor	MFLUCC 12-0276 T	*dead plant material*	China	JX398999	JX399030	-

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
P. verruculosa	MFLUCC 12-0274 T	*dead plant material*	China	JX398996	-	JX399061
P. yanglingensis	LC4553 T	*Camellia sinensis*	China	KX895012	KX895345	KX895231
Pseudopestalotiopsis avucenniae	**MFLUCC 17-0434 T**	***Avicennia marina***	**Thailand**	**MK764287**	**MK764353**	**MK764331**
Ps. curvatispora	**MFLUCC 17-1722 T**	***Rhizophora mucronata***	**Thailand**	**MK764288**	**MK764354**	**MK764332**
Ps. curvatispora	**MFLUCC 17-1723**	***Rhizophora mucronata***	**Thailand**	**MK764289**	**MK764355**	**MK764333**
Ps. curvatispora	**MFLUCC 17-1747**	***Rhizophora mucronata***	**Thailand**	**MK764290**	**MK764356**	**MK764334**
Ps. rhizophorae	**MFLUCC 17-1560 T**	***Rhizophora apiculata***	**Thailand**	**MK764291**	**MK764357**	**MK764335**
Ps. thailandica	**MFLUCC 17-1724 T**	***Rhizophora mucronata***	**Thailand**	**MK764292**	**MK764358**	**MK764336**
Ps. thailandica	**MFLUCC 17-1725**	***Rhizophora mucronata***	**Thailand**	**MK764293**	**MK764359**	**MK764337**
Ps. ampullaceae	LC6618 T	*Camellia sinensis*	China	KX895025	KX895358	KX895244
Ps. camelliae-sinesis	LC3011 T	*Camellia sinensis*	China	KX894985	KX895316	KX895202
Ps. chinensis	LC3011 T	*Camellia sinensis*	China	KX894937	KX895269	KX895154
Ps. cocos	CBS 272.29 T	*Cocos nucifera*	Java, Indonesia	KM199378	KM199467	KM199553

Table 3.2 (continued)

Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
Ps. dawaina	MM14-F0015 [T]	unknown	Dawei, Myanmar	LC324750	LC324751	LC324752
Ps. ignota	NN 42909 [T]	unknown	-	KU500020	-	KU500016
Ps. indica	CBS 459.78 [T]	*Hibiscus rosa-sinensis*	-	KM199381	KM199470	KM199560
Ps. ixorae	NTUCC 17-001.1 [T]	*Ixora* sp.	-	MG816316	MG816326	MG816336
Ps. jiangxiensis	LC4479 [T]	*Eurya* sp.	China	KX895034	KX895343	KX895229
Ps. kawthaungina	MM14-F0083 [T]	unknown	Kawthaung, Myanmar	LC324753	LC324754	LC324755
Ps. kubahensis	UMAS KUB-P20 [T]	*Macaranga* sp.	Sarawak, Malaysia	KT006749	-	-
Ps. myanmarina	NBRC 112264 [T]	*Averrhoa carambola*	Dawei, Myanmar	LC114025	LC114045	LC114065
Ps. simitheae	MFLUCC 12-0121 [T]	*Pandanus odoratissimus*	Thailand	KJ503812	KJ503815	KJ503818
	MFLUCC 12-0125	living leaves of *Pandanus odoratissimus*	Thailand	KJ503813	KJ503816	KJ503819

Table 3.2 (continued)

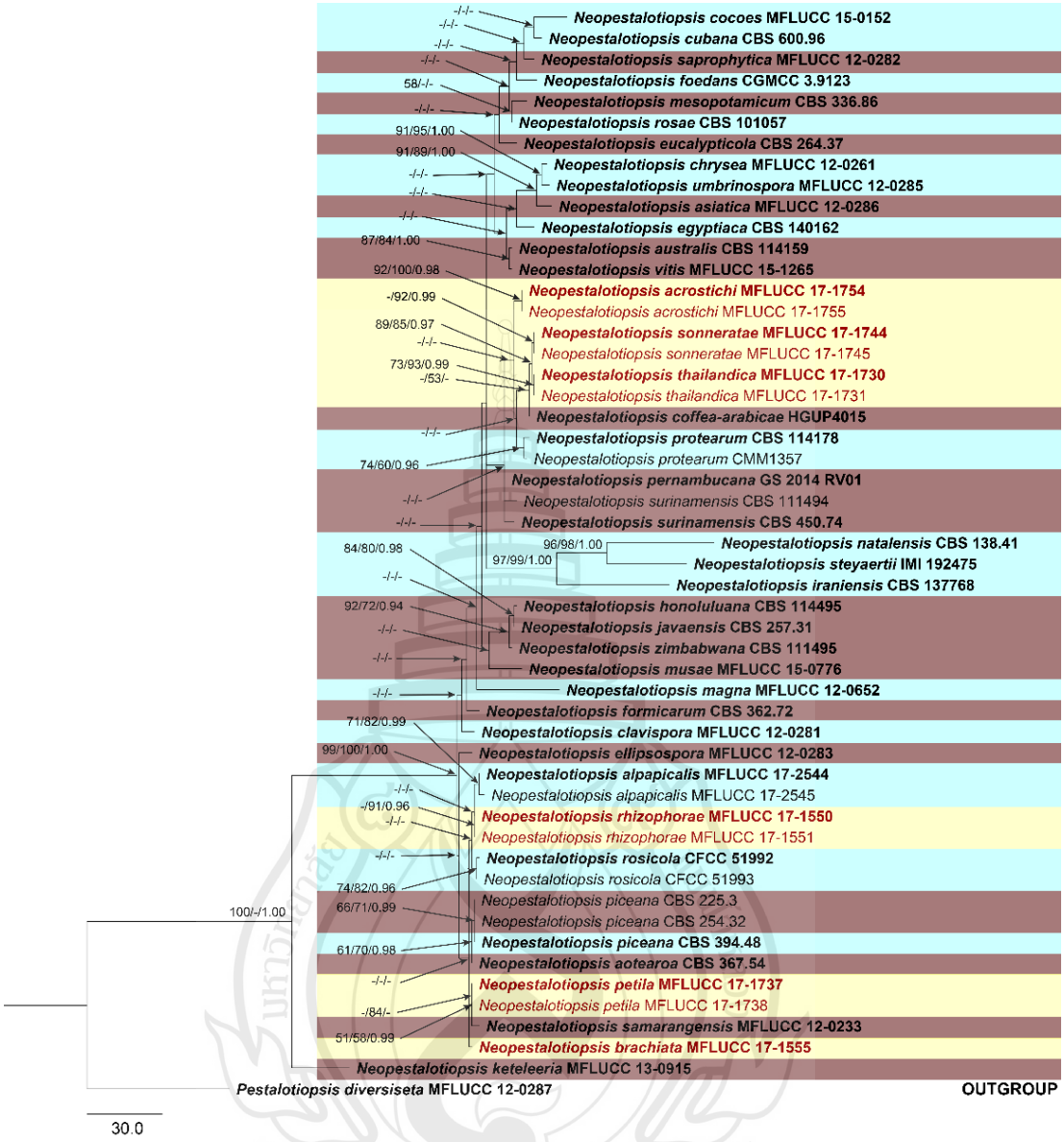
Taxa	Strain number [a]	Host	Country	ITS	*β-tubulin*	*ef1α*
Ps. taiwanensis	NTUCC 17-002.1 [T]	*Ixora* sp.	Taiwan	MG816319	MG816329	MG816339
	NTUCC 17-002.2	*Ixora* sp.	Taiwan	MG816320	MG816330	MG816340
	NTUCC 17-002.3	*Ixora* sp.	Taiwan	MG816321	MG816331	MG816341
	NTUCC 17-002.4	*Ixora* sp.	Taiwan	MG816322	MG816332	MG816342
Ps. theae	MFLUCC 12-0055 [T]	*Camellia sinensis*	Thailand	JQ683727	JQ683711	JQ683743
Ps. vietnamensis	NBRC 112252 [T]	*Fragaria* sp.	Hue, Vietnam	LC114034	LC114054	LC114074

Note [a]BRIP Queensland Plant Pathology Herbarium; CBS CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands; CFCC China Forestry Culture Collection Center; CGMCC China General Microbiological Culture Collection Center; HGUP the Plant Pathology Herbarium of Guizhou University; IFRDCC the International Fungal Research & Development Centre, Kunming, Yunnan (culture collection); ICMP International Collection of Microorganisms from Plants; IMI International Mycological Institute; MFLUCC Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; NBRC the Biological Resource Center, Japan; NTUCC the Department of Plant Pathology and Microbiology, National Taiwan University Culture Collection. [T] Ex-type strains. Strains in this study are in bold.

3.3 Results

The results from the partition homogeneity tests (PHT) for all three phylogenetic trees were not significant (level ≥ 95%), indicating that the individual datasets were congruent and could be combined. The combined alignment of the three phylogeny analyses trees included 22 strains, of which 11 strains belong to *Neopestalotiopsis*, four strains belong to *Pestalotiopsis* and seven strainsbelong to *Pseudopestalotiopsis*.

The alignment of *Neopestalotiopsis* (Figure 3.1) comprised 52 taxa, with the outgroup taxon, *Pestalotiopsis diversiseta* (MFLUCC 12-0287). The total length of the dataset was 1358 characters including alignment gaps, 1–324, 325–482, 483–700, 701–886, 887–1054 and 1055–1358 corresponding to ITS1+ ITS2, 5. 8S, *β-tubulin* (exon), *β-tubulin* (intron), *ef1α* (exon) and *ef1α* (intron), respectively. The combined dataset contained 1001 constant, 175 parsimony uninformative and 182 parsimony informative characters. The combined dataset was analyzedusing MP, ML and BI. The trees generated under different optimality criteria were essentially similar in topology and did not differ significantly (data not shown). The descriptive statistics generated from MP analysis based on the combined dataset of ITS1+ITS2, 5.8S, *β-tubulin* (exon), *β-tubulin* (intron), *ef1α* (exon), and *ef1α* (intron) were TL = 643, CI = 0.673, RI = 0.670, RC = 0.451, HI = 0.327. The best scoring likelihood tree selected with a final value for the combined dataset = -5197.543923.



Note One of the 1000 most parsimonious trees obtained from a heuristic search of combined ITS, *β-tubulin* and *ef1α* sequence data for the genus *Neopestalotiopsis*. The tree is rooted to *Pestalotiopsis diversiseta* (MFLUCC 12-0287). Maximum parsimony and maximum likelihood bootstrap values ≥ 50%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/PPBY) are given at the nodes. The species obtained in this study are in red. Ex-type taxa from other studies are in blackbold.

Figure 3.1 Phylogenetic analysis of *Neopestalotiopsis*

Neopestalotiopsis acrostichi Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.2

Index Fungorum number: IF556434

Facesoffungi number: FoF 05780

Etymology: refers to the host from which the fungus was isolated, *Acrostichum aureum* L.

Holotype: MFLU 19-0774

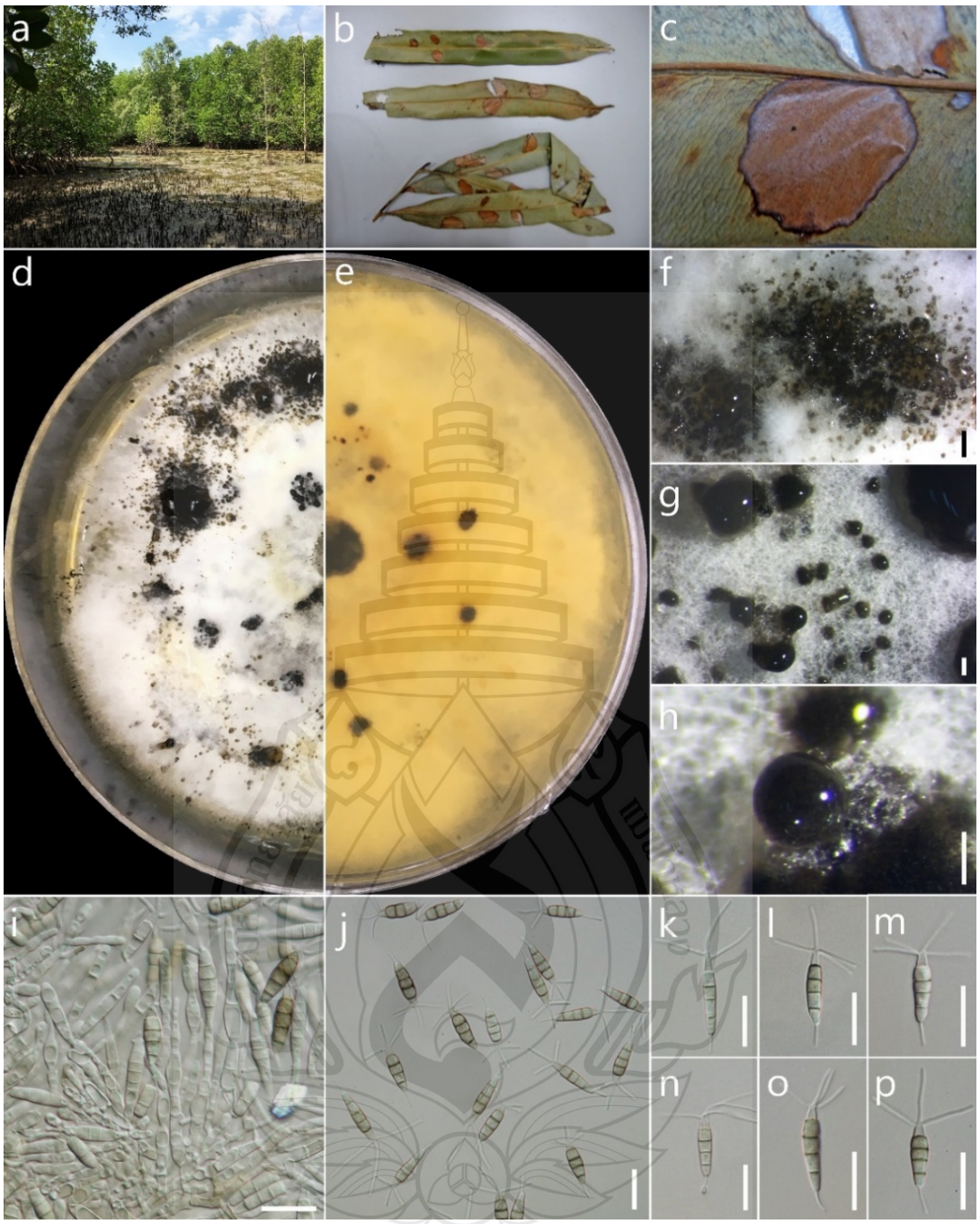
Associated with leaf spots of *Acrostichum aureum* L. *Symptoms* sub circular to irregularshape, pale brown, appear on adaxial surface leaves of *A. aureum*, which later expand outwards (Figure 3.2c). Small brown spots appeared initially and then gradually enlarged, changing to pale browncircular spots with a black border. They were usually 4–5 circular spots occurred on a single affected leaf (Figure 3.2b). Asexual morph: *Conidiomata* pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth, thin-walled, proliferating once percurrently, collarette present and not flared, 10–25 × 2–5 μm. *Conidia* (22–)23–26(–27) × (5–)5.5–6.5(–7) μm, (mean ± SD = 24.3 ± 1.3 × 6 ± 0.6 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (4.5–)5–6(–7) μm long (mean ± SD = 5.5 ± 0.8 μm); three median cells (14–)15–16(–18) μm long (mean ± SD = 15. 9 ± 1 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (4. 5–)5–6(–6. 5) μm long (mean ± SD = 5.6 ± 0.6 μm); third cell brown, 4.5–6 μm long (mean ± SD = 4.9 ± 0.5 μm); fourth cell brown, (4–)4.5–5(–6.5) μm long (mean ± SD = 5.4 ± 0.6 μm); apical cell (3–)4.5–5(–6) μm long (mean ± SD = 4. 9 ± 0. 8 μm), hyaline, conic to acute, with 3–5 tubular appendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (16–)19–28. 5(–33. 5) μm long (mean ± SD = 24. 5 ± 4. 7 μm); single basal appendage, tubular, unbranched, centric, (4.5–)5–7(–12) μm long, (mean ± SD = 7.1 ± 2 μm).

Culture characteristics: Colonies on PDA reaching 6–8 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Chanthaburi Province, leaf spots of *Acrostichum aureum* L., 25 April 2017, Norphanphoun Chada JT12-1 (MFLU 19-0774 dried culture, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1754, TNCC. THAILAND, Chanthaburi Province, leaf spots of *Acrostichum aureum* L., 25 April 2017, Norphanphoun Chada JT12-2 (MFLU 19-0775 dried culture, paratype); ex-type-living cultures, MFLUCC 17-1755.

Notes: *Neopestalotiopsis acrostichi* was isolated from a leaf spot of *Acrostichum aureum*. The new species resembles several other *Neopestalotiopsis* species. The combined phylogenetic tree indicated that *N. acrostichi* is sister to *N. protearum* (CBS 114178) and *N. surinamensis* (CBS 450. 74) (Figure 3.1), but they differ in morphology. *Neopestalotiopsis acrostichi* have larger conidia than *N. protearum* (*N. protearum*: (14–)16–17(–18) × (6.5–)8–9(–10)). *Neopestalotiopsis acrostichi* is very much similar to *N. surinamensis* (Crous et al. 2011, Maharachchikumbura et al. 2014). However, *N. acrostichi* differs from this species by having smaller conidia (*N. surinamensis*:(23–)24–28(–29) × (7–)7. 5–9(–9. 5)) with four apical tubular appendages (*N. surinamensis*: (15–)18–27(–28)) (Table 3.3; Maharachchikumbura et al. 2014). This is the first report of *Neopestalotiopsis* on *A. aureum*.



Note *Neopestalotiopsis acrostichi* (MFLU 19-0774, holotype). a Habitat. b, c Leaf spots on *Acrostichum aureum*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA.i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: f–h = 200 µm, i–p = 20 µm.

Figure 3.2 Morphological characters of *Neopestalotiopsis acrostichi* (MFLU 19-0774, holotype)

Neopestalotiopsis brachiata Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.3

Index Fungorum number: IF556435

Facesoffungi number: FoF 05771

Etymology: the specific epithet "brachiata" refers to the character of apical appendages (Latin 'brachiata' means 'branches').

Holotype: MFLU 19-0776

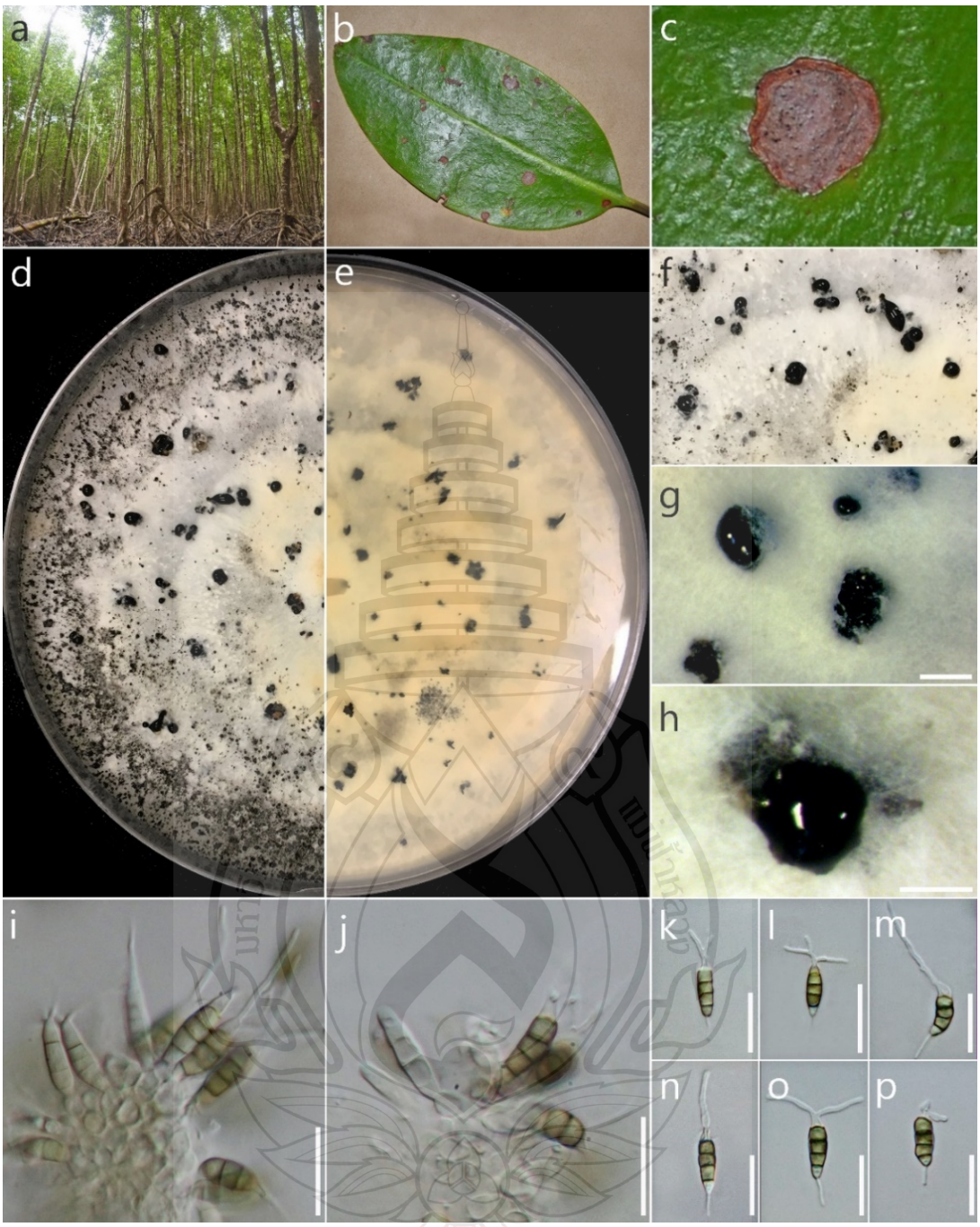
Associated with leaf spots of *Rhizophora apiculata* Blume. *Symptoms* circular or sub circular shape, grayish brown, slightly sunken spots appear on adaxial surface leaves of *R. apiculata*, which later expand outwards (Figure 3.3c). Small auburn spots appeared initially and then gradually enlarged, changing to grayish brown circular ring spots with a dark brown border. They were usually >5 circulars, which occurred on a single affected leaf. In severe cases, lesions spreaded evenly on the leaves (Figure 3.3b). Asexual morph: *Conidiomata* pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to ampulliform to lageniform, hyaline, smooth- and thin-walled,simple, proliferating 1–2 times percurrently, collarette present and not flared, 5–10 × 5–8 μm. *Conidia* (18–)18.5–25(–26) × (5–)5.5–6(–6.5) μm (mean ± SD = 21 ± 2.2 × 5.5 ± 0.6 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (3–)3.5–4(–5) μm long (mean ± SD = 3.8 ± 0.7 μm); three median cells (10–)10.5–15(–16) μm long (mean ± SD = 12.7 ± 1.7 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (3–)4–5(–6) μm long (mean ± SD = 4.4 ± 0.8 μm); third cell brown, (3.5–)4–5(–6) μm long (mean ± SD = 4.2 ± 0.7 μm); fourth cell brown, (3–)4–5(–5.5) μm long (mean ± SD = 4.1 ± 0.5 μm); apical cell (4–)4.5–5(–6) μm long (mean ± SD = 4.5 ± 0.7 μm), hyaline, conic to acute; with 1–3 tubular appendages on apical cell, inserted at different loci in a crest at the apex of the apical cell, branched, flexuous, (8.5–)9.5–33(–34) μm long (mean ± SD =20 ± 7.6 μm); single basalappendage, tubular, unbranched, centric, (3.5–)4–9(–10) μm long (mean ± SD = 6.5 ± 1.6 μm).

Culture characteristics: Colonies on PDA reaching 6–7 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Ngao, Ranong Province, Ngao Mangrove Forest Research Centre, leaf spots of *Rhizophora apiculata*, 6 December 2016, Norphanphoun Chada NG33 (MFLU19-0776 dried culture, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1555, TNCC.

Notes: *Neopestalotiopsis brachiata* is similar to *N. rosicola* (strain CFCC 51992) in conidial size (*N. brachiata* (18–)18.5–25(–26) × (5–)5.5–6(–6.5) μm *vs. N. rosicola*: (19−)20−25.5(−26) × (5−)5.5−8(−8.5) μm) but phylogenetically distinct (Jiang et al., 2018). In the multigene phylogeneticanalysis presented here, the new species formed a sister clade to *N. aotearoa* (strain CBS 367.54), *N. piceanae* (strain CBS 394.48) and *N. petila* (in this study), which appear to be phylogenetically distinct (Figure 3.1). The conidia of *N. brachiata* are different from *N. aotearoa* ((19.5–)21–28(–29) × (6–)6.5–8.5(–9) μm), *N. piceanae* ((19–)19.5–25(–26) × (7–)7.5–9(–9.5) μm) and *N. petila* ((20–)21–26.5(–27.5) × (5.5–)6–7(–8) μm) and also differs by having branched, flexuous apical tubular appendages (Maharachchikumbura et al., 2014).



Note *Neopestalotiopsis brachiata* (MFLU 19-0776, holotype). a Habitat. b, c Leaf spots on *Rhizophora apiculata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA.i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: g = 1000 µm, h = 500 µm, i–p = 20 µm.

Figure 3.3 Morphological characters of *Neopestalotiopsis brachiate* (MFLU 19-0776, holotype)

Neopestalotiopsis petila Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.4

Index Fungorum number: IF556436

Facesoffungi number: FoF 05772

Etymology: the latin "petilus" meaning slander/slim, which refers to the shape of conidia.

Holotype: MFLU 19-0777

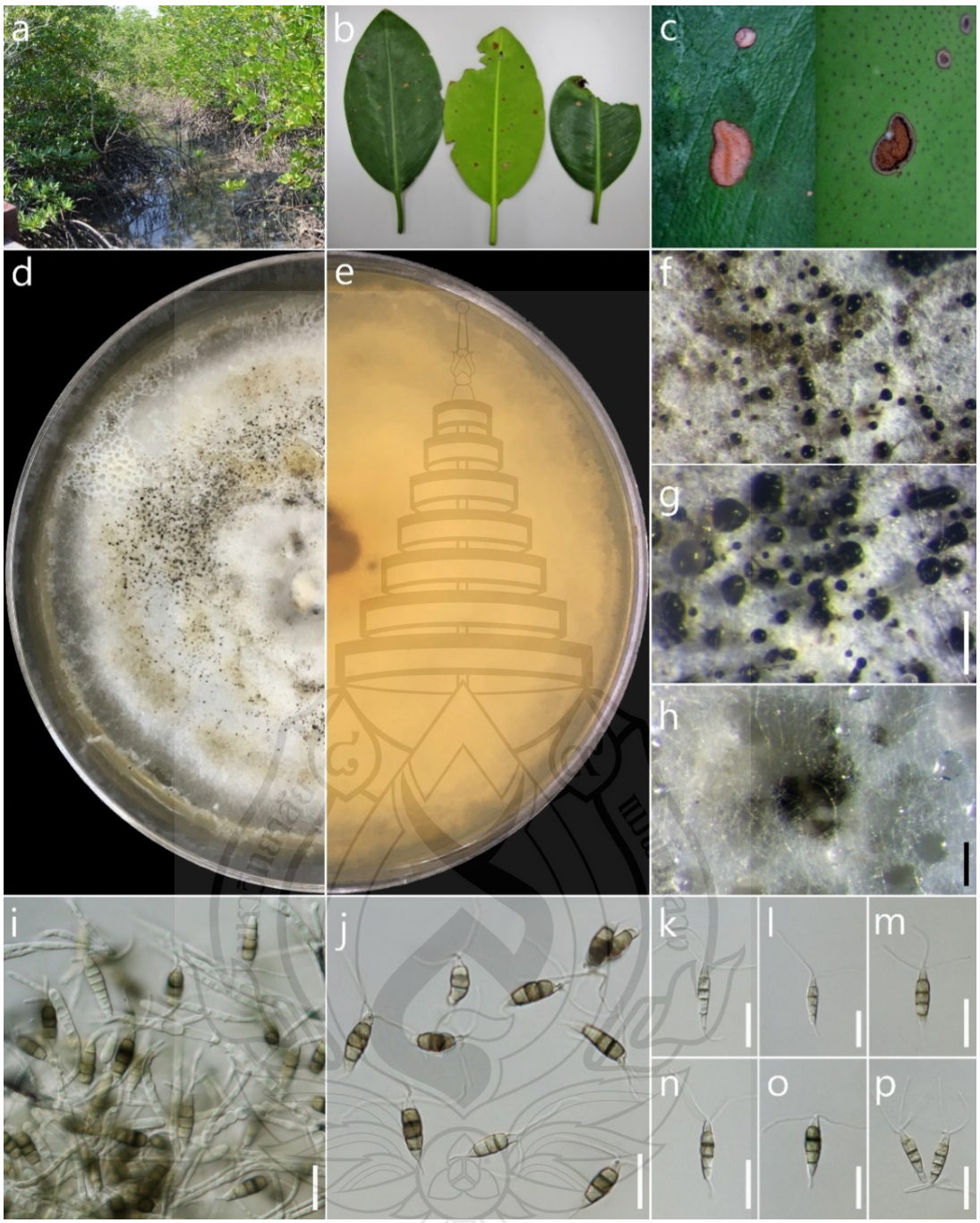
Associated with leaf spots of *Rhizophora mucronata* Lam. *Symptoms* subcircular to the irregular shape, pale brown, slightly sunken spots appear on adaxial surface leaves of *R. mucronata*, which later expand outwards (Figure 3.4c). Small auburn spots appeared initially and then gradually enlarged, changing to pale-aubum circular ring spots with a dark auburn border. They were usually >5 circulars, which occurred on a single affected leaf. In severe cases, lesions spread evenly on the leaves (Figure 3.4b). Asexual morph: *Conidiomata* pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* distinct. *Conidiogenous cells* discrete to integrated, hyaline, smooth- and thin-walled, proliferating one time percurrently, collarette present and not flared. *Conidia* (20–)21–26.5(–27.5) × (5.5–)6–7(–8) μm (mean ± SD = 24.5 ± 2.0 × 6.7 ± 0.7 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (3–)4–5.5(–6) μm long (mean ± SD = 4.52 ± 0.8 μm); three median cells (12.5–)13.5–15(–17) μm long (mean ± SD = 15.3 ± 1.0 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (4.5–)5–6(–7) μm long (mean ± SD = 5.2 ± 0.5 μm); third cell brown, (3.5–)4–5(–5.5) μm long (mean ± SD = 4.8 ± 0.5 μm); fourth cell brown, (4.5–)5–5.5(–6) μm long (mean ± SD = 5.3 ± 0.5 μm); apical cell (3–)4–5(–7) μm long (mean ± SD = 4.6 ± 1.0 μm), hyaline, conic to acute; with2–3 tubular appendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (21–)22–29(–33) μm long (mean ± SD = 25.5 ± 3.1 μm); single basal appendage, tubular, unbranched, centric, (2–)3–8(–9) μm long (mean ± SD = 6 ± 2.1 μm).

Culture characteristics: Colonies on PDA reaching 5–6 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Kor Chang, Trat Province, leaf spots of *Rhizophoramucronata*, 27 April 2017, Norphanphoun Chada KC05-1 (MFLU 19-0777 dried culture, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1737, TNCC. THAILAND, Kor Chang, Trat Province, leaf spots of *R. mucronata*, 27 April 2017, Norphanphoun Chada KC05-2 (MFLU 19- 0778 dried culture, paratype); living cultures, MFLUCC 17-1738.

Notes: Based on multigene analyses, *Neopestalotiopsis petila* is closely related to *N. aotearoa* (strain CBS 367.54), *N. piceana* (strain CBS 394.48), *N. brachiata* (in this study) and *N. samarangensis* (strain MFLUCC 12-0233) (Figure 3.1). However, *N. petila* differs from *N. aotearoa* in having long apical appendages (*N. petila*: (21–)22–29(–33) *vs. N. aotearoa*: (3–)5–12(–13)) and differs from *N. piceana* by having 2–3 apical appendages (*N. piceana* containing only 3 appendages) and short basal appendage (*N. petila*: (2–)3–8(–9) *vs. N. piceana*: 6–23) and larger conidia than *N. samarangensis* (*N. petila*: (20–)21–26.5(–27.5) × (5.6–)6–7(–7.8) *vs. N. samarangensis*: 18–21 × 6.5–7.5) (Maharachchikumbura et al., 2014, 2013). The morphological differences between *N. petila* and *N. brachiata* have been mentioned above as notes of *N. brachiata*. Thus, *N. petila* is considered a novel species.



Note *Neopestalotiopsis petila* (MFLU 19-0777, holotype). a Habitat. b, c Leaf spots on *Rhizophora mucronata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA. i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: g–h = 200 µm, i–p = 20 µm.

Figure 3.4 Morphological characters of *Neopestalotiopsis petila* (MFLU 19-0777, holotype)

Neopestalotiopsis rhizophorae Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.5

Index Fungorum number: IF556437

Facesoffungi number: FoF 05773

Etymology: refers to the host from which the fungus was collected, *Rhizophora mucronate* Lam.

Holotype: MFLU 19-0779

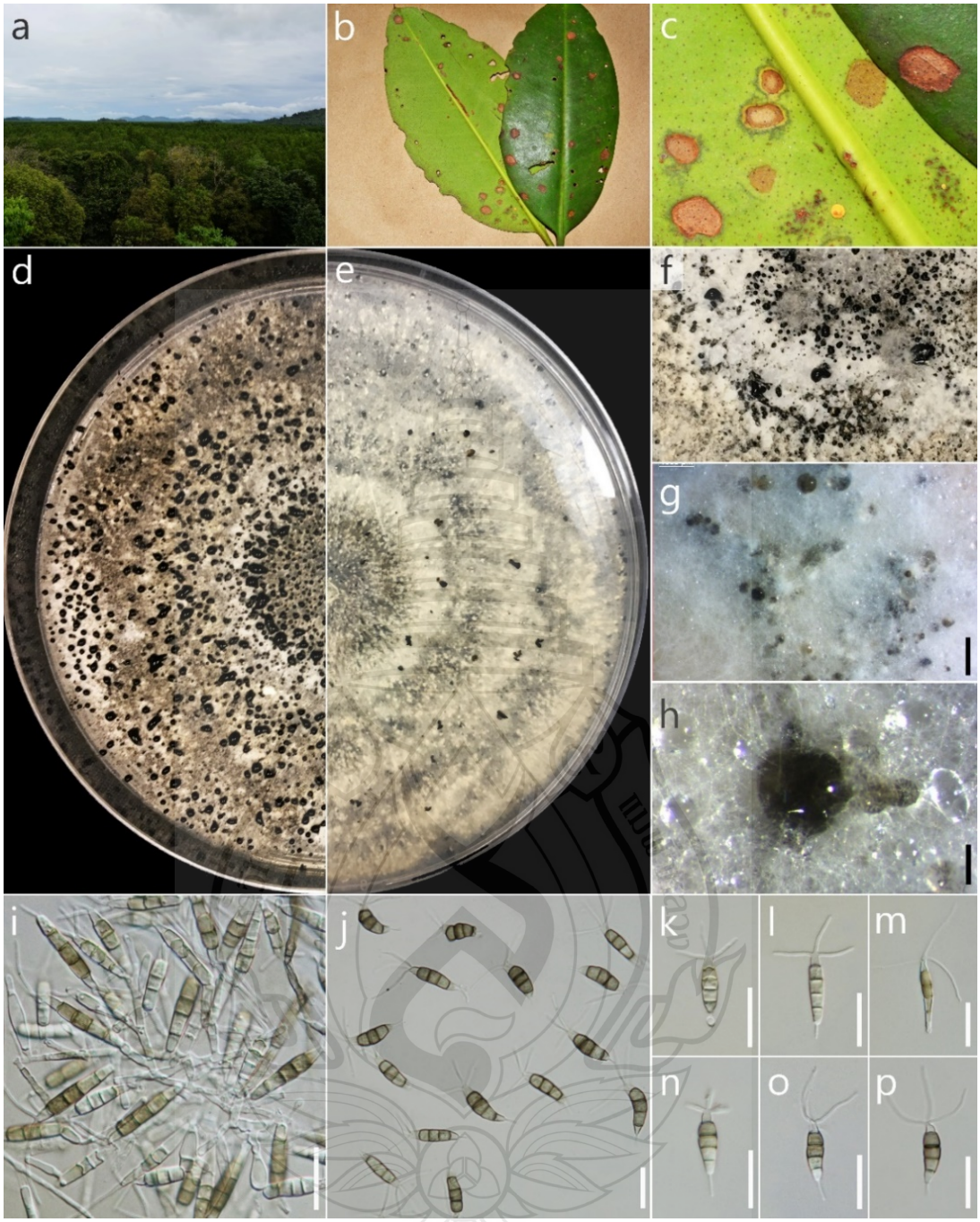
Associated with leaf spots of *Rhizophora mucronata* Lam. *Symptoms* irregular to subcircular shape, brown, slightly sunken spots appear on adaxial surface leaves of *R. mucronata*, which later expand outwards on the surface of the leaves (Figure 3.5c). Small auburn spots appeared initially and then gradually enlarged, changing to tawny circular ring spots with a dark mahogany border and jagged edge. They were usually >5 circulars, which occurred on a single affected leaf. In severe cases, lesions spread evenly on the leaves (Figure 3.5b). Asexual morph: *Conidiomata* pycnidial,globose, brown, semi-immersed on PDA releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* distinct. *Conidiogenous cells* discrete or integrated, ampulliform, clavate or subcylindrical, hyaline, smooth, 8–20 × 4–8 μm. *Conidia* (20–)20. 5–27(–27. 5) × (6–)6. 5–7. 5(–8) μm (mean ± SD = 24.5 ± 0.3 × 7.2 ± 0.6 μm), fusiform to clavate, straight to slightly curved, 4- septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- andsmooth-walled, (2–)3–4(–5) μm long (mean ± SD = 3.7 ± 0.6 μm); three median cells (14–)15.5– 17(–19.5) μm long (mean ± SD = 16.7 ± 1.4 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (4. 5–)5–6(–7) μm long (mean ± SD = 5.9 ± 0.7 μm); third cell brown, (4–)5–7(–10) μm long (mean ± SD = 5.2 ± 0.6 μm); fourth cell brown, (4–)5–5.5(–6.5) μm long (mean ± SD = 5.5 ± 0.6 μm); apical cell (3–)3.5–4(– 5.5) μm long (mean ± SD = 4.1 ± 0.7 μm), hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (6–)12. 5–22(–24) μm long (mean ± SD = 17. 5 ± 4. 4 μm); single basal appendage, tubular, unbranched, centric, with or without knob (2.5–)3–9.5(–10) μm long (mean ± SD = 5.2 ± 1.8 μm).

Culture characteristics: Colonies on PDA reaching 7–8 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Ngao, Ranong Province, Ngao Mangrove Forest Research Centre, leaf spots of *Rhizophora mucronata*, 6 December 2016, Norphanphoun Chada NG16a (MFLU 19-0779 dried culture, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1550, TNCC. THAILAND, Ngao, Ranong Province, Ngao Mangrove Forest Research Centre, leaf spots of *Rhizophora mucronata*, 6 December 2016, Norphanphoun Chada NG16b (MFLU 19-0780 dried culture, paratype); ex-type-living cultures, MFLUCC 17-1551.

Notes: The new species *Neopestalotiopsis rhizophorae* (MFLUCC 17-1550, MFLUCC 17-1551) is isolated from *R. mucronata*, from Ranong province in Thailand. *Neopestalotiopsis rhizophorae* is most similar to *N. petila* and *N. thailandica* (this study) in its conidial size (*N. petila*:(20–)21–26.5(–27.5) × (5.5–)6–7(–8) µm, *N. thailandica*: (20–)21–25(–25.5) × (5.5–)6–7(–7.5) µm) (Table 3.3). However, based on combined gene phylogenetic analysis, *N. rhizophorae* is separated from *N. petila* and *N. thailandica*, and nested between these two species; *N. alpapicalis* (MFLUCC 17-2544, MFLUCC 17-2545), the collections from *R. mucronata* in Phuket, Thailand and *N. rosicola* (strain CFCC 51992, CFCC 51993), the collections from *Rosa chinensis* in China (Figure 3.1). *Neopestalotiopsis rhizophorae* can be distinguished from *N. alpapicalis* by larger conidia and longer appendages (*N. alpapicalis*: conidial size 14–22.5 × 5–7 µm, apical appendages 5.5–15 µm, basal appendages 3–6.5 µm, Table 3.3) with polymorphic nucleotide differences of *β-tubulin* (5- bp) and *ef1α* (3-bp) sequence data. It differs from *N. rosicola* by ITS (4-bp) and *ef1α* (4-bp) sequence data.



Note *Neopestalotiopsis rhizophorae* (MFLU 19-0779, holotype). a Habitat. b, c Leaf spots on*Rhizophora mucronata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA. i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: g = 1000 µm, h = 100 µm, i = 50 µm, j–p = 20 µm.

Figure 3.5 Morphological characters of *Neopestalotiopsis rhizophorae* (MFLU 19-0779, holotype)

Neopestalotiopsis sonneratae Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.6

Index Fungorum number: IF556438

Facesoffungi number: FoF 05774

Etymology: refers to the host from which the fungus was isolated, *Sonneronata alba* L.

Holotype: MFLU 19-0781

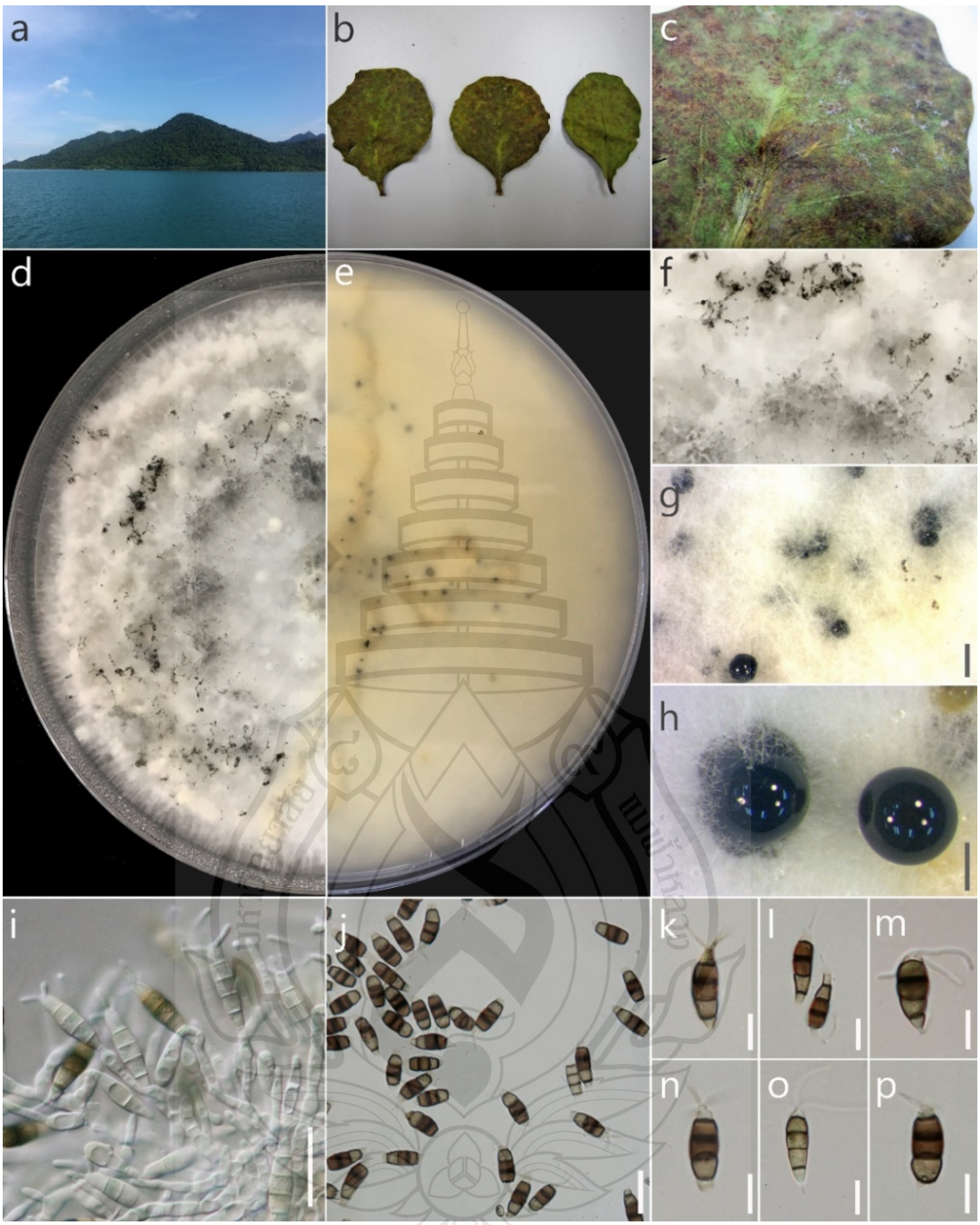
Associated with leaf spots on *Sonneronata alba* L. *Symptoms* small circular shape, auburn, slightly spots appear on adaxial surface leaves of *S. alba*, which later expand outwards on the surface of the leaves (Figure 3.6c). Small auburn spots appeared initially and then gradually enlarged, changing to dark brown circular spots and border with blurred edge. They were usually > 5 circulars, which occurred on a single affected leaf (Figure 3.6b). Asexual morph: *Conidiomata* pycnidial, 200–400 μm diam, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, 3–8 × 2–6 μm, proliferating one time percurrently, collarette present and not flared. *Conidia* (21.5–)24–26(–28) × 7–7.5(–8), (mean ± SD = 24 ± 1.6 × 7.51 ± 0.4 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (2–)3–3.5(–4) μm long (mean ± SD = 3 ± 0.6); three median cells (14.5–)15–16.5(–17.5) μm long (mean ± SD = 15.8 ± 0.9), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; secondcell from base pale brown, (4.5–)5–6(–7) μm long (mean ± SD =5.6 ± 0.8 μm); third cell brown, (4–)5–5.5(–6) μm long (mean ± SD = 5.2 ± 0.7 μm); fourth cell brown, (4–)5–6(–7) μm long (mean ± SD = 5.1 ± 0.7 μm); apical cell (3.5–)4–4.5(–5) μm long (mean ± SD =4 ± 0.6 μm), hyaline,conic to acute; with 1–3 tubular appendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (5.5–)7–8(–14) μm long (mean ± SD = 8.5 ± 2); single basal appendage, tubular, unbranched, centric, (2.5–)3–4(–5) μm long (mean ± SD = 3.4 ± 0.9) long.

Culture characteristics: Colonies on PDA reaching 5–6 cm diam after 7 d at room temperature(±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense, aerial mycelium on surface flat or raised, with filiform margin (curled margin), moderate-to-strongly fluffy, fluffy to floccose, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Kor Chang, Trat Province, leaf spots of *Sonneronata alba*,27 April 2017, Norphanphoun Chada KC01-1 (MFLU 19-0781 dried culture, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1744, TNCC. THAILAND, Kor Chang, Trat Province, leaf spots of *Sonneronata alba*, 27 April 2017, Norphanphoun Chada KC01-2 (MFLU 19-0782 dried culture, paratype); ex-type-living cultures, MFLUCC 17-1745.

Notes: *Neopestalotiopsis sonneratae* was isolated from a leaf spot of *Sonneronata alba* in Thailand. In the phylogenetic analyses of combined genes, *N. sonneratae* forms a sister group to *N. coffea-arabicae* (strain HGUP4015) and *N. thailandica* (in this study) (Figure 3.1). However, there are significant differences in morphological characteristics; *N. coffea-arabicae* and *N. thailandica* conidia are smaller (*N. coffea-arabicae*: 16–20 × 5–7 μm, *N. thailandica*: (20–)21–25(–25. 5) × (5. 7–)6–7(–7.3) μm) with both species containing longer apical appendages (*N. coffea-arabicae*: 11–16 μm, *N. thailandica*: (30–)32. 5–38(–40) μm) and *N. thailandica* having two apical appendages (Song et al., 2013).



Note *Neopestalotiopsis sonneratae* (MFLU 19-0781, holotype). a Habitat. b, c Leaf spots on *Sonneronata alba*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA.i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: g = 1000 µm, h = 500 µm,i, j = 20 µm, k–p = 10 µm.

Figure 3.6 Morphological characters of *Neopestalotiopsis sonneratae* (MFLU 19-0781, holotype)

Neopestalotiopsis thailandica Norphanphoun & K.D. Hyde, sp. nov., Figure 3.7

Index Fungorum number: IF556439

Facesoffungi number: FoF 05775

Etymology: refers to the country where the fungus was collected, Thailand.

Holotype: MFLU 19-0783

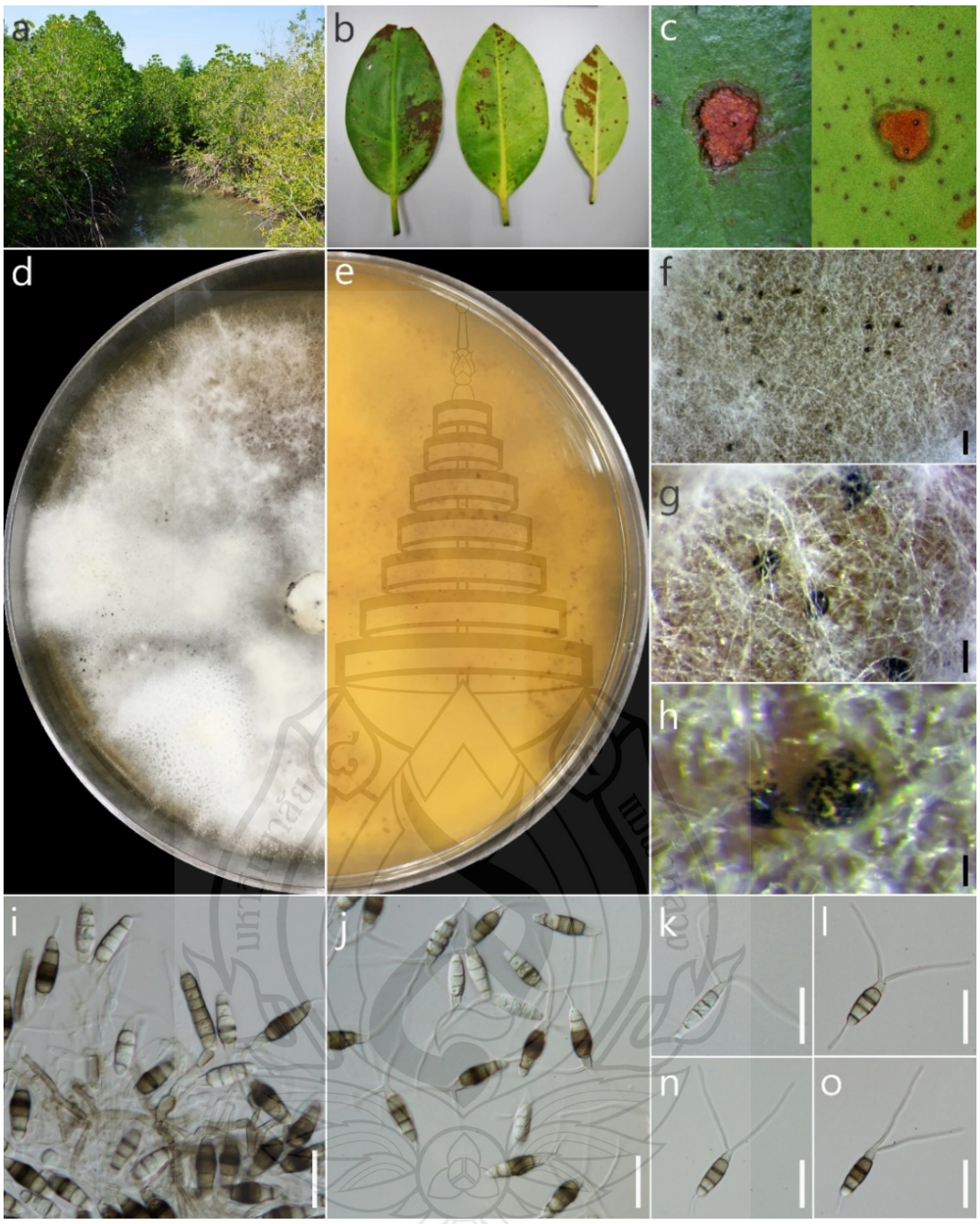
Associated with leaf spots of *Rhizophora mucronata* Lam. *Symptoms* small irregular to subcircular shape, brown, slightly sunken spots appear on adaxial surface leaves of *R. mucronata*, which later expand outwards on the surface of the leaves (Figure 3.7c). Small auburn spots appeared initially and then gradually enlarged, changing to tawny circular ring spots with a dark mahogany border and jagged edge. They were usually >5 circulars, which occurred on a single affected leaf.In severe cases, lesions spread evenly on the leaves (Figure 3.7b). Asexual morph: *Conidiomata* pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* distinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, proliferating 1–2 times percurrently, collarette present and not flared. *Conidia* (20–)21–25(–25.5) × 6–7(–7.5) µm (mean ± SD = 22.6 ± 1.3 × 6.6 ± 0.5 µm), fusiform to clavate, straight to slightly curved, 4(–7)-septate; basal cell obconic with a truncate base, hyaline orsometimes pale brown, thin- and smooth-walled, (2.5–)3–4(–4.5) µm long (mean ± SD = 3.7 ± 0.5 µm); threemedian cells (12–)12.5–15(–16) µm long (mean ± SD = 14.2 ± 0.9 µm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (4–)4.5–5(–5.5) µm long (mean ± SD = 4.6 ± 0.3 µm); third cell brown, (3.5–)11–26(–27.5)µm long (mean ± SD = 4.5 ± 0.4 µm); fourth cell brown, (4–)5–5.5(–6) µm long (mean ± SD = 5.1 ± 0. 6 µm); apical cell (3. 5–)4–5. 5(–6) µm long (mean ± SD = 4. 7 ± 0. 6 µm), hyaline, conic to acute; with 1–2 tubular appendages on apical cell, inserted at different loci but in a crest at the apexof the apical cell, unbranched, flexuous, (30–)32.5–38(–40) µm long (mean ± SD = 34.5 ± 3.7 µm); single basal appendage, tubular, unbranched, centric, (3–)6–9(–10) µm long (mean ± SD = 7. 6 ± 2.2 µm).

Culture characteristics: Colonies on PDA reaching 5–6 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Kor Chang, Trat Province, leaf spots of *Rhizophoramucronata*, 27 April 2017, Norphanphoun Chada KC11-1 (MFLU 19-0783 dried culture, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1730, TNCC.THAILAND, Kor Chang, Trat Province, leaf spots of *Rhizophora mucronata*, 27 April 2017, Norphanphoun Chada KC11-2 (MFLU 19-0784 dried culture, paratype); ex-type-living cultures, MFLUCC 17-1731.

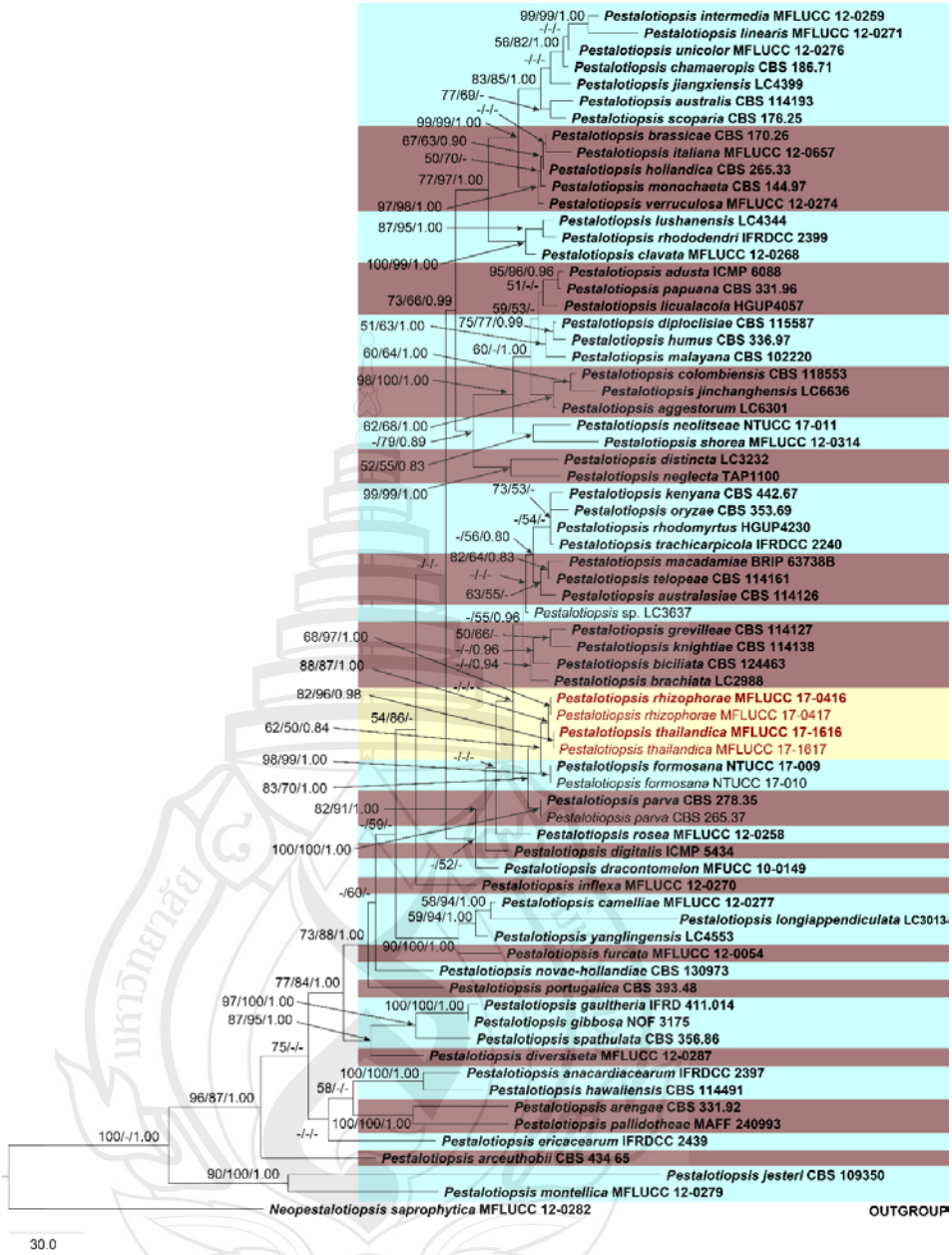
Notes: The collections (MFLUCC 17-1730, MFLUCC 17-1731) were observed and introduced as *N. thailandica*. The new species is introduced with the type from *Rhizophora mucronata* from Trat Province in Thailand. *Neopestalotiopsis thailandica* is most similar to *N. petila* and *N. rhizophorae* (both species are introduced in this study) with its conidial size. The morphological differences between *N. petila* and *N. rhizophorae* have been mentioned above as notes of *N. rhizophorae* (Table 3.3). However, based on the combined gene phylogenetic analysis, *N. thailandica* is separated from other species in the genus and is sister to *N. coffea-arabicae* (HGUP4015, Song et al., 2013), which was isolated from leaves of *Coffea arabica* L. and *N. sonneratae* (in this study) from leaf spots of *Sonneronata alba* (Figure 3.1). However, their morphologyis different. *Neopestalotiopsis thailandica* differs from *N. coffea-arabicae* by having larger conidia (*N. thailandica*: (20–)21–25(–25.5) × 6–7(–7.5) *vs. N. coffea-arabicae*: 16–20 × 5–7)), and longer apical appendages (*N. thailandica*: (30–)32.5–38(–40) *vs. N. coffea-arabicae*:11–16) (Table 3.3). The morphological differences between *N. thailandica* and *N. sonneratae* are mentioned above under the notes of *N. sonneratae*. Thus, based on morphology and phylogeny it is considered that *N. thailandica* is a novel species.



Note *Neopestalotiopsis thailandica* (MFLU 19-0783, holotype). a Habitat. b, c Leaf spots on *Rhizophora mucronata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA. i Conidiogenous cells giving rise to conidia. j–o Conidia. Scale bars: f = 500 µm, g = 200 µm,h = 50 µm, i–o = 20 µm.

Figure 3.7 Morphological characters of *Neopestalotiopsis thailandica* (MFLU 19-0783, holotype)

The second phylogenetic tree (*Pestalotiopsis*) comprised 70 taxa with the outgroup, *Neopestalotiopsis saprophytica* (MFLUCC 12-0282). The total length of the dataset was 1440 characters including alignment gaps, 1–380, 381–538, 539–779, 780–979, 980–1147, and 1148– 1440 corresponding to ITS1+ ITS2, 5. 8S, *β-tubulin* (exon), *β-tubulin* (intron), *ef1α* (exon), and *ef1α* (intron), respectively. The combined dataset contained 887 constant, 174 parsimony uninformative and 379 parsimony informative characters. The combined dataset was analyzedusing MP, ML and BI. The trees generated under different optimality criteria were essentially similar in topology and did not differ significantly (data not shown). The descriptive statistics generated from MP analysis based on the combined dataset of ITS1+ITS2, 5.8S, *β-tubulin* (exon), *β-tubulin* (intron), *ef1α* (exon), and *ef1α* (intron) were TL = 1664, CI = 0.510, RI = 0.685, RC = 0. 349, HI = 0. 490. The best scoring likelihood tree selected with a final value for the combined dataset = -10362.397645.



Note One of the 1000 most parsimonious trees obtained from a heuristic search of combined ITS, *β-tubulin* and *ef1α* sequence data for the genus *Pestalotiopsis*. The tree is rooted to *Neopestalotiopsis saprophytica* (MFLUCC 12-0282). Maximum parsimony and maximum likelihood bootstrap values ≥ 50%. Bayesian posterior probabilities ≥ 0.90 (MPBS/ MLBS/ PPBY) are given at the nodes. The species obtained in this study are in red font. Ex-type taxa from other studies are in black bold.

Figure 3.8 Phylogenetic analysis of *Pestalotiopsis*

Pestalotiopsis rhizophorae Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.9

Index Fungorum number: IF556440

Facesoffungi number: FoF 05781

Etymology: refers to the host from which the fungus was isolated, *Rhizophora apiculate* Blume.

Holotype: MFLU 19-0785

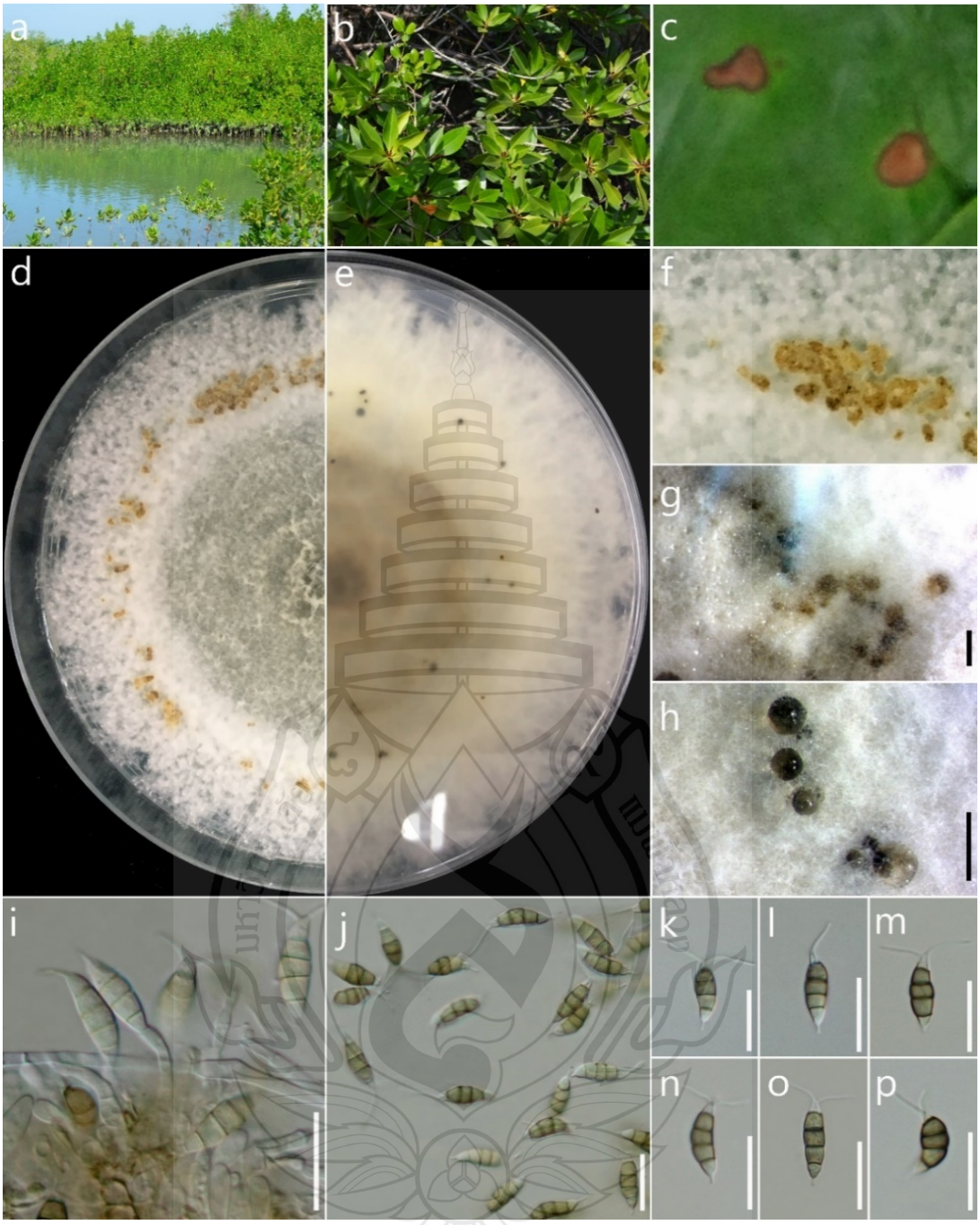
Associated with leaf spots of *Rhizophora apiculata* Blume. *Symptoms* small irregular spots shape, rufous, slightly sunken spots adaxial surface leaves of *R. apiculata*, which later expand outwards on the surface of the leaves (Figure 3.9c). Small rufous spots appeared initially and then gradually enlarged, changing to tawny circular ring spots with a dark brown border and smooth edge. They were usually few circulars, which occurred on a single affected leaf (Figure 3.9b). Asexual morph: *Conidiomata* 2 0–7 0 μm diam, pycnidial, globose, brown, semi-immersed on PDA, rreleasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct.*Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, 10 –20 × 1 –2 μm, proliferating 1–2 times percurrently, collarette present and not flared. *Conidia* (17–)17.5–23(–23.5) × (5. 5–)6–6. 5(–7) μm (mean ± SD = 20 ± 1. 6 × 6. 3 ± 0. 5 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes palebrown, thin- and smooth-walled, (2–)3–3.5(–5) μm long (mean ± SD = 3.7 ± 0.7 μm); three mediancells (11–)11.5–14(–14.5) μm long (mean ± SD = 13.2 ± 1.2 μm), brown, septa and periclinal walls darker than rest of the cell, concolorous, wall rugose; second cell from base pale brown, (3.5–)4–5(–5.5) μm long (mean ± SD = 4.6 ± 0.6 μm); third cell brown, (3–)4–4.5(–5) μm long (mean ± SD = 4.1 ± 0.6 μm); fourth cell brown, (3.5–)4–5(–5.5) μm long (mean ± SD = 4.6 ± 0.5 μm); apical cell (1.8–)2–3(–4.5) μm long (mean ± SD = 3.1 ± 0.5 μm), hyaline, conic to acute; with 1–2 tubularappendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (7. 5–)8–13(–14. 5) μm long (mean ± SD = 11. 4 ± 2. 4 μm); single basal appendage, tubular, unbranched, centric, 1.5–4.5(–5) μm long (mean ± SD = 2.5 ± 1.1 μm).

Culture characteristics: Colonies on PDA reaching 5–6 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, The Sirindhorn International Environmental Park, Cha-am District, Phetchaburi Province, leaf spots on *Rhizophora apiculata*, 30 November 2016,Norphanphoun Chada NNS28a (MFLU 19-0785, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-0416, TNCC. THAILAND, The Sirindhorn International Environmental Park, Cha-am District, Phetchaburi Province, leaf spots on *Rhizophora apiculata*, 30 November 2016, Norphanphoun Chada NNS28b (MFLU 19-0786, paratype); living cultures, MFLUCC 17-0417.

Notes: *Pestalotiopsis rhizophorae* formed a distinct clade in the multi-locus tree and is sister to *P. formosana* (strain NTUCC 17-009), *P. parva* (strain CBS 265.37) and *P thailandica* (in this study) (Figure 3.2). *Pestalotiopsis rhizophorae* differs from *P thailandica* and *P. formosana* by shorter conidia (*P. rhizophorae*: (17–)17. 5–23(–23. 5) μm *vs. P thailandica*: (17–)17. 5–28(–29) μm, *P. formosana*: (15–)18–22(–26) × (5–)6–7 μm); shorter apical appendages (*P. rhizophorae*: (7.5–)8– 13(–14. 5) μm *vs. P thailandica*: (5. 5–)11–34(–38) μm) and basal appendages (*P. rhizophorae*: (1. 3–)1. 5–4. 5(–5) μm *vs. P thailandica*: (2–)2. 5–9. 5(–10) μm, *P. formosana*: (2–)3–5(–6) μm) (Table 3.4, Ariyawansa & Hyde, 2018; Maharachchikumbura et al., 2014). *Pestalotiopsis rhizophorae* is similar to *P. parva* in conidial size (*P. parva*: (16–)16.5–20(–21) × 5–7(–7.5) μm) but differs by having 1–2 apical appendages (Table 3.4; Ariyawansa & Hyde, 2018; Maharachchikumbura et al., 2014). The two species (*P. rhizophorae, P. thailandica*) are also different in four base pairs in ITS, one base pair in *β-tubulin* and *ef1α*. Therefore, the collection in the present study is designated as a new species.



Note *Pestalotiopsis rhizophorae* (MFLU 19-0785, holotype). a Habitat b, c Leaf spots of *Rhizophera apiculata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA.i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: f–h = 100 µm, i–p = 20 µm.

Figure 3.9 Morphological characters of *Pestalotiopsis rhizophorae* (MFLU 19-0785, holotype)

Pestalotiopsis thailandica Norphanphoun, Doilom & K.D. Hyde, sp. nov., Figure 3.10

Index Fungorum number: IF556441

Facesoffungi number: FoF 05782

Etymology: refers to the country where the fungus was collected, Thailand.

Holotype: MFLU 19-0787

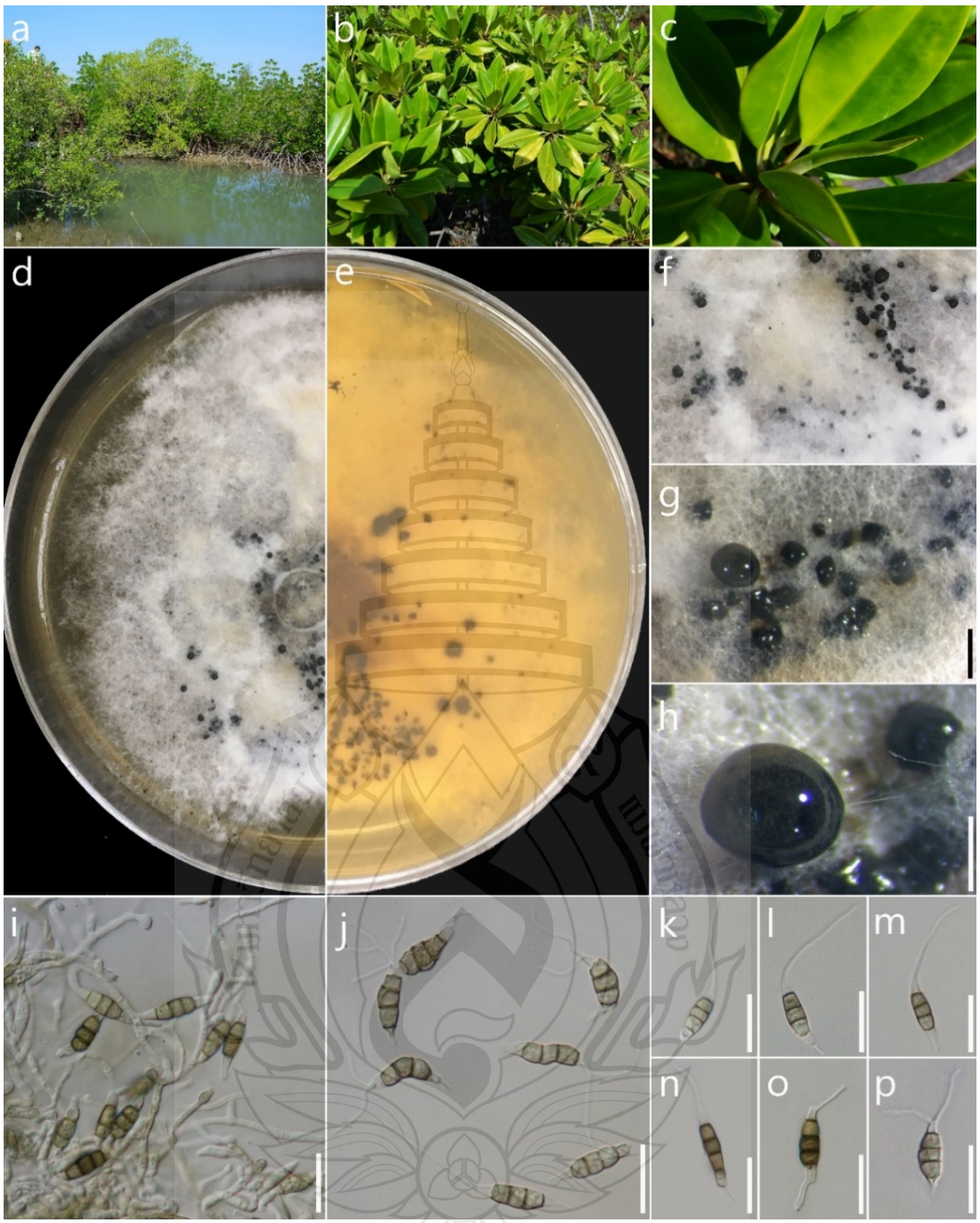
Isolated from asymptomatic leaf of *Rhizophora apiculata* Blume. Asexual morph: *Conidiomata* pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, proliferating 1–2 times percurrently, collarette present and not flared. *Conidia* (17–)17.5–28(–29) × (4.9–)5.5–6.5(–7.1) μm (mean ± SD = 23.3 ± 3.0 × 5.8 ± 0.5 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (1.8–)2–4(–6) μm long (mean ± SD = 3.9 ± 1.3 μm); three median cells (12–)12.5–16(–18) μm long (mean ± SD = 15. 3 ± 1. 5 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (4–)4. 5–6(–7) μm long (mean ± SD = 5. 6 ± 0. 8 μm); third cell brown, (3.5–)4–4.5(–5.5) μm long (mean ± SD = 4.6 ± 0.5 μm); fourth cell brown, (3.5–)4–5(–6.5) μm long (mean ± SD = 5.1 ± 0.7 μm); apical cell (2–)3.5–4(–6) μm long (mean ± SD = 4.2 ± 1.0 μm), hyaline, conic to acute; with 1–2 tubular appendages on apical cell, inserted at same loci at the apex of the apical cell, unbranched, flexuous, (5.5–)11–34(–38) μm long (mean ± SD = 22. 2 ± 8. 5 μm); single basal appendage, tubular, unbranched, centric, (2–)2. 5–9. 5(–10) μm long (mean ± SD = 4 ± 2.0 μm).

Culture characteristics: Colonies on PDA reaching 5–6 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, The Sirindhorn International Environmental Park, Cha- am, Cha-am District, Phetchaburi Province, asymptomatic leaf of *Rhizophora apiculata*, 30 November 2016, Mingkwan Doilom NNSE03AL (MFLU 19-0787, holotype; PDD, isotype); ex- type-living cultures, MFLUCC 17-1616,

TNCC. THAILAND, The Sirindhorn International Environmental Park, Cha-am, Cha-am District, Phetchaburi Province, asymptomatic leaf of *Rhizophora apiculata*, 30 November 2016, Mingkwan Doilom NNSE03DL (MFLU 19-0788, paratype); living cultures, MFLUCC 17-1617.

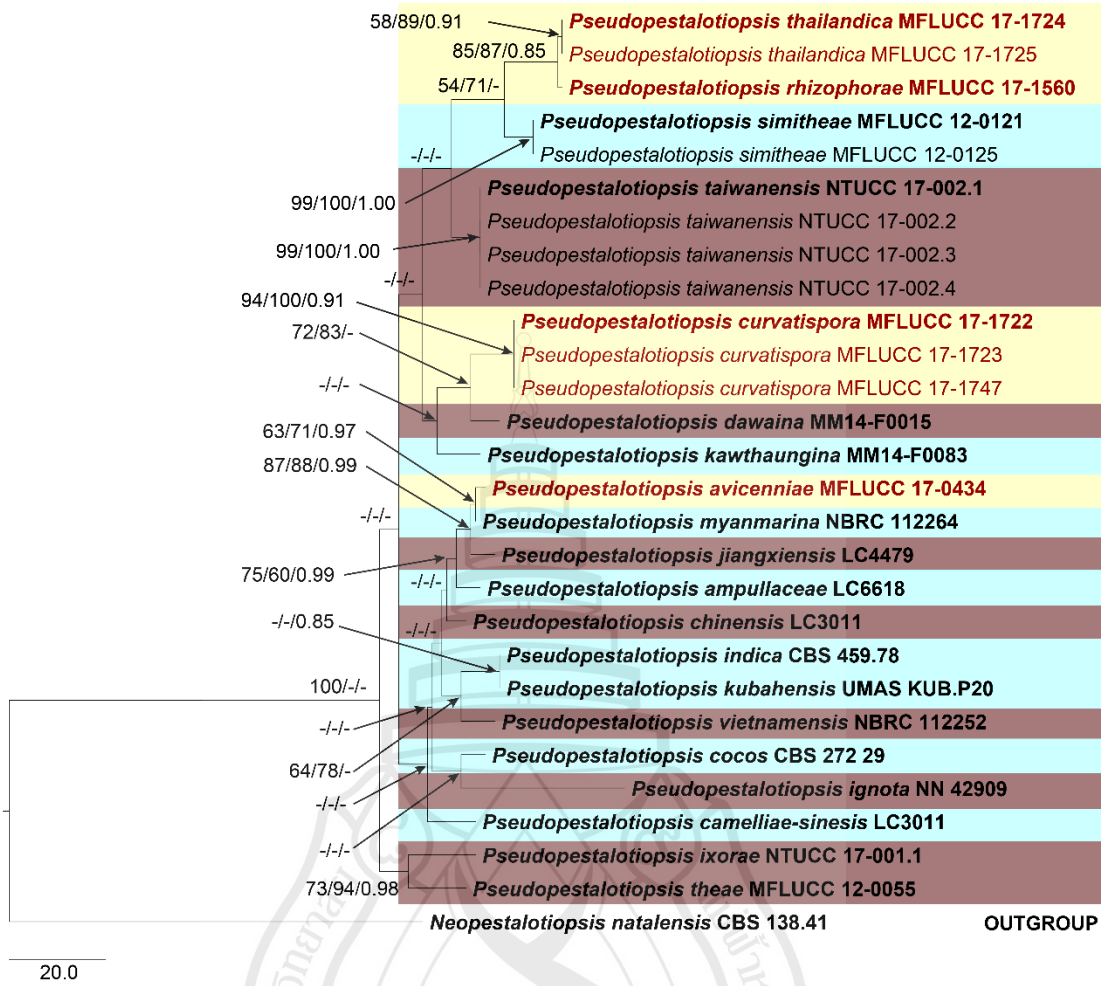
Notes: *Pestalotiopsis thailandica* isolated as an endophyte from a living leaf of *Rhizophora apiculata* is introduced here as a new species. In the phylogenetic analyses based on combined genes, the species appeared as a distinct species represented by two strains and is sister to *P. rhizophorae* (in this study) (Figure 3.2). Although these two species are found on the same host and location, *P. thailandica* differs by having larger conidia (*P. rhizophorae*: (17–)17. 5–23(–23. 5) × (5.5–)6–6.5(–7) μm) and longer apical appendages (*P. rhizophorae*: (7.5–)8–13(–14.5) μm) than *P. rhizophorae* (Table 3.4) (see notes under *P. rhizophorae*). In the phylogenetic analyses, *P. rhizophorae* is also related to *P. formosana* (NTUCC 17-009) and *P. parva* (CBS 265. 37). However, *Pestalotiopsis formosana* and *P. parva* are different from *P. thailandica* by having smaller conidia (*P. formosana*: (15–)18–22(–26) μm, *P. parva*: (16–)16.5–20(–21) μm) and shorter apical appendages (*P. formosana*: (8–)11–16(–20) μm, *P. parva*: (6–)6. 5–12(–13) μm) with 2–3 tubular apical appendages (Table 3.4; Ariyawansa & Hyde, 2018; Maharachchikumbura et al., 2014).



Note *Pestalotiopsis thailandica* (MFLU 19-0787, holotype). a Habitat. b, c Leaf of *Rhizophera apiculata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA.i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: g = 1000 µm, h = 100 µm, i–p = 20 µm.

Figure 3.10 Morphological characters of *Pestalotiopsis thailandica* (MFLU 19-0787, holotype)

The third phylogenetic tree comprised 27 taxa, with *Neopestalotiopsis natalensis* (CBS 138. 41) as the outgroup taxon. The total length of the dataset was 1404 characters including alignment gaps, 1–335, 336–493, 494–742, 743–925, 926–1093 and 1094–1404 corresponding to ITS1+ ITS2, 5. 8S, *β-tubulin* (exon), *β-tubulin* (intron), *ef1α* (exon), and *ef1α* (intron), respectively). The combined dataset contained 1122 constant, 193 parsimony uninformative and 89 parsimony informative characters. The combined dataset was analyzed using MP, ML and BI. The trees generated under different optimality criteria were essentially similar in topology and did not differ significantly (data not shown). The descriptive statistics generated from MP analysis based on the combined dataset of ITS1+ ITS2, 5. 8S, *β-tubulin* (exon), *β-tubulin* (intron), *ef1α* (exon), and *ef1α* (intron) were TL = 386, CI = 0.832, RI = 0.823, RC = 0.685, HI = 0.168. The best scoring likelihood tree selected with a final value for the combined dataset = -3905.071762.



Note One of the 93 most parsimonious trees obtained from a heuristic search of combined ITS, *β-tubulin* and *ef1α* sequence data of the genus *Pseudopestalotiopsis*. The tree is rooted with *Neopestalotiopsis natalensis* (CBS 138. 41). Maximum parsimony and maximum likelihood bootstrap values ≥ 50%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/PPBY) are given at the nodes. The species obtained in this study are in red font. Ex-type taxa from other studies are in black bold.

Figure 3.11 Phylogenetic analysis of *Pseudopestalotiopsis*

Pseudopestalotiopsis avicenniae Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.12

Index Fungorum number: IF556442

Facesoffungi number: FoF 05776

Etymology: refers to the host from which the fungus was isolated, *Avicennia marina* (Forssk.) Vierh.

Holotype: MFLU 19-0789

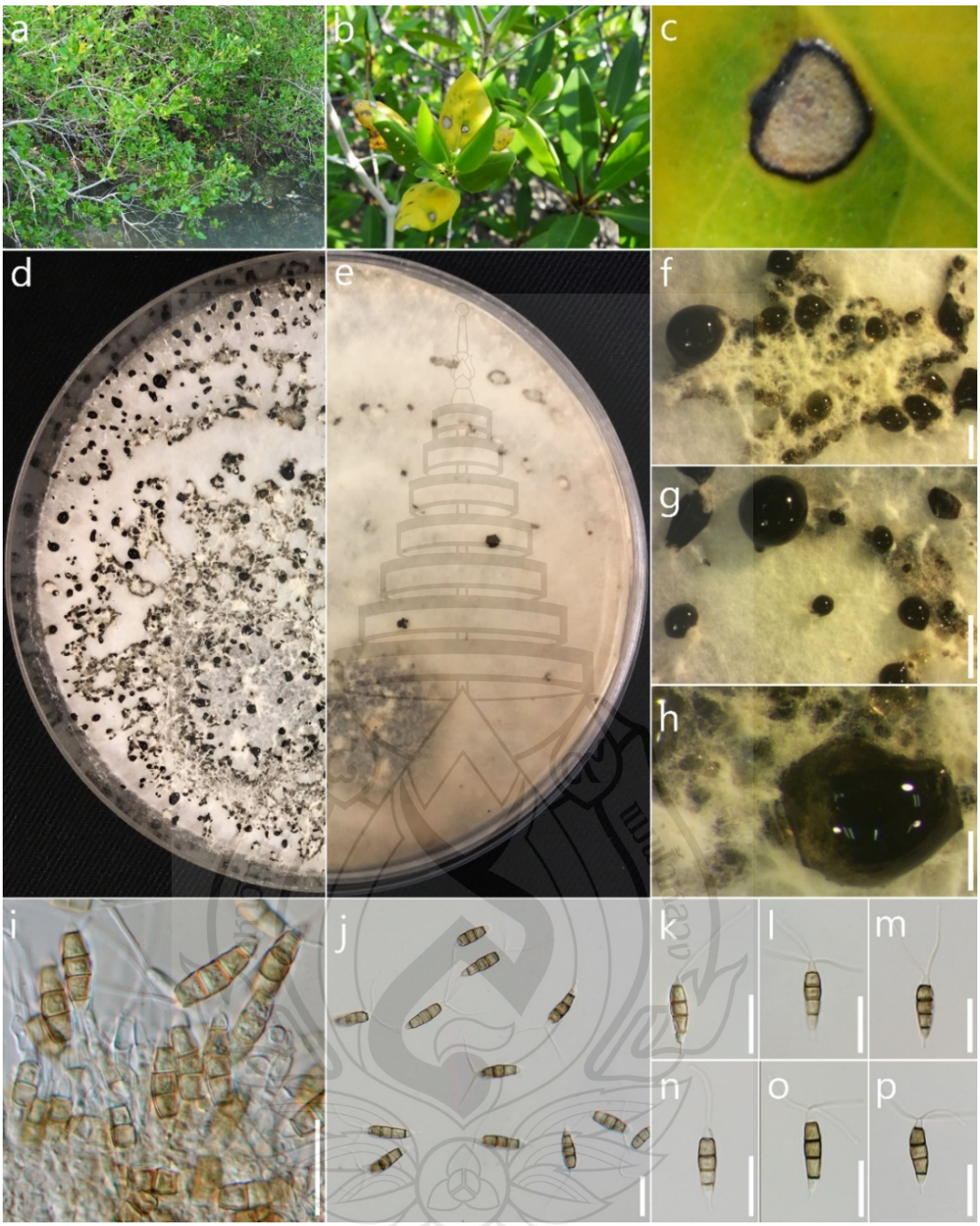
Associated with leaf spots of *Avicennia marina* (Forssk.) Vierh. *Symptoms* circular to irregular, grayish-brown, slightly sunken spots adaxial surface leaves of *A. marina*, which later expand outwards on the surface of the leaves (Figure 3.12c). Small black spots appeared initially and then gradually enlarged, changing to beige circular ring spots with a black border and smooth edge.They were usually >5 circulars, which occurred on a single affected leaf. In severe cases, lesions spread evenly on the leaves (Figure 3.12b). Asexual morph: *Conidiomata* 300–1000 μm diam, pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, 3–6 × 2–56 μm, proliferating 1–2 times percurrently, collarette presentand not flared. *Conidia* (22–)22.5–26.5(–27) × (5–)5.5–6(–6.5) μm (mean ± SD = 23.9 ± 1.4 × 6 ± 0.4 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncatebase, hyaline or sometimes pale brown, thin- and smooth-walled, (3–)4–4.5(–6) μm long (mean ± SD = 4 ± 0.7 μm); three median cells (15–)15.5–17(–18) μm long (mean ± SD = 16.3 ± 0.8 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (4. 5–)5–6(–6. 5) μm long (mean ± SD = 5. 5 ± 0. 5 μm); third cell brown, (4.5–)5–5.5(–6) μm long (mean ± SD = 4.9 ± 0.4 μm); fourth cell brown, (5–)5.5–6(–7) μm long (mean ± SD = 5. 9 ± 0. 5 μm); apical cell (2–)2. 5–4(–5) μm long (mean ± SD = 3. 5 ± 1. 0 μm), hyaline, conic to acute; with 1–3 tubular appendages on apical cell, inserted at different loci but in acrest at the apex of the apical cell, unbranched, flexuous, (14–)15.5–28.5(–35.5) μm long (mean ± SD = 21.3 ± 5.9 μm); single basal appendage, tubular, unbranched, centric, (2–)3–4(–4.5) μm long (mean ± SD = 3.1 ± 0.7 μm).

Culture characteristics: Colonies on PDA reaching 5–7 cm diam after 7 d at

room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, The Sirindhorn International Environmental Park, Cha- am, Cha-am District, Phetchaburi Province, leaf spots of *Avicennia marina*, 30 November 2016, Norphanphoun Chada NNS05-1 (MFLU 19-0789, holotype; PDD, isotype); ex-type-living cultures,MFLUCC 17-0434, TNCC.

Notes: The combined phylogenetic tree showed that *Ps. avicenniae* is sister to *Ps. jiangxiensis* (strain LC4479) and *Ps. elaeidis* (=*Ps. myanmarina*, strain NBRC 112264) (Figure 3.1, Liu et al., 2017; Nozawa et al., 2017). *Pseudopestalotiopsis avicenniae* is morphologically similar to *Ps. jiangxiensis*, but phylogenetically clearly distinct as an independent lineage (Figure 3.3). *Pseudopestalotiopsis avicenniae* is phylogenetically closer to *Ps. elaeidis* (strain NBRC 112264), which was collected from *Averrhoa carambola* in Myanmar, but can be distinguished by its larger conidia (*Ps. elaeidis*: 31–38. 5 × 6. 5–9 µm) and 2–3 apical appendages (Table 3.5, Nozava et al., 2017).



Note *Pseudopestalotiopsis avicenniae* (MFLU 19-0789, holotype). a Habitat. b, c Leaf spotson *Avicennia marina*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA.i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: f = 1000 µm, g = 200 µm,h = 500 µm, i–p = 20 µm.

Figure 3.12 Morphological characters of *Pseudopestalotiopsis avicenniae* (MFLU 19-0789, holotype)

Pseudopestalotiopsis curvatispora Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.13

Index Fungorum number: IF556443

Facesoffungi number: FoF 05777

Etymology: in reference to the Latin word "curvatus" in reference to the shape of the conidia.

Holotype: MFLU 19-0790

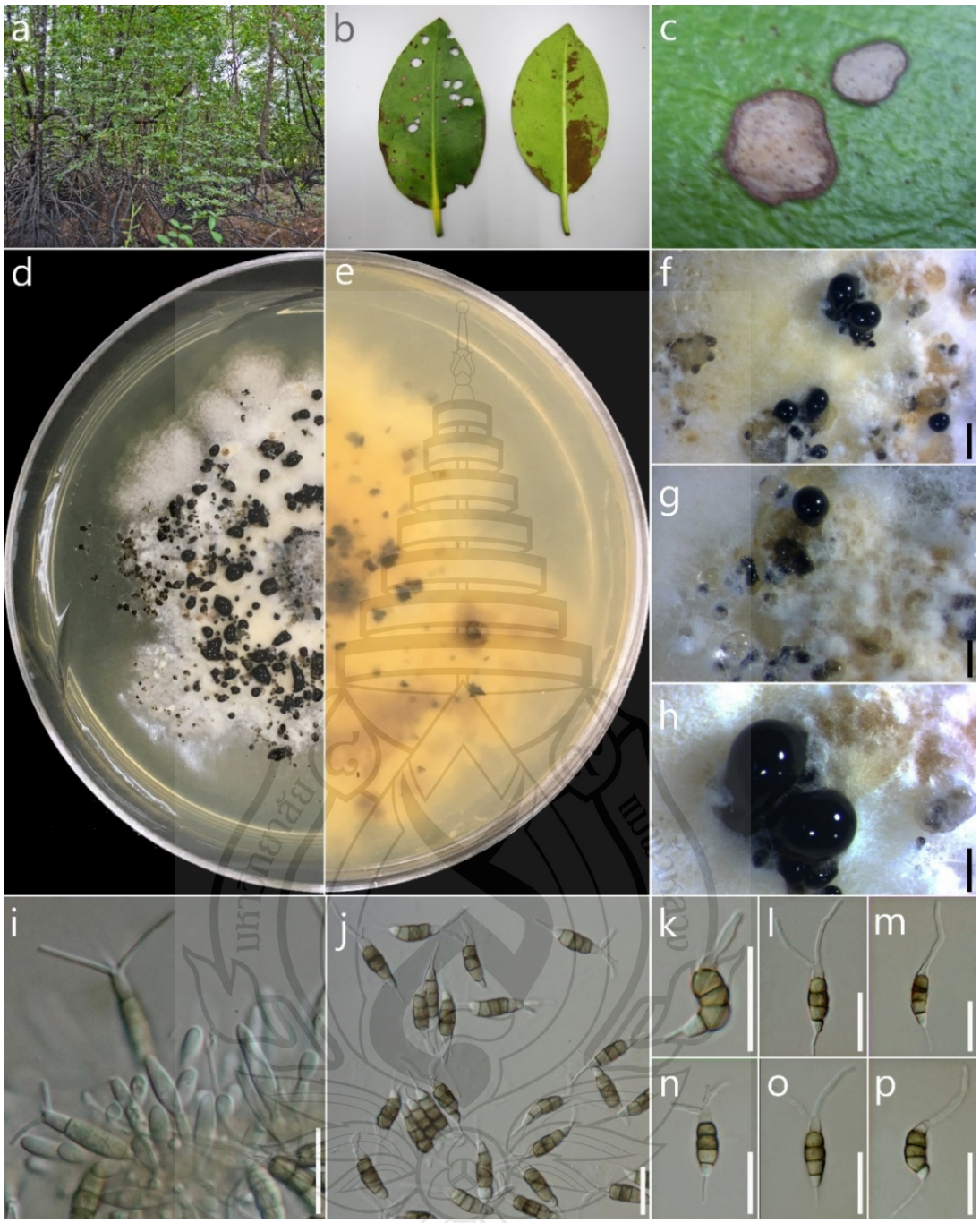
Associated with leaf spots of *Rhizophora mucronata* Blume. *Symptoms* small subcircular, grayish brown, slightly sunken spots adaxial surface leaves of *R. mucronata*, which later expand outwards on the surface of the leaves (Figure 3.13c). Small brown spots appeared initially and then gradually enlarged, changing to beige circular ring spots with a dark brown border and smoothedge. They were usually >5 circulars, which occurred on a single affected leaf. In severe cases, lesions spread evenly on the leaves (Figure 3.13b). Asexual morph: *Conidiomata* 200–400 μm diam, pycnidial, globose, brown, semi-immersed on PDA, rreleasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, 5. 5–11 × 3–5. 5 μm, proliferating 1–2 times percurrently, collarette present and not flared. *Conidia* (18.5–)22–25(–26.5) × (6–)6.5–7 μm (mean ± SD = 23.5 ± 2 × 6.6 ± 0. 4 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (3–)3. 5–4(–5) μm long (mean ± SD = 4.3 ± 0.7 μm); three median cells (11–)13–14(–15) μm long (mean ± SD = 13.8 ± 1.1 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, 4–5 μm long (mean ± SD = 4.5 ± 0.5 μm); third cell brown, (3.5–)4–5(– 5.5) μm long (mean ± SD = 4.4 ± 0.6 μm); fourth cell brown, (3.5–)4–5(–5.5) μm long (mean ± SD = 4.6 ± 0.6 μm); apical cell (3.5–)4–6(–7) μm long (mean ± SD = 5.1 ± 1.1 μm), hyaline, conic to acute; with 1–2 tubular appendages on an apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched or branched irregularly along their length resulting in 1–2 branches, flexuous, (10–)20–29(–35) μm long (mean ± SD = 22. 7 ± 8. 1μm); single basal appendage, tubular, unbranched, centric, (5.5–)9–12(–13.5) μm long (mean ± SD = 9.2 ± 2 μm).

Culture characteristics: Colonies on PDA reaching 3–4 cm diam after 7 d at

room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Trat Province, leaf spots of *Rhizophora mucronata*, 27 April 2017, Norphanphoun Chada KC12-1, (MFLU 19-0791, holotype; PDD, isotype); ex-type- living cultures, MFLUCC 17-1722, TNCC. THAILAND, Trat Province, leaf spots of *Rhizophora mucronata*, 27 April 2017, Norphanphoun Chada KC12-2, (MFLU 19-0792, paratype); living cultures, MFLUCC 17-1723. THAILAND, Trat Province, leaf spots of *Rhizophora apiculata*, 27 April 2017, Norphanphoun Chada KC18-2 (MFLU 19-0790, paratype); ex-type-living cultures, MFLUCC 17-1747.

Notes: The new species *Pseudopestalotiopsis curvatispora* is introduced, which was isolatedfrom a leaf spot on *Rhizophora mucronata*, with the morphology of curved conidia and flexuous branched apical appendages. Based on combined gene phylogenetic analyses, it showed that *Ps. curvatispora* is nested in between *Ps. simitheae* (MFLUCC 12-0121) and *Ps. thailandica* (in this study), which are morphologically different (Table 3.5). *Pseudopestalotiopsis simitheae* is (MFLUCC 12-0121), distinct from other species by forming a well-separated clade (Figure 3.3). This is also supported by morphological differences (larger conidia (22–30 µm) and 2–4 tubular, shorter apical and basal appendages (apical appendages: 14.5–26.5 µm, basal appendages: 4–6.5 µm; Song et al. 2014)). *Pseudopestalotiopsis thailandica* is different from *Ps. simitheae* by having larger conidia ((24–)24.5–30(–30.5) µm), longer apical appendages ((26.5–)28–36(–39.5) µm) and shorterbasal appendages ((3.5–)4.5–5(–6.5) µm) (Table 3.5; Song et al., 2014).



Note *Pseudopestalotiopsis curvatispora* (MFLU 19-0791, holotype). a Habitat. b, c Leaf spots of *Rhizophera mucronata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA. i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: f = 1000 µm,g, h = 500 µm, i–p = 20 µm.

Figure 3.13 Morphological characters of *Pseudopestalotiopsis curvatispora* (MFLU 19-0791, holotype)

Pseudopestalotiopsis rhizophorae Norphanphoun, T.C. Wen & K.D. Hyde, sp. nov., Figure 3.14

Index Fungorum number: IF556444

Facesoffungi number: FoF 05778

Etymology: refers to the host from which the fungus was isolated, *Rhizophora apiculate* Blume.

Holotype: MFLU 19-0793

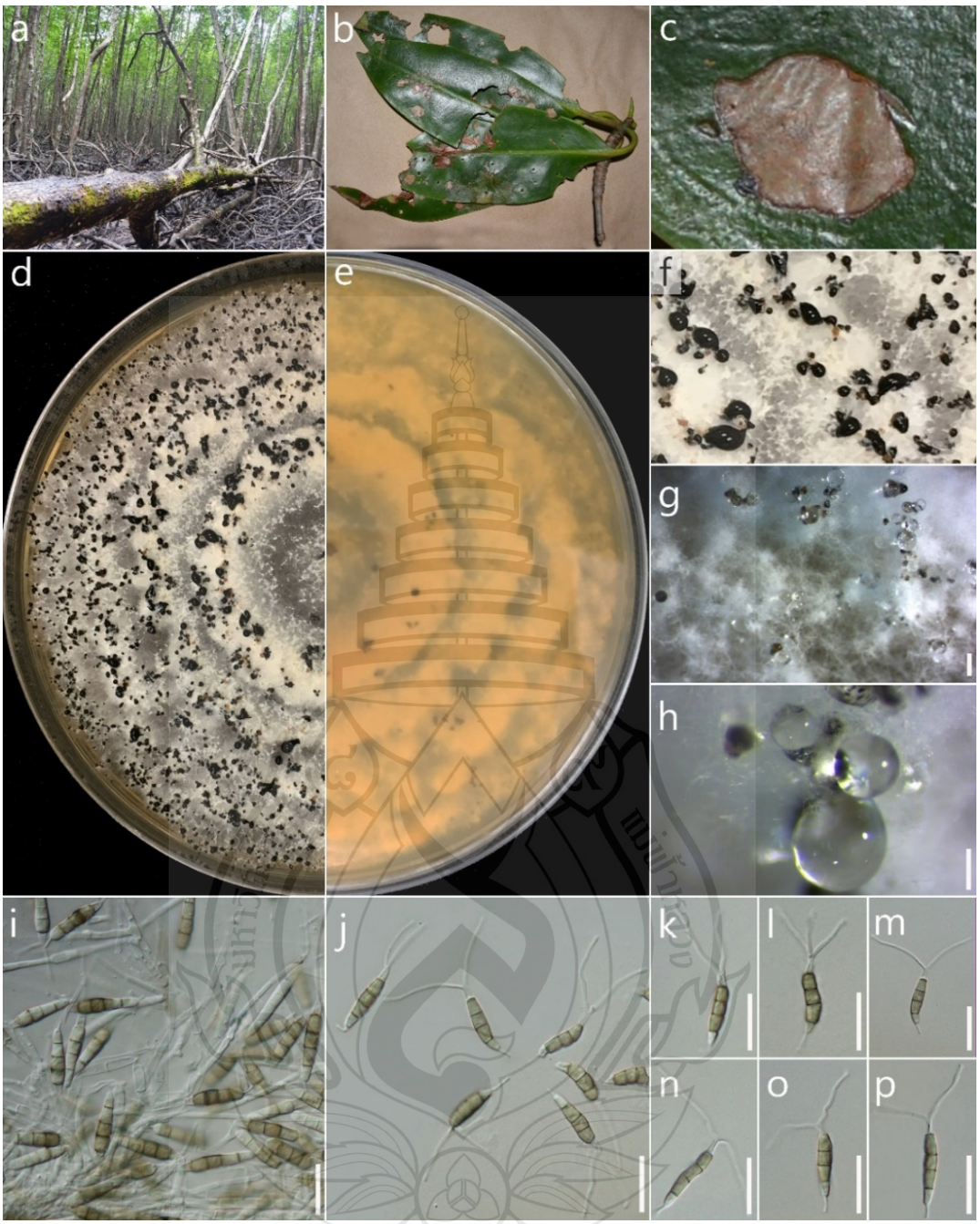
Associated with leaf spots of *Rhizophora apiculata* Blume. *Symptoms* irregular shape, pale brown, slightly sunken spots adaxial surface leaves of *R. apiculata*, which later expand outwards onthe surface of the leaves (Figure 3.14c). Small brown spots appeared initially and then gradually enlarged, changing to pale brown irregular spots with auburn border. They were usually >5 circular spots occurred on a single affected leaf. In severe cases, lesions spread evenly on the leaves with defected leaves (Figure 3.14b). Asexual morph: *Conidiomata* 100–200 μm diam, pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, 5–8 × 5–6 μm, proliferating 1–2 times percurrently, collarette present and not flared. *Conidia* (23–)24–29.5(–30) × 5–5.5(–6) μm (mean ± SD = 26 ± 2.5 × 5.4 ± 0.4 μm), fusiform to clavate, straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (3–)4–5(–6) μm long (mean ± SD = 4. 5 ± 0. 9 μm); three median cells (14.5–)15–19(–19.5) μm long (mean ± SD = 16.4 ± 2 μm), brown, septa and periclinal walls darker than rest of the cell, versicolored, wall rugose; second cell from basepale brown, (4–)5–5.5(–7) μm long (mean ± SD = 5.8 ± 1 μm); third cell brown, 4–5(–5.5) μm long(mean ± SD = 4.7 ± 0.4 μm); fourth cell brown, (4.5–)5.5–6(–7.5) μm long (mean ± SD = 5.9 ± 1.0 μm); apical cell (3.5–)4–5(–7) μm long (mean ± SD = 5.2 ± 0.8 μm), hyaline, conic to acute; with 2–3 tubular appendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (16.5–)18–25(–26) μm long (mean ± SD = 22 ± 3.1 μm); single basal appendage, tubular, unbranched, centric, (3–)3.5–6(–7) μm long (mean ± SD = 5 ± 1.2 μm).

Culture characteristics: Colonies on PDA reaching 5–6 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to

circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin (curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Ngao, Ranong Province, Ngao Mangrove Forest Research Centre, leaf spots of *Rhizophora apiculata*, 6 December 2016, Norphanphoun Chada NG38a (MFLU 19-0793, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1560, TNCC.

Notes: *Pseudopestalotiopsis rhizophorae* formed an independent branch in the phylogeny presented here (Figure 3.3) and is closely related to *Ps. dawaina* (MM14-F0015) and *Ps. kubahensisa* (UMAS KUB-P20). *Pseudopestalotiopsis rhizophorae* differs from *Ps. dawaina* and *Ps. kubahensisa* in length of appendage in both ends: shorter apical appendage (*Ps. dawaina*: 20.5–33.5µm, *Ps. kubahensisa*: 16 –29. 5 µm) and longer basal appendage (*Ps. dawaina*: 2. 5–6. 5 µm, *Ps. kubahensisa*: 3–6 µm) (Table 3.5). Thus, *Ps. rhizophorae* is introduced as a new species.



Note *Pseudopestalotiopsis rhizophorae* (MFLU 19-0793, holotype). a Habitat. b, c Leaf spots of *Rhizophora apiculata*. d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulatingon PDA. i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: g = 500 µm, h = 200 µm, i–p = 20 µm.

Figure 3.14 Morphological characters of *Pseudopestalotiopsis rhizophorae* (MFLU 19-0793, holotype)

Pseudopestalotiopsis thailandica Norphanphoun & K.D. Hyde, sp. nov., Figure 3.15

Index Fungorum number: IF556445

Facesoffungi number: FoF 05779

Etymology: refers to the country where the fungus was collected, Thailand.

Holotype: MFLU 19-0794

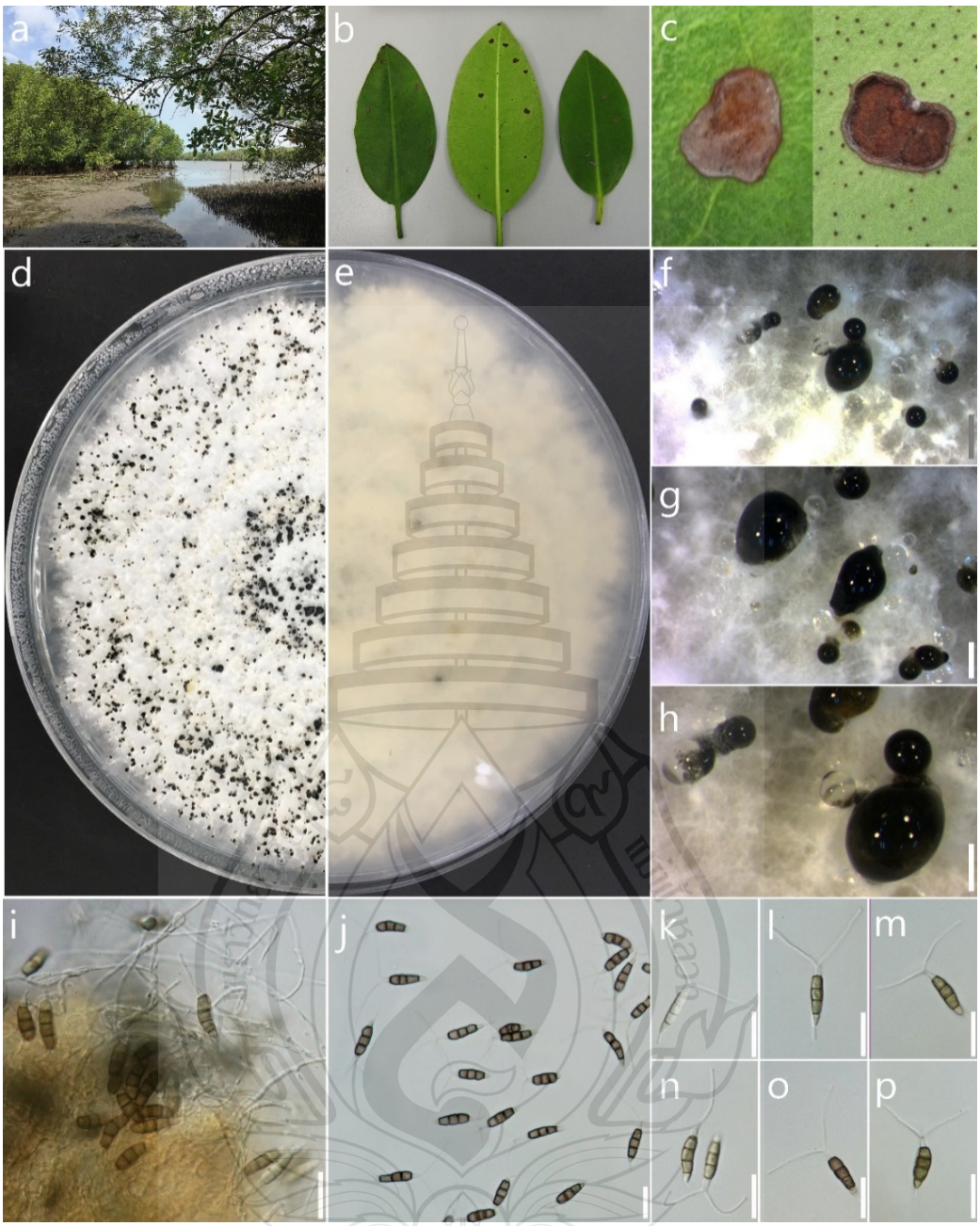
Associated with leaf spots of *Rhizophora mucronata* Blume. *Symptoms* subcircular to the irregular shape, pale brown, slightly sunken spots adaxial surface leaves of *R. mucronata*, which later expand outwards on the surface of the leaves (Figure 3.15c). Small auburn spots appeared initially and then gradually enlarged, changing to pale-auburn circular ring spots with a dark auburn border. They were usually >5 circulars, which occurred on a single affected leaf. In severe cases, lesions spread evenly on the leaves (Figure 3.15b). Asexual morph: *Conidiomata* 250–500 μm diam, pycnidial, globose, brown, semi-immersed on PDA, releasing conidia in a black, slimy, globose, glistening mass. *Conidiophores* indistinct. *Conidiogenous cells* discrete to lageniform, hyaline, smooth- and thin-walled, proliferating 1–2 times percurrently, collarette present and not flared. *Conidia* (24–)24.5–30(–30.5) × (5–)5.5–6(–6.7) μm (mean ± SD = 26.6 ± 2.2 × 5.9±0.3 μm), fusiform to clavate,straight to slightly curved, 4-septate; basal cell obconic with a truncate base, hyaline or sometimes pale brown, thin- and smooth-walled, (3.5–)4–5(–6.6) μm long (mean ± SD = 4.4 ± 1 μm); three median cells (13.5–)16–18(–19) μm long (mean ± SD = 17.2 ± 1.5 μm), brown, septa and periclinalwalls darker than rest of the cell, versicolored, wall rugose; second cell from base pale brown, (5–)5.5–6(–7.5) μm long (mean ± SD = 5.8 ± 0.9 μm); third cell brown, (5–)5.5–6(–6.2) μm long(mean ± SD = 5.6 ± 0.5 μm); fourth cell brown, (5.5–)6–6.5(–7) μm long (mean ± SD = 6.2 ± 0.6 μm); apical cell (3.5–)4.5–5(–7) μm long (mean ± SD = 4.5 ± 1.1 μm), hyaline, conic to acute; with1–2 tubular appendages on apical cell, inserted at different loci but in a crest at the apex of the apical cell, unbranched, flexuous, (26.5–)28–36(–39.5) μm long (mean ± SD = 31.3 ± 3.9μm); single basal appendage, tubular, unbranched, centric, (3.5–)4.5–5(–6.5) μm long (mean ± SD = 4.8 ± 1 μm).

Culture characteristics: Colonies on PDA reaching 5–6 cm diam after 7 d at room temperature (±25 °C), under light 12 hr/dark 12 hr, colonies filamentous to circular, medium dense,aerial mycelium on surface flat or raised, with filiform margin

(curled margin), fluffy, white from above and reverse; fruiting bodies black.

Material examined: THAILAND, Chanthaburi Province, leaf spots of *Rhizophora mucronata*, 27 April 2017, Norphanphoun Chada KC21-1 (MFLU 19-0794, holotype; PDD, isotype); ex-type-living cultures, MFLUCC 17-1724, TNCC. THAILAND, Chanthaburi Province, leaf spots of *Rhizophora mucronata*, 27 April 2017, Norphanphoun Chada KC21-12 (MFLU 19-0795, paratype); ex-type-living cultures, MFLUCC 17-1725.

Notes: The new species, *Pseudopestalotiopsis thailandica* was isolated from a leaf spot from*Rhizophora mucronata* from Chanthaburi Province, Thailand. Based on the combined gene phylogenetic analysis, it showed that *Ps. thailandica* is sister to *Ps. curvatispora* (in this study), andmorphology differences as mentioned in the notes of *Ps. curvatispora*. Thus, it is considered that *Ps. thailandica* is a novel species.



Note *Pseudopestalotiopsis thailandica* (MFLU 19-0794, holotype). a Habitat. b, c Leaf spots on *Rhizophora mucronata.* d, e Culture on PDA (d-above, e-reverse). f–h Colony sporulating on PDA. i Conidiogenous cells giving rise to conidia. j–p Conidia. Scale bars: f = 1000 µm,g, h = 500 µm, i–p = 20 µm.

Figure 3.15 Morphological characters of *Pseudopestalotiopsis thailandica* (MFLU 19-0794, holotype)

3.4 Discussion

Mangrove forests occurring at the interface of terrestrial and marine ecosystems harbour a rich biological diversity of plants, animals, and microorganisms (Beger et al., 2010). However, the phylogenetic and functional description of microbial diversity in mangrove ecosystems has not been addressed to the same extent as for other environments. A previous study on mangrove fungi reported some pathogenic fungi causing leaf spots on *Rhizophora*, e. g. leaf spots on *Rhizophora mangle* in Puerto Rico caused by *Anthostomella* (Stevens, 1920), leaf spots on *R. mangle* in Florida caused by *Cercospora* (McMillan, 1964), leaf spots on *Rhizophora* sp. caused by *Pestalotiopsis* sp., *Colletotrichum* sp. and *Polystigma sonneratiae* (Hyde & Cannon, 1992; Xu et al., 2009). Heart and butt rot disease on *Rhizophora* sp. caused by *Heterobasidion annosum*, *Ganoderma*, *Phellinus* sp., and *Inonotus* sp. (Ryvarden, 2000; Fox, 2001; Sakayaroj et al., 2012) and canker and dieback on *Rhizophora* sp. caused by *Phytophthora cinnamomi* (Vollbrecht et al., 1995; Barnard, 2000; Kinge & Mih, 2011) have also been reported. A leaf spot of *Avicennia marina* caused by *Pseudocercospora avicenniae* (Shivas et al., 2009) was recorded in Queensland, Australia. Thatoi et al. (2013) reportedmore than 200 species of endophytic fungi from mangroves in India. Norphanphoun et al. (2018) reported three novel species of *Cytospora* (*C. lumnitzericola*, *C. thailandica*, *C. xylocarpi*) from*Lumnitzera racemosa*, *Xylocarpus granatum*, and *X. moluccensis* from Phetchaburi and Ranong provinces in Thailand, and Kumar et al. (2019) reported an endophytic species, *Neopestalotiopsis alpapicalis* on *R. apiculata* and *R. mucronata* from Krabi Province, Thailand.

In this study, we examined 22 strains isolated from leaf collections from Phetchaburi, Ranongand Trat Provinces in Thailand. As a result of these sampling endeavors, we described 12 novel species, including six novel species of *Neopestalotiopsis* (*N. acrostichi*, *N. brachiata*, *N. petila*, *N. rhizophorae*, *N. sonneratae*, *N. thailandica*), two novel species of *Pestalotiopsis* (*P. rhizophorae, P. thailandica*) and four novel species of *Pseudopestalotiopsis* (*Ps. avicenniae*, *Ps. curvatispora*,*Ps. rhizophorae*,*Ps. thailandica*), based on morphological and molecular phylogenetic evidence, which clearly differentiated these new species from known

species. As many pestalotioid species have overlapping morphological traits, sequence data is essential to resolve these three genera and introduce new species. Combined gene sequences of ITS, *β-tubulin* and *ef1α* can provide a better resolution for *Pestalotiopsis* and *Pesudopestalotiopsis*. However, more genes are needed to provide better resolution and support in *Neopestalotiopsis*. Furthermore, this is the first report of *Neopestalotiopsis, Pestalotiopsis* and *Pseudopestalotiopsis* fungi associated on mangrove plants in Thailand (*Acrostichum aureum, Avicennia marina, Rhizophora mucronata, R.* apiculate, *Sonneronata alba*), which indicates that there may be a high undescribed diversity of fungi in this ecosystem as has been shown elsewhere in terrestrial habitats in northern Thailand (Hyde et al., 2018). We found 12 new species from mangrove ecosystems, however further study is needed to establish whether these species are unique to such hosts and habitats.

Table 3.3 Comparison of conidia of *Neopestalotiopsis* species related to this study

Species	Strain	Conidial size (µm)	Apical appendages		Basal appendage
			Number	Length (µm)	Length (µm)
N. acrostichi	MFLUCC 17-1754/ MFLUCC 17-1755	(22–)23–26(–27.2) × (5–)5.5–6.5(–7.1)	3–4 (4)	(16–)19–65(–69.5)	(7–)12.5–36(–37)
N. alpapicalis[g]	MFLUCC 17-2544	14–22.3 × 5–6.8	1–4(1, 2)	5.6–15	3.1–6.4
N. aotearoa[d]	CBS 367.54	(19.5–)21–28(–29) × (6–)6.5–8.5(–9)	2–3	(3–)5–12(–13)	1.5–4
N. coffea-arabicae[f]	HGUP4015	16–20 × 5–7	2–4	11–16	3–5
N. musae[b]	MFLUCC 15-0776	18.6–25 9 4.1–5	2–3	16.3–25	4.6–10.3
N. piceana[d]	CBS 394.48	(19–)19.5–25(–26) × (7–)7.5–9(–9.5)	3	(19–)21–31(–33)	6–23
N. protearum[a]	CBS 114178	(14–)16–17(–18) × (6.5–)8–9(–10)	2–4	(10–)15–17(– 22)	(2–)3–3.5(–5)
N. brachiata	MFLUCC 17-1555	(18–)18.5–25(–26) × (4.7–)5.5–6(–6.3)	1–3	(8.5–)9.5–33(–34)	(3.5–)4–9(–10)
N. rhizophorae	MFLUCC 17-1550/ MFLUCC 17-1551	(20–)20.5–27(–27.5) × (6–)6.5–7.5(–8.2)	1–4 (3)	(6–)12.5–22(–24)	(2.5–)4–9.5(–10)

Table 3.3 (continued)

Species	Strain	Conidial size (µm)	Apical appendages		Basal appendage Length (µm)
			Number	Length (µm)	
N. rosicola[c]	CFCC 51992	(18.9−)20.2−25.5(−26.2) × (5−)5.5−8(−8.5)	2–4 (2, 3)	(16.5−)17−22.8 (−25.9)	2−9.5
N. samarangensis[e]	MFLUCC 12-0233	18–21 × 6.5–7.5	3	12–18	3.5–5.2
N. sonneratae	MFLUCC 17-1744/ MFLUCC 17-1745	(21.6–)24–26(–28.2) × (6.8–)7–7.5(–8.1)	1–3	(5.3–)7–8(–13.8)	(2.5–)3–4(–4.7)
N. surinamensis[d]	CBS 450.74	(23–) 24–28(–29) × (7–)7.5–9(–9.5)	2–3	(15–)18–27(–28)	Up to 5–7
N. thailandica	MFLUCC 17-1730/ MFLUCC 17-1731	(20–)21–25(–25.5) × (5.7–)6–7(–7.3)	1–2	(30–)32.5–38(–40)	(3–)6–9(–10)
N. petila	MFLUCC 17-1737/ MFLUCC 17-1738	(20–)21–26.5(–27.5) × (5.6–)6–7(–7.8)	2–3	(21–)22–29(–33)	(2–)3–8(–9)

Note Strains in this study are in bold.

Soure [a]Crous et al. (2011); [b]Hyde et al. (2016); [c]Jiang et al. (2018); [d]Maharachchikumbura et al. (2014); [e]Maharachchikumbura et al. (2013); [f]Song et al. (2013); [g]Kumar et al. (2019)

Table 3.4 Comparison of conidia of *Pestalotiopsis* species related to this study

Species	Strain	Conidial size (µm)	Apical appendages		Basal appendage (µm)
			Number	Length (µm)	
P. formosana [a]	NTUCC 17-009	(15–)18–22(–26) × (5–)6–7	2–3	(8–)11–16(–20)	(2–)3–5(–6)
P. parva [b]	CBS 265.37	(16–)16.5–20(–21) × 5–7(–7.5)	2–3	(6–)6.5–12(–13)	2–4
P. rhizophorae	MFLUCC 17-0416/ MFLUCC 17-0417	(17–)17.5–23(–23.5) × (5.5–)6–6.5(–7)	1–2	(7.5–)8–13(–14.5)	(1.3–)1.5–4.5(–5)
P. thailandica	MFLUCC 17-1616/ MFLUCC 17-1617	(17–)17.5–28(–29) × (4.9–)5.5–6.5(–7.1)	1–2	(5.5–)11–34(–38)	(2–)2.5–9.5(–10)

Note Strains in this study are in bold.

Soure [a]Ariyawansa & Hyde (2018); [b]Maharachchikumbura et al. (2014)

Table 3.5 Comparison of conidia of *Pseudopestalotiopsis* species related to this study

Species	Strain	Conidial size (µm)	Apical appendages		Basal appendage (µm)
			Number	Length (µm)	
Ps. ampullacea[b]	LC6618	21–31.5 × 6.5–9	2–3	17–25	3.5–7
Ps. avicenniae	MFLUCC 17-0434	(22–)22.5–26.5(–27) × (5–)5.5–6(–6.4)	1–3	(14–)15.5–28.5(–35.5)	(2–)3–4(–4.5)
Ps. chinensis[b]	LC3011	25.5–35.5 × 6–9	2–3	24–41	5–12
Ps. rhizophorae	MFLUCC 17-1560	(18.5–)22–25(–26.5) × (6.2–)6.5–7(–7.2)	1–2	(10.2–)20–29(–35)	(5.5–)9–12(–13.5)
Ps. dawaina[d]	MM14-F0015	22–31 × 8–9.5	3	20.5–33.5	2.5–6.5
Ps. elaeidis (=*Ps. myanmarina*)[c]	NBRC 112264 LC4479	31–38.5 × 6.5–9 22–29 × 6–9	2–3 2–4(3)	22.5–38.5 16.5–32	unbranched 6.5–19.5
Ps. jiangxiensis[b]					
Ps. kawthaungina[d]	MM14-F0083	29.5–34.5 × 7–9	3	28–41	4.5–9
Ps. kubahensis[a]	UMAS KUB-P20	(26–)27–30(–33) × 5.6–7.3	2–4(3)	15.9–29.4	3.1–6.0

Table 3.5 (continued)

Species	Strain	Conidial size (µm)	Apical appendages		Basal appendage (µm)
			Number	Length (µm)	
Ps. curvatispora	MFLUCC 17-1722/	(18.6–)19–26(–26.4) × (5.5–)6–7(–7.4)	2–3	(5.5–)6–24(–26.6)	(5.8–)5–11(–12.2)
Ps. simitheae[e]	MFLUCC 17-1723 MFLUCC 12-0121	22–30 × 5–6.5	2–4	14.5–26.5	4–6.5
Ps. taiwanensis[f]	NTUCC 17-002.1	21–26 × 6–7	2–5	16–25	3–7
Ps. thailandica	MFLUCC 17-1724/ MFLUCC 17-1725	(24–)24.5–30(–30.5) × (5–)5.5–6(–6.7)	1–3	(26.5–)28–36(–39.5)	(3.5–)4.5–5(–6.6)

Note Strain in this study are in bold.

Soure [a]Lateef et al. (2015); [b]Liu et al. (2017); [c]Nozawa et al. (2017); [d]Nozawa et al. (2018); [e]Song et al. 2014; [f]Tsai et al. (2018)

Table 3.6 Nucleotides differences in the ITS, *β-tubulin* and *ef1α* sequences of *Neopestalotiopsis* discussed in the paper

Taxon	Strain	ITS										*β-tubulin*			
		68	85	100	370	372	373	374	375	449	487	163	169	201	205
Neopestalotiopsis acrostichi	MFLUCC 17-1754	T	A	T	T	C	A	T	T	T	T	C	T	T	A
N. alpapicalis	MFLUCC 17-2544	-	A	T	T	-	-	A	T	T	T	-	-	-	-
N. aotearoa	CBS 367.54	T	G	T	T	-	-	A	T	T	T	C	T	C	T
N. brachiata	MFLUCC 17-1555	T	A	T	T	-	-	A	T	T	T	T	T	C	T
N. coffea-arabicae	HGUP4015	T	A	T	T	-	-	A	T	T	T	-	-	-	-
N. ellipsospora	MFLUCC 12-0283	T	A	T	C	-	-	G	G	T	T	-	-	-	-
N. petila	MFLUCC 17-1737	T	A	T	T	-	-	A	T	T	T	T	T	C	T
N. piceana	CBS 394.48	T	G	T	T	-	-	A	T	T	T	T	T	C	T
N. protearum	CBS 114178	T	A	T	C	-	-	G	G	T	C	C	T	T	A
N. rhizophorae	MFLUCC 17-1550	T	A	T	T	-	-	A	T	T	T	T	T	C	T
N. rosicola	CFCC 51992	T	A	T	T	-	-	T	A	C	T	T	T	C	T
N. samarangensis	MFLUCC 12-0233	T	A	T	T	-	-	A	T	T	T	-	-	-	-
N. sonneratae	MFLUCC 17-1744	T	A	T	T	-	-	A	T	T	T	C	T	T	A
N. surinamensis	CBS 450.74	T	A	T	T	-	-	T	T	T	T	C	A	T	A
N. thailandica	MFLUCC 17-1730	T	A	C	T	-	-	A	T	T	T	C	T	T	A

Taxon	Strain	*β-tubulin*													
		218	341	355	364	369	370	373	374	375	376	378	379	382	383
Neopestalotiopsis acrostichi	MFLUCC 17-1754	G	C	C	C	G	G	T	G	T	T	C	C	T	C
N. alpapicalis	MFLUCC 17-2544	-	-	C	T	G	G	T	G	T	A	T	C	T	C
N. aotearoa	CBS 367.54	T	C	T	C	G	G	T	G	T	A	T	C	T	C
N. brachiata	MFLUCC 17-1555	T	C	T	C	G	G	T	G	T	A	T	C	T	C
N. coffea-arabicae	HGUP4015	-	-	-	-	A	A	C	A	C	A	C	G	A	T
N. ellipsospora	MFLUCC 12-0283	-	-	C	T	G	G	T	G	T	A	T	C	T	C
N. petila	MFLUCC 17-1737	T	C	T	C	G	G	T	G	T	A	T	C	T	C
N. piceana	CBS 394.48	T	C	T	C	G	G	T	G	T	A	T	C	T	C
N. protearum	CBS 114178	G	C	C	C	G	G	T	G	T	T	C	C	T	C
N. rhizophorae	MFLUCC 17-1550	T	C	T	C	G	G	T	G	T	A	T	C	T	C
N. rosicola	CFCC 51992	T	C	T	C	G	G	T	G	T	A	T	C	T	C
N. samarangensis	MFLUCC 12-0233	-	-	C	T	G	G	T	G	T	A	T	C	T	C
N. sonneratae	MFLUCC 17-1744	T	T	C	C	G	G	T	G	T	T	C	C	T	C
N. surinamensis	CBS 450.74	T	C	C	C	G	G	T	G	T	T	C	C	T	C
N. thailandica	MFLUCC 17-1730	T	T	C	C	G	G	T	G	T	T	C	C	T	C

Table 3.6 (continued)

Taxon	Strain	*β-tubulin*													
		384	385	386	393	402	428	437	438	441	446	459	469	471	472
Neopestalotiopsis acrostichi	MFLUCC 17-1754	T	G	C	A	C	C	A	C	-	A	G	G	T	A
N. alpapicalis	MFLUCC 17-2544	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. aotearoa	CBS 367.54	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. brachiata	MFLUCC 17-1555	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. coffea-arabicae	HGUP4015	C	T	G	-	A	C	A	C	T	A	G	A	G	A
N. ellipsospora	MFLUCC 12-0283	T	G	C	A	A	T	T	C	-	T	C	G	T	G
N. petila	MFLUCC 17-1737	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. piceana	CBS 394.48	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. protearum	CBS 114178	T	G	C	A	C	C	A	A	-	A	G	G	T	A
N. rhizophorae	MFLUCC 17-1550	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. rosicola	CFCC 51992	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. samarangensis	MFLUCC 12-0233	T	G	C	A	A	C	T	C	-	T	C	G	T	G
N. sonneratae	MFLUCC 17-1744	T	G	C	A	A	C	A	C	T	A	G	A	T	A
N. surinamensis	CBS 450.74	T	G	C	A	C	C	A	C	-	A	G	G	T	A
N. thailandica	MFLUCC 17-1730	T	G	C	A	A	C	A	C	T	A	G	A	G	A

Taxon	Strain	*β-tubulin*				*ef1α*									
		543	544	571	674	683	70	81	84	85	86	87	88	89	90
Neopestalotiopsis acrostichi	MFLUCC 17-1754	A	C	T	T	C	T	C	C	A	T	-	-	-	-
N. alpapicalis	MFLUCC 17-2544	T	T	C	T	C	-	-	C	A	T	-	-	-	-
N. aotearoa	CBS 367.54	T	T	C	T	C	T	C	C	A	T	-	-	-	-
N. brachiata	MFLUCC 17-1555	T	T	C	T	C	T	C	C	A	T	-	-	-	-
N. coffea-arabicae	HGUP4015	A	C	C	T	T	T	C	C	A	T	-	-	-	-
N. ellipsospora	MFLUCC 12-0283	T	T	C	T	C	T	A	C	A	T	-	-	-	-
N. petila	MFLUCC 17-1737	T	T	C	C	C	T	C	C	A	T	-	-	-	-
N. piceana	CBS 394.48	T	T	C	T	C	T	C	C	A	T	-	-	-	-
N. protearum	CBS 114178	A	C	T	T	C	T	C	-	-	-	-	-	-	-
N. rhizophorae	MFLUCC 17-1550	T	T	C	T	C	T	C	C	A	T	-	-	-	-
N. rosicola	CFCC 51992	T	T	C	T	C	T	C	C	A	T	-	-	-	-
N. samarangensis	MFLUCC 12-0233	T	T	C	C	C	T	C	C	A	T	-	-	-	-
N. sonneratae	MFLUCC 17-1744	A	C	C	T	T	T	C	C	A	T	C	A	T	C
N. surinamensis	CBS 450.74	A	C	T	T	C	C	C	C	A	T	-	-	-	-
N. thailandica	MFLUCC 17-1730	A	C	C	T	T	T	C	C	A	T	C	A	T	C

Table 3.6 (continued)

Taxon	Strain	*ef1α*													
		91	92	93	97	104	105	112	113	114	118	120	124	133	167
Neopestalotiopsis acrostichi	MFLUCC 17-1754	-	-	-	C	C	A	C	A	T	A	T	T	T	T
N. alpapicalis	MFLUCC 17-2544	-	-	-	C	C	A	-	-	-	A	T	C	T	T
N. aotearoa	CBS 367.54	-	-	-	C	C	A	C	A	T	A	T	C	T	T
N. brachiata	MFLUCC 17-1555	-	-	-	C	C	A	C	A	T	A	A	C	T	T
N. coffea-arabicae	HGUP4015	-	-	-	C	C	A	C	A	T	A	T	C	T	T
N. ellipsospora	MFLUCC 12-0283	-	-	-	C	C	A	C	A	T	A	T	C	T	T
N. petila	MFLUCC 17-1737	-	-	-	C	C	A	C	A	T	A	T	C	T	T
N. piceana	CBS 394.48	-	-	-	C	C	A	C	A	T	A	T	C	T	G
N. protearum	CBS 114178	-	-	-	C	C	A	C	A	T	A	T	C	T	T
N. rhizophorae	MFLUCC 17-1550	-	-	-	C	C	A	-	-	-	A	T	C	T	T
N. rosicola	CFCC 51992	-	-	-	C	C	A	C	A	T	A	T	C	T	T
N. samarangensis	MFLUCC 12-0233	-	-	-	C	G	A	C	A	T	A	T	C	T	T
N. sonneratae	MFLUCC 17-1744	C	C	C	C	C	A	C	A	T	A	T	C	T	T
N. surinamensis	CBS 450.74	-	-	-	T	C	T	C	G	T	G	T	C	C	T
N. thailandica	MFLUCC 17-1730	C	C	C	C	C	A	C	A	T	A	T	C	T	T

Taxon	Strain	*ef1α*										
		169	186	210	246	287	290	407	456	462	480	485
Neopestalotiopsis acrostichi	MFLUCC 17-1754	-	G	G	G	A	T	T	C	A	A	A
N. alpapicalis	MFLUCC 17-2544	-	G	G	G	A	T	C	T	A	A	G
N. aotearoa	CBS 367.54	-	G	G	G	A	T	C	C	A	T	A
N. brachiata	MFLUCC 17-1555	-	G	G	G	A	T	C	C	A	T	A
N. coffea-arabicae	HGUP4015	-	G	G	G	A	T	C	C	A	T	A
N. ellipsospora	MFLUCC 12-0283	-	A	A	A	A	T	C	C	A	T	A
N. petila	MFLUCC 17-1737	-	G	G	G	A	T	C	C	A	T	A
N. piceana	CBS 394.48	-	G	G	G	A	T	C	C	A	T	A
N. protearum	CBS 114178	T	G	G	G	A	T	C	C	A	T	A
N. rhizophorae	MFLUCC 17-1550	-	G	G	G	A	T	C	C	A	A	G
N. rosicola	CFCC 51992	-	G	G	G	A	T	C	C	A	A	A
N. samarangensis	MFLUCC 12-0233	-	G	G	G	A	T	C	C	T	A	A
N. sonneratae	MFLUCC 17-1744	C	G	G	G	A	C	C	C	T	A	A
N. surinamensis	CBS 450.74	-	G	G	T	G	T	C	C	T	A	A
N. thailandica	MFLUCC 17-1730	C	G	G	G	A	C	C	C	T	A	A

Table 3.7 Nucleotides differences in the ITS, *β-tubulin* and *ef1α* sequences of *Pestalotiopsis* discussed in the paper

Taxon	Strain	ITS											*β-tubulin*		
		14	23	162	164	433	491	539	547	551	558	559	14	36	38
Pestalotiopsis rhizophorae	MFLUCC 17-0416	A	T	C	A	A	A	T	T	T	T	G	A	T	C
P. thailandica	MFLUCC 17-1616	A	T	C	G	G	-	C	T	T	T	G	T	T	C
P. formosana	NTUCC 17-009	-	-	T	G	A	-	C	T	-	G	T	-	-	-
P. parva	CBS 278.35	T	A	T	G	A	-	C	C	-	T	G	A	G	G

Taxon	Strain	*β-tubulin*													
		39	43	130	131	132	153	174	260	360	368	372	403	428	430
Pestalotiopsis rhizophorae	MFLUCC 17-0416	C	C	A	A	G	C	C	C	C	T	A	G	A	T
P. thailandica	MFLUCC 17-1616	C	C	A	A	G	C	C	C	C	T	A	G	A	T
P. formosana	NTUCC 17-009	-	-	-	-	-	-	-	-	-	-	C	G	A	T
P. parva	CBS 278.35	A	C	-	-	-	G	T	A	T	C	A	A	T	C

Taxon	Strain	*ef1α*													
		762	33	34	36	56	57	58	71	81	123	126	226	261	434
Pestalotiopsis rhizophorae	MFLUCC 17-0416	A	T	C	C	C	C	A	C	C	A	C	T	C	G
P. thailandica	MFLUCC 17-1616	G	T	C	C	C	C	A	C	C	A	C	T	C	G
P. formosana	NTUCC 17-009	A	T	C	C	-	-	-	G	T	G	A	C	C	A
P. parva	CBS 278.35	A	A	T	T	T	C	A	G	C	A	C	T	T	A

Table 3.8 Nucleotides differences in the ITS, *β-tubulin* and *ef1α* sequences of *Pseudopestalotiopsis* discussed in the paper

Taxon	Strain	ITS													
		30	39	75	119	147	409	410	482	527	545	546	549	553	554
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	A	T	A	G	A	-	-	T	T	G	A	A	G	C
Ps. curvatispora	MFLUCC 17-1722	A	T	A	G	G	-	-	C	T	G	A	A	G	C
Ps. dawaina	MM14 F0015	T	A	A	T	G	-	-	C	T	G	A	A	G	C
Ps. jiangxiensis	LC4479	-	-	-	G	A	-	-	T	T	G	A	A	G	C
Ps. kawthaungina	MM14 F0083	T	A	A	G	A	-	-	T	T	G	A	A	G	C
Ps. myanmarina	NBRC 112264	T	A	A	G	A	-	-	T	T	G	A	A	G	C
Ps. rhizophorae	MFLUCC 17-560	A	T	A	G	G	A	A	C	T	G	A	A	G	C
Ps. simitheae	MFLUCC 12-0121	T	A	A	G	A	-	-	T	-	-	-	G	A	T
Ps. taiwanensis	NTUCC 17-002.1	T	A	A	G	A	-	-	T	-	-	-	-	-	-
Ps. thailandica	MFLUCC 17-1724	A	T	A	G	G	A	A	C	T	G	A	A	G	C
Taxon	**Strain**	**ITS**	***β-tubulin***												
		556	22	107	125	134	148	149	150	151	153	158	183	192	194
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	G	G	T	A	C	T	-	-	-	T	C	A	A	A
Ps. curvatispora	MFLUCC 17-1722	G	G	G	C	C	G	C	A	G	C	C	G	G	A
Ps. dawaina	MM14 F0015	G	-	-	-	-	-	-	-	-	-	-	-	-	-
Ps. jiangxiensis	LC4479	G	G	T	A	C	T	-	-	-	T	C	A	A	A
Ps. kawthaungina	MM14 F0083	G	-	-	-	-	-	-	-	-	-	-	-	-	-
Ps. myanmarina	NBRC 112264	G	-	-	-	-	-	-	-	-	-	-	-	-	-
Ps. rhizophorae	MFLUCC 17-560	G	A	T	C	T	G	C	A	G	T	A	A	G	G
Ps. simitheae	MFLUCC 12-0121	C	-	-	-	-	-	-	-	-	-	-	-	-	-
Ps. taiwanensis	NTUCC 17-002.1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Ps. thailandica	MFLUCC 17-1724	G	A	T	C	T	G	-	-	-	T	A	A	G	G

Table 3.8 (continued)

Taxon	Strain	*β-tubulin*													
		198	206	223	225	250	302	330	355	361	362	363	364	365	372
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	A	G	A	G	C	G	A	C	G	T	A	T	G	A
Ps. curvatispora	MFLUCC 17-1722	T	A	G	A	T	G	G	C	G	T	A	T	G	A
Ps. dawaina	MM14 F0015	-	-	-	-	-	-	-	-	G	T	A	T	G	A
Ps. jiangxiensis	LC4479	A	G	A	G	C	G	A	C	G	T	A	T	G	A
Ps. kawthaungina	MM14 F0083	-	-	-	-	-	-	-	-	G	T	A	T	G	A
Ps. myanmarina	NBRC 112264	-	-	-	-	-	-	-	-	-	-	-	-	-	A
Ps. rhizophorae	MFLUCC 17-560	T	A	A	A	T	A	A	C	G	T	A	T	G	A
Ps. simitheae	MFLUCC 12-0121	-	-	-	-	-	-	-	-	A	G	T	C	A	-
Ps. taiwanensis	NTUCC 17-002.1	-	-	-	-	-	-	-	T	G	T	A	T	G	A
Ps. thailandica	MFLUCC 17-1724	T	A	A	A	T	G	A	C	G	T	A	T	G	A

Taxon	Strain	*β-tubulin*													
		376	413	434	435	445	453	459	505	538	539	540	558	559	560
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	A	T	T	G	C	-	G	T	-	-	-	C	A	T
Ps. curvatispora	MFLUCC 17-1722	A	T	T	A	A	G	G	T	C	C	C	T	C	C
Ps. dawaina	MM14 F0015	A	T	T	A	A	G	G	T	C	C	C	T	C	C
Ps. jiangxiensis	LC4479	A	T	T	G	C	-	G	T	-	-	-	C	A	C
Ps. kawthaungina	MM14 F0083	A	T	T	A	A	G	G	T	C	C	C	T	C	C
Ps. myanmarina	NBRC 112264	A	T	T	G	C	-	G	T	-	-	-	C	A	T
Ps. rhizophorae	MFLUCC 17-560	C	C	G	A	A	G	G	C	T	T	C	C	A	C
Ps. simitheae	MFLUCC 12-0121	-	C	G	A	A	G	G	T	T	T	C	C	A	C
Ps. taiwanensis	NTUCC 17-002.1	C	C	G	A	A	G	G	T	T	T	C	C	A	C
Ps. thailandica	MFLUCC 17-1724	C	C	G	A	A	G	A	C	T	T	C	C	A	C

Table 3.8 (continued)

Taxon	Strain	*β-tubulin*										*ef1α*			
		571	572	573	581	625	628	691	715	739	772	88	89	93	95
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	T	T	G	G	T	C	T	C	T	C	A	C	T	T
Ps. curvatispora	MFLUCC 17-1722	T	C	A	T	T	C	C	T	C	T	A	T	T	C
Ps. dawaina	MM14 F0015	T	C	A	T	T	C	C	T	C	T	A	C	T	T
Ps. jiangxiensis	LC4479	T	T	G	G	T	C	T	C	T	C	A	C	T	T
Ps. kawthaungina	MM14 F0083	T	C	A	T	T	C	C	T	C	T	A	C	T	T
Ps. myanmarina	NBRC 112264	T	T	G	G	T	C	T	C	T	C	A	C	T	T
Ps. rhizophorae	MFLUCC 17-560	T	C	A	T	C	G	C	T	C	T	C	C	T	T
Ps. simitheae	MFLUCC 12-0121	C	C	A	T	T	C	C	T	C	T	G	C	A	T
Ps. taiwanensis	NTUCC 17-002.1	C	C	A	T	T	C	C	T	C	T	A	C	T	T
Ps. thailandica	MFLUCC 17-1724	T	C	A	T	C	C	C	T	C	T	C	C	T	T

Taxon	Strain	*ef1α*													
		99	100	102	105	114	115	123	125	127	128	134	137	140	150
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	T	C	A	G	-	-	A	C	T	C	C	G	C	C
Ps. curvatispora	MFLUCC 17-1722	T	G	T	A	A	A	A	T	C	C	A	A	T	C
Ps. dawaina	MM14 F0015	C	-	-	A	-	-	T	C	C	C	C	A	T	A
Ps. jiangxiensis	LC4479	T	C	A	G	-	-	A	C	T	C	C	G	C	C
Ps. kawthaungina	MM14 F0083	T	C	A	G	-	-	A	C	T	C	C	G	C	C
Ps. myanmarina	NBRC 112264	T	C	A	G	-	-	A	C	T	C	C	G	C	C
Ps. rhizophorae	MFLUCC 17-560	T	C	T	A	-	-	G	C	C	C	C	A	T	C
Ps. simitheae	MFLUCC 12-0121	T	C	T	A	-	-	G	C	C	C	C	A	T	C
Ps. taiwanensis	NTUCC 17-002.1	T	C	T	A	A	-	A	C	T	T	C	G	T	C
Ps. thailandica	MFLUCC 17-1724	T	C	T	A	-	-	G	C	C	C	C	A	T	C

Table 3.8 (continued)

Taxon	Strain	*ef1α*													
		151	152	157	167	172	176	186	252	267	268	269	270	271	272
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	C	A	A	C	A	G	T	A	C	A	G	C	A	A
Ps. curvatispora	MFLUCC 17-1722	-	-	C	T	A	C	C	A	C	A	G	C	A	A
Ps. dawaina	MM14 F0015	G	A	A	T	A	C	C	A	C	A	G	C	A	A
Ps. jiangxiensis	LC4479	C	A	A	T	A	C	T	T	C	A	G	C	A	A
Ps. kawthaungina	MM14 F0083	C	N	A	T	A	C	T	A	C	A	G	C	A	A
Ps. myanmarina	NBRC 112264	C	A	A	T	A	C	T	A	C	A	G	C	A	A
Ps. rhizophorae	MFLUCC 17-560	G	A	A	T	C	C	C	A	-	-	-	-	-	-
Ps. simitheae	MFLUCC 12-0121	G	A	A	T	C	C	C	A	-	-	-	-	-	-
Ps. taiwanensis	NTUCC 17-002.1	A	A	A	T	A	C	T	A	C	A	G	C	A	A
Ps. thailandica	MFLUCC 17-1724	G	A	A	T	C	C	C	A	-	-	-	-	-	-
Taxon	**Strain**	***ef1α***													
		273	274	275	276	277	278	279	280	281	282	283	286	290	304
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	C	-	-	-	C	A	T	G	C	A	C	C	T	A
Ps. curvatispora	MFLUCC 17-1722	C	-	-	-	C	A	T	G	C	A	C	T	T	A
Ps. dawaina	MM14 F0015	C	T	A	C	C	A	T	G	C	A	C	C	T	A
Ps. jiangxiensis	LC4479	C	-	-	-	C	A	T	G	C	A	C	C	T	A
Ps. kawthaungina	MM14 F0083	C	-	-	-	C	A	T	G	C	A	C	C	T	A
Ps. myanmarina	NBRC 112264	C	-	-	-	C	A	T	G	C	A	C	C	T	A
Ps. rhizophorae	MFLUCC 17-560	-	-	-	-	-	-	-	-	-	-	-	C	C	A
Ps. simitheae	MFLUCC 12-0121	-	-	-	-	-	-	-	-	-	-	-	C	T	C
Ps. taiwanensis	NTUCC 17-002.1	C	-	-	-	C	A	T	G	C	A	C	C	T	A
Ps. thailandica	MFLUCC 17-1724	-	-	-	-	-	-	-	-	-	-	-	C	C	A

Table 3.8 (continued)

Taxon	Strain	*ef1α*													
		306	308	312	318	321	343	475	476	478	479	480	484	487	488
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	T	A	C	C	C	C	G	T	C	C	T	C	G	C
Ps. curvatispora	MFLUCC 17-1722	C	A	C	C	C	C	T	T	C	C	T	A	A	C
Ps. dawaina	MM14 F0015	C	A	C	C	C	C	T	T	C	T	T	C	A	C
Ps. jiangxiensis	LC4479	T	A	C	C	C	C	G	T	C	C	T	C	G	C
Ps. kawthaungina	MM14 F0083	C	A	C	C	C	C	T	T	A	C	T	C	G	T
Ps. myanmarina	NBRC 112264	T	A	C	C	C	C	G	T	C	C	T	C	G	C
Ps. rhizophorae	MFLUCC 17-560	C	G	C	T	A	T	T	C	C	T	C	C	G	C
Ps. simitheae	MFLUCC 12-0121	C	A	C	C	C	C	T	C	C	T	T	C	G	C
Ps. taiwanensis	NTUCC 17-002.1	C	A	T	C	C	C	T	T	C	C	C	C	A	C
Ps. thailandica	MFLUCC 17-1724	C	G	C	T	A	T	T	C	C	T	C	C	G	C

Taxon	Strain	*ef1α*										
		491	492	493	496	500	501	504	510	512	521	524
Pseudopestalotiopsis avucenniae	MFLUCC 17-0434	A	G	C	C	G	A	T	T	-	T	C
Ps. curvatispora	MFLUCC 17-1722	A	G	C	C	G	C	T	C	-	T	T
Ps. dawaina	MM14 F0015	A	G	T	C	G	A	T	T	T	T	T
Ps. jiangxiensis	LC4479	A	G	C	C	G	A	T	T	-	T	C
Ps. kawthaungina	MM14 F0083	A	A	C	C	G	A	G	T	-	T	C
Ps. myanmarina	NBRC 112264	A	G	C	C	G	A	T	T	-	T	C
Ps. rhizophorae	MFLUCC 17-560	T	C	C	C	G	A	T	T	-	C	C
Ps. simitheae	MFLUCC 12-0121	A	C	G	C	A	A	T	T	-	C	C
Ps. taiwanensis	NTUCC 17-002.1	A	G	C	T	G	A	T	T	-	T	G
Ps. thailandica	MFLUCC 17-1724	T	C	C	C	G	A	T	T	-	C	C

CHAPTER 4

FICUS MICROCARPA (MORACEAE) AND *KANDELIA CANDEL* (RHIZOPHORACEAE), TWO NEW HOST RECORDS FOR *ALTERNARIA GAISEN* FROM TAIWAN[3]

Abstract

Mangroves grow adjacent to estuarine regions of the tropics and subtropics. Fungi cause diseases in mangroves; however, it is not clear if the diseases are unique to mangrove species or ubiquitous. In this study, we identified a species of *Alternaria*, a genus comprising with saprobic and pathogenic species of a large number of plants. The genus is currently divided into 28 sections based on phylogenetic and morphological evidence. *Alternaria* is characterized by macronematous conidiophores, sympodial, polytretic conidiogenous cells, and obclavate to obovoid, muriform conidia gradually tapering towards beaked apex. We found *A. gaisen* associated with leaf blight of *Ficus microcarpa* and leaf spots of *Kandelia candel* from Taiwan. Phylogenetic analysis of combined SSU, LSU, ITS, *gapdh*, *rpb2*, *ef1α*, *Alta1*, *endoPG* and OPA10-2 sequence data supports positioning of our isolates as *A. gaisen* in section *Alternaria*. This species was first reported from Japanese pear causing black spot disease. This is also a new host record of *A. gaisen* from mangroves in Taiwan.

Keywords: new host record, mangroves, microfungi, phylogenetic analyses, pleosporaceae, *Alternaria gaisen*

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4.1 Introduction

Alternaria Nees is a genus composed of many important plant pathogens as well as endophytic and saprobic species with a worldwide distribution (Ariyawansa et al., 2015; Woudenberg et al., 2013). Species of *Alternaria* mainly inflict damage to pre- and post-harvest agricultural products (Patriarca & Pinto, 2018). Some *Alternaria* species produce secondary metabolites considered as phytotoxins (harmful to plants), and mycotoxins (harmful to humans and animals) (Patriarca & Pinto, 2018). *Alternaria* was introduced by Nees von Esenbeck (1816) to accommodate the type species, *A. alternata* (Fr.) Keissl. (=*A. tenuis* Nees). It is currently placed in the family Pleosporaceae, Pleosporales, Dothideomycetes, based on taxonomy and phylogenetic evidence (Bhunjun et al., 2020; Wijayawardene et al., 2018, 2020). *Alternaria* species produce concatenated conidia, typically ovoid to obclavate, observed singly or in chains, darkly pigmented, muriform, with the basal end of the conidium being rounded, while it tapers towards the apex and gives a typical beak or club-like appearance of the conidium (Lawrence et al., 2014). Over 700 species of this genus are listed in Index Fungorum (accessed January 23, 2021). The classification of *Alternaria* has been confusing in most cases and so far conidial size and shape were used to determine the distinction between different species. Phylogenetic analyses indicated that, there are 28 internal clades of the *Alternaria* complex i.e. sect. *Alternantherae*, sect. *Alternaria*, sect. *Brassicicola*, sect. *Chalastospora*, sect. *Cheiranthus*, sect. *Crivellia*, sect. *Dianthicola*, sect. *Embellisia*, sect. *Embellisioides*, sect. *Euphorbiicola*, sect. *Eureka*, sect. *Gypsophilae*, sect. *Infectoriae*, sect. *Japonicae*, sect. *Nimbya*, sect. *Omanenses*, sect. *Panax*, sect. *Phragmosporae*, sect. *Porri*, sect. *Pseudoalternaria*, sect. *Pseudoulocladium*, sect. *Radicina*, sect. *Soda*, sect. *Sonchi*, sect. *Teretispora*, sect. *Ulocladioides*, sect. *Ulocladium*, and sect. *Undifilum* (Al Ghafri et al., 2019; Lawrence et al., 2013, 2014, 2016; Woudenberg et al., 2013).

The sect. *Alternaria* was formalized to a section by Lawrence et al. (2013), with *A. alternata* (Fr.) Keissl. as the type species, while seven sections were introduced in the same study. Section *Alternaria* includes many important species causing diseases on economic plants, as well as post-harvest pathogens, and human pathogens, *viz*. *A.*

arborescens Simmons, *A. alternata* (Fr.) Keissl., *A. gaisen* Nagano ex Hara, *A. longipes*, *A. mali* (Ellis & Everh.) Mason, and *A. tenuissima* (Kunze) Wiltshire (Simmons, 1995; Woudenberg et al., 2015). This section is characterized by transversely and longitudinally septate, obclavate to ellipsoidal conidia, produced on simple or branched conidiophores, with some forming conidial chains and bearing one or several tretic conidiogenous cells (with sympodial proliferations) (Lawrence et al., 2013; Woudenberg et al., 2013).

Mangroves occur in estuarine regions in the tropics and subtropics Hyde et al., (1988) and suffer from diseases cause by fungi (Barnard, 2000; Fox, 2001; Hyde & Cannon, 1992; Kinge & Mih, 2011; McMillan, 1964; Ryvarden, 2000; Sakayaroj et al., 2012; Shivas et al., 2009; Stevens, 1920; Vollbrecht et al., 1995; Xu et al., 2009). This paper introduces a new host record of *Alternaria gaisen*, associated with leaf blight of *Ficus microcarpa* L.f. (Moraceae), plant species that occur mainly at low elevations and natural habitats including tropical rainforests, river edges, coasts, swamps, and mangrove areas (Ferrer-Gallego & Boisset, 2017) and leaf spots of *Kandelia candel* (L.) Druce (Rhizophoraceae), an abundant mangrove plant in Taiwan that occurs around the coasts and saline-brackish habitats of South Asia and Southeast Asia, which was planted in order to check winds, control sand and protect dikes (Sheue et al., 2003).

4.2 Materials and Methods

4.2.1 Sample Collection and Specimen Examination

Fresh samples with leaf blight and leaf-spot symptoms were collected in July, 2018, from *Ficus microcarpa* and *Kandelia candel*. Fresh specimens were taken to the laboratory in paper bags, examined and described. Mega-morphological characters were examined using a Zeiss Axioskop 2 *plus* stereo microscope (Carl Zeiss Microscopy, LLC, NY, USA). Micro-morphology was examined using a Zeiss Axioskop 2 mot *plus* compound microscope (Carl Zeiss Microscopy, LLC, NY, USA). Images' measurements were made using ZEN2 (blue edition) software. Adobe Photoshop CC 2019 version: 20.0.1 was used to prepare fungal photo-plates (Adobe

Systems, CA, USA) (Senanayake et al., 2020).

Pure cultures were obtained by single spore isolation for fungi from *Ficus microcarpa*. A conidial suspension was prepared by scraping spore masses from the surface of substrate using a sterilized needle into a drop of sterile water on a small glass container. The conidial suspension was examined using a stereo microscope, sucked by a Pasteur pipette or syringe and placed in drops on 2% water agar (WA) at the center of squares marked in a grid on the bottom of Petri dish and incubated at room temperature (25 °C ± 2) overnight. Single germinating spores observed using a dissecting microscope were transferred aseptically into 2% potato dextrose agar (PDA) and incubated at room temperature for one-week under a daily light/dark cycle. Tissue isolation method of Norphanphoun et al. (2018) was used to isolate the fungus from leaf spot of *Kandelia candel*. Based on Simmons (2007), fungal isolations in this study were cultured into PDA, potato-carrot agar (PCA), and V-8 juice agar (V-8 agar) Petri-dish and incubated at room temperature for one-week period under a daily light/dark cycle. Culture characters were examined and recorded at intervals of 5, 7, 14 and 30 d. Morphological characters of fungi on media were examined, r+ecorded, and compared with other species published based on *Alternaria* species keying system in Simmons (2007). Pure cultures were maintained for further studies in PDA, PCA and V-8 agar. The dried and living cultures are deposited in the Department of Plant Medicine, National Chiayi University (NCYU) and duplicates in culture collection Mae Fah Luang University (MFLUCC), Chiang Rai, Thailand.

4.2.2 DNA Extraction, PCR Amplification and Sequencing

DNA extraction was performed with fresh fungal mycelia growing on PDA at room temperature (25 °C ± 2) for one week using a E.Z.N.A ® Fungal DNA Mini Kit, D3390-02,(Omega Bio-tek, Inc., GA) and following the manufacturer's protocols. The small subunit rRNA (SSU) was amplified using primer pairs NS1/NS4 (White et al., 1990); the 28S large subunit ribosomal RNA gene (LSU) amplified by primers LROR/LR5, (White et al., 1990); the internal transcribed spacer region (ITS) using primers ITS1/ ITS4 (White et al., 1990); translation elongation factor 1-α (*ef1α*) using primers 728f/986r (Carbone & Kohn, 1999); glyceraldehyde-3-phosphate dehydrogenase (*gapdh*) using primers gpd1/gpd2 (Berbee et al., 1999); RNA

polymerase II subunit (*rpb2*) using primers 5f2/7cr (Woudenberg et al., 2013); *Alternaria* major allergen (*Alta1*) using primers Alt-for/ Alt-rev (Hong et al., 2005); the endopolygalacturonase (*endoPG*) was amplified using the primers PG3 and PG2b; and an anonymous gene region (OPA10-2)was amplified using the primers OPA10-2L and OPA10-2R (Andrew et al., 2009).

The polymerase chain reactions (PCR) were carried out with 50 µL reaction volume (2 µL of DNA template, 2 µL of each forward and reverseprimers, 25 µL of 2×Power Taq PCR MasterMix (Tri-I Biotech, Taipei, Taiwan) and 19 µL of double-distilled water (ddH_2O)). The PCR thermal cycle programs was carried out for each gene as, SSU: 95 °C (3 min), 40 cycles of 95 °C (30 s), 52 °C (50 s), 72 °C (1 min), final extension at 72 °C (7 min); LSU: 95 °C (3 min), 34 cycles of 95 °C (30 s), 51 °C (50 s), 72 °C (1 min), final extension at 72 °C (10 min); ITS: 95 °C (3 min), 40 cycles of 95 °C (30 s), 55 °C (50 s), 72 °C (1 min), final extension at 72 °C (7 min); *efl1α*: 94 °C (3 min), 40 cycles of 94 °C (45 s), 52 °C (30 s), 72 °C (30 s), final extension at 72 °C (6 min). *gapdh* PCR thermal cycle programs was followed Al Ghafri et al. (2019); *rpb2* was followed from Woudenberg et al. (2013); Alt a 1 was followed from Hong et al. (2005); *endoPG* was followed from Andrew et al. (2009) and Woudenberg et al. (2015). OPA10-2: 94 °C (5 min), 35 cycles of 94 °C (30 s), 50 °C (30 s), 72 °C (45 s), final extension at 72 °C (10 min). PCR products were analyzed with 1.5% agarose gel containing the Safeview DNA stain (GeneMark, Taipei, Taiwan). Purification and sequencing were carried out at Tri-I Biotech, Taipei, Taiwan.

4.2.3 Phylogenetic Analysis

Geneious® 11.1.5 (http://www.geneious.com) was used to assemble sequence data. Multiple alignments derived in this study were analyzed with similar sequences, acquired from GenBank BLASTn included recently published (Al Ghafri et al., 2019; Woudenberg et al., 2015). ITSx 1.1 a Perl based software tool was used to extract SSU, ITS1, 5.8S, ITS2 and LSU (Bengtsson-Palme et al., 2013). BioEdit 7.2.3 (Hall, 1999) was used to extract the partition of *gapdh*, *efl1α*, and *Alta1* based on nucleotide BLAST in GenBank. Combined sequence data of Figure 4.1 (SSU, LSU, ITS1+ ITS2, 5.8S, *gapdh*-exon, *rpb2*, *efl1α*-exon, *Alta1*-exon, *gapdh*-intron, *efl1α*-intron, and *Alta1*-intron) and Figure 4.2 (SSU, LSU, ITS1+ITS2, 5.8S, *gapdh*-exon, *rpb2*, *efl1α*-exon,

Alta1-exon, *endoPG*, OPA10-2, *gapdh*-intron, *ef1α*-intron, and *Alta1*-intron) were performed with maximum parsimony (MP), maximum likelihood(ML) and Bayesian analysis (BI). NEXUS file was converted by using Geneious Prime® 2019.2.1 (http://www.geneious.com). MrModeltest v. 2.2 (Nylander, 2004) was prepared in PAUP* v.4.0b10 (Swofford, 1979). Dataset of phylogenetic tree in Figure 4.1 consisted 99 taxa, included outgroup strains (*Stemphylium herbarum* strain CBS 191.86 and *Pleospora tarda* strain CBS 714.68). This tree was used to determine all *Alternaria* sections (28 sections). Dataset of Figure 4.2 consisted 41 taxa of *Alternaria* sect. *Alternaria* and outgroup from *Alternaria* sect. *Alternantherae* (*A. perpunctulata* strain CBS 115267 and *A. alternantherae* strain CBS124392). Ingroup taxa were selected based on preliminary analyses (not shown) and Figure 4.1. Alignments of each gene region were aligned in MAFFT v.7.110 online program (http://mafft.cbrc.jp/alignment/server/; Katoh & Standley, 2013); Phylemon 2.0 were used to exclude ambiguously aligned positions alignments (Sánchez et al., 2011) and manual adjustments were made wherever necessary in BioEdit v. 7.0.5.3 (Hall, 1999). MEGA v. 10.1.0 was used to combine sequence (Kumar et al., 2018). Missing data were coded as Question mark (?). The phylogram was visualized in FigTree v1.4.0 (http://tree.bio.ed.ac. uk/software /figtree/; Rambaut, 2012) and performed by using Adobe Illustrator CC version 23.0.1 (Adobe Systems, CA, USA). Newly generated sequences in this study are deposited in GenBank (Table 4.1). The finalized alignments and tree topology were deposited in TreeBASE, Figure 4.1: submission ID: 26854, Figure 4.2: submission ID: 26855.

Maximum parsimony (MP), Maximum likelihood (ML) and Bayesian inference (BI) analyses were partitioned analysis and performed for Figure 4.1 with 11 partitions: SSU, LSU, ITS1+ITS2, 5.8S, *gapdh*-exon, *rpb2*, *ef1α*-exon, *Alta1*-exon, *gapdh*-intron, *ef1α*-intron, and *Alta1*-intron) and for Figure 4.2 with 13 partitions: SSU, LSU, ITS1+ITS2, 5.8S, *gapdh*-exon, *rpb2*, *ef1α*-exon, *Alta1*-exon, *endoPG*, OPA10-2, *gapdh*-intron, *ef1α*-intron, and *Alta1*-intron. Analyses were implemented in CIPRES Science Gateway web server with tool selected, PAUP on XSEDE, RAxML-HPC2on XSEDE, and MrBayes on XSEDE respectively (Miller et al., 2010). 1000 bootstrap replicates using heuristic search with random stepwise addition and tree-bisection reconnection (TBR) for Maximum parsimony. 1000 rapid bootstrap replicates were run

with GTRGAMMA model of nucleotide evolution was set for Maximum likelihood and bootstrap values for MP and ML were equal or greater than 50% are presented in both trees.

Bayesian inference (BI) analysis was performed using the Markov Chain Monte Carlo (MCMC) with best-fit nucleotide substitution model foreach gene and dataset were determined using MrModel test version 2.2 with selected by AIC (Nylander, 2004). In Figure 4.1: HKY+I was selected as a best-fitmodel for SSU; GTR+I+G was selected for LSU, ITS1+ITS2, *gapdh*-exon, and *rpb2*; JC for 5.8S; K80 for *ef1α*-exon; HKY+G for *Alta1*-exon; HKY+I+G for *gapdh*-intron, and *ef1α*-intron; and GTR+I was selected as a best-fit model for *Alta1*-intron. In Figure 4.2: HKY was selected as a best-fit model for SSU, *ef1α*-intron, and *Alta1*-intron; HKY+I for LSU, *Alta1*-exon, and *gapdh*-intron; K80 forITS1+ITS2, 5.8S, and *ef1α*-exon; GTR+I for *gapdh*-exon; SYM+G for *rpb2*; SYM+I for *endoPG*; and K80+G for OPA10-2;The MCMC analyses and four chains random tree topology were run between 10,000,000 and 1,000,000 generations respectively for each combined dataset. Treeswere sampled every 100 generations with 25.0% of relative burn-in value.

Table 4.1 GenBank accession numbers of the sequences used in this study

Species	Strain *	Location	Host	GenBank accession numbers								
				SSU	LSU	ITS	*gapdh*	*rpb2*	*ef1α*	*Alta1*	*endoPG*	OPA10-2
Alternaria abundans	CBS 534.83 ^{T}	New Zealand	*Fragaria*	KC584581	KC584323	JN383485	KC584154	KC584448	KC584707	JN383503	-	-
A. alstroemeriae	CBS 118808	USA	*Alstroemeria* sp.	KP124917	KP124447	KP124296	KP124153	KP124764	KP125071	KP123845	KP123993	KP124601
A. alstroemeriae	CBS 118809^{T}	Australia	*Alstroemeria* sp.	KP124918	KP124448	KP124297	KP124154	KP124765	KP125072	-	KP123994	KP124602
A. alternantherae	CBS 124392	China	*Solanum melongena*	KC584506	KC584251	KC584179	KC584096	KC584374	KC584633	KP123846	-	-
A. alternariae	CBS 126989	USA	*Daucus carota*	KC584604	KC584346	AF229485	-	KC584470	KC584730	-	-	-
A. alternata	CBS 117.44	Denmark	*Godetia* sp.	KP124925	KP124455	KP124303	KP124160	KP124772	KP125079	KP123854	KP124001	KP124609
A. alternata	CBS 174.52	USA	*Anemone occidentalis*	KC584578	DQ678068	KC584228	KC584152	DQ677964	KC584704	KP123856	KP124003	KP124611
A. alternata	CBS 686.68	Sahara	desert sand	KP124928	KP124458	KP124306	KP124163	KP124775	KP125082	KP123859	KP124006	KP124614
A. alternata	CBS 826.68	Germany	*Lolium* sp.	KP124929	KP124459	KP124307	KP124164	KP124776	KP125083	KP123860	KP124007	
A. alternata	CBS 916.96^{T}	India	*Arachis hypogaea*	KC584507	DQ678082	KF465761	-	KC584375	KC584634	AY563301	JQ811978	KP124632
A. alternata	CBS 102595	USA	*Citrus jambhiri*	KC584540	KC584284	FJ266476	AY562411	KC584408	KC584666	AY563306	KP124029	KP124636
A. alternata	CBS 116749	Netherlands	unknown	KP124975	KP124505	KP124353	KP124207	KP124821	KP125129	KP123901	KP124054	KP124664
A. alternata	CBS 118812	USA	*Daucus carota*	KC584525	KC584269	KC584193	KC584112	KC584393	KC584652	KP123905	KP124058	KP124668
A. arborescens	CBS 101.13	Switzerland	peat soil	KP125016	KP124546	KP124392	KP124244	KP124862	KP125170	KP123940	KP124096	KP124705
A. arborescens	CBS 102605^{T}	USA	*Solanum lycopersicum*	KC584509	KC584253	NR_135927	AY278810	KC584377	KC584636	AY563303	AY295028	KP124712
A. arborescens	CPC 4244	South Africa	*Malus domestica*	KP125023	KP124553	KP124400	KP124252	KP124870	KP125178	KP123947	KP124104	KP124714
A. arborescens	CBS 119544	New Zealand	*Avena sativa*	KP125031	KP124561	KP124408	JQ646321	KP124878	KP125186	KP123955	KP124112	KP124722
A. arborescens	CBS 123235	Denmark	*human toenail*	KP125033	KP124563	KP124410	KP124261	KP124880	KP125188	KP123957	KP124114	KP124724
A. arborescens	CBS 124283	Russia	*Oryza* sp.	KP125039	KP124569	KP124416	KP124267	KP124885	KP125194	KP123963	KP124120	KP124730
A. argyranthemi	CBS 116530	New Zealand	*Argyranthemum* sp.	KC584510	KC584254	KC584181	KC584098	KC584378	KC584637	-	-	-
A. arrhenatheri	BMP 0514	-	-	-	-	JQ693680	JQ693629	-	-	-	-	-
A. aspera	CBS 115269 ^{T}	Japan	*Pistacia vera*	KC584607	KC584349	KC584242	KC584166	KC584474	KC584734	KF533899	-	-
A. axiaeriisporifera	CBS 118715 ^{T}	New Zealand	*Gypsophila paniculata*	KC584513	KC584257	KC584184	KC584101	KC584381	KC584640	-	-	-
A. betae-kenyensis	CBS 118810^{T}	Kenya	*Beta vulgaris* var. *cicla*	KP125042	KP124572	KP124419	KP124270	KP124888	KP125197	KP123966	KP124123	KP124733
A. bornmueller	DAOM 231361	Austria	*Securigera varia*	KC584624	KC584366	FJ357317	FJ357305	KC584491	KC584751	JN383516	-	-
A. botryospora	CBS 478.90 ^{T}	New Zealand	*Leptinella dioica*	KC584594	KC584336	MH862228	AY278831	KC584461	KC584720	-	-	-
A. botrytis	CBS 197.67 ^{T}	USA	-	KC584609	KC584351	KC584243	KC584168	KC584476	KC584736	-	-	-

Table 4.1 (continued)

Species	Strain *	Location	Host	GenBank accession numbers								
				SSU	LSU	ITS	*gapdh*	*rpb2*	*ef1α*	*Alta1*	*endoPG*	OPA10-2
A. brassicae	CBS 116528	USA	*Brassica oleracea*	KC584514	KC584258	KC584185	KC584102	KC584382	KC584641	-	-	-
A. brassicae-pekinensis	CBS 121493 T	China	*Brassica rapa* subsp. *Pekinensis*	KC584611	KC584353	KC584244	KC584170	KC584478	KC584738	KF533892	-	-
A. brassicicola	CBS 118699	USA	*Brassica oleracea*	KC584515	KC584259	JX499031	KC584103	KC584383	KC584642	-	-	-
A. breviramosa	CBS 121331 T	Australia	*Triticum* sp.	KC584574	KC584318	FJ839608	KC584148	KC584442	KC584700	-	-	-
A. burnsii	CBS 107.38 T	India	*Cuminum cyminum*	KP125043	KP124573	KP124420	JQ646305	KP124889	KP125198	KP123967	KP124124	KP124734
A. burnsii	CBS 110.50	Mozambique	*Gossypium* sp.	KP125044	KP124574	KP124421	KP124271	KP124890	KP125199	KP123968	KP124125	KP124735
A. calycipyricola	CBS 121545 T	China	-	KC584516	KC584260	KC584186	KC584104	KC584384	KC584643	-	-	-
A. capsici-annui	CBS 504.74	-	*Capsicum annuum*	KC584517	KC584261	KC584187	KC584105	KC584385	KC584644	-	-	-
A. caricis	CBS 480.90 T	USA	*Carex hoodii*	NG_062917	NG_057022	NR_135934	AY278826	KC584467	KC584726	-	-	-
A. carotiincultae	CBS 109381 T	USA	*Daucus carota*	KC584518	KC584262	KC584188	KC584106	KC584386	KC584645	-	-	-
A. cetera	CBS 121340 T	Australia	*Elymus scabrus*	KC584573	KC584317	FJ839607	AY562398	KC584441	KC584699	-	-	-
A. chartarum	CBS 200.67 T	Canada	*Populus* sp.	KC584614	KC584356	AF229488	KC584172	KC584481	KC584741	-	-	-
A. cheiranthi	CBS 109384	Italy	*Erysimum cheiri*	KC584519	KC584263	AF229457	KC584107	KC584387	KC584646	JQ905106	-	-
A. chlamydospora	CBS 491.72 T	Egypt	soil	KC584520	KC584264	KC584189	KC584108	KC584388	KC584647	JQ646367	-	-
A. chlamydosporigena	CBS 341.71	USA	air	KC584584	KC584326	KC584231	KC584156	KC584451	KC584710	-	-	-
A. cinerariae	CBS 116495	USA	*Ligularia* sp.	KC584521	KC584265	KC584190	KC584109	KC584389	KC584648	-	-	-
A. concatenata	CBS 120006 T	-	-	KC584613	KC584355	KC584246	-	KC584480	KC584740	-	-	-
A. conjuncta	CBS 196.86 T	Switzerland	*Pastinaca sativa*	KC584522	KC584266	FJ266475	AY562401	KC584390	KC584649	-	-	-
A. conoidea	CBS 132.89	Saudi Arabia	*Ricinus communis*	KC584585	KC584327	FJ348226	FJ348227	KC584452	KC584711	FJ348228	-	-
A. cucurbitae	CBS 483.81	New Zealand	*Cucumis sativus*	KC584616	KC584358	FJ266483	AY562418	KC584483	KC584743	-	-	-
A. cumini	CBS 121329	India	*Cuminum cyminum*	KC584523	KC584267	KC584191	KC584110	KC584391	KC584650	-	-	-
A. dennisii	CBS 110533	New Zealand	*Jacobaea vulgaris*	KC584586	KC584328	KC584232	KC584157	KC584453	KC584712	-	-	-
A. dennisii	CBS 476.90 T	Isle of Man	*Jacobaea vulgaris*	KC584587	KC584329	JN383488	JN383469	KC584454	KC584713	-	-	-
A. dianthicola	CBS 116491	New Zealand	*Dianthus x allwoodii*	KC584526	KC584270	KC584194	KC584113	KC584394	KC584653	-	-	-
A. didymospora	CBS 766.79	Mediterranean	seawater	KC584588	KC584330	FJ357312	FJ357300	KC584455	KC584714	-	-	-
A. eichhorniae	CBS 489.92 T	India	*Eichhornia crassipes*	KP125049	NG_042763	NR_111832	KP124276	KP124895	KP125204	KP123973	KP124130	KP124740

Table 4.1 (continued)

Species	Strain *	Location	Host	GenBank accession numbers								
				SSU	LSU	ITS	*gapdh*	*rpb2*	*ef1α*	*Alta1*	*endoPG*	OPA10-2
A. eichhorniae	CBS 119778	Indonesia	*Eichhornia crassipes*	KP125050	KP124580	KP124426	KP124277	KP124896	KP125205	-	KP124131	KP124741
A. elegans	CBS 109159 ^{T}	Burkina Faso	*Solanum lycopersicum*	KC584527	KC584271	KC584195	KC584114	KC584395	KC584654	-	-	-
A. embellisia	CBS 339.71	USA	*Allium sativum*	KC584582	KC584324	KC584230	KC584155	KC584449	KC584708	-	-	-
A. eryngii	CBS 121339	-	*Eryngium* sp.	KC584529	KC584273	JQ693661	AY562416	KC584397	KC584656	-	-	-
A. euphorbiicola	CBS 198.86	USA	*Euphorbia pulcherrima*	-	-	KJ718172	KJ718017	KJ718345	KJ718520	KJ718686	-	-
A. euphorbiicola	CBS 109410	-	*Beta vulgaris*	MK249665	MK249662	KJ718173	-	-	KJ718521	-	-	-
A. eureka	CBS 193.86 ^{T}	Australia	*Medicago rugosa*	KC584589	KC584331	JN383490	JN383471	KC584456	KC584715	-	-	-
A. gaisen	CBS 632.93	Japan	*Pyrus pyrifolia*	KC584531	KC584275	KC584197	KC584116	KC584399	KC584658	KP123974	AY295033	KP124742
A. gaisen	CBS 118488^{T}	Japan	*Pyrus pyrifolia*	KP125051	KP124581	KP124427	KP124278	KP124897	KP125206	KP123975	KP124132	KP124743
A. gaisen	CPC 25268	Portugal	unknown	KP125052	KP124582	KP124428	KP124279	KP124898	KP125207	KP123976	KP124133	KP124744
A. gaisen	MAFF 731001	Japan	*Fragaria* sp.	-	-	LC164854	LC169125	LC169131	LC167148	LC276235	LC276246	-
A. gaisen	**NCYUCC 19-0351**	**Taiwan**	***Ficus microcarpa***	**MT416127**	**MT416136**	**MT416122**	**MT945064**	**MT945070**	**MT420727**	**MT945062**	**MT945066**	**MT945068**
A. gaisen	**NCYUCC 19-0353**	**Taiwan**	***Kandelia candel***	**MT416128**	**MT416137**	**MT416123**	**MT945065**	**MT945071**	**MT420728**	**MT945063**	**MT945067**	**MT945069**
A. geniostomatis	CBS 118701 ^{T}	New Zealand	*Geniostoma* sp.	KC584532	KC584276	KC584198	KC584117	KC584400	KC584659	-	-	-
A. gossypina	CBS 104.32 ^{T}	Zimbabwe	*Gossypium* sp.	KP125054	KP124584	KP124430	JQ646312	KP124900	KP125209	JQ646395	KP124135	KP124746
A. gossypina	CBS 102597^{T}	USA	*Minneola tangelo*	KP125056	KP124586	KP124432	KP124281	KP124902	KP125211	KP123978	KP124137	KP124748
A. gypsophilae	CBS 107.41 ^{T}	Netherlands	*Gypsophila elegans*	KC584533	KC584277	KC584199	KC584118	KC584401	KC584660	JQ646387	-	-
A. helianthiinficiens	CBS 117370	England	*Helianthus annuus*	KC584534	KC584278	KC584200	KC584119	KC584402	KC584661	-	-	-
A. helianthiinficiens	CBS 208.86 ^{T}	USA	*Helianthus annuus*	KC584535	KC584279	JX101649	KC584120	KC584403	EU130548	-	-	-
A. heterospora	CBS 123376	China	*Solanum lycopersicum*	KC584621	KC584363	KC584248	KC584176	KC584488	KC584748	-	-	-
A. hyacinthi	CBS 416.71 ^{T}	Netherlands	*Hyacinthus orientalis*	KC584590	KC584332	KC584233	KC584158	KC584457	KC584716	-	-	-
A. indefessa	CBS 536.83 ^{T}	USA	soil	KC584591	KC584333	KC584234	KC584159	KC584458	KC584717	-	-	-
A. infectoria	CBS 210.86 ^{T}	England	*Triticum aestivum*	KC584536	KC584280	DQ323697	AY278793	KC584404	KC584662	-	-	-
A. iridiaustralis	CBS 118486 ^{T}	Australia	*Iris* sp.	KP125059	KP124589	KP124435	KP124284	KP124905	KP125214	KP123981	KP124140	KP124751
A. iridiaustralis	CBS 118487	Australia	*Iris* sp.	KP125060	KP124590	KP124436	KP124285	KP124906	KP125215	KP123982	KP124141	KP124752
A. iridicola	MAFF 246890 ^{T}	Japan	*Iris japonica*	-	-	LC269974	LC270142	LC275240	LC275060	LC276238	LC276253	-
A. iridicola	MUCC 2149	Japan	*Iris japonica*	-	-	LC269975	LC270143	LC275241	LC275061	LC276239	LC276254	-

Table 4.1 (continued)

Species	Strain *	Location	Host	GenBank accession numbers								
				SSU	LSU	ITS	*gapdh*	*rpb2*	*ef1α*	*Alta1*	*endoPG*	OPA10-2
A. jacinthicola	CBS 133751[T]	Mali	*Eichhornia crassipes*	KP125062	KP124592	KP124438	KP124287	KP124908	KP125217	KP123984	KP124143	KP124754
A. jacinthicola	CPC 25267	Unknown	*Cucumis melo* var. *inodorus*	KP125063	KP124593	KP124439	KP124288	KP124909	KP125218	KP123985	KP124144	KP124755
A. japonica	CBS 118390	USA	*Brassica rapa* subsp. *Chinensis*	KC584537	KC584281	KC584201	KC584121	KC584405	KC584663	-	-	-
A. kulundii	M313	Russia	soil	KJ443087	KJ443132	KJ443262	KJ649618	KJ443176	-	-	-	-
A. leucanthemi	CBS 421.65 [T]	Netherlands	*Leucanthemum maximum*	KC584605	KC584347	KC584240	KC584164	KC584472	KC584732	-	-	-
A. leucanthemi	CBS 422.65	USA	-	KC584606	KC584348	KC584241	KC584165	KC584473	KC584733	-	-	-
A. limaciformis	CBS 481.81	England	-	KC584539	KC584283	KC584203	KC584123	KC584407	KC584665	JQ646368	-	-
A. longipes	CBS 113.35	Unknown	*Nicotiana tabacum*	KP125064	KP124594	KP124440	KP124289	KP124910	KP125219	KP123986	KP124145	KP124756
A. longipes	CBS 121333	USA	*Nicotiana tabacum*	KP125068	KP124598	KP124444	KP124293	KP124914	KP125223	KP123990	KP124150	KP124761
A. macrospora	CBS 117228 [T]	USA	*Gossypium barbadense*	KC584542	KC584286	KC584204	KC584124	KC584410	KC584668	KJ718702	-	-
A. nepalensis	CBS 118700 [T]	Nepal	*Brassica* sp.	KC584546	KC584290	KC584207	KC584126	KC584414	KC584672	-	-	-
A. nobilis	CBS 116490	New Zealand	*Dianthus caryophyllus*	KC584547	KC584291	KC584208	KC584127	KC584415	KC584673	JQ646385	-	-
A. obclavata	CBS 124120 [T]	USA	air	KC584575	FJ839651	KC584225	KC584149	KC584443	KC584701	-	-	-
A. omanensis	SQUCC 13580 [T]	Oman	dead woods	MK878559	MK878556	MK878562	MK880899	MK880893	MK880896	-	-	-
A. omanensis	SQUCC 15561	Oman	dead woods	MK878561	MK878558	MK878564	MK880901	MK880895	MK880898	-	-	-
A. oudemansii	CBS 114.07 [T]	-	-	KC584619	KC584361	FJ266488	KC584175	KC584486	KC584746	FJ266514	-	-
A. panax	CBS 482.81	USA	*Aralia racemosa*	KC584549	KC584293	KC584209	KC584128	KC584417	KC584675	-	-	-
A. papavericola	CBS 116606 [T]	USA	*Papaver somniferum*	KC584579	KC584321	MH862999	FJ357298	KC584446	KC584705	-	-	-
A. penicillata	CBS 116608	Austria	*Papaver rhoeas*	KC584572	KC584316	FJ357311	FJ357299	KC584440	KC584698	-	-	-
A. penicillata	CBS 116607 [T]	Austria	*Papaver rhoeas*	KC584580	KC584322	KC584229	KC584153	KC584447	KC584706	-	-	-
A. perpunctulata	CBS 115267	USA	*Alternanthera philoxeroides*	NG_062895	KC584294	NR_151838	KC584129	KC584418	KC584676	JQ905111	-	-
A. petroselini	CBS 112.41	-	*Petroselinum crispum*	KC584551	KC584295	KC584211	KC584130	KC584419	KC584677	-	-	-
A. petuchovskii	M304	Russia	alkaline soil	KJ443079	KJ443124	KJ443254	KJ649616	KJ443170	-	-	-	-
A. photistica	CBS 212.86 [T]	England	*Digitalis purpurea*	KC584552	KC584296	KC584212	KC584131	KC584420	KC584678	-	-	-
A. phragmospora	CBS 274.70 [T]	Netherlands	soil	KC584595	KC584337	MH859605	-	KC584462	KC584721	-	-	-
A. porri	CBS 116698	USA	*Allium cepa*	KC584553	KC584297	DQ323700	KC584132	KC584421	KC584679	KJ718726	-	-

Table 4.1 (continued)

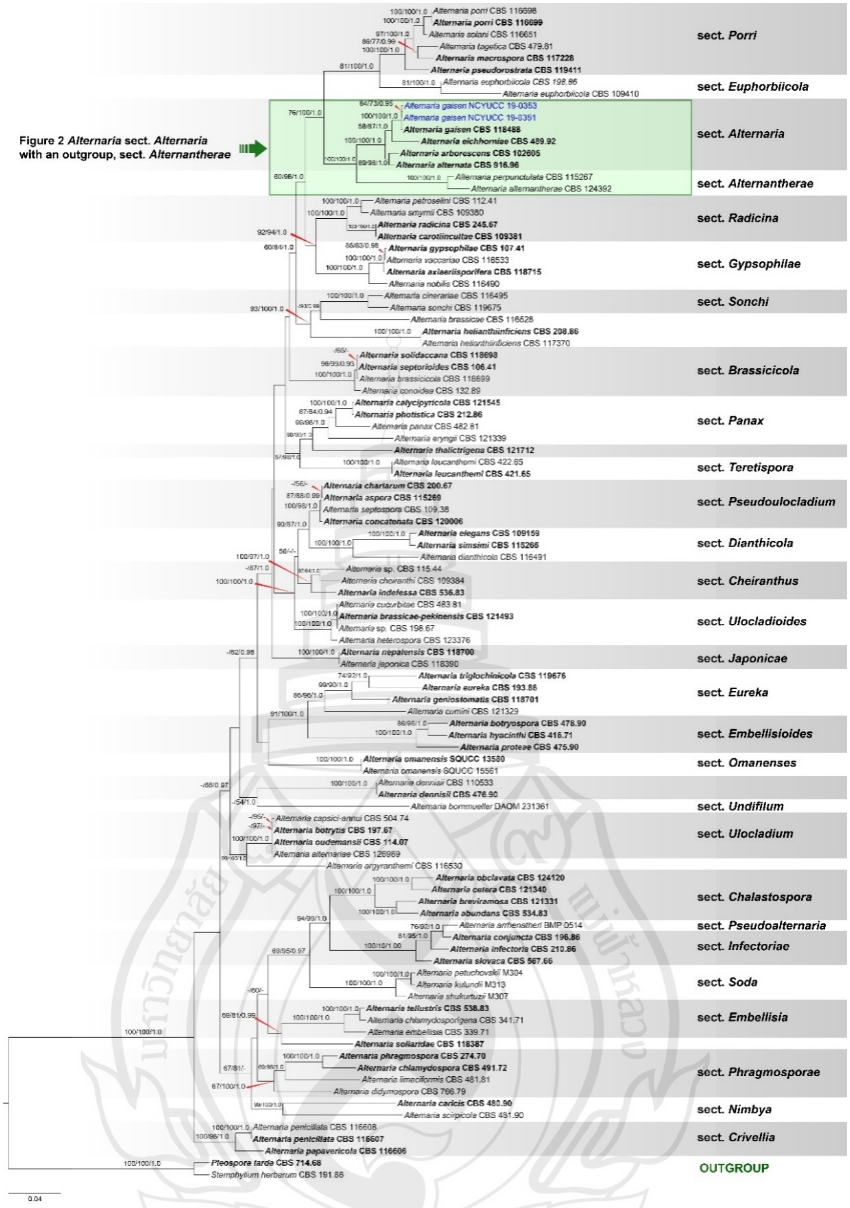
Species	Strain *	Location	Host	GenBank accession numbers								
				SSU	LSU	ITS	*gapdh*	*rpb2*	*ef1α*	*Alta1*	*endoPG*	OPA10-2
A. porri	CBS 116699 [T]			-	-	KJ718218	KJ718053	KJ718391	KJ718564	KJ718727	-	-
A. proteae	CBS 475.90 [T]	Australia	*Protea*	KC584597	KC584339	AY278842	KC584161	KC584464	KC584723	FJ266505	-	-
A. pseudorostrata	CBS 119411 [T]	USA	*Euphorbia pulcherrima*	KC584554	KC584298	JN383483	AY562406	KC584422	KC584680	AY563295	-	-
A. radicina	CBS 245.67 [T]	USA	*Daucus carota*	KC584555	KC584299	KC584213	KC584133	KC584423	KC584681	FN689405	-	-
A. scirpicola	CBS 481.90	England	*Scirpus* sp.	KC584602	KC584344	KC584237	KC584163	KC584469	KC584728	-	-	-
A. septorioides	CBS 106.41 [T]	Netherlands	*Reseda odorata*	KC584559	KC584303	KC584216	KC584136	KC584427	KC584685	-	-	-
A. septospora	CBS 109.38	Italy	wood	KC584620	KC584362	FJ266489	FJ266500	KC584487	KC584747	FJ266515	-	-
A. shukurtuzii	M307	Russia	alkaline soil	KJ443082	KJ443127	KJ443257	KJ649620	KJ443172	-	-	-	-
A. simsimi	CBS 115265 [T]	Argentina	*Sesamum indicum*	KC584560	KC584304	JF780937	KC584137	KC584428	KC584686	JQ905110	-	-
A. slovaca	CBS 567.66 [T]	Slovakia	*Homo sapiens*	KC584576	KC584319	KC584226	KC584150	KC584444	KC584702	-	-	-
A. smyrnii	CBS 109380	England	*Smyrnium olusatrum*	KC584561	KC584305	AF229456	KC584138	KC584429	KC584687	-	-	-
A. solani	CBS 116651	USA	*Solanum tuberosum*	KC584562	KC584306	KC584217	KC584139	KC584430	KC584688	-	-	-
A. soliaridae	CBS 118387 [T]	USA	soil	KC584563	KC584307	KC584218	KC584140	KC584431	KC584689	-	-	-
A. solidaccana	CBS 118698 [T]	Bangladesh	soil	KC584564	KC584308	KC584219	KC584141	KC584432	KC584690	-	-	-
A. sonchi	CBS 119675	Canada	*Sonchus asper*	KC584565	KC584309	KC584220	KC584142	KC584433	KC584691	-	-	-
A. tagetica	CBS 479.81	England	*Tagetes erecta*	KC584566	KC584310	KC584221	KC584143	KC584434	KC584692	KJ718761	-	-
A. tellustris	CBS 538.83 [T]	USA	soil	KC584598	KC584340	MH861643	AY562419	KC584465	KC584724	AY563325	-	-
A. thalictrigena	CBS 121712 [T]	Germany	*Thalictrum* sp.	KC584568	KC584312	EU040211	KC584144	KC584436	KC584694	-	-	-
A. tomato	CBS 103.30	Unknown	*Solanum lycopersicum*	KP125069	KP124599	KP124445	KP124294	KP124915	KP125224	KP123991	KP124151	KP124762
A. tomato	CBS 114.35	Unknown	*Solanum lycopersicum*	KP125070	KP124600	KP124446	KP124295	KP124916	KP125225	KP123992	KP124152	KP124763
A. triglochinicola	CBS 119676 [T]	Australia	*Cycnogeton procerum*	KC584569	KC584313	KC584222	KC584145	KC584437	KC584695	-	-	-
A. vaccariae	CBS 116533	USA	*Vaccaria hispanica*	KC584570	KC584314	KC584223	KC584146	KC584438	KC584696	JQ646386	-	-
Alternaria sp.	CBS 198.67	USA	soil	KC584610	KC584352	AF229487	KC584169	KC584477	KC584737	-	-	-
Alternaria sp.	CBS 115.44	-	*Reseda odorata*	KC584556	KC584300	KC584214	KC584134	KC584424	KC584682	-	-	-
Pleospora tarda	CBS 714.68 [T]	Canada	-	KC584603	KC584345	KC584238	-	-	KC584729	-	-	-
Stemphylium herbarum	CBS 191.86	India	-	GU238232	GU238160	KC584239	-	KC584471	KC584731	-	-	-

Note [T] ex-type strain, strains in this study are in bold.

4.3 Results

4.3.1 Phylogenetic Analysis

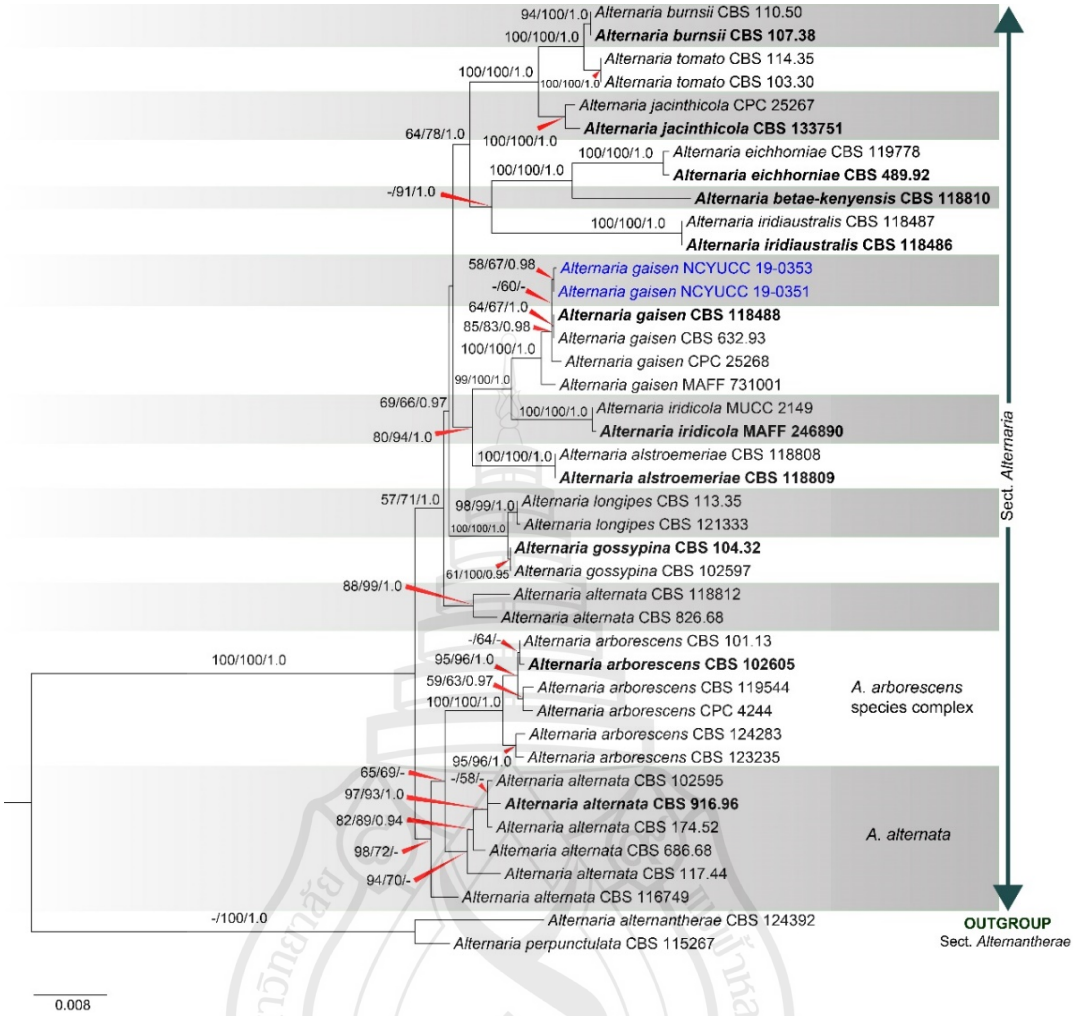
The phylogenetic tree in Figure 4.1 included 99 strains with *Stemphylium herbarum* (CBS 191.86) and *Pleospora tarda* (CBS 714.68) as outgroup. The total number of characters in the dataset was 4352, including alignment gaps, with 1–1010, 1011–1847, 1848–2171, 2172–2329, 2330–2740, 2741–3475, 3476–3490, 3491–3901, 3902–4069, 4070–4293, and 4294–4352 corresponding to SSU, LSU, ITS1+ ITS2, 5.8S, *gapdh*-exon, *rpb2*, *ef1α*-exon, *Alta1*- exon, *gapdh*-intron, *ef1α*-intron, and *Alta1*-intron, respectively. 3063 constant characters, 246 variable characters are parsimony-uninformative, and 1043 characters are parsimony-informative. The trees generated under different optimality criteria based on MP, ML and BI analysis were essentially similar in topology and not significantly different (data not shown). The descriptive statistics generated from MP analysis, TL = 5208, CI = 0.382, RI = 0.709, RC = 0.271, and HI = 0.618. The best scoring likelihood tree selected with a final value for the combined dataset = -31969.718266.



Note Phylogram generated from maximum likelihood analysis based on SSU, LSU, ITS1+ ITS2, 5.8S, gapdh-exon, rpb2, ef1α-exon, Alta1-exon, gapdh-intron, ef1α-intron, and Alta1-intron sequence data of 28 *Alternaria* sections (97 *Alternaria* strains). The tree is rooted to *Stemphylium herbarum* strain CBS 191.86 and *Pleospora tarda* strain CBS 714.68. Maximum parsimony and maximum likelihood bootstrap values ≥50%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/BIPP) are given at the nodes. The species obtained in this study are in blue. Ex-type strains are in bold.

Figure 4.1 Phylogenetic analysis of *Alternaria* sections

The phylogenetic tree in Figure 4.2 included 41 strains, with *Alternaria perpunctulata* (CBS 115267) and *A. alternantherae* (CBS 124392) as outgroup taxa. The total length of the Figure 4.2 dataset was 5293 characters including alignment gaps, 1–1020, 1021–1585, 1586–1912, 1913–2070, 2071–2478, 2479–3338, 3339–3353, 3354–3764, 3765–4208, 4209–4842, 4843–5008, 5009–5233, and 5234–5293 corresponding to SSU, LSU, ITS1+ITS, 5.8S, *gapdh*-exon, *rpb2*, *ef1α*-exon, *Alta1*-exon, *endoPG*, OPA10-2, *gapdh*-intron, *ef1α*-intron, and *Alta1*-intron, respectively. The combined dataset contained 4734 constant, 114 parsimony-uninformative and 445 parsimony-informative characters. The combined dataset was analyzed using MP, ML and BI. The trees generated under different optimality criteria were essentially similar in topology and not significantly different (data not shown). The descriptive statistics generated from MP analysis based on the combined dataset were TL = 791, CI = 0.774, RI = 0.890, RC = 0.688, HI = 0.226. The best scoring likelihood tree selected with a final value for the combined dataset = -12352.288546.



Note Phylogram generated from maximum likelihood analysis based on combined SSU, LSU, ITS1+ ITS2, 5.8S, gapdh-exon, rpb2, ef1α-exon, Alta1-exon, endoPG, OPA10-2, gapdh-intron, ef1α-intron, and Alta1-intron, sequence data for 41 *Alternaria* stains in section *Alternaria*. The tree is rooted to two *Alternaria* stains in section *Alternantherae* (*A. perpunctulata* strain CBS 115267 and *A. alternantherae* strain CBS 124392). Maximum parsimony and maximum likelihood bootstrap values ≥50%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/BIPP) are given at the nodes. The species obtained in this study are in blue. Ex-type strains are in bold.

Figure 4.2 Phylogenetic analysis of *Alternaria* section *Alternaria*

4.3.2 Taxonomy

Alternaria gaisen Nagano ex Hara, Sakumotsubyorigaku, Edn 4: 263 (1928) (Figures 4.3 and 4.4)

MycoBank no: MB 252306

Index Fungorum number: IF252306

Facesoffungi number: FoF08022

≡ *Alternaria gaisen* Nagano, J. Hort. Soc. Japan32(3): 16-19 (1920)

= *Alternaria kikuchiana* S. Tanaka, Memoirs of the Coll. Agric. Kyoto Imper. Univers., Phytopathol. Ser. 28: 27 (1933)

= *Macrosporium nashi* Miura, Flora of Manchuria and East Mongolia, III Cryptogams, Fungi (Industr. Contr. S. Manch. Rly 27): 513 (1928)

Fungus associated with leaf blight of *Ficus microcarpa*. *Symptoms* appeared as circular spots on adaxial and abaxial surface of the leaves, light brown with a pale light center, with fungus spores forming concentric brown rings as they enlarge, with lesions tending to appear first on the margin of leaves as small circular spots. Asexual morph: Hyphomycete. *Conidiophores* 50–100 µm long, septate, simple or sparingly branched, straight to slightly curved, pale to medium brown, with series of 6–12 short, geniculate, sympodial proliferations, gradually enlarging near the apex into a clavate conidiogenous cell, commonly with a terminal cluster of 1–3 conidia. *Conidiogenous cells* mono- to polytretic, clavate, smooth, pale brown, withmedium brown cicatrized conidiogenous loci, produce concatenated conidia, 1–3+ conidia. *Conidia* (15–)20–30(–43) × (9–)11–13(–14) µm ($\bar{x}$ = 24 µm × 11.5 µm, n=30), conspicuously obovoid to spheroid, beaked, pale to dark brown, with 2–6 transverse septa and 1–2 longitudinal or oblique septa, constricted at the septa, usually solitary, straight or slightly curved, with a long ellipsoid to obclavate, simple, pale brown, up to 10–12 µm long and 2–3 µm wide, tapering to beaked apex.

Associated with leaf spot of *Kandelia candel*. *Symptoms* small irregular to subcircular shape, pale brown, slightly sunken spots appear on adaxial surface leaves of *K. candel*, which later expand outwards on the surface of the leaves. Small auburn spots appeared initially and then gradually enlarged, changing to tawny circular ring spots with a dark mahogany border and jagged edge. They were usually >3 circulars, which

occurred on a single affected leaf. In severe cases, lesionsspread evenly on the leaves. Not produce fungalstructure on leaf spot symptom.

Culture characteristics: Colonies on PDA develop well, attaining a diameter of 7.3–7.5 cm under adaily fluorescent light/dark cycle of 8/16 h at 25 °C in 7 d, circular, with evident concentricrings and a whitish aerial-mycelial margin, cottony, greenish to light grey, secreting an orangish pigment into the medium (Figure 4.3P). *Mycelium* 3–4 μm diam, hyaline to pale-brown, smooth,septate. *Conidiophores* arise singly from vegetativehyphae, branches, 1–2 conidiogenous loci, each conidiogenous branch with concatenatedconidia, 1–5+ conidia, the obvious branching is initiated within the chain when a few secondary conidiophores, intercalary conidial pseudorostra, develop with 2–3 conidiogenous loci. *Conidia* inculture (15–)22–28(–44) × (6–)9–12(–18) μm ($\bar{x}$ = 25 × 11.5 μm, n = 30) arising beneath theagar surface or directly from hyphae, formed acropetal chains, conspicuously obovoid to spheroid,tapering to beaked apex, pale to dark brown, with 2–4 transverse septa and 1–2 longitudinal oroblique septa, with outer wall usually smooth, but sometimes are detectably rough (pusticulate) and occasionally definitely tuberculate (Figure 4.3Q–T).

Colonies on PCA similar to those observed on PDA lesion, attaining a diameter of 7.8–8.2 cm under a daily fluorescent light/dark cycle of 8/16 h at 25 °C in 7 d, circular, with evident concentricrings and a whitish aerial-mycelial margin, greenish to light grey. *Mycelium* 2–4 μm diam., pale-brown, smooth, septate. *Conidiophores* arise singly from vegetative hyphae, branches, 1–3 conidiogenous loci(therefore 1–3 conidial chains), each conidiogenousbranch with concatenated conidia, 1–10+ conidia.*Conidia* (10–)22–25(–30) × (6–)10–12(–13) μm ($\bar{x}$ = 22 × 10 μm, n=30), formed acropetal chains, ellipsoid when transverse-septate beginningto form, obovoid to spheroid at stage of distalcell produces 2–3 transverse septa, with 1–3 longitudinal septate (almost 1-septate), smooth, secondary conidiophore with short beaked apex (Figure 4.4A–F).

Colonies on V-8 agar develop well, attaininga diameter of 7.5–8 cm under a daily fluorescent light/dark cycle of 8/16 h at 25 °C in 7 d, circular, with evident concentric rings and a whitish aerial-mycelial margin, cottony, greenish light grey to white at above, secreting an greenish to light grey pigment into the medium. *Mycelium* 3–5 μm diam., hyaline to pale-brown, smooth,septate. *Conidiophores* arise singly from vegetative hyphae, branches, 1–2 conidiogenous loci with conidial chains, each

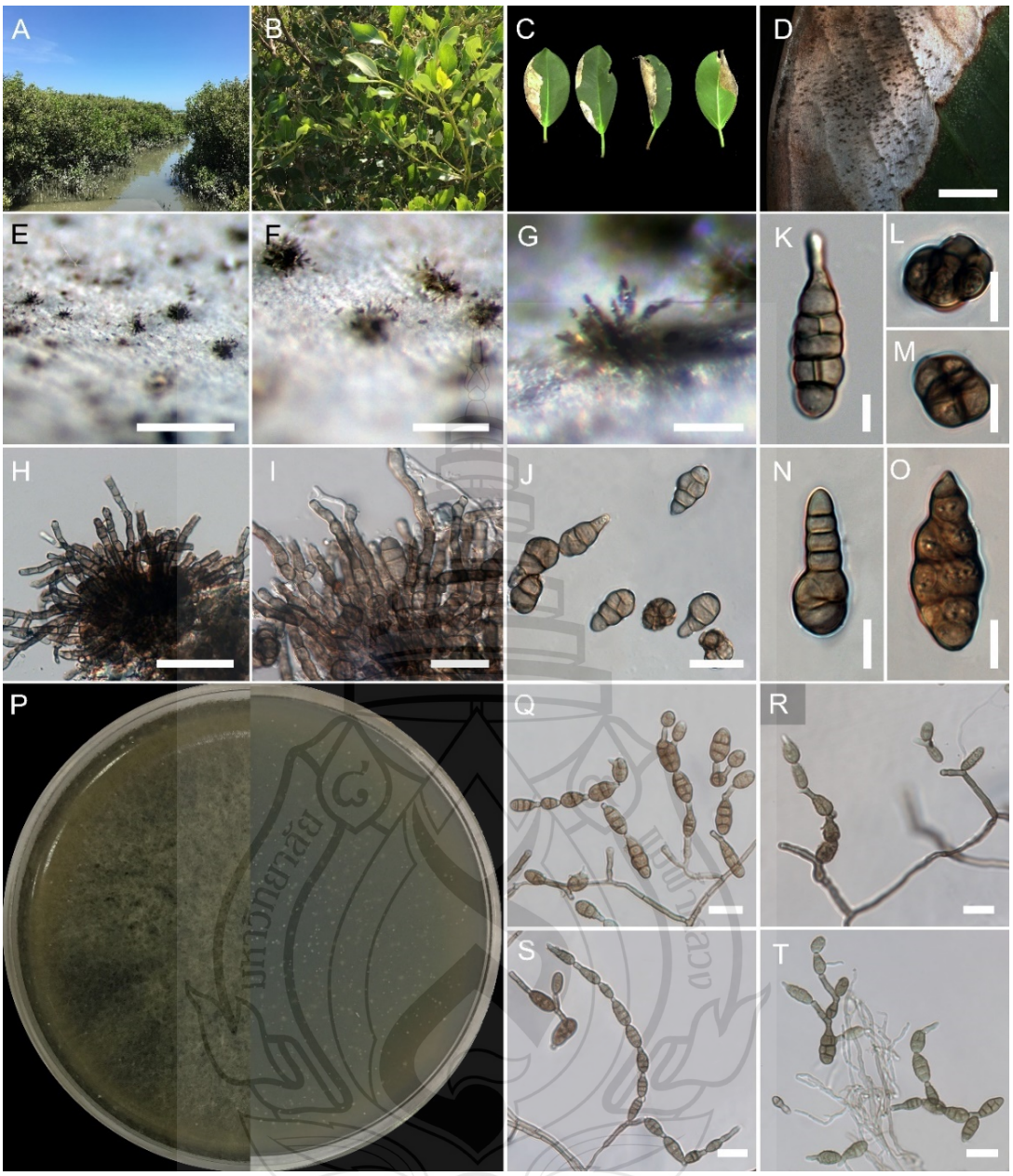
conidiogenous branch with concatenated conidia, 1–5+. *Conidia* (15–)22–25(–35) × (6–)10–12(–13) µm ($\bar{x}$ = 24 × 11 µm, n=30), formed acropetal chains, ellipsoid when transverse septate beginning to form, obovoid to spheroid at stage of distal cell produces 2–5 transverse septate (mostly 3-septate), 1–2 longitudinal septate (almost 1-septate), secondary conidiophore, with smooth, short beaked apex (Figure 4.4G–L).

Material examined: TAIWAN, Tainan, Bei Men Mangrove Reserve, on leaf of *Ficus microcarpa*, 15 Jul 2018, Chada Norphanphoun BM2, dried culture (NCYUCC 19-0351); Taichung, on leaves of *Kandelia candel*, 15 Jul 2018, Chada Norphanphoun TC1-B (NCYUCC 19-0353,), dried culture NCYU herbarium.

Hosts and distributions: *Chimonanthus praecox* (CHINA, Tian et al., 2020), *Fragaria* × *ananassa* (JAPAN, Nishikawa & Nakashima, 2019; Nishikawa & Nakashima, 2020), *Oryza sativa* (PAKISTAN, Akhtar et al., 2014), *Pyrus aromatica* (JAPAN, Watson, 1971), *P. bretschneideri* (CHINA, Wang & Zhang, 2003), (CHINA, Tai, 1979), *P. communis* (UNITED STATES, Wang & Zhang, 2003), *P. pyrifolia* (JAPAN, Andersen et al., 2001; Gobashy et al., 2018; Moslemi et al., 2017; Simmons, 2007; Woudenberg et al., 2013; Woudenberg et al., 2015), (KOREA Andersen et al., 2001; Yu, 2001), (TAIWAN, Andersen et al., 2001), *P. pyrifolia* var. *culta* (JAPAN, Nishikawa & Nakashima, 2019; Nishikawa & Nakashima, 2020), *P. serotina* (FRANCE, Baudry et al., 1993), (JAPAN, Andrew et al., 2009; Watson, 1971), (KOREA, Cho & Shin, 2004), *Pyrus* sp. (CHINA, Zhang, 2003; Zhuang, 2005), (UNITED STATES, Sun & Zhang, 2008), (TAIWAN), *P. ussuriensis* (CHINA, Tai, 1979).

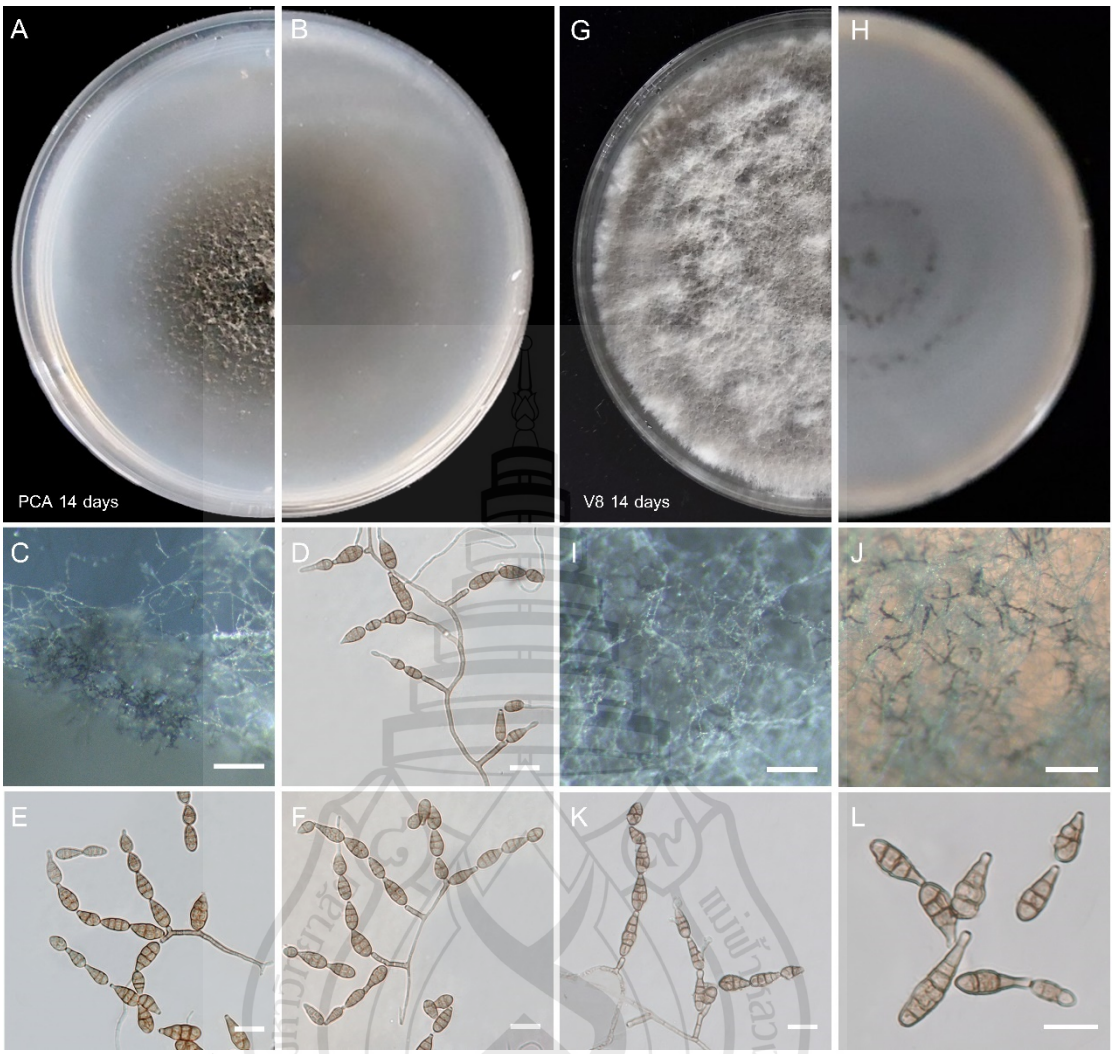
Notes: *Alternaria gaisen* was first reported from black spot disease of Japanese pear (*Pyrus pyrifolia*) by Nagano (1920). Later, it was reported with a wide host range as fungal invaders of fruits and leaves on *Chimonanthus praecox* (Calycanthaceae), *Oryza sativa* (Poaceae), and *Pyrus* spp. (Rosaceae). This species was placed in the section *Alternaria* based on molecular analysis (Lawrence et al., 2013). Our isolates were collected from Bei-Men Mangrove Reserve, a mangrove restoration area in Tainan, and mangrove area in Taichung, Taiwan. Phylogenetic analyses demonstrated that the new isolates are a known species, *A. gaisen*, with high bootstrap support (Figures 4.1 and 4.2). The morphology of the new isolates is similar to *A. gaisen* with Alternaria- shape and short beaked conidia in chain was produced with 8–10 conidia,

and branched at 1–3 conidiogenous loci (Table 4.2). However, the conidial size of the new isolates was smaller than *A. gaisen*, which is listed in Table 4.2. Phylogenetic analyses and morphological characters indicated that our isolates are *A. gaisen*. The morphological characters of species related in this study are mentioned in Table 4.2 (Nishikawa & Nakashima, 2020; Simmons, 1999).



Note *Alternaria gaisen* (NCYUCC 19-0351). a, b Habitat. c Leaf blight on *Ficus macrocarpa*. d-g Conidiomata on host surface. h, i Conidiomata. j-o Conidia. p Culture characters on PDA (leftabove, right-reverse). q-t Mycelium with conidia from cultures on PDA. Bars: d 2000 mm; e 500 μm; f 300 μm; g 100 μm; h 50 μm; i, j, q, s, t 20 μm; k-o, r 10 μm.

Figure 4.3 Morphological characters of *Alternaria gaisen* (NCYUCC 19-0351)



Note *Alternaria gaisen* (NCYUCC 19-0351). a, b Culture characters on PCA with 14 days (a-above, b-reverse). c Mycelium with conidia from cultures on PCA. d-f Conidia, conidiophores, and sporulation patterns from cultures on PCA. g, h Culture characters on V-8 agar with 14 days (g-above, h-reverse). i, j Mycelium with conidia from cultures on V-8 agar. k, l Conidia, conidiophores, and sporulation patterns from culture on V-8 agar. Bars: c, i, j 200 μm; d–f, k, l 20 μm.

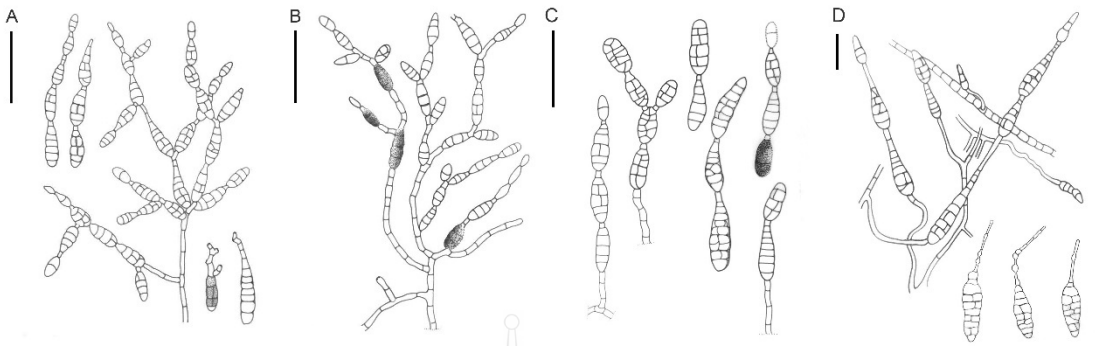
Figure 4.4 Morphological characters of *Alternaria gaisen* (NCYUCC 19-0351)

Table 4.2 Comparison of morphological characteristics of *Alternaria* species related to this study

Species	Conidia			Media	References
	Size (µm)	Shape	Septation		
A. arborescens	12–30(–42) ×7–11	Ovoid to ellipsoid, pale brown to brown, formed conidial chains with branched	1–4 transverse, 0–2 longitudinal septa	PCA	Simmons (2007)
A. alternata	10–30 × 5–12	Ovoid to ellipsoid, pale-yellow to golden brown, formed conidial chains with short secondary conidiophore, branched	4–7 transverse septa, a few, or no longitudinal septa	PCA	Simmons (2007)
A. gaisen	(10–)22–25(–30) × (6–)10–12(–13)	Ellipsoid when transverse septate beginning to form, obovoid to spheroid at stage of distal cell produces secondary conidiophores, pale to dark brown, formed conidial chains of 1–10+ conidia and branched (1–3 conidial chain)	2–4 transverse septa, with 1–3 longitudinal septate (almost 1-septate)	PCA	This study
A. gaisen	30–45(–55) × 13–15(–18)	Obclavate, oblong-ovate or rarely, smooth, or sometimes verrucose, olive-brown, formed conidial chains of 5–8 conidia and branched, 1–3 conidiogenous loci	5–8 transverse, 0–1(–2) longitudinal septa in each transverse	PCA	Simmons (2007)
A. iridicola	28–311 × 7–38 (total) 21–127 × 7–38 (bodies)	Ovoid, ellipsoid to broadly obclavate, or sometimes beakless small oval, pale brown to yellowish brown, formed conidial chains of 3–4 conidia, unbranched	2–16 transverse septa, 0–11 longitudinal septa	PCA	Nishikawa and Nakashima (2014)

Table 4.3 GenBank BLAST search of *Alternaria gaisen,* a new record species in this study

Genes	GenBank BLAST search against type material			
	Species identified	**Strain no.**	**Accession no.**	**Identities (I), Query cover (QC)**
SSU	*A. oudemansii* (sect. *Ulocladium*)	CBS 114.07	NG_067644	100% (I), 100% (QC)
	A. botrytis (sect. *Ulocladium*)	CBS 197.67	NG_067640	100% (I), 100% (QC)
	A. leucanthemi (sect. *Teretispora*)	CBS 421.65	NG_067639	100% (I), 100% (QC)
	A. papavericola (sect. *Crivellia*)	CBS 116606	NG_067636	100% (I), 100% (QC)
	A. iridiaustralis (sect. *Alternaria*)	CBS 118486	NG_063035	100% (I), 100% (QC)
LSU	*A. alstroemeriae* (sect. *Alternaria*)	CBS 118809	MH874589	100%(I), 99% (QC)
	A. aspera (sect. *Pseudoulocladium*)	CBS 115269	MH874542	99.66%(I), 99% (QC)
	A. alternata (= *A. angustiovoidea*, sect. *Alternaria*)	CBS 195.86	MH873628	99.89%(I), 99% (QC)
	A. helianthiinficiens	CBS 208.86	MH873632	99.66%(I), 99% (QC)
	A. planifunda (sect. *Embellisia*)	CBS 537.83	MH873356	99.55%(I), 99% (QC)
ITS	*A. perpunctulata* (sect. *Alternantherae*)	CBS 115267	NR_151838	100% (I), 100% (QC)
	A. alternata (= *A. angustiovoidea*, sect. *Alternaria*)	CBS 195.86	MH861939	94.46% (I), 100% (QC)
	A. alternata (= *A. destruens*, sect. *Alternaria*)	ATCC 204363	NR_137143	94.46% (I), 100% (QC)
	A. iridiaustralis (sect. *Alternaria*)	CBS 118486	NR_136120	94.26% (I), 100% (QC)
	A. alstroemeriae (sect. *Alternaria*)	CBS 118809	NR_163686	94.26% (I), 100% (QC)
gapdh	*A. arborescens* (sect. *Alternaria*)	CBS 102605	AY278810	99.66% (I), 97% (QC)
	A. alternata (= *A. daucifolii*, sect. *Alternaria*)	CBS 118812	KC584112	99.65% (I), 97% (QC)
	A. alstroemeriae (sect. *Alternaria*)	CBS 118809	KP124154	99.48% (I), 97% (QC)
	A. alternata (= *A. rhadina*, sect. *Alternaria*)	CBS 595.93	JQ646316	99.65% (I), 97% (QC)
	A. alternata (= *A. citriarbusti*, sect. *Alternaria*)	SH-MIL-8s	JQ646322	99.65% (I), 97% (QC)
rpb2	*A. pseudoeichhorniae* (sect. *Alternaria*)	MFLUCC 18-1589	MH853717	98.5% (I), 87% (QC)
	A. arborescens (sect. *Alternaria*)	CBS 102605	KC584377	98.5% (I), 87% (QC)
	A. alternata (= *A. daucifolii*, sect. *Alternaria*)	CBS 118812	KC584393	98.15% (I), 87% (QC)
	A. prunicola (sect. *Alternaria*)	MFLUCC 18-1597	MH853722	98.03% (I), 87% (QC)
	A. alstroemeriae (sect. *Alternaria*)	CBS 118809	KP124765	98.8% (I), 75% (QC)
ef1α	*A. alternata* (= *A. daucifolii*, sect. *Alternaria*)	CBS 118812	KC584652	98.33% (I), 99% (QC)
	A. iridiaustralis (sect. *Alternaria*)	CBS 118486	KP125214	97.88% (I), 98% (QC)
	A. betae-kenyensis (sect. *Alternaria*)	CBS 118810	KP125197	97.49% (I), 99% (QC)
	A. burnsii (sect. *Alternaria*)	CBS 107.38	KP125198	97.49% (I), 99% (QC)
	A. eichhorniae (sect. *Alternaria*)	CBS 489.92	KP125204	97.07% (I), 99% (QC)
Alt a 1	*A. alstroemeriae* (sect. *Alternaria*)	CBS 118809	MH084526	97.46% (I), 89% (QC)
	A. acalyphicola (sect. *Porri*)	CBS 541.94	JQ905109	97.25% (I), 89% (QC)
	A. agripestis (sect. *Porri*)	CBS 577.94	JQ905112	97.03% (I), 89% (QC)
	A. aragakii (sect. *Porri*)	CBS 594.93	JQ905107	97.03% (I), 89% (QC)
	A. alternata (= *A. rhadina*, sect. *Alternaria*)	CBS 595.93	JQ646399	97.03% (I), 89% (QC)
endoPG	*A. arborescens* (sect. *Alternaria*)	EGS 39.128	AY295028	96.95% (I), 100% (QC)
	A. alstroemeriae (sect. *Alternaria*)	CBS 118809	KP123994	97.32% (I), 97% (QC)
	A. burnsii (sect. *Alternaria*)	CBS 107.38	KP124124	97.1% (I), 97% (QC)
	A. cerealis (sect. *Alternaria*)	CBS 119544	KP124112	96.88% (I), 97% (QC)
	A. arborescens (sect. *Alternaria*)	EGS 39.128	KP275780	96.86% (I), 97% (QC)
OPA10-2	*A. alternata* (= *A. citriarbusti*, sect. *Alternaria*)	SH-MIL-8s	EF504044	99.21% (I), 100% (QC)
	A. arborescens (sect. *Alternaria*)	CBS 102605	KP124712	96.53% (I), 100% (QC)
	A. arborescens (sect. *Alternaria*)	EGS 39.128	EF504052	96.53% (I), 100% (QC)
	A. alstroemeriae (sect. *Alternaria*)	CBS 118809	KP124602	96.21% (I), 100% (QC)
	A. burnsii (sect. *Alternaria*)	CBS 107.38	KP124734	96.05% (I), 99% (QC)



Note Drawing of morphological characteristics comparison of *Alternaria* species related to this study. a-c redrawn from Simmons (2007). d redrawn from Elliott (1917) and Nishikawa and Nakashima (2019). a *A. alternata*. b *A. arborescens*. c *A. gaisen*. d *A. iridicola*. Bars: a-d 50 μm.

Figure 4.5 Morphological characters of *Alternaria* species related to this study

4.4 Discussion

The new host record of *Alternaria gaisen* was isolated from leaf blight of *Ficus microcarpa* and leaf spots of *Kandelia candel* in Taiwan mangroves. *Alternaria* species have overlapping morphological traits even within section and species level. Sequence data is therefore essential to identify these species and clarify species sections. Previous studies used multi-gene sequence data to provide a better resolution for *Alternaria* species *viz*. SSU, LSU, ITS, *gapdh*, *rpb2*, *ef1α*, *Alta1*, *endoPG*, and OPA10-2 gene regions and else (Al Ghafri et al., 2019; Lawrence et al., 2013, 2014, 2016; Nishikawa & Nakashima, 2020; Woudenberg et al., 2015). In this study the combined gene trees were considered, while greatly facilitated species level identification provided better resolution. Morphological and phylogenetic evidence with a MEGA BLAST search showing percent of identities (I), and query cover (QC) (Table 4.3). Based on the results of our phylogenetic analyses the new isolates clustered within sect. *Alternaria* in Figure 4.1, and also grouped with *A. gaisen* and *A. iridicola* species group with a high moderate suport in Figure 4.2 (99% MP/100% ML/1.0 BS), which is the phylogenetic tree that included only strains of sect. *Alternaria*. *Alternaria iridicola* was

distinguished from our isolates based on morphology of ovoid, ellipsoid to broadly obclavate shapedwith sometimes beakless small oval and large conidia (28–311 × 7–38 µm), and multi-transverse septa (2–16), and longitudinal septa (0–11), with unbranched conidial chains. The morphology of *A. alternata*, and *A. arborescens* were compared to determine the species identification, which weresimilar to our isolates with conidial size (10–30 × 5–12 µm, 12–30(–42) ×7–11 µm, respectively), number of transverse and longitudinal conidia septa (Table 4.2, Figure 4.4). The comparison was based on an identification manual of *Alternaria* by Simmons (2007). However, our isolates can easily be distinguished from *A. alternata* and *A. arborescens* using molecular data (Figure 4.2). Thus, our isolates are identified as *A. gaisen* as mentioned the evidencein notes of species.

This study has located a species of *Alternaria* that associated with leaf blight of *F. microcarpa* and leaf spot of *K. candel* in Taiwan mangroves. This indicates that fungi on mangroves may act as aninoculum for adjacent agricultural and horticultural crops. It would be interesting to establish if other fungi on mangroves can also act in this way. The new collections of *A. gaisen* described in this paper was found from mangrove plants in Taiwan and this is the first record of *A. gaisen* on *F. microcarpa* and *K. candel* in Taiwan. Many fungal species were found in Taiwan's mangroves in recent years especially marine mangrove fungi (Hyde et al., 2020a; Pang, 2009). Pathogenicity testing on various hosts is needed to confirm the pathogenic affinity of the taxon.

CHAPTER 5

DIFFERENTIATION OF SPECIES COMPLEXES IN *PHYLLOSTICTA* ENABLES BETTER SPECIES RESOLUTION[4]

Abstract

Phyllosticta species have worldwide distribution and are pathogens, endophytes, and saprobes. Taxa have also been isolated from leaf spots and black spots of fruits. Taxonomic identification of *Phyllosticta* species is challenging due to overlapping morphological traits and host associations. Herein, we have assembled a comprehensive dataset and reconstructed a phylogenetic tree. We introduce six species complexes of *Phyllosticta* to aid the future resolution of species. We also introduce a new species, *Phyllosticta rhizophorae* isolated from spotted leaves of *Rhizophora stylosa* in mangrove forests of Taiwan. Phylogenetic analysis based on combined sequence data of ITS, LSU, *efl*α, *act* and *gapdh* loci coupled with morphological evidence support the establishment of the new species. We synonymize strains of *P. capitalensis* (CPC 20508 and CPC20509) under the new species. Six strains (CBS 173.77, CBS 119720, CPC 17748, CPC 20252, CPC 20269, and CBS 123404) are unnamed species based on phylogenetic analyses and nucleotide polymorphisms and probably represent new species. The phylogenetic relationships of *Phyllosticta* species are reappraised and suggestions are given for future work.

Keywords: 1 New Species, Microfungi, Morphology, Phylogenetic Analysis, Phyllostictaceae, Rhizophoraceae, Synonym, Taxonomy

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5.1 Introduction

Mangroves are forests situated in intertidal zones in tropical and subtropical backwaters, estuaries, deltas, and lagoons. They are important for wetland ecosystems providing numerous valuable services to the marine environment. Mangroves provide protection to coastal communities against natural hazards such as cyclones, tsunamis, and shoreline erosion (Saenger, 2002; FAO 2007). Mangroves are found in Africa, North and Central America and Asia, including Taiwan (Alias & Jones, 2009; Alias et al., 2010). The fungi in mangoves are important in nutrient cycling helping to provide detritus and nutrients for mangrove inhabitants (Hyde & Jones, 1988; Hyde & Lee, 1998; Hyde et al., 1998; Thatoi et al., 2012). However, there have been no detailed diversity studies of terrestrial mangrove ecosystems in comparison to other environments (Beger et al., 2010).Previous studies have reported endophytic fungi on mangrove trees (Doilom et al., 2017; Rashmi et al., 2019). For example, Thatoi et al. (2013) reported more than 200 species of endophytic fungi from mangroves in India, Kumar et al. (2019) described *Neopestalotiopsis alpapicalis* on *Rhizophora apiculata* and *R. mucronata* from Thailand, and Norphanphoun et al. (2019) established new species of *Neopestalotiopsis*, *Pestalotiopsis*, and *Pseudopestalotiopsis* speciesfrom leaf spot and asymptomatic leaves from mangrove plants in Thailand. Several studies have also reported on fungal pathogens of mangroves. For example, leaf spots disease caused by pathogenic fungi include *Anthostomella* on *Rhizophora mangle* in Puerto Rico (Stevens, 1920), *Cercospora* on *R. mangle* in Florida (McMillan, 1964), *Pestalotiopsis* sp., *Colletotrichum* sp., and *Polystigma sonneratiae* on *Rhizophora* sp. (Hyde & Cannon, 1992; Xu et al., 2009), and *Pseudocercospora avicenniae* on *Avicennia marina* (Shivas et al., 2009). Other diseases include heart and butt rot disease caused by *Heterobasidion annosum, Ganoderma, Phellinus* sp., and *Inonotus* sp. on *Rhizophora* sp. (Ryvarden, 2000; Fox, 2001; Sakayaroj et al., 2012), canker and dieback caused by *Phytophthora cinnamomi* on *Rhizophora* sp. (Vollbrecht et al., 1995; Barnard, 2000; Kinge & Mih, 2011). *Cytospora* species have been associated with dead branches of *Lumnitzera racemosa, Xylocarpus granatum* and *X. moluccensis* in Thailand (Norphanphoun et al., 2018).

In 1995, mangrove areas in Taiwan covered 287 ha, which represents only a tiny proportion of the total area of mangroves worldwide (Hsueh, 1995). Four mangrove plant species are found in Taiwan, all of which have been declared endangered. These are *Avicennia marina*, *Lumnitzera racemose*, *Kandelia candel* and *Rhizophora stylosa* (Fan, 2002; Pang et al., 2011). Previous restoration efforts of mangroves in Taiwan have been only partially successful and deforestation continues with annual declines of mangrove cover. One of the reasons for the decline is ineffective disease management (Hsueh, 1995; Fan, 2002; Pang et al., 2011). Several organisms are responsible for causing diseases of mangrove plants, including fungi. Fungi associated with the intertidal part of mangroves in Taiwan are relatively poorly studied and data on diseases of mangroves are sparse. The taxa collected from mangrove areas in Taiwan have mostly been saprobic marine fungi (Panget al., 2011). Since mangroves in Taiwan represent a negligible proportion of the total mangrove area worldwide, therefore, very few authors have focused on mangrove research in the area (Fan, 2002; Pang et al., 2011).

Phyllosticta was introduced by Persoon (1818) and belongs to Phyllostictaceae in Botryosphaeriales (Hongsanan et al., 2020a; Wijayawardene et al., 2020). *Phyllosticta* is an earlier name of the asexual morph *Guignardia* introduced by Viala and Ravaz (1892). The earlier nametakes precedence based on the International Code for Nomenclature of Algae, Fungi and Plants (http://www.iapttaxon.org/nomen/main.php?page=title). Currently, the number of records of *Phyllosticta* in search engines is higher than that of *Guignardia* (Google Scholar, Index Fungorum, Species Fungorum, MycoBank and GenBank). *Phyllosticta* species are endophytes but are also associated with leaf spots of numerous plants and have a worldwide distribution on a wide range of plants (Okane et al., 2003; Glienke et al., 2011; Wikee et al., 2011, 2013b; Rashmi et al., 2019). Thereare 3,210 epithets of *Phyllosticta* listed in Index Fungorum 2020 (April 18, 2020). van der Aa (1973) described 46 species of *Phyllosticta* with 12 sexual and 17 spermatial morphs. van der Aa and Vanev (2002) revised all species of *Phyllosticta* and accepted 190 epithets. Wikee et al. (2013b) recognized 170 species names based on multi-locus analysis and introduced Phyllostictaceae to accommodate *Phyllosticta*. Previously, many examined isolates of *Phyllosticta* were identified based on a combination of morphological data and

phylogenetic analysis (Guarnaccia et al., 2017; Tran et al., 2019). However, sequence data from type material is not available for many species of *Phyllosticta*, and thus additional research studies focusing on neo- or epitypification are required in order to clarify their taxonomic placement. Evolutionary relationships within *Phyllosticta* are also unclear, despite intensive study (Delsuc et al., 2005). Thus, further analyses using larger datasets in terms of both taxa and loci are necessary to improve phylogenetic resolution within *Phyllosticta*. These approaches have been used successfully for other fungal taxa (Rokas & Carroll, 2005).

Herein, we have assembled a comprehensive dataset of five loci containing all species denoted as *Phyllosticta* in GenBank. Based on the resulting phylogenetic tree, we introduce six workable species complex clades. A new species, *Phyllosticta rhizophorae* is also introduced from Taiwan. Two published strains of *P. capitalensis* are synonymized under the new species. Six strains of *P. capitalensis* are treated as unnamed species based on nucleotide polymorphisms and phylogenetic evidence. Seventeen strains are excluded from *Phyllosticta* based on BLAST searches and phylogenetic placement.

5.2 Materials and Methods

5.2.1 Sample Collection and Specimen Examination

Fresh leaf samples were collected in 2018, from *Rhizophora stylosa* from Shicao, Taiwan. Fresh specimens were taken to the laboratory in paper bags, examined and described following the methods in Norphanphoun et al. (2017). Morphological characters of conidiomata were examined using a Zeiss Axioskop 2 *plus* compound microscope (Carl Zeiss Microscopy, LLC, NY, USA). Micro-morphology was studied using a Zeiss Axioskop 2 mot *plus* compound microscope (Carl Zeiss Microscopy, LLC, NY, USA). All image measurements were made with the ZEN2 (blue edition) software. Photo-plates were made using Adobe Photoshop CC 2019 version: 20.0.1 20181029.r.41 2018/010/29: 1197484 × 64 (Adobe Systems, CA, USA).

Cultures were obtained using the tissue isolation method outlined in Norphanphoun et al. (2018). Single hyphal tips were transferred onto 2% potato agar

(PA) plates and flasks at room temperature (25 °C ± 2) throughout a two-week period: 24hr dark for asexual morph, and 24hr light for sexual morph. Culture characteristics were examined and recorded after 5, 7, 14 and 30 days. Morphological characters in culture were examined throughout the cultivation period. Pure cultures were maintained on PA for further studies. Dried and living cultures have been deposited in the Department of Plant Medicine, National Chiayi University, Taiwan (NCYU) and duplicates in culture collection at Mae Fah Luang University (MFLUCC), Chiang Rai, Thailand. Facesoffungi numbers were obtained as in Jayasiri et al. (2015).

5.2.2 Pathogenicity Testing

Healthy leaves (leaves attached on branches) of *Rhizophora stylosa* were washed with distilled water, wiped with 70% ethanol, dried with sterile tissue paper, and covered with sterile wet cotton at the base of branch stalks. To test Koch's postulates, we followed the inoculation methods of Than et al. (2008). Eight experiments with three replications each were designed for this study. Of these, four were conducted using wounded leaves by pricking them with a pin, and another four using unwounded leaves. Mycelium plugs (0.7 mm diam) of 14-day-old colonies on PDA were used for experiment 1: wounded leaves + mycelium plugs; experiment 2: unwounded leaves + mycelium plugs; experiment 3: spore suspension (5×10^4/ml) from 14-day-old colonies on PA was used for wounded + spores suspension; and experiment 4: unwounded + spores suspension. Sterile water and PDA agar plugs served as control treatments as follows; experiment 5: wounded + PDA agar; experiment 6: unwounded + PDA agar; experiment 7: wounded + sterile water; and experiment 8: unwounded + sterile water. All experiments were kept individually in moist chambers for 1 week and observed for symptom expression every other day. After 7 days, if positive, the fungus was re-isolated from any tissue showing lesions and the isolate was considered to be pathogenic; absence of symptoms on leaves classified the isolate as non-pathogenic.

5.2.3 DNA Extraction, PCR Amplification and Sequencing

Genomic DNA was extracted from fresh fungal mycelia growing on PA at room temperature (25 °C ± 2) for two weeks using an E.Z.N.A ® Fungal DNA Mini Kit, D3390-02, (Omega Bio-tek, Inc., GA) following the manufacturer' s protocols. Polymerase chain reactions (PCR) were carried out using the following primer pairs:

ITS1/ITS4 to amplify the internal transcribed spacer region (ITS) (White et al., 1990), LROR/LR5 for the 28S large subunit ribosomal RNA gene (LSU) (White et al., 1990), act512F/act738R for *actin* (*act*) (Carbone & Kohn, 1999), Gpd1-LM/Gpd2-LM for partial glyceraldehyde-3-phosphate dehydrogenase region (*gapdh*) (Myllys et al., 2002).

The amplification reactions were carried out using the following protocol: 50 µL reaction volume containing 2 µl of DNA template, 2 µL (10 µM stock concentration) of each forward and reverse primers, 25 µl of 2 × Power Taq PCR MasterMix (Tri-I Biotech, Taipei, Taiwan) and 19 µl of double-distilled water (ddH_2O). The PCR thermal cycling program for each locus is described in Table 5.1. PCR products were analysed using 1.5% agarose gels containing the Safeview DNA stain (GeneMark, Taipei, Taiwan) to confirm presence of amplicons at the expected molecular weight. Purification and sequencing of PCR products with the amplification primers mentioned above were carried out at Tri-I Biotech, Taipei, Taiwan.

Table 5.1 Polymerase chain reactions (PCR) thermal cycling programs for each locus

Gene	Primers	PCR thermal cycle protocols*
ITS	ITS1/ ITS4	ID 95 °C for 3 min, 40 cycles of D at 95 °C for 30 s, A at 55 °C for 50 s, E at 72 °C for 1 min, FE at 72 °C for 7 min
LSU	LROR/ LR5	ID 95 °C for 3 min, 34 cycles of D at 95 °C for 30 s, A at 51 °C for 50 s, E at 72 °C for 1 min, FE at 72 °C for 10 min
act	act512F/ act738R	ID 95 °C for 5 min, 40 cycles of D at 95 °C for 40 s, A at 58 °C for 30 s, E at 72 °C for 1 min, FE at 72 °C for 5 min
gapdh	Gpd1-LM/ Gpd2-LM	ID 94 °C for 5 min, 40 cycles of D at 94 °C for 30 s, A at 52 °C for 30 s, E at 72 °C for 30s, FE at 72 °C for 7 min

Note *ID: initial denaturation; D = denaturation; A = annealing; E = elongation; FE = final extension

5.2.4 Phylogenetic Analysis

Raw reads were edited and assembled into contigs using Geneious® version 11.1.5 (http://www.geneious.com). The new sequences were used as queries to perform BLASTn against the nr database in GenBank. Similar sequences were retrieved, and multiple alignments were built. GenBank taxonomy browser was also used to check all sequences assigned as *Phyllosticta* in the database. ITSx 1.1, a Perl based software tool was used to extract ITS1, 5.8S and ITS2 sequences (Bengtsson-Palme et al., 2013). BioEdit version 7.2.3 (Hall, 1999) was used to assign open reading frames of protein coding sequence of β-tubulin, and *ef1α*, according to reference sequences in GenBank database. Combined sequence data of all loci were used to perform maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference analysis (BI). Two datasets were created. Dataset one consisted of 195 taxa (outgroup: *Botryosphaeria obtusa* strain CMW 8232 and *B. stevensii* strain CBS 112553), while dataset two was a subset of dataset one containing 74 strains (outgroup: *P. cordylinophila* strain MFLUCC 10-0166 and *P. cordylinophila* strain MFLUCC 12-0014). Outgroup sequences were selected based on preliminary analysis and results from the multigene phylogeny of dataset one. All taxa used for these analyses can be found in Table 5.3. *Phyllosticta abietis* (AF312012) was not included in the analyses because only the ITS locus was available.

Sequences were aligned for each locus separately using the MAFFT v. 7.110 online program (http://mafft.cbrc.jp/alignment/server/; Katoh & Standley, 2013). TrimAl (available on Phylemon 2.0 platform, Sánchez et al., 2011) was used to trim ambiguously aligned positions. BioEdit v. 7.0.5.3 was used for further manual adjustments wherever necessary (Hall, 1999). A partition homogeneity test (PHT) was performed with PAUP* 4.0b10 to determine congruency of genes and whether they could be combined (Swofford, 2002). The combined sequence alignments were obtained from MEGA v. 7.0.14 and v. 10.1.0 (Kumar et al., 2018). Geneious Prime® 2019.2.1 was used to convert file format to NEXUS for MP and BI analyses (http://www.geneious.com).

Maximum parsimony analysis was performed using the CIPRES Science Gateway web server (PAUP on XSEDE; Miller et al., 2010), with 1000 bootstrap replicates using heuristic search with random stepwise addition and tree-bisection

reconnection (TBR) algorithm. Maximum trees were set to 1000 and branches of zero length were collapsed. The following descriptive tree statistics were calculated: parsimony tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC) and homoplasy index (HI). For ML and BI analyses, the data were partitioned as follows: ITS1+ITS2, 5.8S, LSU, *ef1α*-exon, *act*-exon, *gapdh*, *ef1α*-intron, *act*-intron. The software RAxML-HPC2 on XSEDE (Miller et al., 2010) was used to run ML analysis as implemented in the CIPRES Science Gateway web server, 1000 rapid bootstrap replicates were run using the GTRGAMMA model of nucleotide evolution. Bayesian inference analysis was performed using the Markov Chain Monte Carlo (MCMC) algorithm as implemented in CIPRES Science Gateway web server (MrBayes on XSEDE; Miller et al., 2010). The best-fit nucleotide substitution model for each partition was separately determined using MrModeltest version 2.2 (Table 5.2; Nylander, 2004). Posterior probabilities were computed by running two runs with four chains each starting from random tree topology. 20,000,000 and 2,500,000 generations were run for dataset one and two, respectively. Trees were sampled every 100 generations. 25% of the trees were discarded as burn-in value with average standard deviation of split frequencies converged under 0.01 (Ronquist et al., 2012).

The phylogram was visualized in FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software /figtree/; Rambaut, 2014) and made in Adobe Illustrator CC version 23.0.1 (64-bit) and Adobe Photoshop CC version 20.0.1 release (Adobe Systems, CA, the USA). Newly generated sequences in this study are deposited in GenBank (Table 5.3). The finalized alignments and trees were deposited in TreeBASE, Figure 5.1: submission ID: 26535, Figure 5.2: submission ID: 26536.

Table 5.2 The best-fit nucleotide substitution model for each dataset, selected by AIC in MrModeltest 2.2

Genes / Models	ITS1+ ITS2	5.8S	LSU	*ef1α* (exon)	*act* (exon)	*gapdh*	*ef1α* (intron)	*act* (intron)
F81					●			●
F81+I			●					
GTR						●		
GTR+G					○			
GTR+I+G	○		○			○	○	
HKY							●	
HKY+G								○
JC		●						
K80				●				
SYM	●							
SYM+G		○		○				

Note ○ Best-fit nucleotide substitution model for Figure 5.1

● Best-fit nucleotide substitution model for Figure 5.2

Table 5.3 GenBank Accession numbers of the sequences used for phylogenetic analysis in this study

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
Botryosphaeria obtusa	CMW 8232	Conifers	South Africa	AY972105	-	DQ280419	AY972111	-
B. stevensii	CBS 112553	culture from isotype of *Diplodia mutila*	Not given	AY259093	AY928049	AY573219	-	-
Phyllosticta abieticola	CBS 112067	*Abies concolor*	Canada	KF170306	EU754193	-	KF289238	-
P. acaciigena	CPC 28295 T	*Acacia suaveolens*	Australia	KY173433	KY173523	-	KY173570	-
P. aloeicola	CPC 21020 T	*Aloe ferox*	South Africa	KF154280	KF206214	KF289193	KF289311	KF289124
P. aloeicola	CPC 21021	*Aloe ferox*	South Africa	KF154281	KF206213	KF289194	KF289312	KF289125
P. ardisiicola	NBRC 102261 T	*Ardisia crenata*	Japan	AB454274	-	-	AB704216	-
P. aristolochiicola	BRIP 53316 T	*Aristolochia acuminata*	Australia	JX486129	-	-	-	-
P. aspidistricola	NBRC 102244 T	*Aspidistra elatior*	Japan	AB454314	-	-	AB704204	-
P. aucubae-japonicae	MAFF 236703 T	*Aucuba japonica*	Japan	KR233300	-	KR233310	KR233305	-
P. austroafricana	CBS 144593 T	leaf spots of unidentified deciduous tree	South Africa	MK442613	MK442549	MK442704	MK442640	-
P. azevinhi	MUCC0088	*Ilex pedunculosa*	Japan	AB454302	-	-	AB704226	-
P. beaumarisii	CBS 535.87	*Muehlenbekia adpressa*	Australia	NR_145235	NG_058040	KF766429	KF306232	KF289074
P. bifrenariae	CBS 128855 T	*Bifrenaria harrisoniae*	Brazil	JF343565	KF206209	JF343586	JF343649	JF343744
P. bifrenariae	CPC 17467	*Bifrenaria harrisoniae*	Brazil	KF170299	KF206260	KF289207	KF289283	KF289138
P. brazilianiae	LGMF 330 T	*Mangifera indica*	Brazil	JF343572	KF206217	JF343593	JF343656	JF343758
P. brazilianiae	LGMF 334	*Mangifera indica*	Brazil	JF343566	KF206215	JF343587	JF343650	JF343752
P. camelliae	MUCC0059	*Camellia japonica*	Japan	AB454290	-	-	AB704223	-

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. capitalensis	CBS 226.77	*Paphiopedilum callosum*	Germany	FJ538336	KF206289	FJ538394	FJ538452	JF343718
P. capitalensis	CBS 356.52	*Ilex* sp.	Not given	FJ538342	KF206300	FJ538400	FJ538458	KF289087
P. capitalensis	CBS 100175	*Citrus* sp.	Brazil	FJ538320	KF206327	FJ538378	FJ538436	JF343699
P. capitalensis	CBS 101228	*Nephelium lappaceum*	Hawaii	FJ538319	KF206325	FJ538377	FJ538435	KF289086
P. capitalensis	CBS 114751	*Vaccinium* sp.	New Zealand	EU167584	EU167584	FJ538407	FJ538465	KF289088
P. capitalensis	CBS 115047	*Aspidosperma polyneuron*	Brazil	FJ538323	KF206318	FJ538381	FJ538439	KF289077
P. capitalensis	CBS 115049	*Bowdichia nitida*	Brazil	FJ538324	KF206317	FJ538382	FJ538440	KF289084
P. capitalensis	CBS 117118	*Musa acuminata*	Indonesia	FJ538339	JQ743603	FJ538397	FJ538455	KF289090
P. capitalensis	CBS 120428	*Sansevieria* sp.	Netherlands	JN692544	KF206315	JN692532	JN692520	JN692509
P. capitalensis	CBS 123373	*Musa paradisiaca*	Thailand	FJ538341	JQ743604	FJ538399	FJ538457	JF343703
P. capitalensis	CBS 128856 T	*Stanhopea* sp.	Brazil	JF261465	KF206304	JF261507	JF343647	JF343776
P. capitalensis	CPC 11867	*Acacia crassicarpa*	Thailand	KF206181	KF206283	KF289184	KF289260	KF289108
P. capitalensis	CPC 13987	*Protea repens*	Portugal	KF206183	KF206281	KF289176	KF289263	KF289083
P. capitalensis	CPC 14609	*Zyzygium* sp.	Republic of Madagascar	KF206184	KF206280	KF289175	KF289264	KF289081
P. capitalensis	CPC 16590	*Citrus limon*	Argentina	KF206185	KF206272	KF289177	KF289271	KF289091
P. capitalensis	CPC 16591	*Citrus limon*	Argentina	KF206186	KF206271	KF289179	KF289272	KF289093
P. capitalensis	CPC 16592	*Citrus limon*	Argentina	KF206187	KF206270	KF289178	KF289273	KF289092
P. capitalensis	CPC 17468	*Cymbidium* sp.	Brazil	KF206188	KF206259	KF289189	KF289284	KF289120
P. capitalensis	CPC 20251	Wild plant	Thailand	KC291333	KF206252	KC342553	KC342530	KF289101
P. capitalensis	CPC 20253	*Scheffera venulosa*	Thailand	KF206192	KF206250	KF289181	KF289293	KF289102
P. capitalensis	CPC 20254	*Saccharum officinarum*	Thailand	KC291335	KF206249	KC342555	KC342532	KF289103
P. capitalensis	CPC 20255	Arecaceae	Thailand	KC291336	KF206248	KC342556	KC342533	KF289115

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. capitalensis	CPC 20256	*Ophiopogon japonicus*	Thailand	KC291337	KF206247	KC342557	KC342534	KF289089
P. capitalensis	CPC 20257	*Ficus benjamina*	Thailand	KC291338	KF206246	KC342558	KC342535	KF289099
P. capitalensis	CPC 20258	*Ophiopogon japonicus*	Thailand	KC291339	KF206245	KC342559	KC342536	KF289094
P. capitalensis	CPC 20259	Orchidaceae	Thailand	KC291340	KF206244	KC342560	KC342537	KF289104
P. capitalensis	CPC 20263	Magnoliaceae	Thailand	KC291341	KF206241	KC342561	KC342538	KF289085
P. capitalensis	CPC 20265	Euphobiaceae	Thailand	KF206194	KF206239	KF289182	KF289297	KF289105
P. capitalensis	CPC 20266	*Polyscias* sp.	Thailand	KC291342	KF206238	KC342562	KC342539	KF289109
P. capitalensis	CPC 20267	*Baccaurea ramiflora*	Thailand	KF206195	KF206237	KF289173	KF306233	KF289078
P. capitalensis	CPC 20268	*Hibiscus syriacus*	Thailand	KC291343	KF206236	KC342563	KC342540	KF289117
P. capitalensis	CPC 20270	*Tectona grandis*	Thailand	KC291345	KF206234	KC342565	KC342542	KF289110
P. capitalensis	CPC 20271	*Crinum asiaticum*	Thailand	KF206196	KF206233	KF289183	KF289298	KF289106
P. capitalensis	CPC 20272	Orchidaceae	Thailand	KC291346	KF206232	KC342566	KC342543	KF289079
P. capitalensis	CPC 20274	*Mangifera indica*	Thailand	KF206197	KF206231	KF289188	KF289299	KF289119
P. capitalensis	CPC 20275	*Polyalthia longifolia*	Thailand	KC291347	KF206230	KC342567	KC342544	KF289107
P. capitalensis	CPC 20278	*Euphorbia milii*	Thailand	KC291348	KF206227	KC342568	KC342545	KF289113
P. capitalensis	CPC 20423	*Philodendron* sp.	Thailand	KC291349	KF206226	KC342569	KC342546	KF289116
P. capitalensis	CPC 20510	*Pyrrosia adnascens*	Thailand	KF206200	KF206223	KF289174	KF289304	KF289080
P. capitalensis	LGMF 219	*Citrus sinensis*	Brazil	KF206202	KF206220	JF261490	KF289306	JF343737
P. capitalensis	LGMF 220	*Citrus sinensis*	Brazil	KF206203	KF206219	JF261488	KF289307	JF343735
P. capitalensis	LGMF 222	*Citrus sinensis*	Brazil	KF206204	KF206218	JF261492	KF289308	JF343739
P. carissicola	CPC 25665T	*Carissa macrocarpa*	South Africa	KT950849	KT950863	KT950879	KT950872	KT950876
P. carochlae	CGMCC 3.17317T	*Caryota ochlandra*	China	K J847422	-	KF289178	KF289273	KF289092
P. carochlae	CGMCC 3.17318	*Caryota ochlandra*	China	KJ847423	-	KJ847444	KJ847430	KJ847438
P. catimbauensis	URM 7672 T	*Mandevilla catimbauensis*	Brazil	MF466160	MF466163	MF466155	MF466157	-

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. catimbauensis	URM 7674	*Mandevilla catimbauensis*	Brazil	MF466161	MF466164	MF466153	MF466158	-
P. cavendishii	BRIP 57384	*Musa* cv. Lady Finger	Australia	KC117644	KU697330	KF009695	KF014059	KU716085
P. cavendishii	BRIP 57383	*Musa* cv. Lady Finger	Australia	KC117643	KU697329	KF009694	KF014058	KU716084
P. citriasiana	CBS 120486T	*Citrus maxima*	Thailand	FJ538360	KF206314	FJ538418	FJ538476	JF343686
P. citriasiana	CBS 120487	*Citrus maxima*	China	FJ538361	KF206313	FJ538419	FJ538477	JF343687
P. citribraziliensis	CBS 100098T	*Citrus limon*	Brazil	FJ538352	KF206221	FJ538410	FJ538468	JF343691
P. citribraziliensis	CPC 17466	*Citrus* sp.	Brazil	KF170302	KF206261	KF289226	KF289282	KF289161
P. citricarpa	CBS 127454T	*Citrus limon*	Australia	JF343583	KF206306	JF343604	JF343667	JF343771
P. citricarpa	CBS 127455	*Citrus sinensis*	Australia	JF343584	KF206305	JF343605	JF343668	JF343772
P. citrichinaensis	ZJUCC 200956T	*Citrus reticulata*	China	JN791620	-	JN791459	JN791533	-
P. citrichinaensis	ZJUCC 2010150	*Citrus maxima*	China	JN791662	-	JN791514	JN791582	-
P. citrimaxima	MFLUCC 10-0137T	*Citrus maxima*	Thailand	KF170304	KF206229	KF289222	KF289300	KF289157
P. concentrica	CBS 937.70	*Hedera helix*	Italy	FJ538350	KF206291	FJ538408	KF289257	JF411745
P. concentrica	CPC 18842T	*Hedera* sp.	Italy	KF170310	KF206256	KF289228	KF289288	KF289163
P. conjac	MUCC0410	*Amorphophallus rivieri*	Japan	AB454342	-	-	AB704239	-
P. cordylinophila	MFLUCC 10-0166T	*Cordyline fruticosa*	Thailand	KF170287	KF206242	KF289172	KF289295	KF289076
P. cordylinophila	MFLUCC 12-0014	*Cordyline fruticosa*	Thailand	KF170288	KF206228	KF289171	KF289301	KF289075
P. cornicola	CBS 111639	*Cornus florida*	USA	KF170307	-	-	KF289234	-
P. cruenta	CBS 858.71	*Polygonatum odoratum*	Czech Republic	MG934458	-	MG934501	MG934465	MG934474
P. cruenta	MUCC0206	*Polygonatum odoratum* var. *pluriflorum*	Japan	AB454331	-	-	AB704237	-
P. cryptomeriae	KACC 48643	*Juniperus chinensis* var. *sargentii*	Not given	MK396559	-	-	-	-
P. cryptomeriae	MUCC0028	*Cryptomeria japonica*	Japan	AB454271	-	-	AB704213	-

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. cussonia	CPC 14873T	*Cussonia* sp.	South Africa	JF343578	KF206279	JF343599	JF343662	JF343764
P. cussonia	CPC 14875	*Cussonia* sp.	South Africa	JF343579	KF206278	JF343600	JF343663	JF343765
P. elongata	CBS 126.22T	*Oxycoccus macrocarpos*	USA	FJ538353	-	FJ538411	FJ538469	KF289164
P. ericarum	CBS 132534T	*Erica gracilis*	South Africa	KF206170	KF206253	KF289227	KF289291	KF289162
P. eugeniae	CBS 445.82T	*Eugenia aromatica*	Indonesia	AY042926	KF206288	KF289208	KF289246	KF289139
P. fallopiae	MUCC0113T	*Fallopia japonica*	Japan	AB454307	-	-	AB704228	-
P. fallopiae	ISOJ61	-	Not given	MF164545	-	-	-	-
P. foliorum	CBS 174.77	*Cryptomeria japonica*	USA	KF170308	KF206290	KF289200	KF289245	KF289131
P. foliorum	CBS 447.68T	*Taxus baccata*	Netherlands	KF170309	KF206287	KF289201	KF289247	KF289132
P. gardeniicola	MUCC0117	*Gardenia jasminoides*	Japan	AB454310	-	-	AB704230	-
P. gardeniicola	MUCC0089	*Gardenia jasminoides*	Japan	AB454303	-	-	-	-
P. gaultheriae	CBS 447.70T	*Gaultheria humifusa*	USA	JN692543	KF206298	JN692531	KF289248	JN692508
P. hagahagaensis	CBS 144592T	*Carissa bispinosa*	South Africa	MK442614	MK442550	MK442705	MK442641	MK442657
P. hakeicola	CBS 143492T	*Hakea* sp.	Australia	MH107907	MH107953	MH108025	MH107984	MH107999
P. hamamelidis	MUCC149	*Hamamelis japonica*	Japan	KF170289	-	-	KF289309	-
P. harai	MUCC0038	*Aucuba japonica*	Japan	AB454277	-	-	AB704218	-
P. harai	MUCC0043	*Aucuba japonica*	Japan	AB454281	-	-	AB704219	-
P. hostae	CGMCC 3.14355T	*Hosta plantaginea*	China	JN692535	-	JN692523	JN692511	JN692503

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. hostae	CGMCC 3.14356	*Hosta plantaginea*	China	JN692536	-	JN692524	JN692512	JN692504
P. hubeiensis	CGMCC 3.14986 T	*Viburnum odoratissimim*	China	JX025037	-	JX025042	JX025032	JX025027
P. hubeiensis	CGMCC 3.14987	*Viburnum odoratissimim*	China	JX025038	-	JX025043	JX025033	JX025028
P. hymenocallidicola	CBS 131309 T	*Hymenocallis littoralis*	Australia	JQ044423	JQ044443	KF289211	KF289242	KF289142
P. hymenocallidicola	CPC 19331	*Hymenocallis littoralis*	Australia	KF170303	KF206254	KF289212	KF289290	KF289143
P. hypoglossi	CBS 101.72	*Ruscus aculeatus*	Italy	FJ538365	KF206326	FJ538423	FJ538481	JF343694
P. hypoglossi	CBS 434.92 T	*Ruscus aculeatus*	Italy	FJ538367	KF206299	FJ538425	FJ538483	JF343695
P. ilicis-aquifolii-aquifolii	CGMCC 3.14358 T	*Ilex aquifolium*	China	JN692538	-	JN692526	JN692514	-
P. ilicis-aquifolii-aquifolii	CGMCC 3.14359	*Ilex aquifolium*	China	JN692539	-	JN692527	JN692515	-
P. illicii	24_1_1 T	*Illicium verum*	China	MF198235	MF198240	MF198237	MF198243	-
P. illicii	16_16_1	*Illicium verum*	China	MF198234	MF198239	MF198236	MF198242	-
P. iridigena	CBS 143410 T	*Iris* sp.	South Africa	MG934459	-	MG934502	MG934466	-
P. kerriae	MAFF 240047 T	*Kerria japonica*	Japan	AB454266	-	-	-	-
P. kobus	MUCC0049	*Magnolia kobus*	Japan	AB454286	-	-	AB704221	-
P. leucothoicola	MUCC553 T	*Leucothoe catesbaei*	Japan	AB454370	AB454370	-	KF289310	-
P. ligustricola	MUCC0024 T	*Ligustrum obtusifolium*	Japan	AB454269	-	-	AB704212	-
P. maculata	CPC 18347 T	*Musa* cv. Golygoly pot-pot	Australia	JQ743570	-	KF009700	KF014016	-
P. maculata	BRIP 46622	*Musa* cv. Golygoly pot-pot	Australia	JQ743567	-	KF009692	KF014013	-
P. mangiferae	IMI 260576 T	*Mangifera indica*	India	JF261459	KF206222	JF261501	JF343641	JF343748
P. mangiferae	CPC 20260	Arecaceae	Thailand	KF206193	KF206243	KF289187	KF289294	KF289114
P. mangifera-indicae	MFLUCC 10-0029 T	*Mangifera indica*	Thailand	KF170305	KF206240	KF289190	KF289296	KF289121
P. mimusopisicola	CBS 138899 T	*Mimusops zeyheri*	South Africa	KP004447	MH878626	-	-	-
P. minima	CBS 585.84 T	*Acer rubrum*	USA	KF206176	KF206286	KF289204	KF289249	KF289135
P. miurae	MUCC0065	*Lindera praecox*	Japan	AB454291	-	-	AB704224	-
P. musaechinensis	GZAAS 6.1247	*Musa*.sp.	China	KF955294	-	KM816639	KM816627	KM816633

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. musaechinensis	GZAAS 6.1384	*Musa*.sp.	China	KF955295	-	KM816640	KM816628	KM816634
P. musarum	BRIP 57803	*Musa* sp	Malaysia	JX997138	-	KF009737	KF014055	-
P. musarum	BRIP 58028	*Musa* sp	Australia	KC988377	-	KF009738	KF014054	-
P. neopyrolae	CPC 21879 T	*Pyrola asarifolia*	Japan	AB454318	AB454318	-	AB704233	-
P. ophiopogonis	KACC 47754	*Ophiopogon japonicus*	South Korea	KP197057	-	-	-	-
P. ophiopogonis	LrLF11	Leaf of *Lycoris radiata*	China	MG543713	-	-	-	-
P. owaniana	CBS 776.97 T	*Brabejum stellatifolium*	South Africa	FJ538368	KF206293	FJ538426	KF289254	JF343767
P. owaniana	CPC 14901	*Brabejum stellatifolium*	South Africa	JF261462	KF206303	JF261504	KF289243	JF343766
P. pachysandricola	MUCC124 T	*Pachysandra terminalis*	Japan	AB454317	AB454317	-	AB704232	-
P. paracapitalensis	CPC 26517 T	*Citrus floridana*	Italy	KY855622	KY855796	KY855951	KY855677	KY855735
P. paracapitalensis	CPC 26518	*Citrus floridana*	Italy	KY855623	KY855797	KY855952	KY855678	KY855736
P. paracapitalensis	CPC 26700	*Citrus floridana*	Italy	KY855624	KY855798	KY855953	KY855679	KY855737
P. paracapitalensis	CPC 26701	*Citrus floridana*	Italy	KY855625	KY855799	KY855954	KY855680	KY855738
P. paracapitalensis	CPC 26805	*Citrus floridana*	Italy	KY855626	KY855800	KY855955	KY855681	KY855739
P. paracapitalensis	CPC 26806	*Citrus floridana*	Italy	KY855627	KY855801	KY855956	KY855682	KY855740
P. paracapitalensis	CPC 28120	*Citrus limon*	Spain	KY855628	KY855802	KY855957	KY855683	KY855741
P. paracapitalensis	CPC 28121	*Citrus limon*	Spain	KY855629	KY855803	KY855958	KY855684	KY855742
P. paracapitalensis	CPC 28122	*Citrus limon*	Spain	KY855630	KY855804	KY855959	KY855685	KY855743
P. paracapitalensis	CPC 28123	*Citrus limon*	Spain	KY855631	KY855805	KY855960	KY855686	KY855744
P. paracapitalensis	CPC 28127	*Citrus limon*	Spain	KY855632	KY855806	KY855961	KY855687	KY855745
P. paracapitalensis	CPC 28128	*Citrus limon*	Spain	KY855633	KY855807	KY855962	KY855688	KY855746
P. paracapitalensis	CPC 28129	*Citrus limon*	Spain	KY855634	KY855808	KY855963	KY855689	KY855747

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. paracitricarpa	CPC 27169 T	*Citrus limon*	Greece	KY855635	KY855809	KY855964	KY855690	KY855748
P. paracitricarpa	ZJUCC 200933	*Citrus sinensis*	China	JN791626	KY855813	JN791468	JN791544	KY855752
P. parthenocissi	CBS 111645 T	*Parthenocissus quinquefolia*	USA	EU683672	-	JN692530	JN692518	-
P. partricuspidatae	NBRC 9466 T	*Parthenocissus tricuspidata*	Japan	KJ847424	-	KJ847446	KJ847432	KJ847440
P. partricuspidatae	NBRC 9757	*Parthenocissus tricuspidata*	Japan	KJ847425	-	KJ847447	KJ847433	KJ847441
P. paxistimae	CBS 112527 T	*Paxistima mysinites*	USA	KF206172	KF206320	KF289209	KF289239	KF289140
P. philoprina	CBS 587.69	*Ilex aquifolium*	Spain	KF154278	KF206297	KF289206	KF289250	KF289137
P. philoprina	CBS 616.72	*Ilex aquifolium*	Germany	KF154279	KF206296	KF289205	KF289251	KF289136
P. podocarpi	CBS 111646	*Podocarpus falcatus*	South Africa	AF312013	KF206323	KC357671	KC357670	KF289169
P. podocarpi	CBS 111647	*Podocarpus lanceolata*	South Africa	KF154276	KF206322	KF289232	KF289235	KF289168
P. podocarpicola	CBS 728.79 T	*Podocarpus maki*	USA	KF206173	KF206295	KF289203	KF289252	KF289134
P. pseudotsugae	CBS 111649	*Pseudotsuga menziesii*	USA	KF154277	KF206321	KF289231	KF289236	KF289167
P. pyrolae	IFO 32652	*Erica carnea*	Not given	AB041242	-	-	-	-
P. rhizophorae	CPC 20508	*Ixora chinensis*	Thailand	KF206198	KF206225	KF289185	KF289302	KF289111
P. rhizophorae	CPC 20509	*Cordyline fruticosa*	Thailand	KF206199	KF206224	KF289186	KF289303	KF289112
P. rhizophorae	**NCYUCC 19-0352 T**	***Rhizophora stylosa***	**Taiwan**	**MT360030**	**MT360039**	**-**	**MT363248**	**MT363250**
P. rhizophorae	**NCYUCC 19-0358**	***Rhizophora stylosa***	**Taiwan**	**MT360031**	**MT360040**	**-**	**MT363249**	**MT363250**
P. rhodorae	CBS 901.69	*Rhododendron* sp.	Netherlands	KF206174	KF206292	KF289230	KF289256	KF289166
P. rubella	CBS 111635 T	*Acer rubrum*	USA	KF206171	EU754194	KF289198	KF289233	KF289129
P. schimae	CGMCC 3.14354 T	*Schima superba*	China	JN692534	-	JN692522	JN692510	JN692506
P. schimicola	CGMCC 3.17319 T	*Schima superba*	China	KJ847426	-	KJ847448	KJ847434	KJ854895
P. schimicola	CGMCC 3.17320	*Schima superba*	China	KJ847427	-	KJ847449	KJ847435	KJ854896

Table 5.3 (continued)

Species	Strain no.*	Host	Country	GenBank no.				
				ITS	LSU	*ef1α*	*act*	*gapdh*
P. speewahensis	BRIP 58044 T	Orchids	Australia	KF017269	-	KF017268	-	-
P. sphaeropsoidea	CBS 756.70	*Aesculus hippocastanum*	Germany	AY042934	KF206294	KF289202	KF289253	KF289133
P. spinarum	CBS 292.90	*Chamaecyparis pisifera*	France	JF343585	KF206301	JF343606	JF343669	JF343773
P. styracicola	CGMCC3.14985 T	*Styrax grandiflorus*	China	JX025040	-	JX025045	JX025035	JX025030
P. styracicola	CGMCC3.14989	*Styrax grandiflorus*	China	JX025041	-	JX025046	JX025036	JX025031
P. telopeae	CBS 777.97 T	*Telopea speciosissima*	Tasmania	KF206205	KF206285	KF289210	KF289255	KF289141
P. vaccinii	ATCC 46255 T	*Vaccinium macrocarpon*	-	KC193585	-	KC193582	KC193580	KC193583
P. vaccinii	LC 2795	*Vitis macrocarpon*	USA	KR233323	-	-	-	-
P. vacciniicola	CPC 18590 T	*Vaccinium macrocarpum*	USA	KF170312	KF206257	KF289229	KF289287	KF289165
P. vitis-rotundifoliae	CGMCC 3.17322 T	*Vitis rotundifolia*	USA	KJ847428	-	KJ847450	KJ847436	KJ847442
P. vitis-rotundifoliae	CGMCC 3.17321	*Vitis rotundifolia*	USA	KJ847429	-	KJ847451	KJ847437	KJ847443
P. yuccae	CBS 112065	*Yucca elephantipes*	USA	KF206175	-	-	KF289237	-
P. yuccae	CBS 117136	*Yucca elephantipes*	New Zealand	JN692541	KF766385	JN692529	JN692517	JN692507
Phyllosticta sp.	CPC 11336	*Eucalyptus globulus*	Spain	KF206177	KF206284	KF289199	KF289258	KF289130
Phyllosticta sp.	MUCC147	*Rhododendron keiskei*	Japan	AB454319	AB454319	-	AB704234	-
Phyllosticta sp.	CPC 20269	*Ophiopogon japonicus*	Thailand	KC291344	KF206235	KC342564	KC342541	KF289118
Phyllosticta sp.	CBS 173.77	*Citrus aurantiifolia*	New Zealand	KF206179	KF306231	FJ538393	KF289244	KF289100
Phyllosticta sp.	CBS 123404	*Musa paradisiaca*	Thailand	FJ538333	JQ743601	FJ538391	FJ538449	KF289095
Phyllosticta sp.	CPC 17748	*Heliconia* sp.	Thailand	KF206190	KF206258	KF289180	KF289286	KF289096
Phyllosticta sp.	CPC 20252	*Punica granatum*	Thailand	KC291334	KF206251	KC342554	KC342531	KF289097
Phyllosticta sp.	CBS 119720	*Musa acuminata*	USA	KF206178	KF206316	FJ538398	KF289240	KF289098

Note *T = ex-type strain.

5.3 Results

5.3.1 Phylogenetic Analysis

The results from the partition homogeneity tests (PHT) were not significant (level ≥95%) for either phylogenetic tree, indicating that the individual datasets were congruent and could be combined. Phylogenetic trees from single loci were also generated (Figures 5.4–5.8) to examine topology and clade support. In this study, we introduce six clades as species complexes containing extant species of *Phyllosticta*.

Phylogenetic analysis using ITS (479 bp) – most species clades were recovered as in the combined gene tree, except for *Phyllosticta mimusopisicola*, which grouped within *P. capitalensis* species complex (Figure 5.4).

Phylogenetic analysis using LSU (763 bp) – species complex clades of *P. rhodorae* and *P. vaccinii* clustered within the *P. capitalensis* species complex. Some members of *P. cruenta* species complex clustered within the *P. capitalensis* species complex. *Phyllosticta concentrica* species complex clade was a well-resolved clade and sister to a clade consisting of the *P. capitalensis, P. cruenta, P. vaccinii*, and *P. rhodorae* species complexes. *Phyllosticta owaniana* species complex was paraphyletic (Figure 5.5).

Phylogenetic analysis using *ef1α* (285 bp) – most species in *P. capitalensis* species complex clustered together, except for *P. brazilianiae, P. ilicis-aquifolii, P. philoprina, P. brazilianiae*, and *P. mangifera-indicae.* Species grouping in *P. cruenta* species complex were dispersed throughout the tree, and clustered with species from other clades. Members of clades *P. concentrica, P. owaniana, P. rhodorae*, and *P. vaccinii* formed a well-resolved cluster (Figure 5.6).

Phylogenetic analysis using *act* (223 bp) – *P. capitalensis* species complex was recovered as in the combined gene tree and included species of *P. vaccinii* species complex (*P. vaccinii*, and *P. vacciniicola*). The *P. rhodorae, P. concentrica,* and *P. owaniana* species complexes were well-resolved and clustered together. Species of *P. cruenta* species complex did not cluster together (Figure 5.7).

Phylogenetic analysis using *gapdh* (623 bp) – Members of *P. capitalensis* species complex dispersed in the tree. However, *Phyllosticta capitalensis, P.*

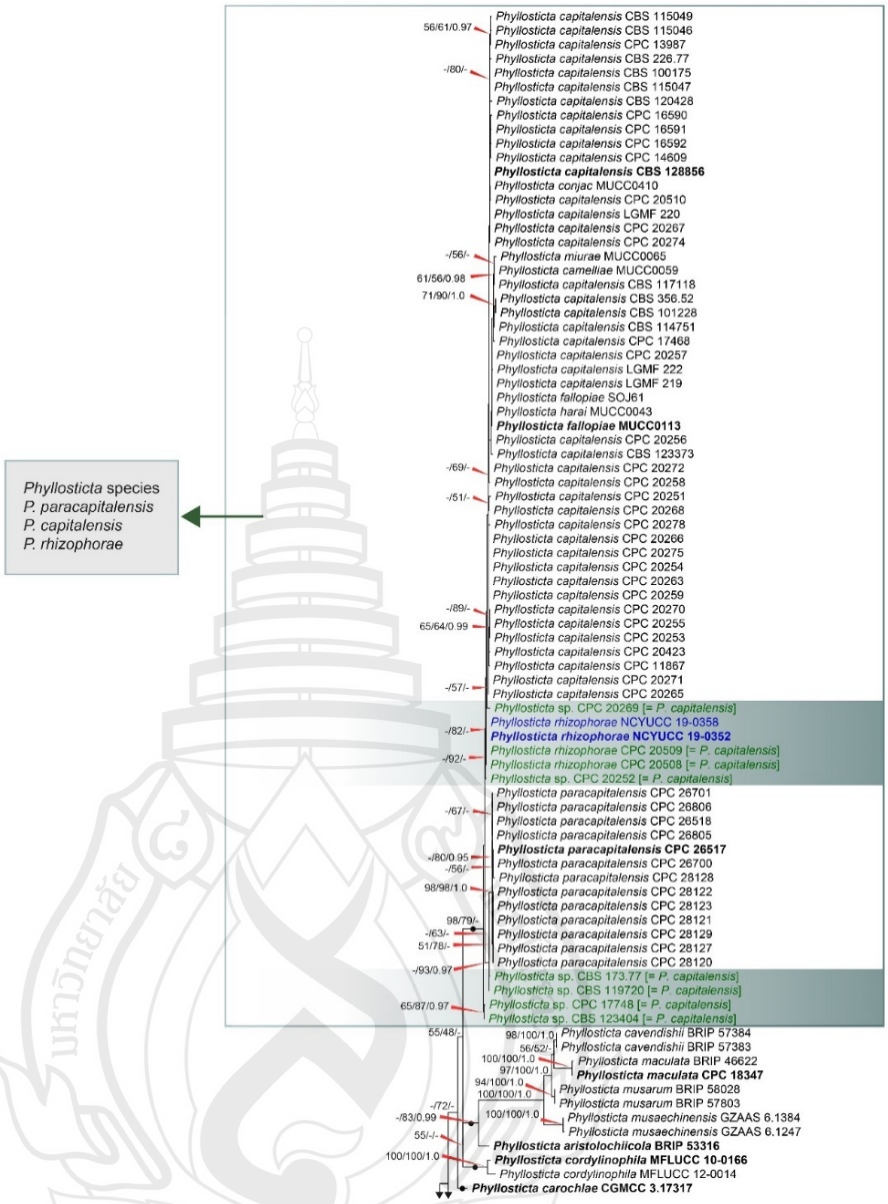
paracapitalensis, and *P. rhizophorae* clustered within the same clade as in other single gene trees. *Phyllosticta cruenta* species complex was paraphyletic with some species grouping with *P. capitalensis* species complex (*P. folliorum*), *P. vaccinii* species complex (*P. vaccinii*, and *P. vacciniicola*) and *P. rhodorae* species complex (*P. rhodorae*). *Phyllosticta podocarpicola* did not cluster within the clade. *Phyllosticta concentrica* species complex formed a well-resolved clade (Figure 5.8).

Phylogenetic analysis using the five-gene combined dataset 1 – consisted of 195 strains and *Botryosphaeria obtusa* (CMW 8232) and *B. stevensii* (CBS 112553) sequences were used as outgroup. The total length of the dataset was 2373 characters including alignment gaps, ITS1+ITS2: 1–321, 5. 8S: 322–479, LSU: 480–1242, *ef1α* (exon): 1243–1296, *act* (exon): 1297–1372, *gapdh*: 1373–1995, *ef1α* (intron): 1996–2226, and *act* (intron): 2227–2373. The combined dataset contained 1493 constant, 156 parsimony uninformative and 724 parsimony informative characters. The combined dataset was analyzed using MP, ML and BI. The trees generated under different optimality criteria were similar in topology and did not differ (data not shown). Descriptive statistics generated from MP analysis based on the combined dataset were TL = 3451, CI = 0.402, RI = 0.839, RC = 0.337, HI = 0.598. The best scoring likelihood tree for the combined dataset had a final value of -20730.513137 (Figure 5.1). The new species grouped within *P. capitalensis* species complex clade along with two other sequences that are denoted as *P. capitalensis* in GenBank. Statistical support for the *P. capitalensis* species complex was 52% ML/0.94 PP. Maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference analysis (BI) of five loci produced a phylogenetic tree that contained six supported clades (Figure 5.1). This study proposes to place all currently and newly described species clades of *Phyllosticta* to six species complexes based on molecular phylogenetic analyses of ITS, LSU, *ef1α*, *act* and *gapdh* loci as follows: 1) *Phyllosticta capitalensis* species complex consisted of 27 species, 2) *Phyllosticta cruenta* species complex comprised 21 species (74% ML /0.94 PP), 3) *Phyllosticta vaccinii* species complex comprised two species (67% MP/ 84% ML/ 0.99 PP), 4) *Phyllosticta rhodorae* species complex consisted of two species and an unnamed species (61% ML/0.96 PP), 5) *Phyllosticta concentrica* species complex included 25 species and was strongly supported (96% MP/ 99% ML/1.0 PP) and 6)

Phyllosticta owaniana species complex included six species and was strongly supported (100% MP/ 99% ML/1.0 PP).

Phylogenetic analysis using five-gene combined dataset 2 – constructed using the 74 strains from *P. capitalensis* species complex and *Phyllosticta cordylinophila* sequences (MFLUCC 10-0166 and MFLUCC 12-0014) were used as outgroup taxa. The total length of the dataset was 2434 characters including alignment gaps, ITS1+ ITS2: 1–392, 5. 8S: 393–550, LSU: 551–1382, *ef1α* (exon): 1383–1417, *act* (exon): 1418–1527, *gapdh*: 1528–2150, *ef1α* (intron): 2151–2349, and *act* (intron): 2350–2496 (Figure 5.2). The combined dataset contained 2357 constant, 50 parsimony uninformative and 89 parsimony informative characters. The combined dataset was analyzed using MP, ML and BI. The trees generated under different optimality criteria were similar in topology and did not differ (data not shown). Descriptive statistics generated from MP analysis based on the combined dataset were TL = 167, CI = 0.850, RI = 0.930, RC = 0.791, HI = 0.150. The best scoring likelihood tree selected for the combined dataset had a final value of -4603.349843 (Figure 5.2).

Phyllosticta paracapitalensis formed a species clade, including the ex-type sequence data (CPC 26517). *Phyllosticta paracapitalensis* species were sister to the *Phyllosticta capitalensis sensu stricto*, within *P. capitalensis* species complex clade based on single-locus and combined gene trees (Figures 5.1, 5.2, 5.4–5.8). *Phyllosticta capitalensis* strains CBS 173.77 and CBS 119720 formed a separate clade from the other strains of *P. capitalensis* and *P. paracapitalensis* (Figures 5.1, 5.2). Nucleotide polymorphism comparisons of *P. capitalensis* (CBS 128856, ex-type) and *P. paracapitalensis* (CPC 26517, ex-type) with strain CBS 173.77 showed the following differences: 2bp ITS, 4bp *ef1α*, 3bp *act* and 0bp *gapdh* between *P. capitalensis* and CBS 173.77; and 4bp ITS, 1bp *ef1α*, 0bp *act* and 2bp *gapdh* between *P. paracapitalensis* and CBS 173.77. CBS 119720 has 0bp ITS, 4bp *ef1α*, 3bp *act* and 0bp *gapdh* differences from *P. capitalensis*, and 2bp ITS, 1bp *ef1α*, 0bp *act* and 2bp *gapdh* differences from *P. paracapitalensis*. Hence, these two strains could be unnamed species of *Phyllosticta* rather than *P. paracapitalensis*. However, because there are no intervening species, these twostrains could also be divergent of *P. paracapitalensis*. Additional data are needed to definitively resolve this issue.



Note Maximum likelihood phylogenetic tree inferred from combined ITS, LSU, *ef1α*, *act* and *gapdh* sequence data from 195 strains of the genus *Phyllosticta*. The tree is artificially rooted to *Botryosphaeria obtusa* strain CMW 8232 and *B. stevensii* strain CBS 112553. Maximum parsimony and maximum likelihood bootstrap values ≥50%, and Bayesian posterior probabilities ≥0.90 are given at the nodes in this order. The species obtained in this study are in blue and species synonymized are in green. Ex-type taxa are in bold.

Figure 5.1 Phylogenetic analysis of the genus *Phyllosticta* based on combined sequence data from 195 strains

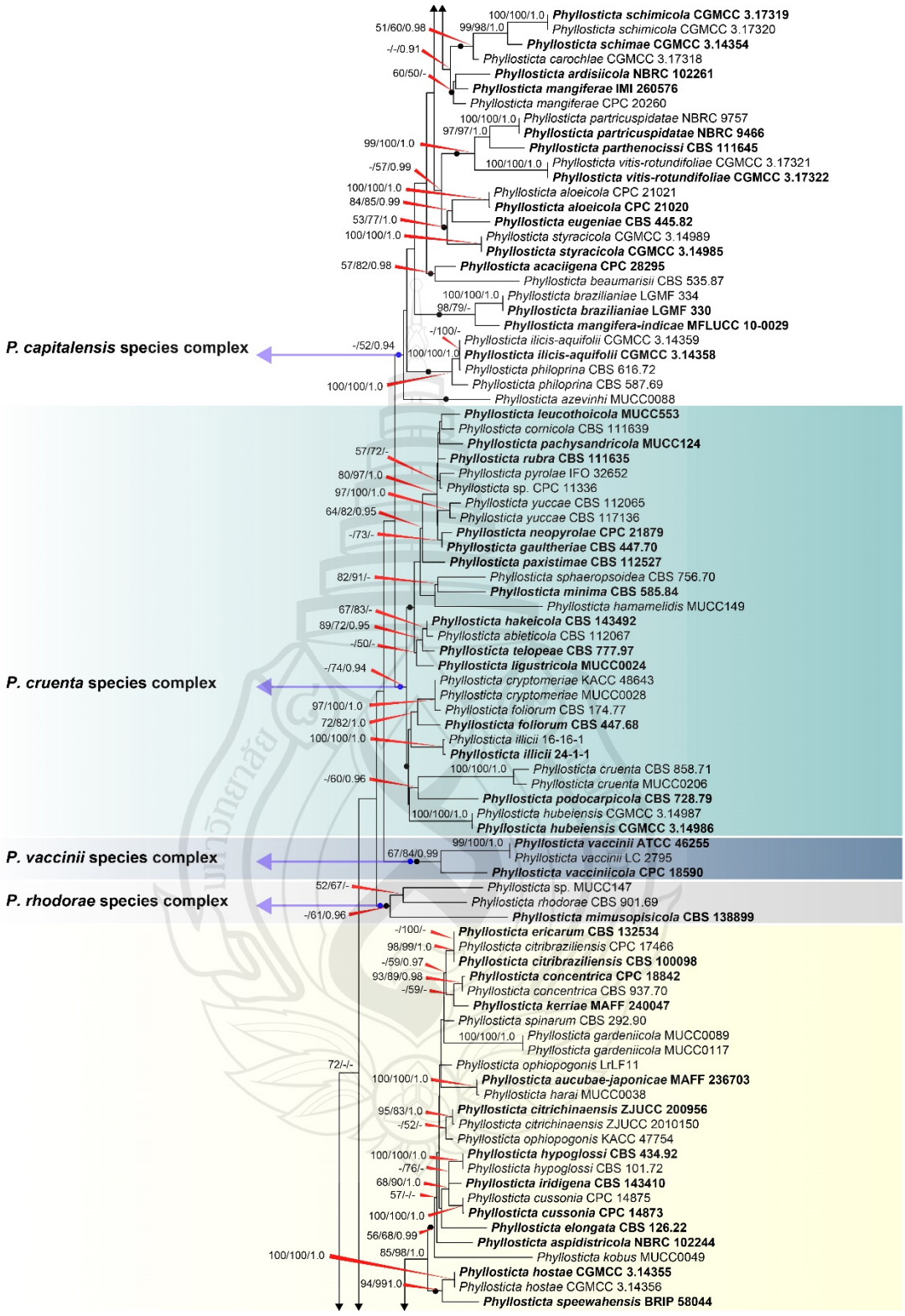


Figure 5.1 (continued)

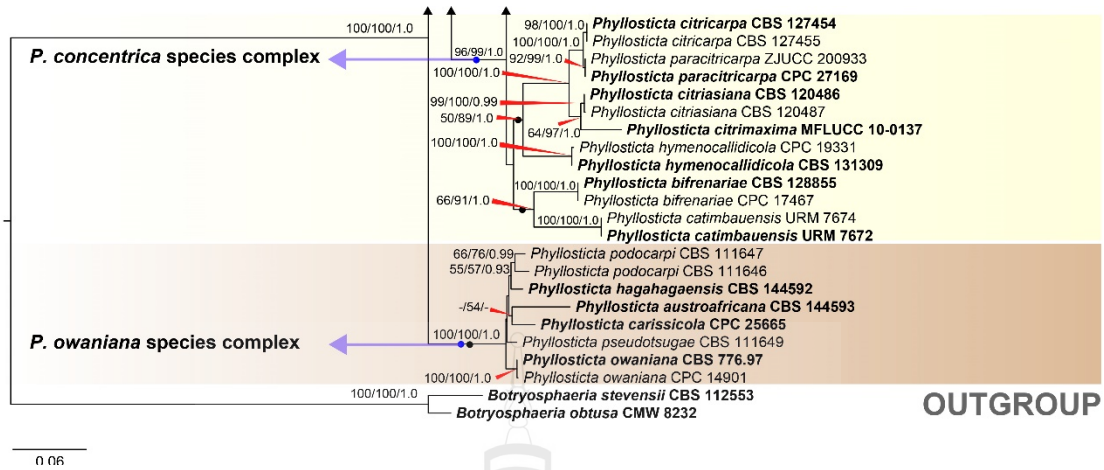
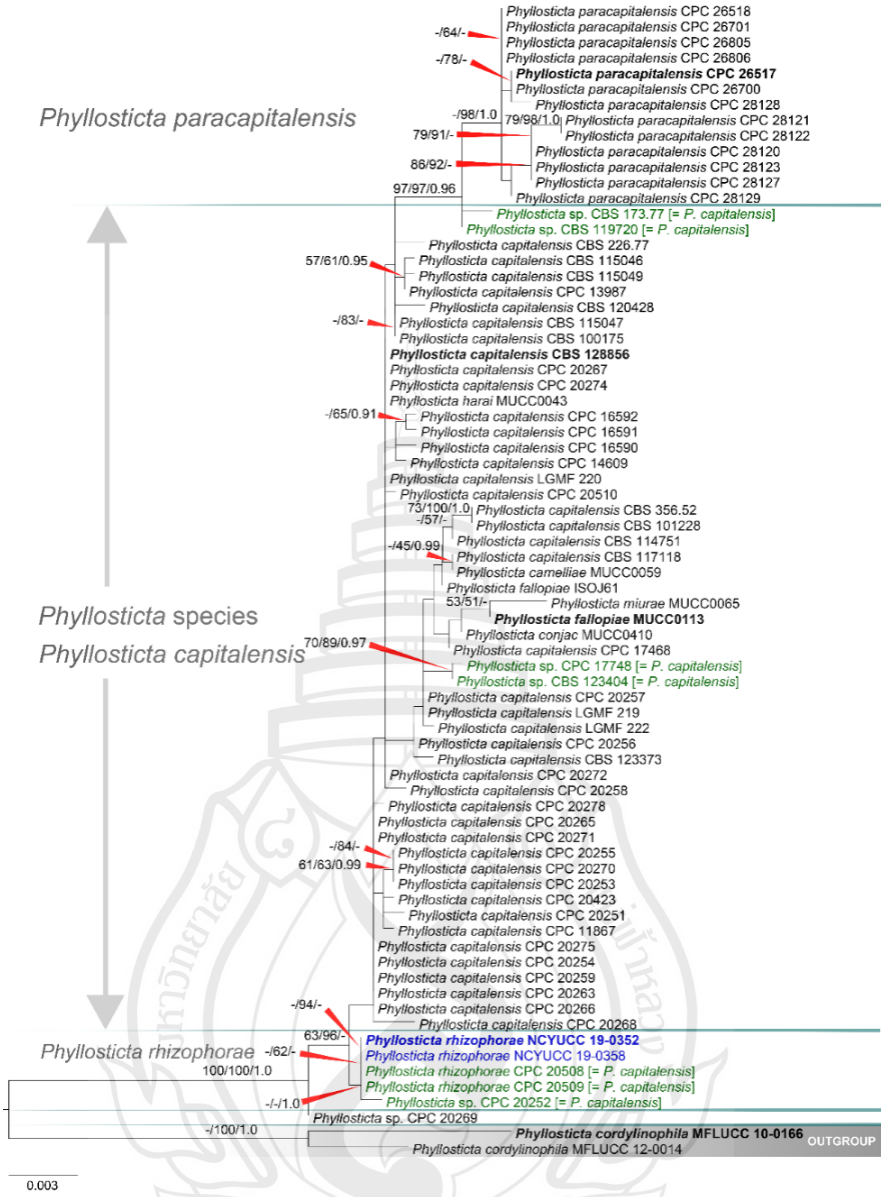


Figure 5.1 (continued)

Phyllosticta camelliae strain MUCC0059 and *P. fallopiae* strain ISOJ61 have unstable placements in the phylogenetic trees (Figures 5.1, 5.2). Based on the polymorphic nucleotide comparison of ITS, *ef1α*, *act* and *gapdh* with *P. capitalensis* (CBS 128856, ex-type) and *P. paracapitalensis* (CPC 26517, ex-type), strain ISOJ61 has 2bp ITS differences from *P. paracapitalensis*, and 0bp ITS differences from *P. capitalensis*. The strain MUCC0059 has 1bp ITS and 0bp *act* differences from *P. capitalensis*, and 3bp ITS and 5bp *act* differences from *P. paracapitalensis*. However, more DNA sequence data are needed for future study to resolve those problematic strains.

Phyllosticta capitalensis sequences formed a large cluster in the tree, which included the ex-type strain (CBS 128856). The newly described taxa (NCYUCC 19-0352 and NCYUCC 19-0358) formed a distinct clade, which grouped with *P. capilalensis* (CPC 20508 and CPC 20509) (Figures 5.1, 5.2). The strains CPC 20508 and CPC 20509 were synonymized under the new species based on phylogenetic analysis and nucleotide comparisons of ITS, *ef1α*, *act* and *gapdh*. Strain CPC 20508 has 2bp ITS, 0bp *ef1α*, 3bp *act*, 0bp *gapdh* differences from *P. capitalensis* (CBS 128856, ex-type) and 4 bp ITS, 5bp *ef1α*, 2bp *act*, 2bp *gapdh* differences from *P. paracapitalensis* (CPC 26517, ex-type). Strain CPC 20509 has 2 bp ITS, 0bp *ef1α*, 3bp *act*, 0bp *gapdh* differences from *P. capitalensis* (CBS 128856, ex-type), and 4 bp ITS, 5bp *ef1α*, 2bp *act*, 2bp *gapdh* differences from *P. paracapitalensis* (CPC 26517, ex-

type). Three strains previously named as *P. capitalensis* (CBS 123404, CPC 20252, CPC 17748) are proposed as unnamed species based on phylogenetic analysis (Figures 5.1, 5.2) and nucleotide comparisons of ITS, *ef1α*, *act* and *gapdh* with the ex-type of *P. capitalensis* (CBS 128856) and *P. paracapitalensis* (strain CBS 123404). Strain CBS 123404 has 0bp ITS, 1bp *ef1α*, 3bp *act*, 3bp *gapdh* differences from *P. capitalensis*, and 2bp ITS, 4bp *ef1α*, 2bp *act*, 5bp *gapdh* from *P. paracapitalensis*; CPC 17748 has 0bp ITS, 1bp *ef1α*, 3bp *act*, 4bp *gapdh* differences from *P. capitalensis*, and 2bp ITS, 4bp *ef1α*, 2bp *act*, 6bp *gapdh* from *P. paracapitalensis*; CPC 20252 has 1 bp ITS, 0bp *ef1α*, 3bp *act*, 0bp *gapdh* differences from *P. capitalensis*, and 3bp ITS, 5bp *ef1α*, 2bp *act*, 2bp *gapdh* differed from *P. paracapitalensis*. *Phyllosticta capitalensis* strain CPC 20269 formed a distinct lineage from other strains of *P. capitalensis* with high bootstrap support (Figure 5.2). It has 4bp ITS, 7bp *ef1α*, 5bp *act*, and 2bp *gapdh* differences from *P. paracapitalensis* (CPC 26517, ex-type), and 2bp ITS, 2bp *ef1α*, 6bp *act*, and 0bp *gapdh* differences from *P. capitalensis* (CBS 128856, ex-type). Hence, we leave it as an unnamed species based on phylogenetic analysis. Nonetheless, in the Figure 5.1, the sequence grouped in a different position, thus further analysis with additional phylogenetic markers is needed to determine exact placement.



Note Phylogenetic tree generated from maximum likelihood analysis based on combined ITS, LSU, *ef1α*, *act* and *gapdh* sequence data from 74 strains of *Phyllosticta*. The tree is rooted to *P. cordylinophila* strain MFLUCC 10-0166 and MFLUCC 12-0014. Maximum parsimony and maximum likelihood bootstrap values ≥50%, and Bayesian posterior probabilities ≥0.90 are given at the nodes in this order. The species obtained in this study are in blue and species synonymized are in green. Ex-type taxa from other studies are in bold.

Figure 5.2 Phylogenetic analysis of the genus *Phyllosticta* based on combined sequence data from 74 strains

5.3.2 Taxonomy

Phyllostictaceae

See Hongsanan et al. (2020a) and Wikee et al. (2013b) for descriptions and illustrations.

Phyllosticta Pers.

For genus description see Wikee et al. (2013b) and Hongsanan et al. (2020a). Herein we introduce six species complexes (*Phyllosticta capitalensis*, *P. concentrica*, *P. cruenta*, *P. owaniana*, *P. rhodorae*, and *P. vaccinii*), which form distinct clades.

***Phyllosticta capitalensis* species complex**

Species included in *Phyllosticta capitalensis* species complex – *P. acaciigena*, *P. aloeicola*, *P. ardisiicola*, *P. aristolochiicola*, *P. azevinhi*, *P. beaumarisii*, *P. brazilianiae*, *P. capitalensis*, *P. carochlae*, *P. cavendishii*, *P. cordylinophila*, *P. eugeniae*, *P. fallopiae*, *P. ilicis-aquifolii*, *P. maculata*, *P. mangiferae*, *P. mangifera-indicae*, *P. musaechinensis*, *P. musarum*, *P. paracapitalensis*, *P. parthenocissi*, *P. partricuspidatae*, *P. philoprina*, *P. rhizophorae*, *P. schimae*, *P. schimicola*, *P. styracicola*, *P. vitis-rotundifoliae*.

Notes – 28 species are included in *Phyllosticta capitalensis* species complex based on molecular analyses and morphological characters. Members of this section are mostly reported as pathogenic and endophytic fungi from a broad range of hosts (Table 5.7). Species of this complex are characterized by conidia that are ellipsoid or ellipsoid to obovoid, ovoid, obpyriform with a mucoid sheath with apical mucoid appendage; ascospores are limoniform with obtuse ends, with distinct hyaline gelatinous caps at both ends, (Table 5.7). Sexual morphs of six species have been reported in this group (*P. cavendishii*, *P. maculata*, *P. musarum*, *P. paracapitalensis*, *P. philoprina*, and *P. rhizophorae*). *Phyllosticta capitalensis* and *P. azevinhi*, most wildly distributed species of *Phyllosticta* was included here. This species complex is recovered in the multilocus tree, as well as in the single locus ITS and *act* trees (Figures 5.1, 5.4, 5.7). *Phyllosticta capitalensis* is used to describe this species complex name based on publication year.

Hennings (1908) described *Phyllosticta capitalensis* on *Stanhopea* sp. (Orchidaceae) from Brazil. The species is commonly isolated as an endophyte and has worldwide distribution (Glienke-Blanco et al., 2002; Silva & Pereira, 2007; Silva et

al., 2008; Rashmi et al., 2019). Wikee et al. (2013a) reported that *P. capitalensis* was found in more than 70 plant families. Many factors affect host infection with *P. capitalensis*, such as environmental conditions, host and non-host organisms, and plant defence mechanisms (Wikee et al., 2013a). Guarnaccia et al. (2017) introduced *Phyllosticta paracapitalensis* from asymptomatic living leaves of *Citrus* sp. from Italy. *Phyllosticta paracapitalensis* is sister species to *P. capitalensis* based on molecular analyses of ITS, *act*, *ef1α*, *gapdh*, LSU and *rpb2* (Guarnaccia et al., 2017).

***Phyllosticta concentrica* species complex**

Species included in the *Phyllosticta concentrica* species complex – *P. aspidistricola, P. aucubae-japonicae, P. bifrenariae, P. catimbauensis, P. citriasiana, P. citribrasiliensis, P. citricarpa, P. citrichinensis, P. citri-maxima, P. concentrica, P. cussonia, P. elongata, P. ericarum, P. gardeniicola, P. harai, P. hostae, P. hymenocallidicola, P. hypoglossi, P. iridigena, P. kerriae, P. kobus, P. ophiopogonis, P. paracitricarpa, P. speewahensis, P. spinarum.*

Notes – 25 species are included in the *P. concentrica* species complex. Members of this species complex have mostly been reported as pathogenic and endophytic fungi from a wide range of hosts (Table 5.7). *Phyllosticta citricarpa*, an important pathogenic fungus causing leaf spot and citrus black spot disease on *Citrus*, *Poncirus*, *Fortunella* and their hybrids are included in this clade (van der Aa, 1973; Guarnaccia et al., 2017; Boughalleb-M'Hamdi et al., 2020). *Phyllosticta concentrica* is used to describe this species complex based on publication year. Species of this complex are characterized by conidia that are globose or ellipsoid to obvoid enclosed in a thin persistent sheath with apical mucoid appendage; ascospore are fusiform to ellipsoid, wider at the mid region, both ends rounded with gelatinous caps (Table 5.7). The sexual morph of *P. citrichinensis* has been reported in this group. The clade for this species complex is robust and recovered in all analyses (Figure 5.1, 5.4–5.8).

Phyllosticta concentrica was introduced by Saccardo for fungi on leaves of *Hedera helix* in Italy (Wikee et al., 2013b). Later, the species was introduced from withering, leaf litter, and living leaves in a wide range of hosts (Table 5.7).

***Phyllosticta cruenta* species complex**

Species included in the *Phyllosticta cruenta* species complex – *P. abieticola*, *P. cornicola*, *P. cruenta*, *P. cryptomeriae*, *P. foliorum*, *P. gaultheriae*, *P. hakeicola*, *P. hamamelidis*, *P. hubeiensis*, *P. illicii*, *P. leucothoicola*, *P. ligustricola*, *P. minima*, *P. neopyrolae*, *P. pachysandricola*, *P. paxistimae*, *P. podocarpicola*, *P. paviae*, *P. pyrolae*, *P. rubella*, *P. telopeae*.

Notes – This species complex consists of 21 species, which have mostly been reported as pathogenic and endophytic from a wide range of hosts (Table 5.7). *Phyllosticta cruenta* is used to describe this species complex name based on the publication year. Species of this complex are characterized by conidia that are globose or elongate, ellipsoid to obovoid with mucoid sheath or some species with mucous sheath (*P. pachysandricola*) with or without apical mucoid appendage; ascospores limoniform with obtuse ends, rarely curved (Table 5.7). Sexual morphs of two species have been reported in this group (*P. abieticola*, *P. rubella*). This clade was not resolved based on single-locus trees of LSU, *ef1α*, and *gapdh*, while ITS and *act* topologies provided better resolution for this species complex as combined gene tree (Figure 5.1, 5.4–5.8).

***Phyllosticta owaniana* species complex**

Species included in the *Phyllosticta owaniana* species complex – *P. austroafricana*, *P. carissicola*, *P. hagahagaensis*, *P. owaniana*, *P. podocarpi*, *P. pseudotsugae*.

Notes – Six species are included in the *P. owaniana* species complex. Members of this species complex are mostly reported as pathogenic causing leaf spots on *Carissa* spp., *Brabejum* sp., *Podocarpus* spp., and endophytic fungi on *Cryptomeria* sp., and *Pseudotsuga* spp. (Table 5.7). *Phyllosticta owaniana* is used to describe this species complex based on the publication year. Species of this complex are characterized by conidia that are ellipsoid to obovoid, tapering towards a narrow truncate base, coarsely guttulate, or with a single large central guttule, enclosed in a thin persistent mucoid sheath and with or without apical mucoid appendage; ascospores are fusiform to ellipsoid, with hyaline gelatinous caps at both ends (Table 5.7). The sexual morph of *P.*

podocarpi has been reported in this group. The complex is recovered in the multilocus and single locus (except for LSU) trees (Figures 5.4–5.8).

Winter (1885) introduced *Phyllosticta owaniana*, which is a pathogenic fungus causing serious leaf spot disease on *Brabejum stellatifolium* in South Africa. The species was mentioned as being a specific species for this host (Doidge, 1950; Swart et al., 1998; Crous et al., 2000; Wulandari et al., 2009; Sultan et al., 2011; Glienke et al., 2011; Wikee et al., 2011, 2013a, b; Miles et al., 2013; Zhou et al., 2015; Hyde et al., 2014).

***Phyllosticta rhodorae* species complex**

Species included in the *Phyllosticta rhodorae* species complex – *P. mimusopisicola*, *P. rhodorae.*

Notes – Two species were included in the *P. rhodorae* species complex. Crous et al. (2014) introduced *Phyllosticta mimusopisicola*, a pathogen causing leaf spot disease on *Mimusops zeyheri* in Aflica. *Phyllosticta rhodorae* is found on *Rhododendron* spp., which was recombined by Tassi (1902) (≡ *Phoma rhodorae* Cooke). *Phyllosticta rhodorae* is used to describe this species complex based on publication year. Species of this complex are characterized by conidia that are ellipsoid to obovoid, tapering towards a narrow truncate base, coarsely guttulate, or with a single large central guttule, persistent mucoid sheath and apical mucoid appendage (Table 5.7). The sexual morph has not been reported for this species complex. The complex is recovered in the mulitlocus and LSU trees.

***Phyllosticta vaccinii* species complex**

Species included in the *Phyllosticta vaccinii* species complex – *P. vaccinii*, *P. vacciniicola*.

Notes – Two species are included in the *P. vaccinii* species complex. Members of this species complex have mostly been reported as pathogenic and endophytic on *Vaccinium* spp. (Table 5.7). *Phyllosticta vaccinii* is used to describe this species complex based on publication year. Earle (1897) introduced *P. vaccinii* from leaf spot of *Vaccinium arboretum* in Alabama. This species has been isolated from a wide range of *Vaccinium* (Hyde et al., 2014; Zhou et al., 2015). Detailed host information and distribution is provided in Table 5.7. This species complex is characterized by conidia

that are ellipsoid to obovoid, obpyriform, tapering towards a narrow truncate base, enclosed in a thin persistent mucoid sheath with a mucoid appendage (Table 5.7). The sexual morph has not been reported for this species complex. The complex is robust and recovered in the multi- and single locus trees (Figures 5.1, 5.4–5.8).

Phyllosticta rhizophorae Norph. & Hyde K.D. sp. nov., Figure 5.3

Index Fungorum number: IF557808

Facesoffungi number: FoF08021

Etymology: refers to the host, *Rhizophora stylosa*, of the type strain.

Holotype: NCYUCC 19-0352

Associated with leaf spots of *Rhizophora stylosa*. *Symptoms* irregular to subcircular shape, brown, slightly sunken spots appear on adaxial surface leaves of *R. stylosa*, which later expand outwards on the surface of the leaves (Figure 5.3b). Small auburn spots appeared initially and then gradually enlarged, changing to tawny circular ring spots with a dark mahogany border and jagged edge. They were usually >5 circulars, which occurred on a single affected leaf. In severe cases, lesions spread evenly on the leaves (Figure 5.3c). Sexual morph: *Ascomata* similar to conidiomata in general anatomy, long neck. *Asci* 33–55 × 4–6.5 μm, bitunicate, clavate to broadly fusoid-ellipsoid, with visible apical chamber, 1–2 μm diam. *Ascospores* (12.5–)14–19(–21.5) × 4.1–7.7 μm, (mean ± SD = 16 ± 2.9 × 6.1 ± 1.2 μm), bi-seriate, hyaline, smooth, aseptate, granular to guttulate, straight and slightly curved, widest in the middle, limoniform with obtuse ends, with distinct hyaline gelatinous caps at both ends, 3.5–5.5 × 1.5–3 μm. Asexual morph: *Conidiomata* pycnidial up to 700 μm diam., solitary, black, erumpent, globose including colorless to opaque conidial masses. *Conidiomata* pycnidial up to 200 μm diam., solitary, black, erumpent, globose to pyriform, including colorless to opaque conidial masses in PA. *Pycnidial wall* of several layers, composed of cells of *textura angularis*, thick, inner wall of hyaline *textura angularis* cells. *Central ostiole*, up to 10 μm diam. *Conidiophores* reduced to conidiogenous cells, 13–25 × 3–5 μm, subcylindrical to ampulliform, or with 1–2 supporting cell, that can be branched at the base. *Conidiogenous cells* 10–17 × 3–5 μm, terminal, subcylindrical, hyaline, smooth, proliferating several times percurrently near apex. *Conidia* (13–)15–17(–19.5) × 6–7(–8) μm, (mean ± SD = 16.7 ± 0.5 × 7.3 ± 1.6 μm), solitary, hyaline, aseptate,

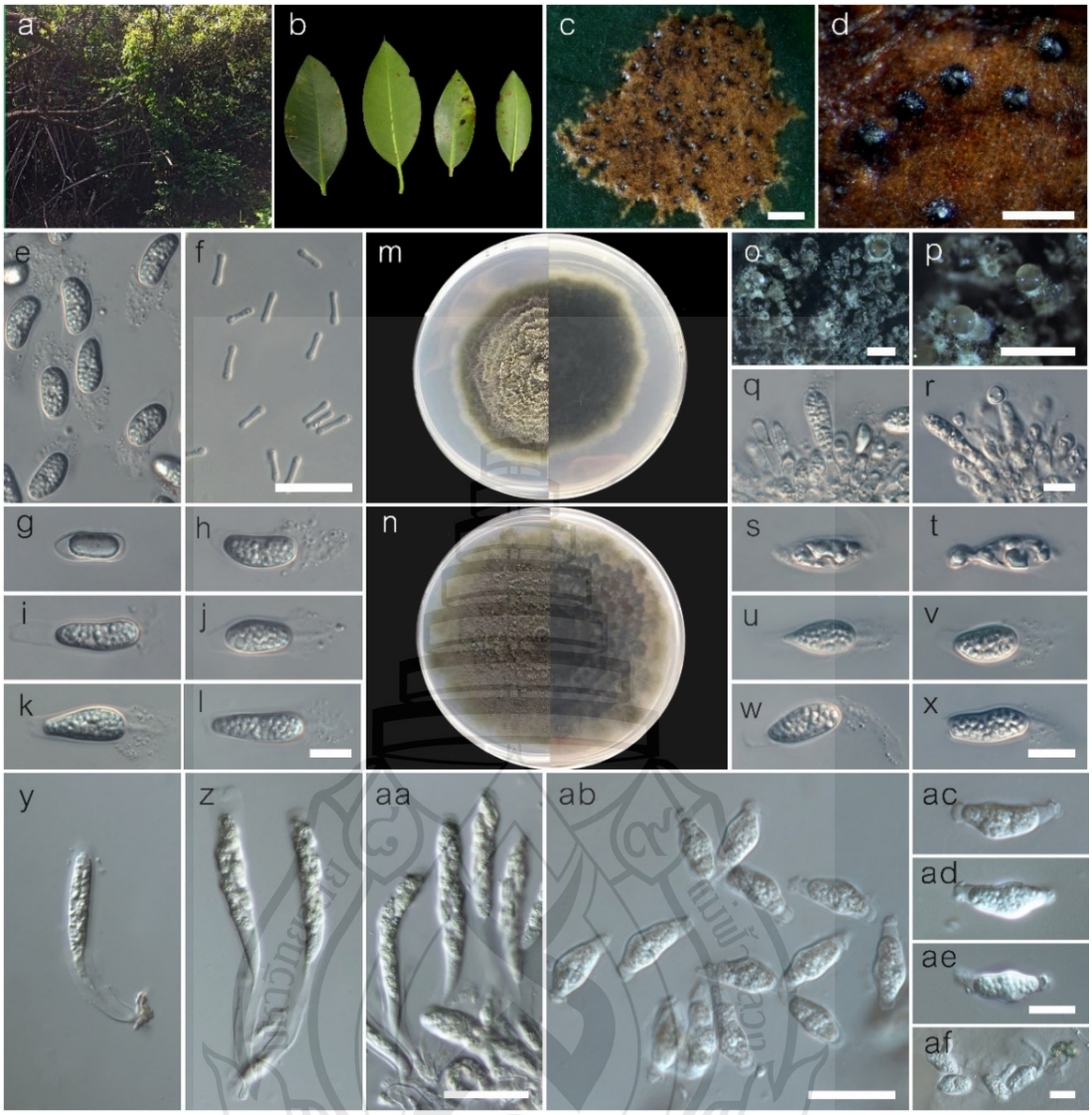
thin and smooth walled, coarsely guttulate, or with a single large central guttulate, broadly ellipsoid or ellipsoid to obovoid, tapering towards a narrow truncate base, enclosed in a persistent mucoid sheath, 1–8 μm thick, and bearing a hyaline, apical mucoid appendage, (5–)9–11(–16) × 6–8(–12) μm, flexible, unbranched, tapering towards an acutely rounded tip, rarely with a short apical appendage. *Spermatia* hyaline, smooth, guttulate to granular, bacilliform, 7.5–11.5 × 1–2 μm, occurring in conidioma with conidia.

Material examined: TAIWAN, Tainan, Shicao, on leaf spot of *Rhizophora stylosa*, July 15, 2018, Chada Norphanphoun SC0 (NCYUCC 19-0352 dried culture, holotype; MFLU, isotype), ex-type living culture NCYUCC 19-0352, NCYUCC 19-0358, MFLUCC.

Distribution: *Cordyline fruticosa* (Thailand), *Heliconia* sp. (Thailand), *Ixora chinensis* (Thailand), *Musa paradisiaca* (Thailand), *Punica granatum* (Thailand), *Rhizophora stylosa* (Taiwan).

Notes: *Phyllosticta rhizophorae* is closely related to *P. capitalensis* based on DNA sequence data in BLAST searches and phylogenetic analysis (Figure 5.1). However, phylogenetic analyses of selected strains in Figure 5.2 indicate that the new taxon groups with five published strains of *P. capitalensis* (CPC 20508, CPC20509, CPC 20252, CBS 123404 and CPC 17748) as a distinct clade, and is separate from *P. capitalensis* species group, which contains the ex-type strain (Figure 5.2). The morphology of *P. rhizophorae* is different from that of *P. capitalensis* (Table 5.4). Hence, *P. rhizophorae* is established based on morphological and molecular data. Two strains of *P. capitalensis* (CPC 20508, CPC20509) are synonymized under *P. rhizophorae* based on phylogenetic analyses (Figure 5.2). The new collection is designated as the type material. Strains CPC 20252, CBS 123404 and CPC 17748 are treated as unnamed species as they form a separate clade from our new collection in both phylogenetic trees (Figures 5.1, 5.2).

Pathogenicity testing: The ability of *Phyllosticta rhizophorae* strains isolated from leaf spots of *Rhizophora stylosa* in Taiwan to induce leaf spot symptoms on *Rhizophora stylosa* was tested through inoculating a spore suspension and mycelial plugs onto wounded and unwounded living leaves. In all cases there was no symptoms on the young healthy plant leaves.



Note *Phyllosticta rhizophorae* (NCYUCC19-0352). a Habitat. b Leaf spots on *Rhizophora stylosa*. c–d Surface of leaf spot with fruiting bodies. e, g–l, s–x Conidia. f Spermatia. m, o–p Colony of asexual morph on PDA. n Colony of sexual morph on PA (left-above, right-reverse). q–r Conidiophore with Conidia developing on conidiogenous cells. y–aa Asci. ab–ae Ascospores. af Ascospores germinating on WA. (a–l morphology from leaf spot, m–af morphology from culture). Scale bars: c, o–p = 1 mm, d= 500 µm, e–f, g–l, q–r, s–x, ac–af = 10 µm, y–aa =15 µm, ab = 20 µm.

Figure 5.3 Morphological characters of *Phyllosticta rhizophorae* (NCYUCC19-0352)

5.4 Discussion

The taxonomy of *Phyllosticta* is challenging. *Phyllosticta* species have overlapping morphological traits, making it difficult to pinpoint taxonomically relevant characters. Reliance on host association for traditional identification of *Phyllosticta* species has further complicated matters. Collectively, these issues have led to taxonomic confusion. Molecular phylogenetic tools have greatly facilitated identification of species and establishment of species complexes (Baayen et al., 2002; Okane et al., 2003; Motohashi et al., 2009; Wikee et al., 2012; Wulandari et al., 2009; Glienke et al., 2011). In this study, both combined and single locus data were considered. Multilocus trees provided better resolution of *Phyllosticta* species than single-locus trees (Figures 5.4–5.8). Adding protein-coding genes to the analysis greatly facilitated species level identification. Based on the results of our phylogenetic analyses we have introduced six species complexes in *Phyllosticta*: *P. capitalensis, P. concentrica, P. cruenta, P. owaniana, P. rhodorae,* and *P. vaccinii*. Splitting of *Phyllosticta* into clades will allow for easier resolution of species. Eighty-four previously described species including a new species were assigned to one of the six species complexes. Given that species delineation in *Phyllosticta* is difficult due to the above-mentioned challenges, the complexes can be used as broader descriptors of the genus. Following the same reasoning and for the sake of communication, species complexes have been introduced successfully for *Colletotrichum* (Cannon et al., 2012; Damm et al., 2019; Jayawardena et al., 2016; da Silva et al., 2020), and *Fusarium* (O'Donnell et al., 2013, 2015; Al-Hatmi et al., 2016).

Multilocus phylogeny and at least two single locus analyses support the six individual *Phyllosticta* species complexes, some of which have strong statistical support (Figure 5.1). Nonetheless, placement of some species remains problematic and additional loci are needed for taxonomic resolution. Results from this study demonstrate that both molecular phylogenetic analyses and morphological data are needed to propose and establish species of *Phyllosticta*, as the latter alone is not sufficient. The molecular boundaries of species of *Phyllosticta* will provide a better

understanding of inter and intraspecific variation within the genus, particularly within the broader species complexes.

Demarcation of individual taxa within the genus is essential so that we develop a better understanding of the lifestyles, ecology, and overall biology of these individual taxa and their impact and control in various ecosystems. Hence, in this study six strains of *P. capitalensis* are unnamed species (strains CBS 173.77, CBS 119720, CPC 17748, CPC 20252, CPC 20269, and CBS 123404) based on nucleotide polymorphisms and phylogenetic analyses. Seventeen strains were excluded from *Phyllosticta*. Seventeen strains – *Phyllosticta alcides* strain P3-4 (Palomares-Rius et al., 2014), *P. artocarpina* strain B5 (Baayen et al., 2002), *P. caprifolii* strain F23 (unpublished), *P. citrullina* strain LrBF12 (unpublished), *P. citrullina* strain LrBF13 (unpublished), *P. coryli* strain CTF324 (Sun et al., 2013), *P. flevolandica* strain AFTOL-ID 1786 (unpublished), *P. flevolandica* strain CBS 998.72 (Vu et al., 2019), *P. heveae* strain NW197 (unpublished), *P. jasmini* strain TS08-19-2 (unpublished), *P. jasmini* strain 6259 (unpublished), *P. juglandis* strain H2 (unpublished), *P. ligustri* strain TS08-20-1 (unpublished), *P. papayae* strain T150 (unpublished), *P. papayae* strain 7AJ-10 (unpublished), *P. populina* strain NW584 (unpublished), and *P. sojicola* strain CBS 301.39 (Vu et al., 2019) – were excluded from *Phyllosticta* based on BLAST searches against type material (Table 5.6). The BLAST results for the above 17 strains denoted as *Phyllosticta* matched other genera to the exclusion of *Phyllosticta*. In the phylogenetic tree, these 17 strains were excluded from the *Phyllosticta* clade (data not shown). Sixteen of these strains were submitted to the database based on sequence data alone without accompanying morphological support. One strain, *P. coryli* CTF324, was published with only the ITS gene region and morphological characters of unicellular conidia, colorless, ovoid to oval, and from 2.4–4.5 × 1.6–2.4 μm (Sun et al., 2013). The morphology of *P. coryli* strain CTF324 corresponds more closely to species of *Didymella* and *Peyronellaea* in Didymellaceae, an observation that is also supported by the BLAST search results (Table 5.6). Finally, a new species, *Phyllosticta rhizophorae*, is introduced in this study. Two strains of *P. capitalensis* (CPC 20508, CPC 20509) were synonymized under the new species.

Description of the new species is based on both morphological and molecular data. The new species was found on mangrove plants in Taiwan (leaf spot of

Rhizophora stylosa) and isolated using tissue isolation. During the research period, a new species and new strains of previously known species from mangroves in Taiwan were reported. For example, *Pestalotiopsis kandelicola*, *P. kenyana*, *P. diploclisiae* were isolated from asymptomatic leaves of *Kandelia candel* (Hyde et al., 2020a, b), while *Alternaria* sp. was associated with leaf blight of *Ficus* sp. and leaf spot of *Kandelia candel* (Norphanphoun et al., 2021). Collectively, these results suggest that there might be a large number of undescribed species, both endophytes and pathogens, in this ecosystem. Pathogenicity testing of *P. rhizophorae* was negative. *Phyllosticta* species have only rarely been isolated from leaf spots and black spots of fruits, but they have also been found as endophytes of diverse host plants, and as saprobes (Okane et al., 2003; Glienke et al., 2011; Guarnaccia et al., 2017; Tran et al., 2019; Wikee et al., 2011, 2013b). Taken together, it seems that *Phyllosticta* species are widely distributed and appear to have different lifestyles, which ranges from pathogens, latent pathogens, and endophytes. Further studies are needed to establish whether these species are host-specific, their habitats and lifestyle, as well as the conditions under which they might switch.

Table 5.4 Morphological characteristics comparison of *Phyllosticta* species related to this study

Species	Strain	Ascomata		Asci		Ascospores		Conidiomata		Conidiogenous cells		Conidia		Spermatia		Reference
		Size*	Shape	Size*	Shape	Size*	Shape	Size*	Shape	Size*	Shape	Size*	Shape	Size*	Shape	
P. capitalensis	CBS 128856 [T]	250	globose to pyriform	58–80 × 11–15	clavate	15–17 × 5–6	limoniform	300 × 250	globose to ampulliform	7–10 × 3–5	subcylindrical to ampulliform to doliiform	(10–)11–12(–14) × (5–)6–7	ellipsoid to obovoid	N/A	N/A	Hennings (1908)
P. fallopiae	MUCC 0113/NBRC 102266 [T]	N/A	N/A	N/A	N/A	N/A	N/A	63.5–98 × 61–98	sub globose to globose	5–10 × 1.2–2.5	cylindrical to subcylindrical	8.5–12.5 × 6–7.5	ellipsoid to obovoid	N/A	N/A	Motohashi et al. (2008)
P. paracapitalensis	CPC 26517 [T]	>300	globose	40–75 × 10–12	subcylindrical to clavate	16–17 × 6 (–7)	limoniform	>250	globose	7–15 × 3–4	subcylindrical	(9–)12–13(–14) × (6–)7	ellipsoid to obovoid	N/A	N/A	Guarnaccia et al. (2017)
P. rhizophorae	NCYUCC 19-0358/19-0352	>200	globose to pyriform	33–55 × 4–6.5	clavate to broadly fusoid-ellipsoid	16 ± 2.9 × 6.1 ± 1.2	limoniform with obtuse ends	>200	globose	10–17 × 3–5	subcylindrical	16.7 ± 0.5 × 7.3 ± 1.6	ellipsoid to obovoid	7.5–11.5 × 1–2	bacilliform	In this study

Note *Size was mentioned in µm; [T] Type species; N/A no morphology mentioned in publication

Table 5.5 GenBank BLAST search results of *Phyllosticta* strains that clustered with *P. capitalensis* in this study

Taxon	Strain**	Host	Country	GenBank accession no.*	GenBank BLAST search results			
					Species identified	Strain**	Accession no.	Identities (I), Query cover (QC)
P. harai	MUCC0043[b]	*Aucuba japonica*	Japan	AB454281▲	*Phyllosticta fallopiae*	MUCC0113[b]	AB454307	100.00% (I), 100% (QC)
					Guignardia philoprina	MUCC0027[b]	AB454270	100.00% (I), 100% (QC)
					Phyllosticta elongata	CBS 114751[d]	EU167584	100.00% (I), 100% (QC)
					Phyllosticta sp.	MUCC0547[b]	AB454364	99.92% (I), 100% (QC)
					Guignardia mangiferae	MUCC0207[b]	AB454332	99.92% (I), 100% (QC)
				AB704219●	*Phyllosticta sphaeropsoidea*	MUCC0112[a]	AB704227	100.00% (I), 100% (QC)
					Guignardia sawadae	MUCC0066[a]	AB704225	100.00% (I), 100% (QC)
					Guignardia mangiferae	MUCC0030[a]	AB704215	100.00% (I), 99% (QC)
					Guignardia mangiferae	MUCC0122[a]	AB704231	99.6% (I), 100% (QC)
					Phyllosticta conjac	MUCC0410[a]	AB704239	99.6% (I), 100% (QC)
P. fallopiae	MUCC 0113[b]	*Fallopia japonica*	Japan	AB454307▲	*Phyllosticta elongata*	CBS 114751[d]	EU167584	100.00% (I), 100% (QC)
					Guignardia philoprina	MUCC0027[b]	AB454270	100.00% (I), 99% (QC)
					Phyllosticta sp.	MUCC0547[b]	AB454364	99.92% (I), 99% (QC)
					Guignardia mangiferae	MUCC0207[b]	AB454332	99.92% (I), 99% (QC)
					Guignardia sp.	MUCC0041[b]	AB454279	99.92% (I), 100% (QC)
				AB704228●	*Phyllosticta miurae*	MUCC0065[a]	AB704224	100.00% (I), 100% (QC)

Table 5.5 (continued)

Taxon	Strain**	Host	Country	GenBank accession no.*	GenBank BLAST search results			
					Species identified	Strain**	Accession no.	Identities (I), Query cover (QC)
					Phyllosticta sphaeropsoidea	MUCC0112[a]	AB704227	100.00% (I), 99% (QC)
					Guignardia philoprina	MUCC0012[a]	AB704206	99.6% (I), 100% (QC)
					Phyllosticta conjac	MUCC0410[a]	AB704239	99.6% (I), 100% (QC)
					Guignardia mangiferae	MUCC0122[a]	AB704231	99.6% (I), 99% (QC)
P. conjac	MUCC0410[b]	*Amorphophallus rivieri*	Japan	AB454342▲	*Phyllosticta fallopiae*	MUCC0113[b]	AB454307	100.00% (I), 100% (QC)
					Guignardia philoprina	MUCC0027[b]	AB454270	100.00% (I), 100% (QC)
					Phyllosticta elongata	CBS 114751[b]	EU167584	100.00% (I), 100% (QC)
					Phyllosticta sp.	MUCC0547[b]	AB454364	99.92% (I), 100% (QC)
					Guignardia mangiferae	MUCC0207[b]	AB454332	99.92% (I), 100% (QC)
				AB704239●	*Guignardia philoprina*	MUCC0012[a]	AB704206	100.00%(I), 100% (QC)
					Phyllosticta fallopiae	MUCC0113[a]	AB704228	99.6% (I), 100% (QC)
					Phyllosticta sphaeropsoidea	MUCC0112[a]	AB704227	99.6%(I), 100% (QC)
					Guignardia sawadae	MUCC0066[a]	AB704225	99.6% (I), 100% (QC)
					Phyllosticta miurae	MUCC0065[a]	AB704224	99.6% (I), 100% (QC)

Table 5.5 (continued)

Taxon	Strain**	Host	Country	GenBank accession no.*	GenBank BLAST search results			
					Species identified	Strain**	Accession no.	Identities (I), Query cover (QC)
P. fallopiae	ISOJ61[c]			MF164545▲	*Phyllosticta capitalensis*	A788[u]	MN121397	100.00% (I), 100% (QC)
					Phyllosticta elongata	LCM 886.01[u]	MF495420	100.00% (I), 100% (QC)
					Phyllosticta capitalensis	LCM 826.01[u]	MF495391	100.00% (I), 00% (QC)
					Phyllosticta capitalensis	LCM 818.01[u]	MF495383	100.00% (I), 100% (QC)
					Phyllosticta capitalensis	VPRI41231[u]	MH183391	100.00% (I), 100% (QC)
P. miurae	MUCC0065[b]	*Lindera praecox*	Japan	AB454291▲	*Guignardia alliacea*	MUCC0015[a]	AB454264	100.00% (I), 100% (QC)
					Guignardia alliacea	MUCC0014[a]	AB454263	99.92% (I), 100% (QC)
					Guignardia philoprina	MUCC0012[a]	AB454262	99.83% (I), 100% (QC)
					Guignardia mangiferae	MUCC0122[a]	AB454315	99.83% (I), 100% (QC)
					Phyllosticta fallopiae	MUCC0113[a]	AB454307	99.75% (I), 100% (QC)
				AB704224●	*Phyllosticta fallopiae*	MUCC0113[a]	AB704228	100% (I), 100% (QC)
					Phyllosticta conjac	MUCC0410[a]	AB704239	99.6% (I), 100% (QC)
					Guignardia mangiferae	MUCC0122[a]	AB704231	99.6% (I), 100% (QC)
					Phyllosticta sphaeropsoidea	MUCC0112[a]	AB704227	99.6% (I), 100% (QC)
					Guignardia sawadae	MUCC0066[a]	AB704225	99.6% (I), 100% (QC)

Table 5.5 (continued)

Taxon	Strain**	Host	Country	GenBank accession no.*	GenBank BLAST search results			
					Species identified	Strain**	Accession no.	Identities (I), Query cover (QC)
P. camelliae	MUCC0059[a]	*Camellia japonica* var. *hortensis*	Japan	AB454290▲	*Guignardia philoprina*	MUCC0012[b]	AB454262	100% (I), 100% (QC)
					Guignardia mangiferae	MUCC0122[b]	AB454315	99.92% (I), 100% (QC)
					Phyllosticta fallopiae	MUCC0113[b]	AB454307	99.92% (I), 100% (QC)
					Guignardia philoprina	MUCC0027[b]	AB454270	99.92% (I), 100% (QC)
					Guignardia alliacea	MUCC0015[b]	AB454264	99.92% (I), 100% (QC)
				AB704223●	*Phyllosticta sphaeropsoidea*	MUCC0112[a]	AB704227	100% (I), 100% (QC)
					Guignardia sawadae	MUCC0066[a]	AB704225	100% (I), 100% (QC)
					Phyllosticta harai	MUCC0043[a]	AB704219	100% (I), 100% (QC)
					Guignardia mangiferae	MUCC0030[a]	AB704215	100% ((I), 99% (QC)
					Guignardia mangiferae	MUCC0122[a]	AB704231	99.6% (I), 100% (QC)

Note *Gene: ▲ITS, • *act*

Source ** references: [a]Ando et al. (2013), [b]Motohashi et al. (2009), [c]Rampadarath et al. (2018), [d]Simon et. al. (2009), [U] Unpublished

Table 5.6 GenBank BLAST search results (top five) of 17 strains excluded from *Phyllosticta* in this study

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	Strain	GenBank accession no.	Identities (I), Query cover (QC)
P. alcides	P3-4[s]	Indetermined	Japan	KF590155■	*Paraphoma radicina*	CBS 111.79	EU754191	I = 99.76% / QC = 100%
					Paraphoma rhaphiolepidis	CBS 142524	KY979813	I = 99.64% / QC = 100%
					Paraphoma radicina	CBS 111.79	KF251676	I = 99.76% / QC = 98%
					Neosetophoma rosarum	MFLU 17-0308	MG829036	I = 99.04% / QC = 100%
					Neosulcatispora agaves	CPC 26407	KT950867	I = 99.04% / QC = 100%
P. artocarpina	B5[d]	*Artocarpus heterophyllus*	India	AY042930▲ (ITS2)	*Neomicrosphaeropsis alhagi-pseudalhagi*	TASM 6134	MH069664	I = 99.54% / QC = 100%
					Epicoccum proteae	CBS 114179	MH862956	I = 99.54% / QC = 100%
					Epicoccum poae	CGMCC 3.18363	NR_158266	I = 99.54% / QC = 100%
					Epicoccum layuense	CGMCC 3.18362	NR_158265	I = 99.54% / QC = 100%
					Epicoccum hordei	CGMCC 3.18360	NR_158263	I = 99.54% / QC = 100%
				AY042929▲ (ITS1)	*Epicoccum rosae*	MFLU 15-3639	NR_157517	I = 100.00 % / QC = 100%
					Epicoccum tritici	MFLUCC 16-0276	KX926426	I = 100.00 % / QC = 100%
					Epicoccum dendrobii	CGMCC 3.18359	NR_158261	I = 100.00 % / QC = 100%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	**Strain**	**GenBank accession no.**	**Identities (I), Query cover (QC)**
					Epicoccum layuense	CGMCC 3.18362	NR_158265	I = 100.00 % / QC = 100%
					Ascochyta rabiei	CBS 237.37	MG786925	I = 99.30% / QC = 100%
P. caprifolii	F23 [u]	*Ferula*		KF887044▲	*Macroventuria wentii*	CBS 526.71	MH860250	I = 99.38% / QC = 100%
					Vacuiphoma bulgarica	CBS 357.84	MH861745	I = 99.18% / QC = 100%
					Vacuiphoma oculihominis	UTHSC DI16-308	NR_158281	I = 98.98% / QC = 100%
					Didymellaceae	2 NV-2016	LT592954	I = 98.98% / QC = 100%
					Ascochyta phacae	CBS 184.55	MH857437	I = 98.77% / QC = 100%
P. citrullina	LrBF12	Bulb of *Lycoris radiata*	China	MG543730▲	*Stagonosporopsis ajacis*	CBS 177.93	NR_160049	I = 99.79% / QC = 91%
					Stagonosporopsis ajacis	CBS 177.93	GU237791	I = 99.79% / QC = 91%
					Stagonosporopsis lupini	CBS 101494	NR_160205	I = 98.40% / QC = 95%
					Stagonosporopsis valerianellae	CBS 329.67	NR_160109	I = 98.40% / QC = 95%
					Stagonosporopsis lupini	CBS 101494	MH862737	I = 98.40% / QC = 95%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	Strain	GenBank accession no.	Identities (I), Query cover (QC)
P. citrullina	LrBF13	Bulb of *Lycoris radiata*	China	MG543731▲	*Stagonosporopsis ajacis*	CBS 177.93	NR_160049	I = 99.59% / QC = 93%
					Stagonosporopsis lupini	CBS 101494	NR_160205	I = 99.59% / QC = 93%
					Stagonosporopsis valerianellae	CBS 329.67	NR_160109	I = 98.22% / QC = 97%
					Stagonosporopsis lupini	CBS 101494	MH862737	I = 98.22% / QC = 97%
					Stagonosporopsis valerianellae	CBS 329.67	MH858985	I = 98.22% / QC = 97%
P. coryli	CTF324 [aa]	Hazelnut		KC196068▲	*Peyronellaea prosopidis*	CPC 21698	NR_137836	I = 99.39% / QC = 100%
					Didymella keratinophila	UTHSC DI16-200	NR_158275	I = 99.18% / QC = 100%
					Didymella sp.	UTHSC DI16-200	LT592901	I = 99.18% / QC = 100%
					Didymella pedeiae	CBS 124517	MH863383	I = 98.98% / QC = 100%
					Didymella microchlamydospora	CBS 105.95	MH862504	I = 98.98% / QC = 100%
P. flevolandica	AFTOL-ID 1786 [u]	-		DQ678090■	*Lolia dictyospora*	CBS H-22131	KU726000	I = 98.98% / QC = 100%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	**Strain**	**GenBank accession no.**	**Identities (I), Query cover (QC)**
					Lindgomyces breviappendiculatus	HHUF 28194	NG_056267	I = 98.82% / QC = 100%
					Lindgomyces breviappendiculatus	KT1399	AB521749	I = 98.82% / QC = 100%
					Lindgomyces apiculatus	KT1108	NG_055737	I = 98.74% / QC = 100%
					Lindgomyces ingoldianus	ATCC 200398	NG_042321	I = 98.66% / QC = 100%
P. flevolandica	CBS 998.72[g]	Soil	Netherlands	DQ377927■	*Lindgomyces angustiascus*	ILL A640-1a	NG_042721	I = 98.43% / QC = 100%
					Lindgomyces lemonweirensis	ILL 40793	NG_042580	I = 98.32% / QC = 100%
					Lindgomyces pseudomadisonensis	KT 2742	LC149916	I = 98.08% / QC = 99%
					Lindgomyces madisonensis	CBS 140367	MH878155	I = 99.08% / QC = 99%
					Lolia dictyospora	CBS H-22131	KU726000	I = 99.18% / QC = 95%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	Strain	GenBank accession no.	Identities (I), Query cover (QC)
P. heveae	NW197[u]	Indetermined	China	EU520128▲	*Didymella keratinophila*	UTHSC DI16-200	NR_158275	I = 96.64%% / QC = 96%
					Didymella sp.	1 NV-2016	LT592901	I = 96.64%% / QC = 96%
					Didymella sancta	CBS 281.83	MH861588	I = 96.25% / QC = 96%
					Didymella microchlamydospora	CBS 105.95	MH862504	I = 96.07% / QC = 96%
					Epicoccum huancayense	CBS 105.80	MH861244	I = 96.07% / QC = 95%
P. jasmini	TS08-19-2[u]	*Jasminum nudiflorum*	China	AB470839▲	*Epicoccum huancayense*	CBS 105.80	MH861244	I = 98.12% / QC = 98%
					Neodidymella thailandicum	MFLU 11-0176	NR_156400	I = 98.11% / QC = 98%
					Stagonosporopsis lupini	CBS 101494	NR_160205	I = 97.93% / QC = 97%
					Ascochyta phacae	CBS 184.55	NR_135942	I = 97.05% / QC = 100%
					Ascochyta phacae	CBS 184.55	EU167570	I = 97.05% / QC = 100%
P. jasmini	6259[u]	*Artemisia annua*	China	JN903927▲	*Boeremia trachelospermi*	CGMCC 3.18222	NR_158252	I = 99.58% / QC = 92%
					Boeremia exigua var. *heteromorpha*	CBS 443.94	NR_158238	I = 99.58% / QC = 92%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	Strain	GenBank accession no.	Identities (I), Query cover (QC)
					Boeremia exigua var. *pseudolilacis*	CBS 101207	NR_158232	I = 99.58% / QC = 92%
					Boeremia exigua var. *populi*	CBS 100167	NR_158231	I = 99.58% / QC = 92%
					Boeremia strasseri	CBS 126.93	NR_135985	I = 99.37% / QC = 92%
P. juglandis	H2 [u]	Indetermined		KC168088▲	*Didymella rosea*	BRIP 50788	NR_136125	I = 99.39% / QC = 100%
					Phoma segeticola	CGMCC 3.17489	KP330443	I = 100.00% / QC = 97%
					Didymella suiyangensis	CGMCC 3.18352	NR_158260	I = 99.79% / QC = 97%
					Didymella suiyangensis	LC7439	KY742089	I = 99.79% / QC = 97%
					Didymella brunneospora	CBS 115.58	KT389505	I = 99.37% / QC = 97%
P. ligustri	TS08-20-1 [u]	*Ligustrum* sp.	China	AB470841▲	*Ascochyta rabiei*	CBS 237.37	EU167600	I = 97.79% / QC = 100%
					Ascochyta phacae	CBS 184.55	NR_135942	I = 97.61% / QC = 100%
					Epicoccum huancayense	CBS 105.80	MH861244	I = 97.94% / QC = 97%
					Didymella microchlamydospora	CBS 105.95	MH862504	I = 97.23% / QC = 99%
					Didymella keratinophila	UTHSC DI16-200	NR_158275	I = 97.39% / QC = 98%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	Strain	GenBank accession no.	Identities (I), Query cover (QC)
P. papayae	T150 [u]	Indetermined	China	FJ462748▲	*Diaporthe mahothocarpus*	CGMCC 3.15181	NR_147522	I = 99.81% / QC = 91%
					Diaporthe toxicodendri	TFM FP-10740	NR_158416	I = 96.52% / QC = 98%
					Diaporthe toxicodendri	FFPRI420987	LC275192	I = 96.52% / QC = 98%
					Diaporthe alnea	CBS 146.46	NR_147525	I = 96.83% / QC = 97%
					Diaporthe bohemiae	CPC 28222	NR_164425	I = 96.45% / QC = 97%
P. papayae	7AJ-10 [u]	Mulberry		KR708979▲	*Diaporthe mahothocarpus*	CGMCC 3.15181	NR_147522	I = 99.56% / QC = 79%
					Diaporthe toxicodendri	TFM FP-10740	NR_158416	I = 96.85% / QC = 83%
					Diaporthe toxicodendri	FFPRI420987	LC275192	I = 96.85% / QC = 83%
					Diaporthe alnea	CBS 146.46	NR_147525	I = 96.80% / QC = 82%
					Diaporthe bohemiae	CPC 28222	NR_164425	I = 97.00% / QC = 82%
P. populina	NW584 [u]	Indetermined	China	EU520202▲	*Epicoccum huancayense*	CBS 105.80	MH861244	I = 96.99% / QC = 97%
					Neodidymella thailandicum	MFLU 11-0176	NR_156400	I = 96.82% / QC = 97%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	Strain	GenBank accession no.	Identities (I), Query cover (QC)
					Stagonosporopsis lupini	CBS 101494	NR_160205	I = 96.85% / QC = 97%
					Boeremia trachelospermi	CGMCC 3.18222	NR_158252	I = 100.00% / QC = 88%
					Boeremia exigua var. *heteromorpha*	CBS 443.94	NR_158238	I = 100.00% / QC = 88%
P. sojicola	CBS 301.39 [p]	Indetermined	Germany	EU573029▲	*Epicoccum proteae*	CBS 114179	NR_158240	I = 98.04% / QC = 100%
					Neodidymella thailandicum	MFLU 11-0176	NR_156400	I = 97.85%/ QC = 100%
					Epicoccum huancayense	CBS 105.80	MH861244	I = 97.84% / QC = 100%
					Stagonosporopsis lupini	CBS 101494	NR_160205	I = 97.65% / QC = 99%
					Boeremia trachelospermi	CGMCC 3.18222	NR_158252	I = 99.79% / QC = 93%
				MH867524■	*Stagonosporopsis pini*	C452	MK348019	I = 97.74% / QC = 99%
					Didymella vitalbina	CBS 123707	MH874853	I = 97.63% / QC = 99%
					Didymella anserina	CBS 285.29	MH866534	I = 97.63% / QC = 99%
					Briansuttonomyces eucalypti	CBS 114879	KU728519	I = 97.63% / QC = 99%

Table 5.6 (continued)

Taxon	Strain	Host	Country	GenBank accession no.*	GenBank BLAST search against type material			
					Species identified (top BLAST results)	**Strain**	**GenBank accession no.**	**Identities (I), Query cover (QC)**
					Phoma tamaricicola	MFLUCC 14-0602	KM408754	I = 97.63% / QC = 99%
				EU595356○	*Boeremia exigua* var. *pseudolilacis*	CBS 101207	KY484710	I = 93.87% / QC = 88%
					Boeremia exigua var. *populi*	CBS 100167	KY484706	I = 90.84% / QC = 88%
					Boeremia exigua var. *heteromorpha*	CBS 443.94	KY484700	I = 90.84% / QC = 88%
					Boeremia strasseri	CBS 126.93	KY484735	I = 90.04% / QC = 88%
					Boeremia noackiana	CBS 101203	KY484728	I = 85.77% / QC = 88%

Note *Gene: ▲ITS, ▪LSU, ○*ef1α*

Table 5.7 Recorded geographic and host distributions of *Phyllosticta* species

Species record	Host	Locality	References
***Phyllosticta capitalensis* species complex**			
P. acaciigena	*Acacia suaveolens*	Australia	Crous et al. (2016)
P. aloeicola	*Aloe ferox*	South Africa	Wikee et al. (2013b)
P. ardisiicola	*Ardisia crenata*	Japan	Motohashi et al. (2008)
P. aristolochiicola	*Aristolochia acuminata*	Australia	Crous et al. (2012a)
	Aristolochia clematitis	Australia	Wulandari et al. (2013)
	Aristolochia sempervirens	Australia	Wulandari et al. (2013)
P. azevinhi	*Ilex azevinho*	Madeira Islands	Spaulding (1961)
	Ilex pedunculosa	Japan	Kobayashi (2007), Kobayashi and Sasaki (1975), Motohashi et al. (2009)
P. beaumarisii	*Muehlenbeckia adpressa*	Australia	Paul et al. (1986)
P. brazilianiae	*Mangifera indica*	Brazil	Glienke et al. (2011)
P. capitalensis	*Acacia crassicarpa*	Thailand	Wikee et al. (2013b)
	Acer rubrum	Japan	Okane et al. (2003)
	Acer sp.	Japan	Motohashi et al. (2009)
	Aleurites fordii	Georgia	Wulandari et al. (2013)
	Allamanda cathartica	India	Wulandari et al. (2013)
	Allophylus sp.	South Africa	Wikee et al. (2013a)
	Alnus serrulatoides	Japan	Okane et al. (2003)
	Alocasia sp.	Thailand	Wikee et al. (2013a)
	Amomum siamense	Thailand	Okane et al. (2003)
	Amomum sp.	Thailand	Okane et al. (2003), Wikee et al. (2013a)

Table 5.7 (continued)

Species record	Host	Locality	References
	Amomum uliginosum	Thailand	Okane et al. (2003)
	Ampelopsis sp.	United States	Wikee et al. (2013a)
	Anacardium giganteum	Brazil	Rodrigues et al. (2004), Wulandari et al. (2009), Glienke et al. (2011)
	Anacardium sp.	Brazil	Wikee et al. (2013a)
	Anarcardium giganteum	Brazil	Sultan et al. (2011)
	Anogeissus latifolia	India	Murali et al. (2007)
	Anthocleista sp.	South Africa	Wikee et al. (2013a)
	Anthurium sp.	Thailand	Wikee et al. (2013a)
	Artocarpus sp.	Thailand	Shaw et al. (2006), Wikee et al. (2013a)
	Arundina bambusifolia	Costa Rica	Cash and Watson (1955), Thaung (2008a)
	Arundina graminifolia	Japan	Okane et al. (2003)
	Arundina sp.	Japan	Wikee et al. (2013a)
	Aspidistra elatior	Japan	Motohashi et al. (2009)
	Aspidosperma polyneuron	Brazil	Rodrigues et al. (2004), Wulandari et al. (2009), Wikee et al. (2011), Glienke et al. (2011), Wikee et al. (2013a, b)
	Aspidosperma sp.	Brazil	Wikee et al. (2013a)
	Atropis distans	Georgia	Wulandari et al. (2013)
	Baccaurea ramiflora	Thailand	Wikee et al. (2013b)
	Banksia dryandroides	Hawaii	Crous et al. (2004)
	Barringtonia racemosa	South Africa, KwaZulu-Natal	Shaw et al. (2006)
	Barringtonia sp.	South Africa	Wikee et al. (2013a)

Table 5.7 (continued)

Species record	Host	Locality	References
	Bauhinia racemosa	India	Murali et al. (2007)
	Berberis thunbergii	Japan	Okane et al. (2003)
	Bifrenaria harrisoniae	Brazil	Silva et al. (2008)
	Botrychium sp.	United States	Wikee et al. (2013a)
	Bowdichia nitida	Brazil	Rodrigues et al. (2004), Wulandari et al. (2009), Wikee et al. (2011), Glienke et al. (2011), Wikee et al. (2013a, b)
	Bowdichia sp.	Brazil	Wikee et al. (2013a)
	Brassolaeliocattleya sp.	Florida	Alfieri Jr. et al. (1984)
	Bumelia lycioides	Georgia, United States	Wulandari et al. (2013)
	Butea monosperma	India	Murali et al. (2007)
	Caesalpinia crista	Japan	Okane et al. (2003)
	Caesalpinia sp.	Japan	Wikee et al. (2013a)
	Calophyllum sp.	Thailand	Wikee et al. (2013a)
	Camellia sinensis	China, India, Japan, Malawi, Papua New Guinea, Taiwan	Mathur (1979), Kobayashi (2007), Wiehe (1953), Shaw (1984), Anonymous (1979), Cheng et al. (2019)
	Camellia sp.	United States	Wikee et al. (2013a)
	Canthium sp.	South Africa	Wikee et al. (2013a)
	Capsicum sp.	Dominican Republic	Wulandari et al. (2009), Glienke et al. (2011), Wikee et al. (2013a)
	Careya arborea	India	Murali et al. (2007)
	Cariniana estrellensis	Brazil	Lisboa et al. (2016)
	Cassia fistula	India	Murali et al. (2007)

Table 5.7 (continued)

Species record	Host	Locality	References
	Cassia occidentalis	Brazil	Rodrigues et al. (2004)
	Cattleya skinneri	Guatemala	Cash and Watson (1955)
	Cattleya sp.	Florida	Alfieri Jr. et al. (1984)
	Cerbera manghas	Japan	Okane et al. (2003)
	Cerbera sp.	Japan	Wikee et al. (2013a)
	Cercidiphyllum japonicum	Japan	Motohashi et al. (2009)
	Cercidiphyllum sp.	Japan	Wikee et al. (2013a)
	Cercis canadensis	Japan	Motohashi et al. (2009)
	Cercis sp.	Japan	Wikee et al. (2013a)
	Cinnamomum camphora	Japan	Okane et al. (2003)
	Cinnamomum japonicum	Japan	Okane et al. (2003)
	Cinnamomum sp.	Japan	Wikee et al. (2013a)
	Citrus × *paradisi*	Florida, South Africa, KwaZulu-Natal, South Africa, Mpumalanga	Peres et al. (2007), Meyer et al. (2006)
	Citrus × *paradisi-reticulata*	New Zealand	Everett and Rees-George (2006)
	Citrus aurantifolia	Italy, New Zealand	Guarnaccia et al. (2017), Tran et al. (2019), Wikee et al. (2013b), Wulandari et al. (2009), Glienke et al. (2011)
	Citrus aurantium	Australia, Brazil, Thailand	Rodrigues et al. (2004), Wulandari et al. (2009), Miles et al. (2013), Tran et al. (2019), Glienke et al. (2011), Guarnaccia et al. (2017)
	Citrus latifolia	Brazil	Glienke et al. (2011), Wikee et al. (2013a)

Table 5.7 (continued)

Species record	Host	Locality	References
	Citrus limon	South Africa, Eastern Cape, Taiwan, Argentina, Australia, Greece, Italy, Malta, Portugal, Spain	Meyer et al. (2006), Wulandari et al. (2009), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014), Miles et al. (2013), Tran et al. (2019), Guarnaccia et al. (2017)
	Citrus limonia	Brazil	Glienke et al. (2011)
	Citrus medica var. *sarcodactylis*	Italy	Guarnaccia et al. (2017)
	Citrus paradisi	Florida	Wulandari et al. (2009), Glienke et al. (2011)
	Citrus reticulata	Australia, Brazil	Miles et al. (2013), Tran et al. (2019), Glienke et al. (2011), Wikee et al. (2013a)
	Citrus sinensis	Brazil, Florida	Glienke et al. (2011), Wikee et al. (2013a, b), Guarnaccia et al. (2017)
	Citrus sp.	Argentina, Australia, Brazil, China, Hong Kong, New Zealand, South Africa, Taiwan, Thailand, United States	Wulandari et al. (2009), Wikee et al. (2011, 2013a), Glienke et al. (2011), Guarnaccia et al. (2017)
	Clethra barbinervis	Japan	Okane et al. (2003)
	Cliffortia sp.	South Africa	Wikee et al. (2013a)
	Clutia sp.	South Africa	Wikee et al. (2013a)
	Cocculus sp.	United States	Wikee et al. (2013a)
	Codiaeum sp.	Thailand	Wikee et al. (2013a)
	Coelogyne sp.	Philippines, Thailand	Cash and Watson (1955), Shaw et al. (2006), Wikee et al. (2013a)
	Combretum sp.	South Africa	Wikee et al. (2013a)
	Comocladia sp.	Puerto Rico	Wikee et al. (2013a)
	Coprosma sp.	Hawaii	Wikee et al. (2013a)

Table 5.7 (continued)

Species record	Host	Locality	References
	Cordia obliqua	India	Murali et al. (2007)
	Cordia sp.	South Africa	Wikee et al. (2013a)
	Cordia wallichii	India	Murali et al. (2007)
	Cordyline fruticosa	Thailand	Wikee et al. (2013b)
	Coriaria terminalis	Japan	Okane et al. (2003)
	Cornus kousa	Japan	Okane et al. (2003)
	Corylopsis sinensis	Japan	Okane et al. (2003)
	Corylus sieboldiana	Japan	Okane et al. (2003)
	Cotinus coggygria var. *cinerea*	Japan	Okane et al. (2003)
	Crinum asiaticum	Thailand	Wikee et al. (2013b)
	Crinum sp.	Thailand	Liu et al. (2012)
	Croton sp.	South Africa	Wikee et al. (2013a)
	Ctenomeria sp.	South Africa	Wikee et al. (2013a)
	Curtisia sp.	South Africa	Wikee et al. (2013a)
	Cussonia sp.	South Africa, Gauteng	Meyer et al. (2006), Wikee et al. (2013a)
	Cymbidium sp.	Brazil, Florida, India	Alfieri Jr. et al. (1984), Silva and Pereira (2007), Glienke et al. (2011), Wikee et al. (2013b)
	Cyphostemma sp.	South Africa	Wikee et al. (2013a)
	Cypripedium insigne	India	Cash and Watson (1955)
	Cypripedium sp.	Japan	Cash and Watson (1955)
	Dalbergia lanceolaria	India	Murali et al. (2007)

Table 5.7 (continued)

Species record	Host	Locality	References
	Daphniphyllum teijsmanni	Japan	Okane et al. (2003)
	Davidia involucrata	Japan	Okane et al. (2003), Motohashi et al. (2009)
	Davidia sp.	Japan	Wikee et al. (2013a)
	Dendrobium canaliculatum	Australia	Cash and Watson (1955)
	Dendrobium phalaenopsis	Australia, Belgium, Philippines	Nag Raj (1993), Cash and Watson (1955)
	Dendrobium schuetzei	Philippines	Cash and Watson (1955)
	Dendrobium sp.	Brunei Darussalam, Thailand, Florida, Haiti, Samoa	Peregrine and Ahmad (1982), Wikee et al. (2013a), Alfieri Jr. et al. (1984), Benjamin and Slot (1969), Cash and Watson (1955)
	Dendrobium undulatum	Australia	Cash and Watson (1955)
	Dendropanax trifidus	Japan	Motohashi et al. (2009)
	Dieffenbachia sp.	Thailand	Wikee et al. (2013a)
	Diospyros kaki	Taiwan	Duan et al. (2017)
	Diospyros montana	India	Murali et al. (2007)
	Diospyros sp.	South Africa	Wikee et al. (2013a)
	Dodonaea sp.	Hawaii	Wikee et al. (2013a)
	Dovyalis sp.	South Africa	Wikee et al. (2013a)
	Dracontomelon mangiferum	Myanmar	Thaung (2008b)
	Ekebergia sp.	South Africa	Wikee et al. (2013a)
	Elaeis guineensis	Malaysia	Nasehi et al. (2020)
	Elaeocarpus glabripetalus	China	Lou et al. (2009)
	Elaeodendron glaucum	India	Murali et al. (2007)

Table 5.7 (continued)

Species record	Host	Locality	References
	Encephalartos ferox	South Africa	Glienke et al. (2011)
	Encephalartos sp.	South Africa	Wikee et al. (2013a)
	Enkianthus sp.	Japan	Wikee et al. (2013a)
	Epidendrum fragrans	Jamaica	Cash and Watson (1955)
	Epidendrum sp.	Florida, Mexico	Alfieri Jr. et al. (1984), Cash and Watson (1955)
	Eriobotrya japonica	Japan	Motohashi et al. (2009)
	Eriobotrya sp.	Japan	Wikee et al. (2013a)
	Erythroxylum monogynum	India	Murali et al. (2007)
	Eucalyptus dives	South Africa	Wulandari et al. (2013)
	Eucalyptus grandis	Brazil	Wikee et al. (2013b)
	Eucalyptus sp.	Brazil, South Africa	Wikee et al. (2013a)
	Euclea sp.	South Africa	Wikee et al. (2013a)
	Euonymus alatus	Japan	Okane et al. (2003)
	Euphorbia milii	Thailand	Wikee et al. (2013a, b), Guarnaccia et al. (2017)
	Euphorbia sp.	Thailand	Wikee et al. (2013a)
	Eurya japonica	Japan	Okane et al. (2003)
	Fagus crenata	Japan	Okane et al. (2003)
	Fagus japonica	Japan	Okane et al. (2003)
	Ficus benjamina	Thailand	Wikee et al. (2013a, b)
	Ficus sp.	Thailand	Wikee et al. (2013a)
	Forsythia koreana	Japan	Okane et al. (2003)

Table 5.7 (continued)

Species record	Host	Locality	References
	Forsythia viridissima	Japan	Okane et al. (2003)
	Fortunella sp.	South Africa, Mpumalanga, United States	Meyer et al. (2006), Wikee et al. (2013a)
	Gardenia jasminoides var. *radicans*	Japan	Okane et al. (2003)
	Gardenia sp.	South Africa	Wikee et al. (2013a)
	Ginkgo biloba	Japan, Taiwan	Motohashi et al. (2009), Kirschner (2018)
	Ginkgo sp.	Japan	Wikee et al. (2013a)
	Givotia rottleriformis	India	Murali et al. (2007)
	Gmelina arborea	India	Murali et al. (2007)
	Grevillea robusta	Hawaii	Crous et al. (2004, 2013)
	Grevillea sp.	Australia, Tasmania	Crous et al. (2004, 2013)
	Grewia sp.	South Africa	Wikee et al. (2013a)
	Grewia tiliifolia	India	Murali et al. (2007)
	Guzmania sp.	Florida	Alfieri Jr. et al. (1984)
	Hebe sp.	South Africa	Wikee et al. (2013a)
	Hedera helix	Italy	Wulandari et al. (2009)
	Hedera sp.	South Africa	Wikee et al. (2013a)
	Heliconia sp.	Thailand	Wikee et al. (2013b)
	Helicteres isora	India	Murali et al. (2007)
	Helicteres jamaicensis	Puerto Rico	Wulandari et al. (2013)
	Helicteres sp.	Puerto Rico	Wulandari et al. (2013)
	Heptapleurum venulosum	Pakistan	Wulandari et al. (2013)

Table 5.7 (continued)

Species record	Host	Locality	References
	Hibiscus sp.	Thailand	Wikee et al. (2013a)
	Hibiscus syriacus	Thailand	Wikee et al. (2013a, b), Guarnaccia et al. (2017)
	Hydrangea quercifolia	Japan	Motohashi et al. (2009)
	Hypericum androsaemum	Japan	Okane et al. (2003)
	Ilex rotunda	Japan	Okane et al. (2003)
	Ilex serrata	Japan	Okane et al. (2003)
	Ilex sp.	United States	Wikee et al. (2013a)
	Ipomoea sp.	Malaysia	Wikee et al. (2013a)
	Itea sp.	United States	Wikee et al. (2013a)
	Ixora chinensis	Thailand	Wikee et al. (2013b), Guarnaccia et al. (2017)
	Ixora nigricans	India	Murali et al. (2007)
	Jacquiniella sp.	Panama	Cash and Watson (1955), Piepenbring (2006)
	Juglans mandshurica	Japan	Okane et al. (2003)
	Kandelia candel	Japan	Okane et al. (2003)
	Kandelia sp.	Japan	Wikee et al. (2013a)
	Koelreuteria paniculata	Japan	Okane et al. (2003)
	Kydia calycina	India	Murali et al. (2007)
	Laelia anceps	Mexico	Cash and Watson (1955)
	Laelia sp.	Florida	Alfieri Jr. et al. (1984)
	Laeliocattleya sp.	Florida	Alfieri Jr. et al. (1984)
	Lagerstroemia microcarpa	India	Murali et al. (2007)

Table 5.7 (continued)

Species record	Host	Locality	References
	Lagerstroemia parviflora	India	Murali et al. (2007)
	Leucadendron × *laureolum-salignum*	Hawaii	Crous et al. (2013)
	Leucadendron sp.	Australia, Hawaii, Tasmania	Crous et al. (2004, 2013)
	Leucospermum cordifolium-glabrum	Hawaii	Crous et al. (2013)
	Leucospermum cordifolium-patersonii	Hawaii	Crous et al. (2013)
	Leucospermum sp.	Australia, Hawaii, Tasmania	Wikee et al. (2013a), Crous et al. (2004, 2013)
	Ligustrum lucidum	Japan	Motohashi et al. (2009)
	Ligustrum sp.	Japan	Wikee et al. (2013a)
	Lindera strychnifolia	Japan	Okane et al. (2003)
	Lindera umbellata	Japan	Okane et al. (2003)
	Litchi sp.	South Africa	Wikee et al. (2013a)
	Lithocarpus edulis	Japan	Motohashi et al. (2009)
	Lithocarpus sp.	Japan	Wikee et al. (2013a)
	Livistona sp.	Thailand	Wikee et al. (2013a)
	Lonicera morrowii	Japan	Okane et al. (2003)
	Loxostylis sp.	South Africa	Wikee et al. (2013a)
	Macfadyena unguis-cati	Brazil	da Silva et al. (2012)
	Mackaya sp.	South Africa	Wikee et al. (2013a)
	Maerua sp.	South Africa	Wikee et al. (2013a)
	Magnolia grandiflora	Iran	Esmaeilzadeh et al. (2020)
	Magnolia liliifera	Thailand	Wulandari et al. (2009), Glienke et al. (2011), Wikee et al. (2011)

Table 5.7 (continued)

Species record	Host	Locality	References
	Magnolia praecocissima	Japan	Okane et al. (2003)
	Magnolia salicifolia	Japan	Okane et al. (2003)
	Magnolia sp.	Thailand, United States	Wikee et al. (2013a)
	Mangifera indica	Brazil, Florida, Japan, India, Malaysia, Mexico, Myanmar, South Africa, Mpumalanga, Taiwan	Sivanesan (1984), Watson (1971), Roy (1967), Glienke et al. (2011), Wikee et al. (2011, 2013a), Miles et al. (2013), Zhou et al. (2015), Hyde et al. (2014), Liu (1977), Thaung (2008b), Meyer et al. (2006), Sivanesan and Hsieh (1989), Nag Raj (1993), van der Aa (1973), Kobayashi (2007), Alfieri Jr. et al. (1984), McGuire and Crandall (1967)
	Mangifera sp.	Brazil, Ghana	Wikee et al. (2013a)
	Michelia fuscata	Japan	Okane et al. (2003)
	Michelia sp.	Thailand	Wikee et al. (2013a)
	Monanthotaxis sp.	South Africa	Wikee et al. (2013a)
	Morus alba	Japan	Okane et al. (2003)
	Morus latifolia	Japan	Okane et al. (2003)
	Morus sp.	Thailand	Wikee et al. (2013a)
	Musa acuminata	China, Hawaii, Indonesia, Indonesia, South Africa, KwaZulu-Natal, South Africa, Mpumalanga, Thailand	Okane et al. (2003), Meyer et al. (2006), Wulandari et al. (2009), Sun et al. (2016), Wikee et al. (2013b), Glienke et al. (2011), Wikee et al. (2013b), Miles et al. (2013)

Table 5.7 (continued)

Species record	Host	Locality	References
	Musa paradisiaca	Thailand	Wulandari et al. (2009), Glienke et al. (2011), Wikee et al. (2011), Wikee et al. (2013a, b), Guarnaccia et al. (2017)
	Musa sp.	Hawaii, Indonesia, Thailand, United States	Crous et al. (2004), Glienke et al. (2011), Wikee et al. (2013a)
	Myracrodruon sp.	Brazil	Wikee et al. (2013a)
	Myracrodruon urundeuva	Brazil	Rodrigues et al. (2004), Wulandari et al. (2009), Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Miles et al. (2013)
	Myrica rubra	Japan	Okane et al. (2003)
	Nandina domestica	Japan	Okane et al. (2003)
	Nandina domestica var. *leucocarpa*	Japan	Okane et al. (2003)
	Naringi crenulata	India	Murali et al. (2007)
	Nephelium lappaceum	Hawaii	Wulandari et al. (2009), Glienke et al. (2011), Wikee et al. (2013b), Guarnaccia et al. (2017)
	Nephelium sp.	United States	Wikee et al. (2013a)
	Nerium oleander var. *indicum*	Japan	Motohashi et al. (2009)
	Nerium sp.	Japan	Wikee et al. (2013a)
	Nidularium sp.	Florida	Alfieri Jr. et al. (1984)
	Ocotea sp.	South Africa	Wikee et al. (2013a)
	Odontoglossum sp.	Florida	Alfieri Jr. et al. (1984)
	Oncidium sp.	Florida, Panama	Alfieri Jr. et al. (1984), Cash and Watson (1955), Piepenbring (2006)
	Ophiopogon sp.	Thailand	Wikee et al. (2013a)

Table 5.7 (continued)

Species record	Host	Locality	References
	Orchidaceae	Florida	Alfieri Jr. et al. (1984)
	Orchidaceae	Japan	Okane et al. (2003)
	Orixa japonica	Japan	Okane et al. (2003)
	Osmanthus fragrans var. *aurantiacus f. aurantiacus*	Japan	Motohashi et al. (2009)
	Ougeinia oojeinensis	India	Murali et al. (2007)
	Pandanus sp.	Thailand	Hyde et al. (2018)
	Paphiopedilum callosum	Germany	Wulandari et al. (2009), Glienke et al. (2011), Wikee et al. (2013a, b), Guarnaccia et al. (2017)
	Paphiopedilum sp.	Germany	Wikee et al. (2013a)
	Parinari sp.	South Africa	Wikee et al. (2013a)
	Paullinia cupana	Brazil	Wikee et al. (2013a)
	Pavetta sp.	South Africa	Wikee et al. (2013a)
	Persea americana	South Africa, Mpumalanga	Meyer et al. (2006)
	Phalaenopsis sp.	Florida	Alfieri Jr. et al. (1984)
	Phellodendron amurense	Japan	Okane et al. (2003)
	Philodendron sp.	Thailand	Wikee et al. (2013a, b)
	Picrasma quassioides	Japan	Okane et al. (2003)
	Piper sp.	Puerto Rico	Wulandari et al. (2013)
	Pittosporum sp.	Hawaii, Japan	Wikee et al. (2013a)
	Pittosporum tobira	Japan	Motohashi et al. (2009)

Table 5.7 (continued)

Species record	Host	Locality	References
	Podocarpus macrophyllus	Japan	Okane et al. (2003)
	Podocarpus sp.	South Africa	Wikee et al. (2013a)
	Polyalthia longifolia	Thailand	Wikee et al. (2013a, b), Guarnaccia et al. (2017)
	Polyalthia sp.	Thailand	Wikee et al. (2013a)
	Polyscias sp.	Thailand	Wikee et al. (2013a, b)
	Premna tomentosa	India	Murali et al. (2007)
	Protea × *compacta-susannae*	Hawaii	Crous et al. (2013)
	Protea cynaroides	Hawaii	Crous et al. (2004, 2013)
	Protea repens	Portugal	Wikee et al. (2013b)
	Protea sp.	Hawaii	Wikee et al. (2013a)
	Prunus cerasoides	Thailand	Okane et al. (2003)
	Prunus laurocerasus var. *angustifolia*	Japan	Okane et al. (2003)
	Prunus sp.	Japan	Wikee et al. (2013a)
	Psidium guajava	Brazil, India, Venezuela	Wulandari et al. (2009), Wikee et al. (2011), Glienke et al. (2011), Pande (2008), Gonzalez and Rondon (2005)
	Psidium sp.	Brazil	Wikee et al. (2013a)
	Punica granatum	Japan, Thailand	Okane et al. (2003), Wikee et al. (2013a, b)
	Punica granatum var. *nana*	Japan	Okane et al. (2003)
	Punica sp.	Thailand	Wikee et al. (2013a)
	Putterlickia sp.	South Africa	Wikee et al. (2013a)
	Pyrrosia adnascens	Thailand	Wikee et al. (2013b)

Table 5.7 (continued)

Species record	Host	Locality	References
	Quercus dentata	Japan	Okane et al. (2003)
	Quercus variabilis	Japan	Okane et al. (2003)
	Rauvolfia sp.	South Africa	Wikee et al. (2013a)
	Rhododendron × *pulchrum*	Japan	Wulandari et al. (2013)
	Rhododendron indicum	Japan	Okane et al. (2003)
	Rhododendron simsii	Japan	Okane et al. (2003)
	Rhododendron sp.	Brazil, Japan	Rodrigues et al. (2004), Sultan et al. (2011), Wikee et al. (2013a)
	Rhoicissus sp.	South Africa	Wikee et al. (2013a)
	Rhus sp.	South Africa	Wikee et al. (2013a)
	Rhynchostylis sp.	Malaysia	Liu (1977), Wikee et al. (2013a)
	Ricinus communis	China	Tang et al. (2020)
	Robinia pseudoacacia	Japan	Motohashi et al. (2009)
	Rothmannia sp.	South Africa	Wikee et al. (2013a)
	Rubus croceacanthus	Japan	Okane et al. (2003)
	Rubus sp.	Japan	Wikee et al. (2013a)
	Saccharum officinarum	Thailand	Wikee et al. (2013a, b)
	Saccharum sp.	Thailand	Wikee et al. (2013a)
	Sambucus nigra	Japan	Okane et al. (2003)
	Sansevieria hyacinthoides	Thailand	Wikee et al. (2013a)
	Sansevieria sp.	Netherlands, Thailand	Wulandari et al. (2009), Wikee et al. (2013a, b)
	Schefflera venulosa	Thailand	Wikee et al. (2013b)

Table 5.7 (continued)

Species record	Host	Locality	References
	Schomburgkia sp.	Cayman, Islands, West Indies	Cash and Watson (1955)
	Schomburgkia tibicinis	Mexico	Cash and Watson (1955)
	Schrebera sp.	South Africa	Wikee et al. (2013a)
	Sclerocarya sp.	South Africa	Wikee et al. (2013a)
	Scutia sp.	South Africa	Wikee et al. (2013a)
	Secamone sp.	South Africa	Wikee et al. (2013a)
	Smilax aspera	India	Wulandari et al. (2013)
	Smilax china	Japan	Okane et al. (2003)
	Smilax kraussiana	South Africa	Glienke et al. (2011)
	Smilax sp.	South Africa	Wikee et al. (2013a)
	Sophora japonica	Japan	Okane et al. (2003)
	Sorbus commixta	Japan	Okane et al. (2003)
	Spathiphyllum sp.	Japan	Motohashi et al. (2009), Wikee et al. (2013a)
	Spondias mombin	Brazil, Indonesia	Rodrigues et al. (2004), Wulandari et al. (2009), Wikee et al. (2011), Glienke et al. (2011), Ismail et al. (2012, 2013), Miles et al. (2013)
	Spondias sp.	Brazil	Wikee et al. (2013a)
	Stangeria sp.	South Africa	Wikee et al. (2013a)
	Stanhopea graveolens	Brazil	Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Miles et al. (2013)
	Stanhopea sp.	Brazil, Costa Rica	Cash and Watson (1955), Nag Raj (1993), Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Zhou et al. (2015), Guarnaccia et al. (2017), Tran et al. (2019), Hyde et al. (2014)

Table 5.7 (continued)

Species record	Host	Locality	References
	Sterculia sp.	Puerto Rico	Wikee et al. (2013a)
	Stereospermum angustifolium	India	Murali et al. (2007)
	Strychnos potatorum	India	Murali et al. (2007)
	Strychnos sp.	South Africa	Wikee et al. (2013a)
	Sumbaviopsis albicans	Puerto Rico	Wulandari et al. (2013)
	Syringa reticulata	Iran	Esmaeilzadeh et al. (2020)
	Syzygium cumini	India	Murali et al. (2007)
	Syzygium sp.	Madagascar	Wikee et al. (2013b)
	Tectona grandis	India, Thailand	Murali et al. (2007), Wikee et al. (2013a, b), Hyde et al. (2018)
	Telopea sp.	Australia, Hawaii, Tasmania, Thailand	Wikee et al. (2013a), Crous et al. (2004, 2013)
	Terminalia crenulata	India	Murali et al. (2007)
	Thea sinensis	China, USSR	Watson (1971), Jin (2011)
	Thujopsis dolabrata var. *hondai*	Japan	Okane et al. (2003)
	Tilia miqueliana	Japan	Okane et al. (2003)
	Tinospora crispa	Thailand	Wikee et al. (2013a)
	Tinospora sp.	Thailand	Wikee et al. (2013a)
	Trema sp.	South Africa	Wikee et al. (2013a)
	Trichilia sp.	South Africa	Wikee et al. (2013a)
	Tsuga sieboldii	Japan	Okane et al. (2003)
	unknown, Pteridophyta	Japan	Okane et al. (2003)

Table 5.7 (continued)

Species record	Host	Locality	References
	Vaccinium sp.	New Zealand	Wulandari et al. (2009), Glienke et al. (2011), Wikee et al. (2013a, b), Guarnaccia et al. (2017), Tran et al. (2019)
	Vagnera stellata	New York, United States	Wulandari et al. (2013), Wulandari et al. (2013)
	Vanda sp.	Brunei Darussalam, Florida	Peregrine and Ahmad (1982), Alfieri Jr. et al. (1984)
	Vinca minor	South Africa	Shaw et al. (2006)
	Viscum sp.	South Africa	Wikee et al. (2013a)
	Vitex agnus-castus	Japan	Okane et al. (2003)
	Vitex cannabifolia	Japan	Okane et al. (2003)
	Vitex sp.	Malaysia, South Africa	Wikee et al. (2013a)
	Xymalos sp.	South Africa	Wikee et al. (2013a)
	Zanthoxylum armatum	Japan	Okane et al. (2003)
	Zanthoxylum sp.	Japan, Puerto Rico	Wikee et al. (2013a)
	Zingiber officinale	Thailand	Okane et al. (2003)
	Ziziphus sp.	South Africa, Thailand	Wikee et al. (2013a)
	Ziziphus xylopyrus	India	Murali et al. (2007)
P. carochlae	*Caryota ochlandra*	China	Zhou et al. (2015)
P. cavendishii	*Musa* sp.	Australia	Wong et al. (2013)
P. cordylinophila	*Cordyline atropurpurea*	Japan	Wikee et al. (2013b)
	Cordyline australis	Hawaii, New Zealand	Nag Raj (1993), Pennycook (1989)
	Cordyline banksii	New Zealand	Pennycook (1989)
	Cordyline dracaenoides	Argentina	Farr (1973)

Table 5.7 (continued)

Species record	Host	Locality	References
	Cordyline fruticosa	Japan, Thailand	Motohashi et al. (2009), Wikee et al. (2013b)
	Cordyline terminalis	Hawaii, India, Japan, Samoa, Tonga	Dingley et al. (1981), Mathur (1979), Raabe (1981), Kobayashi (2007)
	Crinum pedunculatum	Australia	Simmonds (1966)
	Dracaena sp.	Puerto Rico, Virgin Islands, West Indies	Stevenson (1975), Minter et al. (2001)
P. eugeniae	Eugenia aromatica	Indonesia	Sultan et al. (2011)
	Eugenia cumini	Taiwan	Anonymous (1979)
	Eugenia maleolens	Puerto Rico, Virgin Islands	Stevenson (1975)
	Eugenia sp.	Florida	Alfieri Jr et al. (1984)
	Eugenia uniflora	Florida	Alfieri Jr et al. (1984)
	Syzygium cumini	Florida	Alfieri Jr et al. (1984)
	Syzygium jambos	Florida	Alfieri Jr et al. (1984)
P. fallopiae	*Fallopia japonica*	Japan	Motohashi et al. (2008, 2009), Wikee et al. (2011), Zhou et al. (2015), Hyde et al. (2014)
P. ilicis-aquifolii	*Ilex aquifolium*	China, United Kingdom	Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014), Su and Cai (2012)
P. maculata	*Musa acuminata*	Australia, Hawaii, Indonesia	Shivas (1989), Raabe et al. (1981), Wulandari et al. (2010)
	Musa sapientum	Thailand	Giatgong (1980)
	Musa sp.	Australia, Bangladesh, Bhutan, Brunei Darussalam, China, Christmas Island,	Hyde and Alcorn (1993), Wulandari et al. (2010), Sivanesan (1984), Photita et al. (2002), Dingley et al. (1981), Meredith (1969), Raabe et al. (1981), Stevens (1925), Thaung (2008b), Shaw (1984), McKenzie (1996), Ebbels and Allen (1979)

Table 5.7 (continued)

Species record	Host	Locality	References
		Territory of, Congo, Democratic Republic of the, Cook Islands, Fiji, Hawaii, Hong Kong, India,Indonesia, Malaysia, Micronesia, Myanmar, Nepal, New Caledonia, New Guinea, New Zealand, Niue, Pakistan, Palau, Papua New Guinea, Philippines, Samoa, Solomon Islands, Sri Lanka, Taiwan, Tanzania, Thailand, Tonga, Vanuatu, Vietnam	
	Musa × *paradisiaca*	Hawaii, Indonesia	Anonymous (1960), Goos and Gowing (1992), Photita et al. (2002)
	Musa × *sapientum*	Malaysia	Williams and Liu (1976)
	Musa cavendishii	Taiwan	Yen (1972), Photita et al. (2002)
	Musa acuminata	Indonesia	Wong et al. (2012), Wulandari et al. (2013)
	Musa sp.	Australia, Fiji, Indonesia, Malaysia, Palau, Papua New Guinea, Philippines, Samoa, Solomon Islands	Wong et al. (2012, 2013), Wulandari et al. (2013), Hyde et al. (2014)

Table 5.7 (continued)

Species record	Host	Locality	References
P. mangiferae	*Mangifera indica*	Tanzania	Ebbels and Allen (1979)
P. mangifera-indica	*Mangifera indica*	Thailand	Wikee et al. (2013b)
P. musaechinensis	*Musa* sp.	China	Wu et al. (2014)
P. musarum	*Camellia oleifera*	China	Yu et al. (2018)
	Lycopersicon esculentum	India	Mathur (1979)
	Musa acuminata	Hawaii	Raabe et al. (1981)
	Musa basjoo	China	Tai (1979)
	Musa cavendishii	Taiwan	Anonymous (1979)
	Musa nana	Hawaii	Anonymous (1960)
	Musa sapientum	Thailand	Giatgong (1980)
	Musa sp.	India, New Caledonia	Mathur (1979), Huguenin (1966)
	Musa textilis	Philippines	Reinking (1918, 1919)
	Musa × *paradisiaca*	Dominican Republic, Hawaii, India	Ciferri (1929), Anonymous (1960), Mathur (1979), Kamal (2010)
	Musa × *paradisiaca* var. *sapientum*	China	Tai (1979)
	Musa × *sapientum*	India, Japan, Mexico, New Caledonia, Philippines, Taiwan	Mathur (1979), Kobayashi (2007), Alvarez (1976), Huguenin (1966), Reinking (1918, 1919), Anonymous (1979)
	Musa × *sapientum* var. *paradisiaca*	Dominican Republic	Ciferri (1961)
	Erythrina variegata	Guam	Lenne (1990), Boa and Lenné (1994)
	Musa acuminata	Hawaii	Raabe et al. (1981)

Table 5.7 (continued)

Species record	Host	Locality	References
	Musa sp.	France, Hawaii	Photita et al. (2002), Stevens (1925)
	Musa × *sapientum*	Dominican Republic	Ciferri (1929)
	Prosopis pallida	Hawaii	Raabe et al. (1981)
	Musa nana	China	Zhuang (2001)
	Musa paradisiaca	India, Thailand	Wong et al. (2012)
	Musa sp.	Australia, Brunei Darussalam, China, India, Malaysia, Myanmar, Nepal, Sri Lanka, Thailand	Wulandari et al. (2010), Wong et al. (2013), Thaung (2008b)
	Musa × *paradisiaca*	India	Ali and Saikia (1997)
	Musa × *sapientum*	Brunei Darussalam	Peregrine and Ahmad (1982)
	Musa × *paradisiaca*	Dominican Republic	Ciferri (1961)
	Musa acuminata	Hawaii	Teodoro (1937)
	Musa sp.	Hawaii	Meredith (1969)
	Musa × *sapientum*	Fiji, Malaysia, Philippines	Firman (1972), Johnston (1960), Williams and Liu (1976), Turner (1971), van der Aa (1973), Petrak and Sydow (1931), Teodoro (1937)
	Musa humilis	Philippines	Teodoro (1937)
	Musa sp.	Philippines	Teodoro (1937)
	Musa textilis	Philippines	Teodoro (1937)
	Musa × *paradisiaca*	India, Philippines	Teodoro (1937)
	Musa × *sapientum*	Philippines	Teodoro (1937)

Table 5.7 (continued)

Species record	Host	Locality	References
	Musa × *sapientum* var. *cinerea*	Philippines	Teodoro (1937)
	Musa × *sapientum* var. *compressa*	Philippines	Teodoro (1937)
	Musa × *sapientum* var. *lacatan*	Philippines	Teodoro (1937)
P. paracapitalensis	*Citrus aurantifolia*	New Zealand	Guarnaccia et al. (2017)
	Citrus aurantiifolia	New Zealand	Tran et al. (2019)
	Citrus aurantium	Australia	Tran et al. (2019)
	Citrus australasica	Australia	Tran et al. (2019)
	Citrus floridana	Italy	Guarnaccia et al. (2017), Tran et al. (2019)
	Citrus hystrix	Australia	Tran et al. (2019)
	Citrus japonica	Australia	Tran et al. (2019)
	Citrus limon	Spain	Guarnaccia et al. (2017), Tran et al. (2019)
	Citrus maxima	Australia	Tran et al. (2019)
	Citrus maxima-reticulata	Australia	Tran et al. (2019)
	Citrus reticulata	Australia	Tran et al. (2019)
	Citrus wintersii	Australia	Tran et al. (2019)
P. parthenocissi	*Parthenocissus quinquefolia*	Missouri, United States	Zhang et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
P. partricuspidatae	*Parthenocissus tricuspidata*	Japan	Zhou et al. (2015)
P. philoprina	*Ilex aquifolium*	California, New Jersey, Washington	Shaw (1973), Anonymous (1960)
	Ilex coriacea	Florida	Alfieri Jr. et al. (1984), Anonymous (1960)
	Ilex cornuta	North Carolina	Grand (1985)

Table 5.7 (continued)

Species record	Host	Locality	References
	Ilex crenata	North Carolina	Grand (1985)
	Ilex opaca	North Carolina, New Jersey, New York, South Carolina, Texas, West Virginia	Anonymous (1960), Grand (1985)
	Ilex sp.	Asia, Europe, Florida, North America, United Kingdom	Alfieri Jr. et al. (1984), von Arx and Muelle (1954), Cannon et al. (1985)
	Manihot glaziovii	India	Rao and Mani Varghese (1988), Pande (2008)
	Yucca sp.	Illinois	Cooke (1969)
	Rhododendron catawbiense	Canada	Ginns (1986)
	Rhododendron sp.	California, Canada, Nova Scotia, Ontario, Massachusetts, North Carolina, New Hampshire, New York, United Kingdom	Barr (1970), Pirozynski (1974), Ginns (1986), Grand (1985), Cannon et al. (1985)
	Ilex aquifolium	California	French (1989)
	Macrophoma ilicella	Georgia	Dzhalagonia (1965)
	Cryptomeria japonica	Netherlands	Sultan et al. (2011)
	Hedera helix	Switzerland	Luginbuehl and Mueller (1980)
	Ilex aquifolium	Switzerland	Luginbuehl and Mueller (1980)
	Ilex cinerea	Hong Kong	Lu et al. (2000), Zhuang (2001)
	Ilex paraguariensis	Brazil	Takeda et al. (2003)
	Juniperus communis	Switzerland	Luginbuehl and Mueller (1980)
	Taxus baccata	Germany, Netherlands, Poland, United States	Slippers et al. (2004), Phillips et al. (2005), Phillips and Alves (2009), Begoude et al. (2010), McDonald and Eskalen (2011), Lynch et al. (2013)

Table 5.7 (continued)

Species record	Host	Locality	References
			Adesemoye et al. (2014), Chen et al. (2014), Zhou et al. (2015), Nogueira et al. (2016), Hyde et al. (2014), Mulenko et al. (2008), Sultan et al. (2011), Nouri et al. (2018)
	Taxus baccata var. *fastigiata*	Poland	Mulenko et al. (2008)
	Taxus cuspidata	Poland	Mulenko et al. (2008)
	Rhododendron carolinianum	Connecticut, North Carolina, New Jersey, New York	Anonymous (1960)
	Rhododendron catawbiense	Connecticut, Massachusetts, Maryland, New Jersey, New York, Pennsylvania, Virginia	Anonymous (1960)
	Rhododendron macrophyllum	New Jersey, Oregon, Washington	Anonymous (1960), Shaw (1973)
	Rhododendron maximum	Connecticut, Massachusetts, Maryland, New Jersey, New York, Pennsylvania, Virginia	Anonymous (1960)
	Rhododendron sp.	California, Connecticut, Florida, Massachusetts, Maryland, Netherlands, New Zealand, New Jersey, New York, Pennsylvania, Virginia, Washington	Anonymous (1931-1970, 1960), Alfieri Jr. et al. (1984), Wikee et al. (2013b), Pennycook (1989), Eglitis et al. (1966)
	Rhododendron × *hybridum*	Netherlands	BPI n/a.)
	Chamaecyparis obtusa	Japan	Kobayashi (2007)
	Cryptomeria japonica	Japan	Kobayashi and Sasaki (1975), Sivanesan (1984), Kobayashi (2007), Motohashi et al. (2009)

Table 5.7 (continued)

Species record	Host	Locality	References
	Larix leptolepis	Japan	Kobayashi (2007)
	Ilex aquifolium	Germany, Netherlands, Spain	Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014), Zhu et al. (2018)
	Ilex latifolia	China	Tai (1979), Chen (2002), Teng (1996)
	Ilex cornuta	China	Tai (1979), Teng (1996)
	Ilex crenata	New Jersey	Anonymous (1960)
	Ilex crenata cv. Rotundifolia	Georgia	Driver (1952)
	Ilex opaca	North Carolina, New Jersey, New York, South Carolina, Texas, West Virginia	Anonymous (1960), Williams and Hayne (1982)
	Ilex sp.	California, United Kingdom	Anonymous (1960), Cannon et al. (1985)
	Ilex verticillata	New York	Anonymous (1960)
	Hedera helix	Portugal	Unamuno (1941)
	Ilex aquifolium	Portugal	Unamuno (1941)
	Rhododendron sp.	England	Davis (1946)
	Rhododendron sp.	Austria	von Hoehnel (1931)
P. rhizophorae	*Cordyline fruticosa*	Thailand	In this study
	Heliconia sp.	Thailand	In this study
	Ixora chinensis	Thailand	In this study

Table 5.7 (continued)

Species record	Host	Locality	References
	Musa paradisiaca	Thailand	In this study
	Punica granatum	Thailand	In this study
	Rhizophora stylosa	Thailand	In this study
P. schimae	*Schima superba*	China	Su and Cai (2012), Zhou et al. (2015), Hyde et al. (2014)
P. schimicola	*Schima superba*	China	Zhou et al. (2015)
P. styracicola	*Styrax grandiflorus*	China, France	Zhang et al. (2013a), Wikee (2013b), Zhou et al. (2015), Hyde et al. (2014)
P. vitis-rotundifoliae	*Vitis rotundifolia*	United States	Zhou et al. (2015)
***P. cruenta* species complex**			
P. abieticola	*Abies concolor*	Canada	Hyde et al. (2014)
	Aloe ferox	South Africa	Wikee et al. (2013b), Zhou et al. (2015)
P. cornicola	*Cornus alternifolia*	US, Wisconsin	Anonymous (1960)
	Cornus asperifolia	US	Anonymous (1960)
	Cornus florida	Australia, Florida, North Carolina, United States	Sampson and Walker (1982), Grand (1985), Grand et al. (1975), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
	Cornus hemsleyi	Armenia	Simonyan (1981)
	Cornus mas	Ukraine	Dudka et al. (2004)
	Cornus occidentalis	US	Anonymous (1960)
	Cornus racemosa	US	Anonymous (1960)
	Cornus sp.	US	Anonymous (1960)
	Cornus stolonifera	US	Anonymous (1960)
	Cornus alba	Canada, Iowa, Ohio, Poland	Conners (1967), Gilman and Archer (1929), Farr (1991), Mulenko et al. (2008)

Table 5.7 (continued)

Species record	Host	Locality	References
	Cornus alternifolia	Canada, Iowa, US	Conners (1967), Gilman and Archer (1929), Anonymous (1960)
	Cornus amomum	Iowa, Missouri	Farr (1991), Gilman and Archer (1929), Maneval (1937)
	Cornus asperifolia	Iowa, Kansas, Oklahoma, Range of host	Gilman and Archer (1929), Rogerson (1953), Preston (1945), Anonymous (1960)
	Cornus australis	Iran	Jorstad (1960)
	Cornus californica	California, Canada	French (1989), Ginns (1986)
	Cornus canadensis	Canada	Ginns (1986)
	Cornus controversa	Japan	Kobayashi (2007)
	Cornus coreana	China	Bai (2003)
	Cornus florida	Eastern states, Florida, Georgia, Iowa, Missouri, North Carolina, Oklahoma	Anonymous (1960), Alfieri et al. (1984), Miller et al. (1954), Anonymous (1960), Maneval (1937), Grand (1985), Preston (1947)
	Cornus hemsleyi	China	Bai (2003)
	Cornus mas	Bulgaria, Greece, Poland, Ukraine	Vanev et al. (1997), Pantidou (1973), Mulenko et al. (2008), Dudka et al. (2004)
	Cornus nuttallii	Canada	Ginns (1986)
	Cornus occidentalis	US	Anonymous (1960)
	Cornus paniculata	Iowa	Gilman and Archer (1929)
	Cornus racemosa	Canada, Iowa, Kansas, New York, Oklahoma, Range of host, Virginia, Wisconsin	Farr (1991), Mix (1954), Preston (1947), Anonymous (1960)

Table 5.7 (continued)

Species record	Host	Locality	References
	Cornus sanguinea	Austria, Bulgaria, Czechoslovakia, England, France, Germany, Iran, Italy, Poland, Portugal, Romania, Sweden, United States, USSR	Farr (1991), Vanev et al. (1997), Arzanlou and Torbati (2013), Mulenko et al. (2008), de Sousa Dias et al. (1987), Ge et al. (2016)
	*Cornus sanguinea sub*sp. *australis*	Bulgaria, Iran	Vanev et al. (1997), Arzanlou and Torbati (2013)
	Cornus sericea	Canada, Italy, Missouri, Poland	Ginns (1986), Garibaldi et al. (2003), Maneval (1937), Mulenko et al. (2008)
	Cornus sp.	Bulgaria, China, Georgia, Germany, Iowa, Mississippi, Netherlands, US	Bobev (2009), Tai (1979), Chen (2002), Zhuang (2005), Guo (1997), Dzhalagonia (1965), Farr (1991), Gilman and Arche (1929), Parris (1959), Ge et al. (2016), Anonymous (1960)
	Cornus stolonifera	Canada, Canada, Quebec, Iowa, Montana, North Dakota, Oklahoma, Range of host, South Dakota, Washington, Wisconsin	Conners (1967), Parmelee (1988), Feau et al. (2005), Gilman and Archer (1929), Shaw (1973), Brenckle (1918), Preston (1945), Anonymous (1960), Mankin (1969), Greene (1942)
	Cornus stolonifera var. *aurea*	Iowa	Gilman and Archer (1929)
	Cornus stolonifera var. *lutea*	Iowa	Gilman and Archer (1929)
	Cornus walteri	China	Zhuang (2005)

Table 5.7 (continued)

Species record	Host	Locality	References
	Swida australis	Ukraine	Dudka et al. (2004)
	Swida sanguinea subsp. australis	Armenia	Simonyan (1981)
	Cornus obliqua	Wisconsin	Greene (1962)
	Cornus racemosa	Wisconsin	Greene (1962)
	Cornus rugosa	Wisconsin	Greene (1962)
	Cornus sanguinea	Maryland, Netherlands	Verkley et al. (2013)
P. cruenta	*Maianthemum bifolium*	Poland	Mulenko et al. (2008)
	Polygonatum nakaiana	China	Tai (1979)
	Polygonatum odoratum var. *pluriflorum*	China	Tai (1979)
	Polygonatum	Austria	Petrak (1963)
	Lomatium suksdorfii	Washington	Shaw (1973)
	Convallaria majalis	Poland	Adamska (2001)
	Maianthemum bifolium	Poland	Adamska (2001)
	Polygonatum multiflorum	Poland	Adamska (2001)
	Polygonatum sp.	Sweden, Ukraine	Dudka et al. (2004), Eriksson (2014)
	Disporum viridescens	China	Tai (1979)
	Polygonatum humile	China	Tai (1979)
	Polygonatum odoratum var. *pluriflorum*	China	Tai (1979)
	Polygonatum officinale	China	Tai (1979)
	Smilacina japonica	China	Tai (1979)
	Tovara japonica	China	Tai (1979)

Table 5.7 (continued)

Species record	Host	Locality	References
	Bambuseae	Dominican Republic	Ciferri (1961)
	Convallaria majalis	Lithuania, Poland, Russia, Scotland	Treigiene (2006), Mulenko et al. (2008), Ruszkiewicz-Michalska et al. (2012), Gasich et al. (1999), Foister (1961)
	Iris sp.	Illinois	Boewe (1964)
	Maianthemum bifolium	Poland	Mulenko et al. (2008)
	Oakesia sp.	Wisconsin	Greene (1949)
	Polygonatum biflorum	United States	Anonymous (1960)
	Polygonatum commutatum	Missouri	Maneval (1937)
	Polygonatum lasianthum	China	Tai (1979)
	Polygonatum latifolium	USSR	van der Aa (1973)
	Polygonatum macropodum	China	Bai (2000)
	Polygonatum multiflorum	India, Lithuania, Poland, Romania, Ukraine	van der Aa (1973), Treigiene (2006), Mulenko et al. (2008), Wulandari et al. (2013), Dudka et al. (2004)
	Polygonatum odoratum	Lithuania, Poland, Romania, Ukraine	Treigiene (2006), Mulenko et al. (2008), van der Aa (1973), Dudka et al. (2004)
	Polygonatum odoratum var. *pluriflorum*	China, Japan	Jin (2011), Motohashi et al. (2009)
	Polygonatum officinale	Austria, China	van der Aa (1973), Tai (1979)
	Polygonatum orientale	Ukraine	Dudka et al. (2004)
	Polygonatum sewerzowii	Uzbekistan	Gafforov (2017)
	Polygonatum sibiricum	China	Tai (1979)
	Polygonatum sp.	China, India, Wisconsin	Teng (1996), Mathu (1979), Greene (1949)

Table 5.7 (continued)

Species record	Host	Locality	References
	Polygonatum vulgare	Spain	Gonzalez Fragoso (1917)
	Smilacina amplexicaulis	New Mexico, United States	Anderson (1919), Anonymous (1960)
	Smilacina racemosa	Missouri, United States	Maneval (1937), Anonymous (1960)
	Smilacina stellata	North Dakota, United States	Anderson (1919), Brenckle (1918), Anonymous (1960)
	Smilax china	Japan	Kobayashi (2007)
	Smilax herbacea	China	Tai (1979)
	Smilax hispida	Missouri	Maneval (1937)
	Smilax sp.	Missouri	Maneval (1937)
	Uvularia sp.	Wisconsin	Greene (1949)
	Maianthemum dilatatum	Washington	Shaw (1973)
	Polygonatum multiflorum	Pakistan	Ahmad (1969), Ahmad et al. (1997)
	Smilacina racemosa	Idaho, Washington	Shaw (1973)
	Smilacina stellata	Idaho, Montana, Oregon, Washington	Shaw (1973)
	Maianthemum dilatatum	Alaska, Washington,	Anonymous (1960)
	Polygonatum biflorum	Connecticut, Indiana, New York, Virginia, Wisconsin,	Anonymous (1960)
	Polygonatum canaliculatum	Iowa, Ohio, Wisconsin	Anonymous (1960)
	Polygonatum commutatum	Iowa	Gilman and Archer (1929)
	Polygonum multiflorum	Greece	Pantidou (1973)
	Smilacina amplexicaulis	California, New Mexico	Anonymous (1960)

Table 5.7 (continued)

Species record	Host	Locality	References
	Smilacina racemosa	Iowa, Illinois, Oklahoma, Range of host	Gilman and Archer (1929), Neely (1959), Preston (1947), Anonymous (1960)
	Smilacina stellata	Mississippi, Range of host	Parris (1959), Anonymous (1960)
	Smilax herbacea	Iowa	Anonymous (1960), Gilman and Archer (1929)
	Smilax hispida	Iowa	Gilman and Archer (1929)
	Smilax rotundifolia	Iowa	Anonymous (1960), Gilman and Archer (1929)
	Smilax tamnoides var. *hispida*	Iowa	Anonymous (1960)
	Uvularia grandiflora	Iowa, Illinois, Missouri, Virginia, Wisconsin	Anonymous (1960)
	Uvularia perfoliata	Indiana	Anonymous (1960)
	Uvularia sessilifolia	Connecticut, New York, Wisconsin	Anonymous (1960)
	Polygonatum officinale	Portugal	Nag Raj (1993), Costa and Camara (1952)
P. cryptomeriae	*Cryptomeria japonica*	District of Columbia, Japan, Korea, Virginia	Brittingham and O'Brien (1978), Leuchtmann et al.1992), Shaw et al. (2006), Motohashi et al. (2009), Cho and Shin (2004)
	Cunninghamia lanceolata	China	Chen (2002)
P. foliorum	*Rhododendron ponticum*	Netherlands	Timmwemans (1957)
	Taxus baccata	England, Europe	Dennis (1978), von Arx and Mueller (1954)
	Taxus sp.	United Kingdom	Cannon et al. (1985)
	Yucca sp.	Mexico	Chacón and Carrion (1984)
	Cryptomeria japonica	United States	Wikee et al. (2013b)

Table 5.7 (continued)

Species record	Host	Locality	References
	Taxus baccata	Italy, Netherlands	Wikee et al. (2013b), Zhou et al. (2015), Mayorquin et al. (2016), Hyde et al. (2014)
	Taxus baccata	Scotland	Spaulding (1961), Foister (1961)
P. gaultheriae	*Gaultheria humifusa*	Netherlands, United States	Sultan et al. (2011), Zhou et al. (2015), Hyde et al. (2014)
	Gaultheria cumingiana	Taiwan	Anonymous (1979)
	Gaultheria humifusa	United States, Washington	Wikee et al. (2013b), van der Aa (1973)
	Gaultheria procumbens	New Jersey, Range of host	van der Aa (1973), Ellis and Everhart (1878−1898), Nag Raj (1993), Cash (1953), Anonymous (1960)
	Gaultheria shallon	California, Canada, Oregon, Washington	Eglitis et al. (1966), Ginns (1986), Shaw (1973), Lambe (1960), Anonymous (1960)
	Gaultheria spp.	North America	Bissett and Darbyshir (1984a), Wulandari et al. (2013), van der Aa (1973), Van Der and Vanev (2002)
P. hakeicola	*Hakea* sp.	Australia	Crous et al. (2018)
P. hamamelidis	*Hamamelis* sp.	United States	Anonymous (1960)
	Hamamelis japonica	Japan	Kobayashi (2007), Motohashi et al. (2009), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
	Hamamelis japonica subsp. megalophylla	Japan	Motohashi et al. (2009)
	Hamamelis japonica var. *discolor* f. *obtusata*	Japan	Motohashi et al. (2009)
	Hamamelis sp.	Eastern states, Mississippi, Tennessee, Wisconsin	Anonymous (1960)

Table 5.7 (continued)

Species record	Host	Locality	References
	Hamamelis virginiana	Canada, Canada, Ontario, North Carolina, South Carolina	Ginns (1986), Bissett and Darbyshir (1984b), van der Aa (1973), Nag Raj (1993)
P. hubeiensis	*Viburnum odoratissimum*	China	Hyde et al. (2014), Wikee et al. (2013b), Wulandari et al. (2013), Zhang et al. (2013a), Zhou et al. (2015)
P. illicii	*Illicium verum*	China	Lin et al. (2017)
P. leucothoicola	*Leucothoe catesbaei*	Japan	Hyde et al. (2014), Wikee et al. (2013b), Zhou et al. (2015)
P. ligustricola	*Ligustrum obtusifolium*	Japan	Hyde et al. (2014), Motohashi et al. (2009), Zhou et al. (2015)
P. minima	*Acer rubrum*	Louisiana, Mississippi, North Carolina	Overholts (1938), Parris (1959), Wolf et al. (1938)
	Acer saccharophorum	Mississippi	Parris (1959)
	Acer sp.	Alabama, Florida, New Jersey	Blain (1931), Alfieri Jr. et al. (1984), Nag Raj (1993), Cash (1953)
	Acer cinnamomifolium	China	Zhuang (2001), Bai (2000)
	Acer negundo	Alabama, China	Anderson (1919), Tai (1979), Chen (2002), Bai (2000)
	Acer campestre	Canada, Ontario, Ukraine	Bissett and Darbyshire (1984c), Dudka et al. (2004)
	Acer crataegifolium	Japan	Motohashi et al. (2009)
	Acer ginnala	Canada, Manitoba, Ontario	Ginns (1986), Bissett and Darbyshire (1984c)
	Acer glabrum	Idaho, Missouri	Anonymous (1960)
	Acer mono	China	Tai (1979), Chen (2002), Zhuang (2005)
	Acer negundo	Missouri, North Carolina, Range of host	Maneval (1937), Grand (1985), Anonymous (1960)
	Acer nigrum	United States	Anonymous (1960)
	Acer palmatum	Connecticut, North Carolina	Anonymous (1960), Grand (1985)

Table 5.7 (continued)

Species record	Host	Locality	References
	Acer platanoides	Canada, Eastern states, Missouri, North Carolina, Wisconsin	Conners (1967), Anonymous (1960), Maneval (1937), Grand (1985), Greene (1958)
	Acer pseudoplatanus	Connecticut, Pennsylvania	Anonymous (1960)
	Acer pycnanthum	Japan	Motohashi et al. (2009)
	Acer rubrum	Canada, Canada, New Brunswick, Canada, Nova Scotia, Canada, Ontario, Canada, Prince Edward Island, Canada, Quebec, Florida, Massachusetts, Mississipp, North Carolina, North Dakota, New Jersey, New York, Oklahoma, Pennsylvania, Range of host, South Dakota, Tennessee, United States, Wisconsin	Conners, (1967), Ginns (1986), Bissett and Darbyshire (1984c), Miller (1991), Schubert (1991), Cooke (1978), Parris (1959), Grand (1985), Grand et al. (1975), Wikee et al. (2013b), van der Aa (1973), Mix (1954), Preston (1945), Fergus (1954), Anonymous (1960), Mankin (1969), Zhou et al. (2015), Hyde et al. (2014), Greene (1966)
	Acer saccharinum	Canada, Canada Ontario, Iowa, Missouri, Mississippi, North Carolina, Oklahoma, Range of host, Wisconsin	Conners (1967), Bissett and Darbyshire (1984c), Gilman and Archer (1929), Maneval (1937), Parris (1959), Grand (1985), Wolf et al. (1938), Preston (1947), Anonymous (1960), Anderson (1919)
	Acer saccharum	Canada, Canada, Ontario, Canada, Quebec, Mississippi, Pennsylvania, Range of host, Wisconsin	Conners (1967), Ginns (1986), Fergus (1954), Anonymous (1960), Anderson (1919)

Table 5.7 (continued)

Species record	Host	Locality	References
	Acer sp.	Canada, Ontario, Canada, Prince Edward Island, China, Mississippi, New Jersey, North America	Bissett and Darbyshire (1984c), Wikee et al. (2013b), Parris (1959), van der Aa (1973), Nag Raj (1993)
	Acer spicatum	Canada, Canada, New Brunswick, Canada, Nova Scotia, New York, Wisconsin	Conners (1967), Ginns (1986), Bissett and Darbyshire (1984c), Anonymous (1960), Anderson (1919)
	Acer tartaricum	Canada, Ontario	Bissett and Darbyshire (1984c)
	Sorbus americana	Canada	Ginns (1986)
P. neopyrolae	*Pyrola asarifolia*	Japan	Zhou et al. (2015), Hyde et al. (2014)
	Pyrola asarifolia subsp. incarnata	Japan	Wikee et al. (2013b)
P. pachysandricola	*Pachysandra terminalis*	Japan	Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
P. paxistimae	*Paxistima myrsinites*	North America	Wikee et al. (2013b)
P. podocarpicola	*Podocarpus maki*	Florida, United States	Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
P. pyrolae	*Chimaphila umbellata*	Canada, Ontario	Bissett and Darbyshire (1984d)
	Chimaphila umbellata var. *cisatlantica*	Canada	Conners (1967)
	Erica carnea	Japan	Sultan et al. (2011)
	Gaultheria shallon	Canada, British Columbia	Leuchtmann et al. (1992)
	Orthilia secunda	Poland	Mulenko et al. (2008)
	Pyrola asarifolia	Canada, New Brunswick, Montana, Oregon	Bissett and Darbyshire (1984d), Shaw (1973), Shaw et al. (2006)

Table 5.7 (continued)

Species record	Host	Locality	References
	Pyrola asarifolia var. *purpurea*	Alaska	Parmelee (1958)
	Pyrola bracteata	Canada, British Columbia	Bissett and Darbyshire (1984d)
	Pyrola elliptica	Wisconsin	Anonymous (1960)
	Pyrola rotundifolia	Delaware, Lithuania, Ukraine, United States	van der Aa (1973), Ellis and Everhart (1889), Nag Raj (1993), Cash (1953), Treigiene (2006), Dudka et al. (2004), Wikee et al. (2013b)
P. rubella	*Pyrola rotundifolia* var. *americana*	Delaware, Montana	Anonymous (1960)
P. paviae	*Pyrola* sp.	United States	Sultan et al. (2011)
P. telopeae	*Vaccinium myrtillus*	Lithuania	Treigiene (2006)
***P. vaccinii* species complex**			
P. vaccinii	*Gaultheria procumbens*	Eastern states	Barr (1970)
	Kalmia latifolia	Eastern states	Barr (1970)
	Kalmia sp.	Rhode Island	Goos (2010)
	Lyonia lucida	Eastern states	Barr (1970)
	Vaccinium ashei	Florida	Alfieri Jr. et al. (1984)
	Vaccinium elliottii	Florida	Alfieri Jr. et al. (1984)
	Vaccinium macrocarpon	Eastern states, Massachusetts, New Jersey, Washington, Wisconsin	Barr (1970), Weidemann and Boone (1983)
	Vaccinium sp.	Rhode Island	Goos (2010)
	Acer truncatum	China	Sun et al. (2011)

Table 5.7 (continued)

Species record	Host	Locality	References
	Arctostaphylos columbiana	British Columbia, Canada	Conners (1967)
	Gaylussacia brachycera	Maryland	Anonymous (1960)
	Kalmia latifolia	Connecticut, New Jersey, New York, Virginia	Anonymous (1960)
	Oxycoccus macrocarpos	Netherlands	Sultan et al. (2011)
	Oxycoccus macrocarpus	United States	Wulandari et al. (2009), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
	Vaccinium macrocarpon	New Jersey, Oregon, Range of host, Washington	Shaw (1973), Eglitis et al. (1966), Anonymous (1960)
	Vaccinium oxycoccos	United States	Anonymous (1960)
	Pieris nitida	Mississippi	Tracy and Earle (1895)
	Vaccinium ovatum	California, Washington	Anonymous (1960), French (1987), Nag Raj (1993), Bona (1928), Shaw (1973), Eglitis et al. (1966)
	Vaccinium arboreum	Alabama, Florida, Mississippi	van der Aa (1973), Anonymous (1960), Weidemann et al. (1982), Nag Raj (1993), Zhang et al. (2013b), Alfieri Jr. et al. (1984), Parris (1959)
	Vaccinium ashei	Mississippi	Parris (1959)
	Vaccinium corymbosum	Florida	Miller (1997)
	Vaccinium macrocarpon	Massachusetts, Michigan, New Jersey, United States, Wisconsin	Weidemann and Boone (1983), Zhang et al. (2013b), Polashock et al. (2009), Olatinwo et al. (2003), Waller et al. (2020), Zhou et al. (2015), Hyde et al. (2014), McManus (1998)
	Vaccinium ovatum	California	French (1989)
	Vaccinium sp.	China, North America	Wikee et al. (2013b)

Table 5.7 (continued)

Species record	Host	Locality	References
	Vaccinium vitis-idaea	China	Bai (2000)
	Vaccinium ashei	Georgia, Maryland, Mississippi, North Carolina	Anonymous (1960)
	Vaccinium corymbosum	Georgia, Maryland, North Carolina	Anonymous (1960)
P. vacciniicola	*Vaccinium macrocarpon*	United States	Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
***P. rhodorae* species complex**			
P. mimusopisicola	*Mimusops zeyheri*	South Africa	Crous et al. (2014)
P. rhodorae	*Rhododendron ponticum*	United Kingdom	Dennis (1986)
	Rhododendron sp.	Denmark, England, Scotland	Lind (1913), Anonymous (1928), Dennis and Foister (1942), Foister (1961)
	Rhododendron californicum	Oregon	Zeller (1934)
	Rhododendron smirnowii	Washington	Eglitis et al. (1966)
	Rhododendron sp.	England, Washington	Eglitis et al. (1966)
***P. concentrica* species complex**			
P. aspidistricola	*Aspidistra elatior*	Japan	Motohashi et al. (2008, 2009), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
P. aucubae-japonicae	*Aucuba japonica*	Japan	Hernandez-Restrepo et al. (2016)
P. bifrenariae	*Bifrenaria harrisoniae*	Brazil	Glienke et al. (2011)
P. catimbauensis	*Mandevilla catimbauensis*	Brazil	Crous et al. (2017)
P. citriasiana	*Citrus maxima*	Thailand, China, Vietnam	Wulandari et al. (2009), Guarnaccia et al. (2017)
P. citribrasiliensis	*Citrus limon*	Brazil	Glienke et al. (2011), Wikee et al. (2011, 2013b), Zhou et al. (2015), Hyde et al. (2014)

Table 5.7 (continued)

Species record	Host	Locality	References
	Citrus sp.	Brazil	Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Miles et al. (2013), Wulandari et al. (2013), Guarnaccia et al. (2017), Tran et al. (2019)
P. citricarpa	*Aegle marmelos*	Myanmar	Thaung (2008b)
	Camellia sinensis	Papua New Guinea	Shaw (1984)
	Cassia emarginata	Cuba	Urtiaga (1986)
	Cedrela mexicana	Cuba	Urtiaga (1986)
	Cedrela odorata	Cuba	Urtiaga (2004)
	Chrysanthemum × *morifolium*	Hong Kong	Lu et al. (2000), Zhuang (2001)
	Citrus × *grandis-reticulata*	New Zealand	Gadgil (2005)
	Citrus × *paradisi*	Australia, South Africa, South Africa, KwaZulu-Natal, South Africa, Mpumalanga, Swaziland	Simmonds (1966), Gorter (1977), Crous et al. (2000), Meyer et al. (2001, 2006)
	Citrus × *tangelo*	New Zealand	Pennycook (1989), Gadgil (2005)
	Citrus aurantiacum	Brazil	Sultan et al. (2011)
	Citrus aurantifolia	Cook Islands, Fiji, Niue, Samoa, Tonga	Dingley et al. (1981)
	Citrus aurantium	Australia, Brazil, China, Myanmar	Wulandari et al. (2009), Phillips et al. (2009), Minnis et al. (2012), Nouri et al. (2018), Thaung (2008b), Tai (1979), Bai (2000), Nag Raj (1993), Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Ismail et al. (2012)
	Citrus decumana	Myanmar	Thaung (2008b)

Table 5.7 (continued)

Species record	Host	Locality	References
	Citrus deliciosa	Australia, Brazil	Nag Raj (1993), Mendes (1998)
	Citrus grandis	China	Tai (1979), Bai (2000)
	Citrus junos	China	Tai (1979), Bai (2000)
	Citrus limon	Argentina, Australia, Brazil, Cook Islands, Fiji, Italy, Nigeria, Niue, Samoa, South Africa, South Africa, Mpumalanga, Tonga, Tunisia, Uruguay, Zimbabwe	Simmonds (1966), Wulandari et al. (2009), Dingley et al. (1981), Meyer et al. (2001, 2006), Whiteside (1966), Wikee et al. (2011, 2013a, b), Guarnaccia et al. (2017), Glienke et al. (2011), Miles et al. (2013), Zhou et al. (2015), Tran et al. (2019), Hyde et al. (2014), Mendes et al. (1998), Boughalleb-M'Hamdi et al. (2020)
	Citrus limon	Australia	Simmonds (1966)
	Citrus limonia	China, Southern Africa, Australia, Brazil	Gorter (1977), Crous et al. (2000), Tai (1979), Bai (2000), Doidge (1950), Nag Raj (1993), Glienke et al. (2011)
	Citrus maxima	Southern Africa, Philippines, Brazil	Reinking (1919, 1918, 1921), Doidge (1950), Glienke et al. (2011)
	Citrus medica	Myanmar	Thaung (2008b)
	Citrus medica var. *limonum*	Myanmar	Thaung (2008b)
	Citrus microcarpa	China	Tai (1979), Bai (2000)
	Citrus natsudaidai	Japan	Kobayashi (2007)
	Citrus nobilis	China, Philippines	Teodoro (1937), Reinking (1921), Tai (1979), Zhuang (2001), Bai (2000)
	Citrus nobilis var. *deliciosa*	Southern Africa	Doidge (1950)
	Citrus paradisi	Cook Islands	Dingley et al. (1981)

Table 5.7 (continued)

Species record	Host	Locality	References
	Citrus reticulata	Australia, Cook Islands, Fiji, Hong Kong, Niue, South Africa, South Africa, Mpumalanga, Tonga	Simmonds (1966), Dingley et al. (1981), Lu et al. (2000), Gorter (1977), Crous et al. (2000), Meyer et al. (2001, 2006), Dingley et al. (1981)
	Citrus reticulata	Australia, Brazil, China, Hong Kong, India, Japan, Philippines	Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Miles et al. (2013), Guarnaccia et al. (2017), Tran et al. (2019), Wang et al. (2012), Lu et al. (2000), Zhuang (2001), Das et al. (2018), Kobayashi (2007), Tai (1979), Bai (2000), Watson (1971), Simmonds (1966), Mendes et al. (1998)
	Citrus reticulata var. *poonensis*	China	Tai (1979), Bai (2000)
	Citrus reticulata var. *suhoiensis*	China	Tai (1979), Bai (2000)
	Citrus reticulata var. *sunki*	China	Tai (1979), Bai (2000)
	Citrus reticulata var. *tankan*	China	Tai (1979), Bai (2000)
	Citrus sinensis	Australia, Brazil, China, Cook Islands, Fiji, Niue, North America, Samoa, South Africa, South Africa, Mpumalanga, Tonga, Uganda, Zimbabwe, Angola, Florida, India, Malta, Portugal, Tunisia	Bassimba et al. (2018), Shivas (1989), Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Miles et al. (2013), Wulandari et al. (2009, 2013), Tran et al. (2019), Mendes et al. (1998), Glienke et al. (2011), Guarnaccia et al. (2017), Das et al. (2018), Boughalleb-M'Hamdi et al. (2020), Simmonds (1966), Tai (1979), Bai (2000), Doidge (1950), Peres et al. (2007), Dingley et al. (1981), Schubert et al. (2012), Gorter (1977), Crous et al. (2000), Meyer et al. (2001, 2006), Reeder et al. (2008), Whiteside (1966)
	Citrus sinensis f. sehkan	Taiwan	Anonymous (1979)
	Citrus sinensis var. *sekkan*	China	Tai (1979), Bai (2000)

Table 5.7 (continued)

Species record	Host	Locality	References
	Citrus sp.	Angola, Argentina, Australia, Bhutan, Brazil, China, Cuba, Florida, Ghana, India, Indonesia, Italy, Japan, Kenya, Malta, Mozambique, Namibia, Nigeria, Philippines, Portugal, South Africa, Swaziland, Taiwan, Uganda, United States, Uruguay, Zambia, Zimbabwe, Africa, Asia, Australia, Fiji, Hong Kong, New Zealand, United States, West Indies	Petrak (1953), Watson (1971), Mendes et al. (1998), Firman (1972), Dingley et al. (1981), Zhuang (2001), Pennycook (1989), Bai (2000), Meyer et al. (2001, 2006), Rossman (2009), Guarnaccia et al. (2019), Wikee et al. (2013b), Guarnaccia et al. (2017), Trakunyingcharoen et al. (2015), Mendes et al. (1998), Kobayashi (2007)
	Citrus tankan	China	Zhuang (2001), Bai (2000)
	Citrus tankan f. koshotankan	China	Bai (2000)
	Citrus tankan var. *koshotankan*	China, Taiwan	Anonymous (1979), Tai (1979)
	Citrus unshiu	Japan, Korea	Kobayashi (2007), Cho and Shin (2004)
	Diospyros halesioides	Cuba, West Indies	Urtiaga (1986, 2004), Minter et al. (2001)
	Elaeis guineensis	Malaysia	Williams and Liu (1976), Turner (1971)
	Elettaria cardamomum	Tanzania	Ebbels and Allen (1979)
	Eucalyptus grandis	Malaysia, South Africa	Crous et al. (1989)
	Fortunella crassifolia	China	Tai (1979), Bai (2000)
	Jatropha podagrica	Cuba	Urtiaga (1986)
	Mangifera indica	Florida	McMillan Jr. (1986)
	Psidium guajava	Myanmar	Thaung (2008b)

Table 5.7 (continued)

Species record	Host	Locality	References
	Senna bicapsularis	Cuba	Lenne (1990), Boa and Lenné (1994)
	Zea mays	Malaysia	Williams and Liu (1976)
P. citrichinansis	*Citrus maxima*	China	Wang et al. (2012)
	Citrus reticulata	China	Wang et al. (2012)
P. citrimaxima	*Citrus maxima*	Thailand	Wikee et al. (2013b)
P. concentrica	*Corynocarpus laevigatus*	New Zealand	Gadgil (2005)
	Cryptomeria japonica	District of Columbia, Japan, Korea, Virginia	Brittingham and O'Brien (1978), Petrini et al. (1991), Leuchtmann et al. (1992), Shaw et al. (2006), Motohashi et al. (2009), Cho and Shin (2004)
	Cunninghamia lanceolata	China	Chen (2002)
	Fatshedera lizei	Florida	Alfieri Jr. et al. (1984)
	Hedera canariensis	California	French (1989)
	Hedera helix	Alabama, Balearic Islands, California, Canada, District of Columbia, Eastern states, Florida, France, Italy, Sicily, Mississippi, North Carolina, Nebraska, New Jersey, Southern Africa, South Carolina, Texas, Ukraine, USSR, Virginia, Washington, West Virginia, Maryland, Texas, India	Cash (1953), Jorstad (1962), Anonymous (1960, 1931-1970), French (1989), Bose et al. (1970), Mathur (1979), Ginns (1986), Alfieri Jr. et al. (1984), Nag Raj (1993), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014), Greuter et al. (1991), Parris (1959) , Grand (1985), van der Aa (1973), Dudka et al. (2004), Shaw (1973), Williams and Hayne (1982), Doidge (1950)
	Hedera nepalensis	Pakistan	Ahmad (1969), Ahmad et al. (1997)

Table 5.7 (continued)

Species record	Host	Locality	References
	Hedera rhombea	Japan	Motohashi et al. (2009)
	Hedera sp.	California, Spain	French (1989), Wikee et al. (2013b)
	Ilex aquifolium	Portugal	Nag Raj (1993)
	Ilex cornuta	Florida	Miller (1990)
	Ilex opaca	Oklahoma	Preston (1945)
	Ilex sp.	Australia, New Jersey	Cash (1954), Nag Raj (1993), Cunnington (2003)
	Ilex verticillata	New York	Nag Raj (1993)
	Ilex vomitoria	Florida	Alfieri Jr. et al. (1984)
	Magnolia kobus	Japan	Nag Raj (1993), Kobayashi (2007), Motohashi et al. (2009)
	Magnolia liliiflora var. *gracilis*	Japan	Motohashi et al. (2009)
	Magnolia sp.	Iran	Esfandiari and Petrak (1950)
	Pieris floribunda	Connecticut	Anonymous (1960)
	Quercus ilex	Ukraine	Dudka et al. (2004)
	Quercus robur	Poland	Mulenko et al. (2008)
	Rhododendron carolinianum	Connecticut	
	Rhododendron catawbiense	New Jersey	Seave (1922)
	Rhododendron caucasicum	Turkey	Huseyinov and Selcuk (2001)
	Rhododendron chrysanthum	USSR	Petrak (1934)
	Rhododendron indicum	Japan	Kobayashi (2007)
	Rhododendron keiskei	Japan	Motohashi et al. (2009)
	Rhododendron macrophyllum	California, Washington	BPI n/a)

Table 5.7 (continued)

Species record	Host	Locality	References
	Rhododendron maximum	Connecticut, District of Columbia, Massachusetts, New York, New Jersey, West Virginia	Clinton (1908, 1934), Ellis and Everhart (1888), Seave (1922), Davis (1946), Nag Raj (1993), Cash (1953), Eglitis et al. (1966)
	Rhododendron maximum	New Jersey, West Virginia	Eglitis et al. (1966)
	Rhododendron micranthum	China	Bai (2000)
	Rhododendron mucronatum	Japan	Kobayashi (2007)
	Rhododendron mucronulatum	Korea	Cho and Shin (2004)
	Rhododendron obtusum	Japan	Kobayashi (2007)
	Rhododendron ponticum	France, Portugal, Turkey, USSR	Vanev and van der Aa (1998), Huseyinov and Selcuk (2001), Jaczewski (1915)
	Rhododendron simsii	Japan	Kobayashi (2007)
	Rhododendron sp.	Canada, Japan, Netherlands, New Jersey, New York, Oklahoma, United States, Virginia, Washington, England, France, New Jersey, Portugal	Brunaud (1890), Martin (1931), Pirone (1939), White (1933), Seaver (1922), Camara (1930), White and Hamilton (1935), Tengwall (1924), Preston (1945), Kobayashi (2007), Motohashi et al. (2009), van der Aa (1973)
	Taxus baccata	Germany, Poland	van der Aa (1973), Lotz-Winter et al. (2011), Mulenko et al. (2008)
	Taxus brevifolia	Idaho, Montana, Washington	Anonymous (1960), Shaw (1973)
	Taxus cuspidata	Poland	Mulenko et al. (2008)

Table 5.7 (continued)

Species record	Host	Locality	References
	Umbellularia californica	California	French (1989)
P. cussonia	*Cussonia* sp.	South Africa	Wikee et al. (2013b)
	Cussonia umbellifera	South Africa	Wikee et al. (2013b)
P. elongata	*Oxycoccus macrocarpos*	United States	Wikee et al. (2013b)
	Vaccinium macrocarpon	Massachusetts, Wisconsin	Weidemann et al. (1982)
P. ericarum	*Erica gracilis*	South Africa, South Africa, Western Cape	Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014), Crous et al. (2012b)
P. gardeniicola	*Gardenia jasminoides*	India, Japan, Taiwan	Sarbhoy et al. (1971), Mathur (1979), Kobayashi (2007), Kobayashi and Sasaki (1975), Motohashi et al. (2009), Anonymous (1979)
	Gardenia jasminoides var. *radicans*	Japan	Kobayashi (2007)
P. harai	*Aucuba japonica*	Japan	Kobayashi (2007), Motohashi et al. (2009)
P. hostae	*Hosta plantaginea*	China	Su and Cai (2012), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
P. hymenocallidicola	*Hymenocallis littoralis*	Australia	Crous et al. (2011), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
P. hypoglossi	*Ruscus aculeatus*	Italy, Sicily, Portugal	Wulandari et al. (2009), Sultan et al. (2011), Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Zhou et al. (2015), Guarnaccia et al. (2017), Zhu et al. (2018), Hyde et al. (2014), Greuter et al. (1991), Nag Raj (1993)
	Ruscus hypoglossum	France, Italy	Wikee et al. (2011, 2013a, b), Wulandari et al. (2009), Glienke et al. (2011)
	Ruscus ponticus	Ukraine	Dudka et al. (2004)
	Ruscus sp.	France, Italy, Portugal, Turkey, Ukraine	Wikee et al. (2011), Nag Raj (1993)
	Ruscus hypoglossum	Portugal	Nag Raj (1993), Costa and Camara (1952)

Table 5.7 (continued)

Species record	Host	Locality	References
P. iridigena	*Iris* sp.	South Africa	Marin-Felix et al. (2019)
P. kerriae	*Kerria japonica*	Japan	Motohashi et al. (2008, 2009), Wikee et al. (2011, 2013a), Zhou et al. (2015), Hyde et al. (2014)
P. kobus	*Magnolia kobus*	Japan	Nag Raj (1993), Motohashi et al. (2009)
P. ophiopogonis	*Ophiopogon japonicus*	South Korea, Thailand	Kwon et al. (2015), Wikee et al. (2012, 2013a, b)
P. paracitricarpa	*Citrus limon*	Greece	Guarnaccia et al. (2017), Tran et al. (2019)
	Citrus sinensis	China	Guarnaccia et al. (2017)
P. speewahensis	*Vanda* sp.	Australia	Shivas et al. (2013)
P. spinarum	*Chamaecyparis lawsoniana*	New Zealand	Gadgil (2005)
	Chamaecyparis pisifera	France	Shaw et al. (2006), Sultan et al. (2011), Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Zhou et al. (2015), Guarnaccia et al. (2017), Hyde et al. (2014)
	Cryptomeria japonica	New Zealand	Gadgil (2005)
	Cupressus arizonica	New Zealand	Gadgil (2005)
	Cupressus macrocarpa	New Zealand	Gadgil (2005)
	Hedera helix	Italy	Glienke et al. (2011), Wikee et al. (2011)
	Juniperus chinensis	New Zealand	Gadgil (2005)
	Juniperus sp.	France, Germany	Wikee et al. (2013b)
	Taxus baccata	Lithuania	Treigiene (2006)
	Thuja plicata	New Zealand	Gadgil (2005)
***P. owaniana* species complex**			
P. austroafricana	*Unidentified host*	South Africa	Crous et al. (2019)

Table 5.7 (continued)

Species record	Host	Locality	References
P. carissicola	*Carissa macrocarpa*	South Africa, Eastern Cape	Crous et al. (2015)
P. hagahagaensis	*Carissa bispinosa*	South Africa	Crous et al. (2019)
P. owaniana	*Brabejum stellatifolium*	South Africa	Swart et al. (1998), Crous et al. (2000), Wulandari et al. (2009), Sultan et al. (2011), Glienke et al. (2011), Wikee et al. (2011, 2013a, b), Miles et al. (2013), Zhou et al. (2015), Hyde et al. (2014), Doidge (1950)
P. podocarpi	*Podocarpus falcatus*	South Africa	Wikee et al. (2013a, b)
	Podocarpus lanceolata	South Africa	Sultan et al. (2011), Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
	Podocarpus latifolia	South Africa, Mpumalanga	Shaw et al. (2006)
P. pseudotsugae	*Cryptomeria japonica*	Japan	Petrini et al. (1991), Leuchtmann et al. (1992)
	Pseudotsuga brevifolia	China	Petrini et al. (1991), Leuchtmann et al. (1992)
	Pseudotsuga gaussenii	China	Petrini et al. (1991), Leuchtmann et al. (1992)
	Pseudotsuga japonica	Japan	Petrini et al. (1991), Leuchtmann et al. (1992)
	Pseudotsuga menziesii	United States	Wikee et al. (2013b), Zhou et al. (2015), Hyde et al. (2014)
	Pseudotsuga sinensis	China	Petrini et al. (1991), Leuchtmann et al. (1992)

Table 5.8 Size of ascospores, conidia, and spermatia of *Phyllosticta* recorded species

Species	Ascospores (µm)	Conidia size (µm)	Spermatia (µm)	Reference
***Phyllosticta cruenta* species complex**				
P. acaciigena	-	7–15 × 3–5	-	Crous et al. (2016)
P. aloeicola	-	5–13 × 3–4	-	Wikee et al. (2013b)
P. ardisiicola	-	7–11 × 5–7.5	-	Motohashi et al. (2008)
P. aristolochiicola	-	7–16 × 6.5–11	-	Crous et al. (2012b)
P. azevinhi	-	8–10 × 4–5	-	Brotéria (1908)
P. beaumarisii	-	7.5–15 × 6.5–8.75	-	Paul and Blackburn (1986)
P. brazilianiae	-	(8–)10–11(–12.5) × (5–)6(–7)	-	Glienke et al. (2011)
P. capitalensis	-	(10–)11–12(–14) × (5–)6–7	-	Glienke et al. (2011)
P. carochlae	-	6–8.5 × (9–) 10–12 (–13)	-	Zhou et al. (2015)
P. cavendishii	(12–)14–17(–18) × (7–)8–9(–10)	(12–)13–16(–17) × 8–9 (–10)	6–7(–8) × (1–)2	Wong et al. (2012)
P. cordylinophila	-	10–17 × 3–6	-	Wikee et al. (2013b)
P. eugeniae	-	12.4–14.8 × 4.3–7.1	-	Chen (1967)
P. fallopiae	-	8.5–12.5 × 6–7.5	-	Motohashi et al. (2008)
P. ilicis-aquifolii	-	10–18 × 6–9	5–8 × 1.5–2.5	Su and Cai (2012)
P. maculata	(17–)19–23(–24) × (8–)9–11(–13)	(15–)16–19(–21) × (9–)10–12(–13)	(10–)11–13(–14) × (1–)2	Wong et al. (2012)
P. mangiferae	-	(8–)10–12 × (5–)6–7	-	Glienke et al. (2011)
P. mangifera-indicae	-	3–5 × 3–4	-	Wikee et al. (2013b)
P. musaechinensis	-	14–18 × 8–12	-	Wu et al. (2014)

Table 5.8 (continued)

Species	Ascospores (µm)	Conidia size (µm)	Spermatia (µm)	Reference
P. musarum	(14–)16–18(–21) × 7–8(–9)	(12–)13–16(–20) × (7–)9–10(–11)	(6–)7–8(–9) × (1–)2	Wong et al. (2012)
P. paracapitalensis	16–17 × 6 (–7)	(9–)12–13(–14) × (6–)7	-	Guarnaccia et al. (2017)
P. parthenocissi	-	7.5–10 × 6–9	-	Zhang et al. (2013b)
P. partricuspidatae	-	5–8.5 × 8–12	3–5 (−7) × 1–2.5	Zhou et al. (2015)
P. philoprina	16–20 × 6–9	10–15 × 7–10	6−15 × 1.5−3	van der Aa (1973)
P. rhizophorae	(12.5–)14–19(–21.5) × 4.1–7.7	(13–)15–17(–19.5) × 6–7(–8)	7.5–11.5 × 1–2	In this study
P. schimae	-	7–13 × 4–7	7–11 × 1–2.5	Su and Cai (2012)
P. schimicola	-	5–8 × 8–11 (−12)	-	Zhou et al. (2015)
P. styracicola	-	9.5–13 × 6.5–9	-	Zhang et al. (2013a)
P. vitis-rotundifoliae	-	6–9.5 × 9–13	-	Zhou et al. (2015)
***P. cruenta* species complex**				
P. abieticola	(15–)16–18(–20) × (6–)7	(11−)13−16(−18) × (7−)8	-	Wikee et al. (2013b)
P. cornicola	-	(6−)7−8 × (5.5−)6(−7)	-	Wikee et al. (2013b)
P. cruenta	-	12−21 × 5−10, mostly 16−19 × 8−10	4–9(–15) × 1–2	van der Aa (1973)
P. cryptomeriae	-	9−13.5 × 6.3−10.5	-	Petrini et al. (1991)
P. foliorum	-	(12−)13−14(−15) × (9−)10(−11)	-	Wikee et al. (2013b)
P. gaultheriae	-	5−7 × 4−5	-	Ellis et al. (1885)
P. hakeicola	-	(9–)10–13(–15) × (6.5–)7	-	Crous et al. (2018)

Table 5.8 (continued)

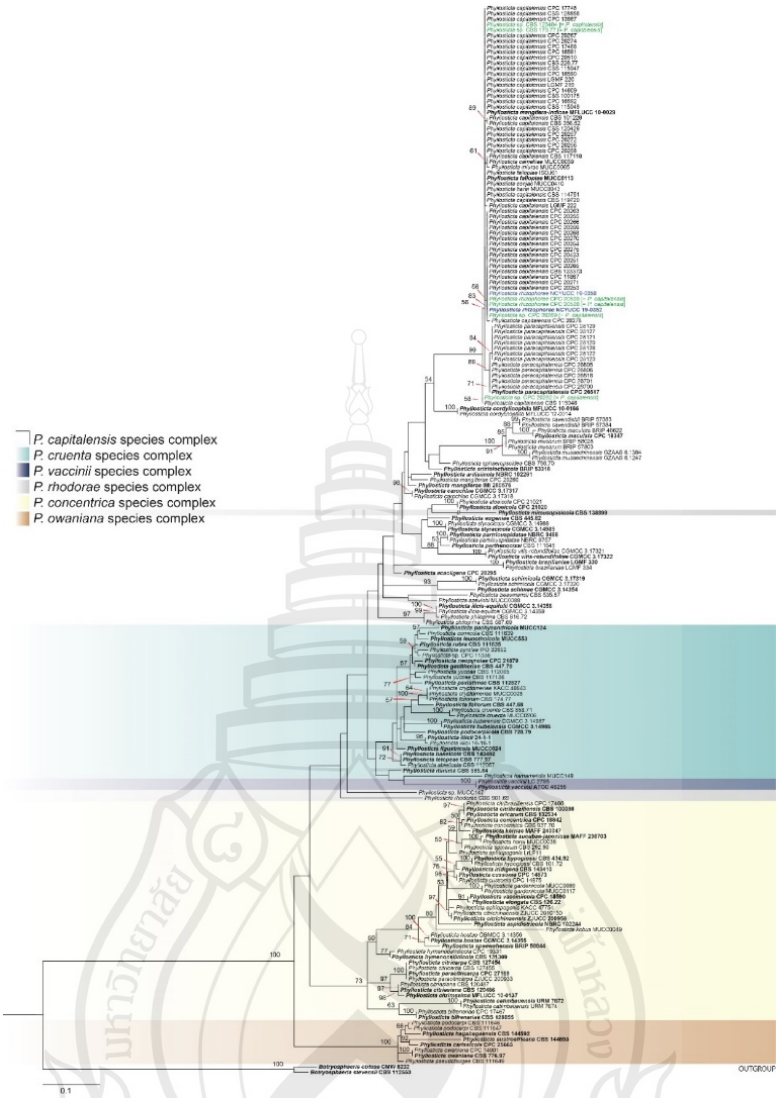
Species	Ascospores (µm)	Conidia size (µm)	Spermatia (µm)	Reference
P. hamamelidis	-	8.4–16.2 × 6.0–10.3	-	Bissett and Darbyshire (1984b)
P. hubeiensis	-	10–14.5 × 6–9	5.5–10 × 1.2–2.3	Zhang et al. (2013a)
P. illicii	-	(12–)13–15(–17) × 7(–9)	7–13 × 2–3	Lin et al. (2017)
P. leucothoicola	-	(6–)7–8(–9) × 6(–7)	5–7 × 2–3	Wikee et al. (2013b)
P. ligustricola	-	7.4–14.7 × 4.9–7.4	-	Motohashi et al. (2008)
P. minima	-	(9–)10–11(–12) × (6–)7(–8)	-	Wikee et al. (2013b)
P. neopyrolae	-	(6–)7(–8) × (5–)6(–7)	-	Wikee et al. (2013b)
P. pachysandricola	-	5.5–8.5 × 4.5–7.5	-	Wikee et al. (2013b)
P. paxistimae	-	(10–)12–14(–16) × 6–7(–8)	-	Wikee et al. (2013b)
P. podocarpicola	-	12–13(–16) × 8–9(–9.5)	-	Wikee et al. (2013b)
P. pyrolae	-	4.5–7.5 × 4–9	4–6 × 1.5–2	van der Aa (1973)
P. rubella	(8–)9–10(–12) × (4–)5	(6–)6.5–7(–8) × (4–)5(–5.5)	-	Wikee et al. (2013b)
P. paviae	-	11–15 × 7–9	-	Jagiełło et al. (2019)
P. telopeae	-	14–16.5 × 8 – 9.5	-	Yip (1989)
***P. vaccinii* species complex**				
P. vaccinii	-	7–11 × 4.5–7	-	Zhang et al. (2013b)
P. vacciniicola	-	(9–)10–12(–13) × (6–)7(–8)	-	Wikee et al. (2013b)

Table 5.8 (continued)

Species	Ascospores (µm)	Conidia size (µm)	Spermatia (µm)	Reference
***Phyllosticta rhodorae* species complex**				
P. mimusopisicola	-	10–11(–12) × (5.5–)6–6.5(–7)	7–15 × 1.5–2	Crous et al. (2014)
P. rhodorae	-	10−14 × 7−8.7	5.0–8.5 × 1–1.5	Davis (1946)
***P. concentrica* species complex**				
P. aspidistricola	-	9.5–12.5 × 8.5–10	-	Motohashi et al. (2008)
P. aucubae-japonicae	-	10–13 × 5–8.5	-	Hernandez-Restrepo et al. (2016)
P. bifrenariae	-	(10–)11–13(–16) × (7–)8–9	5–10 × 1.5–2	Glienke et al. (2011)
P. catimbauensis	-	(8.5–)9.5(–10.5) × 5.5–6	5.5–9.5 × 1.5–2	Crous et al. (2017)
P. citriasiana	-	(10–)12–14(–16) × (5–)6–7(–8)	3–5 × 1–2	Wulandari et al. (2009)
P. citribrasiliensis	-	(8–)10–12(–13) × 6–7(–8)	-	Glienke et al. (2011)
P. citricarpa	-	6–13 × 5–9	5–8 × 0.5–1	van der Aa (1973)
P. citrichinensis	(13–)14–20 (−21) × (6–)7–8(−9)	(7–)8–12(−13) × 6–9	7–9 × 1–2	Wang et al. (2012)
P. citri-maxima	-	5(–8) × (3–)4(–7)	-	Wikee et al. (2013b)
P. concentrica	-	(10–)11–13(–14) × (6–)8(–9)	-	Wikee et al. (2013b)
P. cussonia	-	(10–)12–15(–17) × (6–)7(–8)	7–10 × 2–3	Wikee et al. (2013b)
P. elongata	-	9–14 × 5–8	-	Weidemann et al. (1982)
P. ericarum	-	(8−)9–10(−12) × (6−)7	-	Crous et al. (2012a)
P. gardeniicola	-	3.6–6.0 × 1.5–2.7	-	Mhaiskar (1968)

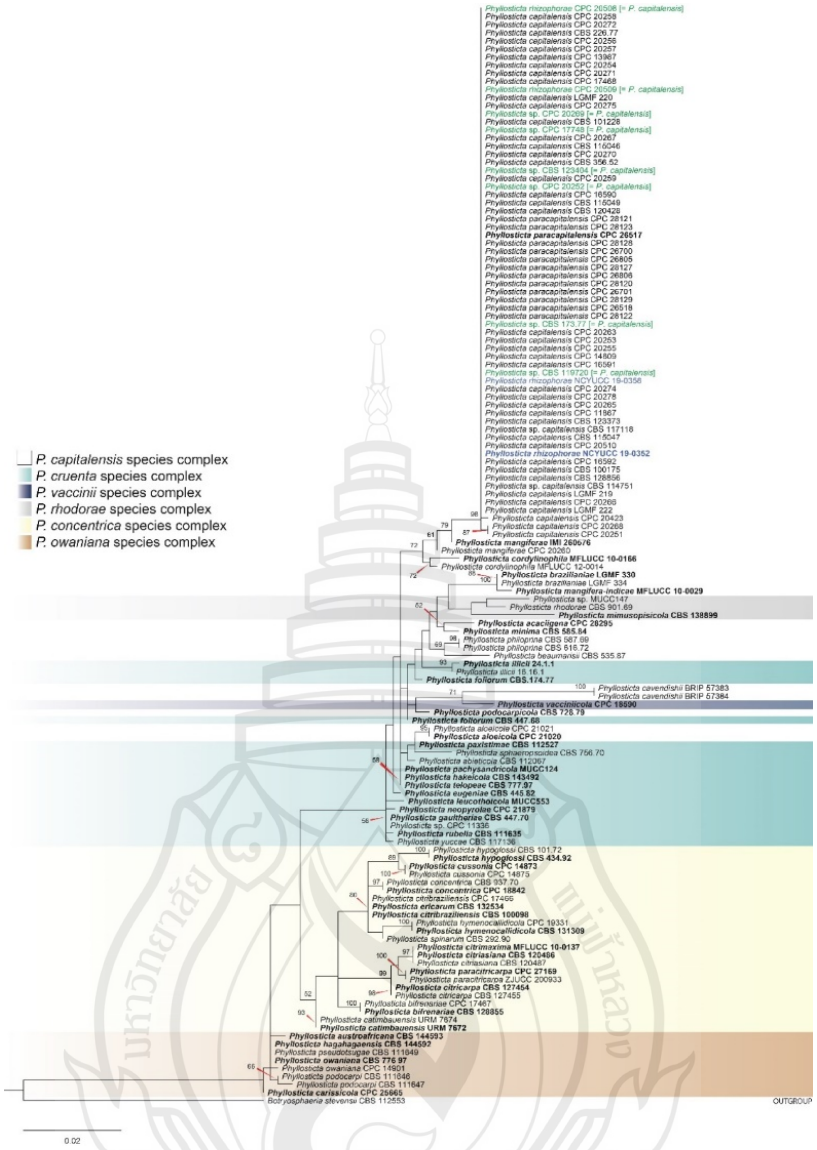
Table 5.8 (continued)

Species	Ascospores (µm)	Conidia size (µm)	Spermatia (µm)	Reference
P. harai	-	-	-	Motohashi et al. (2009) *in valid
P. hostae	-	8–15 × 5–9 (av. 10.9 × 7.6)	-	Su and Cai (2012)
P. hymenocallidicola	-	(8–)9–10(–11) × (6–)6.5–7	-	Crous et al. (2011)
P. hypoglossi	-	8–15(−18) × 6–10	-	Aa (1973)
P. iridigena	-	(10–)12–13(–15) × (7–)8(–9)	-	Marin-Felix et al. (2019)
P. kerriae	-	9.5–12.5 × 6–7.5	-	Motohashi et al. (2008)
P. kobus	-	9–12 × 6–8	-	Hennings (1905)
P. ophiopogonis	-	10–14 × 7–8	6.7–8.3 × 1.3–1.6	Wikee et al. (2013b)
P. paracitricarpa	-	(9–)11–13(–15) × 7–8(–9)	-	Guarnaccia et al. (2017)
P. speewahensis	-	10–13.5 × 7.5–9	-	Shivas et al. (2013b)
P. spinarum	-	(10–)12–14(–15) × (7–)7.5(–8)	-	Wikee et al. (2013b)
***P. owaniana* species complex**				
P. austroafricana	-	(11–)14–17(–23) × (6–)8–10(–11)	6–8 × 2–3	Crous et al. (2019)
P. carissicola	-	(11–)12–14(–15) × (9–) 10(–11)	-	Crous et al. (2015)
P. hagahagaensis	-	(11–)13–14(–15) × (7–) 8(–9)	-	Crous et al. (2019)
P. owaniana	-	(10–)11–12(–13) × (7–)8(–9)	-	Wikee et sl. (2013b)
P. podocarpi	(19–)20(–23) × (7–)8(–9)	(10–)14(–17) × (8–)9(–10)	(6–)10(–11) × (2–)2.5(–3)	Crous et al. (1996)
P. pseudotsugae	-	6.7–13.5 × 5–9	-	Petrini et al. (1991)



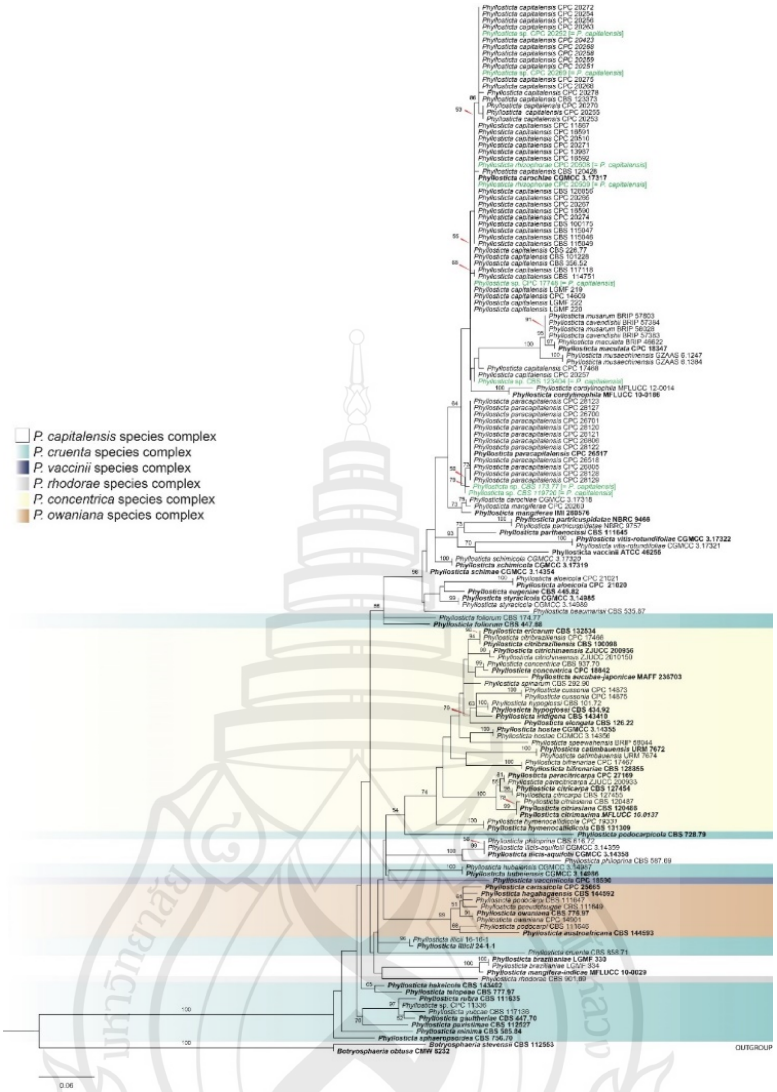
Note Phylogram generated using maximum likelihood analysis based on ITS sequence data from 195 strains. The tree is artificially rooted to Botryosphaeria obtusa strain CMW 8232 and *Botryosphaeria stevensii* strain CBS 112553. Maximum likelihood bootstrap values ≥50% are given at the nodes in this order. Species in six species complexes clades were kept hightlighted according to *P. capitalensis* species complex: White, *P. cruenta* species complex: Green, *P. vaccinii* species complex: Blue, *P. rhodorae* species complex: Gray, *P. concentrica* species complex: Yellow, and *P. owaniana* species complex: Brown. The species obtained in this study are in blue and species synonymized are in green. Ex-type taxa are in bold.

Figure 5.4 Phylogenetic analysis of *Phyllosticta* based on ITS sequence data



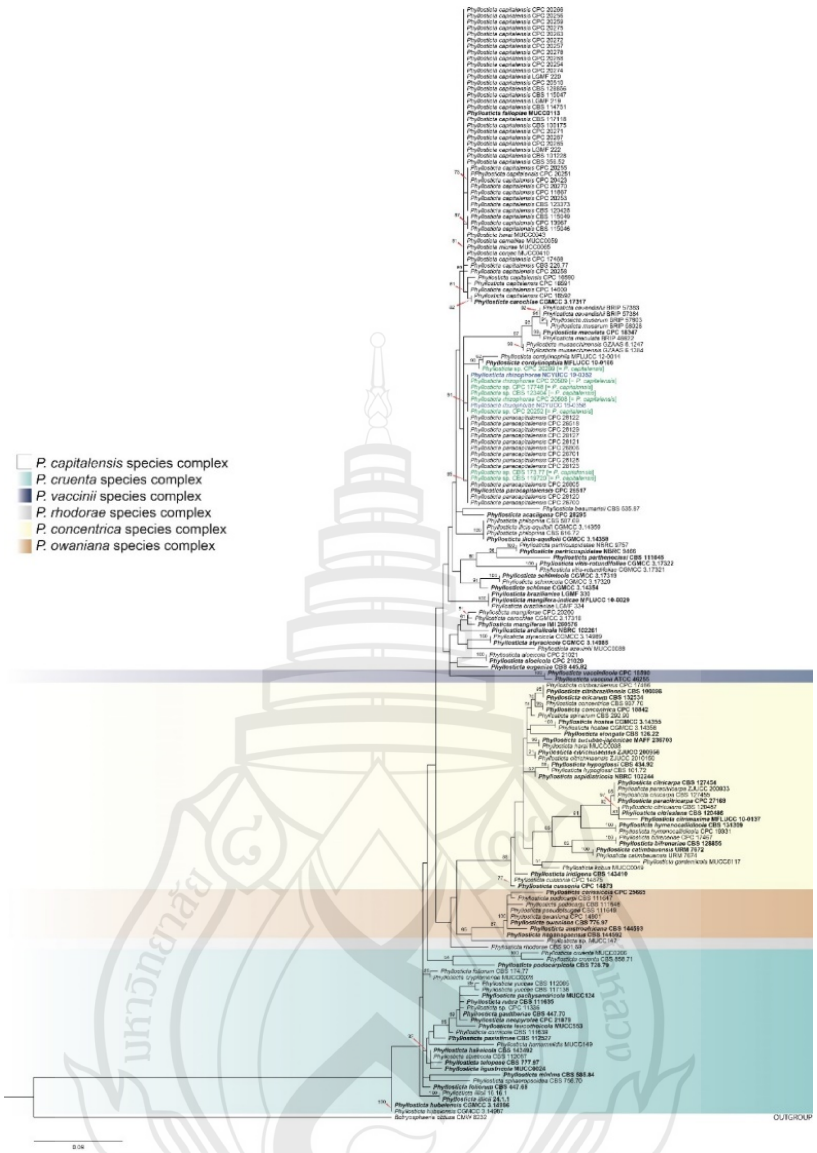
Note Phylogram generated using maximum likelihood analysis based on LSU sequence data from 136 strains. The tree is artificially rooted to *Botryosphaeria stevensii* strain CBS 112553. Maximum likelihood bootstrap values ≥50% are given at the nodes in this order. Species in six species complexes clades were kept hightlighted according to *P. capitalensis* species complex: White, *P. cruenta* species complex: Green, *P. vaccinii* species complex: Blue, *P. rhodorae* species complex: Gray, *P. concentrica* species complex: Yellow, and *P. owaniana* species complex: Brown. The species obtained in this study are in blue and species synonymized are in green. Ex-type taxa are in bold.

Figure 5.5 Phylogenetic analysis of *Phyllosticta* based on LSU sequence data



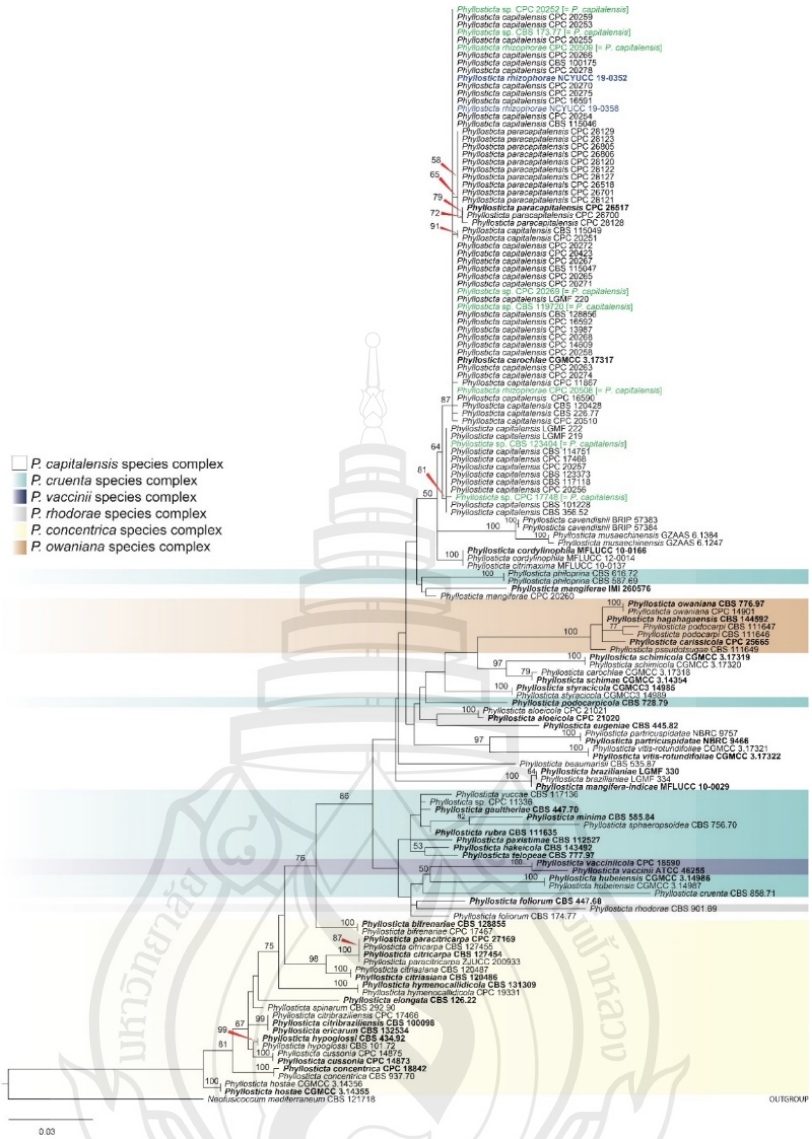
Note Phylogram generated using maximum likelihood analysis based on ef1α sequence data from 160 strains. The tree is artificially rooted to *Botryosphaeria obtusa* strain CMW 8232 and Botryosphaeria stevensii strain CBS 112553. Maximum likelihood bootstrap values ≥50% are given at the nodes in this order. Species in six species complexes clades were kept hightlighted according to *P. capitalensis* species complex: White, *P. cruenta* species complex: Green, *P. vaccinii* species complex: Blue, *P. rhodorae* species complex: Gray, *P. concentrica* species complex: Yellow, and *P. owaniana* species complex: Brown. The species obtained in this study are in blue and species synonymized are in green. Ex-type taxa are in bold.

Figure 5.6 Phylogenetic analysis of *Phyllosticta* based on ef1α sequence data



Note Phylogram generated using maximum likelihood analysis based on *act* sequence data from 183 strains. The tree is artificially rooted to *Botryosphaeria obtusa* strain CMW 8232. Maximum likelihood bootstrap values ≥50% are given at the nodes in this order. Species in six species complexes clades were kept hightlighted according to *P. capitalensis* species complex: White, *P. cruenta* species complex: Green, *P. vaccinii* species complex: Blue, *P. rhodorae* species complex: Gray, *P. concentrica* species complex: Yellow, and *P. owaniana* species complex: Brown. The species obtained in this study are in blue and species synonymized are in green. Ex-type taxa are in bold.

Figure 5.7 Phylogenetic analysis of *Phyllosticta* based on *act* sequence data



Note Phylogram generated using maximum likelihood analysis based on gapdh sequence data from 144 strains. The tree is artificially rooted to *Neofusicoccum mediterraneum* CBS 121718. Maximum likelihood bootstrap values ≥50% are given at the nodes in this order. Species in six species complexes clades were kept hightlighted according to *P. capitalensis* species complex: White, *P. cruenta* species complex: Green, *P. vaccinii* species complex: Blue, *P. rhodorae* species complex: Gray, *P. concentrica* species complex: Yellow, and *P. owaniana* species complex: Brown. The species obtained in this study are in blue and species synonymized are in green. Ex-type taxa are in bold.

Figure 5.8 Phylogenetic analysis of *Phyllosticta* based on gapdh sequence data

CHAPTER 6

DIAPORTHE: FORMALIZING SPECIES-GROUP CONCEPTS[5]

Abstract

Diaporthe species have a worldwide distribution and are associated with economically important hosts as pathogens, endophytes, and saprobes. Taxonomic identification of *Diaporthe* species is challenging due to overlapping morphological traits and host associations. Herein, we have assembled a comprehensive dataset and inferred a phylogenetic tree of Diaporthaceae using combined sequence data of ITS, *ef1 α*, *β-tubulin*, *cal* and *his3*. *Diaporthe* is not monophyletic and splits into several phylogenetically distinct clades. We introduce 13 species complexes of *Diaporthe* to aid identification of species in the genus and to make communication easier. Nine species were kept as singletons. Two taxa of Diaporthaceae, *Ophiodiaporthe cyatheae* and *Chiangraiomyces bauhiniae*, are synonymized under *D. cyatheae* (≡ *O. cyatheae*) and *D. pseudobauhiniae* (≡ *C. bauhiniae*), respectively based on phylogenetic analyses and morphological characters. The phylogenetic relationships of Diaporthaceae are reappraised, and suggestions are given for future work.

Keywords: Diaporthaceae, Morphology, Phylogeny, Plant disease, Species complexes

[5]This paper has been published in *Mycosphere*, 2022, accepted.

6.1 Introduction

Nitschke (1867) established *Diaporthe* as the type of Diaporthaceae to accommodate *Diaporthe eres*, the type species. Saccardo and Roumeguère (1884) introduced *Phomopsis*, the asexual morph. Fungal species with pleomorphic life-cycles had two names until the implementation of one fungus:one name (Taylor, 2011). The name *Diaporthe* (1867) takes precedence over *Phomopsis* (1884) based on the International Code for Nomenclature of Algae, Fungi and Plants (http://www.iapttaxon.org/nomen/main.php?page=title) (Rossman et al., 2014). More than 1000 species have been named under *Diaporthe* in Index Fungorum (http://www.indexfungorum.org/names/Names.asp, November 2021). Dissanayake et al. (2017) provided a backbone phylogenetic tree of 171 species that were introduced from culture or directly sequenced specimens. The authors used molecular data to link species with their type.

Diaporthe has a broad geographic distribution and comprises pathogens, endophytes, and saprobes on a wide range of hosts (Dissanayake et al., 2017; Bhunjun et al., 2022). *Diaporthe* species have been associated with economically important hosts, such as *Citrus* sp. and *Coffea* sp. as well as ornamental plants, such as *Clematis* (Dissanayake et al., 2017; Phukhamsakda et al., 2020). Some species have been reported as pathogens of diebacks, cankers, leaf spots, blights, melanoses, stem-end rot, and gummosis of various hosts (Gomes et al., 2013; Gopal et al., 2014; Manawasinghe et al., 2019; Zapata et al., 2020; Caio et al., 2021). For example, *D. kochmanii* and *D. kongii* have been associated with sunflower stem blight (Thompson et al., 2011), while *D. australafricana* and *D. viticola* have been linked to cane and leaf spot disease of grapevine (Van Niekerk et al., 2005). *Diaporthe citri* induces multiple symptoms in citrus, including stem-end rot and melanose of citrus fruits, gummosis or blight of perennial branches and trunks (Udayanga et al., 2013).

Diaporthe species have been previously identified based on morphology and host specificity (Uecker, 1988; Ferreira et al., 2015). However, overlapping morphological traits and association of several *Diaporthe* species with the same host make it difficult to identify characters that are taxonomically relevant at the species

level (Rehner & Uecker, 1994; Mostert et al., 2001; Gomes et al., 2013; Guarnaccia et al., 2016; Santos et al., 2010; Udayanga et al., 2011, 2014a, b; Dissanayake et al., 2017a, b). Thus, a molecular approach is essential to identify and comprehensively characterize *Diaporthe* (Santos & Phillips, 2009; Diogo et al., 2010; Luongo et al., 2011; Udayanga et al., 2012a, b; Thomidis et al., 2013; Gao et al., 2017). However, sequence data from type material is unavailable for many *Diaporthe* species, while the phylogenetic relationships of genera in Diaporthaceae remain unclear (Delsuc et al., 2005; Manawasinghe et al., 2019). Hence, additional studies are needed focusing on neo- or epi- typification to clarify the taxonomic placement of these taxa. Using all the sequences classified under *Diaporthe*, Bhunjun et al. (2022) demonstrated that several species have been wrongly identified. Therefore, using larger dataset analyses in terms of taxa and loci is necessary to improve the taxonomic and phylogenetic resolution within *Diaporthe*. These approaches have been used successfully for other fungal taxa (Rokas & Carroll, 2005; Norphanphoun et al., 2020; Bhunjun et al., 2020, 2021).

Herein, we have assembled a comprehensive dataset of five loci – nuclear ribosomal internal transcribed spacer (ITS), translation elongation factor 1-alpha (*ef1α*), beta-tubulin (β-tubulin), calmodulin (*cal*), and histone (*his3*) – containing all species denoted as *Diaporthe* (559 strains) and all genera of Diaporthaceae. Different outgroups were also tested including *Diaporthella corylina* strains or *Cytospora disciformis* and *C. leucostoma*. The latter two were selected for the backbone tree. Based on the resulting phylogenetic tree, we introduce 13 workable sections of *Diaporthe*. Several genera and species are synonymised in a separate paper (Norphanphoun et al., 2022), based on phylogenetic analyses and morphological characteristics. A list of *Diaporthe* species that are excluded from the genus is also provided following Species Fungorum (2022) and recent publications.

6.2 Materials and Methods

Raw reads were edited and assembled into contigs using Geneious® version 11.1.5 (http://www.geneious.com). The new sequences were used as queries to perform BLASTn against the nr database in GenBank to check for contamination and retrieve Diaporthaceae sequences. The GenBank taxonomy browser was also used to check all sequences assigned as *Diaporthe* in the database (last accessed in April 2021). The BLASTn against nr and type sequences was used to identify sequences incorrectly assigned to *Diaporthe*. The ITSx 1.1, a Perl based software tool, was used to extract ITS1, 5.8S and ITS2 regions (Bengtsson-Palme et al., 2013). Five genetic markers were used for phylogenetic analyses: *β-tubulin*, *cal*, *ef1α*, *his3* and ITS. Open reading frames of protein-coding genes were determined using reference sequences in BioEdit version 7.2.3 (Hall, 1999). For each genetic marker, two datasets were assembled; one containing *Diaporthella corylina* strains CBS 121124 and CBS 140348 as the outgroup, and the other containing *Cytospora disciformis* strain CBS 116827 and *C. leucostoma* strain SXYLt as the outgroup. For the latter two, genome data were used to extract the sequences needed for the analysis. *Cytospora* taxa were selected as the outgroup as they are closer to Diaporthaceae. The ITS dataset contained 534 taxa, *ef1α* 510, *β-tubulin* 479, *cal* 383, and *his3* 343 taxa. The combined datasets consisted of 535 taxa. Taxa for which a single sequence (ITS) was available were excluded from the combined matrix. When included, most were not stable and impacted the robustness of the tree. Individual datasets for each genetic marker were also assembled. For ITS, an additional dataset was prepared, even including the 50 strains excluded from the initially combined dataset. All taxa used for these analyses are given in Table 1.

Datasets for each genetic marker were aligned separately using the MAFFT v.7.110 online tool (http://mafft.cbrc.jp/alignment/server/; Katoh & Standley, 2013). BioEdit v. 7.0.5.3 was used for performing further manual adjustments where necessary (Hall, 1999). TrimAl (available on Phylemon 2.0 platform, Sánchez et al., 2011) was used to trim ambiguously aligned positions or regions. A partition homogeneity test (PHT) was performed with PAUP* 4.0b10 to determine the congruency of genes and

whether they could be combined (Swofford, 2002). The combined sequence alignments were obtained from MEGA v. 7.0.14 and v. 10.1.0 (Kumar et al., 2018).

Phylogenetic analyses were run on the CIPRES Science Gateway v. 3.3 web server (https://www.phylo.org/, Miller et al., 2010). For the combined dataset, data were partitioned as follows: ITS1+ITS2, 5.8S, *ef1α*-exon, *ef1α*-intron, *β-tubulin*-exon, *β-tubulin*- intron, *cal*-exon, *cal*-intron, *his3*-exon, *his3*-intron. Maximum likelihood (ML) analysis was performed using RAxML-HPC2 on XSEDE v. 8.2.12 (Stamatakis, 2014). Statistical confidence was derived from 1000 rapid bootstrap replicates. The GTRGAMMA model of nucleotide evolution was deemed the most appropriate for all datasets. The phylograms were visualized in FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/; Rambaut, 2014) and edited in Adobe Illustrator CC version 23.0.1 (64-bit) and Adobe Photoshop CC version 20.0.1 (Adobe Systems, CA, the USA). Newly generated sequences were deposited in the GenBank (Table 1).

Table 6.1 GenBank Accession numbers of the sequences used for phylogenetic analysis in this study

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
Cytospora disciformis	CBS 116827 [T]	*Eucalyptus grandis*	Uruguay	KY051801	KX965072	KX964907	N/A	N/A
C. leucostoma	SXYLt*	*Prunus* sp.	China	LKEB00000000				
Diaporthe absenteum	LC3429 [T]	*Camellia sinensis*	China	KP267897	KP267971	KP293477	N/A	KP293547
D. absenteum	LC3564	*Camellia sinensis*	China	KP267912	KP267986	KP293492	N/A	KP293559
D. acaciarum	CBS 138862 [T]	*Acacia tortilis*	Tanzania	KP004460	N/A	KP004509	N/A	KP004504
D. acaciigena	CBS 129521 [T]	*Acacia retinodes*	Australia	KC343005	KC343731	KC343973	KC343247	KC343489
D. acericola	MFLUCC 17-0956 [T]	*Acer negundo*	Italy	KY964224	KY964180	KY964074	KY964137	N/A
D. acerigena	CFCC 52554 [T]	*Acer tataricum*	China	MH121489	MH121531	N/A	MH121413	MH121449
D. acerigena	CFCC 52555	*Acer tataricum*	China	MH121490	MH121532	N/A	MH121414	MH121450
D. acerina	CBS 137.27	*Acer saccharum*	Not stated	KC343006	KC343732	KC343974	KC343248	KC343490
D. actinidiae	ICMP 13683 [T]	*Actinidia deliciosa*	New Zealand	KC145886	KC145941	N/A	N/A	N/A
D. actinidiae	KFRD-7	*Actinidia deliciosa* var. *Miliang*	China	KX346886	KY404088	N/A	N/A	N/A
D. actinidiae	KFRD-8	*Actinidia chinensis* var. *Jinyan*	China	KX346887	KY404089	N/A	N/A	N/A
D. actinidiae	LP-2	*Actinidia* sp.	China	KX457968	KX457965	N/A	N/A	N/A
D. acuta	PSCG045	*Pyrus pyrifolia*	China	MK626956	MK654809	MK691223	MK691123	MK726160
D. acuta	CGMCC 3.19600 [T]	*Pyrus pyrifolia*	China	MK626957	MK654802	MK691225	MK691124	MK726161
D. acutispora	CGMCC 3.18285 [T]	*Coffea* sp.	China	KX986764	KX999155	KX999195	KX999274	N/A
D. alangii	CFCC 52556 [T]	*Alangium kurzii*	China	MH121491	MH121533	MH121573	MH121415	MH121451
D. alleghaniensis	CBS 495.72 [T]	*Betula alleghaniensis*	Canada	KC343007	KC343733	KC343975	KC343249	KC343491
D. alnea	CBS 146.46 [T]	*Alnus* sp.	Netherlands	KC343008	KC343734	KC343976	KC343250	KC343492

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. amaranthophila	MAFF 246900	*Amaranthus tricolor*	Japan	LC459575	LC459577	LC459579	LC459583	LC459581
D. amaranthophila	MAFF 246901	*Amaranthus tricolor*	Japan	LC459576	LC459578	LC459580	LC459584	LC459582
D. ambigua	CBS 114015 [T]	*Pyrus communis*	South Africa	KC343010	KC343736	KC343978	KC343252	KC343494
D. ampelina	CBS 114016 [T]	*Vitis vinifera*	France	AF230751	AY745056	JX275452	AY745026	N/A
D. ampelina	CBS 267.8	*Vitis vinifera*	Italy	KC343018	KC343744	KC343986	KC343260	KC343502
D. amygdali	CBS 115620	*Prunus persica*.	US	KC343020	KC343746	KC343988	KC343262	KC343504
D. amygdali	CBS 111811	*Vitis vinifera*	South Africa	KC343019	KC343745	KC343987	KC343261	KC343503
D. amygdali	CBS 120840	*Prunus salicina*	South Africa	KC343021	KC343747	KC343989	KC343263	KC343505
D. amygdali	CBS 126679 [T]	*Prunus dulcis*	Portugal	KC343022	KC343748	KC343990	KC343264	KC343506
D. anacardii	CBS 720.97 [T]	*Anacardium occidentale*	East Africa	KC343024	KC343750	KC343992	KC343266	KC343508
D. angelicae	CBS 111592 [T]	*Heracleum sphondylium*	Austria	KC343027	KC343753	KC343995	KC343269	KC343511
D. anhuiensis	CNUCC_201901 [T]	*Cunninghamia lanceolata*	China	MN219718	MN224668	MN227008	MN224549	MN224556
D. anhuiensis	CNUCC_201902	*Cunninghamia lanceolata*	China	MN219727	MN224669	MN227009	MN224550	MN224557
D. apiculatum	LC3418 [T]	*Camellia sinensis*	China	KP267896	KP267970	KP293476	N/A	N/A
D. apiculatum	CFCC 53069	*Rhus chinensis*	China	MK432652	MK578128	MK578055	MK442974	MK442999
D. aquatica	IFRDCC 3051 [T]	*Aquatic habitat*	China	JQ797437	N/A	N/A	N/A	N/A
D. aquatica	IFRDCC 3015	*Aquatic habitat*	China	JQ797438	N/A	N/A	N/A	N/A
D. araucanorum	CBS 145285 [T]	*Araucaria araucana*	Chile	NR_169994	MN509733	MN509722	MN974277	N/A
D. araucanorum	CBS 145286	*Araucaria araucana*	Chile	MN509712	MN509734	MN509723	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. arctii	CBS 139280 T	*Arctium lappa*	Austria	KJ590736	KJ590776	KJ610891	KJ612133	KJ659218
D. arecae	CBS 161.64 T	*Areca catechu*	India	KC343032	KC343758	KC344000	KC343274	KC343516
D. arecae	CBS 535.75	*Citrus* sp.	India	KC343033	KC343759	KC344001	KC343275	KC343517
D. arengae	CBS 114979 T	*Arenga engleri*	Hong Kong	KC343034	KC343760	KC344002	KC343276	KC343518
D. aseana	MFLUCC 12-0299a T	Unidentified dead leaf	Thailand	KT459414	KT459448	KT459432	KT459464	N/A
D. asheicola	CBS 136967 T	*Vaccinium ashei*	Chile	KJ160562	KJ160594	KJ160518	KJ160542	N/A
D. asheicola	CBS 136968	*Vaccinium ashei*	Chile	KJ160563	KJ160595	KJ160519	KJ160543	N/A
D. aspalathi	CBS 117169 T	*Aspalathus linearis*	South Africa	KC343036	KC343762	KC344004	KC343278	KC343520
D. aspalathi	CBS 117168	*Aspalathus linearis*	South Africa	KC343035	KC343761	KC344003	KC343277	KC343519
D. australafricana	CBS 111886 T	*Vitis vinifera*	Australia	KC343038	KC343764	KC344006	KC343280	KC343522
D. australafricana	CBS 113487	*Vitis vinifera*	Australia	KC343039	KC343765	KC344007	KC343281	KC343523
D. averrhoae	SCHM 3605 T	*Averrhoa carambola*	China	AY618930	N/A	N/A	N/A	N/A
D. azadirachtae	TN 01	*Azadirachta indica*	India	KC631323	N/A	N/A	N/A	N/A
D. baccae	CBS 136972 T	*Vaccinium* sp.	Italy	KJ160565	KJ160597	N/A	N/A	MF418264
D. baccae	CPC 20585	*Vaccinium* sp.	Italy	KJ160564	KJ160596	N/A	N/A	N/A
D. batatas	CBS 122.21 T	*Ipomoea batatas*	US	KC343040	KC343766	KC344008	KC343282	KC343524
D. bauhiniae	CFCC 53071 T	*Bauhinia purpurea*	China	MK432648	MK578124	MK578051	MK442970	MK442995
D. bauhiniae	CFCC 53072	*Bauhinia purpurea*	China	MK432649	MK578125	MK578052	MK442971	MK442996
D. beckhausii	CBS 138.27	*Viburnum* sp.	Not stated	KC343041	KC343767	KC344009	KC343283	KC343525
D. beilharziae	BRIP 54792 T	*Indigofera australis*	Australia	JX862529	JX862535	KF170921	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. benedicti	SBen914 [T]	*Salix* sp.	US	KM669929	KM669785	N/A	KM669862	N/A
D. betulae	CFCC 50469 [T]	*Betula platyphylla*	China	KT732950	KT733016	KT733020	KT732997	KT732999
D. betulae	CFCC 50470	*Betula platyphylla*	China	KT732951	KT733017	KT733021	KT732998	KT733000
D. betulicola	CFCC 51128 [T]	*Betula albosinensis*	China	KX024653	KX024655	KX024657	KX024659	KX024661
D. betulicola	CFCC 51129	*Betula albosinensis*	China	KX024654	KX024656	KX024658	KX024660	KX024662
D. betulina	CFCC 52560	*Betula albo- sinensis*	China	MH121495	MH121537	MH121577	MH121419	MH121455
D. betulina	CFCC 52561	*Betula costata*	China	MH121496	MH121538	MH121578	MH121420	MH121456
D. bicincta	CBS 121004 [T]	*Juglans* sp.	US	KC343134	KC343860	KC344102	KC343376	KC343618
D. biconispora	CGMCC 3.17252 [T]	*Citrus grandis*	China	KJ490597	KJ490476	KJ490418	MT227578	KJ490539
D. biconispora	CGMCC 3.17251	*Fortunella margarita*	China	KJ490596	KJ490475	KJ490417	N/A	KJ490538
D. biguttulata	CFCC 52584	*Juglans regia*	China	MH121519	MH121561	MH121598	MH121437	MH121477
D. biguttulata	ZJUD47 [T]	*Citrus limon*	China	KJ490582	KJ490461	KJ490403	N/A	KJ490524
D. bohemiae	CBS 143347 [T]	*Vitis vinifera*	Czech Republic	MG281015	MG281536	MG281188	MG281710	MG281361
D. bohemiae	CBS 143348	*Vitis vinifera*	Czech Republic	MG281016	MG281537	MG281189	MG281711	MG281362
D. brasiliensis	CBS 133183 [T]	*Aspidosperma* sp.	Brazil	KC343042	KC343768	KC344010	KC343284	KC343526
D. brasiliensis	LGMF926	*Aspidosperma tomentosum*	Brazil	KC343043	KC343769	KC344011	KC343285	KC343527
D. caatingaensis	CBS 141542 [T]	*Tacinga inamoena*	Brazil	KY085927	KY115603	KY115600	N/A	KY115605
D. caatingaensis	URM7484	*Pilosocereus gounellei* subsp. *Gounellei*	Brazil	KY085928	N/A	KY115602	KY115599	KY115606
D. camelliae-oleiferae	HNZZ027 [T]	*Camellia oleifera*	China	MZ509555	MZ504707	MZ504718	MZ504685	MZ504696
D. camelliae-oleiferae	HNZZ030	*Camellia oleifera*	China	MZ509556	MZ504708	MZ504719	MZ504686	MZ504697

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. camelliae-sinensis	SAUCC194.92 T	*Camellia sinensis*	China	MT822620	MT855932	MT855817	MT855699	MT855588
D. camelliae-sinensis	SAUCC194.103	*Castanea mollissima*	China	MT822631	MT855943	MT855828	MT855710	MT855599
D. camptothecae	SCHM 3611 T	*Camptotheca acuminate*	China	AY622996	N/A	N/A	N/A	N/A
D. canthii	CBS 132533 T	*Canthium inerme*	South Africa	JX069864	KC843120	KC843230	KC843174	N/A
D. caricae-papayae	NIBM-ABIJP	*Carica papaya*	Malaysia	MN335224	N/A	N/A	N/A	N/A
D. carpini	CBS 114437	*Carpinus betulus*	Sweden	KC343044	KC343770	KC344012	KC343286	KC343528
D. carpini	CSB F191	*Brachiaria*	Kenya	KU680350	N/A	N/A	N/A	N/A
D. caryae	CFCC 52563 T	*Carya illinoensis*	China	MH121498	MH121540	MH121580	MH121422	MH121458
D. caryae	CFCC 52564	*Carya illinoensis*	China	MH121499	MH121541	MH121581	MH121423	MH121459
D. cassines	CPC 21916	*Cassine peragua*	South Africa	KF777155	KF777244	N/A	N/A	N/A
D. caulivora	CBS 127268 T	*Glycine max*	Croatia	KC343045	KC343771	KC344013	KC343287	KC343529
D. celastrina	CBS 139.27 T	*Celastrus* sp.	US	KC343047	KC343773	KC344015	KC343289	KC343531
D. celeris	CBS 143349 T	*Vitis vinifera*	Czech Republic	MG281017	MG281538	MG281190	MG281712	MG281363
D. celeris	CBS 143350	*Vitis vinifera*	Czech Republic	MG281018	MG281539	MG281191	MG281713	MG281364
D. ceratozamiae	CBS 131306 T	*Ceratozamia robusta*	Australia	JQ044420	N/A	N/A	N/A	N/A
D. ceratozamiae	HCH260	*Artemisia lavandulifolia*	China	KU360597	N/A	N/A	N/A	N/A
D. cercidis	CFCC 52565 T	*Cercis chinensis*	China	MH121500	MH121542	MH121582	MH121424	MH121460
D. chamaeropis	CBS 454.81 T	*Chamaerops humilis*	Greece	KC343048	KC343774	KC344016	KC343290	KC343532
D. chamaeropis	CBS 753.70	*Spartium junceum*	Croatia	KC343049	KC343775	KC344017	KC343291	KC343533
D. charlesworthii	BRIP 54884m T	*Rapistrum rugostrum*	Australia	KJ197288	KJ197250	KJ197268	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. chensiensis	CFCC 52567 [T]	*Abies chensiensis*	China	MH121502	MH121544	MH121584	MH121426	MH121462
D. chensiensis	CFCC 52568	*Abies chensiensis*	China	MH121503	MH121545	MH121585	MH121427	MH121463
D. chiangraiensis (=*Chiangraiomyces bauhiniae*)	MFLUCC 17–1669 [T]	*Bauhinia* sp.	Thailand	MF190119	MF377598	N/A	N/A	N/A
D. chiangraiensis (=*Ch. bauhiniae*)	MFLUCC 17–1670	*Bauhinia* sp.	Thailand	MF190118	MF377599	N/A	N/A	N/A
D. chimonanthi	SCHM 3614 [T]	*Chimonanthus praecox*	China	AY622993	N/A	N/A	N/A	N/A
D. chimonanthi	G18 A2-24	*Luehea divaricata*	Brazil	EU878426	N/A	N/A	N/A	N/A
D. chongqingensis	CGMCC 3.19603 [T]	*Pyrus pyrifolia*	China	MK626916	MK654866	MK691321	MK691209	MK726257
D. chongqingensis	PSCG 436	*Pyrus pyrifolia*	China	MK626917	MK654867	MK691322	MK691208	MK726256
D. cichorii	MFLUCC 17-1023 [T]	*Cichorium intybus*	Italy	KY964220	KY964176	KY964104	KY964133	N/A
D. cinerascens	CBS 719.96	*Ficus carica*	Bulgaria	KC343050	KC343776	KC344018	KC343292	KC343534
D. cinnamomi	CFCC 52569 [T]	*Cinnamomum* sp.	China	MH121504	MH121546	MH121586	N/A	MH121464
D. cinnamomi	CFCC 52570	*Cinnamomum* sp.	China	MH121505	MH121547	MH121587	N/A	MH121465
D. cissampeli	CBS 141331 [T]	*Cissampelos capensis*	South Africa	KX228273	N/A	KX228384	N/A	KX228366
D. citri	CBS 135422 [T]	*Citrus* sp.	US	KC843311	KC843071	KC843187	KC843157	N/A
D. citri	AR4469	*Citrus* sp.	US	KC843321	KC843081	KC843197	KC843167	N/A
D. citriasiana	CGMCC 3.15224	*Citrus unshiu*	China	JQ954645	JQ954663	KC357459	KC357491	KJ490515
D. citrichinensis	ZJUD34 [T]	*Citrus* sp.	China	JQ954648	JQ954666	KJ490396	KC357494	KJ490516
D. citrichinensis	ZJUD38	*Citrus* sp.	China	KC357558	KC357527	KC357463	KC357495	KJ490517

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. collariana	MFLUCC 17-2636 T	*Magnolia champaca*	Thailand	MG806115	MG783040	MG783041	MG783042	N/A
D. columnaris	ICMP 16836	*Vaccinium vitis-idaea*	US	KC145883	KC145999	N/A	N/A	N/A
D. columnaris	AR3612 T	*Vaccinium vitis-idaea*	US	AF439625	N/A	N/A	N/A	N/A
D. compacta	CGMCC 3.17536 T	*Camellia sinensis*	China	KP267854	KP267928	KP293434	N/A	KP293508
D. conica	CFCC 52571 T	*Alangium chinense*	China	MH121506	MH121548	MH121588	MH121428	MH121466
D. conica	CFCC 52574	*Alangium chinense*	China	MH121509	MH121551	MH121591	MH121431	MH121469
D. conorum	MAFF 410330	*Abies firma*	Japan	AB201443	N/A	N/A	N/A	N/A
D. conorum	UAS002 T	*Nothapodytes nimmoniana*	India	FJ158120	N/A	N/A	N/A	N/A
D. convolvuli	CBS 124654 T	*Convolvulus arvensis*	Turkey	KC343054	KC343780	KC344022	KC343296	KC343538
D. corylicola	CFCC 53986 T	*stems of Corylus heterophylla*	China	MW839880	MW815894	MW883977	MW836684	MW836717
D. crataegi	CBS 114435	*Crataegus rhipidophylla*	Sweden	KC343055	KC343781	KC344023	KC343297	KC343539
D. crotalariae	CBS 162.33 T	*Crotalaria spectabilis*	US	KC343056	KC343782	KC344024	KC343298	KC343540
D. crousii	CAA819 T	*Vaccinium corymbosum*	China	MK792299	MK828071	MK837922	MK883827	MK871440
D. crousii	CAA820	*Vaccinium corymbosum*	China	MK792300	MK828072	MK837923	MK883828	MK871441
D. cucurbitae	CBS 136.25	*Arctium* sp.	Not stated	KC343031	KC343757	KC343999	KC343273	KC343515
D. cucurbitae	DAOM 42078 T	*Cucumis* sp.	Canada	KM453210	KM453211	KP118848	N/A	KM453212
D. cuppatea	CBS 117499 T	*Aspalathus linearis*	South Africa	KC343057	KC343783	KC344025	KC343299	KC343541
D. cyatheae (=*Ophiodiaporthe cyatheae*)	YMJ 1364 T	*Cyathea lepifera*	Taiwan	JX570889	KC465406	KC465403	KC465410	N/A
D. cynaroidis	CBS 122676 T	*Protea cynaroides*	South Africa	KC343058	KC343784	KC344026	KC343300	KC343542

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. cytosporella	FAU461 [T]	*Citrus limon*	Italy	KC843307	KC843116	KC843221	KC843141	MF418283
D. decedens	CBS 109772	*Corylus avellana*	Austria	KC343059	KC343785	KC344027	KC343301	KC343543
D. decedens	CBS 114281	*Corylus avellana*	Austria	KC343060	KC343786	KC344028	KC343302	KC343544
D. decorticans	CBS 114649	*Alnus glutinosa*	Sweden	KC343170	KC343896	KC344138	KC343412	KC343654
D. decorticans	CBS 114200	*Prunus padus*	Sweden	KC343169	KC343895	KC344137	KC343411	KC343653
D. detrusa	CBS 109770	*Berberis vulgaris*	Austria	KC343061	KC343787	KC344029	KC343303	KC343545
D. detrusa	CBS 114652	*Berberis vulgaris*	Sweden	KC343062	KC343788	KC344030	KC343304	KC343546
D. discoidispora	ZJUD89 [T]	*Citrus unshiu*	China	KJ490624	KJ490503	KJ490445	N/A	KJ490566
D. discoidispora	ZJUD87	*Camellia sinensis*	China	KJ490622	KJ490501	KJ490443	N/A	KJ490564
D. elaeagni-glabrae	CGMCC 3.18287 [T]	*Elaeagnus glabra*	China	KX986779	KX999171	KX999212	KX999281	KX999251
D. elaeagni-glabrae	LC4806	*Elaeagnus glabra*	China	KX986780	KX999172	KX999213	KX999282	KX999252
D. elonis	6307	*Prunella vulgaris*	China	JN998101	N/A	N/A	N/A	N/A
D. endocitricola	ZHKUCC20-0012 [T]	*Citrus maxima*	China	MT355682	MT409336	MT409290	MT409312	N/A
D. endocitricola	ZHKUCC20-0013	*Citrus maxima*	China	MT355683	MT409337	MT409291	MT409313	N/A
D. endophytica	CBS 133811 [T]	*Schinus terebinthifolius*	Brazil	KC343065	KC343791	KC344033	KC343307	KC343549
D. endophytica	LGMF911	*Schinus terebinthifolius*	Brazil	KC343066	KC343792	KC344034	KC343308	KC343550
D. eres	AR3519	*Corylus avellana*	Austria	KJ210523	KJ210547	KJ420789	KJ435008	KJ420839
D. eres	CBS 109767	*Acer* sp.	Austria	DQ491514	KC343801	KC344043	KC343317	KC343559
D. eres	AR3560	*Viburnum* sp.	Austria	JQ807425	JQ807351	KJ420795	KJ435011	KJ420846
D. eres	AR4346	*Prunus mume*	Korea	JQ807429	JQ807355	KJ420823	KJ435003	KJ420872

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. eres	AR4348	*Prunus persica*	Korea	JQ807431	JQ807357	KJ420811	KJ435004	KJ420862
D. eres	AR4363	*Malus* sp.	Korea	JQ807436	JQ807362	KJ420809	KJ435033	KJ420860
D. eres	AR4369	*Pyrus pyrifolia*	Korea	JQ807440	JQ807366	KJ420813	KJ435005	KJ420864
D. eres	AR4371	*Malus pumila*	Korea	JQ807441	JQ807367	KJ420796	KJ435034	KJ420847
D. eres	AR5197	*Rhododendron* sp.	Germany	KJ210531	KJ210552	KJ420812	KJ435014	KJ420863
D. eres	CBS 135428	*Juglans cinerea*	US	KC843328	KC843121	KC843229	KC843155	KJ420840
D. eres	CBS 138594 [T]	*Ulmus laevis*	Germany	KJ210529	KJ210550	KJ420799	KJ434999	KJ420850
D. eres	CBS 138595	*Ulmus laevis*	Germany	KJ210533	KJ210554	KJ420817	KJ435006	KJ420866
D. eres	CBS 138597	*Vitis vinifera*	France	KJ210518	KJ210542	KJ420783	KJ434996	KJ420833
D. eres	CBS 138598	*Ulmus* sp.	US	KJ210521	KJ210545	KJ420787	KJ435027	KJ420837
D. eres	CBS 138599	*Acer nugundo*	Germany	KJ210528	KJ210549	KJ420830	KJ435000	KJ420845
D. eres	DP0666	*Juglans cinerea*	US	KJ210522	KJ210546	KJ420788	KJ435007	KJ420838
D. eres	DP0177	*Pyrus pyrifolia*	New Zealand	JQ807450	JQ807381	KJ420820	KJ435041	KJ420869
D. eres	DP0179	*Pyrus pyrifolia*	New Zealand	JQ807452	JQ807383	KJ420803	KJ435028	KJ420854
D. eres	DP0180	*Pyrus pyrifolia*	New Zealand	JQ807453	JQ807384	KJ420804	KJ435029	KJ420855
D. eres	DP0438	*Ulmus minor*	Austria	KJ210532	KJ210553	KJ420816	KJ435016	KJ420886
D. eres	FAU506	*Cornus florida*	US	KJ210526	JQ807403	KJ420792	KJ435012	KJ420842
D. eres	DP0590	*Pyrus pyrifolia*	New Zealand	JQ807464	JQ807394	KJ420810	KJ435037	KJ420861
D. eres	DP0591	*Pyrus pyrifolia*	New Zealand	JQ807465	JQ807395	KJ420821	KJ435018	KJ420870
D. eres	FAU483	*Malus* sp.	Netherlands	KJ210537	KJ210556	KJ420827	KJ435022	KJ420874

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. eres	FAU522	*Sassafras albidum*	US	KJ210525	JQ807406	KJ420791	KJ435010	KJ420841
D. eres	LCM11401b	*Ulmus* sp.	US	KJ210520	KJ210544	KJ420786	KJ435026	KJ420836
D. eres (=*D. biguttusis*)	CGMCC 3.17081 [T]	*Lithocarpus glabra*	China	KF576282	KF576257	KF576306	N/A	N/A
D. eres (=*D. camptothecicola*)	CFCC 51632 [T]	*Camptotheca* sp.	China	KY203726	KY228887	KY228893	KY228877	KY228881
D. eres (=*D. castaneae-mollisimae*)	DNP128 [T]	*Castanea mollissima*	China	JF957786	KJ210561	KJ420801	JX197430	KJ420852
D. eres (=*D. cotoneastri*)	CBS 439.82 [T]	*Cotoneaster* sp.	UK	FJ889450	GQ250341	JX275437	JX197429	N/A
D. eres (=*D. ellipisoidea*)	CGMCC 3.17084 [T]	*Lithocarpus glabra*	China	KF576270	KF576245	KF576294	N/A	N/A
D. eres (=*D. fukushii*)	MAFF625033 [T]	*Pyrus pyrifolia*	Japan	JQ807468	JQ807417	KJ420814	KJ435017	KJ420865
D. eres (=*D. henanensis*)	HHAUP12290 [T]	*Ziziphus jujube*	China	KC898258	N/A	KF600608	N/A	KF600609
D. eres (=*D. longicicola*)	CGMCC 3.17089 [T]	*Lithocarpus glabra*	China	KF576267	KF576242	KF576291	N/A	N/A
D. eres (=*D. lonicerae*)	MFLUCC 17-0963 [T]	*Lonicera* sp.	Italy	KY964190	KY964146	KY964073	KY964116	N/A
D. eres (=*D. mahothocarpus*)	CGMCC 3.15181 [T]	*Lithocarpus glabra*	China	KC153096	KC153087	KF576312	N/A	N/A
D. eres (=*D. momicola*)	MFLUCC 16-0113 [T]	*Prunus persica*	China	KU557563	KU557631	KU557587	KU557611	N/A
D. eres (=*D. nobilis*)	CBS 113470	*Castanea sativa*	Korea	KC343146	KC343872	KC344114	KC343388	KC343630
D. eres (=*D. rosicola*)	MFLU 17-0646 [T]	*Rosa* sp.	UK	MG828895	MG829270	MG843877	MG829274	N/A
D. eucalyptorum	CBS 132525 [T]	*Eucalyptus* sp.	Australia	NR120157	N/A	N/A	N/A	N/A
D. eucommiae	SCHM 0020 [T]	*Eucommia ulmoides*	China	AY601921	N/A	N/A	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. eucommiicola	SCHM 3607 [T]	*Eucommia ulmoides, Styrax hypoglauca*	China	AY578071	N/A	N/A	N/A	N/A
D. eugeniae	DPFT23	*Mangifera indica*	Malaysia	MK110366	MK117267	MK122799	N/A	N/A
D. eugeniae	CBS 444.82 [T]	*Eugenia aromatica*	Indonesia	KC343098	KC343824	KC344066	KC343340	KC343582
D. fibrosa	CBS 109751	*Rhamnus cathartica*	Austria	KC343099	KC343825	KC344067	KC343341	KC343583
D. fibrosa	CBS 113830	*Rhamnus cathartica*	Sweden	KC343100	KC343826	KC344068	KC343342	KC343584
D. foeniculina	CBS 111553 [T]	*Foeniculum vulgare*	Portugal	KC843295	KC843104	KC843209	KC843129	N/A
D. foeniculina	CBS 123208 [T]	*Foeniculum vulgare*	Portugal	KC343104	KC343830	KC344072	KC343346	KC343588
(=*D. foeniculacea*)								
D. foeniculina	CBS 129528 [T]	*Rhus pendulina*	South Africa	JF951146	KC843100	KC843205	KC843124	N/A
(=*D. rhoicola*)								
D. foikelawen	CBS 145289 [T]	*Drimys winteri*	Chile	NR_169995	MN509735	MN509724	MN974278	N/A
D. foikelawen	CBS 145288	*Drimys winteri*	Chile	MN509716	MN509738	MN509727	N/A	N/A
D. forlicesenica	MFLUCC 17-1015 [T]	*Dorycnium hirsutum*	Italy	KY964215	KY964171	KY964099	N/A	N/A
D. fraxini-angustifoliae	BRIP 54781 [T]	*Fraxinus angustifolia*	Australia	JX862528	JX862534	KF170920	N/A	N/A
D. fraxini-angustifoliae	MFLUCC 15-0748	*Vitis vinifera*	China	KT459428	KT459446	KT459430	KT459462	N/A
D. fraxinicola	CFCC 52582 [T]	*Fraxinus chinensis*	China	MH121517	MH121559	N/A	MH121435	N/A
D. fraxinicola	CFCC 52583	*Fraxinus chinensis*	China	MH121518	MH121560	N/A	MH121436	N/A
D. fructicola	MAFF 246408 [T]	*Passiflora edulis* × *P. edulis f. flavicarpa*	Japan	LC342734	LC342735	LC342736	LC342738	LC342737
D. fructicola	MAFF 246409	*Passiflora edulis* × *P. edulis f. flavicarpa*	Japan	LC342739	LC342740	LC342741	LC342743	LC342742
D. fulvicolor	CGMCC 3.19601 [T]	*Pyrus pyrifolia*	China	MK626859	MK654806	MK691236	MK691132	MK726163

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. fulvicolor	PSCG 057	*Pyrus pyrifolia*	China	MK626858	MK654810	MK691233	MK691131	MK726164
D. fusicola	CGMCC 3.17087 [T]	*Lithocarpus glabra*	China	KF576281	KF576256	KF576305	KF576233	N/A
D. fusicola	GH3	Unidentified	China	MT499213	MT506473	MT506474	MT506476	MT506475
D. ganjae	CBS 180.91 [T]	*Cannabis sativa*	US	KC343112	KC343838	KC344080	KC343354	N/A
D. ganjae	PSCG489	*Pyrus pyrifolia*	China	MK626955	MK654897	MK691287	MK691202	MK726204
D. ganzhouensis	CFCC 53087 [T]	Unidentified dead wood	China	MK432665	MK578139	MK578065	MK442985	MK443010
D. ganzhouensis	CFCC 53088	Unidentified dead wood	China	MK432666	MK578140	MK578066	MK442986	MK443011
D. gardeniae	CBS 288.56 [T]	*Gardenia jasminoides*	Italy	KC343113	KC343839	KC344081	KC343355	KC343597
D. gardeniae	step-1	*Gardenia jasminoides*	China	KY797655	MF158048	MF158050	N/A	MF158049
D. garethjonesii	MFLUCC 12-0542a [T]	Unidentified dead leaf	Thailand	KT459423	KT459457	KT459441	KT459470	N/A
D. glabrae	SCHM 3622 [T]	*Bougainvillea glabra*	China	AY601918	N/A	N/A	N/A	N/A
D. goulteri	BRIP 55657a [T]	*Helianthus annuus*	Australia	KJ197290	KJ197252	KJ197270	N/A	N/A
D. grandiflori	SAUCC194.84 [T]	*Heterostemma grandiflorum*	China	MT822612	MT855924	MT855809	MT855691	MT855580
D. guangdongensis	ZHKUCC20-0014 [T]	*Citrus maxima*	China	MT355684	MT409338	MT409292	MT409314	N/A
D. guangdongensis	ZHKUCC20-0015	*Citrus maxima*	China	MT355685	MT409339	MT409293	MT409315	N/A
D. guangxiensis	JZB320094 [T]	*Vitis vinifera*	China	MK335772	MK523566	MK500168	MK736727	N/A
D. guangxiensis	JZB320091	*Vitis vinifera*	China	MK335769	MK523564	MK500165	MK736724	N/A
D. gulyae	BRIP 54025 [T]	*Helianthus annuus*	Australia	JF431299	JN645803	KJ197271	N/A	N/A
D. gulyae	MFLUCC 17-1026	*Heracleum sphondylium*	Italy	KY964223	KY964179	KY964107	KY964136	N/A
D. helianthi	CBS 592.81 [T]	*Helianthus annuus*	Serbia	KC343115	KC343841	KC344083	KC343357	KC343599

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. heliconiae	SAUCC194.77 T	*Heliconia metallica*	China	MT822605	MT855917	MT855802	MT855684	MT855573
D. heliconiae	SAUCC194.75	*Heliconia metallica*	China	MT822603	MT855915	MT855800	MT855682	MT855571
D. heterophyllae	CBS 143769	*Acacia heterohpylla*	France	MG600222	MG600224	MG600226	MG600218	MG600220
D. heterostemmatis	SAUCC194.85 T	*Heterostemma grandiflorum*	China	MT822613	MT855925	MT855810	MT855692	MT855581
D. heterostemmatis	SAUCC194.102	*Camellia sinensis*	China	MT822630	MT855942	MT855827	MT855709	MT855598
D. heveae	B23	*Atta cephalotes*	Brazil	KR812219	N/A	N/A	N/A	N/A
D. hickoriae	CBS 145.26 T	*Carya glabra*	USA	KC343118	KC343844	KC344086	KC343360	KC343602
D. hispaniae	CBS 143351 T	*Vitis vinifera*	Spain	MG281123	MG281644	MG281296	MG281820	MG281471
D. hispaniae	CBS 143352	*Vitis vinifera*	Spain	MG281124	MG281645	MG281297	MG281821	MG281472
D. hongkongensis	CBS 115448 T	*Dichroa febrífuga*	China	KC343119	KC343845	KC344087	KC343361	KC343603
D. hongkongensis	LC3079	*Camellia sinensis*	China	KP267851	KP267925	KP293431	N/A	KP293505
D. hordei	CBS 481.92 T	*Hordeum vulgare*	Norway	KC343120	KC343846	KC344088	KC343362	KC343604
D. hordei	HCH306	*Artemisia lavandulifolia*	China	KU360617	N/A	N/A	N/A	N/A
D. huangshanensis	CNUCC 201903 T	*Camellia oleifera*	China	MN219729	MN224670	MN227010	N/A	MN224558
D. huangshanensis	CNUCC 201904	*Camellia oleifera*	China	MN219730	MN224671	MN227011	N/A	MN224559
D. hubeiensis	JZB320123 T	*Vitis vinifera*	China	MK335809	MK523570	MK500147	MK500235	N/A
D. hubeiensis	JZB320128	*Vitis vinifera*	China	MK335814	MK523573	MK500152	MK500240	N/A
D. hunanensis	HNZZ023 T	*Camellia oleifera*	China	MZ509550	MZ504702	MZ504713	MZ504680	MZ504691
D. hunanensis	HNZZ025	*Camellia oleifera*	China	MZ509551	MZ504703	MZ504714	MZ504681	MZ504692
D. hungariae	CBS 143353 T	*Vitis vinifera*	Hungary	MG281126	MG281647	MG281299	MG281823	MG281474

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. hungariae	CBS 143354	*Vitis vinifera*	Hungary	MG281127	MG281648	MG281300	MG281824	MG281475
D. impulsa	CBS 114434	*Sorbus aucuparia*	Sweden	KC343121	KC343847	KC344089	KC343363	KC343605
D. impulsa	CBS 141.27	*Sorbus americana*	Sweden	KC343122	KC343848	KC344090	KC343364	KC343606
D. incompleta	CGMCC 3.18288 [T]	*Camellia sinensis*	China	KX986794	KX999186	KX999226	KX999289	KX999265
D. incompleta	LC6706	*Camellia sinensis*	China	KX986793	KX999185	N/A	KX999288	KX999264
D. inconspicua	CBS 133813 [T]	*Maytenus ilicifolia*	Brazil	KC343123	KC343849	KC344091	KC343365	KC343607
D. inconspicua	URM7776	*Cenostigma pyramidale*	Brazil	MG696772	MG710414	MG710395	MG710391	MG710410
D. infecunda	CBS 133812 [T]	*Schinus* sp.	Brazil	KC343126	KC343852	KC344094	KC343368	KC343610
D. infecunda	CPC 20293	*Schinus terebinthifolius*	Brazil	KC343129	KC343855	KC344097	KC343371	KC343613
D. infertilis	CBS 230.52 [T]	*Citrus sinensis*	Suriname	KC343052	KC343778	KC344020	KC343294	KC343536
D. infertilis	CPC 20322	*Glycine max*	Brazil	KC343053	KC343779	KC344021	KC343295	KC343537
D. isoberliniae	CPC 22549 [T]	*Isoberlinia angolensis*	Zambia	KJ869133	N/A	KJ869245	N/A	N/A
D. italiana	MFLUCC 18-0091 [T]	*Morus alba*	Italy	NR_165892	MH853687	MH853689	MH853691	N/A
D. italiana	MFLUCC 18-0090	*Morus alba*	Italy	MH846237	MH853686	MH853688	MH853690	N/A
D. juglandicola	CFCC 51134 [T]	*Juglans mandshurica*	China	KU985101	KX024628	KX024634	KX024616	KX024622
D. juglandicola	CFCC 51135	*Juglans mandshurica*	China	KU985102	KX024629	KX024635	KX024617	KX024623
D. kadsurae	CFCC 52587	*Kadsura longipedunculata*	China	MH121522	MH121564	MH121601	MH121440	MH121480
D. kadsurae	CFCC 52586 [T]	*Kadsura longipedunculata*	China	MH121521	MH121563	MH121600	MH121439	MH121479
D. kochmanii	BRIP 54033 [T]	*Helianthus annuus*	Australia	JF431295	JN645809	N/A	N/A	N/A
D. kochmanii	BRIP 54034	*Helianthus annuus*	Australia	JF431296	JN645810	N/A	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. kongii	BRIP 54031 T	*Portulaca grandifla*	Australia	JF431301	JN645797	N/A	N/A	N/A
D. kongii	BRIP 54032	*Portulaca grandifla*	Australia	JF431300	JN645798	N/A	N/A	N/A
D. krabiensis	MFLUCC 17-2481 T	*marine based habitats*	Thailand	MN047101	MN433215	MN431495	N/A	N/A
D. kyushuensis	STE-U2675	*grapevines*	South Africa	AF230749	N/A	N/A	N/A	N/A
D. kyushuensis	ch-D-1 T	*grapevine*	Japan	AB302250	N/A	N/A	N/A	N/A
D. lagerstroemiae	SCHM 3608 T	*Lagerstroemia indica*	China	AY622994	N/A	N/A	N/A	N/A
D. leucospermi	CBS111980 T	*Leucospermum* sp.	Australia	JN712460	KY435632	KY435673	KY435663	KY435653
D. limonicola	CPC 27869	*Citrus limon*	Malta	MF418419	MF418498	MF418579	MF418253	MF418339
D. limonicola	CPC 28200 T	*Citrus limon*	Malta	NR_154980	MF418501	MF418582	MF418256	MF418342
D. liquidambaris	XSD-15	Unidentified	China	EU273505	N/A	N/A	N/A	N/A
D. liquidambaris	SCHM 3621 T	*Liquidambar formosana*	China	AY601919	N/A	N/A	N/A	N/A
D. litchii	SAUCC194.22 T	*Litchi chinensis*	China	MT822550	MT855863	MT855747	MT855635	MT855519
D. litchii	SAUCC194.12	*Elaeagnus conferta*	China	MT822540	MT855854	MT855737	MT855625	MT855509
D. litchiicola	BRIP 54900 T	*Litchi chinensis*	Australia	JX862533	JX862539	KF170925	N/A	N/A
D. lithocarpus	CGMCC 3.15175 T	*Lithocarpus glabra*	China	KC153104	KC153095	KF576311	KF576236	N/A
D. lithocarpus	CGMCC 3.17098	*Lithocarpus glaber*	China	KF576276	KF576251	KF576300	KF576228	N/A
D. litoricola	MFLUCC 16-1195	Unidentified	UK	MF190139	N/A	N/A	N/A	N/A
D. litoricola	MFLUCC 17-1657 T	Unidentified	UK	MF190140	N/A	N/A	N/A	N/A
D. longispora	CBS 194.36 T	*Ribes* sp.	Canada	KC343135	KC343861	KC344103	KC343377	KC343619
D. loropetali	SCHM 3615 T	*Loropetalum chinense*	China	AY601917	N/A	N/A	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. lusitanicae	CBS 123212	*Foeniculum vulgare*	Portugal	KC343136	KC343862	KC344104	KC343378	KC343620
D. lusitanicae	CBS 123213 [T]	*Foeniculum vulgare*	Portugal	MH863280	KC343863	KC344105	KC343379	KC343621
D. lutescens	SAUCC194.36 [T]	*Chrysalidocarpus lutescens*	China	MT822564	MT855877	MT855761	MT855647	MT855533
D. macintoshii	BRIP 55064a [T]	*Rapistrum rugostrum*	Australia	KJ197289	KJ197251	KJ197269	N/A	N/A
D. macintoshii	CAF013	Unidentified	China	KY420947	N/A	N/A	N/A	N/A
D. macintoshii	CAF027	Unidentified	China	KU821458	N/A	N/A	N/A	N/A
D. magnoliicola	SCHM 3001 [T]	*Magnolia coco*	China	AY622995	N/A	N/A	N/A	N/A
D. malorum	CAA734 [T]	*Malus domestica*	Portugal	KY435638	KY435627	KY435668	KY435658	KY435648
D. malorum	CAA953	*Eucalyptus globulus*	Portugal	MN190308	MT309430	MT309456	MT309447	MT309439
D. manihotia	CBS 505.76	*Manihot utilissima*	Rwanda	KC343138	KC343864	KC344106	KC343380	KC343622
D. manihotia	MFLU 19-2826	*Camellia* sp.	China	MT012296	MW014359	MW018927	MW014358	N/A
D. marina	MFLU 17-2622 [T]	*marine based habitats*	Thailand	MN047102	N/A	N/A	N/A	N/A
D. maritima	NB464-3A	*Picea rubens*	Canada	KU552027	KU552022	KU574616	N/A	N/A
D. maritima	DAOM 695742 [T]	*Picea rubens*	Canada	KU552025	KU552023	KU574615	MN136126	MN136175
D. masirevicii	BRIP 57892a [T]	*Helianthus annuus*	Australia	KJ197276	KJ197239	KJ197257	N/A	N/A
D. masirevicii	LC6740	*Camellia sinensis*	China	KY011888	KY011899	N/A	N/A	N/A
D. mayteni	CBS 133185 [T]	*Maytenus ilicifolia*	Brazil	KC343139	KC343865	KC344107	KC343381	KC343623
D. maytenicola	CPC 21896 [T]	*Maytenus acuminata*	South Africa	KF777157	N/A	KF777250	N/A	N/A
D. megalospora	CBS 143.27 [T]	*Sambucus canadensis*	Not stated	KC343140	KC343866	KC344108	KC343382	KC343624
D. melastomatis	SAUCC194.55 [T]	*Melastoma malabathricum*	China	MT822583	MT855896	MT855780	MT855664	MT855551

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. melastomatis	SAUCC194.80	*Millettia reticulata*	China	MT822608	MT855920	MT855805	MT855687	MT855576
D. melitensis	CPC 27873 [T]	*Citrus limon*	Malta	MF418424	MF418503	MF418584	MF418258	MF418344
D. melitensis	CPC 27875	*Citrus limon*	Malta	MF418425	MF418504	MF418585	MF418259	MF418345
D. melonis	CBS 507.78 [T]	*Cucumis melo*	US	KC343142	KC343868	KC344110	KC343384	KC343626
D. melonis	SoyYS1712	soybean	Myanmar	LC360101	LC377213	LC377206	N/A	N/A
D. meridionalis	stc-2	soybean	Not stated	AF001015	N/A	N/A	N/A	N/A
D. meridionalis	90-48	soybean	Not stated	AF000564	N/A	N/A	N/A	N/A
D. michelina	SCHM 3603 [T]	*Michelia alba*	China	AY620820	N/A	N/A	N/A	N/A
D. middletonii	BRIP 54884e [T]	*Rapistrum rugostrum*	Australia	KJ197286	KJ197248	KJ197266	N/A	N/A
D. middletonii	BRIP 57329	*Chrysanthemoides monilifera* subsp. *Rotundata*	Australia	KJ197285	KJ197247	KJ197265	N/A	N/A
D. millettiae	GUCC9167 [T]	*Millettia reticulata*	China	MK398674	MK480609	MK502089	MK502086	N/A
D. minusculata	CGMCC 3.20098 [T]	saprobic on decaying woody	China	MT385957	MT424692	MT424712	MW022475	MW022499
D. minusculata	GZCC 19-0345	saprobic on decaying woody	China	MT797184	MT793027	MT793038	MW022476	MW022500
D. miriciae	BRIP 54736j [T]	*Helianthus annuus*	Australia	KJ197282	KJ197244	KJ197262	N/A	N/A
D. miriciae	CGMHD 1023	*Homo sapiens*	Taiwan	MH268404	MH368012	MH368009	MH368011	MH368010
D. multiguttulata	CGMCC 3.17258 [T]	*Citrus grandis*	China	KJ490633	KJ490512	KJ490454	N/A	KJ490575
D. multiguttulata	CFCC 53099	Unidentified	China	MK573958	MK574633	MK574653	MK574593	MK574613
D. musigena	CBS 129519 [T]	*Musa* sp.	Australia	KC343143	KC343869	KC344111	KC343385	KC343627
D. musigena	HKFZL006	*Khaya senegalensis*	China	MK050110	MK054238	MK079660	N/A	N/A
D. myracrodruonis	URM 7972 [T]	*Astronium urundeuva*	Brazil	MK205289	MK213408	MK205291	MK205290	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. nebulae	PMM1681 [T]	*Vitis vinifera*	South Africa	KY511337	MH708552	KY511369	N/A	N/A
D. nebulae	Phom240	*Vitis vinifera*	South Africa	KY511315	MH708543	KY511346	N/A	N/A
D. neilliae	CBS 144.27 [T]	*Spiraea* sp.	US	KC343144	KC343870	KC344112	KC343386	KC343628
D. nelumbonis	A-SER3	*Persea americana*	Sri Lanka	MK907914	N/A	N/A	N/A	N/A
D. nelumbonis	R. Kirschner 4114 [T]	*Nelumbo nucifera*	Taiwan	KT821501	N/A	LC086652	N/A	N/A
D. neoarctii	CBS 109490 [T]	*Ambrosia trifi*	US	KC343145	KC343871	KC344113	KC343387	KC343629
D. neoraonikayaporum	MFLUCC 14-1136 [T]	*Tectona grandis*	Thailand	KU712449	KU749369	KU743988	KU749356	N/A
D. nigra	JZB320170 [T]	*stem of Ballota nigra*	Italy	MN653009	MN892277	MN887113	N/A	N/A
D. nitschkei	AR5211 [T]	*Hedera helix*	France	KJ210538	KJ210559	KJ420828	KJ435043	KJ420875
D. nomorae	CBS 157.29	*Morus* sp.	Japan	KC343154	KC343880	KC344122	KC343396	KC343638
D. nothofagi	BRIP 54801 [T]	*Nothofagus cunninghamii*	Australia	JX862530	JX862536	KF170922	N/A	N/A
D. obtusifoliae	CPC 32336 [T]	*Acacia obtusifolia*	Australia	MG386072	N/A	N/A	N/A	MG386137
D. ocoteae	CBS 141330 [T]	*Ocotea obtusata*	France	KX228293	N/A	KX228388	N/A	N/A
D. oculi	HHUF 30565 [T]	*Homo sapiens*	Japan	LC373514	LC373516	LC373518	N/A	N/A
D. oncostoma	CBS 589.78	*Robinia pseudoacacia*	France	KC343162	KC343888	KC344130	KC343404	KC343646
D. oncostoma	CBS 100454	*Robinia pseudoacacia*	Germany	KC343160	KC343886	KC344128	KC343402	KC343644
D. oraccinii	CGMCC 3.17531 [T]	*Camellia sinensis*	China	KP267863	KP267937	KP293443	N/A	KP293517
D. oraccinii	LC3296	*Camellia sinensis*	China	KP267884	KP267958	KP293464	N/A	KP293536
D. osmanthi	GUCC9165 [T]	*Osmanthus fragrans*	China	MK398675	MK480610	MK502091	MK502087	N/A
D. ovalispora	CGMCC 3.17256 [T]	*Citrus limon*	China	KJ490628	KJ490507	KJ490449	N/A	KJ490570

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. ovoidea	CGMCC 3.17092 [T]	*Lithocarpus glabra*	China	KF576264	KF576239	KF576288	KF576222	N/A
D. ovoidea	CGMCC 3.17093	*Lithocarpus glaber*	China	KF576265	KF576240	KF576289	KF576223	N/A
D. oxe	CBS 133186 [T]	*Maytenus ilicifolia*	Brazil	KC343164	KC343890	KC344132	KC343406	KC343648
D. oxe	CBS 133187	*Maytenus ilicifolia*	Brazil	KC343165	KC343891	KC344133	KC343407	KC343649
D. padina	CFCC 52590 [T]	*Padus racemosa*	China	MH121525	MH121567	MH121604	MH121443	MH121483
D. padina	CFCC 52591	*Padus racemosa*	China	MH121526	MH121568	MH121605	MH121444	MH121484
D. pandanicola	MFLUCC 17-0607 [T]	*Pandanus* sp.	Thailand	MG646974	N/A	MG646930	N/A	N/A
D. paranensis	CBS 133184 [T]	*Maytenus ilicifolia*	Brazil	KC343171	KC343897	KC344139	KC343413	KC343655
D. paranensis	LMICRO417	*Schinus terebinthifolia*	Brazil	KY461115	KY461116	N/A	N/A	N/A
D. parapterocarpi	CPC 22729 [T]	*Pterocarpus brenanii*	Zambia	KJ869138	N/A	KJ869248	N/A	N/A
D. parva	CGMCC 3.19599 [T]	*Pyrus* × *bretschneideri*	China	MK626919	MK654858	MK691248	N/A	MK726210
D. parva	PSCG035	*Pyrus* × *bretschneideri*	China	MK626920	MK654859	MK691249	MK691169	MK726211
D. pascoei	BRIP 54847 [T]	*Persea americana*	Australia	JX862532	JX862538	KF170924	N/A	N/A
D. pascoei	BPPCA147	*Mangifera indica*	Malaysia	MK111091	MK117255	MK122790	N/A	N/A
D. passiflorae	CBS 132527 [T]	*Passifl a edulis*	South America	JX069860	N/A	N/A	N/A	N/A
D. passiflorae	DJY16A1-5	*Actinidia* sp.	China	MH595929	MH621353	MH621349	N/A	N/A
D. passifloricola	CBS 141329 [T]	*Passiflora foetida*	Malaysia	KX228292	N/A	KX228387	N/A	KX228367
D. passifloricola	NFIF-3-11	*Citrus reticulata* cv. *nanfengmiju*	China	MG786598	MG925401	MG925398	MK238995	MK238998
D. patagonica	CBS 145291 [T]	*Aristotelia chilensis*	Chile	NR_169996	MN509739	MN509728	MN974279	N/A
D. patagonica	CBS 145755	*Aristotelia chilensis*	Chile	MN509718	MN509740	MN509729	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. penetriteum	CGMCC 3.17532 [T]	*Camellia sinensis*	China	KP714505	KP714517	KP714529	N/A	KP714493
D. penetriteum	LC3215	*Camellia sinensis*	China	KP267879	KP267953	KP293459	N/A	KP293532
D. perjuncta	CBS 109745 [T]	*Ulmus glabra*	Austria	KC343172	KC343898	KC344140	KC343414	KC343656
D. perniciosa	ATCC 38578	Unidentified	Not stated	HQ908492	N/A	N/A	N/A	N/A
D. perseae	CBS 151.73 [T]	*Persea gratissima*	Netherlands	KC343173	KC343899	KC344141	KC343415	KC343657
D. perseae	BPPCA257	*Mangifera indica*	Malaysia	MK111098	MK117256	MK122791	N/A	N/A
D. pescicola	MFLUCC 16-0105 [T]	*Prunus persica*	China	KU557555	KU557623	KU557579	KU557603	N/A
D. pescicola	PSCG036	*Pyrus* x *bretschneideri*	China	MK626855	MK654796	MK691226	MK691116	MK726159
D. phaseolorum	AR4203 [T]	*Phaseolus vulgaris*	US	KJ590738	KJ590739	KJ610893	KJ612135	KJ659220
D. phaseolorum	CBS 116019	*Caperonia palustris*	US	KC343175	KC343901	KC344143	KC343417	KC343659
D. phillipsii	CAA817 [T]	*Vaccinium corymbosum*	Portugal	MK792305	MK828076	MN000351	MK883831	MK871445
D. phillipsii	CAA818	*Vaccinium corymbosum*	Portugal	MK792307	MK828078	MN000352	MK883833	MK871447
D. phoenicicola	CBS 161.64 [T]	*Areca catechu*	India	MH858400	GQ250349	JX275440	JX197432	N/A
D. phoenicicola	PBMR345	*Mangifera indica*	Malaysia	MK111088	MK117275	MK122810	N/A	N/A
D. phoenicicola	PBMR340	*Mangifera indica*	Malaysia	MK111086	MK117271	MK122805	N/A	N/A
D. phoenicicola	KUC21243	*Sargassum* sp.	South Korea	KT207761	N/A	KT207659	N/A	N/A
D. phoenicicola	KUC21217	*Sargassum* sp.	South Korea	KT207733	N/A	KT207633	N/A	N/A
D. phragmitis	CBS 138897 [T]	*Phragmites australis*	China	KP004445	N/A	KP004507	N/A	KP004503
D. phyllanthicola	SCHM 3680 [T]	*Phyllanthus emblica*	China	AY620819	N/A	N/A	N/A	N/A
D. phyllanthicola	RS 129	*Medicinal plant*	India	MK398278	N/A	N/A	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. podocarpi-macrophylli	CGMCC 3.18281 [T]	*Podocarpus macrophyllus*	China	KX986774	KX999167	KX999207	KX999278	KX999246
D. podocarpi-macrophylli	LC6229	*Olea europaea*	Italy	KX986771	KX999164	KX999204	KX999277	KX999243
D. poincianellae	URM 7932 [T]	*Cenostigma pyramidale*	Brazil	MH989509	MH989538	MH989537	MH989540	MH989539
D. portugallica	CPC 34247 [T]	*Camellia sinensis*	Portugal	MH063905	MH063911	MH063917	MH063893	MH063899
D. portugallica	CPC 34248	*Camellia sinensis*	Portugal	MH063906	MH063912	MH063918	MH063894	MH063900
D. pseudoalnea	CFCC 54190 [T]	*Alnus glutinosa*	Netherlands	MZ727037	MZ816343	MZ753487	MZ753468	MZ781302
D. pseudoalnea	M2A	*Alnus glutinosa*	Netherlands	MZ727038	MZ816344	MZ753488	MZ753469	MZ753478
D. pseudoinconspicua	URM 7873	*Cenostigma pyramidale*	Brazil	MH122535	MH122530	MH122521	MH122525	MH122518
D. pseudoinconspicua	URM 7874 [T]	*Cenostigma pyramidale*	Brazil	MH122538	MH122533	MH122524	MH122528	MH122517
D. pseudolongicolla (=*D. novem*)	PL42 [T]	*Glycine max*	Serbia	JQ697843	JQ697856	N/A	N/A	N/A
D. pseudolongicolla (=*D. novem*)	CBS 127270	*Glycine max*	Croatia	KC343156	KC343882	KC344124	KC343398	KC343640
D. pseudomangiferae	CBS 101339 [T]	*Mangifera indica*	Dominican Republic	KC343181	KC343907	KC344149	KC343423	KC343665
D. pseudomangiferae	CBS 388.89	*Mangifera indica*	Mexico	KC343182	KC343908	KC344150	KC343424	KC343666
D. pseudooculi	HHUF 30617 [T]	*Homo sapiens*	Japan	NR_161019	LC373517	LC373519	N/A	N/A
D. pseudooculi	B3180	*tamarind*	Malaysia	MT043790	N/A	N/A	N/A	N/A
D. pseudophoenicicola	CBS 462.69 [T]	*Phoenix dactylifera*	Spain	KC343184	KC343910	KC344152	KC343426	KC343668
D. pseudophoenicicola	HNQZ01	*Areca catechu*	China	MN424520	MN424562	MN424534	MN424576	MN424548
D. pseudotsugae	MFLU 15-3228 [T]	*Pseudotsuga menziesii*	Italy	N/A	KY964181	KY964108	KY964138	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. psoraleae	CBS 136412 [T]	*Psoralea pinnata*	South Africa	KF777158	KF777245	KF777251	N/A	N/A
D. psoraleae-pinnatae	CBS 136413 [T]	*Psoralea pinnata*	South Africa	KF777159	N/A	KF777252	N/A	N/A
D. pterocarpi	MFLUCC 10-0571 [T]	*Pterocarpus indicus*	Thailand	JQ619899	JX275416	JX275460	JX197451	N/A
D. pterocarpi	MFLUCC 10-0588	*Pterocarpus indicus*	Thailand	JQ619900	JX275417	JX275461	JX197452	N/A
D. pterocarpicola	MFLUCC 10-0580 [T]	*Pterocarpus indicus*	Thailand	JQ619887	JX275403	JX275441	JX197433	N/A
D. pulla	CBS 338.89 [T]	*Hedera helix*	Yugoslavia	KC343152	KC343878	KC344120	KC343394	KC343636
D. pungensis	SAUCC194.112 [T]	*Elaeagnus pungens*	China	MT822640	MT855952	MT855837	MT855719	MT855607
D. pungensis	SAUCC194.89	*Camellia sinensis*	China	MT822617	MT855929	MT855814	MT855696	MT855585
D. pustulata	CBS 109742	*Acer pseudoplatanus*	Austria	KC343185	KC343911	KC344153	KC343427	KC343669
D. pustulata	CBS 109784	*Prunus padus*	Austria	KC343187	KC343913	KC344155	KC343429	KC343671
D. pyracanthae	CBS 142384 [T]	*Pyracantha coccinea*	Portugal	KY435635	KY435625	KY435666	KY435656	KY435646
D. pyracanthae	CAA487	*Pyracantha coccinea*	Portugal	KY435636	KY435626	KY435667	KY435657	KY435647
D. racemosae	CPC 26646 [T]	*Euclea racemosa*	South Africa	MG600223	MG600225	MG600227	MG600219	MG600221
D. raonikayaporum	CBS 133182 [T]	*Spondias mombin*	Brazil	KC343188	KC343914	KC344156	KC343430	KC343672
D. ravennica	MFLUCC 15-0479 [T]	*Tamarix* sp.	Italy	KU900335	KX365197	KX432254	N/A	N/A
D. ravennica	MFLUCC 17-1029	*Salvia* sp.	Italy	KY964191	KY964147	KY964075	N/A	N/A
D. rhoina	CBS 146.27	*Rhus toxicodendron*	Not stated	MH854907	KC343915	KC344157	KC343431	KC343673
D. rosae	MFLUCC 17-2658 [T]	*Rosa* sp.	Thailand	MG828894	N/A	MG843878	MG829273	N/A
D. rosae	MFLUCC 17-2574	*Senna siamea*	Thailand	MG906793	MG968954	MG968952	N/A	N/A
D. rosiphthora	COAD 2913	*Rosa* sp.	Brazil	MT311196	MT313692	N/A	MT313690	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. rosiphthora	COAD 2914 [T]	*Rosa* sp.	Brazil	MT311197	MT313693	N/A	MT313691	N/A
D. rossmaniae	CAA762 [T]	*Vaccinium corymbosum*	Portugal	MK792290	MK828063	MK837914	MK883822	MK871432
D. rossmaniae	CAA763	*Vaccinium corymbosum*	Portugal	MK792291	MK828064	MK837915	MK883823	MK871433
D. rostrata	CFCC 50062 [T]	*Juglans mandshurica*	China	KP208847	KP208853	KP208855	KP208849	KP208851
D. rostrata	CFCC 50063	*Juglans mandshurica*	China	KP208848	KP208854	KP208856	KP208850	KP208852
D. rudis	AR3422 [T]	*Laburnum anagyroides*	Austria	KC843331	KC843090	KC843177	KC843146	
D. rudis	CBS 113201	*Vitis vinifera*	Portugal	MH862916	KC343960	KC344202	KC343476	KC343718
D. rumicicola	MFLUCC18-0739	*Rumex* sp.	Italy	MH846233	MK049554	MK049555	N/A	N/A
D. rumicicola	JZB320006 [T]	*Scrophularia canina*	Italy	MK066126	MK078545	MK078546	N/A	N/A
D. saccarata	CBS 116311 [T]	*Protea repens*	South Africa	KC343190	KC343916	KC344158	KC343432	KC343674
D. sackstonii	BRIP 54669b [T]	*Helianthus annuus*	Australia	KJ197287	KJ197249	KJ197267	N/A	N/A
D. salicicola	BRIP 54825 [T]	*Salix purpurea*	Australia	JX862531	JX862537	KF170923	N/A	N/A
D. salinicola	MFLU 17-2592	*Xylocarpus* sp.	Thailand	MN047099	MN077074	N/A	N/A	N/A
D. salinicola	MFLU 18-0553 [T]	*Xylocarpus* sp.	Thailand	MN047098	MN077073	N/A	N/A	N/A
D. salsuginosa	NFCCI-4385	*Avicennia marina*	India	MN061372	N/A	MN431500	N/A	N/A
D. sambucusii	CFCC 51986 [T]	*Sambucus williamsii*	China	KY852495	KY852507	KY852511	KY852499	KY852503
D. sambucusii	CFCC 51987	*Sambucus williamsii*	China	KY852496	KY852508	KY852512	KY852500	KY852504
D. schimae	CFCC 53103 [T]	*Schima superba*	China	MK432640	MK578116	MK578043	MK442962	MK442987
D. schimae	CFCC 53104	*Schima superba*	China	MK432641	MK578117	MK578044	MK442963	MK442988
D. schini	CBS 133181 [T]	*Schinus terebinthifolius*	Brazil	KC343191	KC343917	KC344159	KC343433	KC343675

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. schini	CPC 20286	*Schinus terebinthifolius*	Brazil	KC343192	KC343918	KC344160	KC343434	KC343676
D. schisandrae	CFCC 51988 [T]	*Schisandra chinensis*	China	KY852497	KY852509	KY852513	KY852501	KY852505
D. schisandrae	CFCC 51989	*Schisandra chinensis*	China	KY852498	KY852510	KY852514	KY852502	KY852506
D. schoeni	MFLU 15-1279 [T]	*Schoenus nigricans*	Italy	KY964226	KY964182	KY964109	KY964139	N/A
D. schoeni	MFLU 15-2609	*Plantago* sp.	Italy	KY964229	KY964185	KY964112	KY964141	N/A
D. sclerotioides	CBS 296.67 [T]	*Cucumis sativus*	Netherlands	KC343193	KC343919	KC344161	KC343435	KC343677
D. sclerotioides	CBS 710.76	*Cucumis sativus*	Netherlands	KC343194	KC343920	KC344162	KC343436	KC343678
D. scobina	CBS 251.38	*Fraxinus excelsior*	UK	KC343195	KC343921	KC344163	KC343437	KC343679
D. searlei	CBS 146456 [T]	*Macadamia*	Australia	MN708231	N/A	MN696540	N/A	N/A
D. sennae	CFCC 51636 [T]	*Senna bicapsularis*	China	KY203724	KY228885	KY228891	KY228875	N/A
D. sennae	CFCC 51637	*Senna bicapsularis*	China	KY203725	KY228886	KY228892	KY228876	N/A
D. sennicola	CFCC 51634 [T]	*Senna bicapsularis*	China	KY203722	KY228883	KY228889	KY228873	KY228879
D. sennicola	CFCC 51635	*Senna bicapsularis*	China	KY203723	KY228884	KY228890	KY228874	KY228880
D. serafiniae	BRIP 55665a [T]	*Helianthus annuus*	Australia	KJ197274	KJ197236	KJ197254	N/A	N/A
D. serafiniae	BRIP 54136	*Lupinus albus*	Australia	KJ197273	KJ197235	KJ197253	N/A	N/A
D. shaanxiensis	CFCC 53106 [T]	on branches of liana	China	MK432654	MK578130	N/A	MK442976	MK443001
D. shaanxiensis	CFCC 53107	on branches of liana	China	MK432655	MK578131	N/A	MK442977	MK443002
D. shennongjiaensis	CNUCC 201906	*Juglans regia*	China	MN216228	MN224673	MN227013	MN224552	MN224561
D. shennongjiaensis	CNUCC 201905 [T]	*Juglans regia*	China	MN216229	MN224672	MN227012	MN224551	MN224560
D. siamensis	MFLUCC 10-573a [T]	*Dasymaschalon* sp.	Thailand	JQ619879	JX275393	JX275429	JX197422	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. siamensis	MFLUCC 12-0300	*dead leaf*	Thailand	KT459417	KT459451	KT459435	KT459467	N/A
D. silvicola	CFCC 54191 [T]	*Fraxinus excelsior*	Netherlands	MZ727041	MZ816347	MZ753491	MZ753472	MZ753481
D. silvicola	M79	*Fraxinus excelsior*	Netherlands	MZ727042	MZ816348	MZ753492	MZ753473	MZ753482
D. sinensis	ZJUP0033-4 [T]	*Amaranthus* sp.	China	MK637451	MK660449	MK660447	N/A	MK660451
D. sinensis	ZJUP0038-3	*Amaranthus* sp.	China	MN442428	MN448493	MN448494	N/A	MN448492
D. sojae	DP0605	*Glycine max*	US	KJ590707	KJ590750	KJ610863	KJ612104	KJ659196
D. sojae	FAU459	*Stokesia laevis*	US	KJ590709	KJ590752	KJ610865	KJ612106	KJ659198
D. sojae	FAU499	*Asparagus officinalis*	US	KJ590717	KJ590760	KJ610873	KJ612114	KJ659206
D. sojae	FAU604	*Glycine max*	US	KJ590716	KJ590759	KJ610872	KJ612113	KJ659205
D. sojae	FAU635 [T]	*Glycine max*	US	KJ590719	KJ590762	KJ610875	KJ612116	KJ659208
D. sojae	FAU636	*Glycine max*	US	KJ590718	KJ590761	KJ610874	KJ612115	KJ659207
D. sophorae	JAC12639	*Sophora microphylla*	New Zealand	MK432728	N/A	N/A	N/A	N/A
D. sophorae	PDD95984	Unidentified	New Zealand	JQ694115	N/A	N/A	N/A	N/A
D. spartinicola	CBS 140003 [T]	*Spartium junceum*	Spain	KR611879	N/A	N/A	N/A	KR857696
D. spinosa	CGMCC 3.19602 [T]	*Pyrus pyrifolia*	China	MK626849	MK654811	MK691234	MK691129	MK726156
D. spinosa	PSCG388	*Pyrus pyrifolia*	China	MK626860	MK654798	MK691229	MK691128	MK726171
D. sterilis	CBS 136969 [T]	*Vaccinium corymbosum*	Italy	KJ160579	KJ160611	KJ160528	KJ160548	MF418350
D. sterilis	MFLUCC 17-1011	*Cytisus* sp.	Italy	KY964211	KY964167	KY964095	KY964126	N/A
D. stewartii	CBS 193.36 [T]	*Cosmos bipinnatus*	Not stated	MH867279	GQ250324	JX275421	JX197415	N/A
D. stewartii	MN1	*Helianthus annuus*	US	KX668416	KX852355	N/A	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. stictica	CBS 370.54 [T]	*Buxus sampervirens*	Italy	KC343212	KC343938	KC344180	KC343454	KC343696
D. subclavata	ZJUD83	*Citrus maxima* cv. *Shatianyou*	China	KJ490618	KJ490497	KJ490439	N/A	KJ490560
D. subclavata	CGMCC 3.17257 [T]	*Citrus unshiu*	China	KJ490630	KJ490509	KJ490451	N/A	KJ490572
D. subcylindrospora	KUMCC 17-0151 [T]	*Salix* sp.	China	MG746629	MG746630	MG746631	N/A	N/A
D. subellipicola	KUMCC 17-0153 [T]	on dead wood	China	MG746632	MG746633	MG746634	N/A	N/A
D. subordinaria	CBS 464.90 [T]	*Plantago lanceolata*	New Zealand	KC343214	KC343940	KC344182	KC343456	KC343698
D. subordinaria	CBS 101711	*Plantago lanceolata*	New Zealand	KC343213	KC343939	KC344181	KC343455	KC343697
D. taiwanensis	NTUCC 18-105-1 [T]	*Ixora chinensis*	Taiwan	MT241257	MT251199	MT251202	MT251196	N/A
D. taiwanensis	NTUCC 18-105-2	*Ixora chinensis*	Taiwan	MT241258	MT251200	MT251203	MT251197	N/A
D. tanakae	MAFF 410600	*Malus pumila* var. *domestica*	Japan	AB245077	N/A	N/A	N/A	N/A
D. tanakae	MAFF 410127	*Malus pumila* var. *domestica*	Japan	AB245075	N/A	N/A	N/A	N/A
D. taoicola	MFLUCC 16-0117 [T]	*Prunus persica*	China	KU557567	KU557635	KU557591	N/A	N/A
D. taoicola	PSCG485	*Pyrus pyrifolia*	China	MK626869	MK654812	MK691227	MK691120	MK726173
D. tarchonanthi	CBS 146073 [T]	*Tarchonanthus littoralis*	South Africa	MT223794	N/A	MT223733	N/A	MT223759
D. tecomae	CBS 100547 [T]	*Tabebuia* sp.	Brazil	KC343215	KC343941	KC344183	KC343457	KC343699
D. tectonae	MFLUCC 12-0777 [T]	*Tectona grandis*	Thailand	NR147590	KU749359	KU743977	KU749345	N/A
D. tectonae	MFLUCC 14-1139	*Tectona grandis*	Thailand	KU712438	KU749366	KU743985	KU749353	N/A
D. tectonendophytica	MFLUCC 13-0471 [T]	*Tectona grandis*	Thailand	NR_147591	KU749367	KU743986	KU749354	N/A
D. tectonendophytica	LC8115	Unidentified	China	KY491550	KY491560	KY491570	N/A	N/A
D. tectonigena	MFLUCC 12-0767 [T]	*Tectona grandis*	China	KU712429	KU749371	KU743976	KU749358	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. tectonigena	LC6512	*Camellia sinensis*	China	KX986782	KX999174	KX999215	KX999284	KX999254
D. terebinthifolii	CBS 133180 [T]	*Schinus terebinthifolius*	Brazil	KC343216	KC343942	KC344184	KC343458	KC343700
D. terebinthifolii	CPC 20285	*Schinus terebinthifolius*	Brazil	KC343218	KC343944	KC344186	KC343460	KC343702
D. ternstroemia	CGMCC 3.15183 [T]	*Ternstroemia gymnanthera*	China	NR_147523	KC153089	N/A	N/A	N/A
D. ternstroemia	CGMCC 3.15184	*Ternstroemia gymnanthera*	China	KC153099	KC153090	N/A	N/A	N/A
D. tersa	FS441	deep-sea sediments of the Indian Ocean	China	MK592793	N/A	N/A	N/A	N/A
D. tersa	BCKSKMP-8	*Butea monosperma*	India	MG049670	N/A	N/A	N/A	N/A
D. thunbergiae	MFLUCC 10-0576a [T]	*Thunbergia laurifolia*	Thailand	JQ619893	JX275409	JX275449	JX197440	N/A
D. thunbergiae	MFLUCC 10-0576b	Unidentified	Not stated	JQ619894	JX275410	JX275450	JX197441	N/A
D. thunbergiicola	MFLUCC 12-0033 [T]	*Thunbergia laurifolia*	Thailand	KP715097	KP715098	N/A	N/A	N/A
D. tibetensis	CFCC 51999 [T]	*Juglans regia*	China	MF279843	MF279858	MF279873	MF279888	MF279828
D. tibetensis	CFCC 52000	*Juglans regia*	China	MF279844	MF279859	MF279874	MF279889	MF279829
D. torilicola	MFLUCC 17-1051 [T]	*Torilis arvensis*	Italy	KY964212	KY964168	KY964096	KY964127	N/A
D. toxica	CBS 534.93 [T]	*Lupinus angustifolius*	Australia	KC343220	KC343946	KC344188	KC343462	KC343704
D. toxica	CBS 546.93	*Lupinus* sp.	Australia	KC343222	KC343948	KC344190	KC343464	KC343706
D. toxicodendri	TFM FP-10740 [T]	*Toxicodendron vernicifluum*	Japan	NR_158416	N/A	N/A	N/A	N/A
D. toxicodendri	FFPRI420990	*Toxicodendron vernicifluum*	Japan	LC275193	LC275217	LC275225	LC275201	LC275209
D. tulliensis	BRIP 62248a [T]	*Theobroma cacao*	Australia	KR936130	KR936133	KR936132	N/A	N/A
D. tulliensis	RST-1	*Ricinus communis*	China	MN911382	MT121969	N/A	N/A	N/A
D. ueckeri	FAU656 [T]	*Cucumis melo*	USA	KJ590726	KJ590747	KJ610881	KJ612122	KJ659215

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. ueckeri	HNWN01	*Areca catechu*	China	MN424522	MN424564	MN424536	MN424578	MN424550
D. ukurunduensis	CFCC 52592 [T]	*Acer ukurunduense*	China	MH121527	MH121569	N/A	MH121445	MH121485
D. ukurunduensis	CFCC 52593	*Acer ukurunduense*	China	MH121528	MH121570	N/A	MH121446	MH121486
D. undulata	CGMCC 3.18293 [T]	Unidentified leaf	China-Laos border	KX986798	KX999190	KX999230	N/A	KX999269
D. undulata	LC8111	Unidentified	China	KY491546	KY491556	KY491566	N/A	N/A
D. unshiuensis	CGMCC 3.17566 [T]	*Fortunella margarita*	China	KJ490584	KJ490463	KJ490405	N/A	KJ490526
D. unshiuensis	PSCG339	*Pyrus pyrifolia*	China	MK626928	MK654879	MK691300	MK691181	MK726188
D. vaccinii	CBS 160.32 [T]	*Oxycoccus macrocarpos*	USA	KC343228	KC343954	KC344196	KC343470	KC343712
D. vaccinii	CBS 122116	*Vaccinium corymbosum*	USA	KC343227	KC343953	KC344195	KC343469	KC343711
D. vacuae	CAA829 [T]	*Vaccinium corymbosum*	Portugal	MK792306	MK828077	MK837928	MK883832	MK871446
D. vacuae	CAA830	*Vaccinium corymbosum*	Portugal	MK792309	MK828080	MK837931	MK883834	MK871449
D. vangueriae	CPC 22703 [T]	*Vangueria infausta*	Zambia	KJ869137	N/A	KJ869247	N/A	N/A
D. varians	LC8112	*Acer* sp.	Japan	KY491547	KY491557	KY491567	KY491575	N/A
D. varians	LC8113	*Acer* sp.	Japan	KY491548	KY491558	KY491568	KY491576	N/A
D. vawdreyi	BRIP 57887a [T]	*Psidium guajava*	Australia	KR936126	KR936129	KR936128	N/A	N/A
D. velutina	CGMCC 3.18286 [T]	*Neolitsea* sp.	China	KX986790	KX999182	KX999223	N/A	KX999261
D. velutina	LC4419	*Neolitsea* sp.	China	KX986789	KX999181	KX999222	KX999286	KX999260
D. verniciicola	CFCC 53109 [T]	*Vernicia montana*	China	MK573944	MK574619	MK574639	MK574583	MK574599
D. verniciicola	CFCC 53110	*Vernicia montana*	China	MK573945	MK574620	MK574640	MK574584	MK574600
D. vexans	CBS 127.14	*Solanum melongena*	USA	KC343229	KC343955	KC344197	KC343471	KC343713

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
D. vexans	FAU597	*Solanum* sp.	Dominican Republic	KJ590734	KJ590774	KJ610889	KJ612131	KJ659216
D. viburni	CBS 158.29 [T]	Unidentified	Not stated	MH855030	N/A	N/A	N/A	N/A
D. viniferae	JZB320071 [T]	*Vitis vinifera*	China	MK341550	MK500107	MK500112	MK500119	N/A
D. viniferae	JZB320072	*Vitis vinifera*	China	MK341551	MK500108	MK500113	MK500120	N/A
D. virgiliae	CMW40748 [T]	*Virgilia oroboides*	South Africa	KP247566	N/A	KP247575	N/A	N/A
D. virgiliae	CMW40749	Unidentified	Not stated	KP247567	N/A	KP247576	N/A	N/A
D. vochysiae	LGMF1583 [T]	*Vochysia divergens*	Brazil	MG976391	MK007526	MK007527	MK007528	MK033323
D. woodii	CBS 558.93	*Lupinus* sp.	Australia	KC343244	KC343970	KC344212	KC343486	KC343728
D. woolworthii	CBS 148.27	*Ulmus americana*	Not stated	KC343245	KC343971	KC344213	KC343487	KC343729
D. xishuangbanica	CGMCC 3.18283 [T]	*Camellia sinensis*	China	KX986784	KX999176	KX999217	N/A	N/A
D. xishuangbanica	CGMCC 3.18282	*Camellia sinensis*	China	KX986783	KX999175	KX999216	N/A	KX999255
D. xunwuensis	CFCC 53085 [T]	Unidentified dead wood	China	MK432663	MK578137	MK578063	MK442983	MK443008
D. xunwuensis	CFCC 53086	Unidentified dead wood	China	MK432664	MK578138	MK578064	MK442984	MK443009
D. yunnanensis	CGMCC 3.18289 [T]	*Coffea* sp.	China	KX986796	KX999188	KX999228	KX999290	N/A
D. yunnanensis	LC8107	*Coffea* sp.	China	KY491542	KY491552	KY491562	KY491572	N/A
D. zaobaisu	CGMCC 3.19598 [T]	*Pyrus x bretschneideri*	China	MK626922	MK654855	MK691245	N/A	MK726207
D. zaobaisu	PSCG032	*Pyrus x bretschneideri*	China	MK626923	MK654856	MK691246	N/A	MK726208
Hyaliappendispora galii	MFLUCC 16-1208 [T]	*Galium* sp.	Italy	NR_154107	MF377587	N/A	N/A	N/A
H. galii	MFLU 15-2269	*Galium* sp.	Italy	MF190150	MF377588	N/A	N/A	N/A
Massariothea sp.	MFLUCC 15-0452	*Thysanolaena* sp.	Thailand	MG967672	MH137275	N/A	N/A	N/A

Table 6.1 (continued)

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	*ef1α*	*β-tubulin*	*cal*	*his3*
Massariothea sp.	MFLUCC 14-0585	Poaceae sp.	Thailand	MG967671	MH104871	N/A	N/A	N/A
Massariothea sp.	MFLUCC 15-0458	Poaceae sp.	Thailand	MG967674	MH171171	N/A	N/A	N/A
Paradiaporthe artemisiae	MFLUCC 14–0850 [T]	*Artemisia*	Italy	MF190155	MF377583	N/A	N/A	N/A
P. artemisiae	MFLUCC 17–1663	*Artemisia*	Italy	MF190156	MF377584	N/A	N/A	N/A
Phaeocytostroma ambiguum	CFMS 1295	*Zea mays*	Brazil	KU323508	KU351848	N/A	N/A	N/A
Ph. ambiguum	CPC 17079	*Zea mays*	South Africa	FR748043	FR748075	N/A	N/A	N/A
Ph. megalosporum	CBS 284.65	*Rice-field soil*	India	FR748045	FR748077	N/A	N/A	N/A
Ph. plurivorum	CBS 113835	Unidentified	Portugal	MH862945	FR748078	N/A	N/A	N/A
Ph. sacchari	CBS 275.34	Unidentified	Japan	MH855512	FR748079	N/A	N/A	N/A
Phaeodiaporthe appendiculata	CBS 123821 [T]	*Acer campestre*	Austria	NR_154299	N/A	N/A	N/A	N/A
Pustulomyces bambusicola	MFLUCC 11-0436	Poaceae	Thailand	KF806752	KF806755	N/A	N/A	N/A
Stenocarpella macrospora	CBS 117560 [T]	*Zea mays*	South Africa	NR_157418	MG934504	N/A	N/A	N/A
S. macrospora	YZ-1	*Zea mays*	China	KY012337	MF076787	N/A	N/A	N/A
S. maydis	CPC 16789	*Zea mays*	South Africa	FR748064	FR748093	N/A	N/A	N/A
S. maydis	CBS 117559	*Zea mays*	South Africa	FR748052	FR748081	N/A	N/A	N/A
S. maydis	A1-1*	*Zea mays*	US	NQMI00000000				

Note * Whole genomic DNA strain, [T] Type.

6.3 Results

6.3.1 Phylogenetic Analysis

The results from the partition homogeneity tests (PHT) were not significant (level ≥95%), indicating that the individual datasets were congruent and could be combined. Phylogenetic trees from single loci were generated (Figures 6.2–6.7) to examine the overall topology and clade support. In this study, we introduce 13 species complexes containing extant species of *Diaporthe*. Nine singleton species were not assigned to any complex, and their phylogenetic placement was not robust. Almost all Diaporthaceae genera, except for *Paradiaporthe*, grouped and nested within *Diaporthe*. *Hyaliappendispora* and *Phaeodiaporthe* consistently formed a basal clade with strong support.

Phylogenetic analysis of the ITS region (609 bp) consisted of 534 strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the outgroup. Eight species complexes (*D. arecae*, *D. biconispora*, *D. decedens*, *D. eres*, *D. oncostoma*, *D. rudis*, *D. toxica*, and *D. vawdreyi* species complexes) were recovered as in the combined gene tree (Figure 6.1). The *Diaporthe pustulata* species complex formed a well-resolved clade except for *D. obtusifoliae*. *Diaporthe eres* species complex was paraphyletic. Most species in the *D. sojae* species complex clustered, except for some, which dispersed throughout the tree. Species in the *D. varians*, *D. carpini*, and *D. scobina* species complexes were dispersed throughout the tree and clustered with species from other clades (Figure 6.2).

Another phylogenetic analysis was performed using the ITS dataset (609 bp), which included the 50 strains that only have ITS sequence and excluded from the combined dataset (Figure 6.1). This dataset consisted of 784 Diaporthaceae strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the outgroup taxa. The tree topology was similar to the previously obtained ITS tree (Figure 6.2). Those 50 strains dispersed throughout the tree, but placements and memberships in different sections were not impacted (Figure 6.3).

Phylogenetic analysis of the *ef1α* gene (381 bp) consisted of 510 strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the

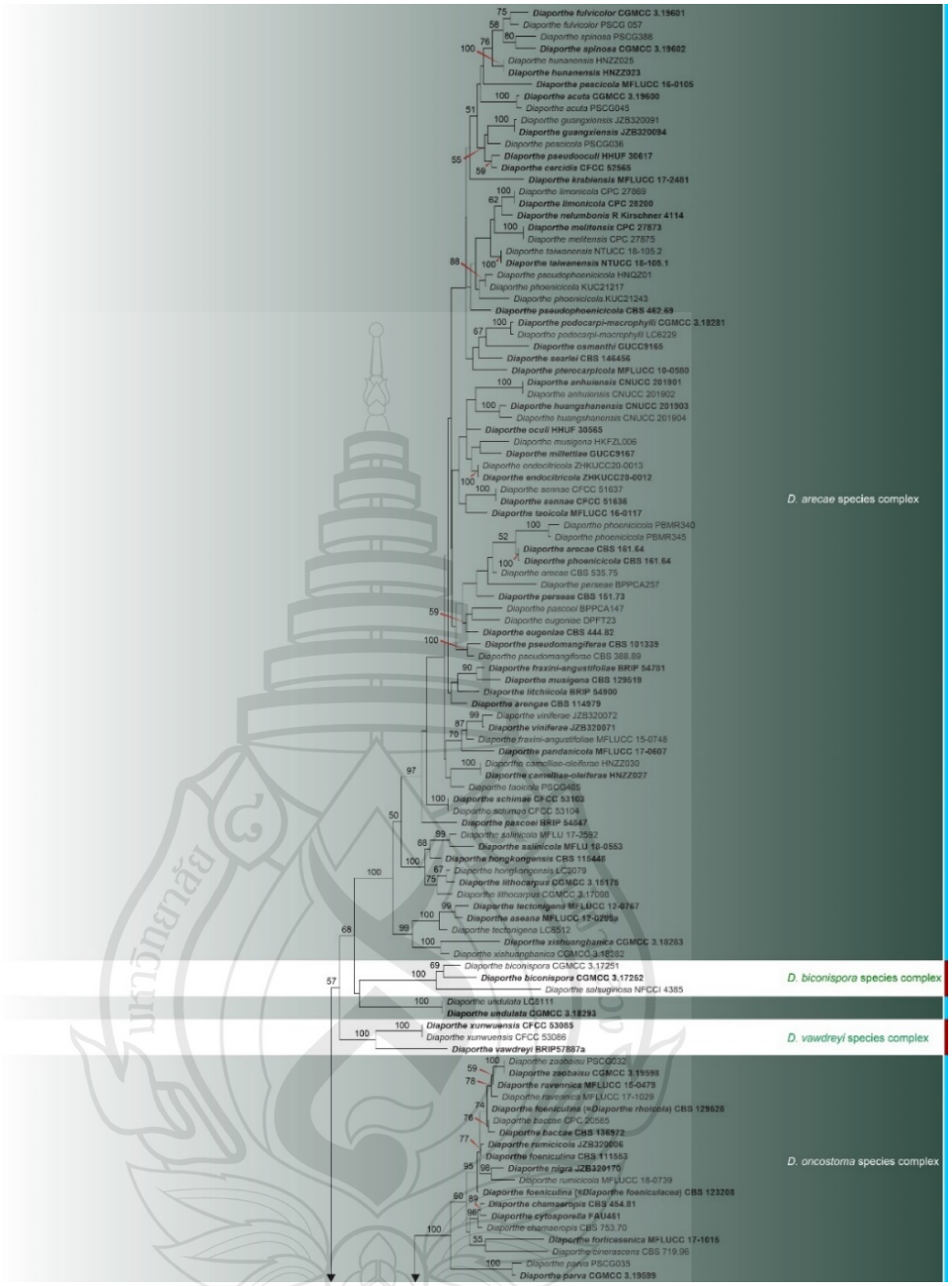
outgroup taxa. The *D. arecae*, *D. biconispora*, *D. carpini*, *D. decedens*, *D. oncostoma*, *D. pustulata*, *D. rudis*, *D. sojae*, *D. varians*, and *D. vawdreyi* species complexes were recovered as in the combined gene tree. The *Diaporthe eres* species complex formed a well-resolved clade except for *D. shennongjiaensis*. *Diaporthe scobina* and *D. toxica* species complexes were dispersed throughout the tree and clustered with species from other clades (Figure 6.4).

Phylogenetic analysis using the *β-tubulin* gene (763 bp) consisted of 479 strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the outgroup taxa. The *D. arecae*, *D. biconispora*, *D. carpini*, *D. decedens*, *D. eres*, *D. oncostoma*, *D. pustulata*, *D. rudis*, *D. toxica*, *D. varians*, and *D. vawdreyi* species complexes were recovered as in the combined gene tree (Figure 6.1). *Diaporthe scobina*, *D. sojae* and *D. varians* species complexes formed a well-resolved species complex except for some species (Figure 6.5).

Phylogenetic analysis using the *cal* gene (694 bp) consisted of 383 strains. *Cytospora leucostoma* (SXYLt) was used as the outgroup taxon. The *D. carpini*, *D. decedens*, *D. eres*, *D. oncostoma*, *D. rudis*, *D. scobina*, *D. toxica*, *D. varians*, and *D. vawdreyi* species complexes were recovered as in the combined gene tree (Figure 6.1). *Diaporthe arecae*, *D. biconispora*, *D. pustulata*, and *D. sojae* species complexes were well-resolved, except for some species (Figure 6.6).

Phylogenetic analysis using the *his3* gene (474 bp) consisted of 343 strains. *Cytospora leucostoma* (SXYLt) was used as the outgroup taxa. The *D. arecae*, *D. oncostoma*, *D. vawdreyi*, *D. carpini*, *D. pustulata*, *D. rudis*, and *D. toxica* species complexes were recovered as in the combined gene tree. *Diaporthe eres* species complex was recovered as in the combined gene tree except for *D. penetriteum*. Similarly, the *D. sojae* species complex was recovered except for *D. tarchonanthi*, which did not cluster within the clade. *Diaporthe varians* species complex formed a well-resolved clade except for *D. incomplete* strain CGMCC 3.18288. This species complex formed a sister clade to *D. sojae* species complex and some genera in Diaporthaceae. One species of the *D. scobina* species complex clustered within the *D. carpini* species complex, and that was the only species with his3 sequence in the clade (Figure 6.7). Species of the *D. biconispora* species complex clustered within *D. arecae* species complex.

Phylogenetic analysis using the five-gene combined dataset consisted of 535 strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) sequences were used as the outgroup taxa. The dataset consisted of 2921 characters including alignment gaps (ITS1+ITS2: 1–451, 5.8S: 452–609, *ef1α* (exon): 610–650, *ef1α* (intron): 651–990, *β-tubulin* (exon): 991–1173, *β-tubulin* (intron): 1174–1753, *cal* (exon): 1754–2028, *cal* (intron): 2029–2447, *his3* (exon): 2448–2780, and *his3* (intron): 2781–2921). The combined dataset was analyzed using the maximum likelihood, and the best scoring likelihood tree for the combined dataset had a final value of -82762.099887 (Figure 6.1). *Diaporthe sojae* species complex formed a large clade in the tree, including the ex-type, CBS 128856. *Ophiodiaporthe* and *Chiangriomyces* were synonymized under *Diaporthe* based on phylogenetic analysis and morphological characteristics (Figure 6.1).



Note Maximum likelihood phylogenetic tree inferred from combined ITS1+ITS2, 5.8S, *ef1α*, *β-tubulin*, *cal*, and *his3* sequence data of 535 strains of Diaporthaceae. The tree is artificially rooted with *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values ≥50% are given at the nodes. The species synonymized are in blue and the ex-type taxa are in bold.

Figure 6.1 Phylogenetic analysis of Diaporthaceae

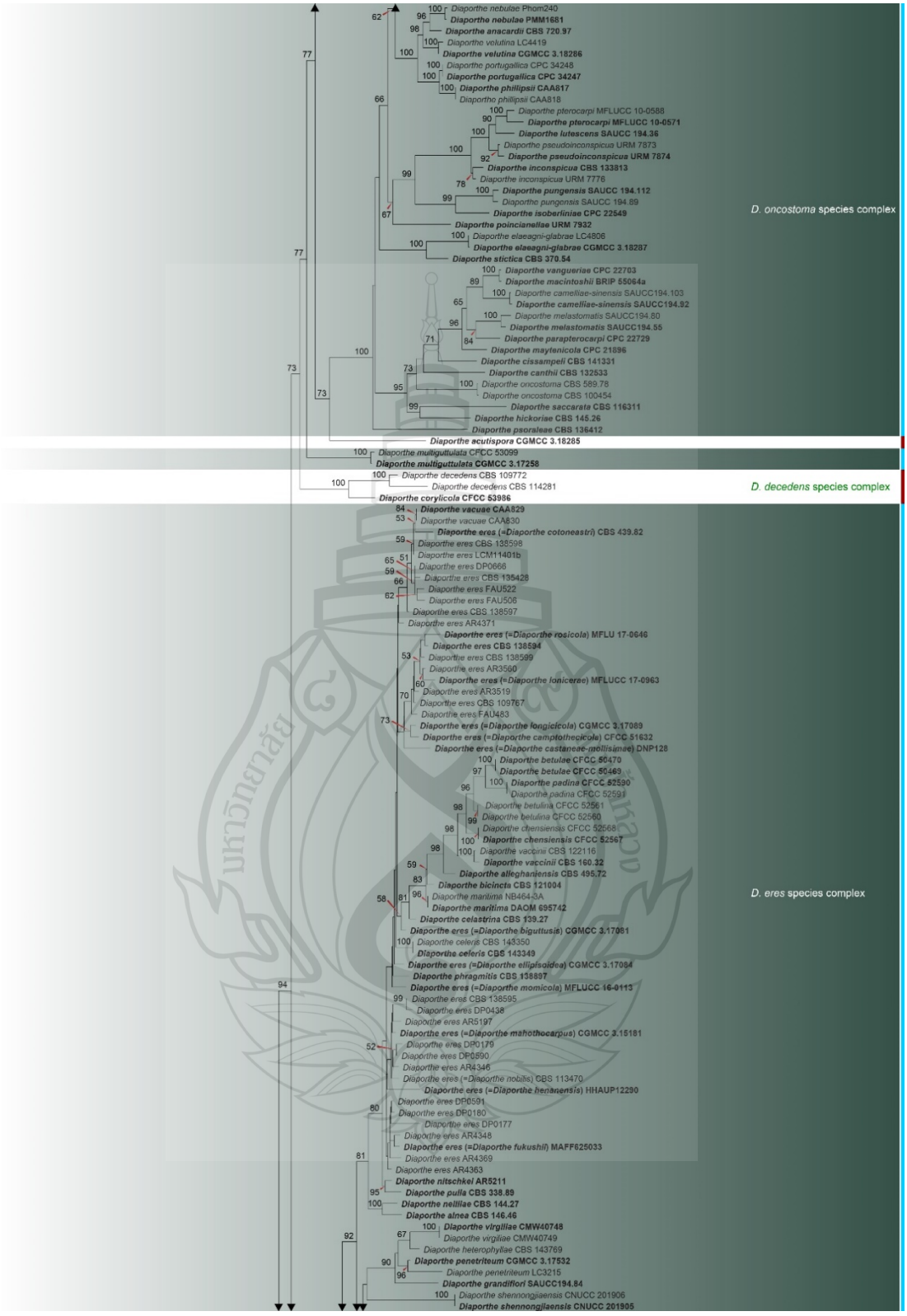


Figure 6.1 (continued)

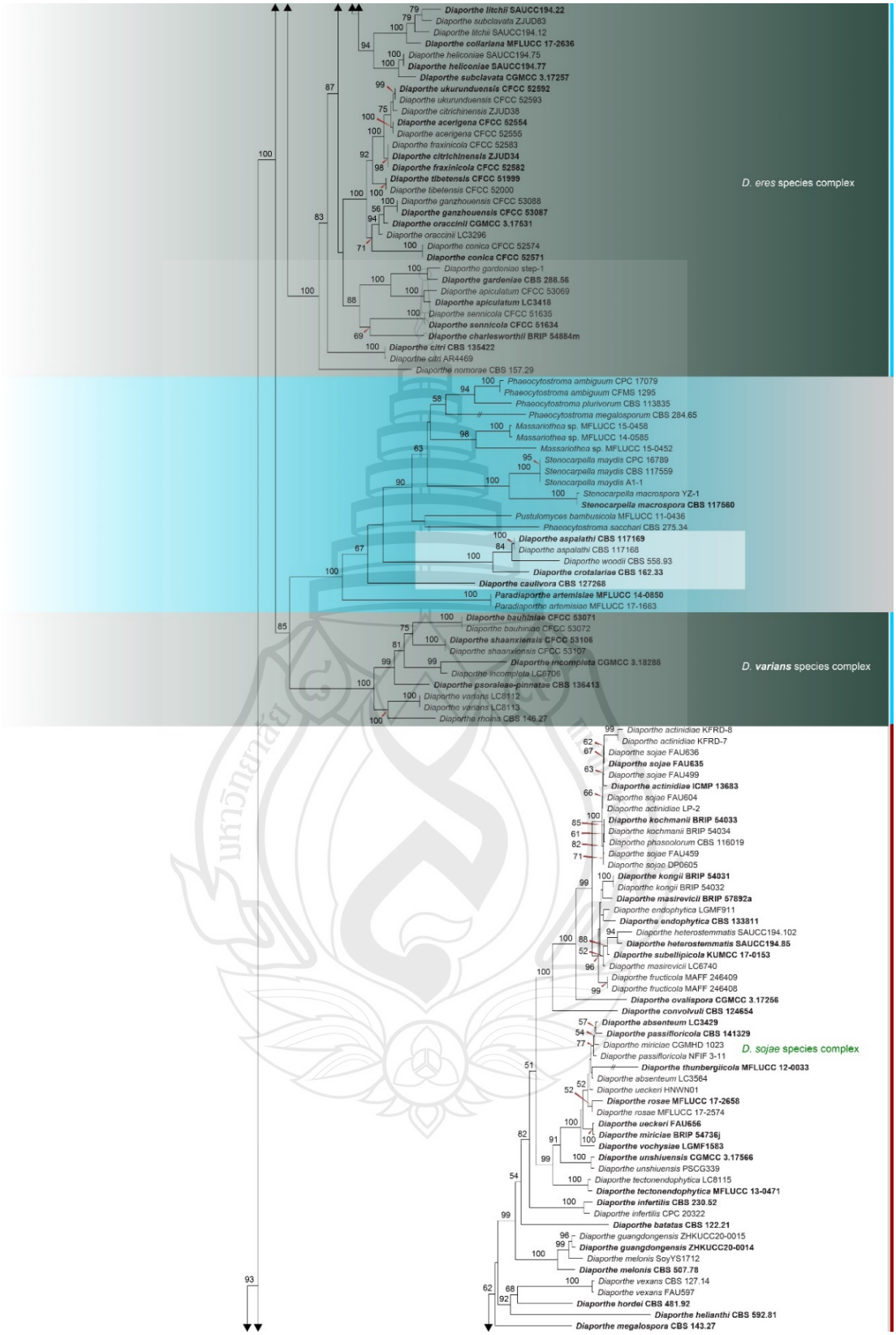


Figure 6.1 (continued)

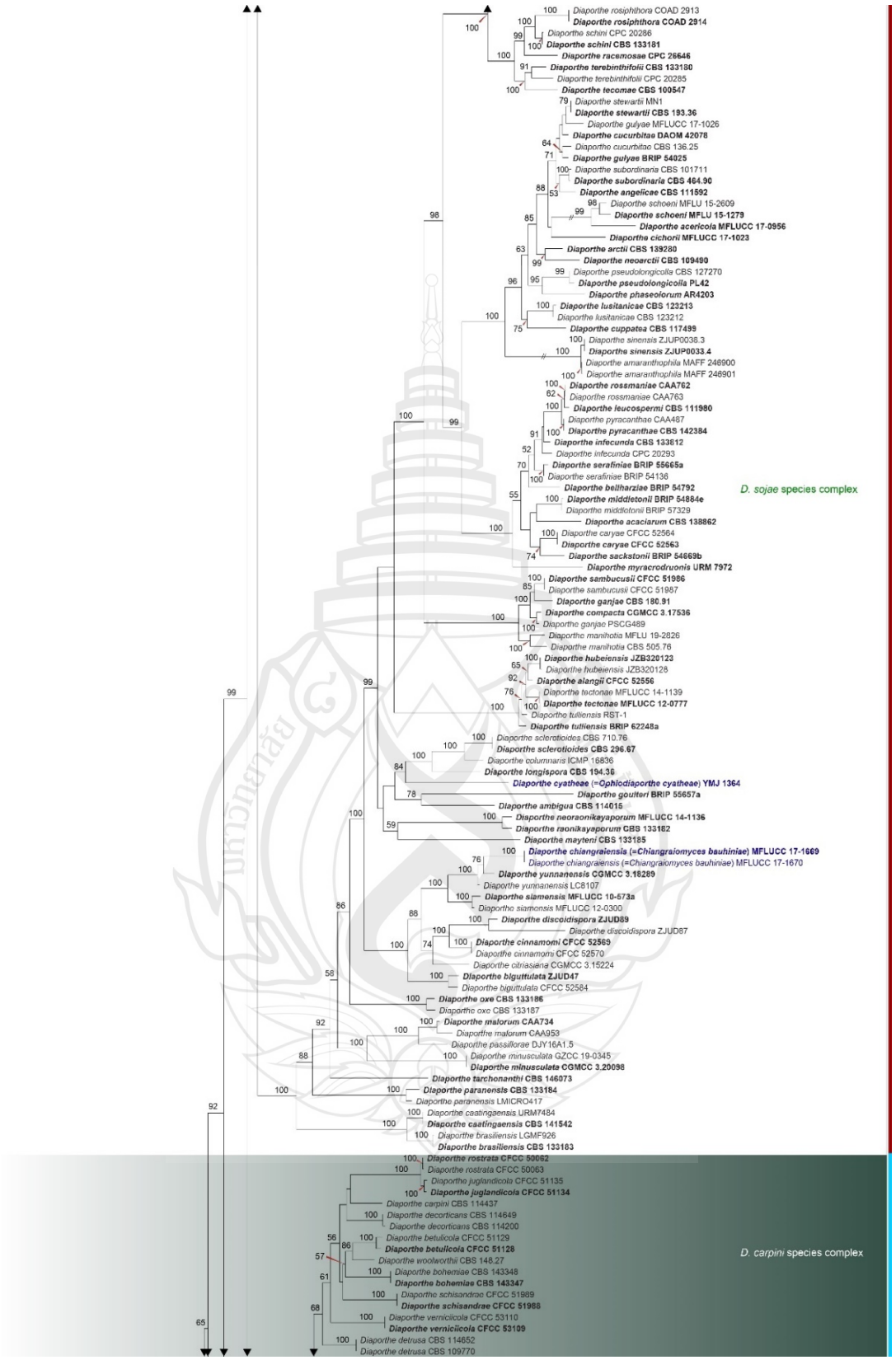


Figure 6.1 (continued)

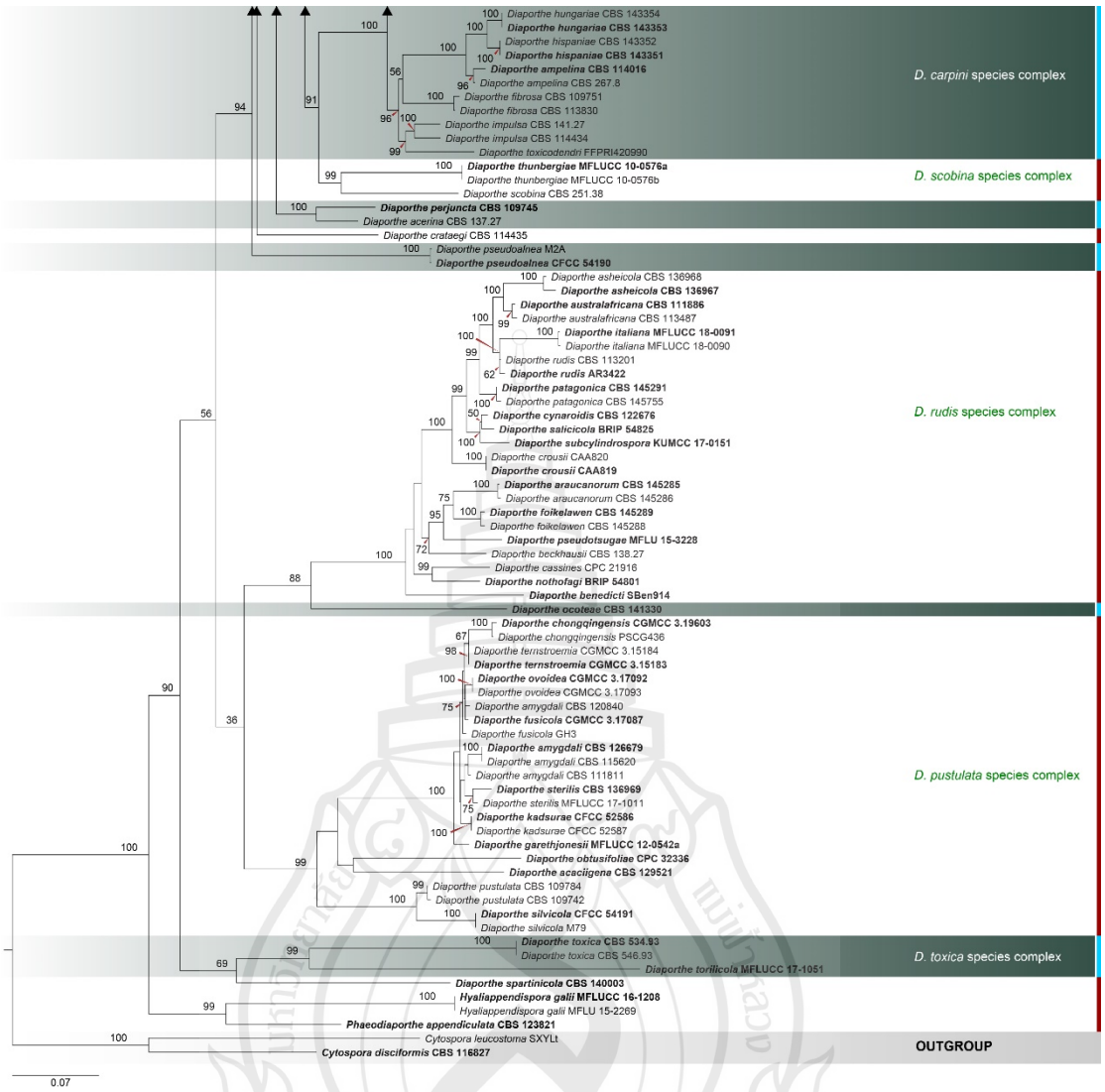


Figure 6.1 (continued)

6.3.2 Species Complexes

There are 13 species complexes:

1) *D. arecae* species complex
2) *D. biconispora* species complex
3) *D. carpini* species complex
4) *D. decedens* species complex
5) *D. eres* species complex
6) *D. oncostoma* species complex
7) *D. pustulata* species complex
8) *D. rudis* species complex
9) *D. scobina* species complex
10) *D. sojae* species complex
11) *D. toxica* species complex
12) *D. varians* species complex
13) *D. vawdreyi* species complex

***Diaporthe arecae* species complex**

Species included in the *D. arecae* species complex – *Diaporthe acuta, D. anhuiensis, D. arecae, D. arengae, D. aseana, D. camelliae-oleiferae, D. cercidis, D. endocitricola, D. eugeniae, D. fraxini-angustifoliae, D. fulvicolor, D. guangxiensis, D. hongkongensis, D. huangshanensis, D. hunanensis, D. krabiensis, D. limonicola, D. litchiicola, D. lithocarpus, D. melitensis, D. millettiae, D. musigena, D. nelumbonis, D. oculi, D. osmanthi, D. pandanicola, D. pascoei, D. perseae, D. pescicola, D. phoenicicola, D. podocarpi-macrophylli, D. pseudomangiferae, D. pseudooculi, D. pseudophoenicicola, D. pterocarpicola, D. salinicola, D. schimae, D. searlei, D. sennae, D. spinosa, D. taiwanensis, D. taoicola, D. tectonigena, D. viniferae, D. xishuangbanica*

Notes: Forty-five species are included in the *Diaporthe arecae* species complex based on maximum likelihood analysis (100%, Figure 6.1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of host plants (Table 1), while some species were described as human pathogens (Arciuolo et al., 2020). *Diaporthe arecae* is used to describe and name this species complex as mentioned in Huang et al.

(2015) and Ozawa et al. (2019). This species complex was recovered in all analyses (Figures 6.1–6.7).

***Diaporthe biconispora* species complex**

Species included in the *D. biconispora* species complex – *Diaporthe biconispora*, *D. salsuginosa*

Notes: Two species are included in the *D. biconispora* species complex based on maximum likelihood analysis (91%, Figure 6.1). Members of this section include a pathogen associated with an unidentified host and an endophyte from *Citrus grandis* and *Fortunella margarita* (Table 1). *Diaporthe biconispora* is used to describe this species complex based on the publication year (2015). Huang et al. (2015) introduced *Diaporthe biconispora*, as an endophytic on *Citrus grandis* in China. This clade was not well-resolved based on single-locus *his3* trees, while ITS, *ef1α*, *β-tubulin*, and *cal* topologies provided better resolution for this species complex, similar to the combined gene tree (Figures 6.1–6.7).

***Diaporthe carpini* species complex**

Species included in the *D. carpini* species complex – *Diaporthe ampelina*, *D. betulicola*, *D. bohemiae*, *D. carpini*, *D. decorticans*, *D. detrusa*, *D. fibrosa*, *D. hispaniae*, *D. hungariae*, *D. impulsa*, *D. juglandicola*, *D. rostrata*, *D. schisandrae*, *D. toxicodendri*, *D. verniciicola*, *D. woolworthii*

Notes: Sixteen species are included in the *D. carpini* species complex based on maximum likelihood analysis of combined gene tree (100%, Figure 6.1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe carpini* is used to describe this species complex. This clade was not well-resolved based on single-locus ITS and *β-tubulin* trees but *ef1α*, *cal*, and *his3* topologies provided a better resolution for this species complex, similar to the combined gene tree (Figures 6.1–6.7).

***Diaporthe decedens* species complex**

Species included in the *D. decedens* species complex – *Diaporthe corylicola*, *D. decedens*

Notes: Two species are included in the *D. decedens* species complex based on maximum likelihood analysis (100%, Figure 6.1). The clade for this species complex is robust and recovered in all analyses (Figures 6.1–6.7), except for the *cal* tree, in which *D. decedens* strain CBS 114281 grouped with the *D. sojae* species complex.

***Diaporthe eres* species complex**

Species included in the *D. eres* species complex – *Diaporthe acerigena, D. alleghaniensis, D. alnea, D. apiculatum, D. betulae, D. betulina, D. bicincta, D. celastrina, D. celeris, D. charlesworthii, D. chensiensis, D. citri, D. citrichinensis, D. collariana, D. conica, D. eres, D. fraxinicola, D. ganzhouensis, D. gardeniae, D. grandiflori, D. heliconiae, D. heterophyllae, D. litchii, D. maritima, D. neilliae, D. nitschkei, D. nomorae, D. oraccinii, D. padina, D. penetriteum, D. phragmitis, D. pulla, D. sennicola, D. shennongjiaensis, D. subclavata, D. tibetensis, D. ukurunduensis, D. vaccinii, D. vacuae, D. virgiliae*

Notes: Forty species are included in the *D. eres* species complex based on the maximum likelihood analysis of the combined gene tree (100%, Figure 6.1). This is the second largest species complex in *Diaporthe* genus. Its members are mostly pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe eres*, the type species of the genus, is used to describe this species complex based on the publication year (1870). Therefore, this clade has been also mentioned in previous publications as a species complex (Petrović et al., 2015; Chaisiri et al., 2021). The clade was not well-resolved in ITS, *ef1α*, *cal*, and *his3* single-locus trees, but *β-tubulin* topology provided a better resolution for this species complex similar to the combined gene tree (Figures 6.1–6.7). *Diaporthe eres* strains collected from different hosts were dispersed in the clade.

***Diaporthe oncostoma* species complex**

Species included in the *D. oncostoma* species complex – *Diaporthe anacardii, D. baccae, D. camelliae-sinensis, D. canthii, D. chamaeropis, D. cinerascens, D. cissampeli, D. cytosporella, D. elaeagni-glabrae, D. foeniculina, D. forlicesenica, D. hickoriae, D. inconspicua, D. isoberliniae, D. lutescens, D. macintoshii, D. maytenicola, D. melastomatis, D. nebulae, D. nigra, D. oncostoma, D. parapterocarpi, D. parva, D. phillipsii, D. poincianellae, D. portugallica, D. pseudoinconspicua, D.*

psoraleae, *D. pterocarpi*, *D. pungensis*, *D. ravennica*, *D. rumicicola*, *D. saccarata*, *D. stictica*, *D. vangueriae*, *D. velutina*, *D. zaobaisu*

Notes: Thirty-seven species are included in the *D. oncostoma* species complex based on the maximum likelihood analysis (100%, Figure 6.1). Members of this section are mostly pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe oncostoma* is used to describe this species complex based on the publication year (1870). The clade for this species complex is robust and recovered in the multi- and single-locus trees (except for the *cal* tree, in which *D. parvae* grouped to *D. eres* species complex) (Figures 6.1–6.7).

***Diaporthe pustulata* species complex**

Species included in the *D. pustulata* species complex – *Diaporthe acaciigena*, *D. amygdali*, *D. chongqingensis*, *D. fusicola*, *D. garethjonesii*, *D. kadsurae*, *D. obtusifoliae*, *D. ovoidea*, *D. pustulata*, *D. silvicola*, *D. sterilis*, *D. ternstroemia*

Notes: Twelve species are included in the *D. pustulata* species complex, which is strongly supported in the combined gene tree (94%, Figure 6.1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe pustulata* is used to describe this species complex based on the publication year. This species complex clade was robust and recovered in all single-locus tree analyses and in the combined gene tree (Figures 6.1–6.7).

***Diaporthe rudis* species complex**

Species included in the *D. rudis* species complex – *Diaporthe araucanorum*, *D. asheicola*, *D. australafricana*, *D. beckhausii*, *D. benedicti*, *D. cassines*, *D. crousii*, *D. cynaroidis*, *D. foikelawen*, *D. italiana*, *D. nothofagi*, *D. patagonica*, *D. pseudotsugae*, *D. rudis*, *D. salicicola*, *D. subcylindrospora*

Notes: Sixteen species are included in the *D. rudis* species complex, which has the maximum statistical support (100%, Figure 6.1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe rudis* is used to describe this species complex based on the publication year. This species complex clade was robust and recovered in most single-locus trees and in the combined gene tree, except for the ITS single-locus tree topology that was not well-resolved (Figures 6.1–6.7).

***Diaporthe scobina* species complex**

Species included in the *D. scobina* species complex – *Diaporthe scobina*, *D. thunbergiae*

Notes: Two species are included in the *D. scobina* species complex based on the maximum likelihood analysis of the combined gene tree (97%, Figure 6.1). Members of this section are associated with *Fraxinus excelsior* and *Thunbergia laurifolia* (Table 1, Mulenko et al., 2008; Udayanga et al., 2012). *Diaporthe scobina* is used to describe this species complex based on the publication year. This clade was not well-resolved based on ITS, *ef1α*, and *his3* single-locus trees, but *β-tubulin* and *cal* topologies provided a better resolution for this species complex similar to the combined gene tree (Figures 6.1–6.7).

***Diaporthe sojae* species complex**

Species included in the *D. sojae* species complex – *Diaporthe absenteum*, *D. acaciarum*, *D. acericola*, *D. actinidiae*, *D. alangii*, *D. amaranthophila*, *D. ambigua*, *D. angelicae*, *D. arctii*, *D. batatas*, *D. beilharziae*, *D. biguttulata*, *D. brasiliensis*, *D. caatingaensis*, *D. caryae*, *D. chiangraiensis* (=*Chiangraiomyces bauhiniae*), *D. cichorii*, *D. cinnamomi*, *D. citriasiana*, *D. columnaris*, *D. compacta*, *D. convolvuli*, *D. cucurbitae*, *D. cuppatea*, *D. cyatheae* (=*Ophiodiaporthe cyatheae*), *D. discoidispora*, *D. endophytica*, *D. fructicola*, *D. ganjae*, *D. goulteri*, *D. guangdongensis*, *D. gulyae*, *D. helianthi*, *D. heterostemmatis*, *D. hordei*, *D. hubeiensis*, *D. infecunda*, *D. infertilis*, *D. kochmanii*, *D. kongii*, *D. leucospermi*, *D. longispora*, *D. lusitanicae*, *D. malorum*, *D. manihotia*, *D. masirevicii*, *D. mayteni*, *D. megalospora*, *D. melonis*, *D. middletonii*, *D. minusculata*, *D. miriciae*, *D. myracrodruonis*, *D. neoarctii*, *D. neoraonikayaporum*, *D. ovalispora*, *D. oxe*, *D. paranensis*, *D. passiflorae*, *D. passifloricola*, *D. phaseolorum*, *D. pseudolongicolla*, *D. pyracanthae*, *D. racemosae*, *D. raonikayaporum*, *D. rosae*, *D. rosiphthora*, *D. rossmaniae*, *D. sackstonii*, *D. sambucusii*, *D. schini*, *D. schoeni*, *D. sclerotioides*, *D. serafiniae*, *D. siamensis*, *D. sinensis*, *D. sojae*, *D. stewartii*, *D. subellipicola*, *D. subordinaria*, *D. tarchonanthi*, *D. tecomae*, *D. tectonae*, *D. tectonendophytica*, *D. terebinthifolii*, *D. thunbergiicola*, *D. tulliensis*, *D. ueckeri*, *D. unshiuensis*, *D. vexans*, *D. vochysiae*, *D. yunnanensis*

Notes: Ninety-two species are included in the *D. sojae* species complex, which is strongly supported in the combined gene tree (99%, Figure 6.1). Members of this section are mostly pathogenic, endophytic, and saprobic on a broad range of host plants (Table 1), and some species are human pathogens (Garcia-Reyne et al., 2011; Iriart et al., 2011; Mattei et al., 2013). *Diaporthe sojae* is used to name this species complex, as in Udayanga et al. (2015). This clade was not well-resolved based on ITS and *β-tubulin* and *his3* single-locus trees, but *ef1α* and *cal* topologies provided a better resolution for this species complex as did the combined gene tree (Figures 6.1–6.7). This is the largest species complex clade of *Diaporthe*. Most species that only have ITS sequence data and not included in the combined gene tree are grouped in this clade (Figure 6.3).

***Diaporthe toxica* species complex**

Species included in the *D. toxica* species complex – *Diaporthe torilicola*, *D. toxica*

Notes: Two species are included in the *D. toxica* species complex based on the maximum likelihood analysis (94%, Figure 6.1). The members are pathogens and endophytes on *Lupinus angustifolius* and *Torilis arvensis* (Dissanayake et al., 2017; Gomes et al., 2013). *Diaporthe toxica* produces secondary metabolites that cause lupinosis in sheep (Williamson et al., 1994; Table 1). *Diaporthe toxica* is used to describe this species complex based on the publication year. This clade was not well-resolved based on the *ef1α* single-locus tree, while ITS, *β-tubulin*, *cal*, and *his3* topologies provided a better resolution for this species complex as did the combined gene tree (Figures 6.1–6.7).

***Diaporthe varians* species complex**

Species included in the *D. varians* species complex – *Diaporthe bauhiniae, D. incompleta, D. psoraleae- pinnatae, D. rhoina, D. shaanxiensis, D. varians*

Notes: Six species are included in the *D. varians* species complex, which has maximum statistical support in the combined gene tree (100%, Figure 6.1). Members of this section are reported as pathogenic and saprobic fungi on a broad range of hosts (*Acer* sp., *Bauhinia purpurea, Camellia sinensis, Psoralea pinnata*, *Rhus toxicodendron*) as mentioned in Table 1. *Diaporthe varians* is used to describe this species complex based on the publication year (1870). This clade was not resolved in

the single-locus trees of ITS and *his3*, but *β-tubulin*, *ef1α*, and *cal* topologies provided a better resolution for this species complex as in the combined gene tree (Figures 6.1–6.7).

***Diaporthe vawdreyi* species complex**

Species included in the *D. vawdreyi* species complex – *Diaporthe vawdreyi*, *D. xunwuensis*

Notes: Two species are included in the *D. vawdreyi* species complex, which is strongly supported (100%, Figure 6.1). Members of this section are pathogenic on *Psidium guajava* and saprobic fungi from unidentified dead wood (Table 1). *Diaporthe vawdreyi* is used to describe this species complex based on the publication year (2015), a pathogenic species that causes fruit rot disease of *Psidium guajava* in Australia (Crous et al., 2015). The clade for this species complex is robust and recovered in all analyses (Figures 6.1–6.7).

6.4 Discussion

Diaporthe species are associated with economically important hosts as pathogens, endophytes, and saprobes on a wide range of hosts and have a broad geographic distribution (Uecker, 1988; Ferreira et al., 2015). *Diaporthe* taxonomy and species descriptions have previously been based on morphology and host-specificity. However, the overlap of morphological traits and association with the same host made the identification of taxonomically relevant characters at the species level difficult and species delimitation based on morphology was problematic (Rehner & Uecker, 1994; Mostert et al., 2001; Gomes et al., 2013; Guarnaccia et al., 2016; Santos et al., 2010; Udayanga et al., 2011, 2014a, b; Dissanayake et al., 2017a, b). Hence, a molecular approach is essential to identify and comprehensively characterize members of *Diaporthe* (Santos & Phillips, 2009; Diogo et al., 2010; Luongo et al., 2011; Udayanga et al., 2012a, b; Thomidis et al., 2013; Gao et al., 2017). However, sequence data from type material is not available for many *Diaporthe* species, and even some known species do not have enough molecular data to justify their introduction as novel taxa.

More than 500 taxa have been recorded and named as species of *Diaporthe* (http://www.indexfungorum.org, accessed on May 5, 2022).

The current study provides a comprehensive phylogenetic analysis of Diaporthaceae, focusing on *Diaporthe*. All valid species of *Diaporthe* with molecular data are included in the phylogenetic analysis along with all genera of Diaporthaceae. There are 317 species with available sequence data, and 30 species (50 strains) only have ITS sequences, some of which are type strains. Single and combined genetic marker trees were inferred. *Diaporthe* separates into deeply divergent, strongly supported clades, whose placements are stable in both the combined and single gene trees. Therefore, to make it more convenient to identify species in the genus, we split *Diaporthe* into 13 workable species complexes: *D. arecae*, *D. biconispora*, *D. carpini*, *D. decedens*, *D. eres*, *D. oncostoma*, *D. pustulata*, *D. rudis*, *D. scobina*, *D. sojae*, *D. toxica*, *D. varians*, and *D. vawdreyi*. In this study, we accepted 287 *Diaporthe* species. Of the 287 species included in the combined analysis, 274 were assigned to one of the 13 species complexes. Four species were nested with other genera, hence were not assigned to any species complex (*D. aspalathi*, *D. caulivora*, *D. crotalariae*, *D. woodii*). Nine species were retained as singletons (*D. acerina*, *D. acutispora*, *D. crataegi*, *D. multiguttulata*, *D. ocoteae*, *D. perjuncta*, *D. pseudoalnea*, *D. spartinicola*, *D. undulata*) based on multilocus and single-gene trees. Given that species delineation in *Diaporthe* is difficult due to the above-mentioned challenges, these complexes can be used as broader descriptors. Following the same reasoning and for ease of communication, species complexes have been introduced successfully for *Fusarium* (O'Donnell et al., 2013, 2015; Al-Hatmi et al., 2016), *Colletotrichum* (Cannon et al., 2012; Damm et al., 2019; Jayawardena et al., 2016; da Silva et al., 2020), and *Phyllosticta* (Norphanphoun et al., 2020).

Using broad sampling in terms of taxa and genes is necessary for improving the phylogenetic resolution at low and high taxonomic levels within Diaporthaceae. Single (Figures 6.2–6.7) and multiple gene phylogenies along with statistical support were considered to introduce the *Diaporthe* species complexes (Figure 6.1). The placement of the proposed species complexes and the species they contain are mostly similar in the single gene trees and the combined gene tree (Figure 6.1). The topology of *ef1α* most closely resembled that of the combined tree with only a handful of incongruences,

followed by *β-tubulin*. Nonetheless, within the complexes, the placement of some species remains problematic, and additional loci are likely needed for taxonomic resolution. These include *D. actinidiae, D. eres, D. foeniculina, D. amygdali, D. phoenicicola,* and *D. sojae*. Delimiting species of *Diaporthe* will not only provide a better understanding of inter and intraspecific variation within the broader species complexes but also at the genus and family levels.

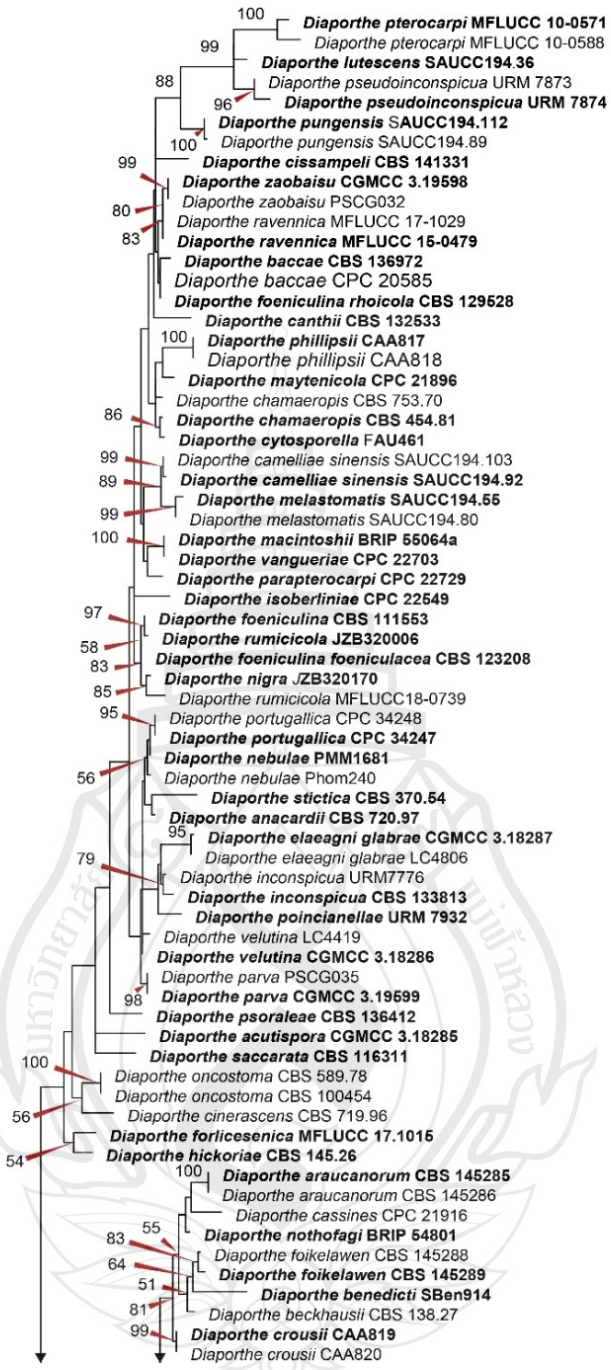
Herein, we used sequence data of *Cytospora disciformis* strain CBS 116827 and of *C. leucostoma* strain SXYLt as the outgroup rather than the commonly used *Diaporthella*, as the former is more phylogenetically closer to Diaporthaceae. The resulting tree was more robust with *Cytospora* as the outgroup, as indicated by the bootstrap support in both the deep and shallow nodes and the stable position of taxa.

In our analysis, *Diaporthe* is not monophyletic similar to previous results (Gao et al., 2017; Huang et al., 2021). *Stenocarpella, Massariothea*, *Phaecytostroma,* and *Pustulomyces* nested within *Diaporthe* in all the single gene trees and the combined gene tree. *Diaporthe caulivora, D. crotalariae, D. woodii,* and *D. aspalathi* formed a strongly supported clade with these genera in the combined gene tree and the *ef1α* tree. These four *Diaporthe* species were not introduced as members of any species complex as their placements are unstable in single gene trees. In contrast, *Hyaliappendispora* and *Phaeodiaporthe* were consistently placed separately from *Diaporthe* and the rest of the genera at the base of the Diaporthaceae tree with high statistical support. (Figures 6.2–6.7).

Demarcation of individual taxa within the genus is essential for a better understanding of the lifestyles, ecology, and overall biology of these individual taxa and their impact and control in various ecosystems. Hence, some strains were excluded from the Diaporthaceae tree, as they do not belong to *Diaporthe* based on BLAST search and phylogenetic analysis, *viz. D. scabra* strain CBS 127746, DCDSL 69/96, DCDSL 11/96, DCDSL 102/96, *D. columnaris* strain CBS 109873, *D. elonis* strain d91, *D. liquidambaris* strain SA1, *D. oncostoma* strain WU 32007, *D. phyllanthicola* strain TW23, msy54, *D. rhoina* strain IPBCC 15.1322, IPBCC 15.1323, and *D. apiculate* strain CGMCC 3.17533, LC3187. Two taxa, *Ophiodiaporthe cyatheae* and *Chiangraiomyces bauhiniae,* are synonymized under *Diaporthe, D. cyatheae* (≡ *O. cyatheae*) and *D. pseudobauhiniae* (≡ *C. bauhiniae*), respectively based on

phylogenetic analysis (Figures 6.1–6.7) (Fu et al., 2013; Senanayake et al., 2017). *Apiosphaeria guaranitica* (UB23801, UB23795, UB23750, UB23561, UB23518, UB23484, UB23393, UB22757, CDUB247), *Chaetoconis polygoni* (CBS 405.95), *Mazzantia galii* (CBS 125529), *M. napelli* (AR 3498, AFTOL-ID 2126) were removed from the Diaporthaceae tree.

The non-monophyly of *Diaporthe* in this (in all single gene trees and the combined gene tree) and other studies challenges its genus status. Sequences split into several distinct and genetically divergent clades, which could represent separate genera. Determining the extent of discordance between morphology and molecular data (dense and broad taxon sampling, careful examination of morphology) and the suitability of genetic markers used (phylogenomic analyses) will help substantially towards resolving this question. Further studies are also needed to establish whether these species are host-specific, determine their habitats and lifestyles, the conditions under which they might switch lifestyle and their interactions with their plant hosts.



Note Phylogram generated using maximum likelihood analysis based on ITS sequence data from 534 strains. The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values ≤50% are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

Figure 6.2 Phylogenetic analysis of Diaporthaceae based on ITS sequence data

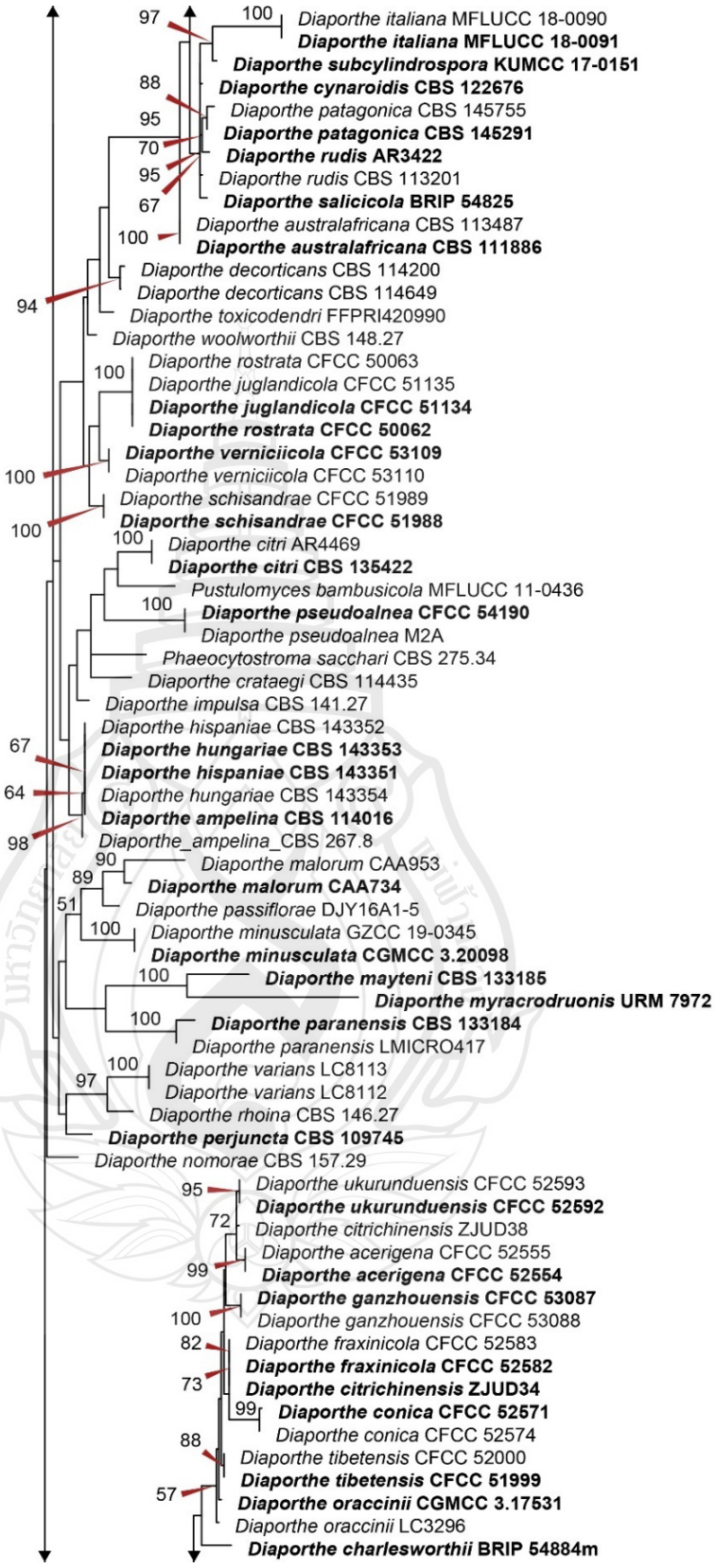


Figure 6.2 (continued)

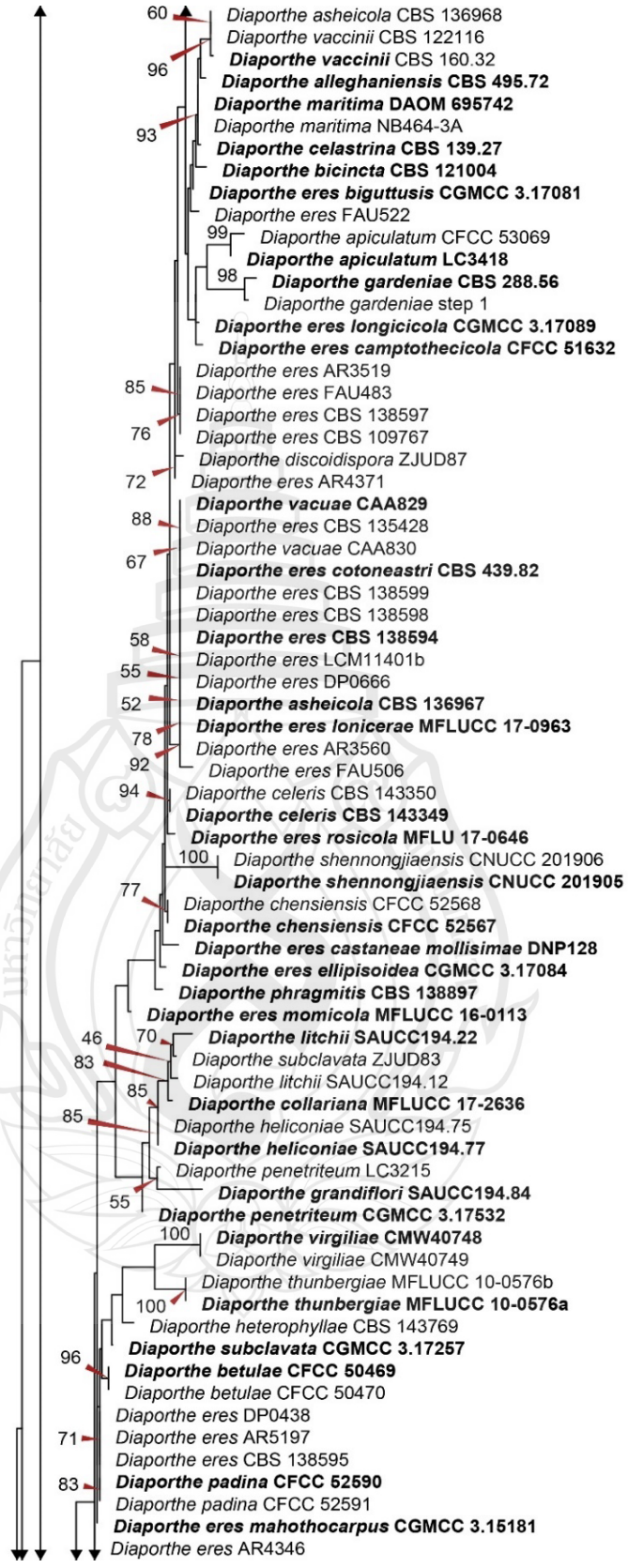


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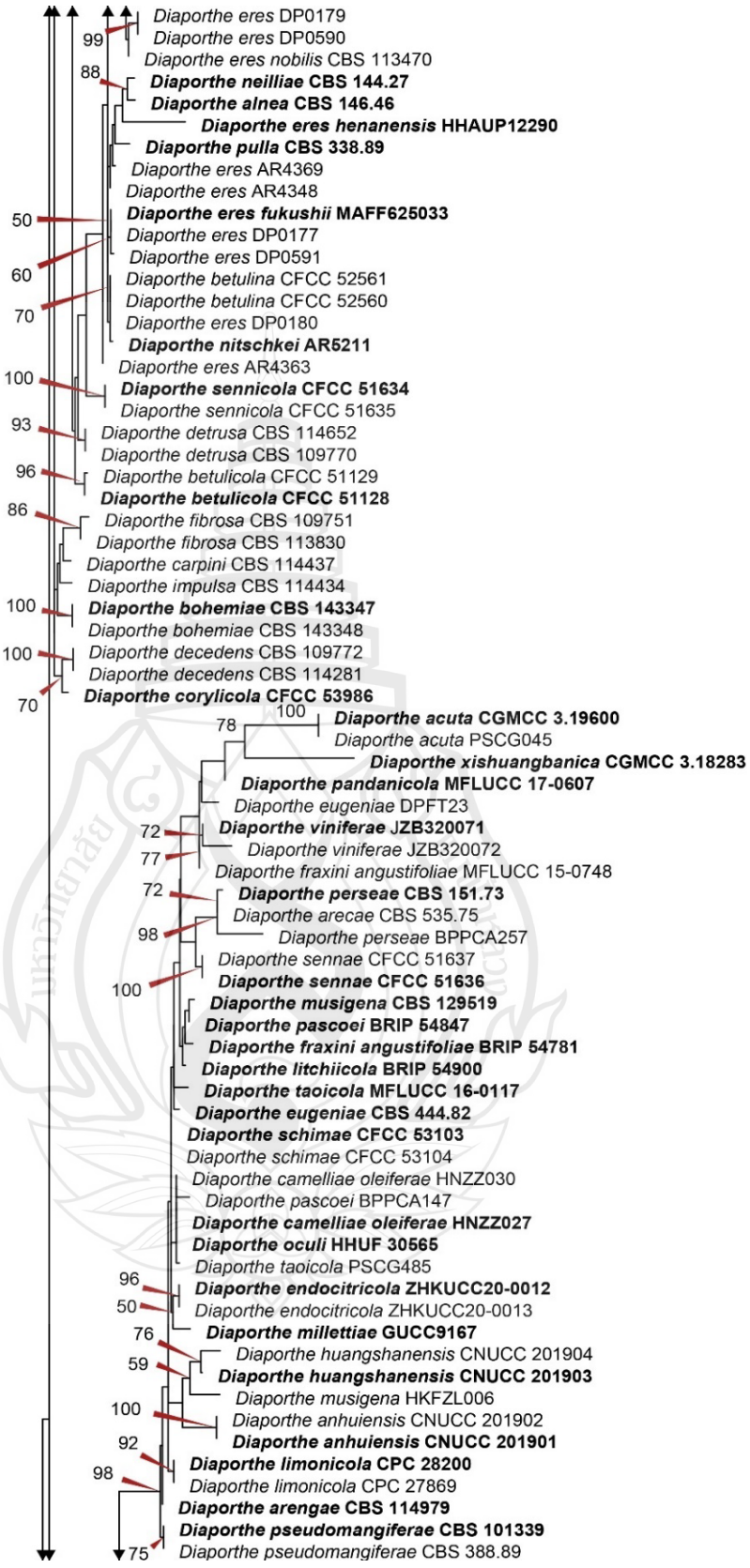


Figure 6.2 (continued)

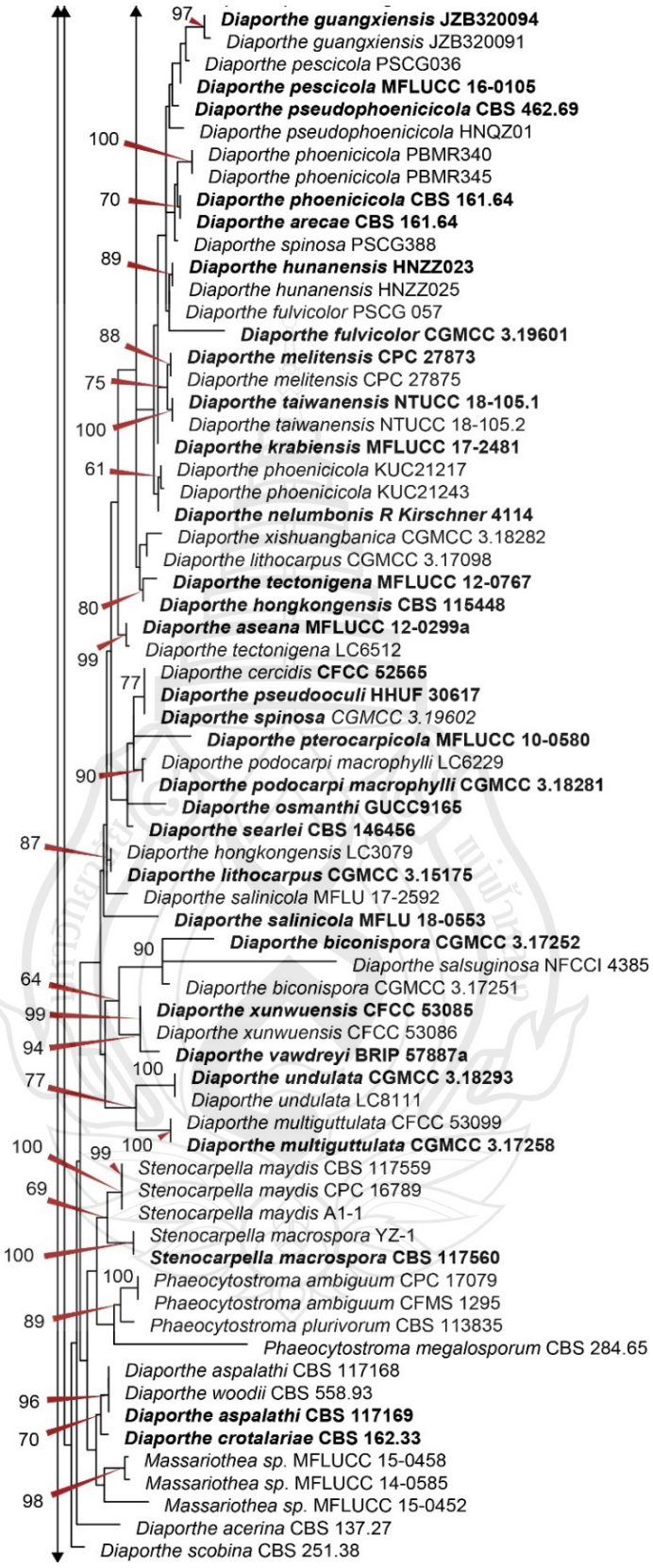


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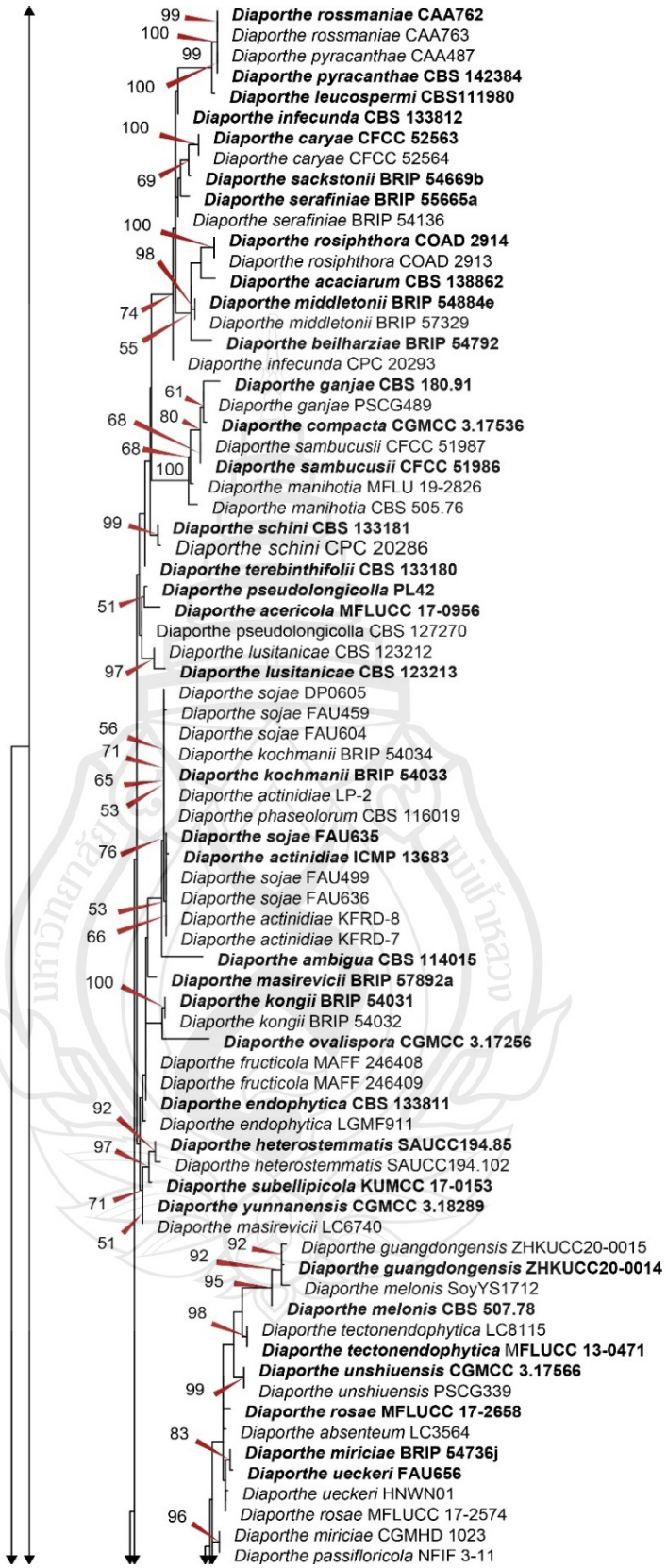


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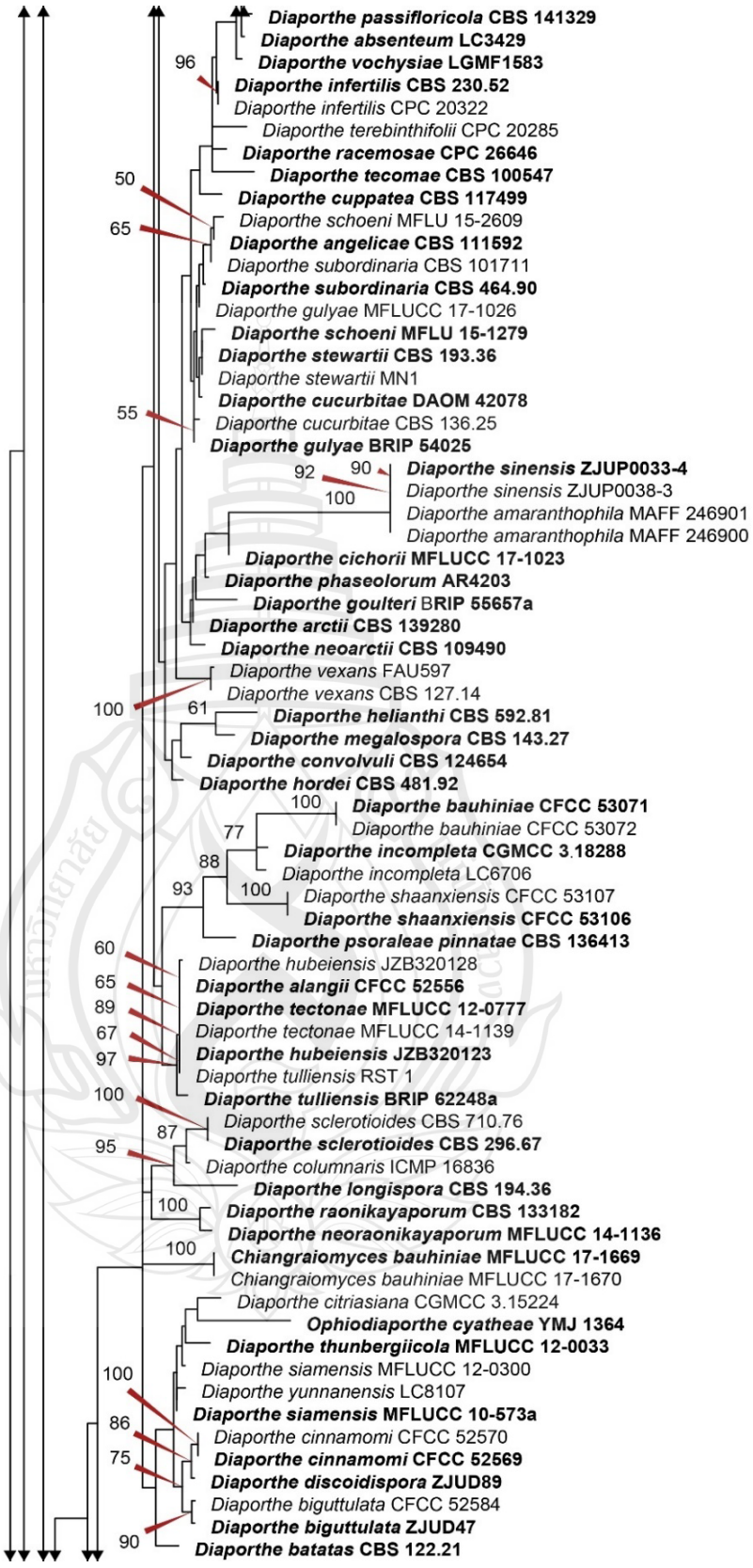


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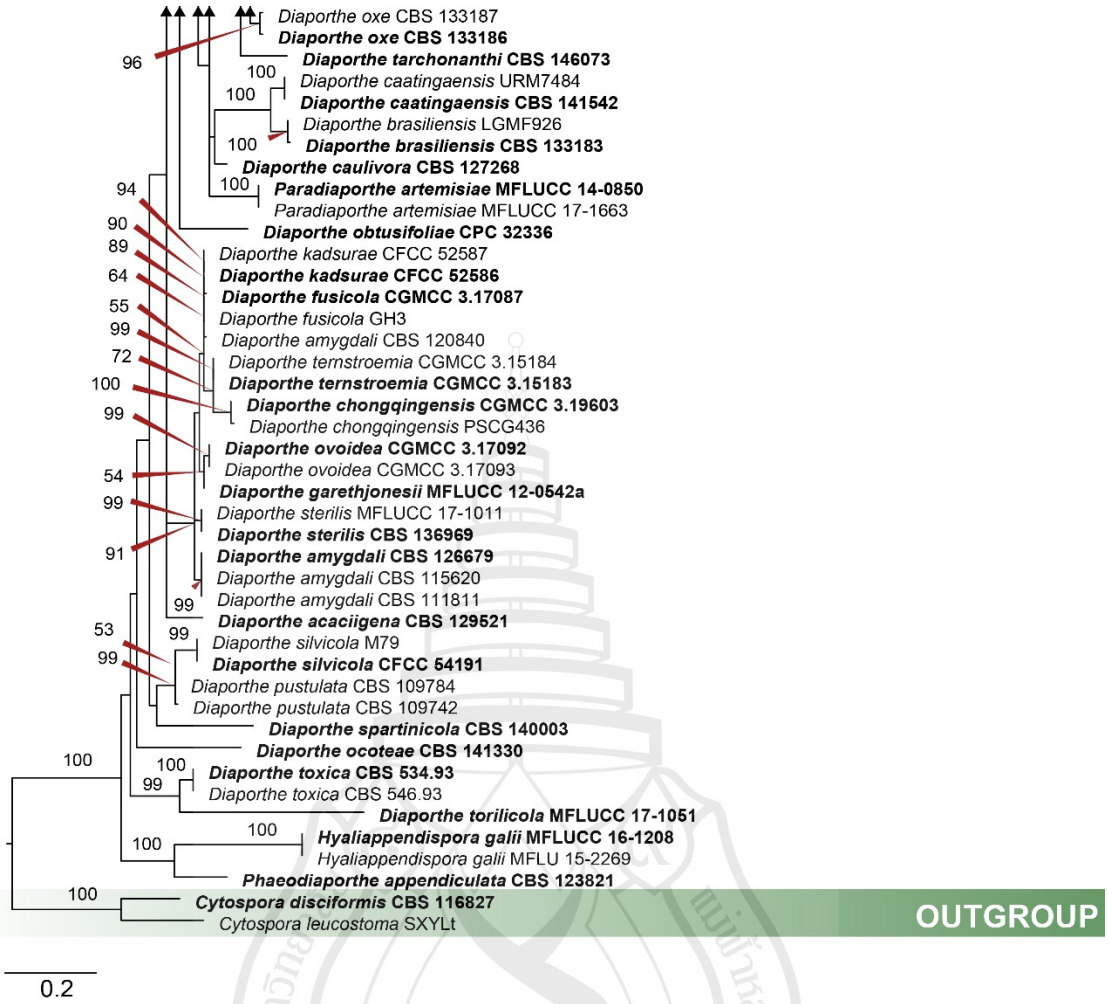
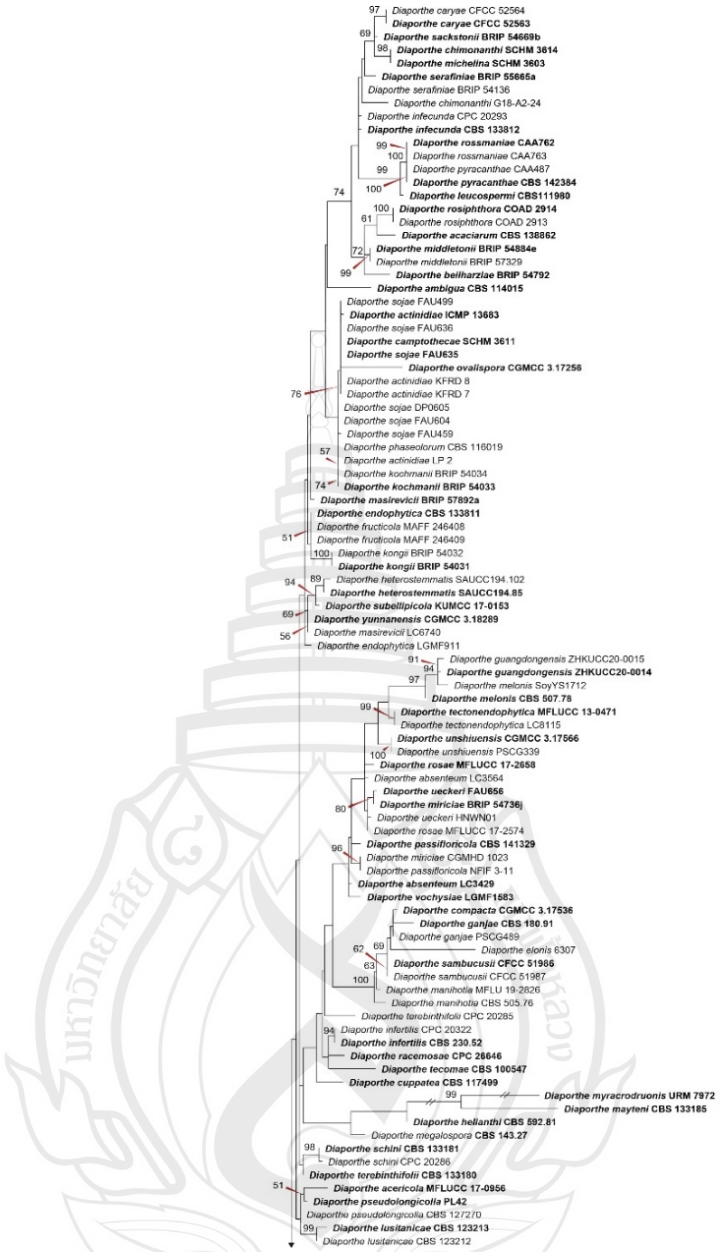


Figure 6.2 (continued)



Note Phylogram generated using maximum likelihood analysis based on ITS sequence data from 584 strains (included 50 strains that only have the ITS region). The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values ≤50% are given at the nodes inthis order. The species synonymized are in blue and ex-type taxa are in bold.

Figure 6.3 Phylogenetic analysis of Diaporthaceae based on ITS sequence data (included strains that only have the ITS region)

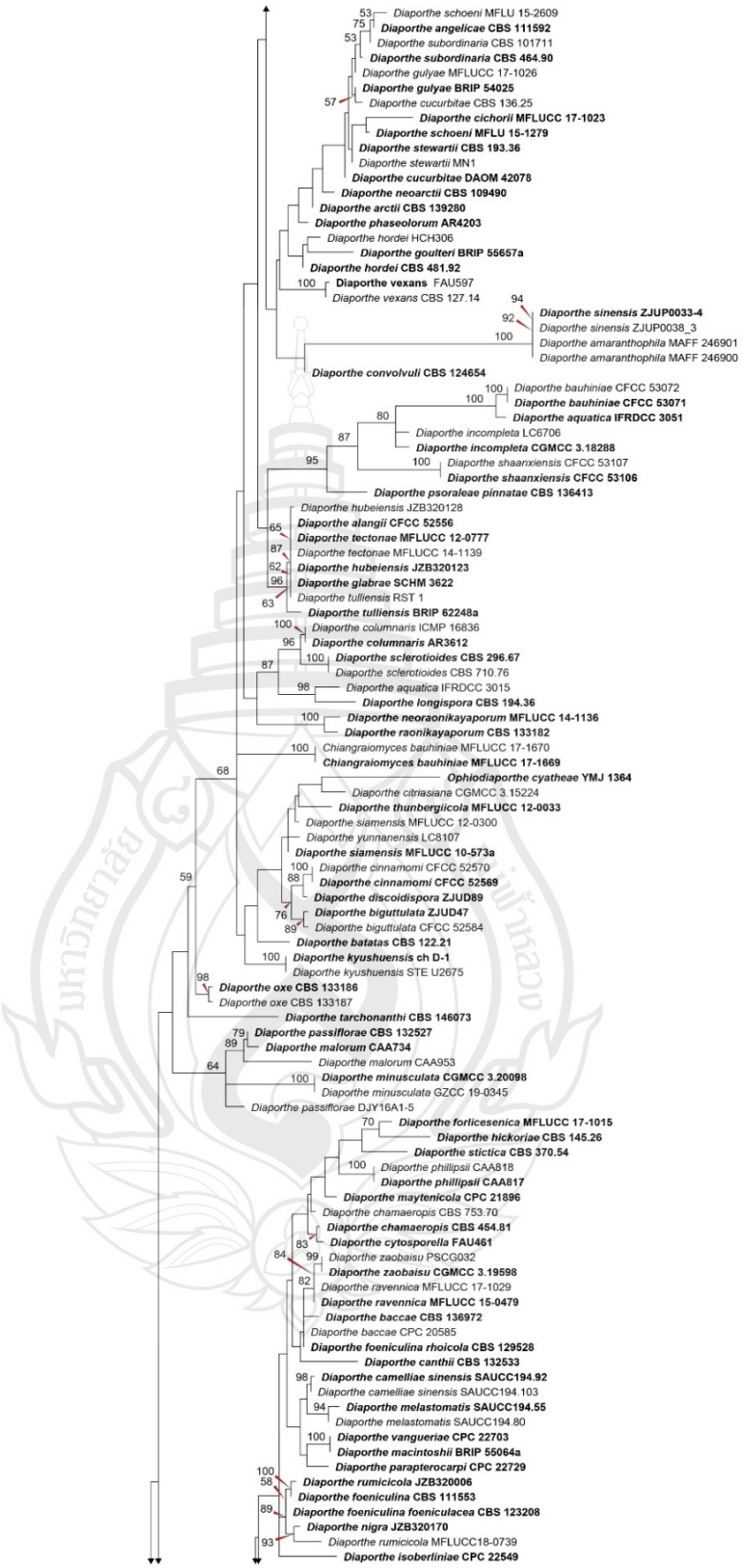


Figure 6.3 (continued)

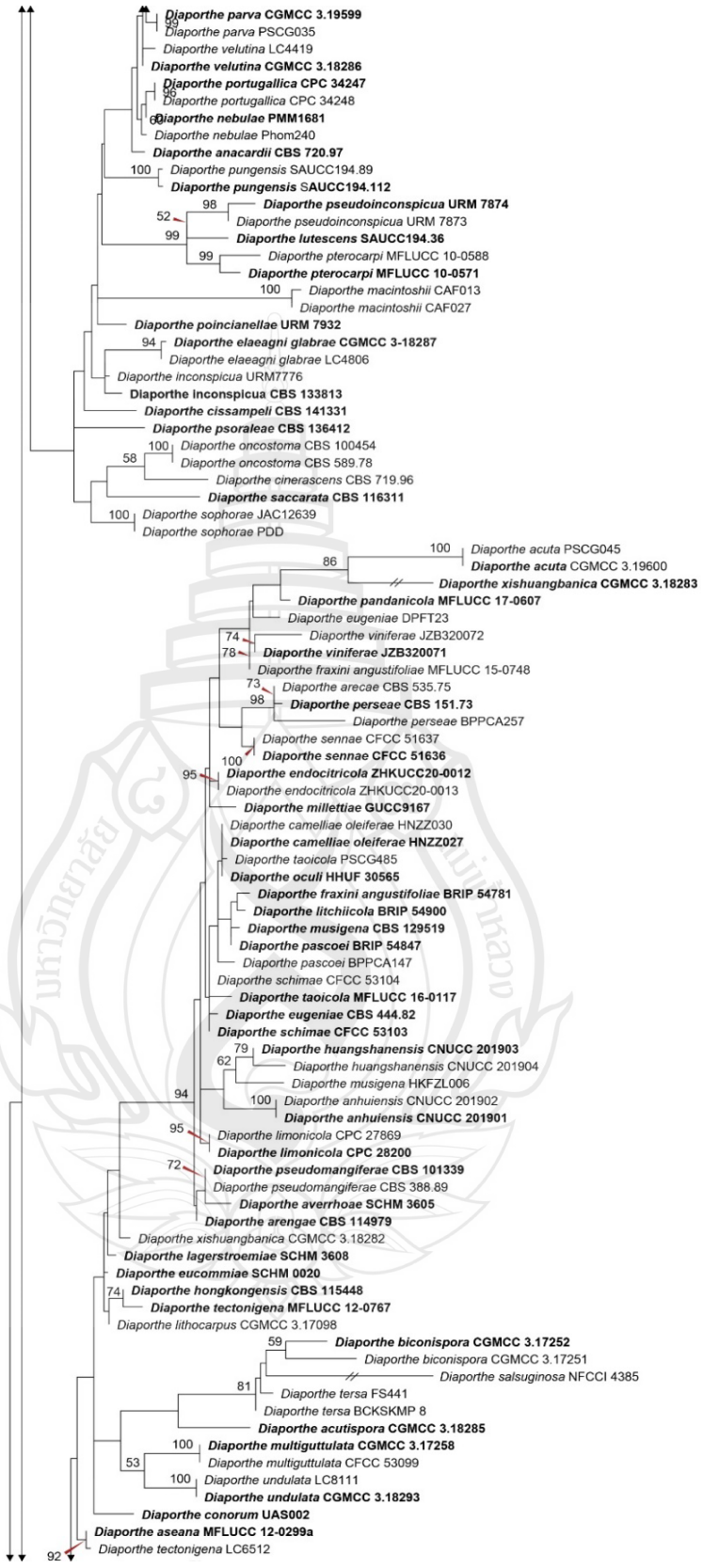


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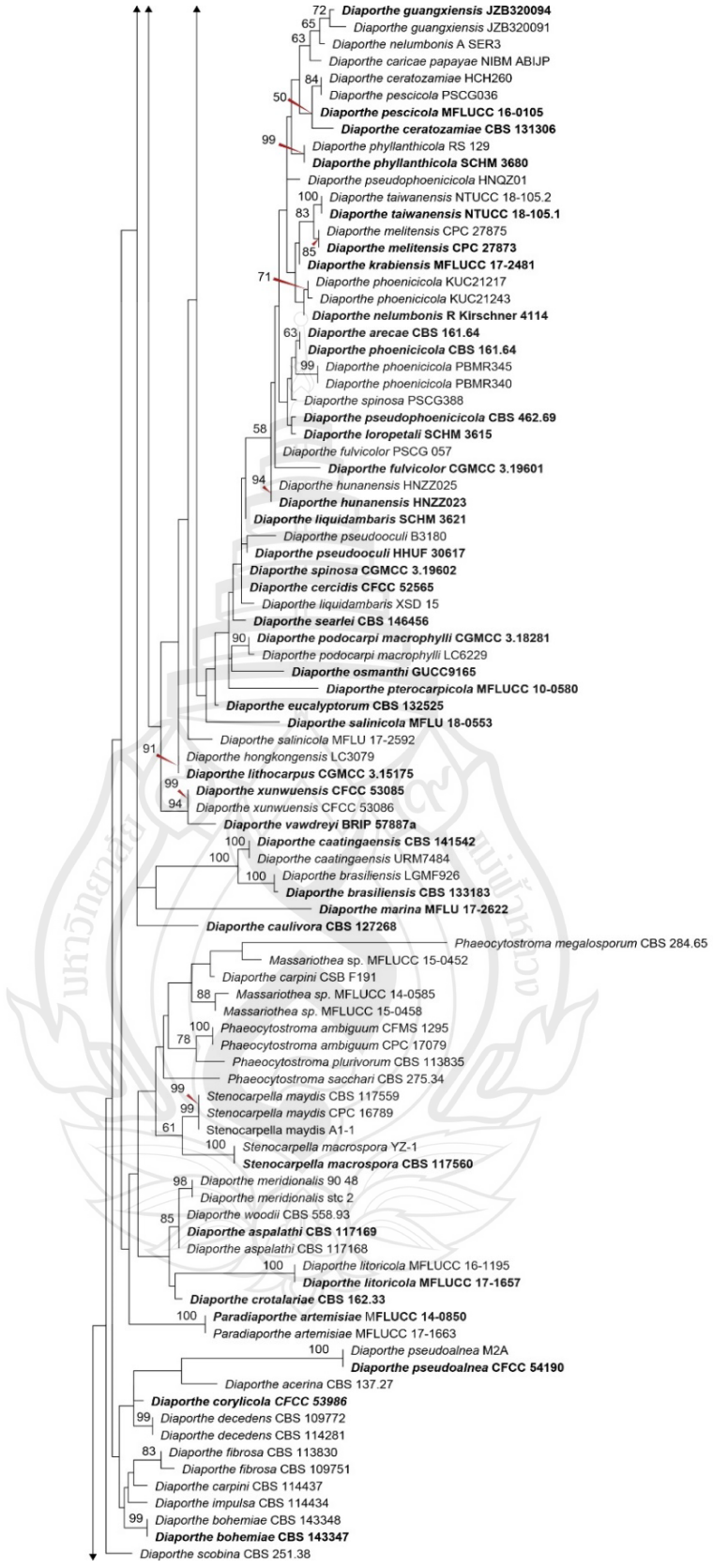


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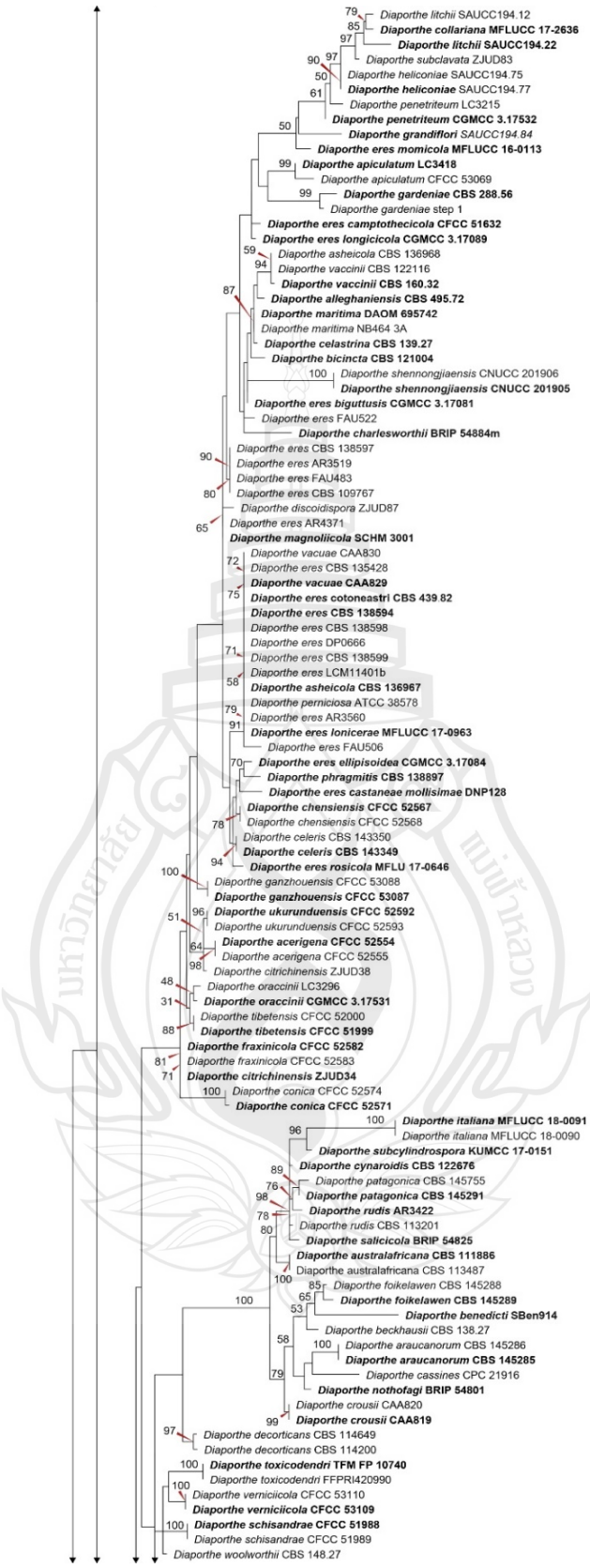


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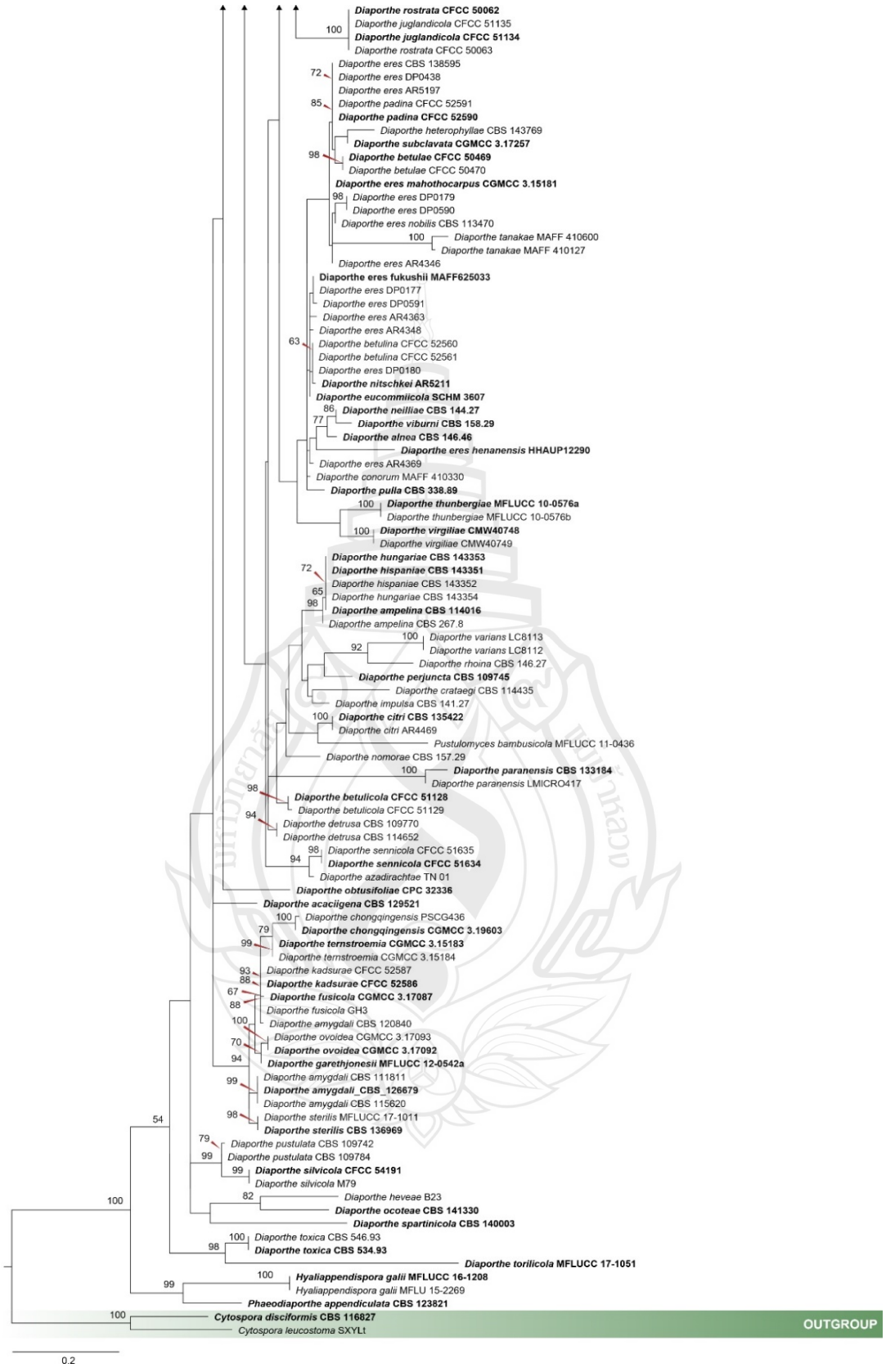
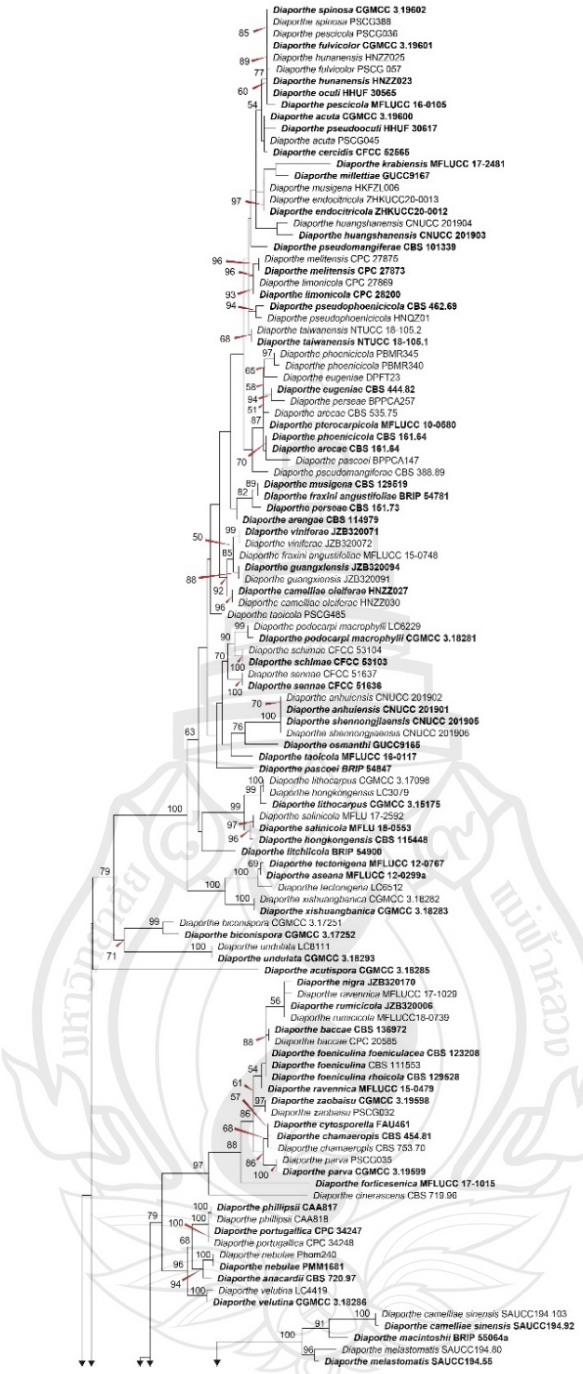


Figure 6.3 (continued)



Note Phylogram generated using maximum likelihood analysis based on *ef1α* sequence data from 510 strains. The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values ≤50% are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

Figure 6.4 Phylogenetic analysis of Diaporthaceae based on ef1α sequence data

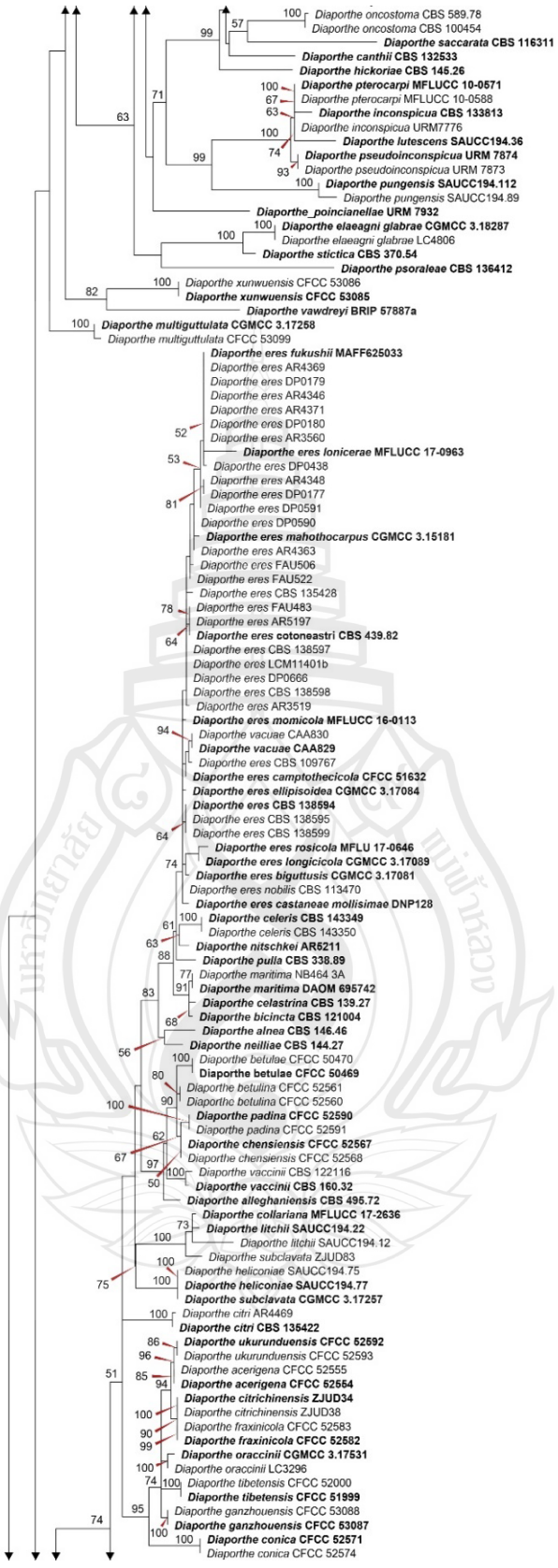


Figure 6.4 (continued)

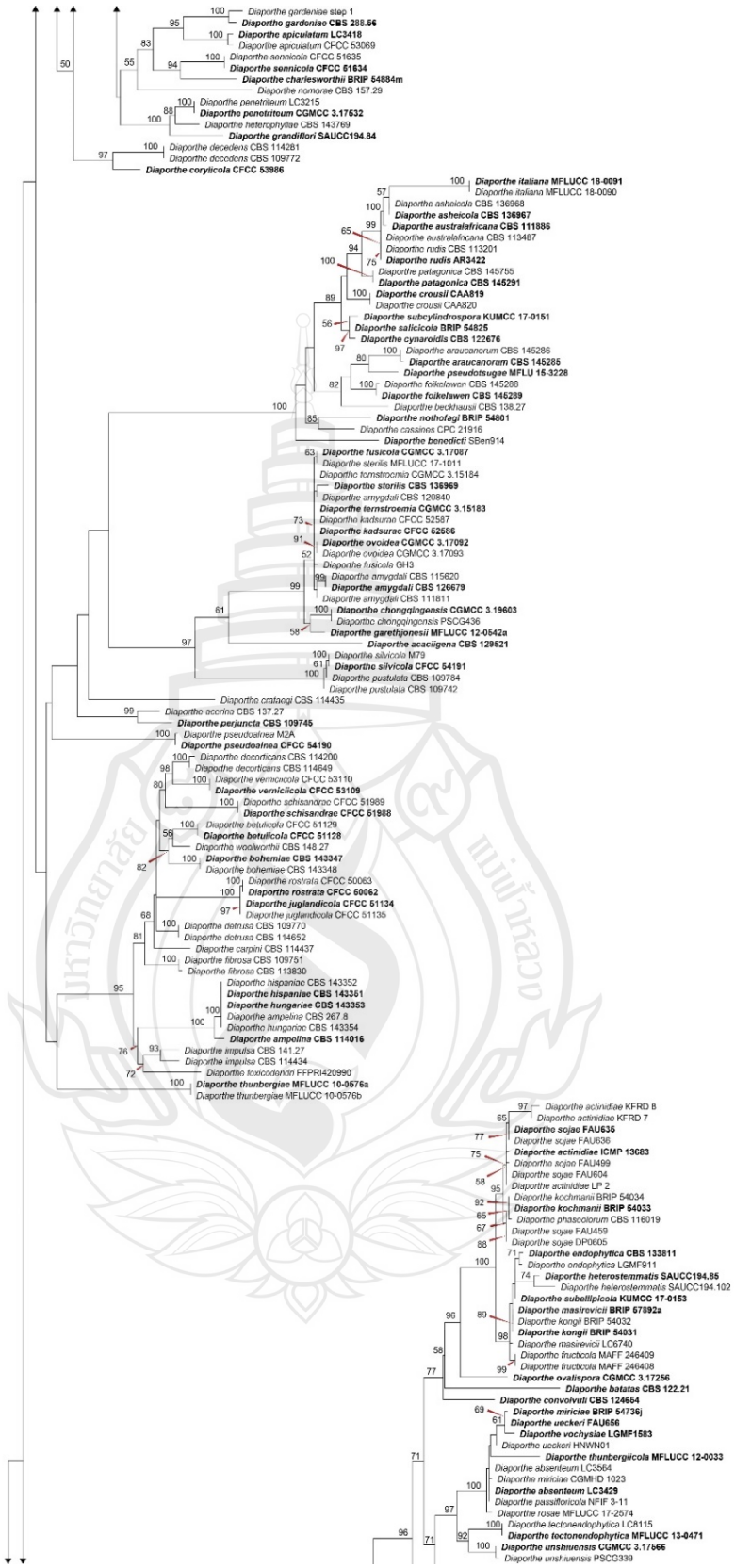


Figure 6.4 (continued)

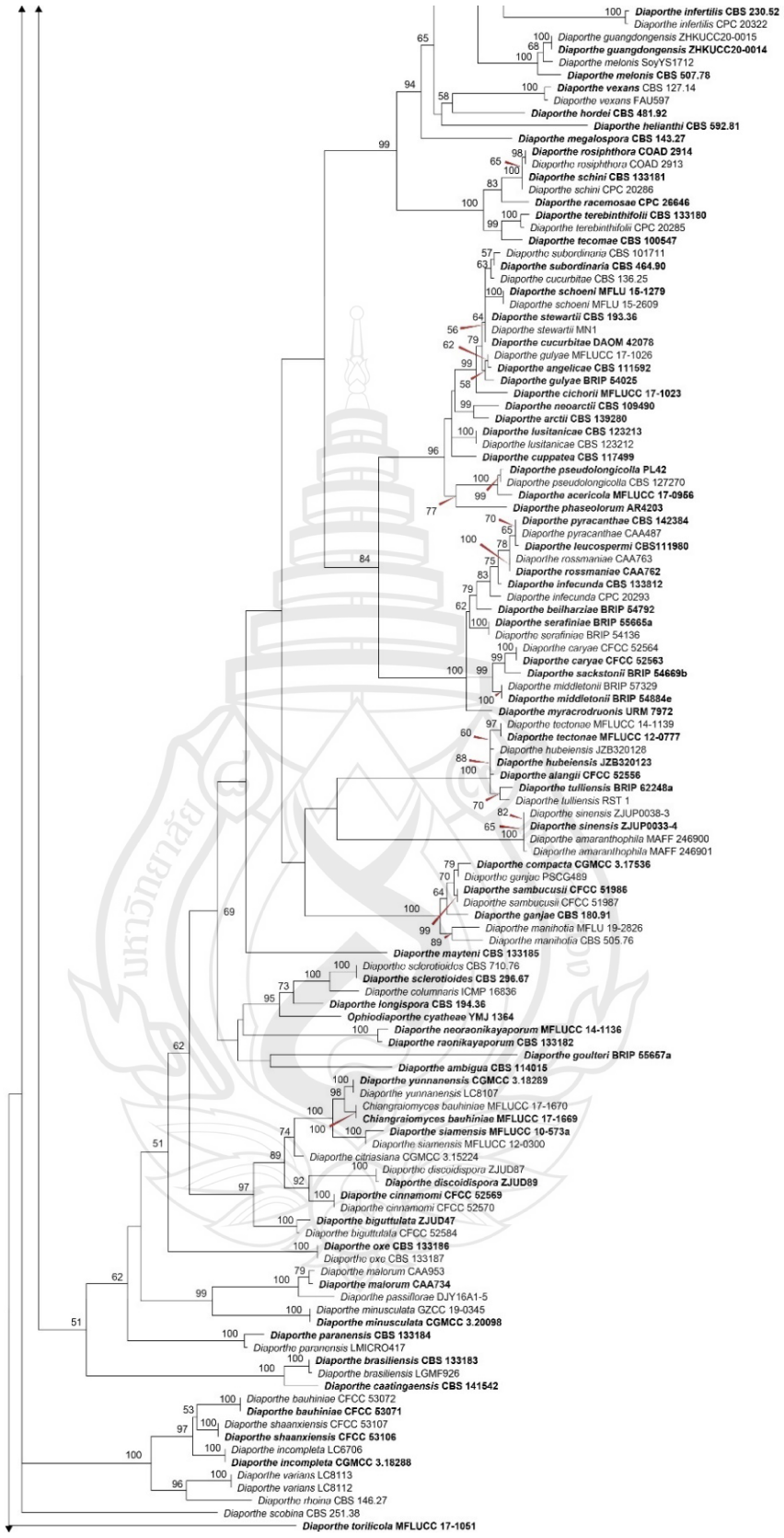


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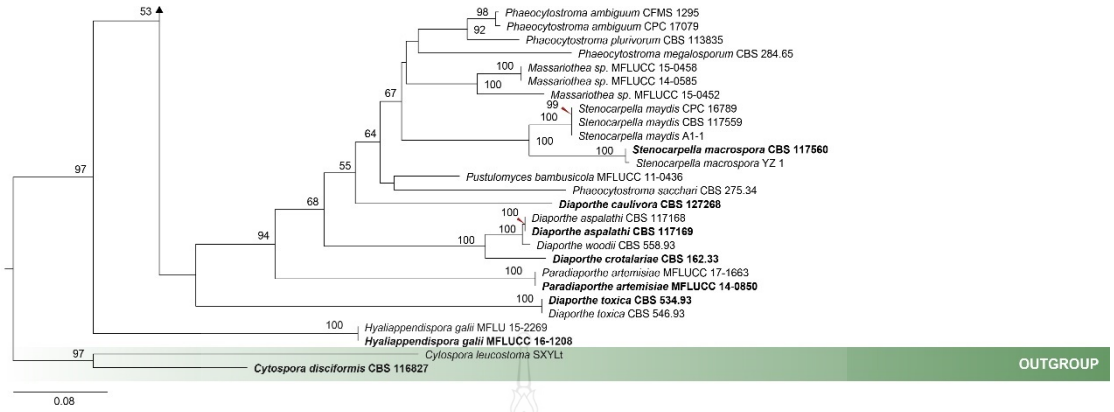
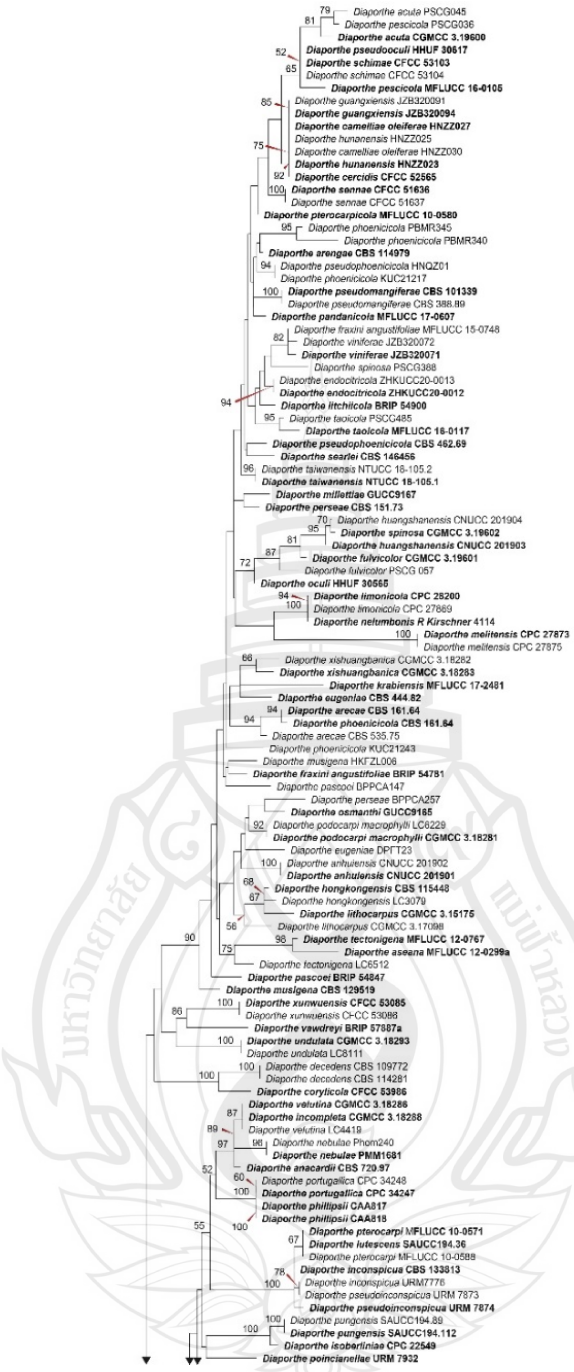


Figure 6.4 (continued)



Note Phylogram generated using maximum likelihood analysis based on *β-tubulin* sequence data from 479 strains. The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values ≤50% are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

Figure 6.5 Phylogenetic analysis of Diaporthaceae based on β-tubulin sequence data

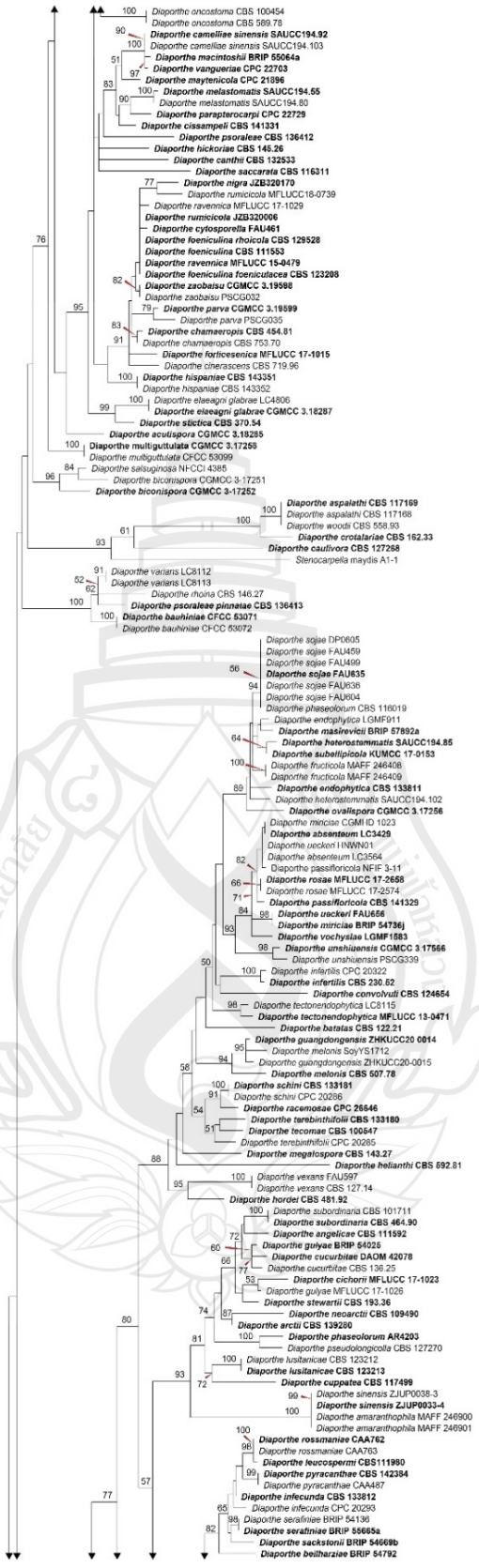


Figure 6.5 (continued)

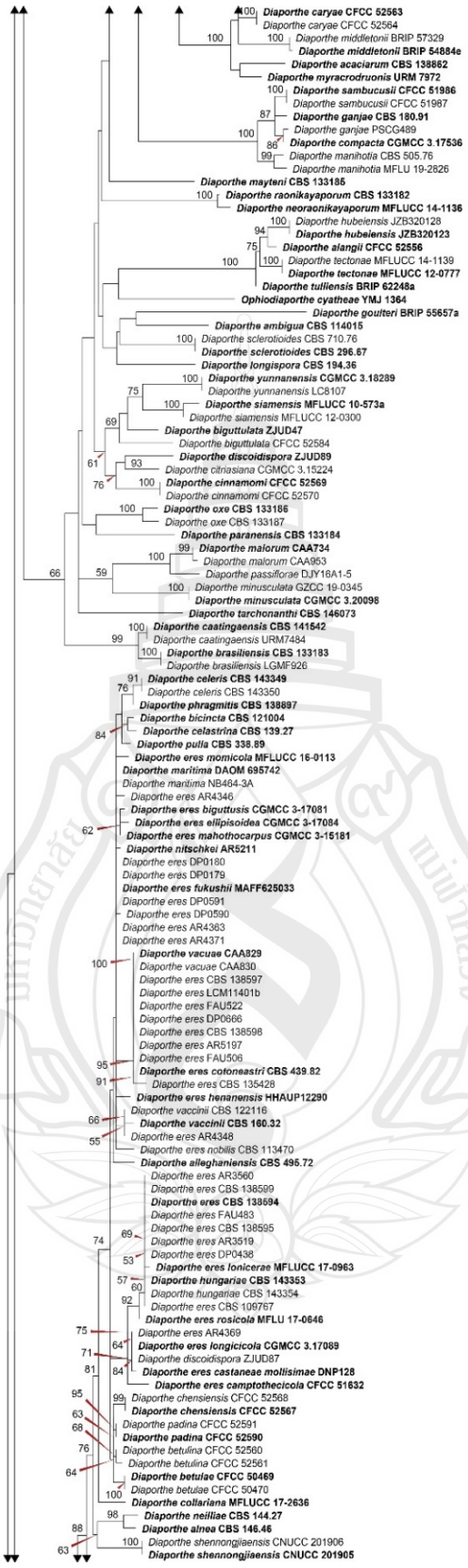


Figure 6.5 (continued)

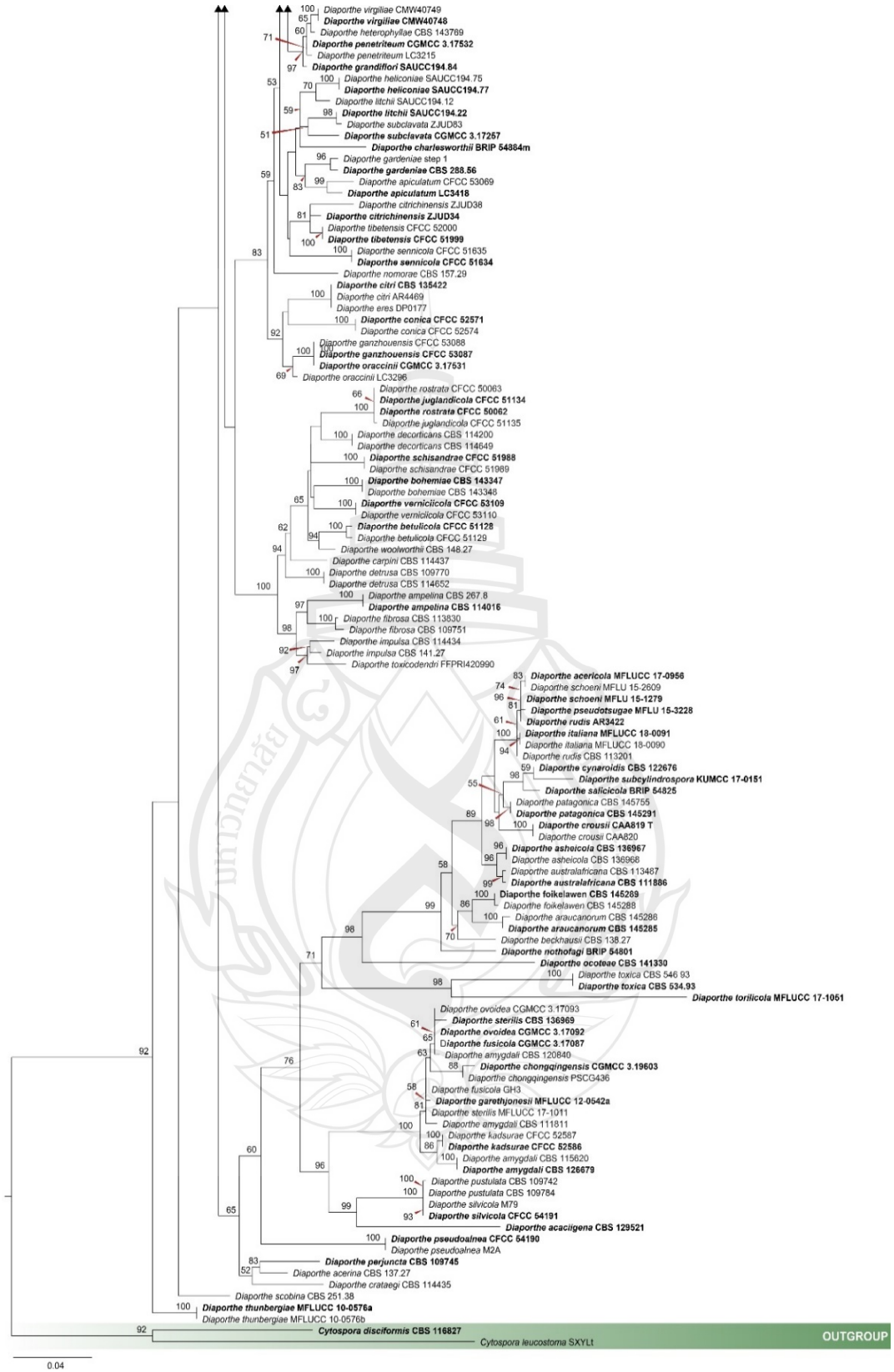
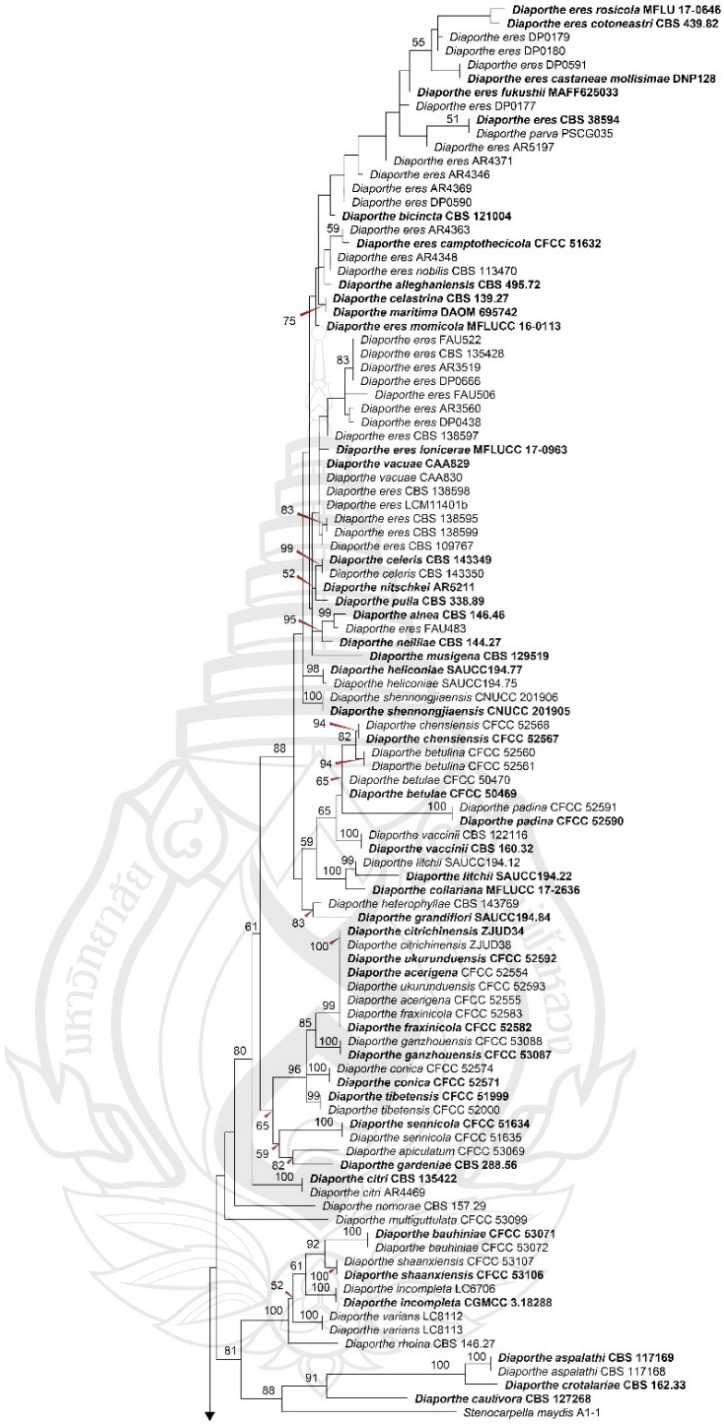


Figure 6.5 (continued)



Note Phylogram generated using maximum likelihood analysis based on *cal* sequence data from 383 strains. The tree is artificially rooted to *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values ≤50% are given at the nodes inthis order. The species synonymized are in blue and ex-type taxa are in bold.

Figure 6.6 Phylogenetic analysis of Diaporthaceae based on cal sequence data

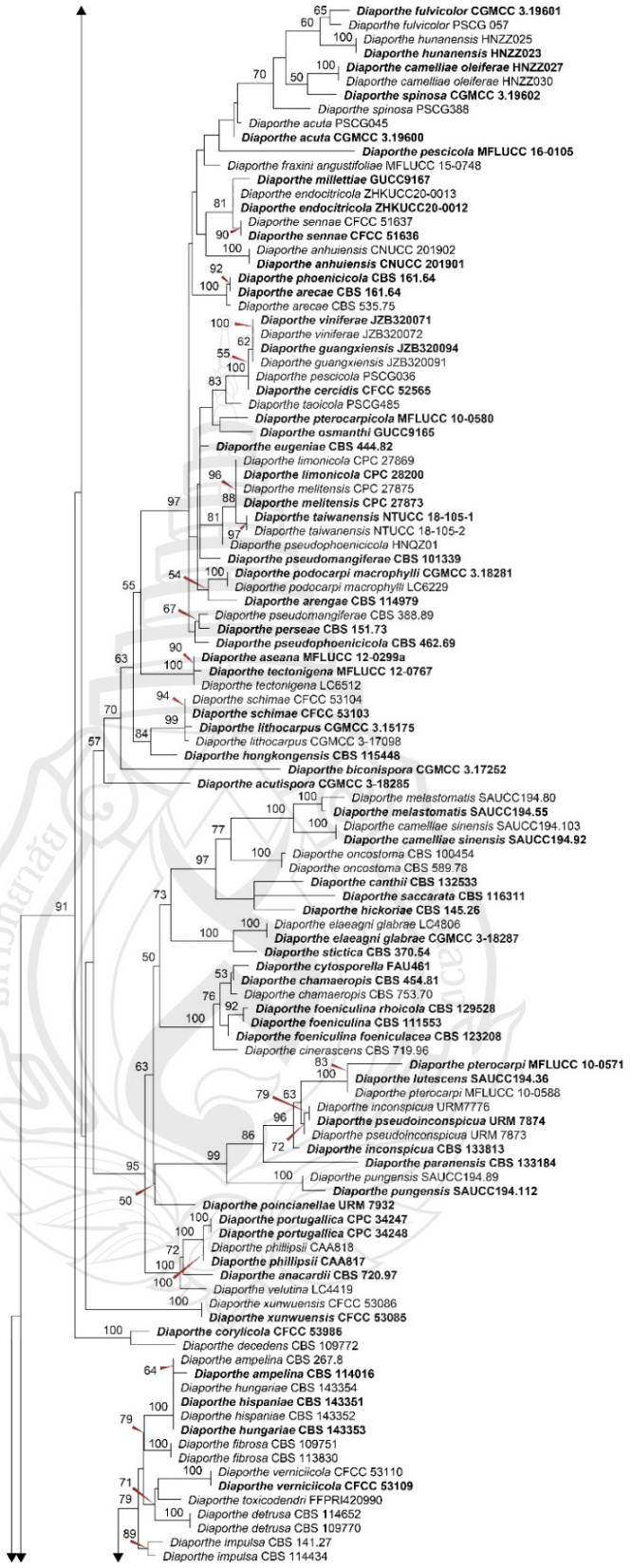


Figure 6.6 (continued)

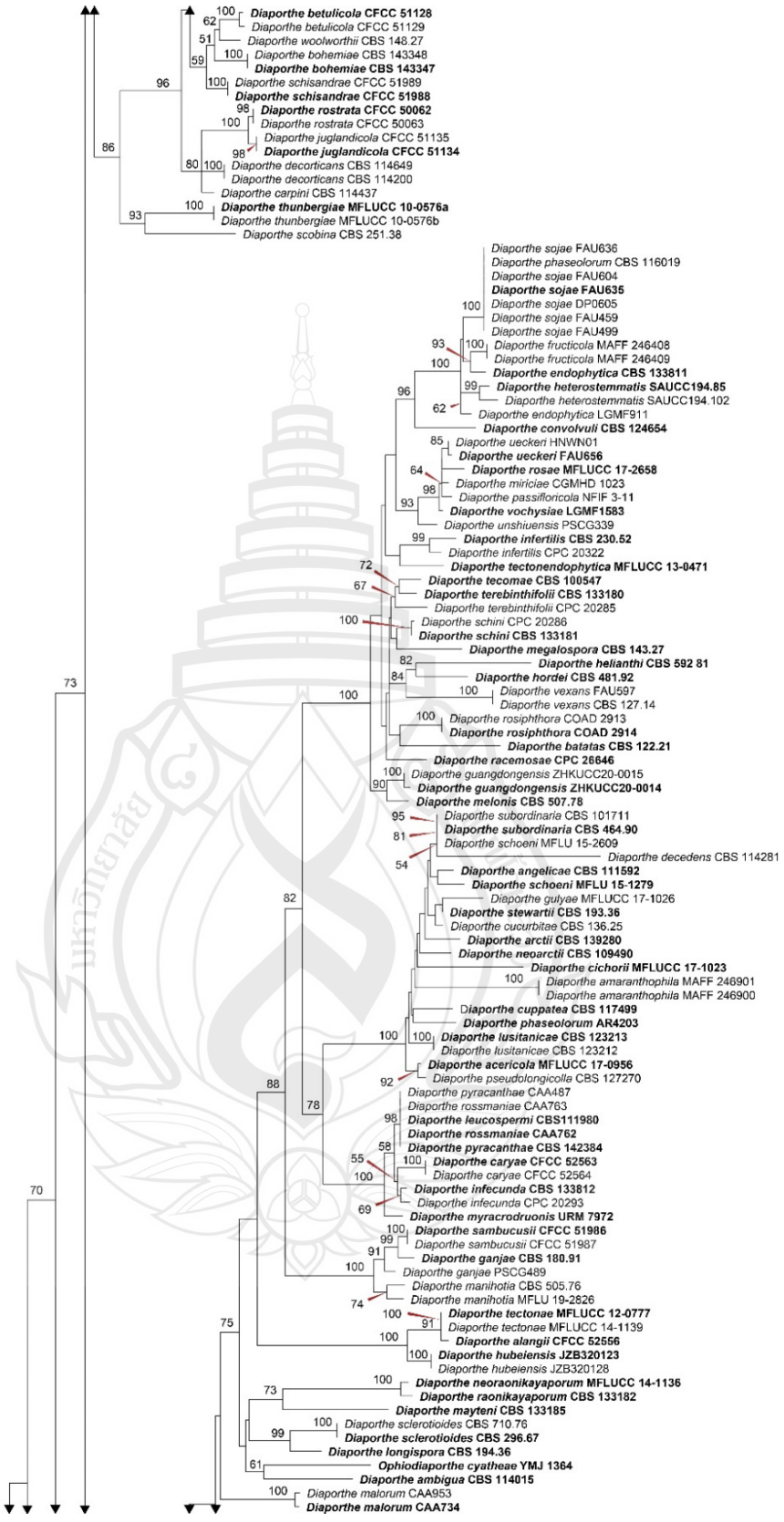
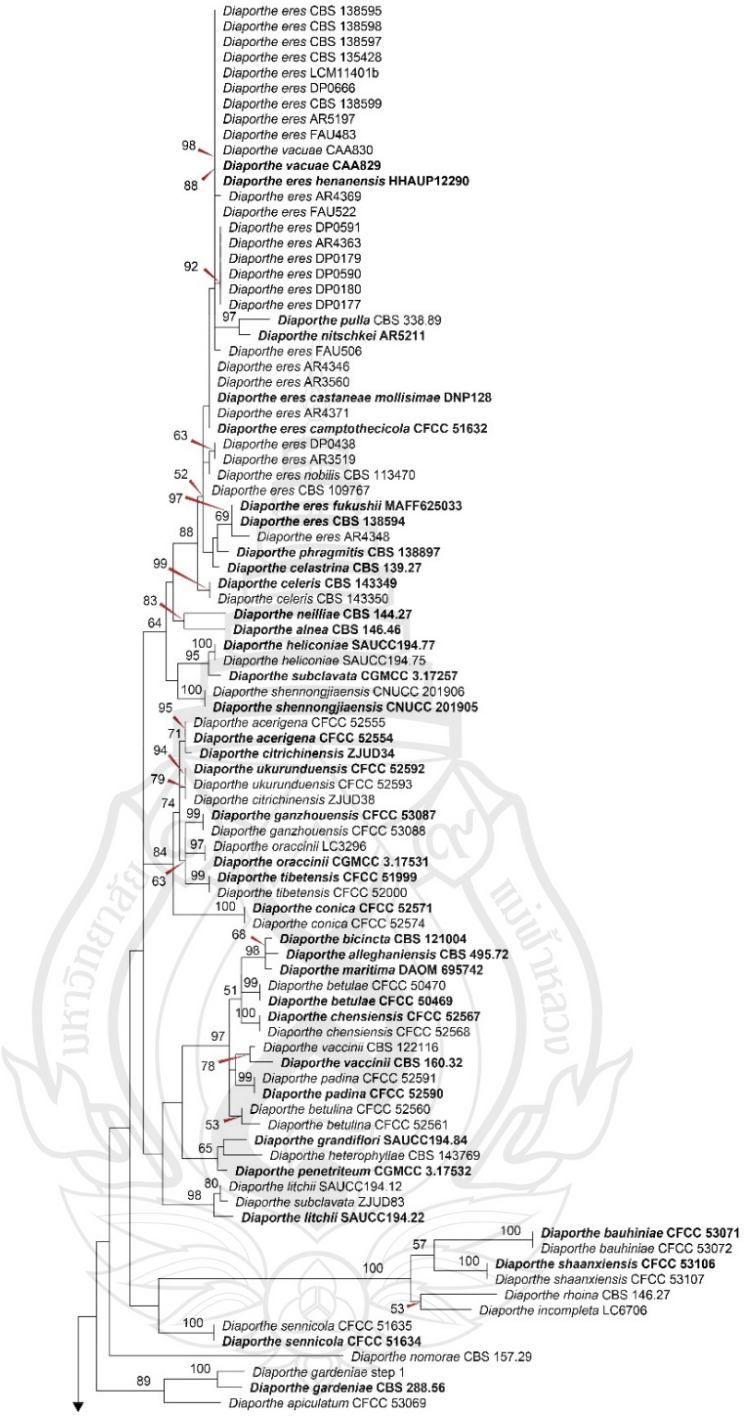


Figure 6.6 (continued)



Figure 6.6 (continued)



Note Phylogram generated using maximum likelihood analysis based on *his*3 sequence data from 343 strains. The tree is artificially rooted to *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values ≤50% are given at the nodes inthis order. The species synonymized are in blue and ex-type taxa are in bold.

Figure 6.7 Phylogenetic analysis of Diaporthaceae based on his3 sequence data

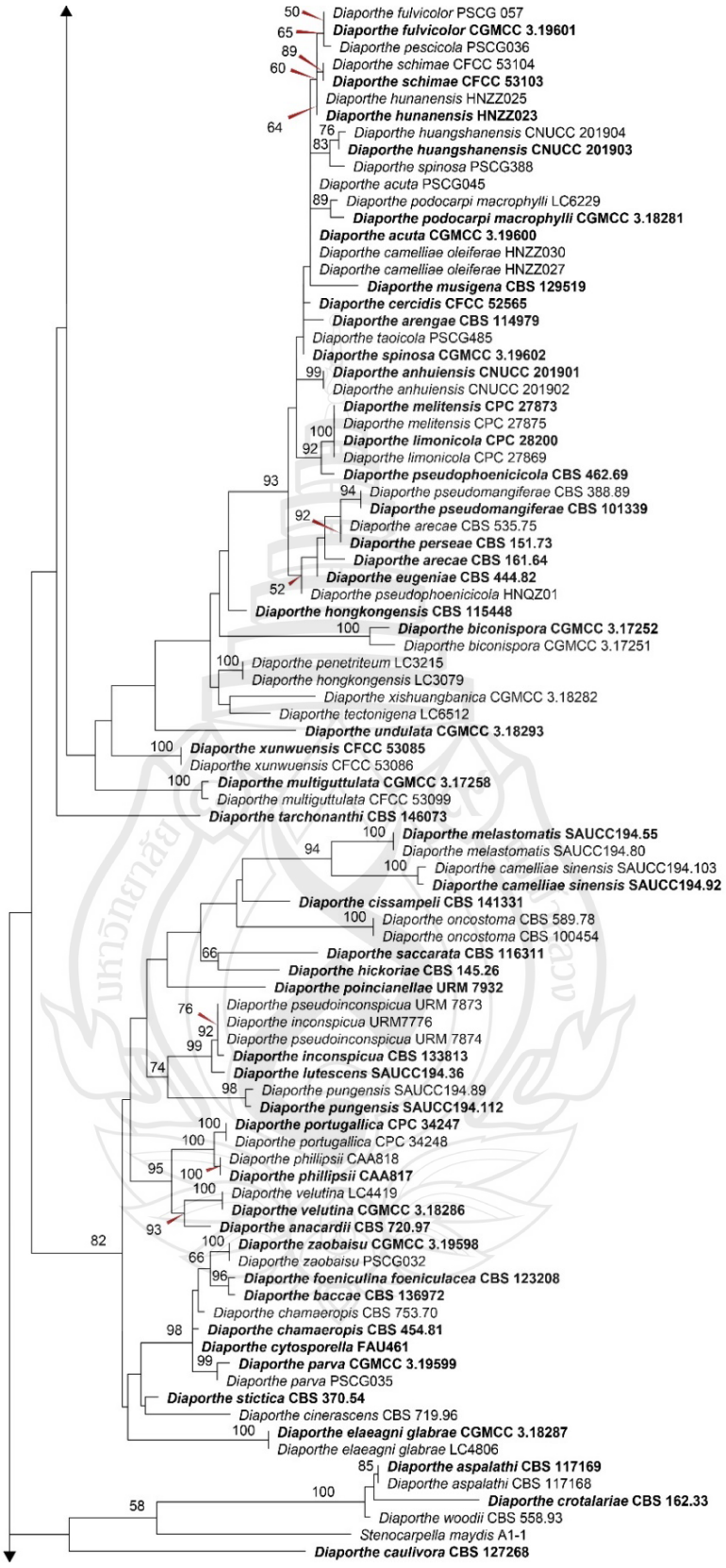


Figure 6.7 (continued)

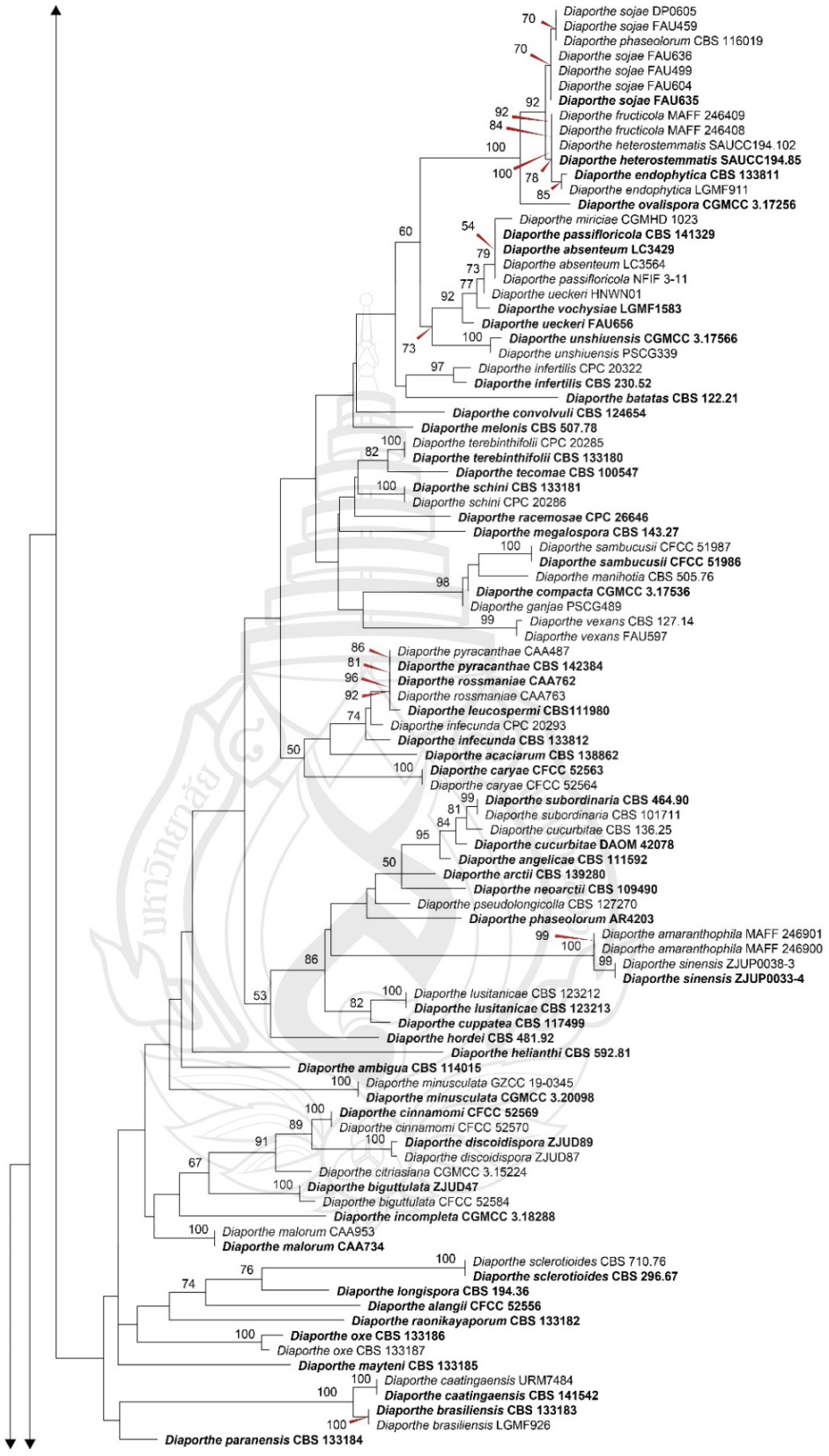


Figure 6.7 (continued)

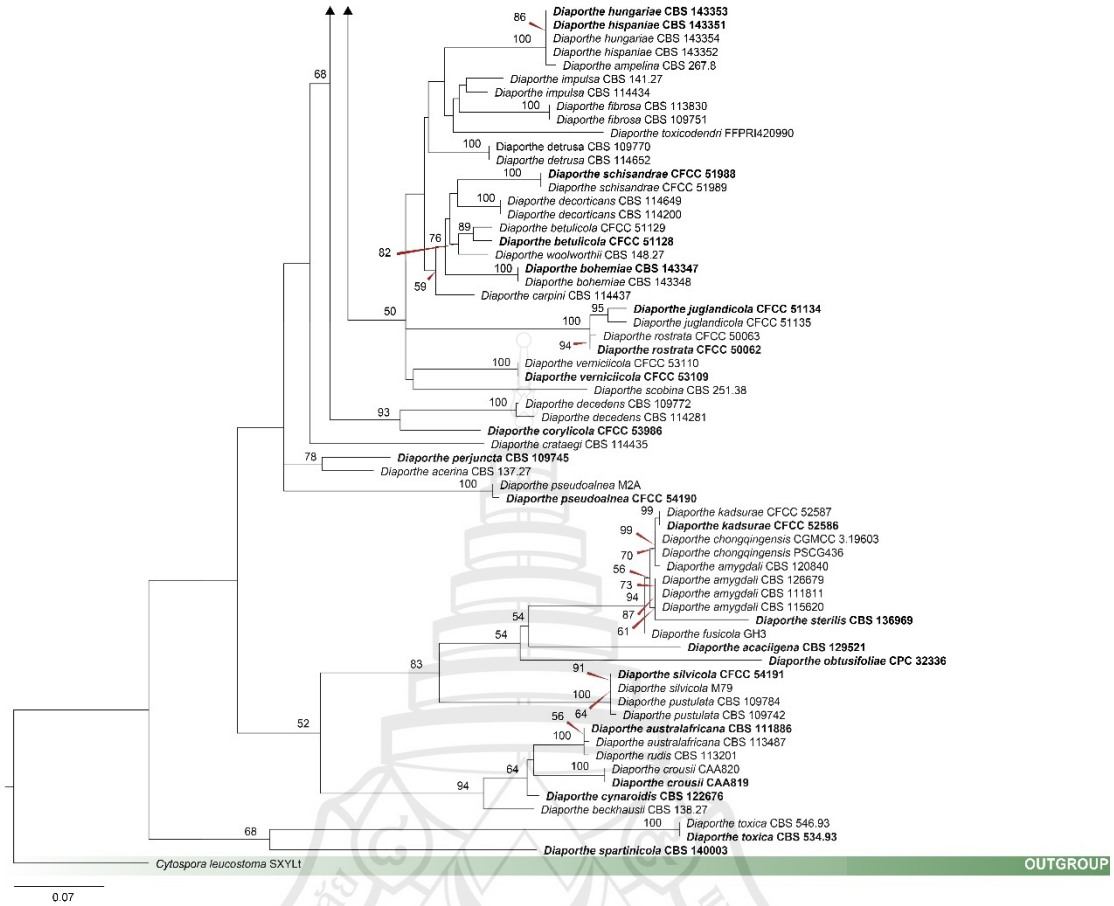


Figure 6.7 (continued)

CHAPTER 7

TOWARDS A BACKBONE TREE FOR *SEIMATOSPORIUM,* WITH *S. PHYSOCARPI* SP. NOV.[6]

Abstract

The genus *Seimatosporium* is saprobic or pathogenic on plants, and are 'pestalotioid fungi'. The genus presently belongs in *Discosiaceae* (*Amphisphaeriales*) and includes 78 species epithets. In this study, we observed three specimens of *Seimatosporium* from Russia and they are characterized by morphological and sequence data. We analyzed combined ITS and LSU gene sequence data of 42 species representing the genera *Discostroma* (7), *Sarcostroma* (2) and *Seimatosporium* (32, including the three new strains) with *Pseudopestalotiopsis theae* as the outgroup taxon. One isolate from dead branches of *Physocarpus opulifolius* is unique and is introduced as *Seimatosporium physocarpi* sp. nov., in this paper. It can be distinguished from similar and related species by phenotypic conidial characters and phylogenetic analyses. A specimen from *Rosa kalmiussica* Chrshan. & Lasebna (often includes in *Rosa canina* sensu lato) is designated as an epitype for *S. rosae*, the type of the genus. In addition, a collection of *S. lichenicola* is described, illustrated, and compared with other species in the genus.

Keywords: *Discosiaceae*, new species, phylogeny, epitype, combine gene, taxonomy

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[6]This paper has been published in *Mycosphere*, 2015, *6*(3), 385–400. https://doi.org/10.5943/mycosphere/6/3/12

7.1 Introduction

The genus *Seimatosporium* was introduced by Corda (1833), with *S. rosae* Corda as the type species. This genus is presently placed in the family the *Discosiaceae, Amphisphaeriales* (Senanayake et al., 2015). The sexual morph of *Seimatosporium* has been identified as *Discostroma* (Hyde et al., 2011) and are known as 'pestalotioid fungi' (Nag Raj, 1993). *Seimatosporium* is a relatively well-known saprobic and plant pathogenic coelomycetous taxon (Sutton, 1980; Tanaka et al., 2011). Based on their conidial features, Nag Raj (1993) provided an account of *Seimatosporium* species and rearranged them into five natural groupings under extant generic names. These are *Seimatosporium sensu stricto* (*S. botan* Sat. Hatak. & Y. Harada), *Sporocadus* (with *S. lichenicola* (Corda) Shoemaker & E. Müll., the generic type), *Sarcostroma* (with *S. foliicola* (Berk.) Shoemaker, as type of the genus), *Diploceras* (with *S. hypericinum* (Ces.) B. Sutton, as type of the genus), and *Vermisporium* (with *S. leptospermi* R.G. Bagn. & Sheridan). Tanaka et al. (2011) re-studied *Diploceras*, *Sporocadus*, *Sarcostroma*, *Diploceras*, and *Vermisporium*, which lack sexual morphs, and concluded that they should be placed under the genus *Seimatosporium*, based on a monophyletic grouping in LSU and ITS phylogenetic analyses. This finding was similar to the large diversity of *Seimatosporium* species as treated in Sutton (1980). According to Index Fungorum (2015) *Seimatosporium* comprises 78 species. The characteristic features of the genus are conidia with pigmented median cells, with or without an apical appendage, and single, branched, or unbranched basal appendage (Nag Raj, 1993).

In the present study, we report on three specimens of *Seimatosporium*, collected in Russia. With evidence from morphological and phylogenetic analyses we introduce a new species *S. physocarpi*; designate an epitype for *S. rosae*, and provide a detailed description for *S. lichenicola* which is the asexual morph of *Discostroma fuscellum*.

7.2 Materials and Methods

7.2.1 Sample Collection and Specimen Examination

Samples were collected during May 2014 from the Rostov region of European Russia and returned to the laboratory in small paper bags. Specimens were examined under a Motic SMZ 168 dissecting microscope for fungal fruiting bodies. Hand sections of the fruiting structures were mounted in water for microscopic studies. The fungi were examined under a Nikon Ni compound microscope and photographed using a Canon EOS 600D digital camera fitted to the microscope. The images were processed with Adobe Photoshop CS5 Extended version 12.0 software (Adobe Systems Inc., The United States) and the Tarosoft (R) Image Framework program v. 0.9.7 was used for measurements. Single spore isolation was followed the method detailed in Chomnunti et al. (2014) and the germinating spores were transferred aseptically to malt extract agar (MEA) plates and incubated at 18 °C. Colony characters were observed and measured after a week and one month.

The herbarium materials are deposited in the Mae Fah Luang University Herbarium, Chiang Rai, Thailand (MFLU) and New Zealand Fungal Herbarium, New Zealand (PDD) and living cultures deposited at Mae Fah Luang University Culture Collection (MFLUCC) and Fungal Biodiversity Centre (CBS). Facesoffungi numbers and Index Fungorum numbers are provided as detailed in Jayasiri et al. (2015) and Index Fungorum (2015).

7.2.2 DNA Extraction, PCR Amplification and Sequencing

Genomic DNA were extracted from the growing mycelium on PDA, following the methods of Telle and Thines (2011). Polymerase chain reactions (PCR) were carried out using primer pairs of ITS5 and ITS4 to amplify the internal transcribed spacers (ITS) (White et al., 1990), and large subunit rDNA (LSU) was amplified using primer pairs of LROR and LR5 (Vilgalys & Hester. 1990). The amplification reaction was performed in a 50 µl reaction volume containing, 5–10 ng DNA, 0.8 units Taq polymerase, 1×PCR buffer, 0.2 mM dNTP, 0.3 µm of each primer with 1.5 mM MgCl2 (Cai et al., 2009). Amplification protocols were followed according to

Maharachchikumbura et al. (2013, 2014). The PCR products were visualized on 1% agarose gel stained with ethidium bromide. Purification and sequencing of PCR product were carried at Shanghai Sangon Biological Engineering Technology & Services Co., Ltd (China). Sequences derived from this study were deposited in GenBank.

7.2.3 Phylogenetic Analysis

Blast searches were made to identify the closest matches in GenBank (Table 7.1) and recently published sequences. Combined analysis of LSU and ITS sequences of 39 taxa of *Discostroma* (7), *Sarcostroma* (2) and *Seimatosporium* (29) were used to confirm the phylogenetic placement of our three strains, with *Pseudopestalotiopsis theae* (MFLUCC 12-0055) as the outgroup taxon. Sequence data were optimized manually to allow best alignment and maximum sequence similarity as detailed in Maharachchikumbura et al. (2012). A maximum parsimony analysis (MP) was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford, 2002). Ambiguously aligned regions were excluded and gaps were treated as missing data. The trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Maxtrees were setup to 5000, branches of zero length were collapsed and all multiple parsimonious trees were saved. Descriptive tree statistics for parsimony Tree Length [TL], Consistency Index [CI], Retention Index [RI], Relative Consistency Index [RC] and Homoplasy Index [HI] were calculated for the Maximum Parsimonious Tree (MPT). The robustness of the most parsimonious trees was evaluated by 100 bootstrap replications resulting from maximum parsimony analysis, each with ten replicates of random stepwise addition of taxa (Felsenstein, 1985). The Kishino-Hasegawa tests (KHT) (Kishino & Hasegawa, 1989) were performed to determine whether the trees were significantly different. Trees were viewed in TreeView v.1.6.6 (Page, 1996)

In addition, Bayesian Analyses (BA) were performed using MrBayes 3.2.0 (MrBayes v. 3.2.1; Ronquist et al., 2012). Suitable models for the Bayesian analysis were first selected using models of nucleotide substitution for each gene, as determined using MrModeltest v. 2.2 (Nylander, 2004), and included for each gene partition. The analyses of four Markov Chain Monte Carlo (MCMC) chains were run from random trees for 1,000,000 generations and sampled every 100 generations. The temperature

value was lowered to 0.15, burn-in was set to 0.10, and the run was automatically stopped as soon as the average standard deviation of split frequencies reached below 0.01.The resulting trees were printed with FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/).

Table 7.1 GenBank Accession numbers of the sequences used in phylogenetic analysis

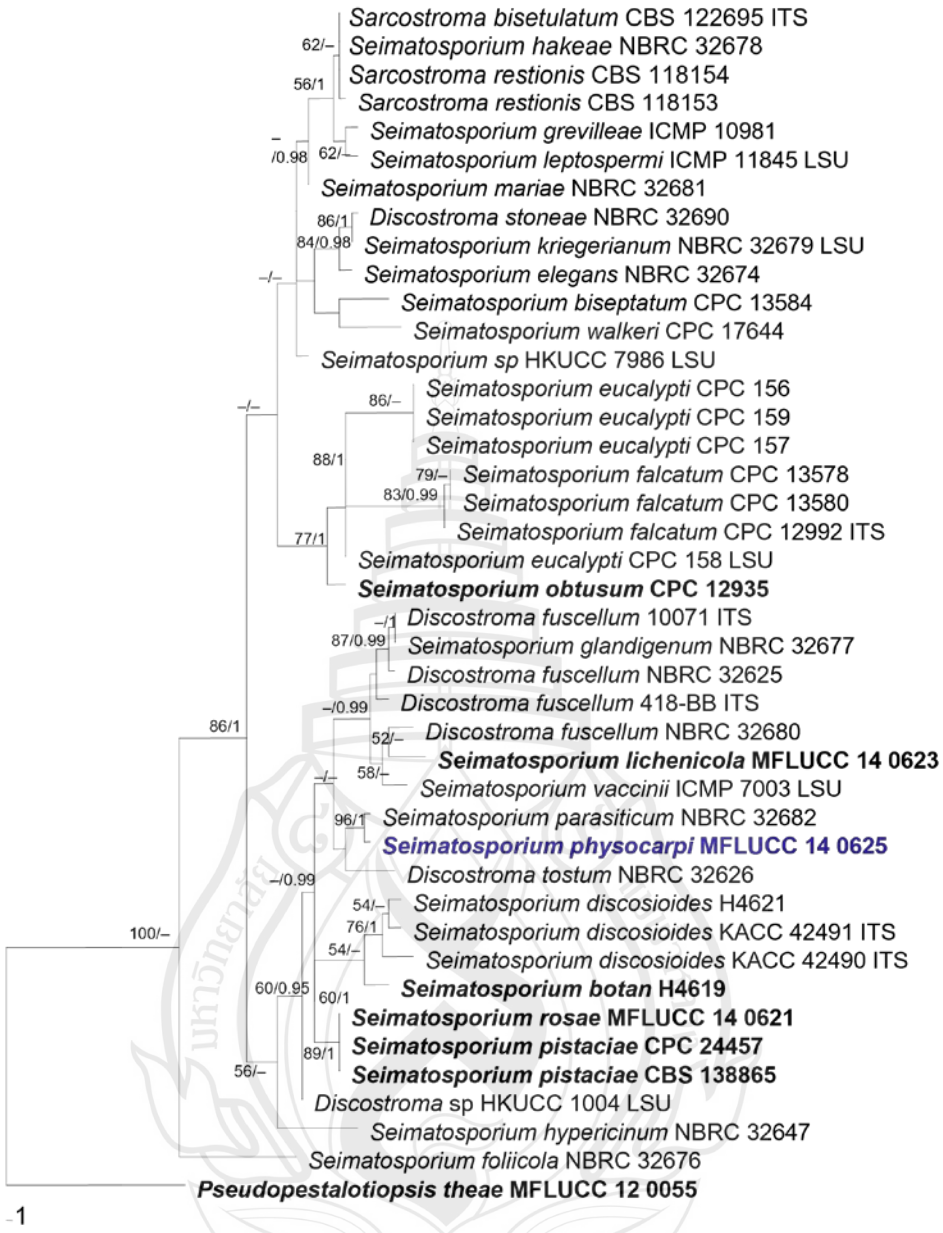
Taxon name	**Strain number**	**GenBank Acc. No.**	
		LSU	**ITS**
Discostroma fuscellum	NBRC 32625	AB593726	AB594794
	NBRC 32680	AB593739	AB594806
	10071	–	AF377284
	418-BB	–	GU244511
Discostroma sp.	HKUCC 1004	AF382380	–
Discostroma stoneae	NBRC 32690	AB593729	AB594797
Discostroma tostum	NBRC 32626	AB593727	AB594795
Pseudopestalotiopsis theae	MFLUCC 12-0055	KM116282	JQ683727
Sarcostroma bisetulatum	CBS 122695	–	EU552155
Sarcostroma restionis	CBS 118153	DQ278925	DQ278923
	CBS 118154	DQ278924	DQ278922
Seimatosporium biseptatum	CPC 13584	JN871208	JN871199
Seimatosporium botan	H4619	AB593731	AB594799
Seimatosporium discosioides	H4621	AB593732	AB594800
	KACC 42490	–	EF600969
	KACC 42491	–	EF600970
Seimatosporium elegans	NBRC 32674	AB593733	AB594801
Seimatosporium eucalypti	CPC 156/ CBS 115131	JN871209	JN871200
	CPC 157/ CBS 110733	JN871210	JN871201
	CPC 158/ CBS 110734	JN871211	–
	CPC 159/ CBS 114876	JN871212	JN871202

Table 7.1 (continued)

Taxon name	Strain number	GenBank Acc. No.	
		LSU	ITS
Seimatosporium falcatum	CPC 13580	JN871214	JN871205
	CPC 12992	–	JN871203
	CPC 13578	JN871213	JN871204
Seimatosporium foliicola	NBRC 32676	AB593734	AB594802
Seimatosporium glandigenum	NBRC 32677	AB593735	AB594803
Seimatosporium grevilleae	ICMP 10981	AF382372	AF405304
Seimatosporium hakeae	NBRC 32678	AB593736	AB594804
Seimatosporium hypericinum	NBRC 32647	AB593737	AB594805
Seimatosporium kriegerianum	NBRC 32679	AB593738	–
Seimatosporium leptospermi	ICMP 11845	AF382373	–
Seimatosporium lichenicola	MFLUCC 14-0623	KT198725	KT198724
Seimatosporium mariae	NBRC 32681	AB593740	AB594807
Seimatosporium obtusum	CPC 12935	JN871215	JN871206
Seimatosporium parasiticum	NBRC 32682	AB593741	AB594808
Seimatosporium physocarpi	MFLUCC 14-0625	KT198723	KT198722
Seimatosporium pistaciae	CPC 24455/ CBS 138865	KP004491	KP004463
	CPC 24457	KP004492	KP004464
Seimatosporium rosae	MFLUCC 14-0621	KT198727	KT198726
Seimatosporium sp.	HKUCC 7986	AF382375	–
Seimatosporium vaccinii	ICMP 7003	AF382374	–
Seimatosporium walkeri	CPC 17644	JN871216	JN871207

Note CBS: Culture collection of the Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands; CPC: Culture collection of Pedro Crous, housed at CBS; H: Finnish Museum of Natural History (University of Helsinki), HKUCC: The University of Hong Kong Culture Collection, Hong Kong, China; ICMP: International Collection of Microorganisms from Plants,

Auckland, New Zealand; KACC: Korean Agricultural Culture Collection, National Institute of Agricultural Biotechnology, Korea; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; NBRC: Biological Resource Center, National Institute of Technology and Evaluation, Chiba, Japan; LSU: large subunit (28S) of the nrRNA gene operon; ITS: internal transcribed spacers and intervening 5.8S nrDNA.



Note Maximum Parsimony (MP) majority rule consensus tree for the analyzed *Seimatosporium* isolates based on a combined dataset of LSU and ITS sequence data. MP bootstrap support values higher than 50% and Bayesian posterior probabilities (PP) above 95% are given at the nodes (MP/PP). The tree is rooted with *Pseudopestalotiopsis theae* (MFLUCC 12−0055). The strain numbers are mentioned after the species names. New strains are in blue bold and ex-type strains are in black bold.

Figure 7.1 Phylogenetic analysis of the *Seimatosporium*

7.3 Results

7.3.1 Phylogenetic Analyses

The combined LSU and ITS alignment was used to resolve the species relationships in *Seimatosporium*. The phylogenetic analyses were obtained from maximum parsimony (MP) and Bayesian analyses. The alignment comprised 42 taxa and 1300 total characters including gaps. Parsimony analyses indicate that 1140 characters were constant, 73 variable characters were parsimony-uninformative and 87 characters were parsimony informative. The parsimony analysis of the data matrix resulted in two equally parsimonious trees and in the first tree (TL= 288, CI=0.670, RI = 0.814, RC = 0.546, HI = 0.330) is shown here. The Bayesian analysis resulted in a tree with the same topology as the MP trees. The phylogenetic results from Figure 7.1 are discussed in the descriptive notes and discussion below.

7.3.2 Taxonomy

Seimatosporium lichenicola (Corda) Shoemaker & E. Müll., Can. J. Bot. 42: 405 (1964), Figure 7.2

Faces of fungi numbers: FoF00793

Asexual morph: *Discostroma fuscellum* (Berk. & Broome) Brockmann 1976

Saprobic and parasitic on dying twigs, leafstalks and leaves, sometimes on living leaves of *Cotinus coggygria* Scop. Sexual morph: Undetermined. Asexual morph: *Conidiomata* 400–600 µm diam. pycnidial, solitary, immersed, unilocular, brown, with a conspicuous apex. *Pycnidial wall* (30–50 µm) multilayered, comprised of light brown-walled cells of *textura angularis*, with inner most layer thin, hyaline. *Conidiophore*s reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, phialidic, hyaline, smooth, formed from the inner most layer of pycnidium wall. *Conidia* (10–)12–14 × 4–5(–6) µm ($\overline{x}$ = 12 × 5 µm, n = 30), initially hyaline, pale brown to dark brown at maturity, fusiform, straight , infrequently slightly curved, with 3 transverse septa, not constricted at the septa, narrowly rounded at both ends, smooth-walled, with thick walls pale brown to dark brown at maturity, narrowly rounded at both ends, smooth-walled, basal cell conic to obconic with a truncate base, subhyaline, 2.5–4 μm long ($\overline{x}$ = 3.5 µm), with two median cells subcylindrical to doliform, with

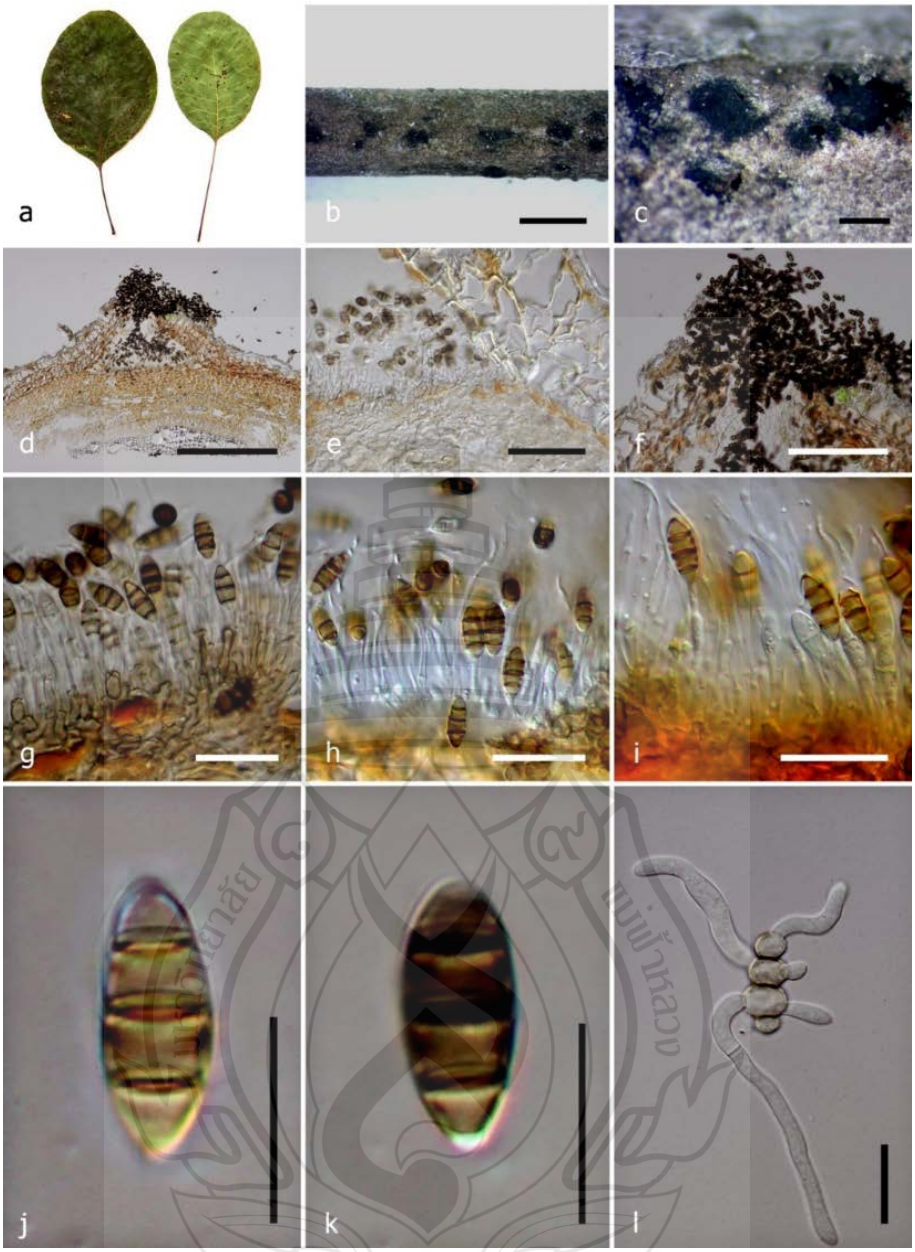
thick verruculose walls, brown to dark brown, 7.5–8 μm long ($\overline{x}$ = 7.5 µm), with apical cell conical and rounded at apex, hyaline, cylindrical to subcylindrical, 3.5–4 μm long ($\overline{x}$ = 3.5 µm)

Culture characters: Colonies on PDA slow growing, reaching 2 cm diam. after 5 days at 25 °C, circular, spreading, with flat mycelium, with fimbriate margins, pale yellow clusters forming in the centre of colonies after 2 days, clustered or effuse in centre of colony, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Oktyabrsky District, Persianovsky Arboretum, on live leaves and dying branches of *Cotinus coggygria* Scop, 4 June 2014, T. Bulgakov T−095 (MFLU 14−0773, reference specimen of *Seimatosporium lichenicola* designated here), living culture, MFLUCC 14−0623, CBS 139966.

Notes: *Seimatosporium lichenicola* was introduced by Shoemaker and Müller (1964) as the sexual morph of *Clethridium corticola* (Fuckel) Shoemaker & E. Müll. The species was described as coelomycetous, producing clavate, mostly 3 transversely septate, non-seteferous conidia. Sutton (1980) reported *S. lichenicola*, with 13–15 × 5.5–6.5 µm, 3-septate, fusiform conidia, which lack appendages. Nag Raj (1993) transferred *S. lichenicola* to *Sporocadus*. The type was from *Rosa canina*, in Lobkowitschen gardens in Prague, Czechoslovakia. Tanaka et al. (2011) reviewed these four genera and as none had a reported sexual morph, they were synonymized under *Seimatosporium*. The sexual morph of *S. lichenicola* is reported to be *Discostroma fuscellum* based on phylogenetic data (Tanaka et al., 2011).

Our collection is consistent with the reports of Shoemaker and Müller (1964), Sutton (1980), Nag Raj (1993) and Tanaka et al. (2011), whereas our collection differs in being found on dead branches of *Cotinus coggygria* in Russia. Based on these findings, we name our collection as *S. lichenicola*. Molecular analyses show our strain to cluster with *Discostroma fuscellum* which is the sexual morph of *S. lichenicola* (Figure 7.1) (Tanaka et al., 2011; Nag Raj, 1993). Sequence data for *S. lichenicola* is not available in GenBank and therefore, we designate our collection as a reference specimen. We do not designate an epitype as the host is different (Ariyawansa et al., 2014).



Note *Seimatosporium lichenicola* (MFLUCC 14-0623). a Leaf spot disease on *Cotinus coggygria* leaf. b Habit on wood. c Fruiting bodies on substrate. The blackened areas are the conidia masses. d Cross section of the conidioma. e Pycnidial wall. f Apex of conidioma. g, h, i Conidiogenous cells. j, k Mature conidia. l Germinating spore on PDA. Bars: d = 300 µm; e = 50 µm; f = 100 µm; g, h, i, l = 20 µm; j, k = 10 µm.

Figure 7.2 Morphological characters of *Seimatosporium lichenicola* (MFLUCC 14-0623)

Seimatosporium physocarpi Norphanphoun, Bulgakov & K.D. Hyde, sp. nov., Figure 7.3

Index Fungorum Number: IF551287

Faces of fungi number: FoF00794

Etymology: *Physocarpi*, refers to the the host genus from which this species was collected.

Holotypus: MFLU 14-0775.

Parasitic (necrotrophic) and saprobic on leaves (leaf spot), twigs and fruits of *Physocarpus opulifolius*. Sexual morph: Undetermined. Asexual morph: *Conidiomata* stromatic, erumpent, initially subglobose, becoming cornuted with an obtuse or subcylindrical head and a broad stalk, up to 350–900 µm diam, 400–900 µm high, globose, pale brown to brown, dehiscing by a rupture in the overlying host epidermis and covered with dark brown conidial masses. *Pycnidial wall* basal stroma up to 200 µm thick, with cell of *textura angularis*, moderately thick-walled, hyaline. *Conidiophores* arising from the upper cells of the basal stroma, branched, hyaline, smooth, up to 20 µm long, invested in mucus. *Conidiogenous cells* lageniform to subcylindrical with moderate apical periclinal thickening, hyaline, smooth, formed from the inner most layer of pycnidial. *Conidia* (10–)15–16 × 3.5–4.8(5) µm ($\overline{x}$ =13 × 4.1 µm, n = 30), hyaline to slightly olivaceous, fusiform, straight to slightly curved, 3–septate, basal cell conic to obconic, slightly olivaceous, thin-walled and verruculose, 2–3 µm long ($\overline{x}$ =2.5 µm), with two median cells, doliiform to cylindrical, with thick verruculose walls, constricted at the septa, concolourous, olivaceous, with septa and periclinal walls darker than the rest of the cell, together 5.5–8 µm long ($\overline{x}$ = 6.75 µm), second cell from base 3.5–4 µm ($\overline{x}$ = 3.7 µm); third cell 2–3.5 µm ($\overline{x}$ = 2.75 µm); apical cell hyaline, cylindrical to subcylindrical 2–3 µm long ($\overline{x}$ = 2.5 µm); with 1 tubular apical appendage, arising from the apex of the apical cell, 7–12 µm long ($\overline{x}$ = 9.5 µm), unequal in length; basal appendage present, rarely one, 12– 14 µm long ($\overline{x}$ = 13 µm).

Culture characteristics: Colonies on PDA slow growing, reaching 2.5 cm diam. after 7 days at 25 °C, later producing dense mycelium, circular, erumpent, spreading, fluffy, with moderate aerial mycelium and smooth, margins lobate, pale yellow in the

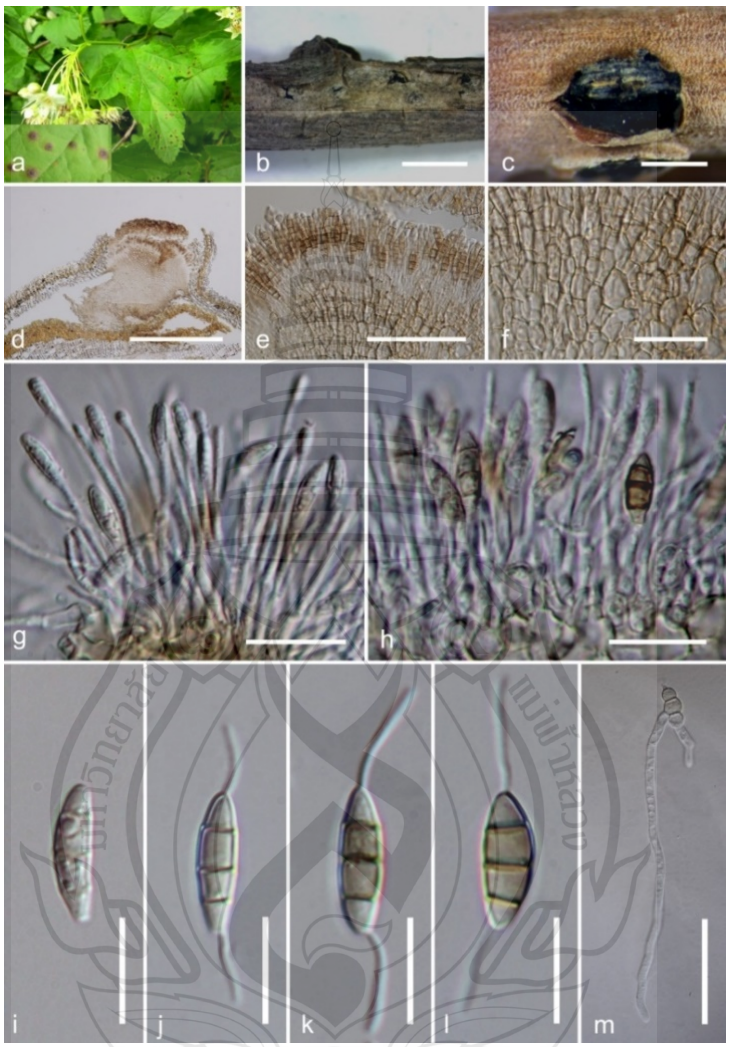
centre of the colony after 4 days, clustered or effuse on center of colony surface, without aerial mycelium.

Material examined: RUSSIA, Rostov Region, Rostov-on-Don city, Botanical Garden of Southern Federal University, Systematic Arboretum, on dead branches of *Physocarpus opulifolius* (L.) Maxim (host family), 8 May 2014, T. Bulgakov T-126 (MFLU 14−0775, holotype); *Ibid.* (PDD, isotype); ex-type living culture, MFLUCC 14−0625, CBS 139968.

Notes: In the phylogenetic tree (Figure 7.1), *S. physocarpi* clustered in the same clade with *S. parasiticum*, *Discostroma tostum* (*S. passerinii*), *S. lichenicola* (*D. fuscellum*), *S. glandigenum* and *S. vacinii*. However, the conidia of *S. passerinii*, *S. lichenicola*, *S. glandigenum* and *S. vacinii* lack appendages, while only *S. parasiticum* has apical and basal appendages (Nag Raj, 1993). Therefore, our species morphologically closely resembles *S. parasiticum*. *Seimatosporium parasiticum* was described from leaves of *Physocarpus opulifolius* (Rosaceae) from Germany (Sutton, 1980). However, *S. physocarpi* can be distinguished by its smaller conidial dimensions (10–16 × 3.5–4.8 µm in *S. physocarpi*, 22–35 × 5–7 µm in *S. parasiticum*) and *S. physocarpi* has longer apical (7–12 µm versus 2–5 µm) and longer basal appendages (12–14 µm versus 2–8 µm) than *S. parasiticum* (Sutton, 1980). Our new species has 3-septate conidia and occurs in European Russia (and Eastern Europe). It is distinct from *S. parasiticum* which occurs in Central Europe, and has 3–5-septate (mostly 5–septate) and often irregularly curved conidia (Sutton, 1980; Tomoshevich, 2012). A detailed morphology comparison of the related species with the new species is provided in Table 7.2.

This species is parasitic usually causes leaf spots of *Physocarpus* species, and also grows on dead twigs as with many necrotrophic fungi. *Seimatosporium* species found on *Physocarpus* spp. in some regions of European Russia (Moscow and Moscow region, St.-Petersburg and Leningrad region, Rostov region, Krasnodar region) and Asian Russia (Western Siberia, Novosibirsk region) (Bulgakov et al., 2014; Tomoshevich, 2012). In some reports, the *Seimatosporium* species on *Physocarpus* were reported as *Seimatosporium lonicerae* (Cooke) Shoemaker, but this species is distinct from *S. physocarpi* by occasionally having 2-septate conidia, with mostly a

single basal appendage, and sometimes with a shorter apical appendage (Melnik, 1997; Nag Raj, 1993).



Note *Seimatosporium physocarpi* (MFLU 14-0775, holotype) a Leaf spot disease on *Physocarpus opulifolius* leaf. b Stromatal habit in wood. c Fruiting bodies on host substrate. d Cross section of the stroma showing perithecia. e, f Peridium. g, h Conidiogenous cells. i Immature conidia. j, k, l Mature conidia. m Germinating spore on PDA. – Bars: c = 600 µm; d = 300 µm; e, m = 50 µm; f= 20 µm; g, h = 15 µm; i, j, k, l = 10 µm.

Figure 7.3 Morphological characters of *Seimatosporium physocarpi* (MFLU 14-0775, holotype)

Seimatosporium rosae Corda, in Sturm, Deutschl. Fl., 3 Abt. (Pilze Deutschl.) 3(13): 79 (1833), Figure 7.4

Index Fungorum Number: IF190497

Epitypification identifier: IF551303

Faces of fungi numbers: FoF00795

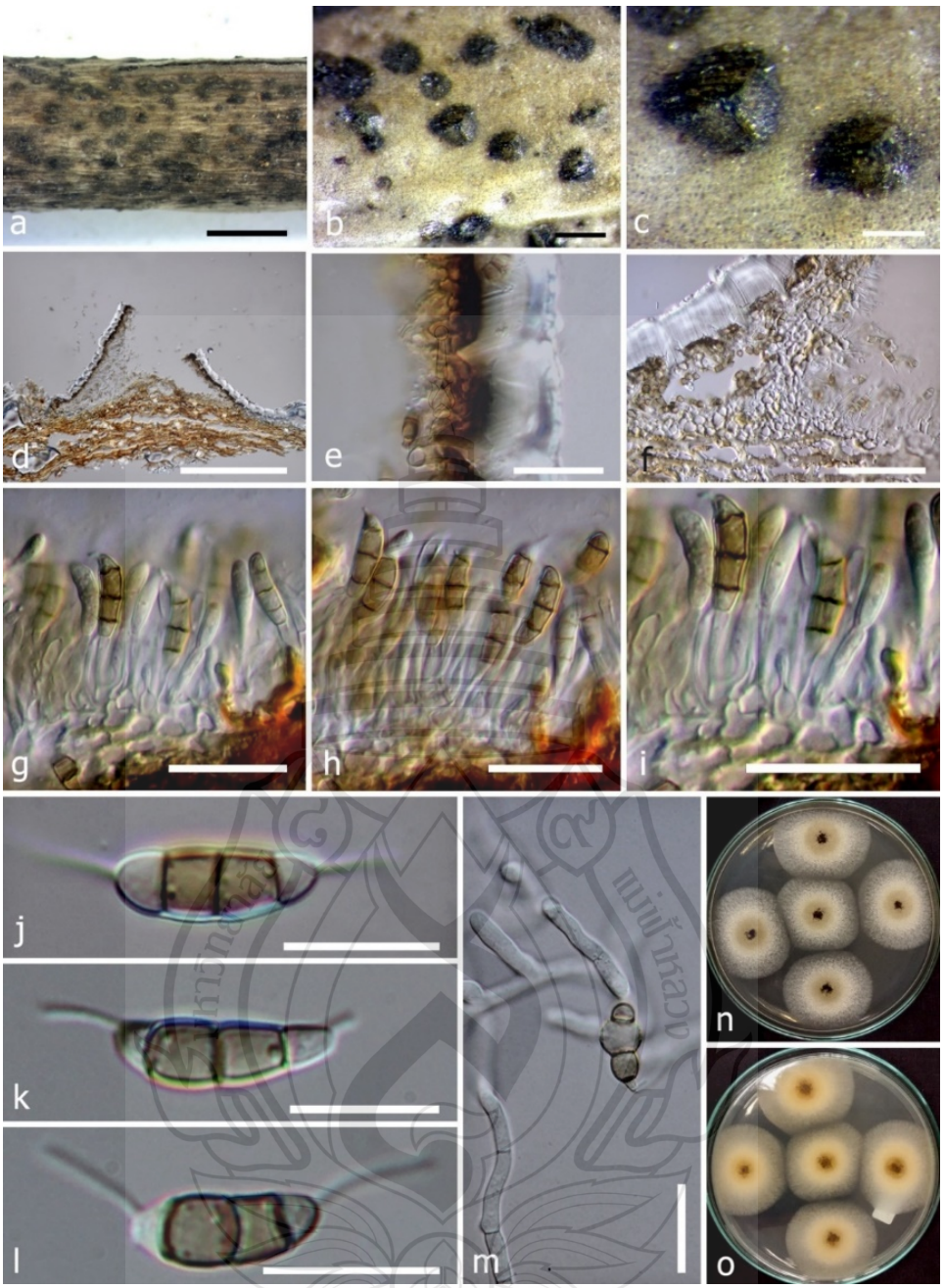
Saprobic and weak parasitic on dead and dying branches of *Rosa kalmiussica* Chrshan. & Lasebna (this species often includes in *Rosa canina* sensu lato) Sexual morph: Undetermined. Asexual morph: *Conidiomata* acervular, intra-epidermal, 250–400 µm diam., 150–170 µm high, unilocular, glabrous, brown, dehiscing by irregular split in the overlying host tissue; basal stroma thin, with cells moderately thick-walled, almost colourless at the base, pale brown in the lateral tissue and cells of *textura angularis*. *Conidiophores* arising from the upper cells of the basal and lateral tissue, sparsely septate and branched, colourless, thin-walled, smooth, up to 10 µm long. *Conidiogenous cells* lageniform to cylindrical, colourless, thin-walled,smooth, formed from the inner most layer of pycnidium wall. *Conidia* (11–)12–15 × 3.5–4.5(–5) µm ($\overline{x}$ = 13.5 × 4.5 µm, n = 30), hyaline or slightly olivaceous, fusiform, straight to slightly curved, 3-septate, basal cell conic to obconic, thin-walled and verruculose, 2–3.5 µm long ($\overline{x}$ = 3µm), with two median cells, doliiform to cylindrical, with thick verruculose walls, constricted at septa, concolourous, olivaceous, with septa and periclinal walls darker than the rest of the cell, together 5–7 µm long ($\overline{x}$ = 17 µm) second cell from base 3–4.5 µm ($\overline{x}$ = 4 µm); third cell 3–4 µm ($\overline{x}$ = 3.5 µm); apical cell hyaline, cylindrical to subcylindrical 2.5–4 µm long ($\overline{x}$ = 3.25 µm); with 1 tubular apical appendage, arising from the apex of the apical cell, 5–10(–10.4) µm long ($\overline{x}$ = 8 µm), unequal in length; basal appendage present, 5–7(–8) µm long ($\overline{x}$ = 5.5 µm).

Culture characteristics: Colonies on PDA slow growing, reaching 3 cm diam. after 13 days at 25 °C, later producing dense mycelium, circular, rough margin white at first with dark green clusters in the center of the colony after 5 days, clustered or effuse on center of colony surface, without aerial mycelium. Hyphae septate branched, hyaline, thin.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye Forestry, edge of ravine forest, on dying and dead branches of *Rosa kalmiussica* Chrshan. & Lasebna, 21 May 2014, T. Bulgakov T−056 (MFLU 14-0771,

epitype of *Seimatosporium rosae* designated here); living cultures MFLUCC 14-0621, CBS 139823.

Notes: *Seimatosporium rosae* is the generic type and was found on *Rosa* sp. in Slovakia. Our isolate was collected on *Rosa kalmiussica* Chrshan. & Lasebna from the Rostov Region of Russia and has the same conidial size range (11–15 × 3.5–5 µm) and same host as *S. rosae*, which is consistent with reports of Sutton (1980), and Nag Raj (1993). In molecular analyses (Figure 7.1), our isolate clusters together with *S. pistaciae*, a species introduced by Crous and Mirab (2014) from buds of *Pistacia vera* from Iran. Although, *S. pistaciae* morphologically closely matches *S. rosae*, Crous & Mirab distinguished these taxa, the former having larger conidia (15–22 × 4–5 µm, Crous et al., 2014). We designate our collection of *S. rosae* as an epitype specimen (sensu Ariyawansa et al., 2014) as was collected on it same host in Europe.



Note *Seimatosporium rosae* (MFLUCC 14-0621, epitype). a Habit in wood. b, c Fruiting bodies on host substrate. d Cross section of fruiting body. e, f Peridium. g, h, i Conidiogenous cells. j, k, l Mature conidia. m Germinating spore on PDA. n from above. o from below. Bars: c = 200 µm; d = 300 µm; e, g, h, i, m = 20 µm; f= 50 µm; j, k, l = 10 µm.

Figure 7.4 Morphological characters of *Seimatosporium rosae* (MFLUCC 14-0621, epitype)

7.4 Discussion

The genus *Seimatosporium* previously belonged in the family *Amphisphaeria--ceae* (Shoemaker & Müller, 1964; Brockmann, 1976; Paulus et al., 2006; Maharachchikumbura et al., 2015) and later transferred to newly introduced *Discosiaceae* (Senanayake et al., 2015). *Amphisphaeriaceae* was established by Winter (1887) as a large heterogeneous family which mainly contains Pestalotiopsis-like asexual morphs (Jeewon et al., 2002). These taxa are characterized by ascomata immersed in the host, with dark peridial walls and asci with amyloid apical apparatii (Barr, 1975b). Their asexual morphs are generally characterized by coelomycetous conidiomata producing septate conidia with filiform apical appendages (Barr, 1990; Nag Raj, 1993). Nag Raj (1993) has reported conidia with pigmented median cells, with or without one apical and basal appendage. The present findings that species of *Vermisporium*, characterized by their falcate to elongate-fusiform conidia with pigmented cells, a beak-like apical cell, and a podiform, tubular, unbranched, eccentric basal appendage, clustering in *Seimatosporium* was rather unexpected. Nag Raj (1993) has reported that one of the main characters used for distinguishing species was the length to width ratio, even though this had previously been found to be inadequate (Swart & Williamson, 1983). The taxonomy has traditionally placed a great deal of emphasis on length and width of conidia, while distinguishing species in *Pestalotiopsis* (Jeewon et al., 2003), and *Seimatosporium*, as a genus sharing many similarities. Spore length has been used as a key character, with many new species of *Pestalotiopsis* being described based on subtle differences in spore size (Mordue, 1985, 1986; Nag Raj, 1985, 1986; Venkatasubbaiah et al., 1991). Further, this finding also questions the value of appendage type *sensu* Nag Raj (1993) as informative features at generic level.

Sutton (1980) treated *Seimatosporium* as heterogeneous with a broad concept. However, Nag Raj (1993) segregated *Seimatosporium* in to five genera based on the conidial morphology. Therefore, the generic concept of *Seimatosporium* remains unresolved and this was discussed by Tanaka et al. (2011) with the support of molecular data. In their study, Tanaka et al. (2011), included isolates representing all the five genera discussed by Nag Raj (1993) and strains representing *Seimatosporium sensu*

stricto. They observed that all *Seimatosporium* species and *Discostroma* sexual morphs clustered in a monophyletic group, but with several subgroups among the *Seimatosporium sensu lato* clade. These may be related to the colour of median cells and may have taxonomic value. For example, in the present study, the clade represented by *Sarcostroma bisetulatum, S. restionis, Seimatosporium hakeae, S. grevilleae, S. leptospermi* and *S. mariae* has coloured median cells. Its sister clade represented by *Seimatosporium kriegerianum, S. elegans, S. biseptatum, Seimatosporium walkeri, S. eucalypti S. falcatum* and *S. obtusum* however, have hyaline median cells. The colour of the median cells in *Pestalotiopsis* (*Amphisphaeriales*) has been shown to have taxonomic value, and based on pigmentation the genus was segregated in *Pestalotiopsis, Neopestalotiopsis* and *Pseudopestalotiopsis* (Maharachchikumbura et al., 2014). The same approach may helpful in the subdivision of *Seimatosporium*. However, further sampling of more genera/species, fresh collection with type strains, and establishing asexual and sexual morph connections are required for reassessment of this genus complex. In addition, species of *Discostroma* and *Seimatosporium* have been linked by molecular data (Tanaka et al., 2011), however the molecular links have not been shown for the types of either genera. Both names should therefore be retained pending fresh collections of the types and further molecular study (Maharachchikumbura et al., 2015).

In the present study, combined LSU and ITS alignment is used to resolve species relationships in *Seimatosporium* (Figure 7.1), following (Tanaka et al., 2011). The phylogenetic tree shows that our collection clearly groups with *Seimatosporium*. The application of molecular data can provide reliable genetic evidence to define species boundaries in taxonomic studies, as shown in this study. Combined multi-gene data phylogenies can better resolve the taxonomy of genera such as *Seimatosporium* (Tanaka et al., 2011).

Seimatosporium species are common as saprobes and pathogens on plants, but are not considered to be destructive foliar pathogens. For example, *Vermisporium acutum* (≡ *Seimatosporium acutum*), was found on a single necrotic lesion on *Eucalyptus nicholii* leaves (Barber et al., 2003). Species of *Seimatosporium* have been reported from necrotic spots and associated with disease on branches, twigs, leaves and fruits (Bulgakov et al., 2014). *Seimatosporium physocarpi* causes leaf spots and grows

on living and dying branches. Thus, the *Seimatosporium* species in this study cannot be considered as saprobic in nature. In temperate arid climate zones, many necrotrophic fungi are specific on host-plants and grow during the cold and wet seasons. Endophytes, may mostly be pathogens, but they often may be treated as saprobes by mycologists, because during the summer they can only be found on dead branches (Bulgakov et al., 2014). Leaf spots of eucalyptus caused by *Vermisporium* have been reported from the Southern Hemisphere (Barber et al., 2011), while *Vermisporium quercinum* was found on the bark of *Quercus suber* (*Fagaceae*) in Sardinia, Italy (Franceschini et al., 1995). *Vermisporium tenzingii* was reported from leaves of *Osbeckia crinita* from Darjeeling, India and *Osbeckia stellata* in Kaltani, Nepal (Wu & Sutton, 1996). Some species such as S. *brevicentrum* and *S. eucalypti* were associated with insect damaged leaves, presumably as secondary invaders of leaf tissue damaged previously by insects or as endophytes sporulating in necrotic tissues (Barber et al., 2011). These results suggest that species of *Seimatosporium* are not likely to be a serious commercial problem.

Table 7.2 Synopsis of morphological features of species of *Seimatosporium* (Related to this research)

Species	Host	Conidiomata (µm)	Conidia					Reference
			Septate	Conidia size (µm)	Two median cell (µm)	Apical appendage (µm)	Basal appendage (µm)	
Seimatosporium botan	*Paeonia suffruticosa* (stems)	–	3 septate	16–20 × 4–5	8–11	4–8	4–8	Duan et al. (2011)
S. discosioides	*Rosa heliophila* (leaves)	100–200	3 septate	11.5–18 × 3.5–5	7.5–10	2–7	2–6	Sutton (1980)
S. glandigenum	*Quercus ballota*,	>250	3 septate	15–18 × 5–6.5	7.5–10	None	None	Sutton (1980)
S. lichenicola	*Rosa* sp.	>350	3 septate	13–15 × 5.5–6.5	–	None	None	Sutton (1980)

Table 7.2 (continued)

Species	Host	Conidiomata (µm)	Conidia					Reference
			Septate	Conidia size (µm)	Two median cell (µm)	Apical appendage (µm)	Basal appendage (µm)	
S. lonicerae	*Physocarpus opulifolius* (twigs)	150	2–3 septate	11–19 × 3–5	6.5–10	4–10	2–9	Sutton (1980)
S. lichenicola (MFLUCC 14-0623)	*Cotinus coggygria* (dying branches, live leaves)	400–600	3 septate	(10–)12–14 × 4–5(–6)	7.5–8	None	None	In this study
S. parasiticum	*Physocarpus opulifolius* (leaves)	>100	3–5 septate	24–31 × 4.5–6.5	17–24	1–8.5	1.5–9	Sutton (1980)

Table 7.2 (continued)

Species	Host	Conidiomata (µm)	Conidia					Reference
			Septate	Conidia size (µm)	Two median cell (µm)	Apical appendage (µm)	Basal appendage (µm)	
S. passerinii	*Epilobium fleischeri*	400–800	3 septate	14–20 × (3–2)–4	–	10–18	None	Syndowia, 28: 320
S. physocarpi (MFLUCC 14-0625)	*Physocarpus opulifolius* (leaves, twigs and fruits)	350–900	3 septate	(10–)15–16 × 3.5–4.8 (5)	5.5–8	7–12	12–14	In this study
S. pistaciae	*Physocarpus opulifolius* (bud)	>150	4 septate	(15–)17–20(–22) × (4–)4.5(–5)	–	10–14	12–20	Persoonia 33 (2014)

Table 7.2 (continued)

Species	Host	Conidiomata (µm)	Conidia					Reference
			Septate	Conidia size (µm)	Two median cell (µm)	Apical appendage (µm)	Basal appendage (µm)	
S. rosae	*Rosa kalmiussica* Chrshan. & Lasebna	250–400	3 septate	12.5–16.5 × 3.5–4	7-10	11-20	9-19	Nag Raj (1993)
				10–15 × 3–4	5–9	1–6.5	1–8	Sutton (1980)
S. rosae (MFLUCC 14–0621)	*Rosa* sp. (branches)	250–400 × 150–170	3 septate	(11–)12–15 × 3.5–4.5(–5)	5–7	5–10(–10.4)	5–7(–8)	In this study
S. vaccinii	*Vaccinium myrtillus*	>100	3 septate	13–18 × 4.5–5.5	–	None	None	Sutton (1980)

Note "–" no result.

CHAPTER 8

LAMPROCONIACEAE FAM. NOV. TO ACCOMMODATE *LAMPROCONIUM DESMAZIERI*[7]

Abstract

The genus *Lamproconium* comprises species that are endophytes, saprobes and pathogens on a wide variety of plants. This genus is currently placed in Diaporthales genera *incertae sedis*. Fresh specimens of *Lamproconium* were collected in Russia and studied to provide morphological and phylogenetic data. Phylogenetic analyses of single spore isolates generated from maximum likelihood, maximum parsimony and Bayesian inference analyses using combined ITS and LSU sequence data, place *L. desmazieri* in the order Diaporthales. *Melanconis desmazieri* is synonymized under *Lamproconium desmazieri*, and Lamproconiaceae is introduced as a new family to accommodate *L. desmazieri* and *Hercospora tiliae*, based on morphology and phylogenetic analyses.

Keywords: Foliar pathogens, genera *incertae sedis*, morphological data, phylogenetic analyses, synonym

[7]This paper has been published in *Phytotaxa*, 2016, *270*(2), 089–102. http://dx.doi.org/10.11646/phytotaxa.270.2.2

8.1 Introduction

Lamproconium (Grove) Grove was introduced as a monotypic genus by Grove (1937) to accommodate *L. desmazieri* (Berk. & Broome) Grove, and was placed in genera *incertae sedis* in the order Diaporthales by Cannon and Minter (2014). This genus is apparently a saprobe with an endophytic lifestyle, or vice versa. Some authors, however, have considered a few species in this genus to be plant pathogens (Grove, 1937; Cannon & Minter, 2014; Sutton, 1980).

The type species of *Lamproconium*, originally described as *Discella desmazieri* Berk. & Broome, was collected from twigs of lime (*Citrus aurantiifolia*) in the UK (Berkeley & Broome, 1850). Grove (1918) transferred the species to *Melanconium* in the subgenus *Lamproconium* as *Melanconium desmazieri* (Berk. & Broome) Sacc. Subsequently, Grove (1937) found that *M. desmazieri* differed from the type species of *Melanconium* (*M. atrum* Link) in having bluish to glistening or dark blue, but not brownish black, 1-septate conidia and accordingly re-circumscribed the species. *Melanconium desmazieri* differed from species of *Discella* by the absence of a true peridium, whereas *Discella* species have a proliferous stratum at the base. Grove (1937) therefore considered *Discella desmazieri* and *Melanconium desmazieri* as conspecific and introduced a new genus *Lamproconium* to accommodate this taxon (Grove, 1937; Sutton, 1980).

Melanconium has been reported as the asexual morph of *Melanconis* Tul. & C. Tul. (Sutton, 1980). The genus *Melanconis* belongs in the family Melanconidaceae in Diaporthales, Sordariomycetes (Maharachchikumbura et al., 2015, 2016). Castlebury et al. (2002) used LSU sequence data from *M. stilbostoma* (Fr.) Tul. & C. Tul., the type species of *Melanconis*, plus *M. alni* Tul. & C. Tul. and *M. marginalis* (Peck) Wehm. in a phylogenetic analysis and showed that *Melanconis desmazieri* Petr. clustered with *Hercospora tiliae* Tul. & C. Tul. However, the group clustered distantly from the family Melanconidaceae. Thus, Castlebury et al. (2002) placed *Melanconis desmazieri* and *Hercospora tiliae* in *Melanconis sensu lato* as genera *incertae sedis* in Diaporthales. This taxonomic treatment was followed by Voglmayr et al. (2012), Voglmayr and Jaklitsch (2014) and Maharachchikumbura et al. (2015, 2016).

Hercospora tiliae differs from *Melanconis desmazieri* in having ellipsoidal to cylindric-ellipsoidal, aseptate, hyaline conidia, while the sexual morph has ellipsoidal to cylindrical, hyaline, 1-septate ascospores (Tulasne & Tulasne, 1863; Petrak, 1938; Sutton, 1980). In *M. desmazieri* conidia are oblong-fusoid, straight, at first acute, and later becoming obtuse at one or both ends (Petrak, 1938; Castlebury et al., 2002; Voglmayr et al., 2012; Voglmayr & Jaklitsch, 2014).

In this study, we provide morphological and phylogenetic data for *Lamproconium* based on five specimens collected in Russia. Furthermore, *Melanconis desmazieri* is synonymized under *Lamproconium desmazieri* based on morphological characters and multi-locus phylogenetic analyses. These taxa form a distinct lineage in Diaporthales and therefore we introduce the family Lamproconiaceae to accommodate them.

8.2 Materials and Methods

8.2.1 Sample Collection and Examination of Specimens

The samples were collected from dead branches of Tilia cordata Mill. in the Rostov region, Russia, in May 2014. The specimens were returned to the laboratory in small paper bags, examined, identified and described following Norphanphoun et al. (2015). Micro-morphological characters were studied using a Motic SMZ 168 dissecting microscope for fungal fruiting bodies. Hand sections of the fruiting structures were mounted in water and examined for morphological details. Fungi were also examined using a Nikon Ni compound microscope and photographed with a Canon EOS 600D digital camera fitted to the microscope. Photo-plates were made by using Adobe Photoshop CS6 Extended version 13.0 × 64 (Adobe Systems, USA), while Tarosoft (R) Image Frame Work program v. 0.9.7 was used for measurements. The contents inside the conidiomata, which comprised conidiophores, conidiogenous cells, conidia and paraphyses, were removed with a sterile needle and soaked in sterile water in a glass container prior to examination.

Cultures were obtained by single spore isolation as described in Chomnunti et al. (2014). Spore germination was observed and photographed using a Nikon Ni

compound microscope fitted with Canon EOS 600D digital camera. Geminated spores were transferred aseptically to fresh malt extract agar (MEA) and incubated at room temperature (18−25°C). Colony characters were observed and measured after one week and also one month.

The Herbarium specimens are deposited in the Mae Fah Luang University Herbarium, Chiang Rai, Thailand (MFLU) and duplicated in New Zealand Fungarium (PDD). Living cultures are deposited at Mae Fah Luang University Culture Collection (MFLUCC) and Kunming Culture Collection (KUMCC). Facesoffungi and Index Fungorum numbers are registered (Jayasiri et al., 2015; Index Fungorum, 2016).

8.2.2 DNA extraction, PCR amplification and sequencing

DNA extraction was performed from fresh fungal mycelia growing on MEA at room temperature (18−25°C) for 3 weeks. The genomic DNA was obtained using a E.Z.N.A.TM Fungal DNA MiniKit (Omega Biotech, CA, USA) following the manufacturer's instructions.

Polymerase chain reactions (PCR) were carried out using primer pairs of ITS5 and ITS4 to amplify the internal transcribed spacer region (ITS1-5.8S-ITS2) (White et al., 1990), and the large subunit rDNA (28S, LSU) was amplified with primers LROR and LR5 (Vilgalys & Hester, 1990). The amplification reaction was performed in 50 µl reaction volume containing 2 µl of DNA template, 2 µl of each forward and reverse primers, 25 µl of 2 × Bench TopTMTaq Master Mix (mixture of Taq DNA Polymerase (recombinant): 0.05 units/µL, MgCl2: 4 mM, and dNTPs (dATP, dCTP, dGTP, dTTP): 0.4 mM) and 19 µl of double-distilled water (ddH2O) (sterilized water). The PCR thermal cycle program for ITS gene amplification were set as: initially 95 °C for 3 min, followed by 30 cycles of denaturation at 95 °C for 1 min, annealing at 51 °C for 1 min, elongation at 72 °C for 45 s, and final extension at 72 °C for 10 min. The PCR thermal cycle program for LSU gene amplification were provided as: initially 95 °C for 3 min, followed by 34 cycles of denaturation at 95 °C for 30 s, annealing at 51 °C for 50 s, elongation at 72 °C for 1 min, and final extension at 72 °C for 10 min. The quality of PCR products were checked by using 1% agarose gel electrophoresis stained with ethidium bromide. Purification and sequencing of PCR product were carried out at Life Biotechnology Co., Shanghai, China.

8.2.3 Phylogenetic analysis

Blast searches were made to identify the closest matches in GenBank and recently published sequences in of Castlebury et al. (2002), Voglmayr et al. (2012), Voglmayr and Jaklitsch (2014) and Maharachchikumbura et al. (2015, 2016). Combined analyses of ITS and LSU sequence data of 62 taxa (Table 8.1) from Diaporthales were downloaded from GenBank and Magnaporthe salvinii (CBS 243.76) and M. grisea (GAD1) were used as outgroup taxa. Additionally, the datasets were optimized manually as detailed in Castlebury et al. (2002), Voglmayr et al. (2012), Voglmayr and Jaklitsch (2014) and Maharachchikumbura et al. (2015, 2016). The combined sequence alignments were obtained from MEGA7 version 7.0.14 (Kumar et al., 2015) and ambiguously aligned regions were excluded, gaps were treated as missing data which performed in BioEdit v. 7.2 (Hall, 1999). Phylogenetic trees were inferred with maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI).

Maximum-likelihood (ML) analysis was performed in RAxML (Stamatakis, 2006) implemented in raxmlGUI v.1.3 (Silvestro & Michalak, 2012). The 1000 rapid bootstrap replicates were run with generalized time reversible GTRGAMMA model of nucleotide substitution and searches for model selected for ML were applied. Trees were visualized using FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/, Rambaut, 2012).

Maximum parsimony (MP) analysis was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford, 2002). The trees were inferred using the heuristic search option with tree bisection-reconnection (TBR) as the branch swapping algorithm and 1000 random sequence additions. Maxtrees were setup to 5000, branches of zero length were collapsed and all multiple parsimonious trees were saved. Descriptive tree statistics for parsimony tree length [TL], consistency index [CI], retention index [RI], rescaled consistency index [RC] and homoplasy index [HI] were calculated for the Maximum Parsimonious Tree (MPT). The robustness of the most parsimonious trees were evaluated by 1000 bootstrap replications, each with ten replicates of random stepwise addition of taxa (Felsenstein, 1985). The Kishino-Hasegawa tests (KHT) (Kishino & Hasegawa, 1989) were performed to determine

whether the trees were significantly different. Trees were viewed in TreeView v.1.6.6 (Page, 1996).

Bayesian inference (BI) analysis was performed using the Markov Chain Monte Carlo (MCMC) method with MrBayes 3.2.2 (Ronquist et al., 2012). The best-fit nucleotide substitution models for each dataset were separately determined using MrModeltest version 2.2 (Nylander, 2004). GTR+I+G were selected as best-fitting models for the ITS and LSU datasets. The Markov Chain Monte Carlo sampling (MCMC) analyses, with four chains, were run, started from random tree topology and lasted 5,000,000 generations and sampled every 100 generations (Nylander et al., 2008). The Tracer v. 1.5.0 program was used to check the effective sampling sizes (ESS) that should be above 200, the stable likelihood plateaus and burn–in value (Rambaut & Drummond, 2009). The first 5000 generations were excluded as burn-in and tree were visualized using FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/, Rambaut 2012). The phylograms are visualized in FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/, Rambaut, 2012) and made in Adobe Illustrator CS6 and Adobe Photoshop CS6 Extended version 13.0 × 64. Sequences data from this study are deposited in GenBank.

Table 8.1 GenBank accession numbers of the sequences used in phylogenetic analyses

Species	**Strain**	**ITS**	**LSU**
Anisogramma anomala	529478	EU683064	EU683066
Anisogramma virgultorum	529479	EU683062	EU683065
Cainiella johansonii	**Kruys 731 (UPS)**	-	**JF701920**
Chapeckia nigrospora	**AR 3809**	-	**EU683068**
Cryphonectria parasitica	CMW 7048	JN942325	JN940858
Cryptodiaporthe aesculi	AFTOL-ID 1238	-	DQ836905
Cryptodiaporthe salicella	AR3455	-	AF408345
Cryptometrion aestuescens	CMW 18790	GQ369458	HQ730869

Table 8.1 (continued)

Species	**Strain**	**ITS**	**LSU**
Cryptometrion parasitica	**ATCC 38755**	**AY141856**	**EU199123**
Cryptosporella hypodermia	**AR3552**	**EU199181**	**AF408346**
Cryptosporella hypodermia	AFTOL-ID 2124	-	DQ862028
Cytospora elaeagni	CFCC 89633	KF765677	KF765693
Cytospora parasitica	**MFLUCC 14-1055**	**KT459408**	**KT459409**
Cytospora tanaitica	**MFLUCC 14-1057**	-	-
Diaporthales sp.	YMJ 1364	JX570889	JX570891
Diaporthales sp.	BCC00200	-	EF622231
Diaporthe eres	AFTOL-ID 935	DQ491514	-
Diaporthe eres	**AR3538**	-	**AF408350**
Diaporthe detrusa	AR3424	-	AF408349
Ditopella ditopa	**AR3423**	-	**AF408360**
Gnomonia gnomon	**CBS 199.53**	**AY818956**	-
Hapalocystis occidentalis	WU 24705	-	AY616231
Harknessia australiensis	CPC 15029	JQ706085	JQ706211
Harknessia ellipsoidea	CPC 17111	JQ706087	JQ706213
Harknessia eucalypti	**CBS 342.97**	**AY720745**	**AF408363**
Harknessia pseudohawaiiensis	CPC 17379	JQ706111	JQ706234
Hercospora tiliae	AR3526	-	AF408365
Lamproconium desmazieri	**MFLUCC 14-1047**	**KX430132**	**KX430133**

Table 8.1 (continued)

Species	Strain	ITS	LSU
Lamproconium desmazieri	MFLUCC 15-0870	KX430134	KX430135
Lamproconium desmazieri	MFLUCC 15-0871	KX430136	KX430137
Lamproconium desmazieri	MFLUCC 15-0872	KX430138	KX430139
Lamproconium desmazieri	MFLUCC 15-0873	KX430140	KX430141
Leucostoma niveum	AR 3413	JX438624	NG_027590
Luteocirrhus shearii	CBS 130776	KC197021	KC197019
Magnaporthe grisea	GAD1	-	JQ920470
Magnaporthe salvinii	CBS 243.76	KM484861	DQ341498
Melanconiella ellisii	BPI 843491	JQ926268	JQ926268
Melanconiella spodiaea	MSH	JQ926298	JQ926298
Melanconiella spodiaea	SPOD	JQ926300	-
Melanconis alni	AR3500	-	AF408371
Melanconis alni	AR3748	EU199195	EU199130
Melanconis desmazieri	AR3525	-	AF408372
Melanconis desmazieri	AR3827	JX522735	-
Melanconis desmazieri	CBS 109780	JX522736	-
Melanconis marginalis	AR3442	-	AF408373
Melanconis stilbostoma	AR3501	-	AF408374
Ophiovalsa betulae	AR3524	-	AF408375
Ophiovalsa suffusa	AR3496	-	AF408376
Phragmoporthe conformis	AR3632	-	AF408377
Pilidiella castaneicola	CBS 143.97	-	AF408378
Pilidiella diplodiella	STE-U 3708	AY339323	AY339284
Pilidiella wangiensis	CPC 19397	JX069873	JX069857

Table 8.1 (continued)

Species	Strain	ITS	LSU
Plagiostoma euphorbiae	CBS 340.78	EU199198	AF408382
Pseudoplagiostoma eucalypti	CBS 124807	GU973512	GU973606
Pseudoplagiostoma oldii	CBS 124808	GU973534	GU973609
Pseudoplagiostoma variabile	CBS 113067	GU973536	GU973611
Pseudovalsa longipes	AR3541	-	EU683072
Pseudovalsa modonia	AR 3558	-	EU683073
Rossmania ukurunduensis	AR 3484	-	EU683075
Schizoparme straminea	CBS 149.22	-	AF362569
Schizoparme straminea	STE-U 3932	AY339348	AY339296
Stegonsporium protopyriforme	CBS 117041	NR_126119	-
Stilbospora macrosperma	CBS 121883	JX517290	JX517299
Stilbospora macrosperma	CBS 121695	JX517288	JX517297
Sydowiella fenestrans	AR 3777	-	EU683078
Thailandiomyces bisetulosus	BCC00018	-	EF622230
Tirisporella beccariana	BCC36737	-	JQ655450

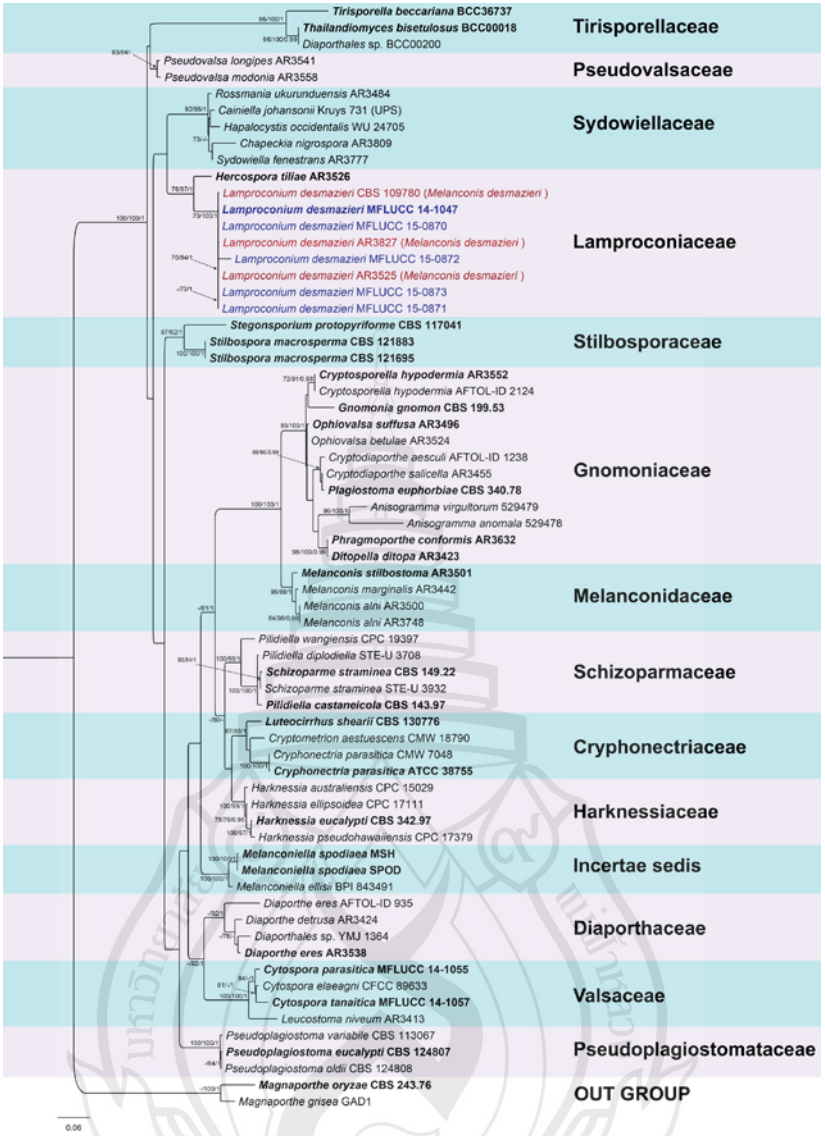
Note The ex-type strains are in bold.

8.3 Results and Discussions

8.3.1 Phylogenetic Analyses

The phylogenetic tree based on combined analysis of ITS and LSU sequence data was used to resolve the relationships in *Lamproconium* in Diaporthales. The phylogenetic analyses were obtained from maximum likelihood (ML), maximum parsimony (MP) and Bayesian analyses. The alignment comprised 67 taxa and 1534 total characters including gaps. Parsimony analyses indicate that 920 characters were constant, 141 variable characters were parsimony uninformative and 473 characters were parsimony informative. The parsimony analysis of the data matrix resulted in two equally parsimonious trees and the first tree (TL = 518, CI = 0.530, RI = 0.801, RC = 0.425, HI = 0.470) is shown in Figure 8.1. The Bayesian analysis resulted in the same topology as the MP trees. The phylogenetic results from Figure 8.1 are discussed in the notes.

Five isolates (MFLUCC 14-1047, MFLUCC 15-0870, MFLUCC 15-0871, MFLUCC 15-0872 and MFLUCC 15-0873) grouped together with three strains of *Melanconis desmazieri* (AR3525, AR3827 and CBS 109780) in the combined phylogeny with 100% ML, 70% MP bootstrap support and 1.0 PP support (Figure 8.1). Our isolate grouped close to *Hercospora tiliae*, but as a distinct lineage with 97% ML, 76% MP support and 1.0 PP in the combined phylogeny (Figure 8.1). There are two genera with nine strains constituting the family Lamproconiaceae, based on the multi-gene phylogeny and with support from morphological observations.



Note Maximum likelihood (ML) majority rule consensus tree of combined ITS and LSU sequence data based on MP, ML and Bayesian analyses. Values above the branches indicate maximum parsimony and maximum likelihood bootstrap ≥70%, (MPBS/MLBS). Values at the third positions, respectively, above or below the branches represent posterior probabilities (BIPP ≥ 0.95) from Bayesian inference analysis. The tree is rooted to *Magnaporthe salvinii* and *M. grisea*. Strain numbers are given following the taxon names. The new sequences resulting from this study are in blue. Synonyms are in red. Ex-type strains are in black bold.

Figure 8.1 Phylogenetic analysis of Lamproconiaceae

8.3.2 Taxonomy

Lamproconiaceae C. Norphanphoun, T.C. Wen & K.D. Hyde, fam. nov.

Index Fungorum number: IF552187

Facesoffungi number: FoF 02248

Pathogen and saprobe on dying twigs and branches. Sexual morph: Undetermined. Asexual morph: Conidiomata pycnidial, solitary, partly immersed in host tissue, uniloculate, multiloculate or convoluted, dark blue (*Lamproconium*), dark blackish brown (*Hercospora*), erumpent in the centre. Pycnidium thick-walled, thin at inner layer, hyaline (*Lamproconium*), dark brown (*Hercospora*), comprising wall cells of *textura angularis* (*Lamproconium*) or *textura intricata* (*Hercospora*). Ostiole absent, dehiscence irregular. Paraphyses interspersed with conidiophores. Conidiophores filiform or cylindrical, pale bluish or hyaline, septate, branched, smooth-walled, formed at the base of conidiomatal wall. Conidiogenous cells holoblastic, cylindrical to subcylindrical, each forming a single conidium at the conidiophore apex, or annellidic, colourless to olivaceous, smooth-walled. Conidia fusiform, ellipsoid, thick- walled, contents granular, aseptate, bluish to glistening dark blue (*Lamproconium*), hyaline (*Hercospora*), smooth- walled, produced in mucilage but without a distinct mucilaginous envelope or appendage.

Type genus: *Lamproconium* (Grove) Grove.

Notes: The order Diaporthales comprises 12 families, viz. Cryphonectriaceae Gryzenh. & M.J. Wingf., Diaporthaceae Höhn. ex Wehm., Gnomoniaceae G. Winter, Harknessiaceae Crous, Melanconidaceae G. Winter, Pseudoplagiostomataceae Cheew., M.J. Wingf. & Crous, Pseudovalsaceae M.E. Barr, Schizoparmaceae Rossman, D.F. Farr & Castl., Stilbosporaceae Link, Sydowiellaceae Lar.N. Vassiljeva, Tirisporellaceae Suetrong et al. and Valsaceae Tul. & C. Tul. (Maharachchikumbura et al., 2015, 2016).

The family Lamproconiaceae is established to accommodate *Lamproconium* and *Hercospora* and is introduced based on morphology and phylogenetic analyses. Lamproconiaceae forms a robust clade basal to Sydowiellaceae and Stilbosporaceae in the combined ITS and LSU phylogeny (Figure 8.1). It is morphologically different in conidial form from the asexual morphs of Sydowiellaceae and Stilbosporaceae.

Species of Sydowiellaceae have been reported as Melanconis-like and is allied with *Hercospora*, as shown in the earlier studies (Castlebury et al., 2002; Rossman et al., 2007). Nevertheless, *Hercospora* is a distinct genus in that the ostioles from individual fruiting bodies converging within the stroma and emerge as one ostiole. *Hercospora tiliae*, with its unusual asexual morph groups with *Melanconis desmazieri*, also from *Tilia* (Castlebury et al., 2002; Rossman et al., 2007; Petrak, 1938; Castlebury et al., 2002; Voglmayr et al., 2012; Voglmayr & Jaklitsch, 2014; Maharachchikumbura et al., 2015, 2016). Thus, *Hercospora* falls outside Sydowiellaceae and belongs in Lamproconiaceae.

The asexual species of Stilbosporaceae and Lamproconiaceae are coelomycetes. The conidia of Lamproconiaceae species are aseptate, fusiform or ellipsoid, with granular contents, and hyaline or bluish to glistening dark blue, while in Stilbosporaceae conidia are cylindrical, clavate to pyriform, eu- or distoseptate, with or without oblique or longitudinal septa and brown (Maharachchikumbura et al., 2016).

Lamproconium (Grove) Grove, British Stem- and Leaf-Fungi (Coelomycetes) (Cambridge) 2: 321 (1937)

Melanconium sect. *Lamproconium* Grove, Bull. Misc. Inf., Kew: 161 (1918)

Type species: *Lamproconium desmazieri* (Berk. & Broome) Grove.

Lamproconium desmazieri (Berk. & Broome) Grove [as 'desmazieri'], British Stem- and Leaf-Fungi (Coelomycetes) (Cambridge) 2: 321 (1937), Figures 8.2–8.4

=*Discella desmazieri* Berk. & Broome, Ann. Mag. nat. Hist., Ser. 2 5: 377 (1850)

=*Melanconium desmazieri* (Berk. & Broome) Sacc., Michelia 2(no. 7): 355 (1881)

=*Melanconis desmazieri* Petr., Annls. mycol. 36(1): 55 (1938)

Facesoffungi number: FoF02249

Pathogen causing canker on branches or twigs of lime trees (*Tilia* spp.). Lime cankers associated with *L. desmazieri*, produced splitting and longitudinal breakage of the outer branches, the symptom will appear as localized, sunken, slightly discolored, dark blue to black lesions on branches discoloration and necrosis of the branches. Branch/top dieback associated with *L. desmazieri* in having black terminal dead shoots,

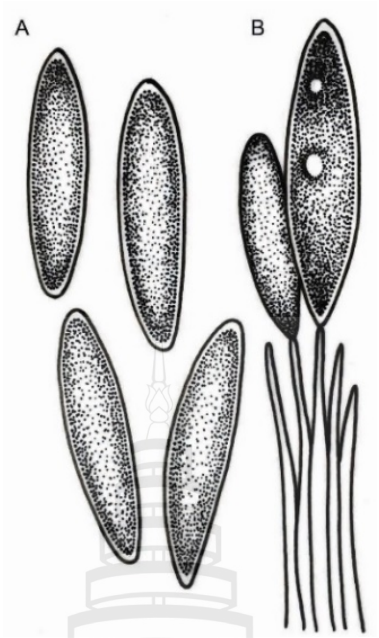
apex downwards initially discoloration; becoming wilted, with brown to dark brown discoloration at the base, midrib, and finally becoming dry and dead. Sexual morph: Undetermined. Asexual morph: Conidiomata 800–1000 × 400–550 μm diam., pycnidial, solitary, partly immersed in host tissue, uniloculate, dark blue, with a raised centre. Pycnidium 50–70 μm, with multi-layered wall, thin at inner layer, hyaline, comprising wall cells of *textura angularis*. Paraphyses interspersed within conidiophores. Conidiophores 30–120 μm, arising from the outermost wall layer at the basal of pycnidium, filiform or cylindrical, pale bluish to hyaline, septate, branched, smooth-walled. Conidiogenous cells cylindrical to subcylindrical, annellidic, with flared periclinal thickenings in the collarette zone, colourless to olivaceous, smooth-walled. Conidia 22–28.5 × 8–10 μm ($\bar{x}$ = 25.25 × 9 μm, n = 30), fusiform, ellipsoid, infrequently slightly curved, aseptate, initially hyaline, bluish to glistening dark blue at maturity, narrowly rounded at ends, smooth-walled.

Material examined: RUSSIA. Rostov region: Krasnosulinsky district, Donskoye forestry, artificial forest, on dead branches of *Tilia cordata* Mill. (Tiliaceae), 21 May 2014, T. Bulgakov (MFLU 14-0780, reference specimen designated here, PDD); living culture, MFLUCC 14-1047, KUMCC. RUSSIA. Rostov region: Shakhty city, Central urban microdistrict, Central Park, parkland, on dying brunches (necrotrophic) of *T. tomentosa* Moench, 9 July 2015, T. Bulgakov (MFLU 15-1940, PDD); living culture, MFLUCC 15-0870, KUMCC. RUSSIA. Rostov region: Krasnosulinsky district, Donskoye forestry, ravine forest, on dead branches of *T. cordata*, 18 June 2015, T. Bulgakov (MFLU 15-2037, PDD); living culture, MFLUCC 15-0871, KUMCC. RUSSIA. Rostov region: Rostov- on-Don city, territory of Southern Federal University, parkland, on dead and dying branches of *T. cordata*, 23 April 2015, T. Bulgakov (MFLU 15-2111, PDD); living culture, MFLUCC 15-0872, KUMCC. RUSSIA. Rostov region: Krasnosulinsky district, Donskoye forestry, ravine forest, on dying branches of *T. cordata*, 18 June 2015, T. Bulgakov (MFLU 15-2192, PDD); living culture, MFLUCC 15-0873, KUMCC.

Notes: *Lamproconium* was introduced as a section of Melanconium by Grove (1918) and as a subgenus (Index Fungorum, 2016), with *Melanconium desmazieri* as the type species. The taxon with bright coloured spores was collected on living twigs of *Tilia* sp. in the UK. Grove (1937) had raised the subgenus to generic rank. In this

study, we have determined our collections as having fusiform, ellipsoid, infrequently slightly curved, aseptate and glistening, dark blue conidia, with narrowly rounded ends (22–28.5 × 8–10 μm). The morphology of our collections is similar to *Lamproconium desmazieri* (Table 8.2). Therefore, we introduce our collections as belonging to the genus *Lamproconium*.

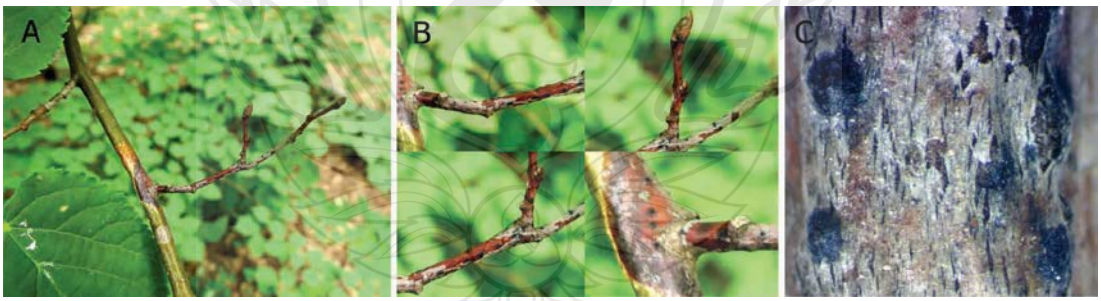
Petrak (1938) reported *Melanconis desmazieri* as the sexual morph of *Melanconium desmazieri*, also from *Tilia* sp. In the phylogenetic study of Castlebury et al. (2002), based on LSU sequence data, *Melanconis desmazieri* fell outside Melanconidaceae sensu stricto and grouped with *Hercospora tiliae*. These taxa were therefore placed in Diaporthales genera incertae sedis (Castlebury et al., 2002; Voglmayr et al., 2012; Voglmayr & Jaklitsch, 2014). Phylogenetic analyses in this study generated from maximum likelihood, maximum parsimony and Bayesian analyses using combined ITS and LSU sequence data from 67 taxa (including our new strains), indicate that *L. desmazieri* belongs with *Hercospora tiliae* as a distinct lineage of Diaporthales (Figure 8.1). Hence, we synonymize *M. desmazieri* under *L. desmazieri* and designate one of our collections as a reference specimen for *L. desmazieri*.



Note *Lamproconium desmazieri* (= *Melaconium desmazieri*) a Conidia. b Conidiophores and developing conidia.

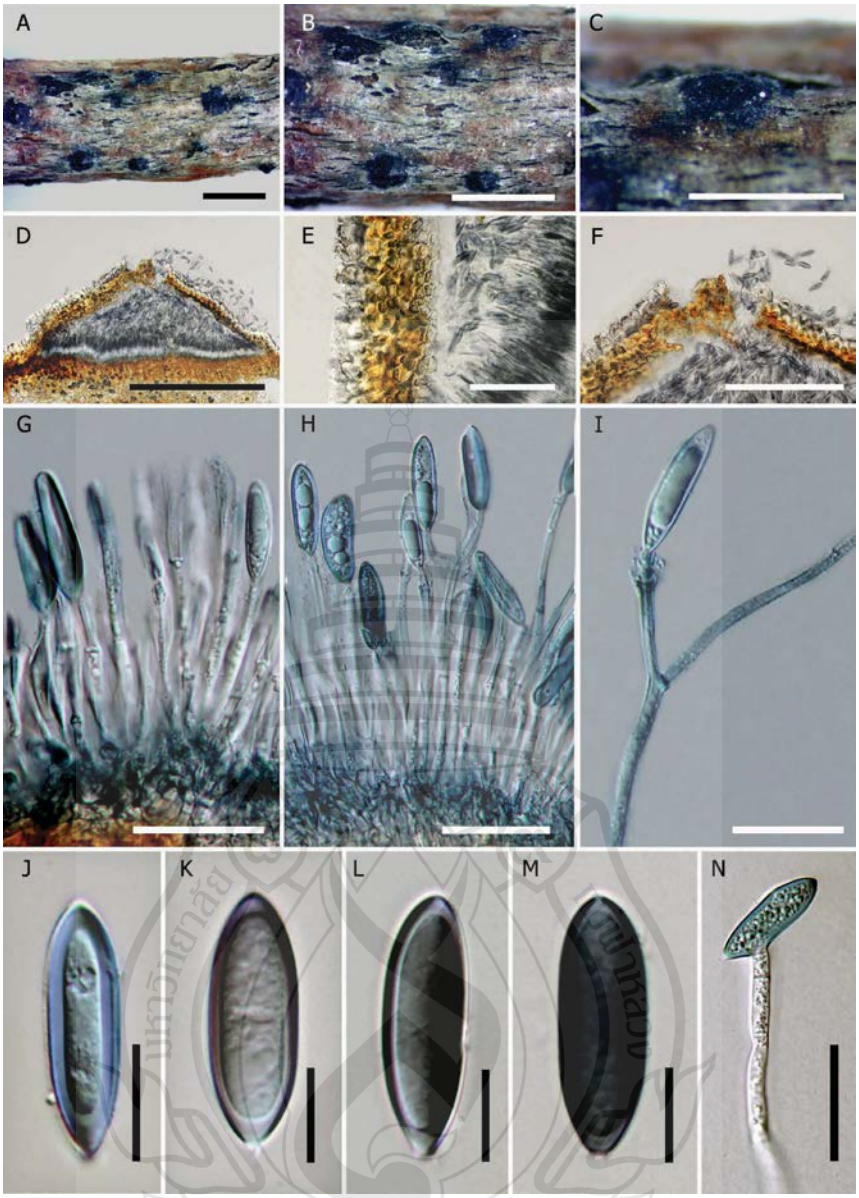
Source Grove (1918)

Figure 8.2 Morphological characters of *Lamproconium desmazieri*



Note Dieback disease caused by *Lamproconium desmazieresi* (MFLU 14-0780, reference specimen). a, b *Tilia cordata* with conidiomata on twigs and branches. c Immersed conidiomata on branch.

Figure 8.3 Morphological characters of dieback disease caused by *Lamproconium desmazieresi* (MFLU 14-0780, reference specimen)



Note *Lamproconium desmazieresi* (MFLU 14-0780, reference specimen). a–c Conidiomata on host. d Cross section of a conidioma. e Peridium and raised host tissue. f Apex of conidioma. g–i Conidiogenous cells with attached conidia (note: annellations at the tip of the conidiogenous cell). j Immature conidium. k–m Mature conidia. n Germinating conidium. Scale bars: a, b = 2 mm, c = 1 mm, d = 500 μm, e = 100 μm, f = 200 μm, g, h = 30 μm, i = 20 μm, j–m = 10 μm, n = 30 μm.

Figure 8.4 Morphological characters of *Lamproconium desmazieresi* (MFLU 14-0780, reference specimen)

Hercospora Fr., Syst. orb. veg. (Lundae) 1: 119 (1825)

Possible synonyms (See Index Fungorum, 2016)

Facesoffungi number: FoF02250

Saprobic on branches and twigs of temperate trees. Sexual morph: Stromatic tissues prosenchymatous around perithecia, delimited externally by blackened dense pseudoparenchymatous zone, interior whitish, composed of interwoven hyphae mixed with substrate cells. Ascomata perithecial, few, small, circinate, beaks converging, becoming united and erumpent through stroma surface as single large opening. Asci 8-spored, unitunicate, broadly cylindrical. Ascospores hyaline, broadly ellipsoid, one septate, wall smooth, without gelcoating, with narrow terminal and median appendages in some species. Asexual morph: *Rabenhorstia* sp., Stromata prosenchymatous. Conidiomata pycnidial, uniloculate, ostiolate, ostiole surrounded by a superficial cap of sterile tissues. Conidiophores elongate. Conidia hyaline ovoid to ellipsoid, one-celled.

Type species: *Hercospora tiliae* (Pers.) Tul. & C. Tul.

Notes: Fries (1825) listed *Sphaeria tiliae* Pers., and *Sphaeria atrovirens* Alb. & Schwein., as two of the species in *Hercospora*. However morphologically *S. tiliae* has hyaline ascospores while *S. atrovirens* comprising opaque ascospores. Tulasne & Tulasne (1863) accepted *H. tiliae* as the type species of *Hercospora*. Petrak (1938) and Ruhland (1900) implicated *Rabenhorstia tiliae* (Pers.) Fr., as the asexual morph of *Hercospora tiliae*. Fourteen species listed under *Hercospora* (Index Fungorum, 2016).

Hercospora tiliae (Pers.) Tul. & C. Tul., Select. fung. carpol. (Paris) 2: 154 (1863), Figures 8.5–8.6

Possible synonyms (See Index Fungorum 2016)

Facesoffungi number: FoF02452

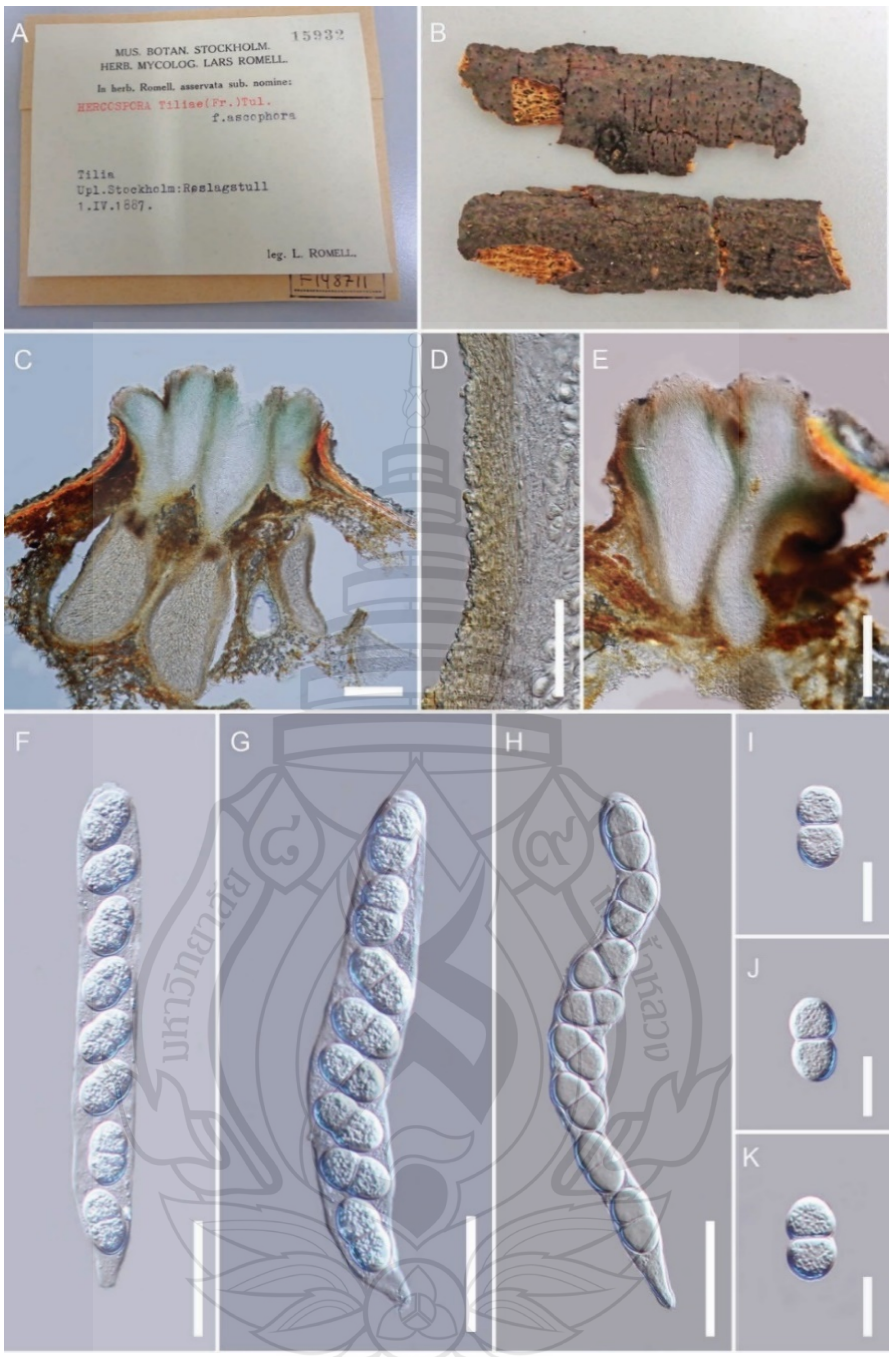
Saprobic on branches and twigs of *Tilia* sp. Sexual morph: Stromata 700–800 μm wide, prosenchymatous around perithecia, delimited externally by greenish-blackened dense pseudoparenchymatous zone, interior whitish, composed of interwoven hyphae mixed with substrate cells, 3–5 ascomata in a stromata. Ascomata 1–1.05 mm high, 0.24–0.34 mm diam., ($\bar{x}$ = 1.02 × 334 μm, n = 10), perithecial, small, aggregated, scattered, globose to subglobose, light brown to dark brown, coriaceous,

ostiolate, papillate. Papilla 625–645 μm high, 190–290 μm diam., ($\bar{x}$ = 640 × 250 μm, n = 10), converging and erumpent through stroma surface as single, large opening, wide at the top, narrowing towards the base, dark brown region around base of papilla. Peridium 10–20 μm wide ($\bar{x}$ = 16 μm, n = 10), comprises light brown, compressed, cells of textura angularis. Asci 140–175 μm × 17–24 μm diam., ($\bar{x}$ = 160 × 21 μm, n = 10), 8- spored, unitunicate, cylindrical, short-stalked, J- apical apparatus. Ascospores 20–25 μm × 9–11 μm diam., ($\bar{x}$ = 23 × 10 μm, n = 10), uniseriate, broadly ellipsoid, 1-septate, not or lightly constricted at the septa, hyaline, smooth. Asexual morph: Stromata prosenchymatous. Conidiomata pycnidial, uniloculate, ostiolate, ostiole surrounded by a superficial cap of sterile tissues. Conidiophores elongate. Conidia 14–16.5 × 4.5–6.5 μm ($\bar{x}$ = 15 × 5 μm, n = 10), hyaline ovoid to ellipsoid, one-celled.

Material examined: SWEDEN. Uppland: Upl. Stockholm: Roslagstull Stockholm, on bark of *Tilia* sp., L. Romell, 1 April 1887, F148711 (S).

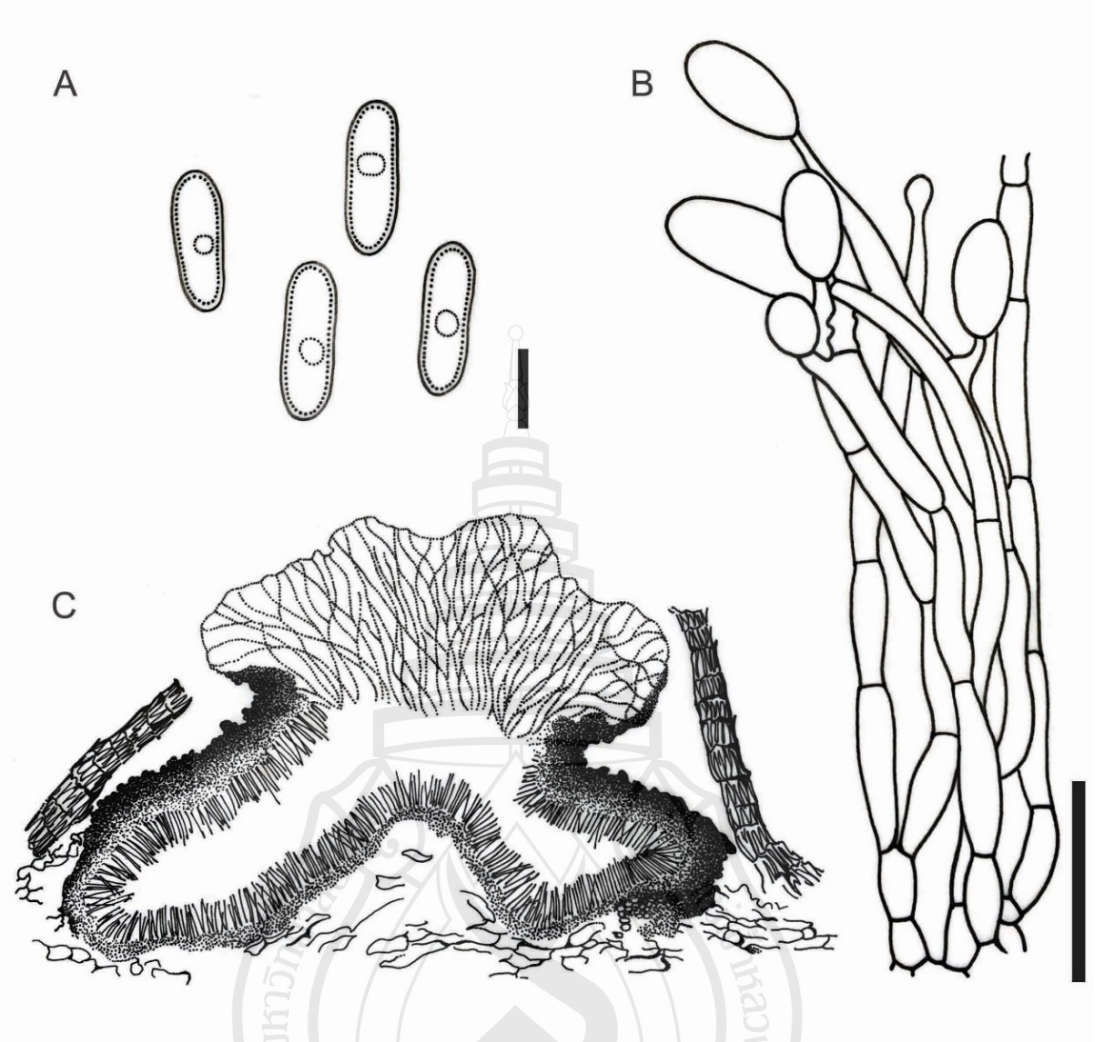
Notes: *Hercospora* Fr. comprises 15 species (Index Fungorum, 2016) with *Hercospora tiliae* as the type. The characters of the genus include eustromatic, immersed, subepidermal, dark blackish brown, separate, uniloculate, multiloculate or convoluted and thick-walled conidiomata; conidiophores branched extensively at the base, less so above, hyaline, septate, smooth, often developing in mucilage, formed at the base and sides of the conidiomatal wall; and ellipsoid, thick-walled, hyaline, aseptate conidia (18–20 × 6–7.5 μm) (Petrak, 1938; Sutton, 1980).

Phylogenetic studies (Castlebury et al., 2002; Rossman et al., 2007; Voglmayr et al., 2012; Voglmayr & Jaklitsch, 2014) based on LSU sequence data, placed *H. tiliae* in Diaporthales, genera incertae sedis, where it grouped with *Melanconis desmazierii*. In the present study based on maximum likelihood, maximum parsimony and Bayesian analyses of combined ITS and LSU sequence data, *Lamproconium desmazierii* (= *Melanconis desmazieri*) and *Hercospora tiliae*, clustered in Lamproconiaceae fam. nov.



Note *Hercospora tiliae* (F148711, reference specimen). a Packet of herbarium specimen. b Herbarium specimens. c Cross section of ascomata. d Peridium. e Papilla. f–h Asci in water. i–k Ascospores. Scale bars: c = 200 μm, d, f–h = 40 μm, e = 100 μm.

Figure 8.5 Morphological characters of *Hercospora tiliae* (F148711, reference specimen)



Note *Hercospora tiliae* a Conidia. b Conidiophores and developing conidia. c Conidioma. Scale bars: a = 10 μm, b = 20 μm.

Source (Sutton 1980)

Figure 8.6 Morphological characters of *Hercospora tiliae*

CHAPTER 9

REVISITING THE GENUS *CYTOSPORA* AND ALLIED SPECIES[8]

Abstract

Cytospora species are important plant pathogens causing dieback and canker diseases on a wide range of hosts, worldwide. However, species level identification is difficult due to poor phylogenetic understanding and lack of sequenced type species. ITS sequence data are only available for most *Cytospora* strains in GenBank. In this study, samples of *Cytospora* were collected from symptomatic twigs and branches in European Russia. A combination of morphological characters and multi-gene phylogenetic analysis (ITS, LSU, *rpb2*, *act*) were used to identify taxa. A total of 34 collections, representing 17 fungal species of *Cytospora* were studied. Of these, 14 new species are described and illustrated. Three species were known taxa and identified as *C. nivea*, *C. parasitica*, and *C. salicicola*. Newly introduced species are *C. ampulliformis*, *C. curvata*, *C. donetzica*, *C. erumpens*, *C. longiostiolata*, *C. melnikii*, *C. parakantschavelii*, *C. paratranslucens*, *C. rusanovii*, *C. salicacearum*, *C. salicina*, *C. sorbi*, *C. sorbicola* and *C. ulmi*. Descriptions, illustrations and notes are provided for all studied taxa in this study. The distribution patterns of *Cytospora* species on different hosts are discussed. The study represents a preliminary study of *Cytospora* species from a small region and provides an initial contribution to the understanding of the genus.

Keywords: Diaporthales, Morphology, Phylogenetic analyses, Plant pathogenic fungi, Russia, Valsaceae

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[8]This paper has been published in *Mycosphere*, 2017, *8*(1), 51–97. https://doi.org/10.5943/mycosphere/8/1/

9.1 Introduction

Cytospora was introduced by Ehrenberg (1818) and is one of the most important forest pathogenic genera causing canker disease on branches of various tree species. The disease often leads to large areas of dieback on a wide range of plants (Adams et al., 2005, 2006). *Cytospora* is the asexual morph of *Valsa*, which is the type genus of Valsaceae Tul. & C. Tul. in Diaporthales Nannf. comprising the genera *Amphicytostroma*, *Chadefaudiomyces*, *Cryptascoma*, *Cytospora*, *Ditopellina*, Durispora, *Harpostroma*, *Hypospilina*, *Kapooria*, *Leptosillia*, *Maculatipalma*, *Pachytrype*, and *Paravalsa* (Adams et al., 2005; Wang et al., 2011; Ariyawansa et al., 2015; Fan et al., 2015a, b; Liu et al., 2015; Maharachchikumbura et al., 2015, 2016; Hyde et al., 2016).

Cytospora has been also considered as the asexual morph of other genera such as, *Leucocytospora*, *Leucostoma*, *Valsella* and *Valseutypella* (Fries, 1823; Saccardo, 1884; Gvritishvili, 1982; Spielman, 1985; Adams et al., 2002, 2005; Castlebury et al., 2002; Bulgakov, 2010; Maharachchikumbura et al., 2015, 2016; Rossman et al., 2015; Yang et al., 2015; Li et al., 2016; Hyde et al., 2016). Therefore, all of these sexual genera were synonymized under *Valsa*, either as a subgenus or species (Adams et al., 2006). The International Code of Nomenclature for Algae, Fungi, and Plants (ICN, McNeill et al., 2012) permits a single name for biological species and genera (Hyde et al., 2009; Wikee et al., 2011; Huang et al., 2013; Wei et al., 2013; Udayanga et al., 2014; Fan et al., 2015a, b). Therefore, *Valsa* (1849) was treated as synonym of *Cytospora* (1818), with the latter being the oldest and most widely used name (Adams et al., 2005; Fotouhifar et al., 2010; Fan et al., 2014; Rossman et al., 2015). Most of the names previously recognized in *Valsa* already have an older epithet in *Cytospora* in the SMML Fungal Database (http://nt.ars- grin.gov/fungaldatabases/), while some new names for the common species of *Cytospora*, previously placed in *Valsa*, were provided by Rossman et al. (2015).

Cytospora species usually produce asexual fruiting bodies and contain a single or labyrinthine of locules, filamentous conidiophores or asci, and allantoid hyaline conidia or allantoid hyaline ascospores (Spielman, 1983, 1985; Adams et al., 2005; Fan

et al., 2015a, b). In moist conditions, the conidia will emerge from the fruiting bodies forming yellow, orange to red gelatinous tendrils (Adams et al., 2005, 2006). Identification of *Cytospora* species has generally been established according to host association, while morphological descriptions generally lack significant differences. Therefore, a single species of *Cytospora* may occur on several unrelated host plants, or a single host plant may support more than one *Cytospora* species (Adams et al., 2005; Wang et al., 2011; Ariyawansa et al., 2015; Fan et al., 2015a, b, Liu et al., 2015; Hyde et al., 2016). Thus, there are 585 epithets for *Cytospora* in Index Fungorum (2017) with an estimated number of 110 species in Kirk et al., (2008). However, ex-type sequence data are available for only 23 species in GenBank (accessed 2017). Thus, it is difficult to identify species from a phylogenetic perspective alone (Ariyawansa et al., 2015; Liu et al., 2015; Hyde et al., 2016; Li et al., 2016) as many taxa are morphologically similar. The have been several recent papers dealing with *Cytospora* with a limited number of multi-gene sequence trees or larger trees based on ITS sequence data, however, there has been no comprehensive multi-gene study for the genus (Adams et al., 2002; Fotouhifar et al., 2010; Hyde et al., 2010, 2014; Ariyawansa et al., 2015; Fan et al., 2015a, b; Liu et al., 2015; Yang et al., 2015; Hyde et al., 2016; Li et al., 2016).

The aim of the present study was to identify *Cytospora* species in a small region of Russia based on morphological studies and phylogenetic analysis, and provide a multi-locus phylogeny using ITS, LSU, *rpb2* and *act* sequence data for resolution of *Cytospora* species. The distribution of *Cytospora* species on hosts is also discussed.

9.2 Materials and Methods

9.2.1 Sample Collection and Specimen Examination

The specimens were collected from Russia during 2015 by Timur Bulgakov. The specimens were returned to the laboratory in small paper bags for observation, examination and description, following the methods described in Norphanphoun et al. (2015, 2016). Micro-morphological characters were studied using a Motic SMZ 168 dissecting microscope. Hand sections of the fruiting structures were mounted in water and examined for morphological details. Specimens were examined under a Nikon Ni

compound microscope and photographed using a Canon EOS 600D digital camera fitted to the microscope. Photo-plates were made by using Adobe Photoshop CS6 Extended version 13.0 × 64 (Adobe Systems Inc., The United States) and the Tarosoft (R) Image Framework program v. 0.9.7 was used for taking measurements. The contents inside the conidiomata were picked with a sterile needle and soaked in sterile water in a glass container for examination.

Cultures were obtained by single spore isolation following the method described in Chomnunti et al. (2014). Spore germination was observed and photographed under a Nikon Ni compound microscope fitted with a Canon EOS 600D digital camera. Geminated spores were transferred aseptically to malt extract agar (MEA) and incubated at 18−25°C. Colony characters were recorded and measured after one week and also one month.

The herbarium specimens were deposited in the Mae Fah Luang University Herbarium, Chiang Rai, Thailand (MFLU) and duplicated in New Zealand Fungal Herbarium, New Zealand (PDD). Living cultures were deposited at Mae Fah Luang University Culture Collection (MFLUCC) and Kunming Culture Collection (KUMCC). Facesoffungi and Index Fungorum numbers were registered (Jayasiri et al., 2015; Index Fungorum, 2017).

9.2.2 DNA Extraction, PCR Amplification and Sequencing

Thirty-four isolates were selected for the molecular analyses (Table 9.1). DNA was amplified from the complete the internal transcribed spacer regions (ITS1-5.8S-ITS2), large nuclear ribosomal RNA subunit region (LSU), RNA polymerase II subunit (*rpb2*), and α-actin (*act*) genes of each *Cytospora* isolate, which were performed using fungal mycelia growing on MEA at 18−25°C for one month. The genomic DNA was obtained using a E.Z.N.A.TM Fungal DNA MiniKit (Omega Biotech, CA, USA) following the manufacturer's protocols.

Polymerase chain reactions (PCR) were carried out using primer pairs of ITS1 and ITS4 to amplify the ITS region (White et al., 1990), the partial LSU region was amplified with primers NL1 and NL4 (O'Donnell, 1993), the partial *rpb2* region was amplified using primers bRPB-6F and bRPB-7.1R (Matheny, 2005), and the partial *act* region was amplified using primers ACT512F and ACT783R (Carbone & Kohn, 1999)

(Table 9.1). The amplification reaction was performed in 50 µl reaction volume containing, 2 µl of DNA template, 2 µl of each forward and reverse primers, 25 µl of 2 × Bench TopTMTaq Master Mix (mixture of Taq DNA Polymerase (recombinant): 0.05 units/µL, MgCl2: 4 mM, and dNTPs: 0.4 mM) and 19 µl of double-distilled water (ddH2O). The PCR conditions used in this study for each gene are shown in Table 9.1. The quality of PCR products were checked by using 1% agarose gel electrophoresis stained with ethidium bromide. Purification and sequencing of PCR product were carried out at Life Biotechnology Co., Shanghai, China.

9.2.3 Phylogenetic Analyses

Blast searches were made to identify the closest matches in GenBank and reliable sequences were downloaded (viz. Fotouhifar et al., 2010; Fan et al., 2014, 2015a, b; Hyde et al., 2016). The phylogenetic analyses were initially performed using ITS sequence data and then determined using combined multi-gene phylogeny (ITS, LSU, *rpb2*, *act*) with 143 and 97 sequences respectively. *Cytospora* species were selected for combined multi-gene phylogeny based on fungal group relationships between closely related taxa of type strains with our strains from the ITS phylogenetic tree. *Phomopsis vaccinii* Shear (ATCC 18451) was selected as the outgroup taxon in individual and combined analyses. The individual datasets were combined as this has been previously found to increase phylogenetic accuracy (Cunningham, 1997; Bull et al., 1993). The combined sequence alignment was obtained from MEGA7 version 7.0.14 (Kumar et al., 2015) and ambiguously aligned regions were excluded and gaps were treated as missing data. Alignments were checked visually and manually adjusted for errors. The partition homogeneity test (PHT) or the Incongruence Length Difference (ILD) test were used to testing the congruence and combinability of the individual datasets (Farris et al., 1995a, b) with 1,000 heuristic search replicates in PAUP v. 4.0b10 (Swofford, 2003). In addition, the datasets were optimized manually where necessary. Phylogenetic trees were reconstructed using maximum parsimony, maximum likelihood and Bayesian inference analyses.

Maximum parsimony (MP) analysis was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford, 2003). The trees were inferred using the heuristic search option with tree bisection-reconnection (TBR) as the branch

swapping algorithm and 1000 random sequence additions. Maxtrees were setup to 1000, branches of zero length were collapsed and all multiple parsimonious trees were saved. Descriptive tree statistics for parsimony tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC) and homoplasy index (HI) were calculated for the maximum parsimonious tree (MPT). The robustness of the most parsimonious trees was evaluated by 1000 bootstrap replications, each with ten replicates of random stepwise addition of taxa (Felsenstein, 1985). The Kishino-Hasegawa tests (KHT) (Kishino & Hasegawa, 1989) were performed to determine whether the trees were significantly different.

The best-fit nucleotide substitution models for each dataset were separately determined using MrModeltest version 2.2 for both ML and Bayesian analyses (Nylander, 2004). Maximum- likelihood (ML) analysis was performed in RAxML (Stamatakis, 2006) implemented in raxmlGUI v.1.3 (Silvestro & Michalak, 2012). The 1000 rapid bootstrap replicates were run with generalized time reversible GTRGAMMA model of nucleotide substitution and searches for model selected for ML were applied.

Bayesian inference (BI) analysis was performed using the Markov Chain Monte Carlo (MCMC) method with MrBayes v.3.2.2 (Ronquist et al., 2012). GTR+I+G was selected as the best- fitting model for individual ITS and combined ITS, LSU, *rpb2* and *act*. The Markov ChainMonte Carlo sampling (MCMC) analyses, with four chains, were started from random tree topology and lasted 5,000,000 generations and sampled every 100 generations. The Tracer v. 1.5.0 program was used to check the effective sampling sizes (ESS) that should be above 200, the stable likelihood plateaus and burn-in value (Rambaut et al., 2013). The first 5000 generations were excluded as burn-in.

Table 9.1 The PCR thermal cycle program in this study

Gene and the primers used	Step	Temp	Time	Cycle
ITS ITS1/ITS4	Initialization	95 °C	3 minutes	40 Cycles
	Denaturation	95 °C	30 seconds	
	Annealing	55 °C	50 seconds	
	Extension/Elongation	72 °C	1 minute	
	Final Elongation	72 °C	7 minutes	
LSU NL1/NL4	Initialization	94 °C	2 minutes	30 Cycles
	Denaturation	94 °C	30 seconds	
	Annealing	52 °C	30 seconds	
	Extension/Elongation	72 °C	1 minute	
	Final Elongation	72 °C	7 minutes	
rpb2 bRPB-6F/ bRPB-7.1R	Initialization	95 °C	5 minutes	40 Cycles
	Denaturation	95 °C	1 minute	
	Annealing	52 °C	2 minutes	
	Extension/Elongation	72 °C	90 seconds	
	Final Elongation	72 °C	10 minutes	
act ACT512F/ACT783R	Initialization	95 °C	5 minutes	40 Cycles
	Denaturation	95 °C	40 seconds	
	Annealing	58 °C	30 seconds	
	Extension/Elongation	72 °C	1 minute	
	Final Elongation	72 °C	5 minutes	

The resulting trees were viewed with FigTree v1.4.0 (Rambaut, 2012) and edited in Adobe Illustrator CS6 and Adobe Photoshop CS6 Extended version 13.0 × 64 (Adobe Systems Inc., The United States). Sequences data from this study were deposited in GenBank (Table 9.2) and alignments were saved in TreeBASE (www.treebase.org) submission ID: 20491 (ITS sequence alignment) and 20492 (combined sequence alignment).

Table 9.2 *Cytospora* species introduced in this study (ex-type strains are bold)

NO	TAXON	STRAIN	HOST	GENBANK ACCESSION NUMBERS			
				ITS	LSU	*rpb2*	*act*
1	***Cytospora ampulliformis***	MFLUCC 16-0583	*Sorbus intermedia* (Ehrh.) Pers.	KY417726	KY417760	KY417794	KY417692
2	*Cytospora ampulliformis*	MFLUCC 16-0629	*Acer platanoides* L.	KY417727	KY417761	KY417795	KY417693
3	***Cytospora curvata***	MFLUCC 15-0865	*Salix alba* L.	KY417728	KY417762	KY417796	KY417694
4	*Cytospora donetzica*	MFLUCC 15-0864	*Crataegus monogyna* Jacq.	KY417729	KY417763	KY417797	KY417695
5	*Cytospora donetzica*	MFLUCC 16-0641	*Pyrus pyraster* (L.) Burgsd	KY417730	KY417764	KY417798	KY417696
6	***Cytospora donetzica***	MFLUCC 16-0574	*Rosa* sp.	KY417731	KY417765	KY417799	KY417697
7	*Cytospora donetzica*	MFLUCC 16-0589	*Salix alba* L.	KY417732	KY417766	KY417800	KY417698
8	***Cytospora erumpens***	MFLUCC 16-0580	*Salix* × *fragilis* L.	KY417733	KY417767	KY417801	KY417699
9	***Cytospora longiostiolata***	MFLUCC 16-0628	*Salix* × *fragilis* L.	KY417734	KY417768	KY417802	KY417700
10	***Cytospora melnikii***	MFLUCC 15-0851	*Malus domestica* Borkh	KY417735	KY417769	KY417803	KY417701
11	*Cytospora melnikii*	MFLUCC 16-0635	*Populus nigra L.* var. *italica* Münchh	KY417736	KY417770	KY417804	KY417702
12	*Cytospora nivea*	MFLUCC 15-0860	*Salix acutifolia* Willd.	KY417737	KY417771	KY417805	KY417703
13	***Cytospora parakantschavelii***	MFLUCC 15-0857	*Populus* × *sibirica* G.V. Krylov & G.V. Grig. ex A.K. Skvortsov	KY417738	KY417772	KY417806	KY417704
14	*Cytospora parakantschavelii*	MFLUCC 16-0575	*Pyrus pyraster* (L.) Burgsd.	KY417739	KY417773	KY417807	KY417705
15	*Cytospora parasitica*	MFLUCC 16-0507	*Malus domestica* Borkh	KY417740	KY417774	KY417808	KY417706
16	***Cytospora paratranslucens***	MFLUCC 16-0506	*Populus alba* L. var. *bolleana* (Lauche) Otto	KY417741	KY417775	KY417809	KY417707
17	*Cytospora paratranslucens*	MFLUCC 16-0627	*Populus alba* L.	KY417742	KY417776	KY417810	KY417708

Table 9.2 (continued)

NO	TAXON	STRAIN	HOST	GENBANK ACCESSION NUMBERS			
				ITS	LSU	*rpb2*	*act*
18	*Cytospora rusanovii*	MFLUCC 15-0853	*Populus* × *sibirica* G.V. Krylov & G.V. Grig. ex A.K. Skvortsov	KY417743	KY417777	KY417811	KY417709
19	***Cytospora rusanovii***	MFLUCC 15-0854	*Salix babylonica* L.	KY417744	KY417778	KY417812	KY417710
20	*Cytospora salicacearum*	MFLUCC 15-0861	*Salix* × *fragilis* L.	KY417745	KY417779	KY417813	KY417711
21	***Cytospora salicacearum***	MFLUCC 16-0509	*Salix alba* L.	KY417746	KY417780	KY417814	KY417712
22	*Cytospora salicacearum*	MFLUCC 16-0576	*Populus nigra* L. var. *italica* Münchh.	KY417747	KY417781	KY417815	KY417713
23	*Cytospora salicacearum*	MFLUCC 16-0587	*Prunus cerasus* L.	KY417748	KY417782	KY417816	KY417714
24	*Cytospora salicicola*	MFLUCC 15-0866	*Salix alba* L.	KY417749	KY417783	KY417817	KY417715
25	***Cytospora salicina***	MFLUCC 15-0862	*Salix alba* L.	KY417750	KY417784	KY417818	KY417716
26	*Cytospora salicina*	MFLUCC 16-0637	*Salix* × *fragilis* L.	KY417751	KY417785	KY417819	KY417717
27	***Cytospora sorbi***	MFLUCC 16-0631	*Sorbus aucuparia* L.	KY417752	KY417786	KY417820	KY417718
28	*Cytospora sorbicola*	MFLUCC 16-0581	*Sorbus aucuparia* L.	KY417753	KY417787	KY417821	KY417719
29	*Cytospora sorbicola*	MFLUCC 16-0582	*Cotoneaster melanocarpus* Fisch. ex Blytt,	KY417754	KY417788	KY417822	KY417720
30	***Cytospora sorbicola***	MFLUCC 16-0584	*Acer pseudoplatanus* L.	KY417755	KY417789	KY417823	KY417721
31	*Cytospora sorbicola*	MFLUCC 16-0585	*Sorbaronia mitschurinii* (A.K. Skvortsov & Maitul.) Sennikov	KY417756	KY417790	KY417824	KY417722
32	*Cytospora sorbicola*	MFLUCC 16-0586	*Prunus cerasus* L.	KY417757	KY417791	KY417825	KY417723
33	*Cytospora sorbicola*	MFLUCC 16-0633	*Cotoneaster melanocarpus* Fisch. ex Blytt	KY417758	KY417792	KY417826	KY417724
34	***Cytospora ulmi***	MFLUCC 15-0863	*Ulmus minor* Mill.	KY417759	KY417793	KY417827	KY417725

9.3 Results

9.3.1 Phylogenetic Analyses

The individual ITS dataset contained 143 sequences. The total alignment length had 609 total characters including alignment gaps. Parsimony analyses indicate that 391 characters were constant, 72 variable characters were parsimony uninformative and 146 characters were parsimony informative. The parsimony analysis of the data matrix resulted in 1000 equally parsimonious trees and the first tree (TL = 773, CI = 0.4373, RI = 0.8446, RC = 0.3693, HI = 0.5627) is shown in Figure 9.1. Based on MP, ML and BI analyses of individual ITS dataset can separate some species of *Cytospora* (Figure 9.1). However, it cannot resolve some species. For example *C. longiostiolata* (MFLUCC 16-0628), *C. melnikii* (MFLUCC 15-0851, MFLUCC 16-0635), *C. salicacearum* (MFLUCC 16-0509, MFLUCC 16-0576, MFLUCC 16-0587, MFLUCC 15-0861), *C. salicina* (MFLUCC 15-0862, MFLUCC 16-0637), *C. chrysosperma* (334, CFCC 89629, CFCC 89630, HMBF CGHs10, HMBF 151, HMBF 158, HMBF 17) and *Cytospora* sp. (30 NC5, 37 NC14) (Figure 9.1). Thus, a combined ITS, LSU, *rpb2* and *act* tree was used to delimit the *Cytospora* species. The combined ITS, LSU, *rpb2* and *act* analysis comprised 97 sequences. The total alignment length of 2337 characters including alignment gaps was used of which 609, 610–1163, 1164–2044 and 2045–2337 were derived from ITS, LSU, *rpb2* and *act* sequence data respectively. The result from the partition homogeneity test (PHT) was not significant level (95%), indicating that the individual data sets were congruent and could be combined. Parsimony analysis indicate that 1545 characters were constant, 240 variable characters were parsimony uninformative and 552 characters were parsimony informative and yielded 1000 most parsimonious trees (TL = 2020, CI = 0.554, RI = 0.864, RC = 0.479, HI = 0.446) (Figure 9.2). The BI and ML tree analyses of individual and combined phylogenies had similar topologies to the MP tree as shown in Figures 9.1 and 9.2 respectively. Bootstrap support values of MP, ML (≥70%) and Bayesian posterior probabilities (≥0.90) are shown on the upper branches (Figures 9.1 and 9.2). The molecular support obtained from phylogenetic topologies are discussed under notes of each species.



Note Phylogram generated from one of 1000 most parsimonious trees based on analysis of ITS sequence data of *Cytospora* isolates. The tree is rooted to *Phomopsis vaccinii* (ATCC 18451). Maximum parsimony and maximum likelihood bootstrap values ≥70%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/PP) are given at the nodes. The species obtained in this study are in blue and ex-types from the study are in blue bold. Ex-type taxa from other studies are in black bold.

Figure 9.1 Phylogenetic analysis of of *Cytospora*, based on ITS sequence data

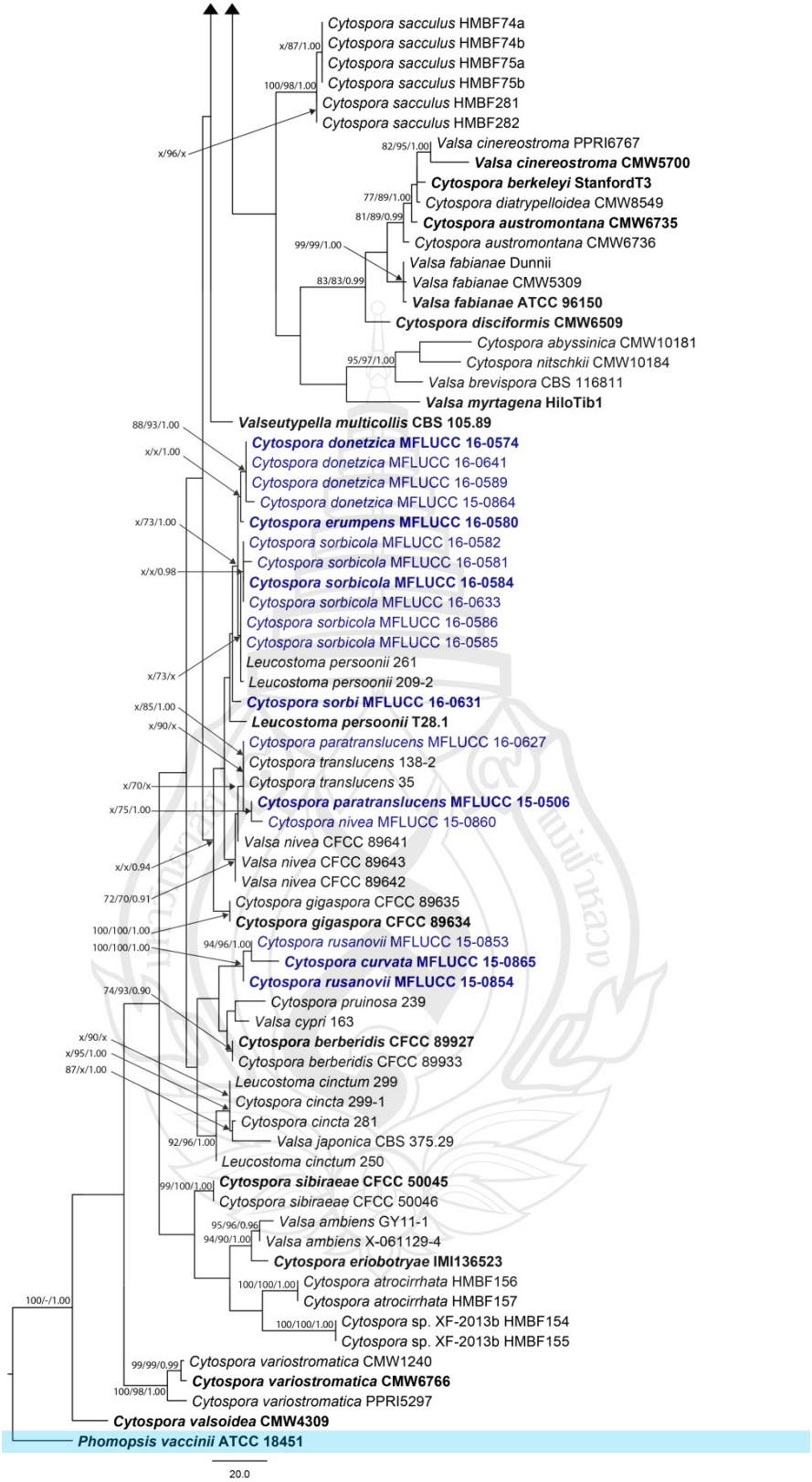
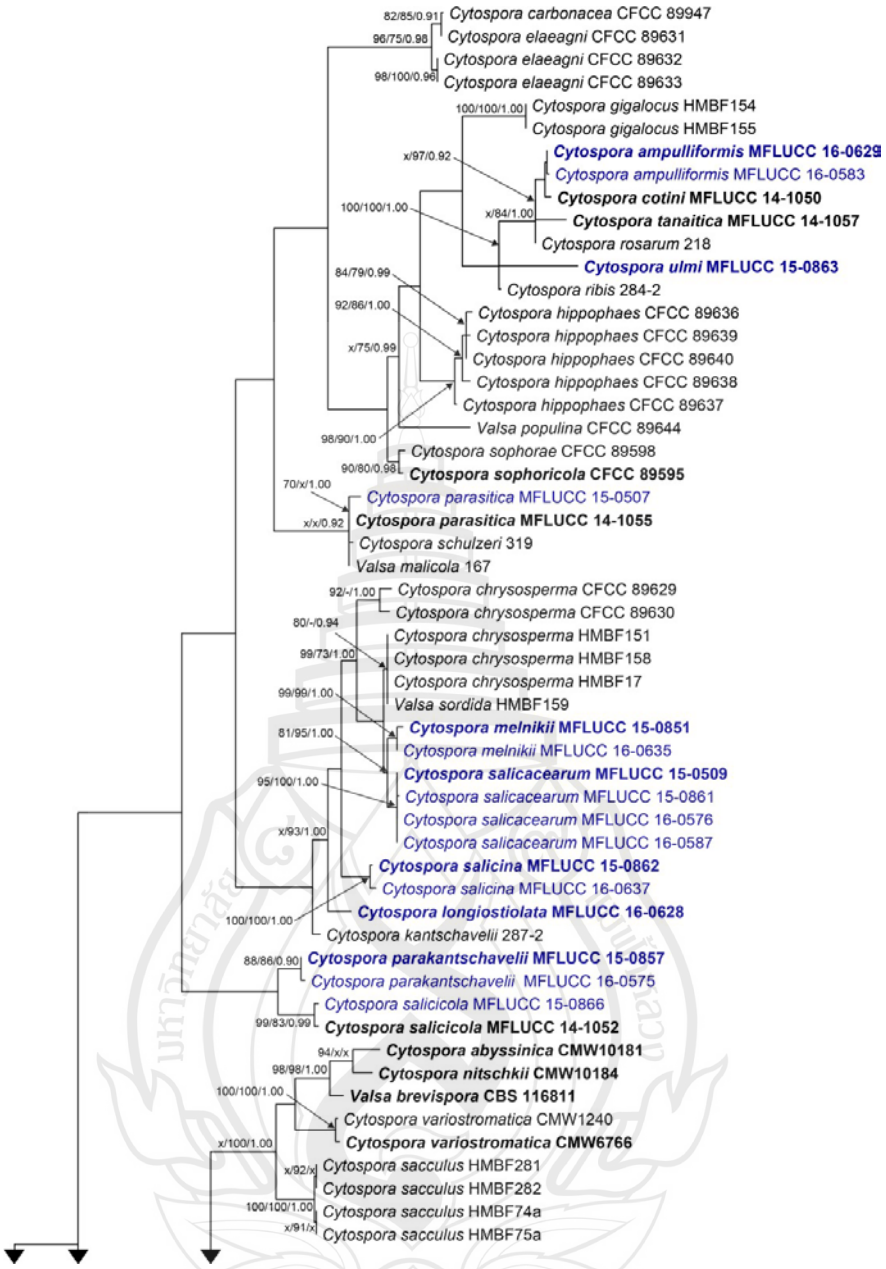


Figure 9.1 (continued)



Note Phylogram generated from one of 1000 most parsimonious trees based on analysis of combined ITS, LSU, *rpb2* and *act* sequence data of *Cytospora* isolates. The tree is rooted to *Phomopsis vaccinii* (ATCC 18451). Maximum parsimony and maximum likelihood bootstrap values ≥70%, Bayesian posterior probabilities ≥0.90 (MPBS/MLBS/PP) are given at the nodes. The species obtained in this study are in blue and ex-types from the study are in blue bold. Ex-type taxa from other studies are in black bold.

Figure 9.2 Phylogenetic analysis of *Cytospora*, based on combined sequence data

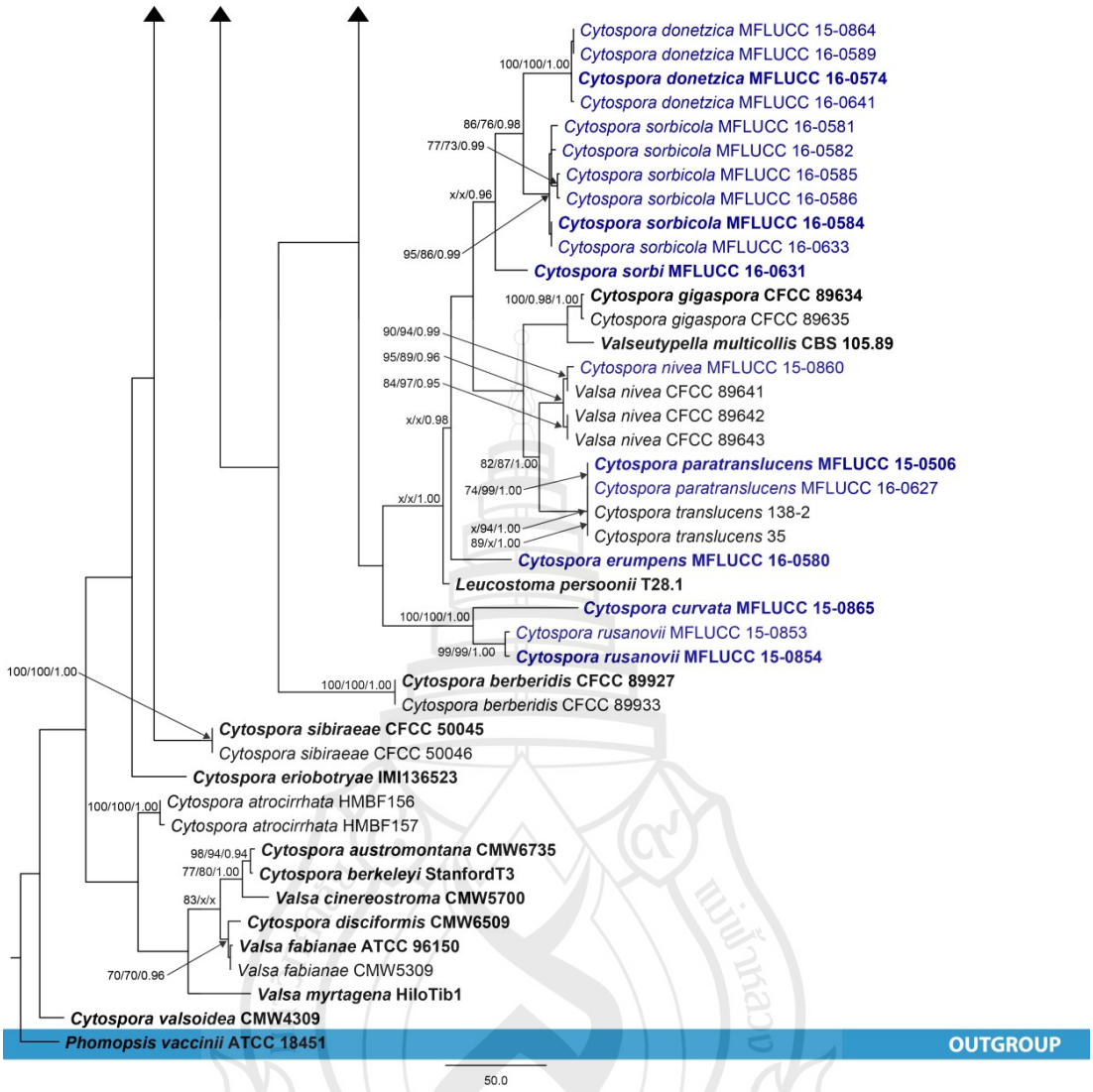


Figure 9.2 (continued)

9.3.2 Taxonomy

In this study, we introduce 14 new species and re-describe three known species. We follow Jeewon and Hyde (2016) for establishing species boundaries and Dayarathne et al. (2016) for using old names.

Cytospora ampulliformis Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.3

Index Fungorum number: IF552601

Facesoffungi Number: FoF 02736

Etymology: The specific epithet 'ampulliformis' refers to the flask-shaped conidiogenous cells.

Holotype: MFLU 15-2187

Associated with twigs and branches of *Sorbus intermedia* (Ehrh.) Pers. Sexual morph: Undetermined. Asexual morph: Conidiomata 680–1200 × 350–480 µm diameter, semi- immersed in host tissue, solitary, erumpent, scattered, discoid, circular to ovoid, with 3–4 locules, and ostiolar neck. Ostioles 200–300 µm long, at the same level as the disc surface. Peridium comprising few to several layers of cells of *textura angularis*, with inner most layer thin, hyaline to pale brown, outer layer brown to dark brown. Conidiophores unbranched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, flask-shaped phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (5–)5.6–9 × 1.3–1.6(–1.7) µm ($\overline{x}$ = 7.5 × 1.6 µm, n = 30), unicellular, subcylindrical, hyaline, smooth-walled.

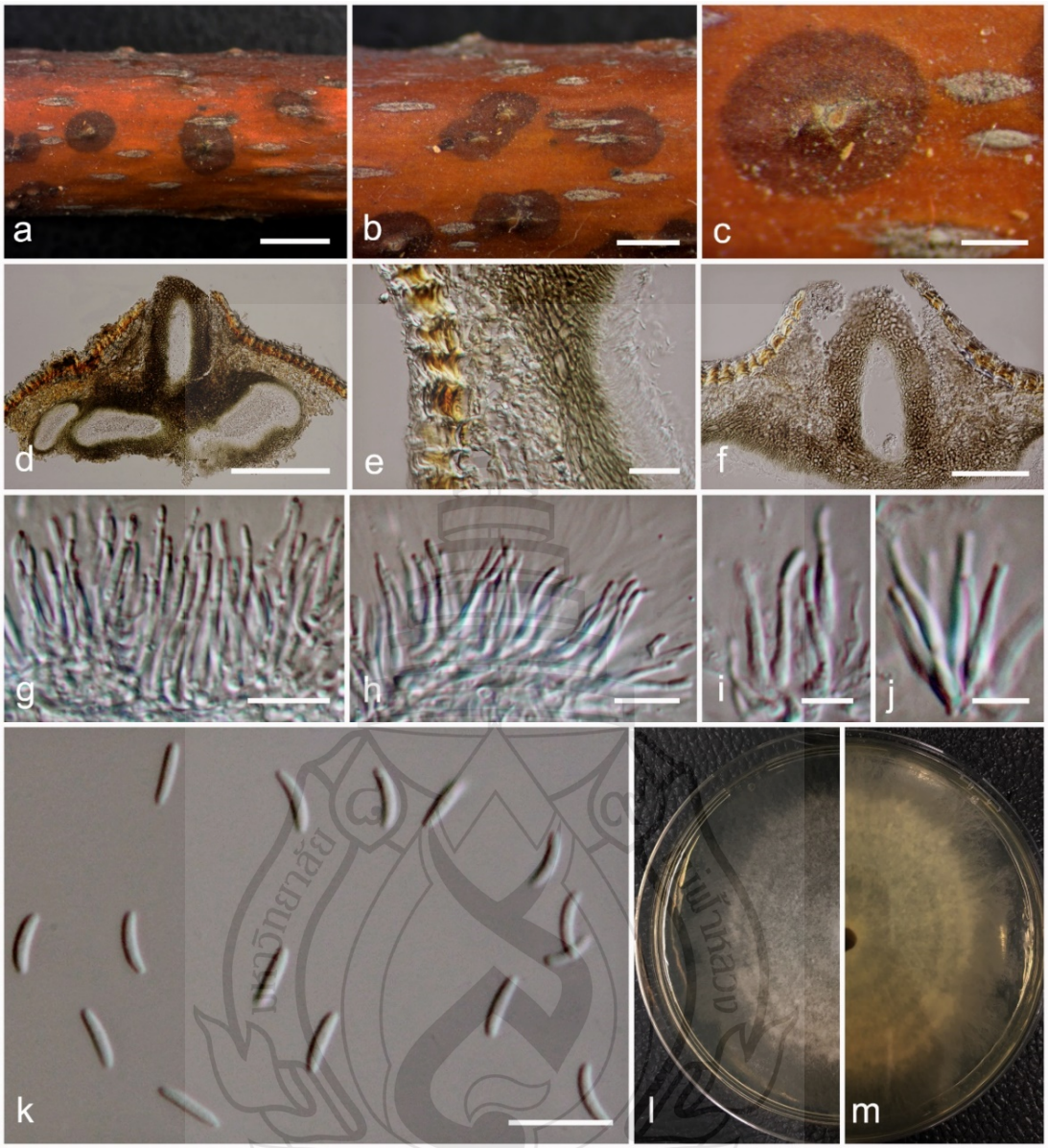
Culture characteristics: Colonies on MEA, reaching 7.5 cm diameter after 7 days at 25 °C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Rostov-on-Don City, Botanical Garden of Southern Federal University, Systematic Arboretum, parkland, dead and dying branches (necrotrophic) of *Sorbus intermedia* (Rosaceae), 30 May 2015, T. Bulgakov, T-483 (MFLU 15-2187, holotype, KUN, isotype), ex-type living culture, MFLUCC 16-0583, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye Forest, artificial forest, dying twigs and branches (necrotrophic) on *Acer platanoides* L. (Sapindaceae), 27 October 2015, T. Bulgakov, T-1094 (MFLU 15-3756, KUN), living culture, MFLUCC 16- 0629, KUMCC.

Notes: *Cytospora* species associated with *Sorbus* sp. were reported in previous studies such as *C. leucostoma* and *Valsa massariana* (Adams et al., 2002, 2005). In this study, *C. ampulliformis*, *C. sorbi* and *C. sorbicola* are also reported from *Sorbus* sp. (Table 9.3). Morphologically, *C. ampulliformis* is similar to *C. sorbi* in its conidiomata having 3–4 locules and in the length of ostiolar neck (*C. ampulliformis*: 200–300 µm versus 250–300 µm: *C. sorbi*). However, *C. ampulliformis* differs from *C. sorbi* in having larger conidia (*C. ampulliformis*: 7.5 × 1.6 µm, versus 6.5 × 1.5 µm: *C. sorbi*).

Based on phylogenetic analyses, both species form separate lineages within the genus *Cytospora* (Figures 9.1 and 9.2).

We obtained two isolates of *Cytospora ampulliformis* (MFLUCC 16-0583, MFLUCC 16-0629) and these formed a close relationship with *C. cotini* (MFLUCC 14-1050) isolated from *Cotinus coggygria, C. tanaitica* (MFLUCC 14-1057) isolated from *Betula pubescens*, *C. rosarum* (218) isolated from *Rosa canina* and *C. ulmi* (MFLUCC 15-0863) isolated from *Ulmus minor*. *Cytospora ampulliformis* (7.5 × 1.6 µm) differs from *C. cotini* in forming black-discoid conidiomata on the host and lobate circular colonies on MEA (Hyde et al., 2016), while it differs from *C. cotini* (5.9 × 1.2 µm), *C. tanatica* (3.4 × 0.7 µm), *C. rosarum* (5–6 × 1.5 µm) and *C. ulmi* (5.4 × 1.4 µm) by its larger conidia.



Note *Cytospora ampulliformis* on *Sorbus intermedia* (MFLU 15-2187, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–j Conidiogenous cells with attached conidia. k Mature conidia. l, m Colonies on MEA (l-from above, m-from below). Scale bars: a = 2000 µm, b = 1000 µm, c= 500 µm, d, f = 200 µm, e = 50 µm, f = 200 µm, g, h, k = 10 µm, i, j = 5 µm.

Figure 9.3 Morphological characters of *Cytospora ampulliformis* (MFLU 15-2187, holotype)

Cytospora curvata Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.4

Index Fungorum number: IF552602

Facesoffungi Number: FoF 02737

Etymology: The specific epithet "curvata" refers to the conidia character (Latin 'curvata' means 'crooked', 'bent', 'curved').

Holotype: MFLU 15-2229

Associated with twigs and branches of *Salix alba* L. Sexual morph: Undetermined. Asexual morph: Conidiomata 900–1100 × 470–580 µm diameter, semi-immersed in host tissue, scattered, erumpent, unilocular, with ostiolar neck. Ostioles 140–160 µm, same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with inner most layer thin, brown, outer later dark brown to black. Conidiophores unbranched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (5.4–)5.8–7.7 ×1.2–1.3(–1.4) µm ($\bar{x}$ = 5.9 × 1.3 µm, n = 30), unicellular, elongate- allantoid, slightly curved, hyaline, smooth-walled.

Culture characteristics: Colonies on MEA, reaching 8 cm diameter after 7 days at 25°C, producing dense mycelium, circular, white, margin rough, lacking aerial mycelium.

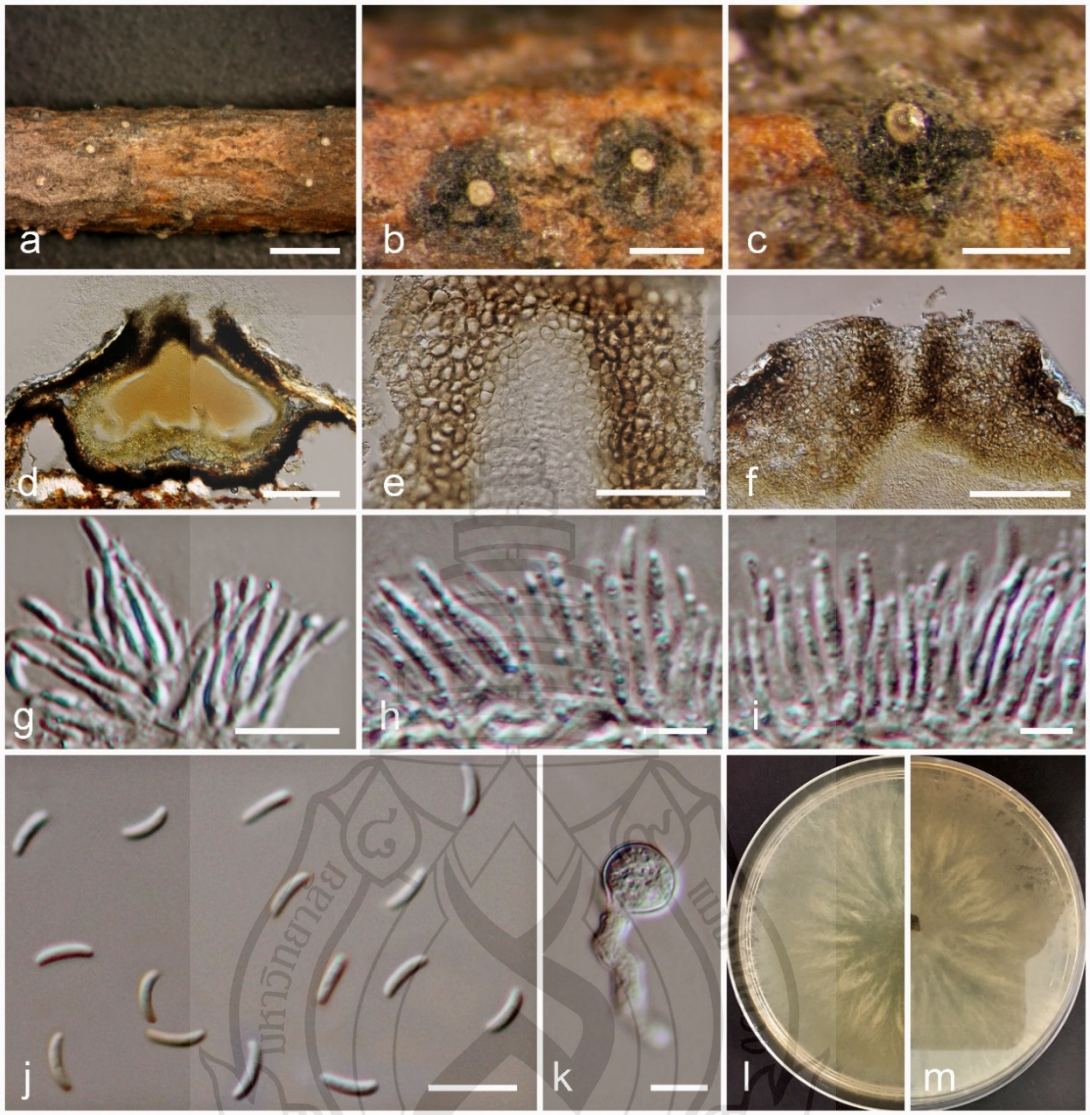
Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye Forest, shore of little pond, on dead and dying branches of *Salix alba* (Salicaceae), 28 June 2015, T. Bulgakov, T-525 (MFLU 15-2229, holotype, KUN, isotype), ex-type living culture, MFLUCC 15-0865, KUMCC.

Notes: Many *Cytospora* species have been reported from *Salix* worldwide (Table 9.3; Adams et al., 2002, 2005, 2006; Défago, 1942; Fotouhifar et al., 2010; Singh et al., 2007). However, they can be distinguished based on phylogenetic analyses (Fan et al., 2014; Wang et al., 2015). Ten novel species are introduced in this study, which were collected from *Salix viz. C. curvata*, *C. donetzica*, *C. erumpens*, *C. longiostiolata*, *C. rusanovii*, *C. salicacearum*, *C. salicina*, *C. salicacearum*, *C. salicicola and C. salicina*. *Cytospora curvata* is most similar to *C. longiostiolata* (MFLUCC 16-0628), but the former species differs in having shorter ostiolar necks (*C. curvata*: 140–160 µm

versus 400–500 µm: *C. longiostiolata*) and larger conidia (*C. curvata*: 5.9 × 1.3 µm versus 5.5 × 1.3 µm: *C. longiostiolata*).

Phylogenetic analysis of combined ITS, LSU, *rpb2* and *act* sequence data indicate that *Cytospora curvata* (MFLUCC 15-0865) forms a separate branch as a sister taxon to *C. rusanovii* (MFLUCC 15-0853, MFLUCC 15-0854) (Figures 9.1 and 9.2). *Cytospora rusanovii* is reported in this study, also from *Salix*. *Cytospora rusanovii* differs from *C. curvata* in having conidiomata with 4–6 locules, long ostioles (410–450 µm), branched conidiophores and conidia that are shorter and wider (5.4 × 1.4 µm) than *C. curvata*.

In ITS, *Cytospora rusanovii* differs from *C. curvata* at six polymorphisms, in *act*, they are different at six polymorphisms. Thus, based on phylogenetic analysis, polymorphic nucleotide comparisons and morphological differences, *C. melnikii* it is considered as a novel species.



Note *Cytospora curvata* on *Salix alba* (MFLU 15-2229, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostioles. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l-from above, m- from below). Scale bars: a = 2000 µm, b, c = 500 µm, d = 200 µm, e = 50 µm, f = 100 µm, g, j, k = 10 µm, h, i = 5 µm.

Figure 9.4 Morphological characters of *Cytospora curvata* (MFLU 15-2229, holotype)

Cytospora donetzica Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.5

Index Fungorum number: IF552603

Facesoffungi Number: FoF 02738

Etymology: The specific epithet "donetzica" refers to biogeographical region of Donets ridge (Donets highland) and Seversky Donets river basin, where the type specimens were collected.

Holotype: MFLU 15-2093

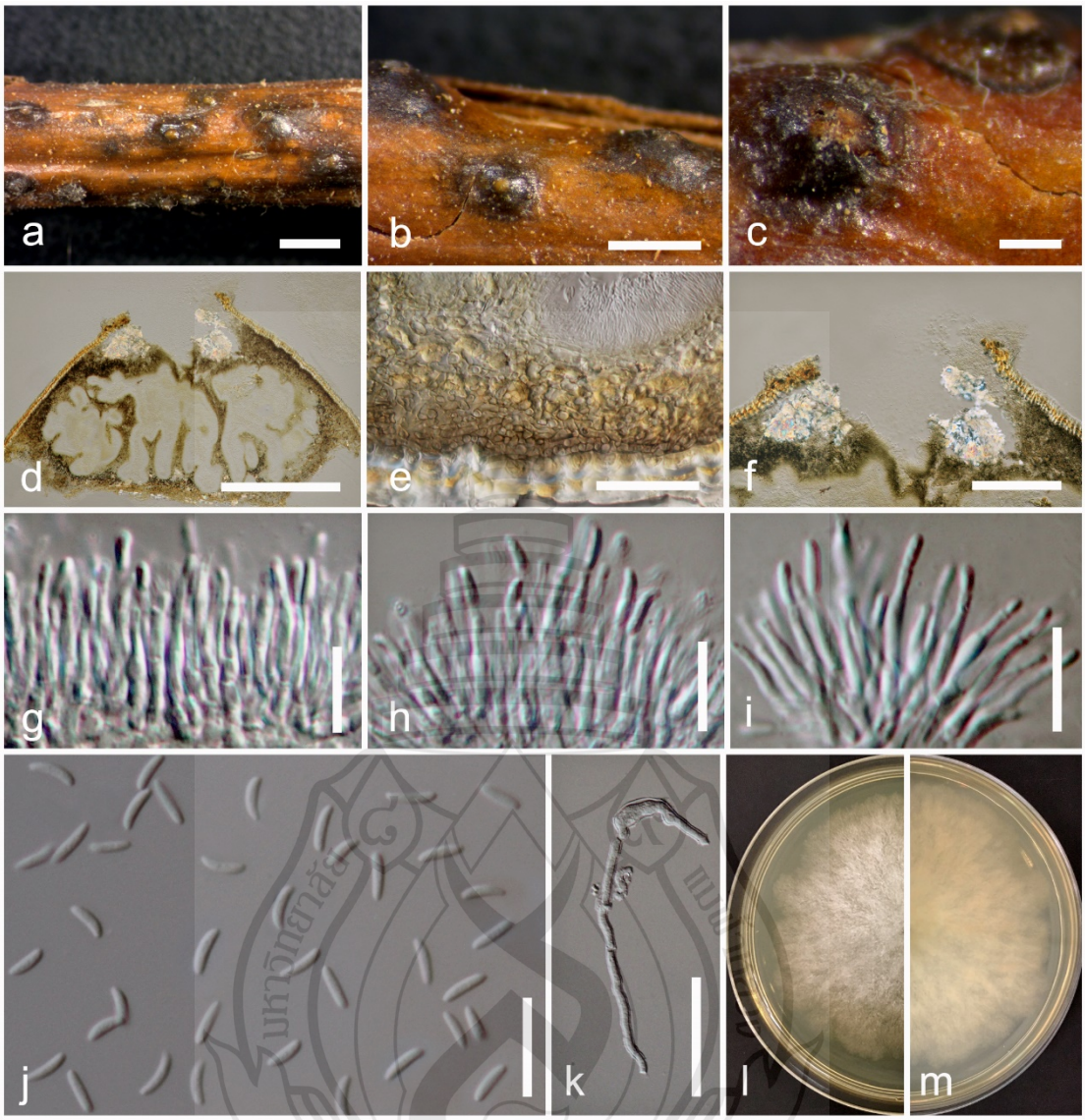
Associated with twigs and branches of *Crataegus monogyna* Jacq., *Pyrus pyraster* (L.) Burgsd., *Rosa* sp. and *Salix alba*. Sexual morph: Undetermined. Asexual morph: Conidiomata 800–1200 × 480–560 µm diameter, semi-immersed in host tissue, scattered, with 3–4 locules, with ostiolate. Ostioles 150–250 µm diameter, at the same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with inner most layer thin, pale brown, outer later brown. Conidiophores branched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (4.6–)5.4–6.4 ×1.2–1.4(– 1.6) µm ($\bar{x}$ = 5.5 × 1.4 µm, n = 30), unicellular, elongate-allantoid, slightly curved, hyaline, smooth-walled.

Culture characteristics: Colonies on MEA, reaching 7 cm diameter after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, with aerial mycelium.

Material examined: RUSSIA, Rostov Region, Shakhty City, Grushevka steppe slopes near Grushevsky pond, ravine shrubbery, on dead and dying branches of *Rosa* sp. (Rosaceae), 14 May 2015, T. Bulgakov, T-389 (MFLU 15-2093, holotype, KUN, isotype), ex-type living culture, MFLUCC 16-0574, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, stony steppe, on dead and dying branches of *Crataegus monogyna* (Rosaceae), 28 June 2015, T. Bulgakov, T-523 (MFLU 15-2227, KUN), living culture, MFLUCC 15-0864, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, riparian forestry, on dead and dying branches of *Salix alba* (Salicaceae), 18 June 2015, T. Bulgakov, T-343 (MFLU 15-2047, KUN), living culture, MFLUCC 16-0589, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, ravine forest, on dying

twigs and branches of *Pyrus pyraster* (Rosaceae), 27 October 2015, T. Bulgakov, T-1102 (MFLU 15-3764, KUN), living culture, MFLUCC 16-0641, KUMCC.

Notes: We observed four isolates of *Cytospora donetzica* (MFLUCC 16-0574, MFLUCC 15-0864, MFLUCC 16-0589, MFLUCC 16-0641) which clustered on a relative independent branch with high bootstrap support (100% MP/ 100% ML/ 1.00 PP, Figure 9.2). The new species is introduced with the type from *Rosa* sp. *Cytospora donetzica* is most similar to *C. ceratosperma* (Tode) G.C. Adams & Rossman in its conidia size (5.5 × 1.4 µm versus 5–6 × 1.4 µm) (Saccardo 1884). However, based on combined gene phylogenetic analysis, *C. donetzica* is clearly separated from *C. ceratosperma* and sister to *C. sorbicola* with high bootstrap support (86% MP/76% ML/0.98 PP) (Figure 9.2). In the polymorphic nucleotides of ITS, *rpb2* and *act* sequence data, *C. donetzica* differs from *C. sorbicola* with five ITS polymorphisms, 23 *rpb2* polymorphisms and seven *act* polymorphisms. Thus, *C. donetzica* is considered as a novel species.



Note *Cytospora donetzica* on *Rosa* sp. (MFLU 15-2093, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostioles. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l-from above, m- from below). Scale bars: a = 2000 µm, b = 1000 µm, c, d = 500 µm, f = 200 µm, e, k = 50 µm, g–j = 10 µm.

Figure 9.5 Morphological characters of *Cytospora donetzica* (MFLU 15-2093, holotype)

Cytospora erumpens Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.6

Index Fungorum number: IF552604

Facesoffungi Number: FoF 02739

Etymology: The specific epithet 'erumpens' refers to the conidiomata characteristic as erumpent.

Holotype: MFLU 15-2165

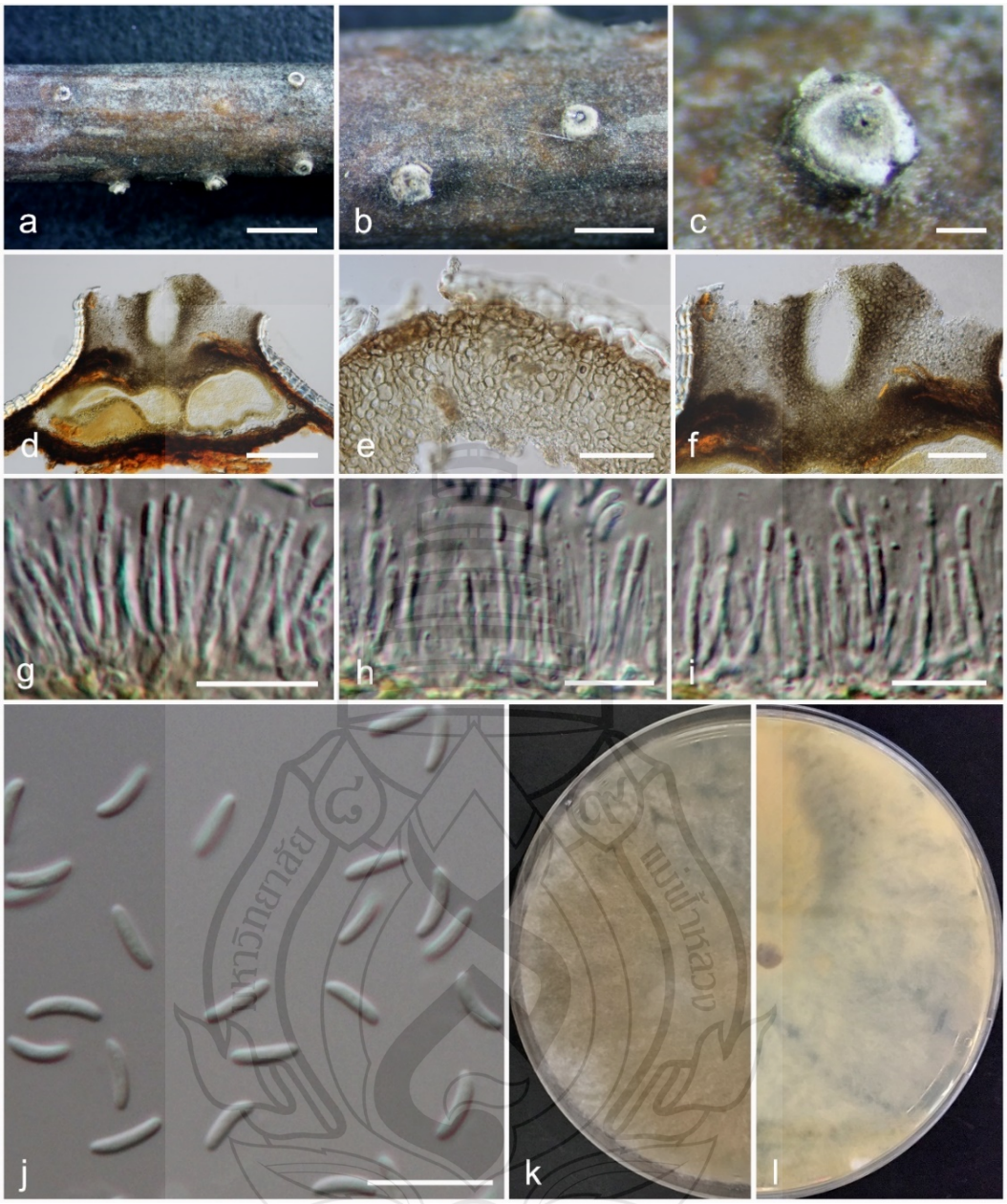
Associated with twigs and branches of *Salix* × *fragilis* L. [*S. alba* L. × *S. euxina* I.V. Belyaeva]. Sexual morph: Undetermined. Asexual morph: Conidiomata 720–1000 × 470–550 µm diameter, semi-immersed in host tissue, solitary, erumpent, with 1–3 locules, with ostiolar neck. Ostioles 280–350 µm, at the same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with inner layer thin, pale brown, outer later brown to dark brown. Conidiophores unbranched or occasionally branched at the base, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (5.6–)6.4–6.7 ×1.3–1.4(–1.7) µm ($\bar{x}$ = 6.4 × 1.5 µm, n = 30), unicellular, elongate- allantoid, hyaline, thin-walled, smooth-walled.

Culture characteristics: Colonies on MEA, reaching 8.5 cm diameter after 7 days at 25 °C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Shakhty City, Grushevka steppe slopes, near Grushevsky pond, osier-bed near pond, on dead and dying branches of *Salix* × *fragilis* L. [*S. alba* L. × *S. euxina* I.V. Belyaeva]. (Salicaceae), 14 May 2015, T. Bulgakov, T-461 (MFLU 15-2165, holotype, PDD isotype), ex-type living culture, MFLUCC 16-0580, KUMCC.

Notes: Morphologically, *Cytospora erumpens* is most similar to *C. sorbi* (MFLUCC 16-0631) with conidia 6.4 × 1.5 µm versus 6.5 × 1.5 µm. However, in the combined gene phylogenetic analysis, *C. erumpens* is clearly separated from *C. sorbi* (Figure 9.2). *Cytospora erumpens* and *C. rusanovii* are similar in morphology and also associated with the same host, *Salix* spp. However, *C. erumpens* differs from *C. rusanovii* in forming black-discoid conidiomata on the host and longer ostiolar necks (*C. erumpens*: 280–350 µm versus 155– 170 µm: *C. rusanovii*).

In phylogenetic study based on the ITS gene show that *Cytospora erumpens* is close to *C. donetzica*, but in the combined gene phylogenetic analysis, *C. erumpens* is separated from *C. donetzica* and some species in the genus (*C. donetzica, C. sorbicola, C. sorbi, C. gigaspora*, *C. nivea*, *C. paratranslucens, C. translucens*) with Bayesian posterior probabilities of 0.98 (Figure 9.2). The ITS, *rpb2* and *act* polymorphic nucleotides of sequence data, *C. erumpens* differs from *C. sorbi* with four ITS polymorphisms, 43 *rpb2* polymorphisms and 13 *act* polymorphisms. Thus, it is considered that *C. erumpens* is a novel species.



Note *Cytospora erumpens* on *Salix* × *fragilis* L. (MFLU 15-2165, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with attached conidia. j Mature conidia. k, l Colonies on MEA (k-from above, l-from below). Scale bars: a = 2000 µm, b = 1000 µm, c, d = 200 µm, e = 50 µm, f = 100 µm, g–j = 10 µm.

Figure 9.6 Morphological characters of *Cytospora erumpens* (MFLU 15-2165, holotype)

Cytospora longiostiolata Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.7

Index Fungorum number: IF552605

Facesoffungi Number: FoF 02740

Etymology: The specific epithet 'longiostiolata' refers to the long ostiolate of conidiomata.

Holotype: MFLU 15-3784

Associated with twigs and branches of *Salix* × *fragilis* L. [*S. alba* L. × *S. euxina* I.V. Belyaeva]. Sexual morph: Undetermined. Asexual morph: Conidiomata 880–1000 × 480–600 µm diameter, semi-immersed in host tissue, solitary, erumpent, discoid, circular to ovoid, unilocular, with long ostiolar neck with ratio of conidiomata (3:4). Ostioles 400–500 µm diameter, at the same level as the disc surface. Peridium comprising several layers of cells of *textura angularis*, with inner most layer thin, pale brown, outer layer brown. Conidiophores unbranched or occasionally branched at the base, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (3.9–)5.4–6.6 ×1.0–1.2(–1.5) µm ($\bar{x}$ = 5.5 × 1.3 µm, n = 30), unicellular, allantoid to subcylindrical, hyaline, smooth-walled.

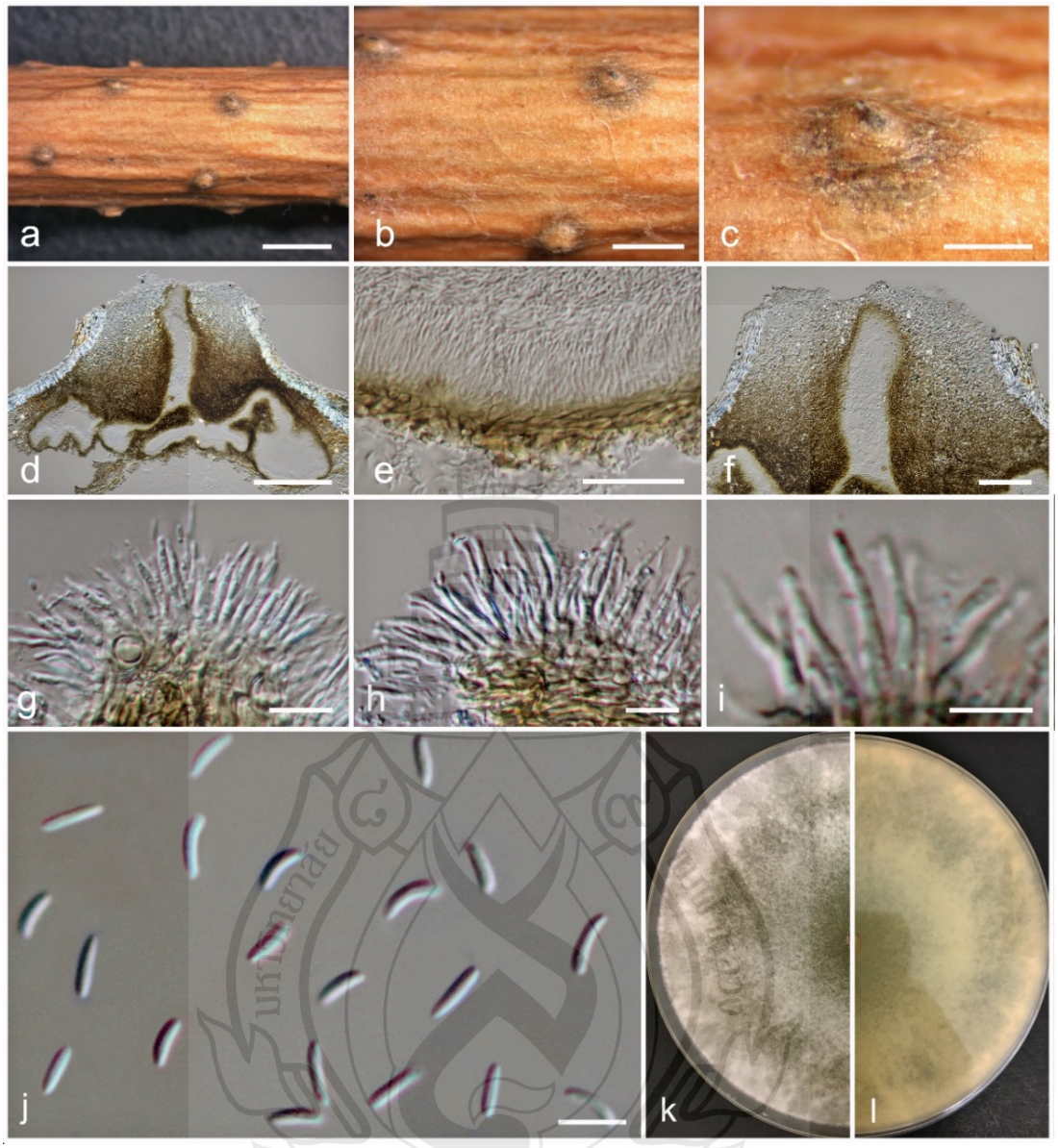
Culture characteristics: Colonies on MEA, reaching 9 cm diameter after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, with aerial mycelium.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, spinney ravine, on dying twigs and branches of *Salix* × *fragilis* L. [*S. alba* L. × *S. euxina* I.V. Belyaeva] (Salicaceae), 27 October 2015, T. Bulgakov, T-1122 (MFLU 15-3784, holotype, KUN, isotype), ex-type living culture, MFLUCC 16-0628, KUMCC.

Notes: *Cytospora longiostiolata* is introduced as new species base on morphological characters and phylogenetic analyses. It has unilocular conidiomata with long ostioles. Phylogenetic analysis using ITS sequence data showed that *C. longiostiolata* is closely related to *C. salicina* (MFLUCC 15-0862, MFLUCC 16-0637) and *C. chrysosperma* species (Figure 9.1). However, *C. salicina* (4.8 × 1.1 µm) and *C. chrysosperma* (4.6 × 1.2 µm) differ from *C. longiostiolata* (5.5 × 1.3 µm) in having

multiloculate conidiomata with smaller conidia. In the phylogenetic analyses based on combined ITS, LSU, *rpb2* and *act* sequence data, *C. longiostiolata* forms a single lineage, separate from these taxa with high bootstrap support (93% ML/ 1.00 PP) (Figure 9.2). *Cytospora longiostiolata* was collected from *Salix* and is most similar to *C. curvata* and the differences are discussed under the species *C. curvata*. The species also resembles *C. donetzica* in conidia size (*C. longiostiolata*: 5.5 × 1.3 versus 5.5 × 1.4 µm: *C. donetzica*). However, *C. donetzica* differs *C. longiostiolata* in having 3–4 locules conidiomata and shorter ostiolar necks (150–250 µm).

In ITS, *Cytospora longiostiolata* differs from *C. chrysosperma* with two polymorphisms, with *C. salicina* in five polymorphisms. In *rpb2* it differs with 21 polymorphisms from *C. chrysosperma*, 19 polymorphisms from *C. salicina*. In *act* it differed in 11 polymorphisms from *C. chrysosperma* and 11 polymorphisms from *C. salicina*.



Note *Cytospora longiostiolata* on *Salix* × *fragilis* (MFLU 15-3784, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with attached conidia. j Mature conidia. k, l Colonies on MEA (k-from above, l-from below). Scale bars: a = 2000 µm, b = 1000 µm, c = 500 µm, d = 200 µm, e = 20 µm, f = 100 µm, g, h = 10 µm, i, j = 5 µm.

Figure 9.7 Morphological characters of *Cytospora longiostiolata* (MFLU 15-3784, holotype)

Cytospora melnikii Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.8

Index Fungorum number: IF552606

Facesoffungi Number: FoF 02741

Etymology: The species named after the famous Russian mycologist Vadim Alexandrovich Melnik, researcher of anamorphic fungi.

Holotype: MFLU 15-1910

Associated with twigs and branches of *Malus domestica* Borkh. and *Populus nigra* L. var. *italica* Münchh. Sexual morph: Undetermined. Asexual morph: Conidiomata 470–520 × 370–420 µm diameter, semi-immersed in host tissue, solitary, scattered, erumpent, discoid, circular to ovoid, unilocular, with long ostiolar neck. Ostioles 200–230 µm long at the same level as the disc surface. Peridium comprising several layers of cells of *textura angularis*, with inner most layer thick, dark brown, outer layer dark brown to black. Conidiophores unbranched or occasionally branched at the base, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (3.1–)4.5–5 ×1–1.2(–1.3) µm ($\bar{x}$ = 4.6 × 1.2 µm, n = 30), unicellular, allantoid to subcylindrical, hyaline, smooth-walled.

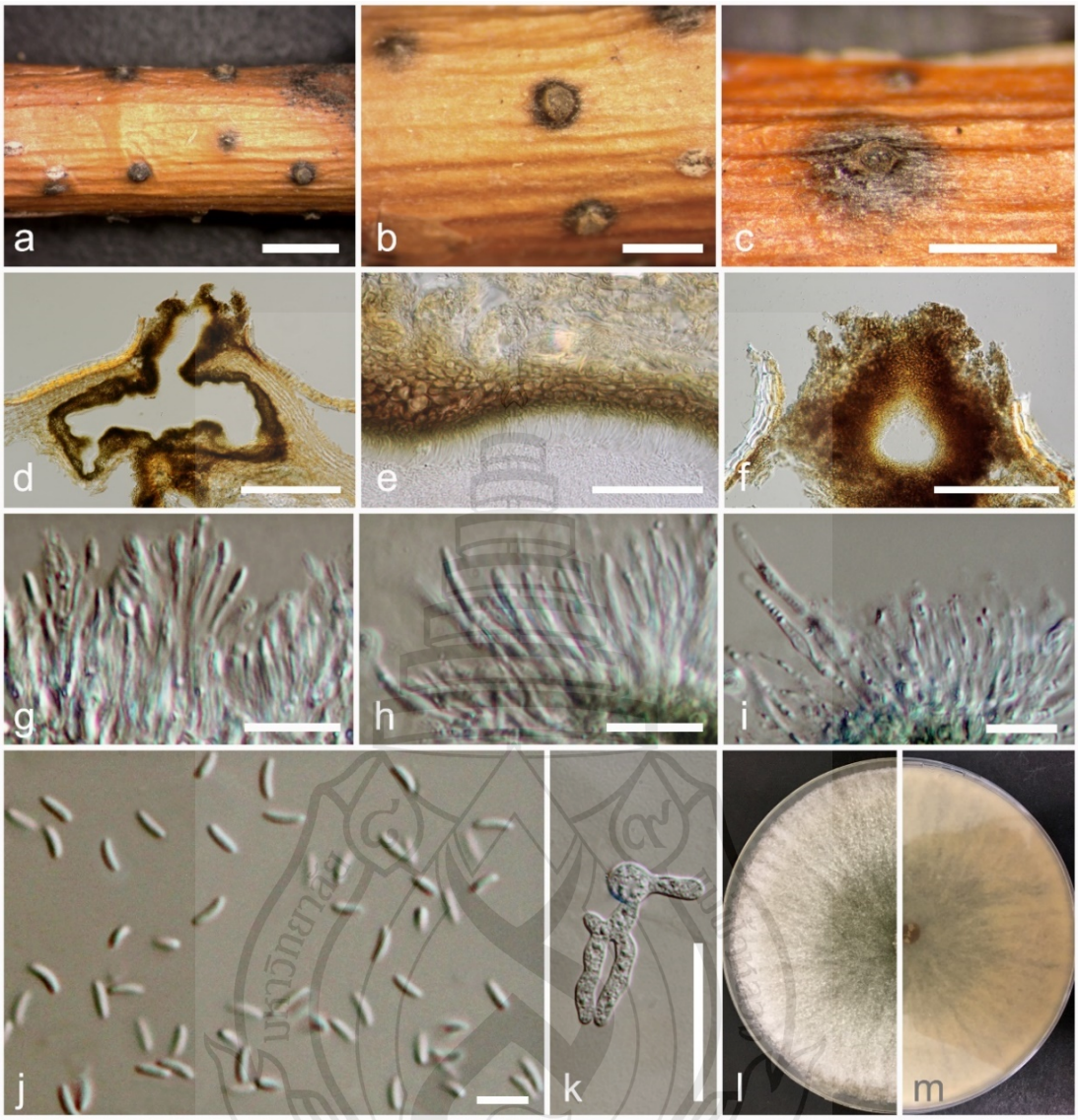
Culture characteristics: Colonies on MEA, reaching the edge of the Petri-dish after 6–7 days at 25 °C, producing dense mycelium, circular, margin rough, white, with aerial mycelium.

Material examined: RUSSIA, Rostov Region, Oktyabrsky District, south edge of Persianovsky settlement, Khoruli gully, field-protecting shelterbelt, on dying branches of *Malus domestica* (Rosaceae), 28 April 2015, T. Bulgakov, T-206 (MFLU 15-1910, holotype, KUN, isotype), ex-type living culture, MFLUCC 15-0851, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, lining-out nursery, trees and shrubs, on dying twigs and branches of *Populus nigra* L. var. italica (Salicaceae), 27 October 2015, T. Bulgakov, T-1104 (MFLU 15-3766, KUN), living culture, MFLUCC 16-0635, KUMCC.

Notes: *Cytospora melnikii* was found on *Malus domestica* and *Populus nigra*, and has semi-immersed, unilocular conidiomata, with long ostioles and shares common walls with the host tissue. *Cytospora melnikii* can be distinguished based on the

characteristics of fruiting bodies, conidia size, cultural characteristics and phylogenetic analyses. *Cytospora melnikii* is most similar to *C. chrysosperma*, which was found Malus. However, *C. chrysosperma* differs in having a multiloculate conidiomata (Mehrabi et al., 2011).

In phylogenetic analyses, using ITS sequence data (Figure 9.1), *C. melnikii* groups with *C. chrysosperma* (HMBF151, HMBF158, HMBF17) and *C. salicacearum* (MFLUCC 16-0509, MFLUCC 16-0587, MFLUCC 15-0861, MFLUCC 16-0576). The tree using ITS, LSU, *rpb2* and *act* sequence data demonstrate that *C. melnikii* is clearly separated from these taxa, with moderate bootstrap support (Figure 9.2). Thus, based on phylogenetic analysis and morphological differences, it is considered that *C. melnikii* is a novel species.



Note *Cytospora melnikii* on *Malus domestica* (MFLU 15-1910, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with attached conidia. j Conidia. k Germinating spore. l, m Colonies on MEA with 7 days (l-from above, m-from below). Scale bars: a =2000 µm, b = 500 µm, c = 500 µm, d = 200 µm, e = 30 µm, f = 100 µm, g, h, i, j = 10 µm.

Figure 9.8 Morphological characters of *Cytospora melnikii* (MFLU 15-1910, holotype)

Cytospora nivea (Hoffm.) Sacc., Michelia 2: 264 (1881), Figure 9.9

For other possible synonyms see Index Fungorum

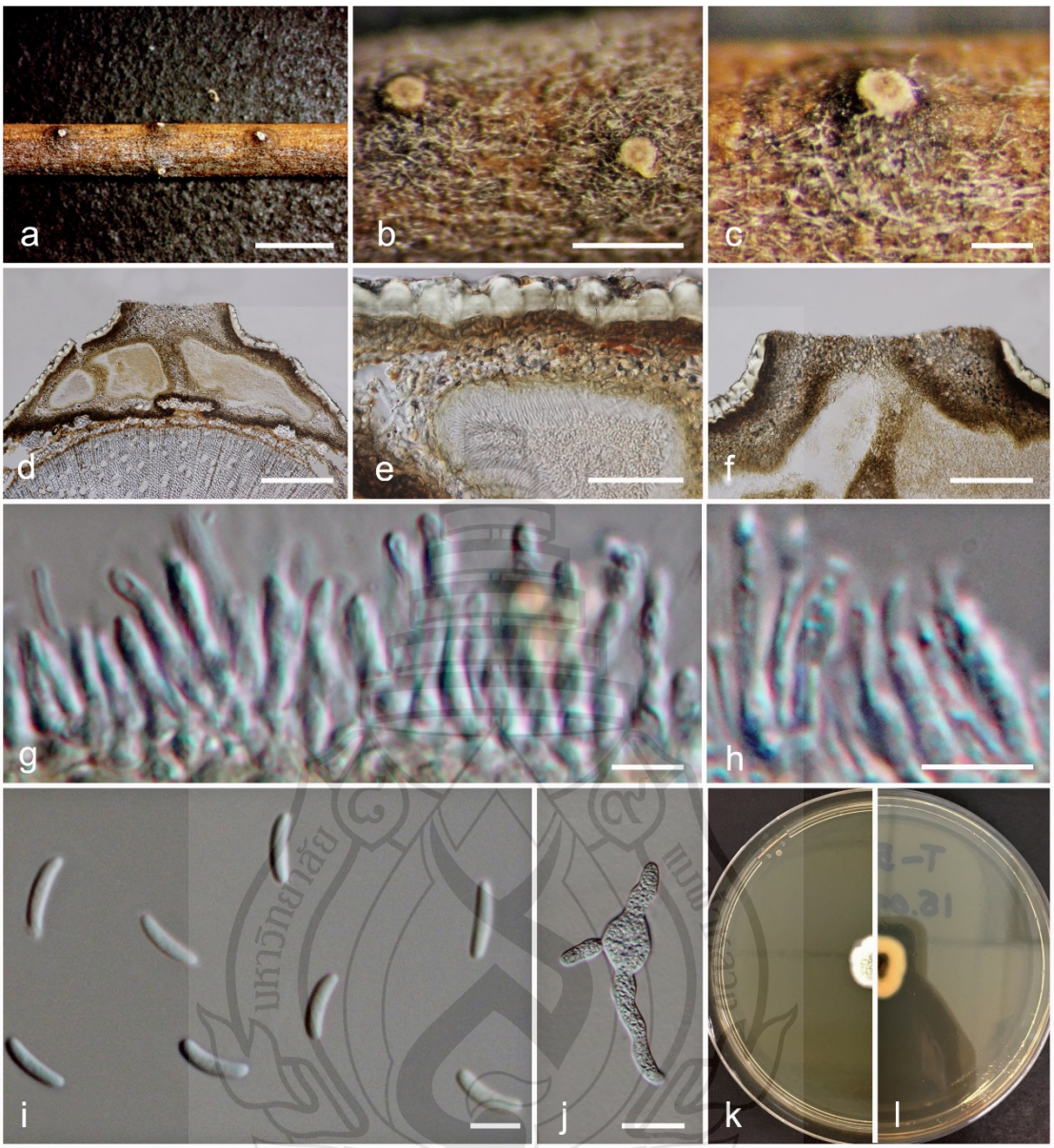
Facesoffungi Number: FoF 02742

Associated with twigs and branches of *Salix acutifolia* Willd. Sexual morph: Undetermined. Asexual morph: Conidiomata 1000–1300 × 340–380 µm diameter, semi- immersed in host tissue, scattered, erumpent, discoid, circular, with 3–4 locules, ostiolate. Ostioles 100–150 µm diameter, at the same level, with flattened top. Peridium comprising a few to several layers of cells of *textura angularis*, inner layer thick, brown, outer later dark brown. Conidiophores unbranched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (7.1–)7.4–8.8 × 1.5–1.6(–1.9) µm ($\bar{x}$ = 7.5 × 1.8 µm, n = 30), unicellular, allantoid, slightly curved ends, hyaline, smooth-walled.

Culture characteristics: Colonies on MEA, reaching 2 cm diameter, after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Ust'-Donestsky District, near Nizhnekundryuchenskaya Village, arenal sandy forest, on dead and dying branches of *Salix acutifolia* (Salicaceae), 17 August 2015, T. Bulgakov, T-506 (MFLU 15-2210, PDD), living culture, MFLUCC 15-0860, KUMCC.

Notes: Fan et al. (2015b) have reported and illustrated *Cytospora nivea* (CFCC 89642). The morphology of our fresh collection resembles *C. nivea* (epitype) in Fan et al. (2015b) in having multiloculate conidiomata, allantoid, slightly curved, hyaline and 7.6 × 1.9 µm conidia and in the combined multi-gene phylogeny (Figures 9.1 and 9.2). This is the first report of *C. nivea* from *Salix a*cutifolia in Russia therefore, details are provided for this species to facilitate identification.



Note *Cytospora nivea* on *Salix acutifolia* (MFLU 15-2210). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing perithecia. e Peridium. f Ostioles. g–h Conidiogenous cells with intact conidia. i Conidia. j Germinating spore. k, l Colonies on MEA (k-from above, l-from below). Scale bars: a = 2000 µm, b = 500 µm, c, d = 200 µm, e, f = 50 µm, j = 20 µm, g, h, i = 5 µm.

Figure 9.9 Morphological characters of *Cytospora nivea* (MFLU 15-2210)

Cytospora parakantschavelii Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.10

Index Fungorum number: IF552607

Facesoffungi Number: FoF 02743

Etymology: The specific epithet is composed from Greek prefix 'para-' meaning 'near' or 'beside' and 'kantschavelii' is from the species name, in reference to the occurrence on *Cytospora* species.

Holotype: MFLU 15-2094

Associated with twigs and branches of *Populus* × *sibirica* G.V. Krylov & G.V. Grig. ex A.K. Skvortsov [*P. balsamifera* L. × *P. nigra* L.] and *Pyrus pyraster* (L.) Burgsd. Sexual morph: Undetermined. Asexual morph: Conidiomata 750–900 × 750–850 µm diameter, semi-immersed in host tissue, solitary, scattered, erumpent, with 3–6 locules, with ostiolar neck. Ostioles 540–680 µm diameter, at the same level as the disc surface. Peridium comprising several layers of cells of *textura angularis*, with inner most layer thin, hyaline to brown, outer layer brown to dark brown. Conidiophores branched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, hyaline, smooth-walled. Conidia (4.5–)5.3–5.7 ×1.1–1.3(–1.6) µm ($\bar{x}$ = 5.3 × 1.4 µm, n = 30), unicellular, elongate-allantoid, hyaline, smooth-walled.

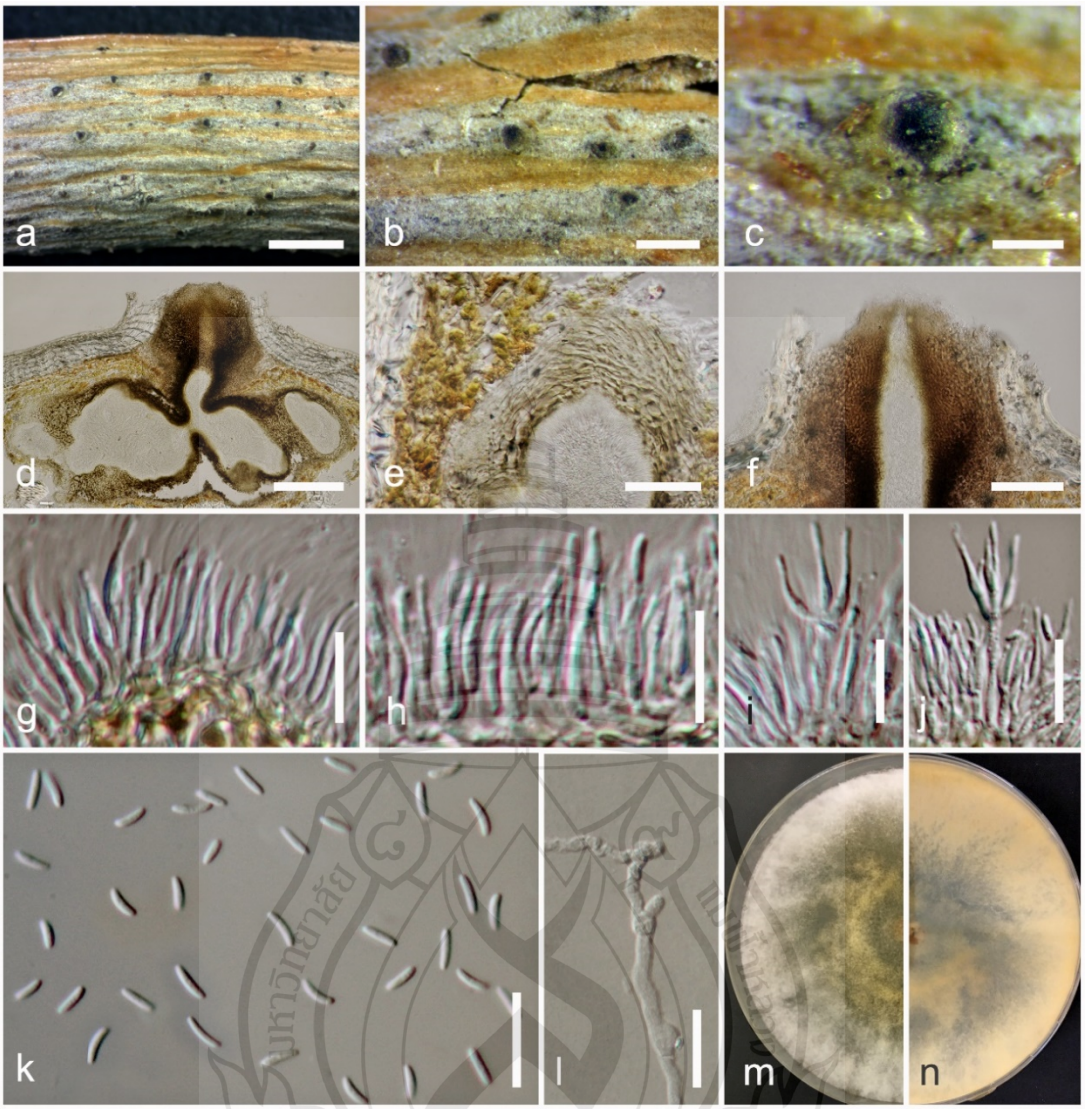
Culture characteristics: Colonies on MEA, reaching 8 cm diameter after 7 days at 25°C, producing dense mycelium, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Shakhty City, steppe slopes near Grushevsky pond, ravine shrubbery, on dead and dying branches of *Pyrus pyraster* (L.) Burgsd. [= *P. communis* auct.] (Rosaceae), 14 May 2015, T. Bulgakov (MFLU 15-2094, holotype, PDD isotype), ex-type living culture, MFLUCC 16-0575, KUMCC; RUSSIA, Rostov Region, Shakhty City, block landpark, on dying branches of *Populus* × *sibirica* G.V. Krylov & G.V. Grig. ex A.K. Skvortsov [*P. balsamifera* L. × *P. nigra* L.] (Salicaceae), 12 May 2015, T. Bulgakov (MFLU 15-1953, PDD), living culture, MFLUCC 15-0857, KUMCC.

Notes: The new species, *Cytospora parakantschavelii* (MFLUCC 16-0575, MFLUCC 15-0857) is similar to *C. kantschavelii* (287-2) in having multiloculate conidiomata. However, conidial dimensions of *C. parakantschavelii* (5.3 × 1.4 µm) are

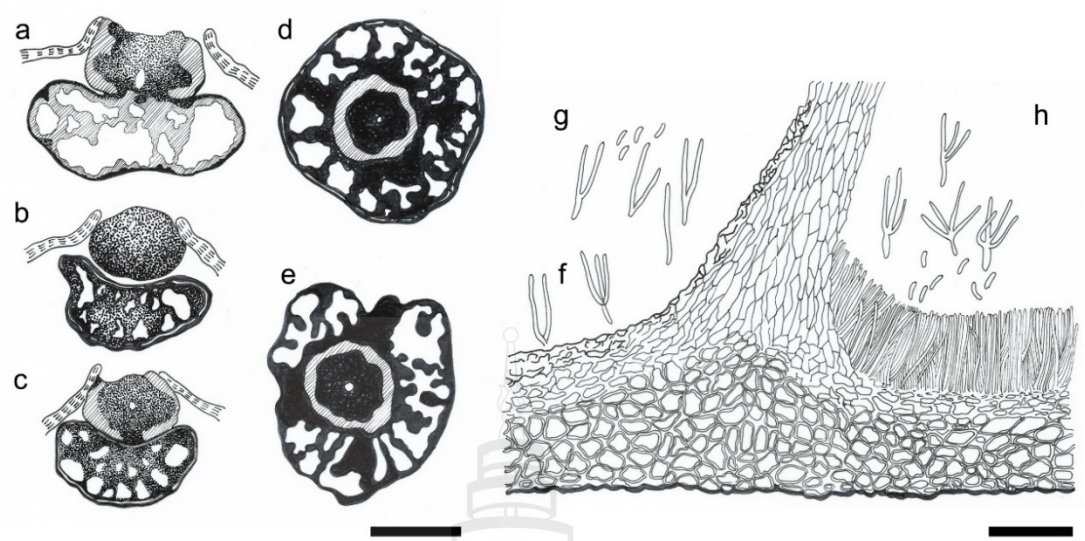
longer and wider than those of *C. kantschavelii* (4–5 × 1.2 µm) (Figure 9.11) (Gvritishvili, 1973).

Phylogenetic analysis of four combined gene loci place *Cytospora parakantschavelii* (MFLUCC 16-0575, MFLUCC 15-0857) on a separate branch from *C. kantschavelii*, forming as a sister taxon to *C. salicicola* Norphanphoun, Bulgakov & Hyde (MFLUCC 14-1052, MFLUCC 15-0866) (Figure 9.2). However, *C. salicicola* differs from *C. parakantschavelii* in having shorter ostioles (170–200 µm), unbranched conidiophores and larger conidia (6.8 × 1.6 µm).



Note *Cytospora parakantschavelii* on *Pyrus pyraster* (L.) Burgsd. (MFLU 15-2094, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–j Conidiogenous cells with attached conidia. k Mature conidia. l Germinating spore. m, n Colonies on MEA (m-from above, n-from below). Scale bars: a = 2000 µm, b = 500 µm, c, d = 200 µm, f = 100 µm, e = 50 µm, l = 20 µm, g–k = 10 µm.

Figure 9.10 Morphological characters of *Cytospora parakantschavelii* (MFLU 15-2094, holotype)



Note *Cytospora kantschavelii* on *Populus nigra* L. a–c Stromata showing conidiomata. d, e Transverse sections through conidiomata. f, g Conidiophores and Conidiogenous cells with attached conidia. h Stroma showing peridium and conidiophores. Scale bars: a, b, c, d, e = 500 µm, g, h = 20 µm.

Source Gvritishvili (1973

Figure 9.11 Morphological characters of *Cytospora kantschavelii*

Cytospora parasitica Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, in Ariyawansa et al., Fungal Diversity: 75(1): 146 (2015), Figure 9.12

Facesoffungi Number: FoF 02744

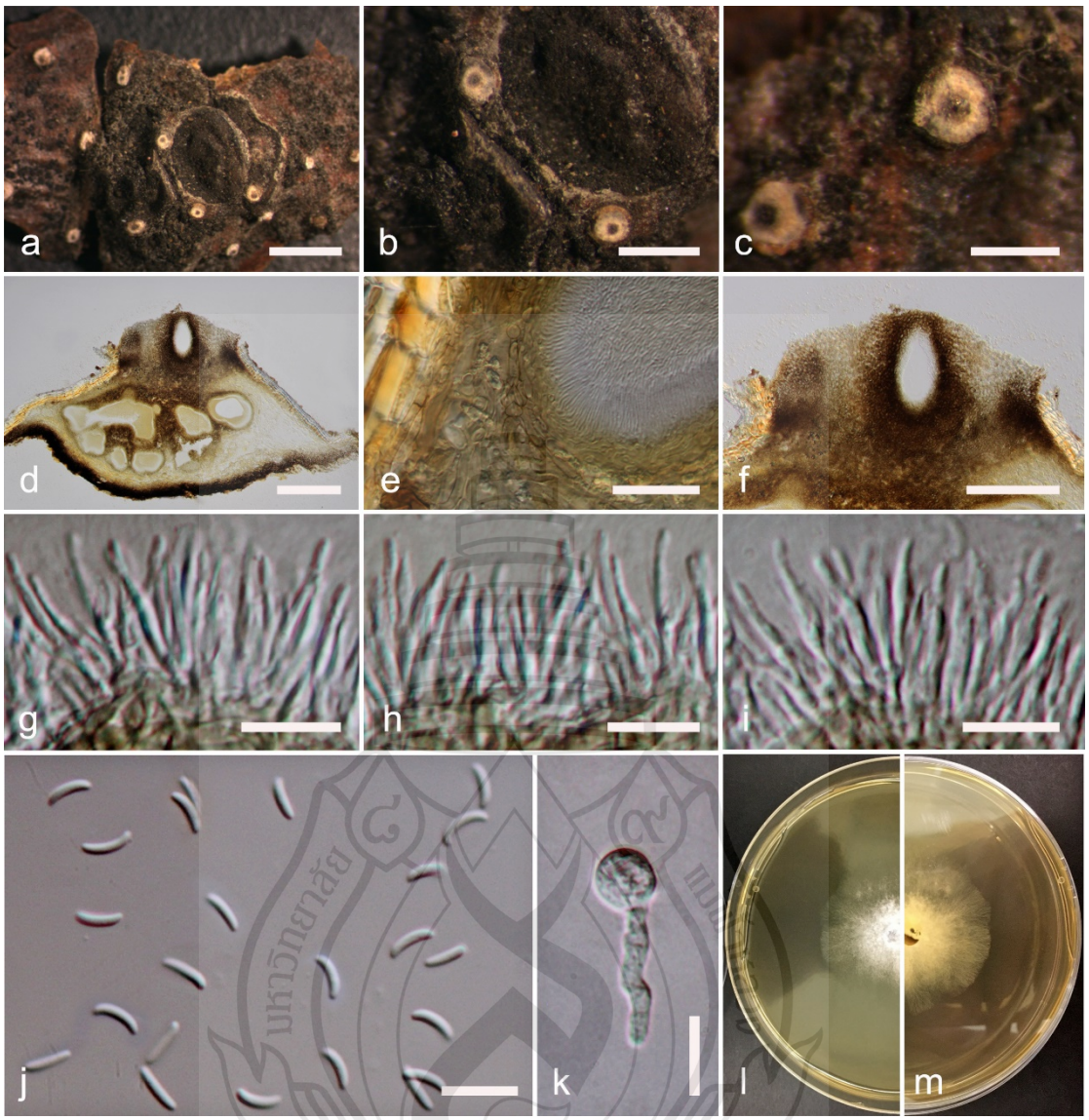
Associated with twigs and branches of *Malus domestica* Borkh. Sexual morph: Undetermined. Asexual morph: Conidiomata 1700–2000 × 900–1200 µm diameter, semi- immersed in host tissue, scattered, erumpent, multi-loculate, with ostiolar neck. Ostioles 320– 400 µm diameter, at same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with most layer thin, brown to dark brown. Conidiophores unbranched or occasionally branched at the base, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (5.5–)6.9–7.3

× 1.5–1.7(–2) µm ($\bar{x}$ = 6.8 × 1.8 µm, n = 30), unicellular, elongate-allantoid, hyaline, smooth-walled.

Culture characteristics: Colonies on MEA, reaching 4 cm diameter, after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Shakhty City, Grushevka steppe slopes near Grushevsky pond, ravine shrubbery, on dying branches (necrotrophic) of *Malus domestica* (Rosaceae), 14 May 2015, T. Bulgakov (MFLU 15-1991, PDD), living culture, MFLUCC 16-0507, KUMCC.

Notes: *Cytospora parasitica* was introduced by Ariyawansa et al. (2015) from *Malus domestica* in Russia (Ariyawansa et al., 2015). The morphology of this collection (MFLUCC 16-0507) is similar to *C. parasitica* (MFLUCC 14- 1055) in having multi-loculate conidiomata and allantoid to slightly curved, unicellular, hyaline, 7 × 1.75 µm conidia (Ariyawansa et al., 2015). In phylogenetic analyses, *C. parasitica* (MFLUCC 16-0507) groups with the ex-type strain (MFLUCC 14-1055) of *C. parasitica* (Figure 9.2).



Note *Cytospora parasitica* on *Malus domestica* Borkh (MFLU 15-1991). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l-from above, m-from below). Scale bars: a = 2000 µm, b = 1000 µm, c= 500 µm, d = 300 µm, e = 30 µm, f = 200 µm, g, h, i, j, k = 10 µm.

Figure 9.12 Morphological characters of *Cytospora parasitica* (MFLU 15-1991)

Cytospora paratranslucens Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.13

Index Fungorum number: IF552608

Facesoffungi Number: FoF 02745

Etymology: The specific epithet is composed from Greek prefix 'para-' meaning 'near' or 'beside' and Latin 'translucens' is from the species name, in reference to the occurrence on *Cytospora*.

Holotype: MFLU 15-1986

Associated with twigs and branches of *Populus alba* L. Sexual morph: Undetermined. Asexual morph: Conidiomata 450–550 × 270–350 µm diameter, semi-immersed in host tissue, scattered, erumpent, breaking through the outer branch, multiloculate, with ostiolar neck. Ostioles 70–150 µm diameter, at same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with inner most layer thin, red-brown, outer later dark brown to black. Conidiophores unbranched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (5.5–)6.5–7.3 × 1.3–1.5(–1.8) µm ($\bar{x}$ = 6.8 × 1.6 µm, n = 30), unicellular, allantoid, slightly curved, hyaline, smooth-walled.

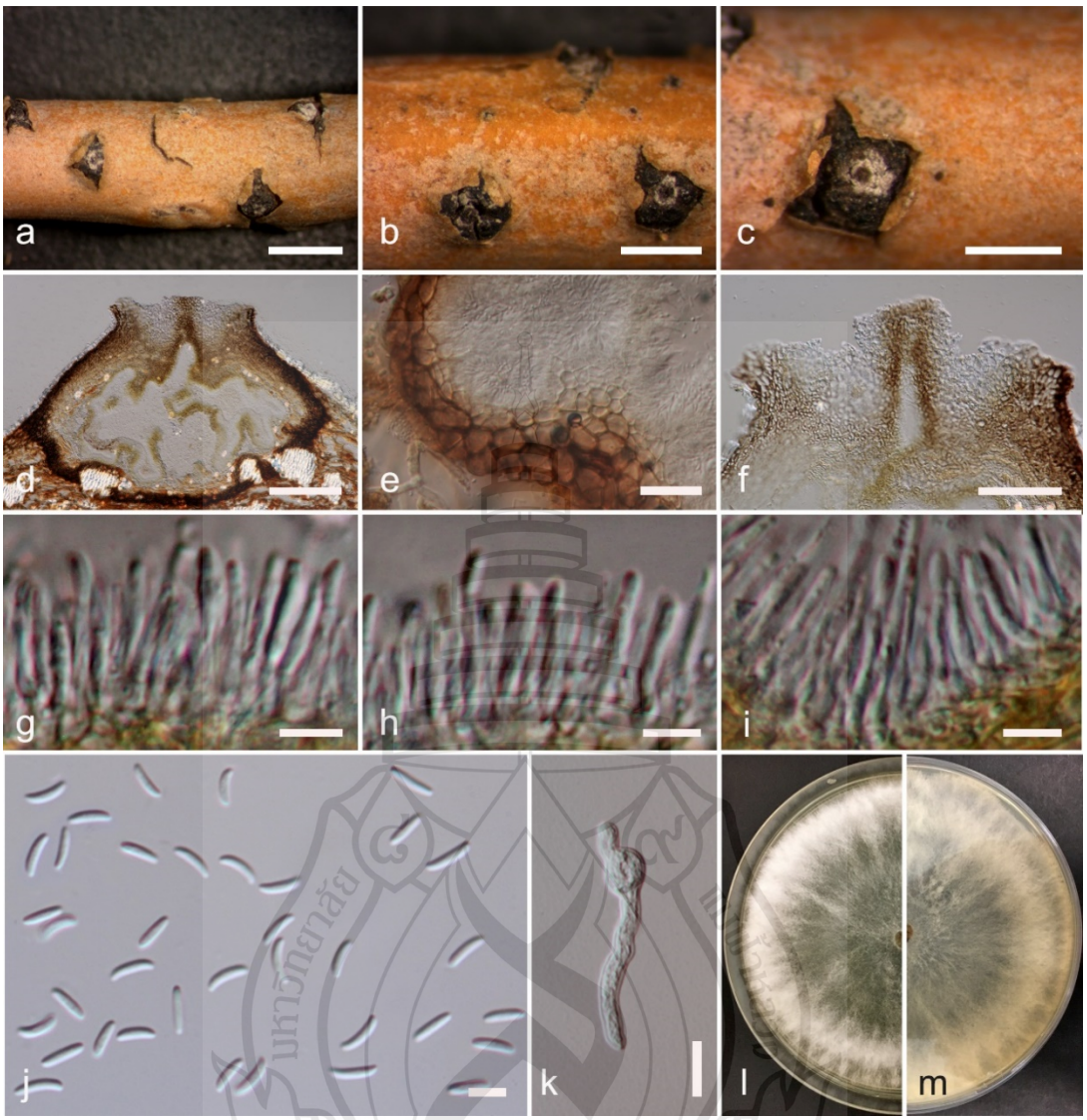
Culture characteristics: Colonies on MEA, reaching 8.5 cm diameter after 7 days at 25 °C, producing dense mycelium, circular, margin rough, white, with aerial mycelium.

Material examined: RUSSIA, Rostov Region, Shakhty City, Grushevka steppe slopes near Grushevsky pond, riparian grove, on dead and dying branches of *Populus alba*, 14 May 2015, T. Bulgakov, T-282 (MFLU 15-1986, holotype, PDD, isotype), ex-type living culture, MFLUCC 16-0506, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, lining-out nursery, trees and shrubs, dying twigs and branches on *Populus alba* L. var. *bolleana* (Lauche) Otto, 27 October 2015, T. Bulgakov, T-1016 (MFLU 15-3678, PDD), living culture, MFLUCC 16-0627, KUMCC.

Notes: *Cytospora* species associated with *Populus* have been reported worldwide (Table 9.3; Adams et al., 2002, 2005, 2006; Défago, 1942; Fotouhifar et al., 2010; Singh et al., 2007). In this study, five novel species are introduced, which were

collected from *Populus viz. C. melnikii, C. parakantschavelii, C. paratranslucens, C. rusanovii and C. salicacearum. Cytospora paratranslucens* is most similar to *C. germanica* and *C. nivea* (Adams et al., 2006). However, they can be distinguished by conidia size (6.8 × 1.6 versus 5 × 1, 6–7.5 × 1.2 µm respectively) (Adams et al., 2006). Furthermore, *C. paratranslucens* has multiloculate conidiomata sharing a single ostiole, while *C. germanica* and *C. nivea* have multiloculate conidiomata with individual or compressed ostioles in the conidiostromata.

In the ITS phylogenetic analyses, *Cytospora paratranslucens* groups with *C. translucens* Sacc. (138-2 and 35) with high bootstrap support (94% ML/ 1.00 PP). ITS sequence data is only available for *C. translucens* in GenBank. Therefore, we compare morphology of *C. paratranslucens* and *C. translucens*, from the original description in Saccardo (1884). *Cytospora paratranslucens* can be distinguished from *C. translucens* in having multiloculate conidiomata, while in *C. translucens* they are uniloculate. The conidia of *C. paratranslucens* are larger than those of *C. translucens* (6.8 × 1.6 µm versus 4.6 × 1.2 µm).



Note *Cytospora paratranslucens* on *Populus alba* (MFLU 15-1986, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l- from above, m-from below). Scale bars: a = 2000 µm, b = 1000 µm, c = 1000 µm, d = 200 µm, e = 20 µm, f = 100 µm, g, h, i, j = 5 µm, k = 10 µm.

Figure 9.13 Morphological characters of *Cytospora paratranslucens* (MFLU 15-1986, holotype)

Cytospora rusanovii Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.14

Index Fungorum number: IF552609

Facesoffungi Number: FoF 02746

Etymology: The specific named after the Russian mycologist Victor Andreyevich Rusanov, researcher of plant pathogenic fungi in Rostov region of Russia.

Holotype: MFLU 15-1931

Associated with twigs and branches of *Salix babylonica* L. and *Populus* × *sibirica* G.V. Krylov & G.V. Grig. ex A.K. Skvortsov [*P. balsamifera* L. × *P. nigra* L.]. Sexual morph: Undetermined. Asexual morph: Conidiomata 530–800 × 280–350 µm diameter, semi-immersed in host tissue, solitary, scattered, erumpent, discoid, circular to ovoid, with 1– 3 locules, and long ostiolar neck. Ostioles 155–170 µm diameter, at the same level as the disc surface. Peridium comprising several layers of cells of *textura angularis*, with inner most layer thick, dark brown, outer layer dark brown to black. Conidiophores unbranched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (6–)6.5–7.1 ×1.4–1.5(– 1.6) µm ($\overline{x}$ = 6.7 × 1.5 µm, n = 30), unicellular, elongate-allantoid, hyaline, smooth-walled.

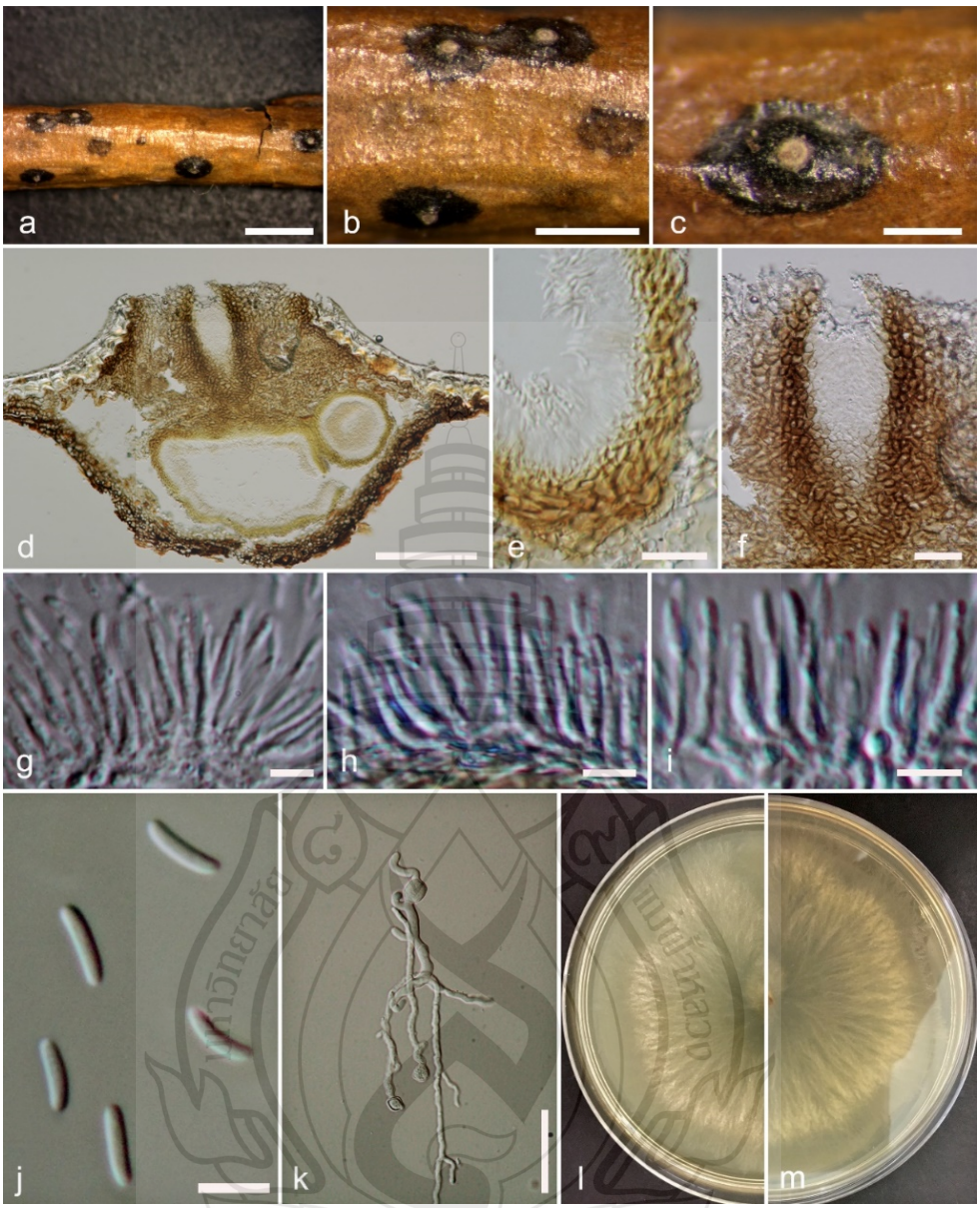
Culture characteristics: Colonies on MEA, reaching 8 cm diameter after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Shakhty City, Central Park, parkland, on dying branches of *Salix babylonica* (Salicaceae), 8 July 2015, T. Bulgakov (MFLU 15-1931, holotype, KUN, isotype), ex-type living culture, MFLUCC 15-0854, KUMCC; RUSSIA, Rostov Region, Shakhty City, Central Park, parkland, on dying branches of *Populus* × *sibirica* G.V. Krylov & G.V. Grig. ex A.K. Skvortsov [*P. balsamifera* L. × *P. nigra* L.] (Salicaceae), 9 July 2015, T. Bulgakov (MFLU 15-1929, KUN), living culture, MFLUCC 15-0853, KUMCC.

Notes: The new species has semi-immersed, 1–3-loculate conidiomata, with long ostioles and 6.7 × 1.5 µm, unicellular conidia. *Cytospora rusanovii* is most similar to *C. microspora* Rabenh. in conidia size (6–7 × 1–1.3) (Saccardo, 1884). However, *C.*

microspora differs from *C. rusanovii* in having multi-loculate conidiomata (>10 locules) (Corda 1839).

Phylogenetic analyses of ITS and multi-gene sequence data (Figures 9.1 and 9.2) indicate that *Cytospora rusanovii* can be distinguished from *C. curvata* (MFLUCC 15-0865) and other species in *Cytospora*, with 98% bootstrap support and 1.00 Bayesian posterior probability in MP, ML and BI analyses (Figure 9.2), while the polymorphic nucleotides differences are discussed under *C. curvata.*



Note *Cytospora rusanovii* on *Salix babylonica* (MFLU 15-1931, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostioles. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l-from above, m-from below). Scale bars: a = 2000 µm, b = 1000 µm, c = 500 µm, d = 100 µm, e = 10 µm, f = 20 µm, g, h, i, j = 5 µm, k = 50 µm.

Figure 9.14 Morphological characters of *Cytospora rusanovii* (MFLU 15-1931, holotype)

Cytospora salicicola Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, in Li et al., Fungal Diversity 78: 78 (2016), Figure 9.15

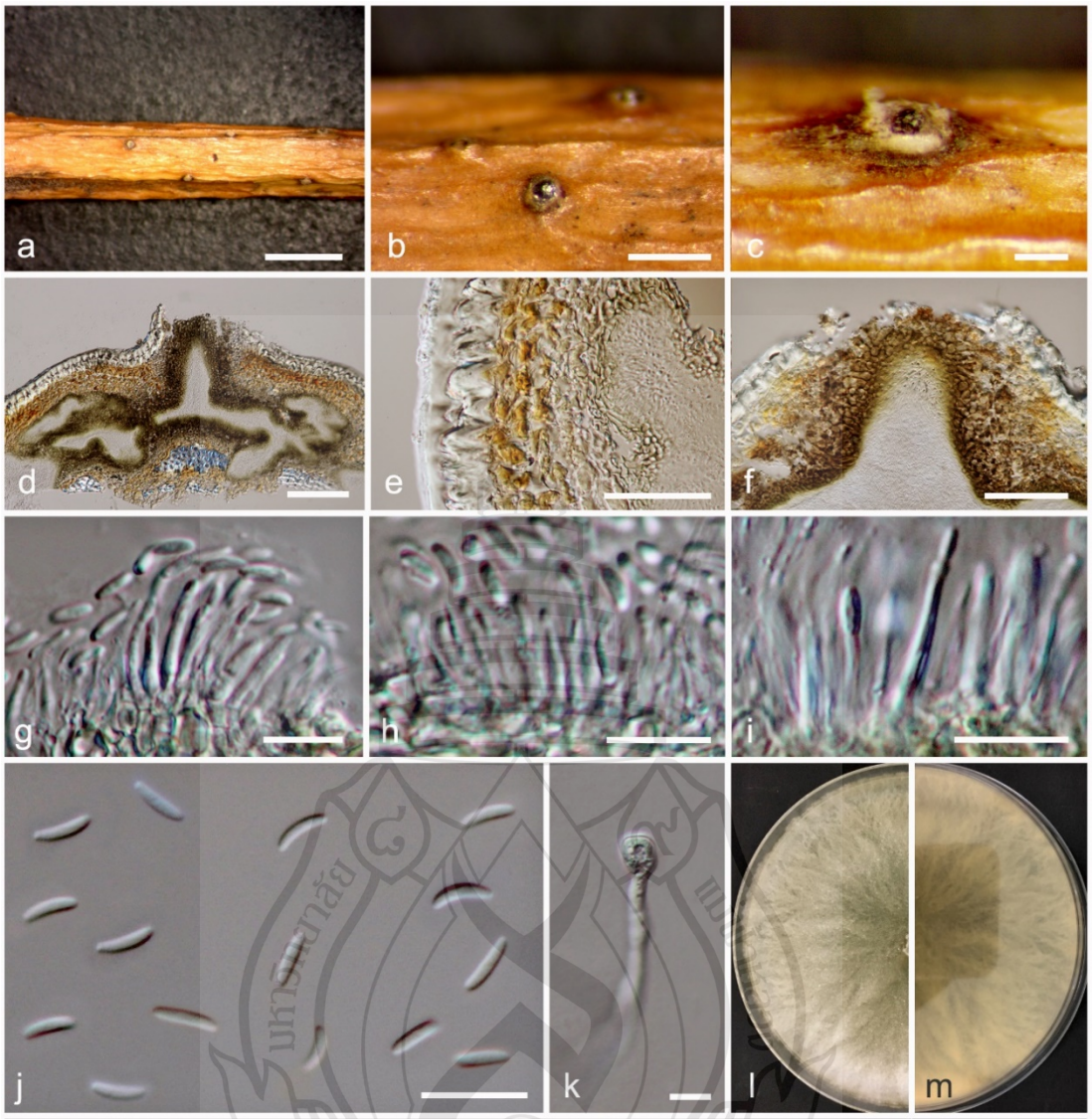
Facesoffungi Number: FoF 02747

Associated with twigs and branches of *Salix alba* L. Sexual morph: Undetermined. Asexual morph: Conidiomata 750–1200 × 300–450 µm diameter, semi-immersed in host tissue, solitary, scattered, visible as raised areas, with 3–4 locules and long ostiolar neck. Ostioles 170–200 µm diameter, at the base, same level as the host surface, black to brown, surrounded by a light coloured ostiolar disk. Peridium comprising several layers of cells of *textura angularis*, with inner most layer thin, hyaline to brown, outer layer brown to dark brown. Conidiophores unbranched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (6.2–)6.9–7.6 × 1.4–1.5(–1.7) µm ($\bar{x}$ = 6.8 × 1.6 µm, n = 30), unicellular, allantoid to subcylindrical, hyaline, smooth-walled.

Culture characteristics: Colonies on MEA, reaching 9 cm diameter, after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, Gremuchaya Balka (Thunderous gully), shore of pond, on dead and dying branches of *Salix alba* (Salicaceae), 28 June 2015, T. Bulgakov, T-527 (MFLU 15-2231, KUN), living culture, MFLUCC 15-0866, KUMCC.

Notes: *Cytospora salicicola* was introduced by Li et al. (2016) from *Salix alba* in Russia (Hyde et al., 2016; Li et al., 2016). In the phylogenetic analyses, our strain MFLUCC 15-0866 groups with the type material of *C. salicicola* (MFLUCC 14-1052) with high bootstrap support from all analyses (99% MP/ 83% ML/ 0.99 PP) (Figure 9.2).



Note *Cytospora salicicola* on *Salix alba* (MFLU 15-2231). a Stromatal habit in wood. b Fruiting bodies on host surface. c Surface of fruiting bodies showing the black Ostioles. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with intact conidia. j Mature conidia. k Germinating conidia. l, m Colonies on MEA (l-from above, m-from below). Scale bars: a = 2000 µm, b = 500 µm, c = 200 µm, d = 100 µm, e = 50 µm, f = 100 µm, g–k = 10 µm.

Figure 9.15 Morphological characters of *Cytospora salicicola* (MFLU 15-2231)

Cytospora salicacearum Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.16

Index Fungorum number: IF552610

Facesoffungi Number: FoF 02748

Etymology: The specific epithet salicacearum refers to host plant family Salicaceae, on which the fungus was first collected.

Holotype: MFLU 15-2061

Associated with twigs and branches of *Salix alba* L., *Salix* × *fragilis* L. [*S. alba* L. × *S. euxina* I.V. Belyaeva], *Populus nigra* L. var. *italica* Münchh. and *Prunus cerasus* L. Sexual morph: Undetermined. Asexual morph: Conidiomata 570–750 × 320–380 µm diameter, semi-immersed in host tissue, solitary, scattered, erumpent, discoid, circular to ovoid, with 1–2 locules, ostiolate. Ostioles 160–200 µm diameter, at the same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with inner most layer thin, dark brown, outer layer dark brown to black. Conidiophores unbranched or occasionally branched at the base, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (3.6–)4.9–6.4 × 0.9–1(–1.1) µm ($\bar{x}$ = 5 × 1 µm, n = 30), unicellular, allantoid to subcylindrical, hyaline, smooth-walled.

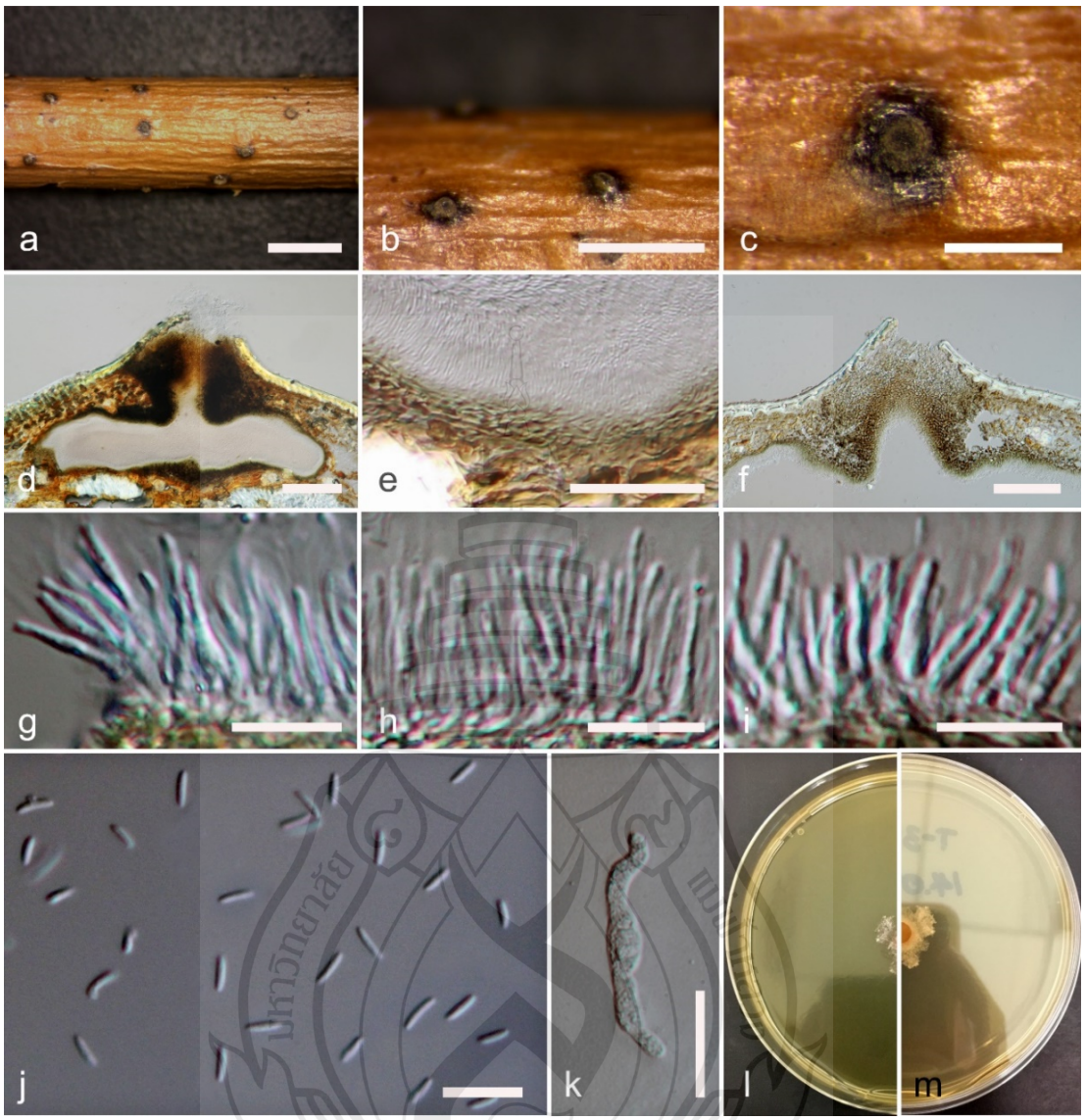
Culture characteristics: Colonies on MEA, reaching 1.5 cm diameter after 7 days at 25 °C, producing rhizoid mycelium, undulate, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Shakhty City, steppe slopes near Grushevsky pond, osier-bed near pond, on dead and dying branches of *Salix alba* (Salicaceae), 14 May 2015, T. Bulgakov, T-357 (MFLU 15-2061, holotype, KUN, isotype), ex-type living culture, MFLUCC 16-0509, KUMCC; RUSSIA, Rostov Region, Shakhty City, steppe slopes near Grushevsky pond, riparian grove, dead and dying branches on *Populus nigra* L. var. *italica* Münchh (Salicaceae), 14 May 2015, T. Bulgakov, T-393 (MFLU 15-2097, KUN), living culture, MFLUCC 16-0576, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, old orchard, dead and dying branches on *Prunus cerasus* L., 18 June 2015, T. Bulgakov, T-503 (MFLU 15-2207, KUN), living culture, MFLUCC 16-0587, KUMCC; RUSSIA,

Rostov Region, Krasnosulinsky District, Donskoye forestry, riparian forest, on dead and dying branches of *Salix* × *rubens* Schrank [S. alba L. × S. fragilis L.] (Salicaceae), 18 June 2015, T. Bulgakov, T-509 (MFLU 15-2213, KUN), living culture, MFLUCC 15-0861, KUMCC.

Notes: *Cytospora salicacearum* has 1–2 loculate conidiomata with a single ostioles and shares common walls. In the phylogenetic analyses based on combined ITS, LSU, *rpb2* and *act* sequence data, *C. salicacearum* is a close relative to *C. melnikii* (MFLUCC 15-0851, MFLUCC 16-0635) and *C. chrysosperma* (HMBF17, HMBF151, HMBF158, HMBF159) (Figure 9.2). However, they are different in morphological characteristics, *C. melnikii* and *C. chrysosperma* differ from *C. salicacearum* in having shorter and wider conidia (4.6 × 1.2 μm, 4.6 × 1.2 μm, 5 × 1 μm, respectively).

Cytospora salicacearum differs from *C. melnikii* and *C. chrysosperma* in the polymorphic nucleotides of the *rpb2* and *act* sequence data. In *rpb2* it differed with 35 polymorphisms from *C. chrysosperma*, four polymorphisms from *C. melnikii*. In *act* it differed with eight polymorphisms from *C. chrysosperma* and differs from *C. melnikii* with four polymorphisms.



Note *Cytospora salicacearum* on *Salix alba* (MFLU 15-2061, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostioles. g–i Conidiogenous cells with intact conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l-from above, m- from below). Scale bars: a = 2000 µm, b = 1000 µm, c= 400 µm, d = 100 µm, e = 50 µm, f = 100 µm, g, h, i, j = 10 µm, k = 20 µm.

Figure 9.16 Morphological characters of *Cytospora salicacearum* (MFLU 15-2061, holotype)

Cytospora salicina Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.17

Index Fungorum number: IF552611

Facesoffungi Number: FoF 02749

Etymology: The specific epithet '*salicina'* refers to the host plant genus Salix, on which the type specimens were collected.

Holotype: MFLU 15-2212

Associated with twigs and branches of *Salix alba* L. and *Salix* × *rubens* Schrank [*S. alba* L. × *S. fragilis* L.]. Sexual morph: Undetermined. Asexual morph: Conidiomata 1200– 1500 × 550–600 µm diameter, semi-immersed in host tissue, solitary, scattered, erumpent, discoid, circular to ovoid, with 2–5 locules, and ostiolar neck. Ostioles 300–350 µm. at the same level as the disc surface. Peridium comprising several layers of cells of *textura angularis*, with inner most layer thick, dark brown, outer layer dark brown to black. Conidiophores branched or occasionally branched at the base, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, hyaline, smooth-walled. Conidia (3.6–)4.2–4.7 × 1–1.1(–1.3) µm ($\bar{x}$ = 4.3 × 1 µm, n = 30), unicellular, allantoid to subcylindrical, hyaline, smooth-walled.

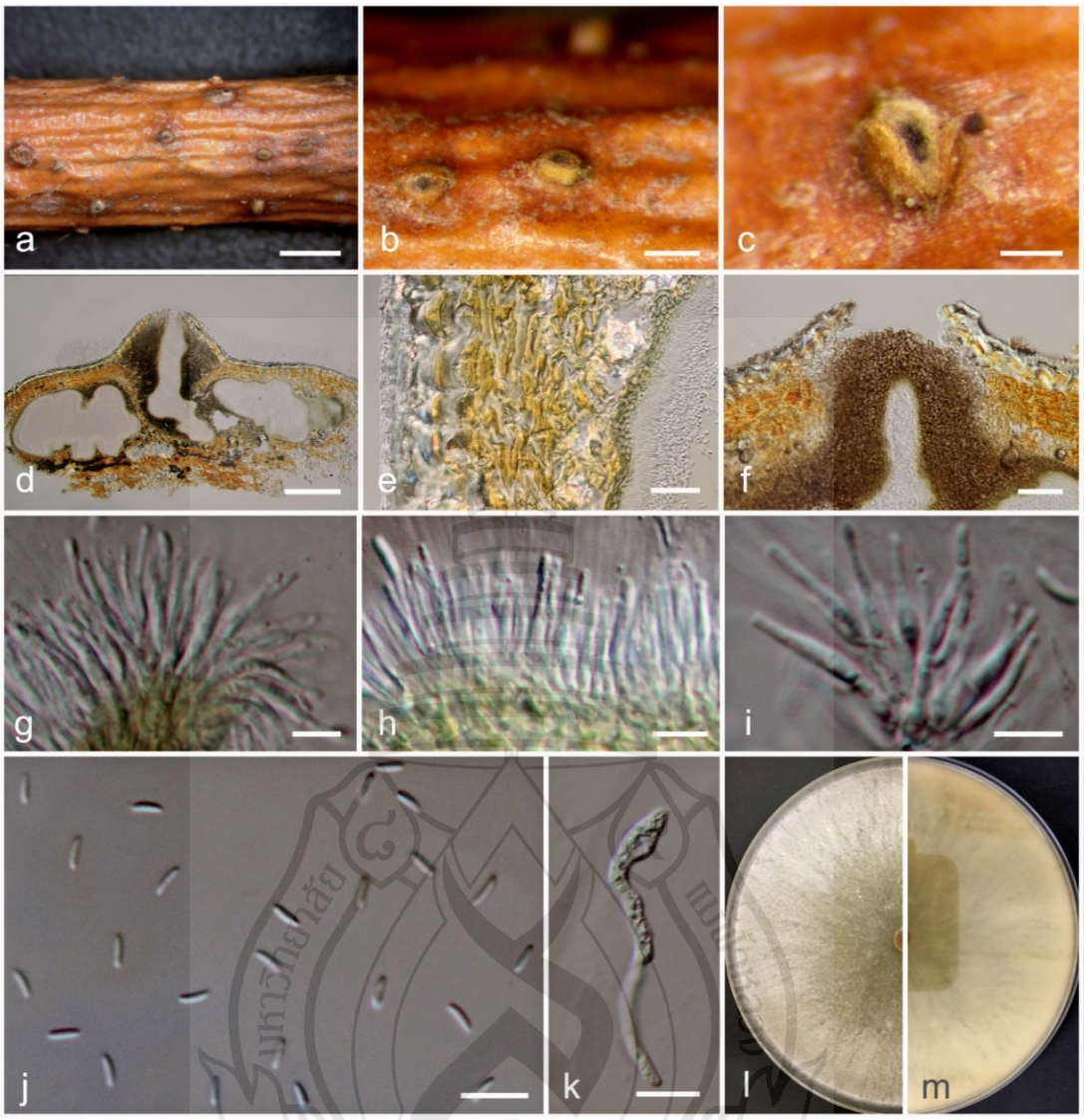
Culture characteristics: Colonies on MEA, reaching 9 cm diameter, after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, riparian forest, on dead and dying branches of *Salix alba* L. (Salicaceae), 18 June 2015, T. Bulgakov, T-508 (MFLU 15-2212, holotype, KUN, isotype), ex-type living culture, MFLUCC 15-0862, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, ravine spinney, on dying twigs and branches of *Salix* × *rubens* Schrank [*S. alba* L. × *S. fragilis* L.] (Salicaceae), 27 October 2015, T. Bulgakov, T-1017 (MFLU 15-3679, KUN), living culture, MFLUCC 16-0637, KUMCC.

Notes: *Cytospora salicina* (MFLUCC 15-0862, MFLUCC 16-0637) was found on *Salix* spp. causing canker disease. *Cytospora salicina* is most similar to *C. chrysosperma* in having multi-locules, but differs in having smaller conidia (4.6 × 1.2 µm) and a peridium comprising several layers. Phylogenetic analysis based of

combined ITS, LSU, *rpb2* and *act* sequence data indicates that *C. salicina* can be distinguished from *C. chrysosperma* (HMBF17, HMBF151, HMBF158, HMBF159), *C. melnikii* (MFLUCC 15-0851, MFLUCC 16-0635) and *C. salicacearum* (MFLUCC 16-0509, MFLUCC 16-0587, MFLUCC 15-0861, MFLUCC 16-0576) (Figure 9.2).

In ITS, *Cytospora salicina* differs from *C. chrysosperma* with 28 polymorphisms, three polymorphisms from *C. melnikii* and a single polymorphism from *C. salicacearum*. In *rpb2* it differs in 32 polymorphisms from *C. chrysosperma*, 30 polymorphisms from *C. melnikii* and 29 polymorphisms from *C. salicacearum*. In *act* it differs with ten polymorphisms from *C. melnikii* and ten polymorphisms from *C. salicacearum*.



Note *Cytospora salicina* on *Salix alba* (MFLU 15-2212, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostioles. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l-from above, m- from below). Scale bars: a = 2000 µm, b = 500 µm, c, d = 200 µm, e = 20 µm, f = 50 µm, j, k = 10 µm, g, h, i = 5 µm.

Figure 9.17 Morphological characters of *Cytospora salicina* (MFLU 15-2212, holotype)

Cytospora sorbi Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.18

Index Fungorum number: IF552612

Facesoffungi Number: FoF 02750

Etymology: The specific epithet "sorbi" refers to the host plant genus Sorbus, on which the type specimen was first collected.

Holotype: MFLU 15-3781

Associated with twigs and branches of *Sorbus aucuparia* L. Sexual morph: Undetermined. Asexual morph: Conidiomata 900–1200 × 420–550 µm diameter, semi-immersed in host tissue, scattered, erumpent, with 3–4 locules, and ostiolar neck. Ostioles 250–300 µm diameter, at the same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with inner most layer thick, brown, outer dark brown. Conidiophores unbranched or occasionally branched at the base, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (6–)6.4–7.6 × 1.4–1.5(– 1.8) µm ($\bar{x}$ = 6.5 × 1.5 µm, n = 30), unicellular, elongate-allantoid, hyaline, smooth-walled.

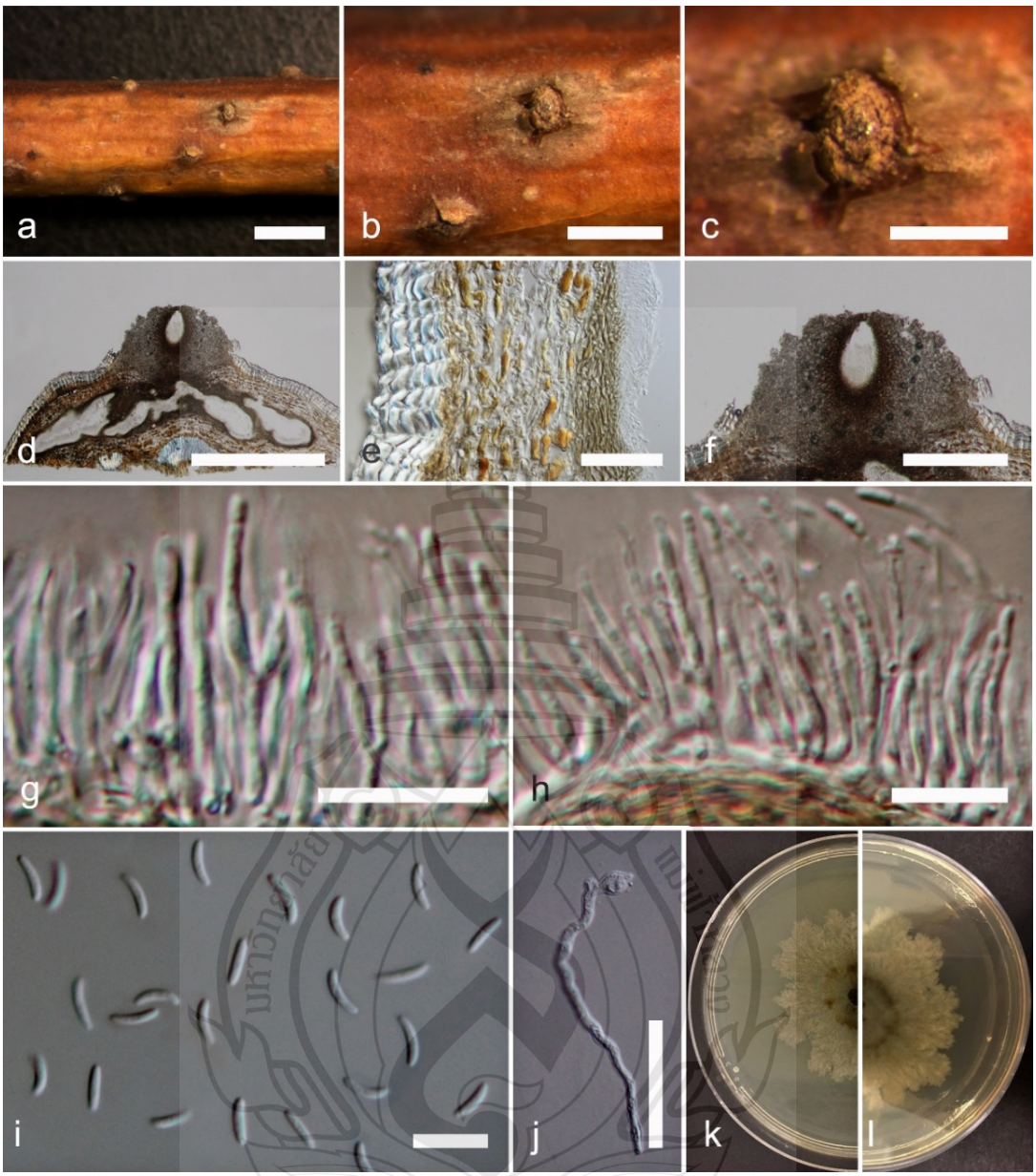
Culture characteristics: Colonies on MEA, reaching 5 cm diameter after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, dying twigs and branches on *Sorbus aucuparia* (Rosaceae), 27 October 2015, T. Bulgakov, T-1119 (MFLU 15-3781, holotype, KUN, isotype), ex-type living culture, MFLUCC 16-0631, KUMCC.

Notes: *Cytospora sorbi* was collected from *Sorbus aucuparia*. In phylogenetic analysis (Figures 9.1 and 9.2) *C. sorbi* forms a separate branch as a sister taxon to *C. sorbicola* and *C. donetzica* (Figure 9.2). *Cytospora sorbicola* and *C. donetzica* differs from *C. sorbi* in having smaller conidia (5.6 × 1.5 µm, 5.5 × 1.4 µm, 6.5 × 1.5 µm, respectively).

In ITS, *Cytospora sorbi* differs from *C. sorbicola* in eleven polymorphisms and eight polymorphisms from *C. donetzica*. In *rpb2* it differs from *C. sorbicola* with 20

polymorphisms and 28 polymorphisms from *C. donetzica*. In *act*, it differs from *C. sorbicola* with nine polymorphisms and eight polymorphisms from *C. donetzica*.



Note *Cytospora sorbi* on *Sorbus aucuparia* L. (MFLU 15-3781, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–h Conidiogenous cells with attached conidia. i Mature conidia. j Germinating spore. k, l Colonies on MEA (k-from above, l-from below). Scale bars: a = 2000 µm, b = 1000 µm, c = 500 µm, d = 500 µm, e = 50 µm, f = 200 µm, g = 10 µm, h = 10 µm, i = 10 µm and j = 40 µm.

Figure 9.18 Morphological characters of *Cytospora sorbi* (MFLU 15-3781, holotype)

Cytospora sorbicola Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.19

Index Fungorum number: IF552613

Facesoffungi Number: FoF 02751

Etymology: The specific epithet "sorbicola" refers to the host plant genus Sorbus, on which the type specimens were collected.

Holotype: MFLU 15-2203

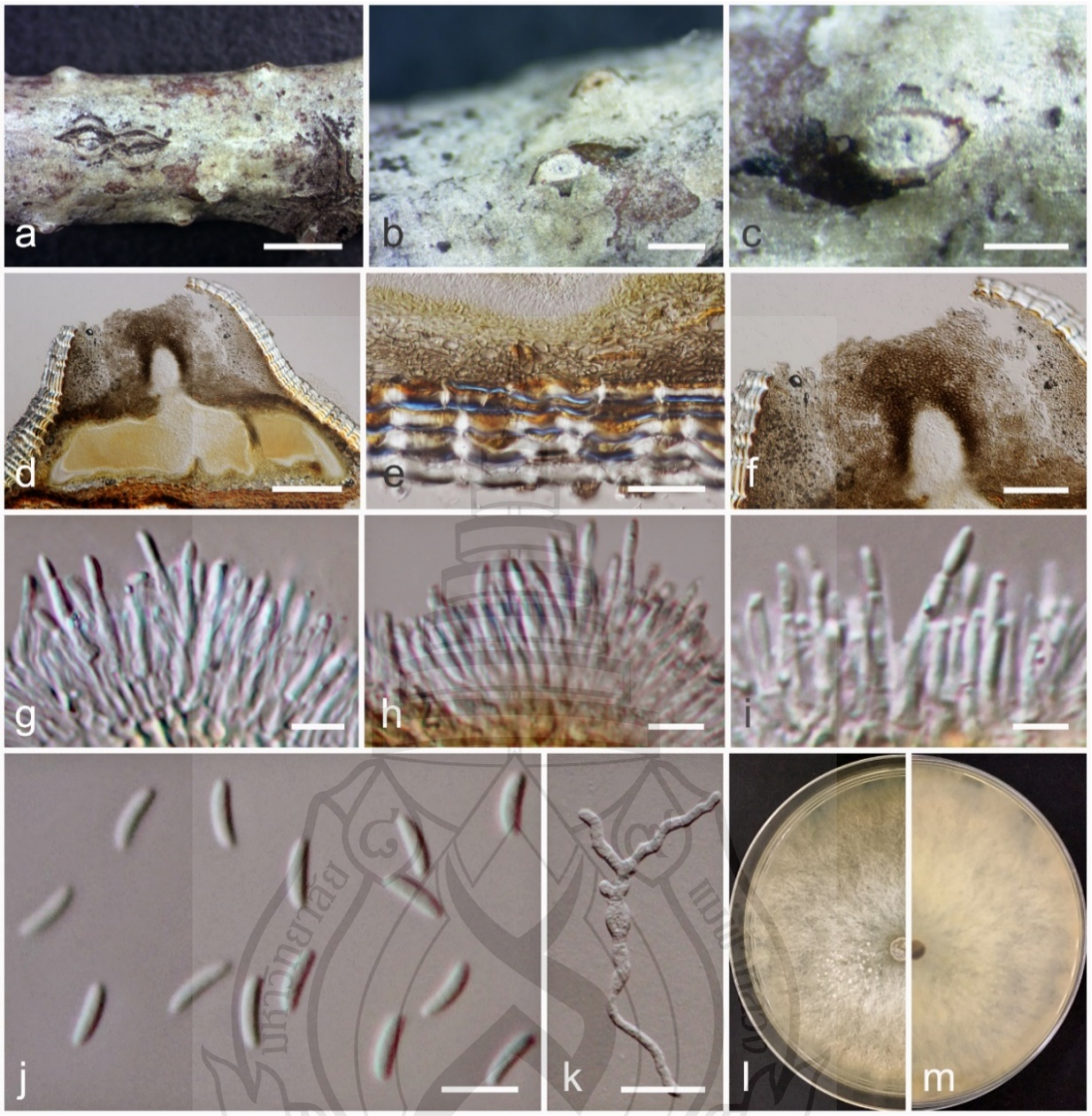
Associated with twigs and branches of *Acer pseudoplatanus* L. and *Cotoneaster melanocarpus* (Bunge) Loudon, *Prunus cerasus* L., *Sorbus aucuparia* L. and × *Sorbaronia mitschurinii* (Skvortsov & Maitul.) Sennikov. Sexual morph: Undetermined. Asexual morph: Conidiomata 850–1200 × 480–600 µm diameter, semi-immersed in bark, solitary, erumpent, with 1–2 locules, ostiolate. Ostioles 250–350 µm diameter, at the same level as the disc surface. Peridium comprising several layers of cells of *textura angularis*, with inner most layer thick, pale brown, outer later dark brown. Conidiophores unbranched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, formed from the inner most layer of pycnidial wall, hyaline, smooth-walled. Conidia (4.4–)5.6–6.1 × 1.3– 1.5(–1.6) µm ($\bar{x}$ = 5.6 × 1.5 µm, n = 30), unicellular, elongate-allantoid, slightly curved, hyaline, smooth-walled.

Culture characteristics: Colonies on MEA, reaching 8 cm diameter after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, artificial forest, dead and dying branches on *Acer pseudoplatanus* (Sapindaceae), 18 June 2015, T. Bulgakov, T-499 (MFLU 15-2203, holotype, KUN, isotype), ex-type living culture, MFLUCC 16-0584, KUMCC; RUSSIA, Rostov Region, Rostov-on-Don City, Botanical Garden of Southern Federal University, parkland, on dead and dying branches on *Sorbus aucuparia* L. (Rosaceae), 30 May 2015, T. Bulgakov, T-472 (MFLU 15-2176, KUN), living culture, MFLUCC 16-0581, KUMCC; RUSSIA, Rostov Region, Rostov-on-Don City, Botanical Garden of Southern Federal University, Systematic Arboretum, on dead and dying branches on Cotoneaster melanocarpus (Bunge) Loudon (Rosaceae), 30 May 2015, T. Bulgakov, T-476 (MFLU 15-2180, KUN), living culture, MFLUCC 16-0582, KUMCC; RUSSIA,

Rostov Region, Krasnosulinsky District, Donskoye forestry, old orchard, on dead and dying branches on Sorbaronia mitschurinii (Skvortsov & Maitul.) Sennikov (Rosaceae), 18 June 2015, T. Bulgakov, T-501 (MFLU 15-2205, KUN), living culture, MFLUCC 16- 0585, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, artificial forest platation, forest nursery, dead and dying branches on Prunus cerasus L. (Rosaceae), 18 June 2015, T. Bulgakov, T-502 (MFLU 15-2206, KUN), living culture, MFLUCC 16-0586, KUMCC; RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, Kabanya Balka (Boar gully), steppe on slope of gully, dying twigs and branches (necrotrophic) on Cotoneaster melanocarpus Lodd., G. Lodd. & W. Lodd., 27 October 2015, T. Bulgakov (MFLU 15-3768, KUN), living culture, MFLUCC 16-0633, KUMCC.

Notes: Six collections of *Cytospora sorbicola* (MFLUCC 16-0581, MFLUCC 16- 0582, MFLUCC 16-0584, MFLUCC 16-0585, MFLUCC 16-0586, MFLUCC 16-0633) were made. *Cytospora sorbicola* is similar to *C. donetzica* and *C. ceratosperma* (Tode) G.C. Adams & Rossman in conidia size (5.6 × 1.5 µm, 5.5 × 1.4 µm, 5–6 × 1.4 µm, respectively) (Saccardo, 1884), but *C. donetzica* differs in having multiloculate conidiomata and shorter ostiolar necks (150–250 µm). Phylogenetic analysis (Figures 9.1 and 9.2) place *C. sorbicola* in a separate clade from *C. ceratosperma* which is sister to *C. donetzica* (MFLUCC 16-0574, MFLUCC 15-0864, MFLUCC 16-0589, MFLUCC 16-0641) with bootstrap support (86% MP/ 76% ML/ 0.98 PP). *Cytospora sorbicola* differs from *C. donetzica* with five ITS polymorphisms, 23 *rpb2* polymorphisms and seven *act* polymorphisms.



Note *Cytospora sorbicola* on *Acer pseudoplatanus* (MFLU 15-2203, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of stroma. d Vertical section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l- from above, m-from below). Scale bars: a = 2000 µm, b, c = 500 µm, d = 200 µm, e = 50 µm, f = 100 µm, g, h, i, j = 5 µm, k = 10 µm.

Figure 9.19 Morphological characters of *Cytospora sorbicola* (MFLU 15-2203, holotype)

Cytospora ulmi Norphanphoun, Bulgakov, T.C. Wen & K.D. Hyde, sp. nov., Figure 9.20

Index Fungorum number: IF552614

Facesoffungi Number: FoF 02752

Etymology: Name refers to the host genus *Ulmus*

Holotype: MFLU 15-1910

Associatd with twigs and branches of Ulmus minor. Sexual morph: Undetermined. Asexual morph: Conidiomata 980–1200 × 500–600 µm diameter, semi-immersed in host tissue, solitary, erumpent, scattered, discoid, circular to ovoid, with 4–6 locules, with long ostiolar neck. Ostioles 410–450 µm, at the same level as the disc surface. Peridium comprising a few to several layers of cells of *textura angularis*, with inner most layer thin, pale brown. Conidiophores branched, reduced to conidiogenous cells. Conidiogenous cells blastic, enteroblastic, phialidic, hyaline, smooth-walled. Conidia (4.8–)5.4–6.4 × 1.3–1.5(–1.6) µm ($\bar{x}$ = 5.4 × 1.4 µm, n = 30), unicellular, elongate-allantoid, hyaline, smooth-walled.

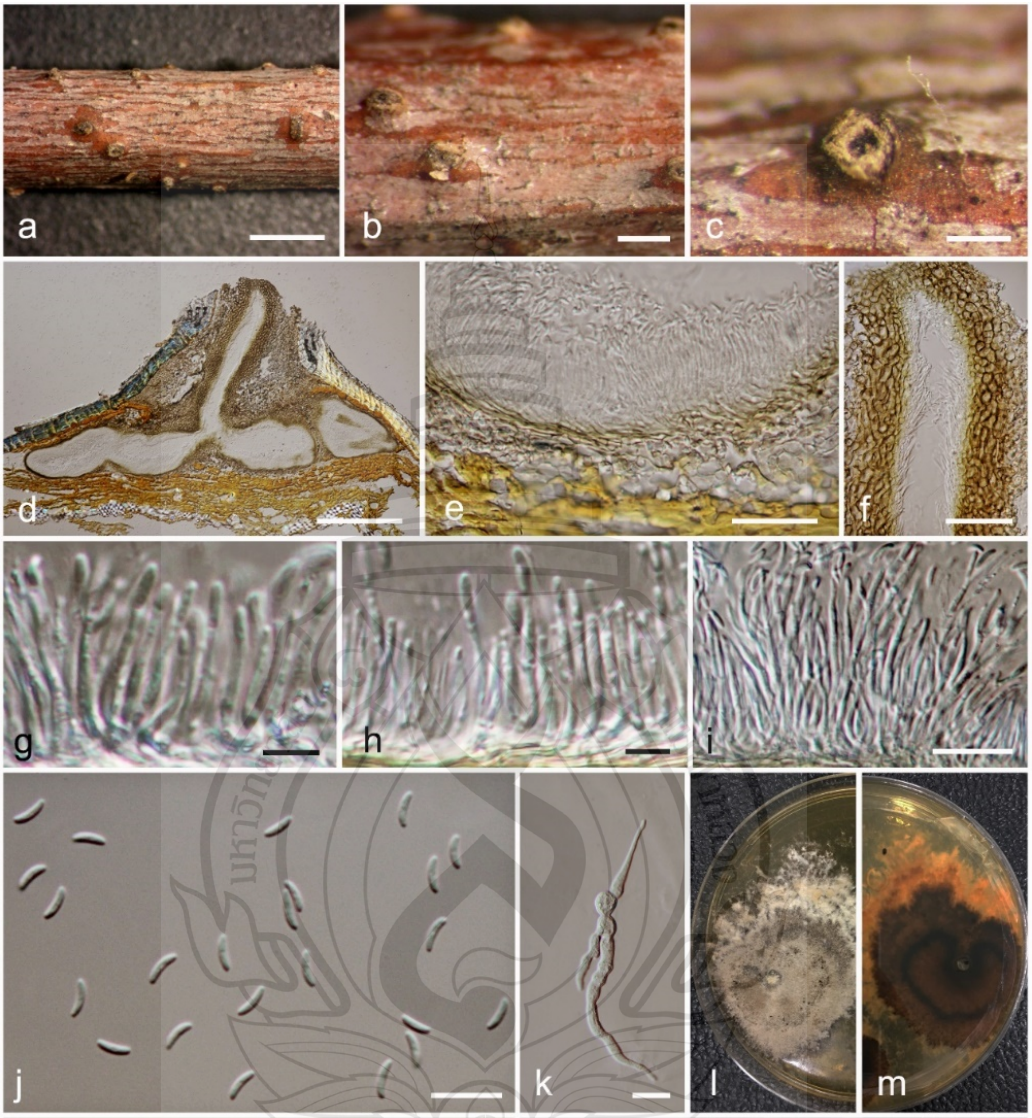
Culture characteristics: Colonies on MEA, reaching 6 cm diameter after 7 days at 25°C, producing dense mycelium, circular, margin rough, white, lacking aerial mycelium.

Material examined: RUSSIA, Rostov Region, Krasnosulinsky District, Donskoye forestry, ravine forest, on dead and dying branches (necrotrophic/saprobic) of *Ulmus minor* Mill., 28 June 2015, T. Bulgakov, T-521 (MFLU 15-2225, holotype, KUN, isotype), ex-type living culture, MFLUCC 15-0863, KUMCC.

Notes: Phylogenetic analysis of four combined gene loci indicate that *Cytospora ulmi* (MFLUCC 15-0863), forms a distinct branch as a sister taxon to *C. ribis* Ehrenb. (284-2) isolated from *Thuja orientalis* L., *C. rosarum* Grev. (218) isolated from *Rosa canina* L. and *C. tanaitica* Norphanphoun, Bulgakov & Hyde (MFLUCC 14-1057) isolated from *Betula pubescens* Ehrh. (Figure 9.2) (Adams et al., 2002; Ariyawansa et al., 2015; Fotouhifar et al., 2010).

Cytospora ulmi is most similar to *C. rosarum* in having long conidia ((4.8–)5.4–6.4 µm versus 4.5–6.7 µm), but has narrower conidia (1.3–1.5(–1.6) µm versus 0.9–1.1 µm). *Cytospora ribis* and *C. tanaitica* are similar to *C. ulmi* in having multi-loculate conidiomata. However, *C. ulmi* (5.4 × 1.4 µm) has larger conidia than *C. ribis* (4 × 1

μm) and *C. tanaitica* (3.4 × 0.7 μm) (Adams et al., 2002; Fotouhifar et al., 2010; Ariyawansa et al., 2015).



Note *Cytospora ulmi* (MFLU 15-2225, holotype). a Stromatal habit in wood. b Fruiting bodies on substrate. c Surface of fruiting bodies. d Cross section of the stroma showing conidiomata. e Peridium. f Ostiolar neck. g–i Conidiogenous cells with attached conidia. j Mature conidia. k Germinating spore. l, m Colonies on MEA (l-from above, m-from below). Scale bars: a = 2000 μm, b= 500 μm, c, d = 200 μm, e, f = 50 μm, g, h = 5 μm, i, j = 10 μm, k = 20 μm.

Figure 9.20 Morphological characters of *Cytospora ulmi* (MFLU 15-2225, holotype)

9.4 Discussion

Cytospora species are important plant pathogens causing dieback and canker disease with a worldwide distribution and host range including *Armeniaca*, *Eucalyptus*, *Fraxinus*, *Ligustrum*, *Malus*, *Mangifera*, *Platanus*, *Populus*, *Punus*, *Robinia*, *Salix* and *Ulmus* to name a few (Adam et al., 2006; Fotouhifar et al., 2010; Ariyawansa et al., 2015; Fan et al., 2015a, 2015b; Liu et al., 2015; Li et al., 2016; Maharachchikumbura et al., 2015, 2016; Hyde et al., 2016). In this study, all samples were collected from European Russia from dying twigs and symptomatic branches. A phylogenetic analysis was constructed using maximum parsimony, maximum likelihood and Bayesian inference for an individual ITS dataset and was able to resolve some species of *Cytospora* (Figure 9.1). However, the combined analysis of ITS, LSU, *rpb2* and *act* sequence was more appropriate for resolving *Cytospora* species (Figure 9.2). It has repeatedly been shown that multi-gene dataset will resolve species in pathogenic (e.g. *Colletotrichum*, Cai et al., 2009; *Diaporthe*, Udayanga et al., 2011, 2015; *Pestalotiopsis*, Maharachchikumbura et al., 2011, 2012) and other genera (e.g. *Stachybotrys*, Lombard et al., 2016; *Nodulosphaeria*, Mapook et al., 2016; *Lasiodiplodia*, Doilom et al., 2017), better than single genes.

Species of *Cytospora* may be relatively host-specific (Zhou et al., 2001), such as *C. australiae* Speg., *C. eucalyptina* Speg., *C. eucalypticola* Van der Westh., and *C. agarwalii* Soni, Dadwal & Jamaluddin which have only been reported from *Eucalyptus* sp. (Adams et al., 2005). Previous reports have however, indicated that many *Cytospora* species have broad host ranges. However, those reports lacked identifications based on molecular data (Fries, 1823; Deng, 1963; Saccardo, 1884; Tai, 1979; Wei, 1979). Some widespread species have been identified and verified by molecular data to occur in many host species, such as *C. chrysosperma* and *C. nivea* (Adams et al., 2005; Fan et al., 2014; Ariyawansa et al., 2015; Fan et al., 2015a, 2015b; Liu et al., 2015; Maharachchikumbura et al., 2015, 2016; Hyde et al., 2016; Li et al., 2016). In Table 9.3 we summarize the species (identified with sequence data) and their host distribution.

Our study provides data on the distribution of 17 *Cytospora* species with a multi-gene phylogeny. Several hosts appear to support several *Cytospora* species and

several *Cytospora* species are known from several hosts (Table 9.3). Some taxa on the other hand, are only known from a single host. Thus, we regard the data we provide on *Cytospora* are preliminary and future studies are likely established numerous new species and further resolve their distribution.

Table 9.3 Occurrence of *Cytospora* species on hosts (species identifications confirmed with molecular data)

Host	Species record	Genes used	References
Abies	*Valsa abietis*	ITS	Adams et al. (2005)
	Valsa friesii	ITS	Défago (1942)
Acacia	*Cytospora* sp. "Uncertain lineage"	ITS	Adams et al. (2006)
Acer	*Cytospora ampulliformis*	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora rosarum	ITS, LSU, *rpb2*, *act*	Tibpromma et al. (personal comm)
	Cytospora sorbicola	ITS, LSU, *rpb2*, *act*	In this study
	Valsa ambiens subsp. *ambiens*	ITS	Spielman (1985)
	Valsa ambiens subsp. *leucostomoides*	ITS	Spielman (1985)
Amygdalus	*Cytospora cincta*	ITS	Fotouhifar et al. (2010)
	Cytospora leucosperma	ITS	Fotouhifar et al. (2010)
Armeniaca	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora cincta	ITS	Fotouhifar et al. (2010)
	Cytospora cinctum	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)
	Cytospora leucostoma	ITS	Fotouhifar et al. (2010)
Berberis	*Cytospora berberidis*	ITS, LSU, *rpb2*, *act*	Liu et al. (2015)

Table 9.3 (continued)

Host	Species record	Genes used	References
Betula	*Cytospora tanaitica*	ITS, LSU, *act*	Ariyawansa et al. (2015)
Celtis	*Cytospora translucens*	ITS	Fotouhifar et al. (2010)
Cerasus	*Cytospora cincta*	ITS	Fotouhifar et al. (2010)
	Cytospora schulzeri	ITS	Fotouhifar et al. (2010)
Ceratonia	*Cytospora acacia* African-Mediterranean lineage	ITS	Adams et al. (2006)
Cercis	*Valsa viridistroma* comb. nov.	ITS	Wehmeyer (1936)
Chamaecyparis	*Valsa abietis* sp. complex 1 (syn. *Valsa weiriana*)	ITS	Adams et al. (2002)
Colutea	*Cytospora schulzeri*	ITS	Fotouhifar et al. (2010)
Cotinus	*Cytospora cotini*	ITS, LSU, *rpb2*, *act*	Hyde et al. (2016)
	Cytospora gelida	ITS, LSU, *rpb2*, *act*	Tibpromma et al. (personal comm)
Cotoneaster	*Cytospora sorbicola*	ITS, LSU, *rpb2*, *act*	In this study
Crataegus	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora cincta	ITS	Fotouhifar et al. (2010)
	Cytospora donetzica	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora malicola	ITS	Fotouhifar et al. (2010)

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora schulzeri	ITS	Fotouhifar et al. (2010)
Cydonia	*Cytospora cincta*	ITS	Fotouhifar et al. (2010)
	Cytospora cinctum	ITS	Fotouhifar et al. (2010)
Elaeagnus	*Cytospora elaeagni*	ITS, LSU, *rpb2*, *act*	Fan et al. (2015b)
	Cytospora nivra	ITS, LSU, *rpb2*, *act*	Fan et al. (2015b)
	Cytospora ribis	ITS	Fotouhifar et al. (2010)
Eriobotrya	*Cytospora eriobotryae*	ITS	Adams et al. (2005, 2006)
Eucaliptus	*Cytospora abyssinica*	ITS	Adams et al. (2005)
	Cytospora aff. austromontana	ITS	Adams et al. (2005)
	Cytospora agarwalii	ITS	Adams et al. (2005)
	Cytospora australiae	ITS	Adams et al. (2005)
	Cytospora austromontana	ITS	Adams et al. (2005)
	Cytospora berkeleyi	ITS	Adams et al. (2005)
	Cytospora chrysosperma	ITS	Adams et al. (2005)
	Cytospora diatrypelloideae	ITS	Adams et al. (2005)
	Cytospora disciformis	ITS	Adams et al. (2005)

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora eucalypticola	ITS	Adams et al. (2005, 2006)
	Cytospora-like species	ITS	Adams et al. (2005)
	Cytospora nitschkii	ITS	Adams et al. (2005)
	Cytospora putative	ITS	Smith et al. (1996)
	Cytospora putative species 1	ITS	Adams et al. (2005)
	Cytospora valsoidea	ITS	Adams et al. (2005)
	Cytospora variostromatica	ITS	Adams et al. (2005)
	Valsa aff. cinereostroma (Cytospora austealia)	ITS	Crous et al. (1990)
	Valsa brevispora	ITS	Adams et al. (2005)
	Valsa cinereostroma	ITS	Adams et al. (2005)
	Valsa eucalypti	ITS	Adams et al. (2005)
	Valsa eugeniae	ITS	Adams et al. (2005)
	Valsa fabianae	ITS	Adams et al. (2005)
	Valsa luecostoma	ITS	Adams et al. (2002)
	Vala myrtagena	ITS	Adams et al. (2005)

Table 9.3 (continued)

Host	Species record	Genes used	References
	Valsa salicina	ITS	Adams et al. (2006)
Eugenia	*Valsa eugeniae*	ITS	Adams et al. (2005)
	Valsa eugeniae	ITS	Sivanesan and Holliday (19701)
Fagus	*Cytospora decorticans*	ITS	Adams et al. (2005)
Ficus	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
Fraxinus	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora minuta	ITS	Adams et al. (2006)
	Cytospora pruinosa	ITS	Fotouhifar et al. (2010)
	Valsa cypri	ITS	Défago (1942)
Hippophae	*Cytospora hippophaes*	ITS, LSU, *rpb2*, *act*	Fan et al. (2015b)
Jacaranda	*Valsa ceratosperma*	ITS	Adams et al. (2006)
	Cytospora atrocirrhata	ITS, LSU, TUB2, *act*	Fan et al. (2015a)
Juglans	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora chrysosperma	ITS, LSU, TUB2, *act*	Fan et al. (2015a)
	Cytospora cincta	ITS	Fotouhifar et al. (2010)
	Cytospora gigaspora	ITS, LSU, TUB2, *act*	Fan et al. (2015a)

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora leucostoma	ITS	Fotouhifar et al. (2010)
	Cytospora sacculus	ITS, LSU, TUB2, *act*	Fan et al. (2015a)
	Cytospora sordida	ITS	Fotouhifar et al. (2010)
Lepidium	*Cytospora ribis*	ITS	Fotouhifar et al. (2010)
Ligustrum	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
Malus	*Cytospora ceratosperma*	ITS	Adams et al. (2005)
	Cytospora chrysosperma	ITS	Fotouhifar et al. (2010), Mehrabi et al. (2011)
	Cytospora cincta	ITS	Fotouhifar et al. (2010), Mehrabi et al. (2011)
	Cytospora cinctum	ITS	Fotouhifar et al. (2010)
	Cytospora lucostoma	ITS	Mehrabi et al. (2011)
	Cytospora malicola	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)
	Cytospora melnikii	ITS, LSU, *rpb2*, *act*	In this study

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora parasitica	ITS, LSU, *rpb2*, *act*	In this study, Ariyawansa et al. (2015)
	Cytospora schulzeri	ITS	Fotouhifar et al. (2010), Mehrabi et al. (2011)
	Valsa cincta	ITS	Adams et al. (2002)
	Valsa mali	ITS	Adams et al. (2002)
	Valsa malicola	ITS	Adams et al. (2002)
	Valsa melostoma	ITS	Adams et al. (2002)
	Valsa nivea	ITS	Adams et al. (2006)
Mangifera	*Valsa cinereostroma (Cytospora)*	ITS	Adams et al. (2005)
Morus	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora cypsi	ITS	Fotouhifar et al. (2010)
	Cytospora pruinosa	ITS	Fotouhifar et al. (2010)
Olea	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Valsa cypri	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)

Table 9.3 (continued)

Host	Species record	Genes used	References
Persica	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora leucostoma	ITS	Fotouhifar et al. (2010)
Picea	*Cytospora mougeotii*	ITS	Adams et al. (2005)
	Valsa kunzei	ITS	Adams et al. (2005)
	Valsa kunzei var. *piceae*	ITS	Proffer and Hart (1988)
Pistacia	*Cytospora terebinthi*	ITS	Fotouhifar et al. (2010)
Pinus	*Valsa friesii*	ITS	Adams et al. (2005)
	Valsa kunzei	ITS	Adams et al. (2006)
	Valsa pini	ITS	Adams et al. (2005), Défago (1942)
Platanus	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora gutnerae	ITS	Fotouhifar et al. (2010)
	Cytospora nivea	ITS	Fotouhifar et al. (2010)
	Cytospora ribis	ITS	Fotouhifar et al. (2010)
Populus	*Cytospora atrocirrhata*	ITS	Fotouhifar et al. (2010)
	Cytospora chrysosperma	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora fugax	ITS	Fotouhifar et al. (2010)
	Cytospora germanica	ITS	Adams et al. (2006)
	Cytospora hariotii	ITS	Adams et al. (2006)
	Cytospora kantschavelii	ITS	Fotouhifar et al. (2010)
	Cytospora melnikii	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora nivea	ITS	Adams et al. (2006)
	Cytospora parakantschavelii	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora paratranslucens	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora rusanovii	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora salicacearum	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora sordida	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)
	Cytospora translucens	ITS	Fotouhifar et al. (2010)
	Cytospora variostromatica	ITS	Adams et al. (2006)
	Valsa nivea	ITS	Défago (1942), Fotouhifar et al. (2010)
Prunus (Sakura)	*Cytospora salicacearum*	ITS, LSU, *rpb2*, *act*	In this study

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora sorbicola	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora chrysosperma	ITS	Fotouhifar et al. (2010)
	Cytospora cincta	ITS	Fotouhifar et al. (2010)
	Cytospora cinctum	ITS	Fotouhifar et al. (2010)
	Cytospora persoonii	ITS	Fotouhifar et al. (2010)
	Cytospora leucostoma	ITS	Adams et al. (2002)
	Valsa cincta	ITS	Adams et al. (2002)
	Valsa leucostoma f. sp. *insititiae*	ITS	Défago (1942)
	Cytospora eutypelloides	ITS	Adams et al. (2006)
	Valsa parapersoonii comb. Nov.	ITS	Adams et al. (2006)
Pseudotsuga	*Valsa abietis* sp. complex 1 (syn. *Valsa weiriana*)	ITS	Adams et al. (2002)
Pyrus	*Cytospora donetzica*	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora parakantschavelii	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora sacculus	ITS	Fotouhifar et al. (2010)
	Valsa ceratosperma	ITS	Fotouhifar et al. (2010)

Table 9.3 (continued)

Host	Species record	Genes used	References
Quercus	*Cytospora intermedia*	ITS	Fotouhifar et al. (2010)
	Cytospora sacculus	ITS	Adams et al. (2005)
	Valseutypella multicollis	ITS	Adams et al. (2006)
Rhododendron	*Valsa subclypeata*	ITS	Adams et al. (2005)
Rhus	*Valsa ceratosperma* s.lat.	ITS	Adams et al. (2005)
Ribes	*Cytospora ribis*	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)
Rosa	*Cytospora cincta*	ITS	Fotouhifar et al. (2010)
	Cytospora donetzica	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora leucostoma	ITS	Fotouhifar et al. (2010)
	Cytospora rhodophila	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)
	Cytospora rosarum	ITS	Fotouhifar et al. (2010)
Robinia	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora leucostoma	ITS	Fotouhifar et al. (2010)
Saccharum	*Cytospora sacchari*	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al. (2010), Singh et al. (2007)
Salix	*Cytospora atrocirrhata*	ITS	Fotouhifar et al. (2010)
	Cytospora aurora	ITS	Fotouhifar et al. (2010)
	Cytospora curvata	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora chrysosperma	ITS, LSU, *rpb2*, *act*	Fan et al. (2015b)
	Cytospora donetzica	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora erumpens	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora fugax	ITS	Fotouhifar et al. (2010)
	Cytospora gigaspora	ITS, LSU, *rpb2*, *act*	Fan et al. (2015b)
	Cytospora longiostiolata	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora nivea	ITS, LSU, *rpb2*, *act*	In this study, Fan et al. (2015b)
	Cytospora populina	ITS, LSU, *rpb2*, *act*	Fan et al. (2015b)
	Cytospora rusanovii	ITS, LSU, *rpb2*, *act*	In this study

Table 9.3 (continued)

Host	Species record	Genes used	References
	Cytospora salicacearum	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora salicina	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora salicacearum	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora salicicola	ITS, LSU, *rpb2*, *act*	In this study, Li et al. (2016)
	Cytospora salicina	ITS, LSU, *rpb2*, *act*	In this study
	Leucostoma translucens	ITS	Fotouhifar et al. (2010)
	Valsa salicina	ITS	Defago (1942), Fotouhifar et al. (2010)
	Valsa sordida	ITS	Adams et al. (2006), Fotouhifar et al. (2010)
	Valsa translucens	ITS	Defago (1942)
Sequoia	*Cytospora eucalypti*	ITS	Adams et al. (2005)
Sibiraea	*Cytospora sibiraeae*	ITS, LSU, *rpb2*, *act*	Liu et al. (2015)
Sophora	*Cytospora chrysosperma*	ITS	Dar and Rai (2014)
	Cytospora sophoricola	ITS	Dar and Rai (2014)
Sorbaronia	*Cytospora sorbicola*	ITS, LSU, *rpb2*, *act*	In this study

Table 9.3 (continued)

Host	Species record	Genes used	References
Sorbus	*Cytospora ampulliformis*	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora leucostoma	ITS	Adams et al. (2005)
	Cytospora sorbicola	ITS, LSU, *rpb2*, *act*	In this study
	Cytospora sorbi	ITS, LSU, *rpb2*, *act*	In this study
	Valsa massariana	ITS	Adams et al. (2002)
Syringa	*Valsa cypri*	ITS	Défago (1942)
Tamarix	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
Taxus	*Valsa ambiens*	ITS	Adams et al. (2005), Défago (1942)
	Valsa ceratophora	ITS	Adams et al. (2005), Défago (1942)
Thuja	*Cytospora chrysosperma*	ITS	Fotouhifar et al. (2010)
	Cytospora ribis	ITS	Fotouhifar et al. (2010)
	Cytospora schulzeri	ITS	Fotouhifar et al. (2010)
Tibouchina	*Valsa eugeniae* (*Cytospora* state)	ITS	Adams et al. (2005)
	Valsa myrtagena	ITS	Fotouhifar et al. (2010)
Triticum	*Cytospora tritici*	ITS	Adams et al. (2006)

Table 9.3 (continued)

Host	Species record	Genes used	References
Ulmus	*Cytospora carbonacea*	ITS	Adams et al. (2002, 2005, 2006), Fotouhifar et al.n(2010), Singh et al. (2007)
	Cytospora eutypelloides	ITS	Défago (1942)
	Cytospora subclypeata	ITS	Adams et al. (2005)
	Cytospora ulmi	ITS, LSU, *rpb2*, *act*	In this study
Vitis	*Cytospora cincta*	ITS	Fotouhifar et al. (2010)
	Cytospora leucostoma	ITS	Fotouhifar et al. (2010)

CHAPTER 10

TAXONOMIC POSITION OF *MELOMASTIA ITALICA* SP. NOV. AND PHYLOGENETIC REAPPRAISAL OF DYFROLOMYCES[9]

Abstract

Melomastia is a genus of saprobic fungal species found on wood, with 29 species epithets listed in Index Fungorum. The classification of species in the genus has been a challenge due to a high degree of morphological overlap and a lack of DNA based phylogenies. The present study clarifies the phylogenetic placement of the genus and with an additional new species based on a fresh collection from Italy. The new species, *Melomastia italica*, is described based on morphological and relationships inferred from phylogenetic analyses of SSU and LSU sequence data. *Melomastia* is accommodated within the family Pleurotremaceae in the class Dothideomycetes. The phylogenetic relationships and intergeneric taxonomy within the family Pleurotremaceae are revisited, while *Dyfrolomyces maolanensis* is transferred to the genus *Melomastia*.

Keywords: *incertae sedis*, Dothideomycetes, Molecular analyses, Morphology, Saprobic fungi

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10.1 Introduction

The genus *Melomastia* Nitschke ex Sacc. was described by Nitschke (1875) to accommodate *Melomastia mastoidea* (Fr.) J. Schröt (= *Melomastia friesii* Nitschke) (Saccardo, 1875). There have been several taxonomic controversies pertaining to the ordinal/familial placement of this genus within the Ascomycota (Barr, 1989, 1994; Hawksworth et al., 1995; Kirk et al., 2008; Hu et al., 2010; Lumbsch & Huhndorf, 2010). It is presently placed in Ascomycetes, genera *incertae sedis* (Lumbsch & Huhndorf, 2010; Maharachchikumbura et al., 2015, 2016; Wijayawardene et al., 2017). Barr (1989) accommodated *Melomastia* in Clypeosphaeriaceae, which is related to Amphisphaeriaceae. Later, Barr (1994) assigned three families with unitunicate asci (Amphisphaeriaceae, Clypeosphaeriaceae, Pleurotremataceae) to the order Xylariales and placed five genera within Pleurotremaceae (*Daruvedia*, *Melomastia*, *Phomatospora*, *Pleurotrema*, *Saccardoella*) based on the non-fissitunicate ascus character.

Hawksworth et al. (1995) retained *Pleurotrema* in the order Pyrenulales. Hu et al. (2010) agreed with Kirk et al. (2008) and placed *Daruvedia* in the Pleosporales (Dothideomycetes) based on type specimen and fresh collections of *Daruvedia*. Senanayake et al. (2016) referred the genus *Phomatospora* to a new family Phomatosporaceae (Phomatosporales) based on DNA sequence data analyses. Presently, *Melomastia* and *Saccardoella* are referred to Ascomycota genera, *incertae sedis* (Kirk et al., 2001; Lumbsch & Huhndorf, 2010). Suetrong et al. (2009) analyzed DNA sequence data of *Saccardoella rhizophorae*, a species known from marine environments, and currently positioned it within the class Dothideomycetes. However, placement of *S. rhizophorae* at an appropriate higher taxonomic level was difficult as the latter did not group with any well-established order/family within the Dothideomycetes (Hyde, 1992; Tsui et al., 1998; Suetrong et al., 2009). Thereafter, Pang et al. (2013) introduced a new family, Dyfrolomycetaceae (Dothideomycetes) to accommodate *Dyfrolomyces tiomanensis*, which grouped with *Saccardoella rhizophorae* based on combined DNA sequence data analyses. This resulted in three

species of *Saccardoella* (*S. mangrovei*, *S. marinospora*, *S. rhizophorae*) being transferred to *Dyfrolomyces* (Pang et al., 2013; Hyde et al., 2013).

Maharachchikumbura et al. (2015) accepted *Pleurotrema* as monotypic in Pleurotremataceae within Chaetosphaeriales without taxonomic justifications and referred *Melomastia* to Sordariomycetes, genera *incertae sedis*. Later, Maharachchikumbura et al. (2016) synonymised Dyfrolomycetaceae under Pleurotremataceae and excluded it from Sordariomycetes based on morphology of the *Pleurotrema* isotype, which are similar to species of *Saccardoella* and *Dyfrolomyces* in Dothideomycetes. To date, 29 epithets of *Melomastia* are recorded in Index Fungorum (2017). During our fungal diversity survey in Italy, we recovered an unusual *Melomastia* species which we described as a new species herein. Phylogenetic investigations also revealed some interesting taxonomic insights pertaining to the intergeneric relationships of *Dyfrolomyces* and *Melomastia*. We provide a more robust phylogeny and resolve some of the taxonomic confusion surrounding the family Pleurotremataceae.

10.2 Materials and Methods

10.2.1 Sample Collection and Examination of Specimens

The samples were collected from dead branches of *Vitis vinifera* in Italy in 2015. The specimens were returned to the laboratory in paper bags, examined and descriptions were carried out following Norphanphoun et al. (2016). Micro-morphological characters were studied using a Motic SMZ 168 dissecting microscope for fungal fruiting bodies. Hand sections of the fruiting structures were mounted in water and examined for morphological details. Fungi were also examined using a Nikon Ni compound microscope and photographed with a Canon EOS 600D digital camera fitted to the microscope. Photo-plates were made using Adobe Photoshop CS6 Extended version 13.0 × 64 (Adobe Systems, USA), while Tarosoft (R) Image Framework program v. 0.9.7 was used for measurements. The contents inside the ascomata, which comprised asci, hamathecium and ascospores, were removed with a sterile needle and soaked in sterile water in a glass container prior to examination.

Cultures were obtained by single spore isolation, following the description in Chomnunti et al. (2014). Spore germination was observed and photographed using a Nikon Ni compound microscope fitted with Canon EOS 600D digital camera. Geminated spores were transferred aseptically to fresh malt extract agar (MEA) and incubated at room temperature (18–25°C).

Herbarium specimens are deposited in the Mae Fah Luang University Herbarium, Chiang Rai, Thailand (MFLU) and duplicated in New Zealand Fungarium (PDD). Living cultures are deposited at Mae Fah Luang University Culture Collection (MFLUCC) and Kunming Culture Collection (KUMCC). Index Fungorum numbers are registered (Jayasiri et al., 2015). New species are established as recommended by Jeewon & Hyde (2016).

10.2.2 DNA Extraction, PCR Amplification and Sequencing

DNA extraction process was followed by Norphanphoun et al. (2017) with fresh fungal mycelia growing on MEA at room temperature (18–25°C) for three weeks. The genomic DNA was obtained using a E.Z.N.A.TM Fungal DNA MiniKit (Omega Biotech, CA, USA) following the manufacturer's instructions.

Polymerase chain reactions (PCR) were carried out using primer pairs of LROR (5′-ACCCGCTGAACTTAAGC-3′) and LR5 (5′-TCCTGAGGGAAACTTCG-3′) to amplify the large subunit rDNA (28S, LSU) (Vilgalys & Hester, 1990), and the small subunit nuclear rDNA (18S, SSU) was amplified with primers (5′-GTAGTCATATGCTTGTCTC-3′) and NS4 (5′-CTTCCGTCAATTCCTTTAAG-3′) (White et al., 1990). The amplification reactions were carried out with the following protocol: 50 µl reaction volume containing 2 µl of DNA template, 2 µl of each forward and reverse primers, 25 µl of 2 × Bench Top™Taq Master Mix (mixture of Taq DNA Polymerase (recombinant): 0.05 units/µL, $MgCl_2$: 4 mM, and dNTPs (dATP, dCTP, dGTP, dTTP): 0.4 mM) and 19 µl of double-distilled water (ddH_2O) (sterilized water). The PCR thermal cycle program for LSU gene amplification are as follows: 95°C for 3 min, followed by 34 cycles of 95°C for 30 s, 51°C for 50 s, 72°C for 1 min, and final extension at 72°C for 10 min. The PCR thermal cycle program for SSU gene amplification were provided as: 95°C for 3 min, followed by 30 cycles of 95°C for 1 min, 51°C for 1 min, 72°C for 45 s, and final extension at 72°C for 10 min. Purification

and sequencing of PCR product with the same primers mentioned above were carried out at Life Biotechnology Co., Shanghai, China.

10.2.3 Phylogenetic Analysis

Blast searches were made to retrieve the closest matches in GenBank and recently published sequences (Suetrong et al., 2009; Pang et al., 2013; Hyde et al., 2016, 2017; Zhang et al., 2017). Combined analyses of SSU and LSU sequence data of 27 taxa (Table 10.1) were analysed under different optimality criteria as suggested by Jeewon et al. (2002, 2003). The combined sequence alignments were obtained from MEGA7 version 7.0.14 (Kumar et al., 2015) and ambiguously aligned regions were excluded, gaps were treated as missing data and further alignments performed in BioEdit v. 7.2 (Hall, 1999). Phylogenetic trees were inferred under maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI).

Maximum-likelihood (ML) analysis was performed in RAxML (Stamatakis, 2006) implemented in raxmlGUI v.1.3 (Silvestro & Michalak, 2012). The 1000 rapid bootstrap replicates were run with generalized time reversible GTRGAMMA model of nucleotide substitution and searches for model selected for ML were applied.

Maximum parsimony (MP) analysis was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford, 2003). The trees were inferred using the heuristic search option with tree bisection-reconnection (TBR) as the branch swapping algorithm and 1000 random sequence additions. Maxtrees were setup to 5000, branches of zero length were collapsed and all multiple parsimonious trees were saved. Descriptive tree statistics for parsimony tree length [TL], consistency index [CI], retention index [RI], rescaled consistency index [RC] and homoplasy index [HI] were calculated for the Maximum Parsimonious Tree (MPT). The robustness of the most parsimonious trees were evaluated by 1000 bootstrap replications, each with ten replicates of random stepwise addition of taxa (Felsenstein, 1985). The Kishino-Hasegawa tests (KHT) were performed to determine whether the trees were significantly different (Kishino & Hasegawa, 1989).

Bayesian inference (BI) analysis was performed using the Markov Chain Monte Carlo (MCMC) method with MrBayes 3.2.2 (Ronquist et al., 2012). The best-fit nucleotide substitution models for each dataset were separately determined using

MrModeltest version 2.2 (Nylander, 2004). GTR+I+G were selected as best-fitting models for the SSU, LSU and TEF datasets. The MCMC analyses, with four chains, were run, started from random tree topology and lasted 5,000,000 generations and sampled every 100 generations (Nylander, 2004). The Tracer v. 1.5.0 program was used to check the effective sampling sizes (ESS) that should be above 200, the stable likelihood plateaus and burn-in value (Rambaut, 2013). The first 5000 generations were excluded as burn-in.

The phylograms are visualized in FigTree v1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/; Rambaut, 2012) and made in Adobe Illustrator CC and Adobe Photoshop CS6 Extended version 13.1.2 × 64. Sequences data from this study are deposited in GenBank.

Table 10.1 GenBank accession numbers of the sequences used in phylogenetic analyses

Taxa	Strain [a]	Genbank accession numbers	
		SSU	LSU
Acrospermum adeanum	M133	EU940031	EU940104
Acrospermum compressum	M151	EU940012	EU940084
Acrospermum gramineum	M152	EU940013	EU940085
Aliquandostipite siamensiae	SS81.02	EF175645	EF175666
Aliquandostipite khaoyaiensis	CBS 118232	AF201453	GU301796
Dendryphiopsis atra	AFTOL-ID 273	DQ677996	DQ678046
Dyfrolomyces thamplaensis	MFLUCC 15-0635	KX925436	KX925435
Dyfrolomyces phetchaburiensis	MFLUCC 15-0951	MF615403	MF615402
Dyfrolomyces rhizophorae	JK 5456A/JK_5349A	GU479766	GU479799
Dyfrolomyces thailandica	MFLUCC 15-0945	KX611367	KX611366
Dyfrolomyces tiomanensis	NTOU3636	KC692155	KC692156
Geoglossum nigritum	AFTOL-ID 56	AY544694	AY544650
Jahnula sangamonensis	A482-1B	EF175640	EF175662
Jahnula seychellensis	SS2113.2	EF175643	EF175664
Kirschsteiniothelia aethiops	CBS 109.53	AY016344	AY016361

Table 10.1 (continued)

Taxa	Strain [a]	Genbank accession numbers	
		SSU	LSU
Kirschsteiniothelia sp.	MFLUCC 10-0036	HQ441569	HQ441568
Lecanora hybocarpa	AFTOL-ID 639	DQ782883	EF105421
Manglicola guatemalensis	BCC20157	FJ743444	FJ743450
Manglicola guatemalensis	BCC24217	FJ743441	FJ743447
Melomastia italica	MFLUCC 15-0160	MG029459	MG029458
Melomastia maolanensis	GZCC 16-0102	KY111906	KY111905
Petriella setifera	AFTOL-ID 956	DQ471020	DQ470969
Rhizocarpon oederi	AFTOL-ID 1372	DQ983486	DQ986804
Roccellographa cretacea	AFTOL-ID 93	DQ883705	DQ883696
Schismatomma decolorans	UKE:47570	NG_013155	NG_027622
Trichoglossum hirsutum	AFTOL-ID 64	AY544697	AY544653
Xylaria acuta	AFTOL-ID 63	AY544719	AY544676

Note [a] *A* Carol Shearer, ascomycetes; *AFTOL-ID* Assembling the Fungal Tree of Life: *BCC* Belgian Coordinated Collections of Microorganisms: *CBS* CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands; *GZCC* Guizhou Culture Collection Guiyang, China; *JK* J. Kohlmeyer; *MFLUCC* Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; *S* working collection of William Quaedvlieg.

10.3 Results

10.3.1 Molecular Phylogeny

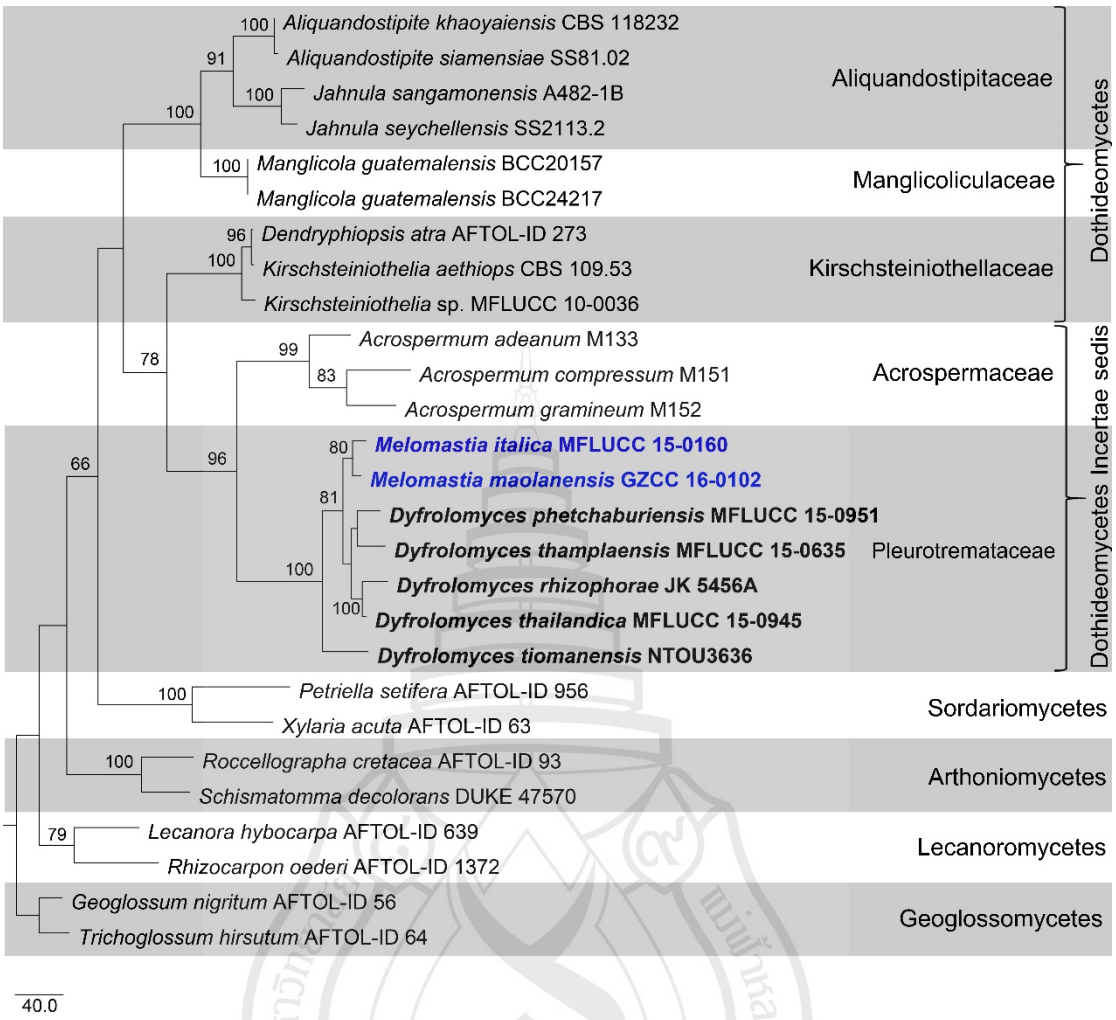
The combined dataset consisted of 27 taxa with a total length of 1909 characters including alignment gaps (1–1007 and 1010–1909 were derived from SSU and LSU sequence data respectively). The result from the partition homogeneity test (PHT) was not significant (level 95%), indicating that the individual data sets were congruent and could be combined. Parsimony analysis indicate that 1909 characters were constant, 146 variable characters were parsimony uninformative and 483 characters were parsimony informative and yielded 1000 most parsimonious trees (TL = 1578, CI = 0.570, RI = 0.749, RC = 0.426, HI = 0.430).

ML, MP and BY analyses of the combined data resulted in phylogenies that can separate genera within Pleurotremaceae (Dothideomycetes) as shown in Figures 1, 2 and 3 respectively. Bootstrap support values of ML, MP (≥ 50%) and Bayesian posterior probabilities (≥ 0.95) are shown on the upper branches (Figures 1, 2, 3). Taxa from Geoglossomycetes were used as outgroups.



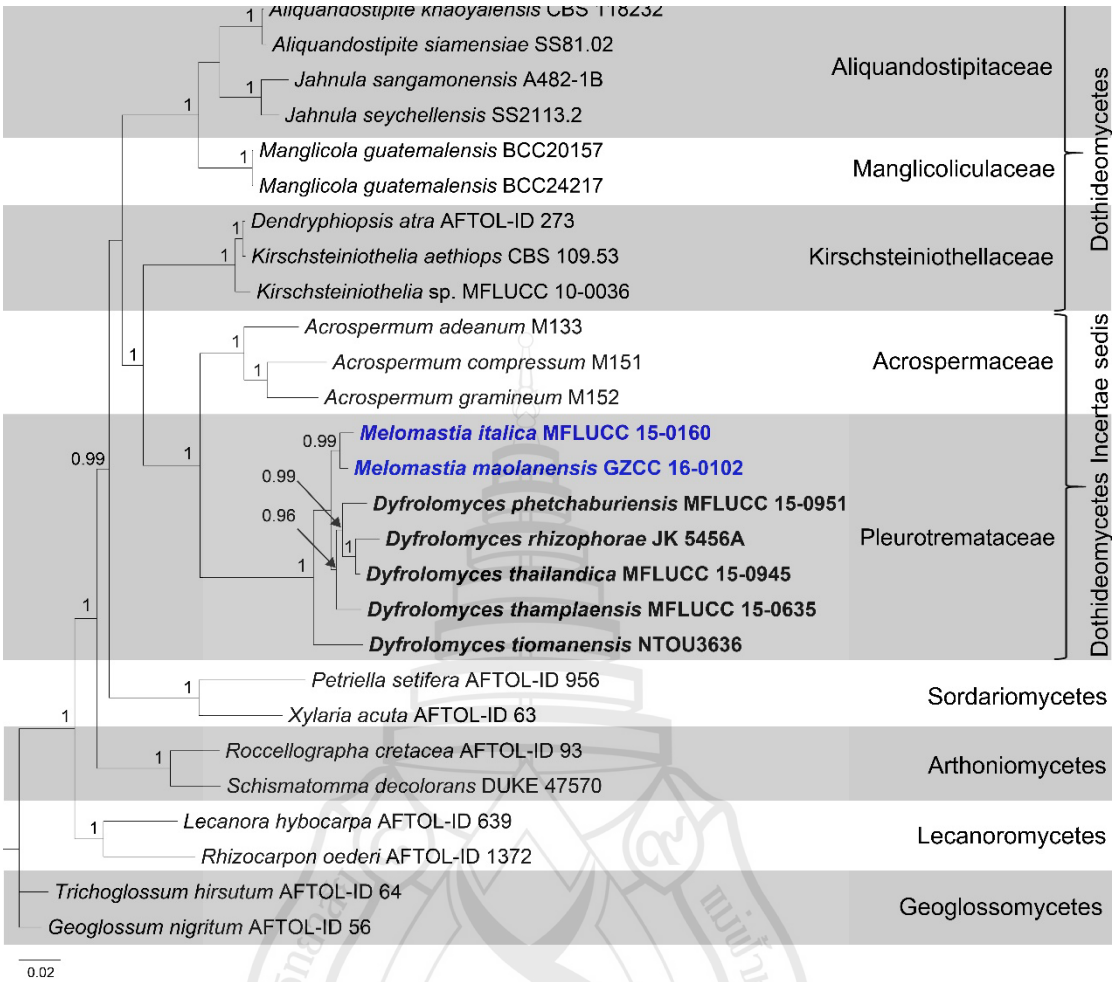
Note Phylogram generated from maximum likelihood (RAxML) based on analysis of a combined SSU and LSU sequence data. Bootstrap values ≥ 50% given at the nodes. The species obtained in this study is in blue bold. Ex-type taxa from other studies are in black bold. *Geoglossum* and *Trichoglossum* were used as outgroups.

Figure 10.1 Phylogenetic analysis of Dothideomycetes incertae sedis generated from maximum likelihood (RAxML)



Note Phylogram generated from maximum parsimony based on analysis of a combined SSU and LSU sequence data. Bootstrap values ≥ 50% given at the nodes. The species obtained in this study is in blue bold. Ex-type taxa from other studies are in black bold. *Geoglossum* and *Trichoglossum* were used as outgroups.

Figure 10.2 Phylogenetic analysis of Dothideomycetes incertae sedis generated from maximum parsimony



Note Phylogram generated from Bayesian analysis based on analysis of a combined SSU and LSU sequence data. Bayesian posterior probabilities ≥ 0.95 (PP) are given at the nodes. The species obtained in this study is in blue bold. Ex-type taxa from other studies are in black bold. *Geoglossum* and *Trichoglossum* were used as outgroups.

Figure 10.3 Phylogenetic analysis of Dothideomycetes incertae sedis generated from Bayesian analysis

10.3.2 Taxonomy

Dyfrolomycetales K.L. Pang, K.D. Hyde & E.B.G. Jones, in Hyde et al., Fungal Diversity 63: 7 (2013)

Pleurotremataceae Walt. Watson, New Phytol. 28: 113 (1929)

=Dyfrolomycetaceae K.D. Hyde, K.L. Pang, Alias, Suetrong & E.B.G. Jones, in Pang, Hyde, Alias, Suetrong, Guo & Jones, Cryptog. Mycol. 34(3): 227 (2013)

For description see Maharachchikumbura et al. (2016)

Type: *Pleurotrema* Müll.

Melomastia Nitschke ex Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 44: 90 (1875)

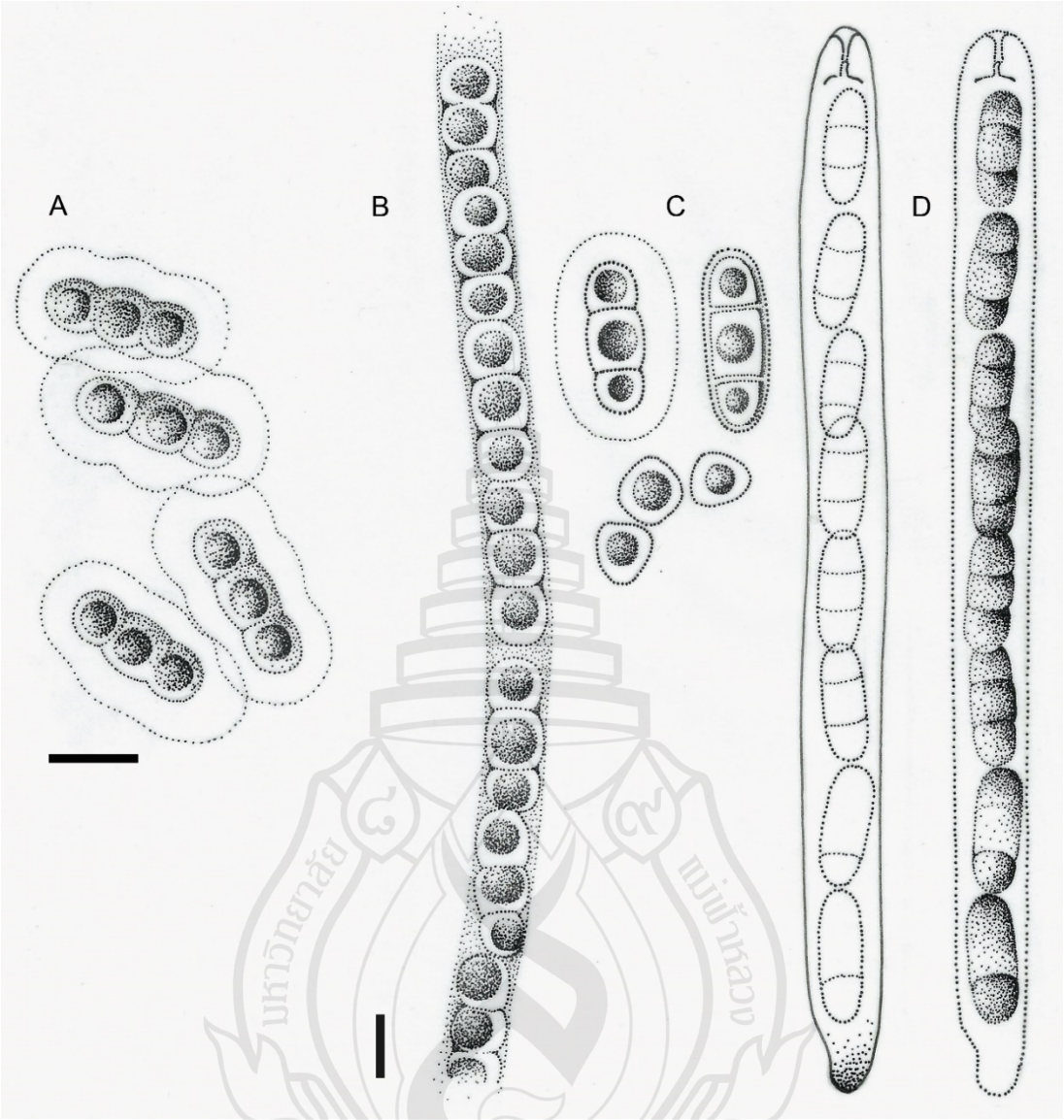
Ascomata raised, immersed, globose, black; in vertical section obpyriform, with a central periphysate ostiolar canal. *Peridium* comprising several layers of brown to dark brown, compressed cells. *Paraphyses* filamentous, flexuose, numerous. *Asci* 8-spored, cylindrical, thick-walled, non fissitunicate, pedicellate, apically rounded, with a J-, subapical ring. *Ascospores* uniseriate, ovoid, hyaline, 2-septate, strongly constricted at the septa, with a lipid globule in each cell, surrounded by a gelatinous sheath.

Type species: *Melomastia friesii* Nitschke

Melomastia mastoidea (Fr.) J. Schröt., in Cohn, Krypt.-Fl. Schlesien (Breslau) 3.2(3): 320 (1894) [1908], Figure 4

= *Melomastia friesii* Nitschke, in Fuckel, Jb. nassau. Ver. Naturk. 25–26: 306 (1871)

For descriptions see Saccardo (1875) and Kang et al. (1999)



Note Morphology of *Melomastia mastoidea*. a, c Ascospores. b, d Asci. Scale bars: a, b = 10 µm.

Source Barr (1994), Kang et al. (1999)

Figure 10.4 Morphological characters of *Melomastia mastoidea*

Melomastia italica Norphanphoun, E. Camporesi, T.C. Wen & K.D. Hyde, sp. nov., Figure 5

Index Fungorum number: IF553984

Facesoffungi number: FoF 03853

Etymology: refers to the country where the fungus was collected.

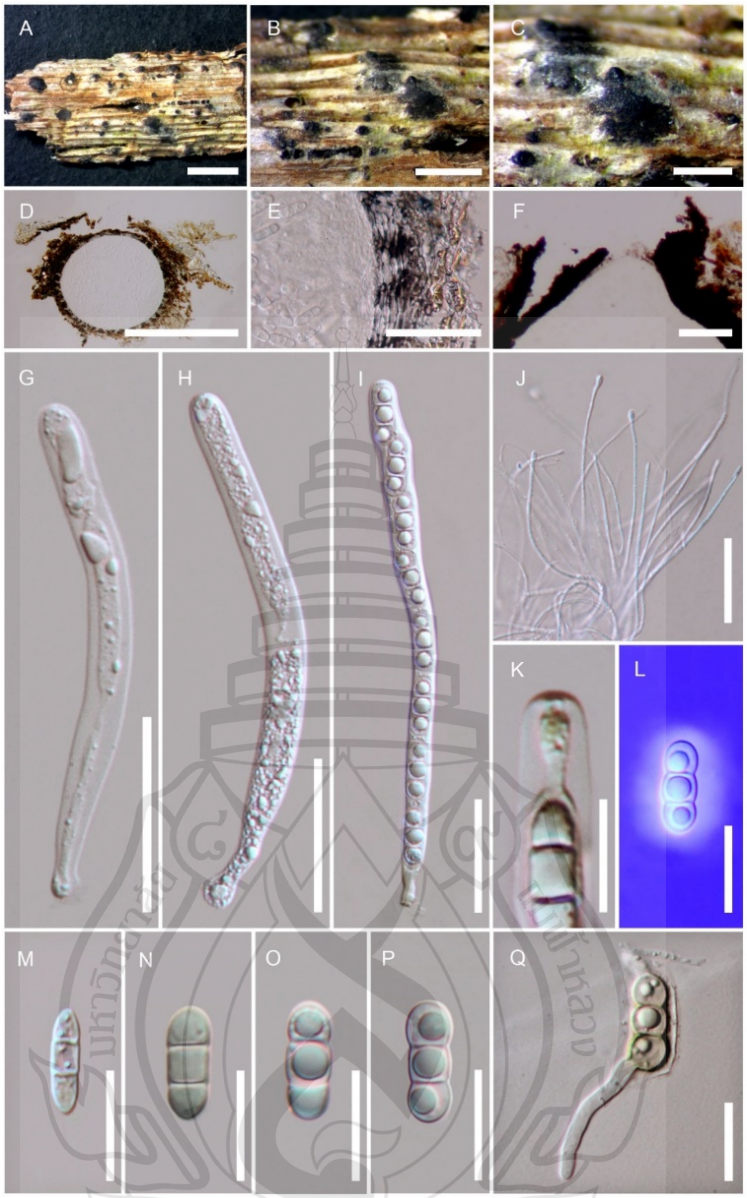
Holotype: MFLU 15-0228

Saprobic on dead branches. Sexual morph: *Ascomata* 400–500 μm high, up to 500 μm diam, perithecial, semi-immersed to immersed in host tissue, subglobose to obpyriform, single, scattered, black, with a short ostiolar neck and erumpent ostiole. *Peridium* thick walled, formed of *textura prismatica*. *Paraphyses* simple, apex inflated at tip. *Asci* 120–190 × 5.1–8.9 μm ($\bar{x}$= 175.5 × 7.5 μm), 8-spored, thick-walled, non fissitunicate, cylindrical or subclavate, undifferentiated at apex, immature asci in Meltzer's reagent showing J-, apical ring. *Ascospores* 8.8–10.5 × 2.8–4.1 μm ($\bar{x}$= 10.1 × 4 μm), uniseriate, ellipsoid, contents granular, 2-septate, constricted at the septa, hyaline glistening, smooth-walled, surrounded by a gelatinous sheath when immature. Asexual morph: Undetermined.

Material examined: ITALY, Province of Forlì-Cesena, near Monte Cavallo - Meldola on dead aerial branches of *Vitis vinifera* L., 1 January 2015, E. Camporesi IT1578 (MFLU 15-0228, holotype; KUN, isotype); ex-type-living cultures, MFLUCC 15-0160, KUMCC.

Notes: *Melomastia* was introduced by Nitschke (1875) with *M. friesii* as the type species found on *Viburnum opulus* L. (Adoxaceae) in Germany. Later, the species was synonymized under *Melomastia mastoidea* (Schröter, 1894). *Melomastia italica* resembles *Melomastia* due to its ellipsoid, granular, 2-septate, hyaline and glistening ascospores, surrounded by a gelatinous sheath (Barr, 1994; Kang et al., 1999). It is most similar to *M. antarctica*, *M. chilensis* and *M. mastoidea*. However, they differ in ascospore size and presence or absence of a gelatinous sheath.

Melomastia antarctica ascospores are 15 × 4.2 μm (without a gelatinous sheath), *M. chilensis* 16–18 × 6–7 μm, *M. mastoidea* 18.1 × 5.4 μm, and *M. italica* 10.1 × 4 μm (Spegazzini, 1887; Petrak, 1921; Barr, 1994; Kang et al., 1999) (Table 10.2).



Note Morphology of *Melomastia italica* (MFLUCC 15-0160, holotype). a Habitat. b, c Habit of ascomata in host. d Section through ascoma. e Peridium. f Ostiole. g–h Immature asci. i Mature ascus. j Paraphyses. k Immature ascus in Meltzer's reagent showing J+, apical apparatus. l Mature ascospore stained in Indian ink. m–n Immature ascospores. o–p Development of mature ascospores. q Germinated ascospore. Scale bars: a = 2 mm, b = 1 mm, c = 500 µm, d = 400 µm, e = 50 µm, f = 100 µm, g–j = 30 µm, k–q = 10 µm.

Figure 10.5 Morphological characters of *Melomastia italica* (MFLUCC 15-0160, holotype)

New combination

Melomastia maolanensis (J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu) Norphanphoun, T.C. Wen & K.D. Hyde, *comb. nov.*

= *Dyfrolomyces maolanensis* J.F. Zhang, J.K. Liu, K.D. Hyde & Z.Y. Liu, *Phytotaxa* 313: 267–277 (2017)

Index Fungorum number: IF554041

Genera included in family Pleurotremaceae

Dyfrolomyces K.D. Hyde, K.L. Pang, Alias, Suetrong & E.B.G. Jones, in Pang, Hyde, Alias, Suetrong, Guo & Jones, Cryptog. Mycol. 34(3): 227 (2013)

Type: *Dyfrolomyces tiomanensis* K.L. Pang et al.

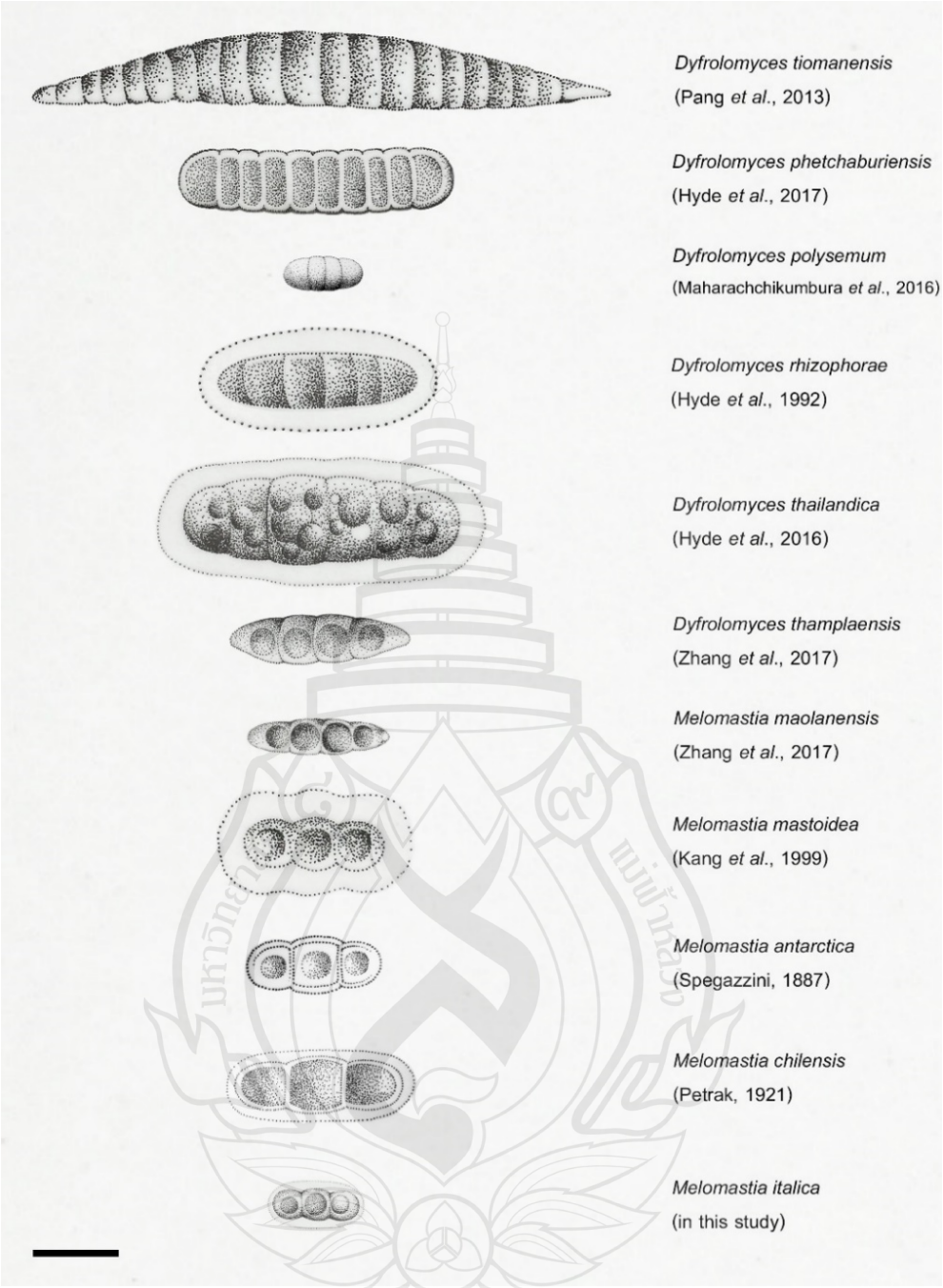
For description see Pang et al. (2013)

Melomastia Nitschke ex Sacc., Atti Soc. Veneto-Trent. Sci. Nat., Padova, Sér. 44: 90 (1875)

Type: *Melomastia mastoidea* (Fr.) J. Schröt.

Pleurotrema Müll. Arg., Bot. Jb. 6: 388 (1885)

Type: *Pleurotrema polysemum* (Nyl.) Müll. Arg., Bot. Jb. 6: 389 (1885) For description see Spegazzini (1879) and Maharachchikumbura et al. (2016)



Note Ascospore of species of Pleurotremaceae discussed in the text. Scale bar 10 µm.

Source Petrak (1921), Spegazzini (1887), Hyde (1992), Pang et al. (2013), Hyde et al. (2016, 2017), Maharachchikumbura et al. (2016), Zhang et al. (2017)

Figure 10.6 Morphological characters of ascospore of species of Pleurotremaceae

Table 10.2 Synopsis of species of Pleurotremaceae discussed in the paper

Species	Habitat/ Host	Ascomata (µm)	Asci (µm)	Ascospores (µm)	Reference
Dyfrolomyces aquatica = *Saccardoella aquatica*	-	560–700	204.2 × 7.9	29.2 × 7, 3-septate with inconspicuous gelatinous sheath	Tsui et al. (1998)
Dyfrolomyces mangrovei ≡ *Saccardoella mangrovei*	Intertidal tertidal mangrove wood	380–585 × 390–485	216 × 8.5–14	26–33 × 6–8, 7–9-septate with mucilaginous sheath	Hyde (1992)
Dyfrolomyces marinospora ≡ *Saccardoella marinospora*	Intertidal mangrove wood	780–1040 × 650–960	190–240 × 10–12	25–31 × 7.5–10, 3-septate with mucilaginous sheath	Hyde (1992)
Dyfrolomyces tiomanensis	On mangrove wood	565−(615)−667 × 283−(374)−446	316−(323)−333 × 12−(16)−17	69−(74)−82 × 9−(10)−11, 20−24-septate without sheath	Pang et al. (2013)
Dyfrolomyces phetchaburiensis	Wood of *Rhizophora apiculata*	300× 264	230 × 10.2	37 × 7.0, 10-septate	Hyde et al. (2017)
Dyfrolomyces rhizophorae	Intertidal mangrove wood of *Rhizophora apiculata*	325–455 × up to 364	135–160 × 8–10	19–26 × 6–8, 4–6-septate with thin sheath	Hyde (1992)

Table 10.2 (continued)

Species	Habitat/ Host	Ascomata (µm)	Asci (µm)	Ascospores (µm)	Reference
Dyfrolomyces thailandica	-	430–350 × 242–280	152 × 8.2	28 × 6.5, 3–5-septate with gelatinous sheath	Hyde et al. (2016)
Dyfrolomyces thamplaensis	Dead branch	-	137 × 7	22 × 5.5, 3-septate without sheath	Zhang et al. (2017)
Melomastia antarctica	*Gaultheria mucronata*	400–900	130–150 × 6	15 × 4.2, 2-septate without sheath	Spegazzini (1887)
Melomastia chilensis	*Sophora macrocarpa*	250–400	160–180 × 9–10	16–18 × 6–7, 2-septate with gelatinous sheath	Petrak (1921)
Melomastia italica	*Vitis vinifera*	400–500 × up to 500	175.5 × 7.5	10.1 × 4, 2-septate with gelatinous sheath	In this study
Melomastia maolanensis = *Dyfrolomyces maolanensis*	Dead branch	-	110.9 × 4.9	16.2 × 3.9, 3-septate without sheath	Zhang et al. (2017), In this study
Melomastia mastoidea	*Rosa*	500–762 × 350–435	198.7 × 8.3	18.1 × 5.4, 2-septate with gelatinous sheath	Barr (1994), Kang (1999)

10.4 Discussion

Melomastia was introduced by Nitschke (1875) and is characterized by globose ascomata with erumpent apex, cylindrical asci and 2-septate ascospores with a gelatinous sheath (Barr et al., 1994; Kang et al., 1999). The genus was re-examined by Barr et al. (1994) and Kang et al. (1999) based on type material, but taxonomic relationships and the position within the Ascomycota remained uncertain. This study, which incorporates a morphological and a phylogenetic approach based on DNA sequence data, partially resolves the taxonomic confusion of *Dyfrolomyces* and *Melomastia* with the genus *Pleurotrema* based on its type species (*Pleurotrema polysemum* (Nyl.) Müll.). Phylogenies clearly indicate that they do not belong in Sordariomycetes as previously postulated by earlier mycologists (Maharachchikum--bura et al., 2015; Hyde et al., 2016; Feng et al., 2017). Instead, they belong in Dothideomycetes. Our phylogenetic results also corroborate those that pertain to the familial placement of *Dyfrolomyces* and *Melomastia*. *Dyfrolomyces*, *Melomastia* and *Pleurotrema* are hereby accommodated in the family Pleurotremaceae and the latter is closely related to the family Acrospermaceae (Figures 1, 2, 3). This relationship is strongly supported and consistent even when the same DNA dataset was subjected to different types of analyses (Figures 1, 2, 3). From a morphological perspective, all of these genera are characterized by thick-walled, non fissitunicate asci, and uniseriate, hyaline ascospores which are constricted at the septum, with a gelatinous sheath, which are typical of the Pleurotremaceae. In all phylogenies, all *Acrospermum* species constitute a well-supported independent lineage, which supports its generic rank in the family Acrospermaceae, sister to the Pleurotremaceae. In addition, results herein confirm that *Melomastia* should be accommodated in Pleurotremaceae (Barr, 1994; Hyde, 1992; Kang et al., 1999; Lumbsch & Huhndorf, 2010; Maharachchikumbura et al., 2015, 2016; Hyde et al., 2016).

Our molecular study revealed interesting taxonomic relationships of the genus *Melomastia*. Both MP and BA derived phylogenies are congruent and indicate that *Melomastia* should be given generic status. Our species sampled herein cluster together with high support and are nested in between *Dyfrolomyces* species (Figures 2, 3).

Analyses of the individual LSU dataset also yielded similar topologies (results not shown). The only discrepancy we noted with respect to *Melomastia* was the placement of the two *Melomastia* species in the ML analyses (Figure 1). *Melomastia italica* segregates in an independent lineage with high support and a similar scenario is observed for *Dyfrolomyces maolanensis* which is nestled between *Melomastia italica* and other *Dyfrolomyces* species, albeit with weak support (Figure 1). Either this depicts a paraphyletic nature of *Melomastia* or simply an artifact during phylogenetic analyses. However, this anomaly reinforces our taxonomic assumption that *Melomastia italica* is a new taxon given its distinct phylogeny. On the other hand, it is worth mentioning that analyses of the LSU gene region only recovered similar phylogeny as the combined dataset (results not shown) and hence we rely mostly on the MP and BA for further taxonomic discussion. Despite a close affinity between *Dyfrolomyces maolanensis* and *Melomastia italica* in other analyses, we consider that *Melomastia italica* is a novel species given its distinct morphological features as compared to *Dyfrolomyces maolanensis*. The latter possesses, *Melomastia italica* is characterized by 2-septate, hyaline and contents granular of ascospores. In addition, comparison of the LSU nucleotides sequenced revealed striking differences in 16 base pairs that justifies it as a new taxon (Jeewon & Hyde, 2016).

There have also been some taxonomic irregularities with respect to the generic status of *Dyfrolomyces*, *Melomastia* and *Pleurotrema*. In fact, if we take a conservative approach, we could combine *Dyfrolomyces* and *Pleurotrema* under the earlier *Melomastia*. However, despite some morphological overlap, our phylogeny supplemented with accurate morphological definitions, indicate that these should be considered as distinct genera. While our molecular data clearly indicates that *Dyfrolomyces* are phylogenetically apart, they are not significantly distinct in morphological characteristics such as septate, variously size ascospores (Figure 6). However, we predict that many more taxa in these genera will be found and they will be supported as distinct in both phylogeny and morphology. Further studies with more Pleurotremaceae collections, especially of *Pleurotrema polysemum* are essential to resolve taxonomic relationships within this family.

Table 10.3 Occurrence of *Melomastia* species on hosts and references

Species	Year	Host records	Location
Melomastia antarctica Speg.	1887	*Pernettya mucronata*	Argentina
Melomastia aquilegiae Domashova	1960	*Aquilegia karelini*	Kirghiz SSR
Melomastia calami Syd.	1928	*Calamus* sp.	Philippine
Melomastia calligoni Kravtzev	1960	*Calligonum* sp.	Central Asia
Melomastia carinata Petr.	1942	*Erhedra*	Iran
Melomastia chilensis Speg.	1921	*Sophora macrocarpa*	Chile
Melomastia clypeata Petr.	1923	*Salix martiana*	Brazil
Melomastia coffeae Saccas	1981	*Coffea robusta*	Central African Republic
Melomastia constricta Frolov	1967	*Malus turkmenorum*	Turkmen SSR
		Cydonia oblonga	Central Asia
Melomastia corylina Feltgen	1901	*Corylus*	Luxemburg
Melomastia graminicola Saccas	1954	*Sorghum vulgare*	French
Melomastia haloxyli Kravtzev	1955	*Haloxylon aphyllum*	Kazakh SSR
Melomastia heteroderma Syd.	1936	-	Cuba
Melomastia heveae Saccas	1954	*Hevea brasiliensis*	Africa
Melomastia hyalostoma Luc	1951	*Cola vera*	Ivory Coast
Melomastia italica Norph. et al.	2015	*Vitis vinifera*	Italy
	2013	*Arundo* spp.	Italy
Melomastia jaapiana Kirschst.	1911	Betulaceae	Germany
Melomastia kazachstanica Kravtzev	1955	*Ammodendron conollyi*	Central Asia
		Haloxylon persicum	
Melomastia lignicola Kirschst.	1910	*Betula pendula*	Germany
Melomastia mastoidea (Fr.) J. Schröt.	1894	*Chaenomeles speciosa*	Ukraine

Table 10.3 (continued)

Species	Year	Host records	Location
		Cornus sanguinea	Denmark
		Deutzia corymbosa	India
		Fraxinus excelsior	Poland
		Fraxinus sp.	Denmark
		Lantana involucrata	Bermuda
		Lonicera periclymenum	Denmark
		Lonicera quinquelocularis	India
		Lonicera xylosteum	Denmark
			Poland
			Russia
		Osmanthus fragrans	Ukraine
		Populus tremula	Denmark
		Rubia peregrina	Portugal
		Sambucus nigra	Denmark
		Symphoricarpos sp.	Denmark
		Syringa sp.	Denmark
			England
		Viburnum opulus	Denmark
			Poland
Melomastia metasequoiae Gucevič	1960	*Metasequoia glyptostroboides*	Ukraine
Melomastia maolanensis (Zhang et al.) Norph., T.C.Wen & Hyde	2016	-	China
Melomastia nigrificans Feltgen	1903	*Salicis*	Luxemburg
Melomastia pallidispora Kirschst.	1911	*Trematosphaeria pallidispora*	Italy

Table 10.3 (continued)

Species	Year	Host records	Location
Melomastia popuschoji Frolov	1967	*Amygdalus turcomanica*	Turkmen SSR
Melomastia prorumpens (Rehm) Kirschst. ≡ *Trematosphaeria prorumpens* Rehm. = *Zignoëlla prorumpens* (Rehm) Sacc.	1939	Pine	Germany
Melomastia salicicola (Fabre) Feltgen ≡ *Zignoëlla salicicola* Fabre.	1901	*Salix alba*	Vaucluse Galliae
Melomastia saxauli Kravtzev	1955	*Haloxylon persicum* *Salsola arbuscula* *Salsola rigida*	Central Asia
Melomastia sedi Gucevič	1967	*Sedum acre*	Crimean SSR
Melomastia shastensis Earle	1905	*Abies magnifica* var. *shastensis*	California
Melomastia yezoensis I. Hino & Katum.	1960	*Sasa kurilensis*	Japan

CHAPTER 11

OVERALL CONCLUSIONS

11.1 Overall Conclusions

In this dissertation, my first objective was to identify species related to mangroves based on their morphology and multi-gene phylogenetic traits. Chapters 2–5 provide well-explained details on sixteen novel species reported from *Acrostichum aureum* (Pteridaceae), *Avicennia marina* (Acanthaceae), *Lumnitzera racernosa* (Combretaceae), *Rhizophora apiculata*, *R. mucronata*, *R. stylosa* (Rhizophoraceae), *Sonneratia alba* (Lythraceae), *Xylocarpus granatum*, and *X. moluccensis* (Meliaceae), and new host records of *Alternaria gaisen* on *Ficus macrocarpa* and *Kandelia candel*. The novel species are *Cytospora lumnitzericola* (Host: *Lumnitzera racernosa*), *C. thailandica* (Host: *Xylocarpus moluccensis*), *C. xylocarpi* (Host: *X. granatum*), *Neopestalotiopsis acrostichi* (Host: *Acrostichum aureum*), *N. brachiate* (Host: *Rhizophora apiculate*), *N. petila* (Host: *R. mucronate*), *N. rhizophorae* (Host: *R. mucronata*), *N. sonneratae* (Host: *Sonneratia alba*), *N. thailandica* (Host: *R. mucronata*), *Pestalotiopsis rhizophorae* (Host: *R. apiculate*), *P. thailandica* (Host: *R. apiculate*), *Pseudopestalotiopsis avucenniae* (Host: *Avicennia marina*), *Ps. curvatispora* (Host: *R. mucronata*), *Ps. rhizophorae* (Host: *R. apiculate*), *Ps. thailandica* (Host: *R. mucronata*), and *Phyllosticta rhizophorae* (Host: *R. stylosa*). In addition, these chapters provide a host-fungal database for future studies and increased the knowledge of fungal diversity in mangrove areas. In particular, a possible reason for the high fungal diversity of selected host species can be the favorable climatic conditions for the fungal communities in mangrove areas.

Furthermore, chapters 5, 6, and 7–10 support the second objective to conduct in-depth genus and family rank revisions for selected taxa and their allied species based on morphology and phylogenetic analysis of ITS and LSU. A new species in *Seimatosporium*

physocarpi sp. nov. was introduced with *S. rosae* was designed here as epitype, and *S. lichenicola* is described as reference specimen, which were mentioned in chapter seven.

Among the selected taxa, a new family, Lamproconiaceae, is introduced to accommodate *Lamproconium desmazieri* and *Hercospora tiliae*, and *Lamproconium desmazieri* (=*Melanconis desmazieri*) is synonymized. Lamproconiaceae forms a robust clade closer to Sydowiellaceae and Stilbosporaceae in the combined phylogeny. However, the morphology characters of Stilbosporaceae and Sydowiellaceae are differ from species in Lamproconiaceae, which were mentioned in chapter eight.

In chapter nine, *Cytospora* (Cytosporaceae) and allied species were revised using a combination of morphology and multi-gene phylogenetic analysis (ITS, LSU, *rpb2*, *act*) to identify taxa. A total of 34 collections were studied, representing 17 fungal species of *Cytospora*. Of these, 14 new species were described and illustrated. Three species are known taxa and identified as *C. nivea*, *C. parasitica*, and *C. salicicola*. New species introduced include *C. ampulliformis*, *C. curvata*, *C. donetzica*, *C. erumpens*, *C. longiostiolata*, *C. melnikii*, *C. parakantschavelii*, *C. paratranslucens*, *C. rusanovii*, *C. salicacearum*, *C. salicina*, *C. sorbi*, *C. sorbicola* and *C. ulmi*. Descriptions, illustrations and notes are provided for all taxa studied in this study. Distribution patterns of *Cytospora* species on different hosts have been discussed. This study is the preliminary study of *Cytospora* species from a small region and provides an initial contribution to understanding the genus.

In chapter ten, *Melomastia* (Pleurotremaceae) was modified based on the type specimen, and taxonomic relationships and its position within the Ascomycota remain uncertain. In this study, *Melomastia italica* sp. nov., a new species from Italy is introduced, using a combined morphological and phylogenetic approach. Multi-gene phylogenies based on DNA sequence data partially resolve the taxonomic confusion of genera *Dyfrolomyces*, *Melomastia*, and *Pleurotrema*. Phylogenies clearly state that they belong to the family Pleurotremaceae in class Dothideomycetes. *Melomastia italica* species sampled here clustered with high support and nested between *Dyfrolomyces* species, and the individual LSU dataset also yielded the same result. Despite the closer affinity between *Dyfrolomyces maolanensis* and *Melomastia italica* in other analyses, we consider that *Melomastia italica* is a novel species given its distinct morphological features compared to *Dyfrolomyces maolanensis*. There have also been some

taxonomic irregularities concerning the generic status of *Dyfrolomyces*, *Melomastia* and *Pleurotrema*. In fact, if we take a conservative approach, we could combine *Dyfrolomyces* and *Pleurotrema* under the earlier *Melomastia*. Despite some morphological overlap, our phylogeny supplemented by precise and accurate morphological definitions indicates that these should be considered as different genera. Although our molecular data clearly show that *Dyfrolomyces* are phylogenetically apart, they are not significantly distinct in morphology. We anticipate that many more taxa will be found in these genera, supported by both phylogeny and morphology. Further studies with more Pleurotremaceae collections, particularly *Pleurotrema polysemum*, are essential to resolving taxonomic relationships within this family. *Phyllosticta* (Botryosphaeriaceae) in chapter five and *Diaporthe* (Diaporthaceae) in chapter six are also linked to the third objective.

Chapters five and six supported my third objective to update the multi-gene phylogenies of complex genera, including *Phyllosticta* (Botryosphaeriaceae) and *Diaporthe* (Diaporthaceae). The taxonomy of those fungi is challenging because their morphological features overlap and make it difficult to identify traits for the taxonomic arrangement. The reliance on host associations to identify native species is also a more complicated matter. Overall, these issues are confusing to categorize. Molecular phylogenetic tools greatly facilitate the identification of species and the formation of species complexes. In this research study, both combined and single locus data were considered, and the multi-locus trees provided a better resolution for both genera than the single-locus trees. The addition of protein-coding genes to the analysis greatly facilitated the identification at the species level. Following the same reason and for the sake of communication, species complexes have been successfully introduced for some genera (*Colletotrichum* (Glomerellaceae), *Fusarium* (Nectriaceae), etc.). In chapters five, the six species complexes established for *Phyllosticta* are *Phyllosticta capitalensis*, *P. concentrica*, *P. cruenta*, *P. owaniana*, *P. rhodorae*, and *P. vaccinii*. Eighty-four previously described species including a new species from Taiwan, *P. rhizophorae*, were assigned to one of six species complexes. We synonymized the strains of *P. capitalensis* (CPC 20508 and CPC20509) under the new species. Six strains (CBS 173.77, CBS 119720, CPC 17748, CPC 20252, CPC 20269, and CBS 123404) are unnamed based on phylogenetic analysis and nucleotide polymorphisms and may

represent new species. Seventeen strains were excluded from *Phyllosticta* based on BLAST searches against type sequences (Table 8.6). BLAST results for the 17 strains of *Phyllosticta* were matched another genus, therefore it was assigned to exclusion from *Phyllosticta*. Seventeen excluded strains are *Phyllosticta alcides* strain P3-4, *P. artocarpina* strain B5, *P. caprifolii* strain F23, *P. citrullina* strain LrBF12, *P. citrullina* strain LrBF13, *P. coryli* strain CTF324, *P. flevolandica* strain AFTOL-ID 1786, *P. flevolandica* strain CBS 998.72, *P. heveae* strain NW197, *P. jasmini* strain TS08-19-2, *P. jasmini* strain 6259, *P. juglandis* strain H2, *P. ligustri* strain TS08-20-1, *P. papayae* strain T150, *P. papayae* strain 7AJ-10, *P. populina* strain NW584, and *P. sojicola* strain CBS 301.39.

To giving species delineation in genera *Phyllosticta* is difficult due to the above-mentioned challenges. Therefore, the splitting of complex species into clades will facilitate species resolution. The complex can be used as a broader descriptor of the genus. Multi-locus phylogeny or at least two single locus analysis supported all the six *Phyllosticta* species complexes, some of which had strong statistical support. However, the placements of some species remain problematic and require additional loci for taxonomic resolution. The results of this study demonstrate that both molecular phylogenetic analyses and morphological data are necessary to propose and establish species of *Phyllosticta*, as the latter alone is not sufficient. The molecular boundaries of *Phyllosticta* species will provide a better understanding of inter and intraspecific variations within the genus, especially within the broader species complexes. The demarcation of each taxon in the genus is essential for us to develop a better understanding of the lifestyle, ecology, and overall biology of these individual taxa, including impact and control in various ecosystems. The phylogenetic relationships of *Phyllosticta* species will be re-evaluated and suggested for future work.

In chapters six, based on the results of phylogenetic analysis, we introduced 13 workable species complexes for *Diaporthe* and another six species complexes for *Phyllosticta*. In chapters 10, the 13 workable species complexes established for *Diaporthe* are *Diaporthe arecae, D. biconispora, D. carpini, D. decedens, D. eres, D. oncostoma, D. pustulata, D. rudis, D. scobina, D. sojae, D. toxica, D. varians*, and *D. vawdreyi*. The study provides a comprehensive phylogenetic analysis of Diaporthaceae while focusing on *Diaporthe*. All valid species of *Diaporthe* with molecular data are

included in the phylogenetic analysis along with all genera of Diaporthaceae. There are 317 species with available sequence data, while for 30 species only the ITS region was available, some of which are type strains and some not. Single and combined genetic marker trees were inferred. *Diaporthe* separates into deeply divergent, strongly supported clades, whose membership is mostly stable in both the combined and single gene trees. In addition, nine species were kept as singletons (*D. acerina*, *D. acutispora*, *D. crataegi*, *D. multiguttulata*, *D. ocoteae*, *D. perjuncta*, *D. pseudoalnea*, *D. spartinicola*, *D. undulata*). In this study, we accepted 287 *Diaporthe* species. Of the 287 species included in the combined analysis, 274 species were assigned to one of the 13 species complexes. Two genera of Diaporthaceae, *Ophiodiaporthe cyatheae* and *Chiangraiomyces bauhiniae* were synonymized under *D. cyatheae* (≡ *O. cyatheae*) and *D. pseudobauhiniae* (≡ *C. bauhiniae*), respectively. Four species were nested with other genera, so these are not assigned to any species complex (*D. aspalathi*, *D. caulivora*, *D. crotalariae*, *D. woodii*).

The non-monophyly of *Diaporthe* in this study and other studies challenges its genus status. Sequences split into several distinct and genetically divergent clades, which could represent separate genera. Determining the extent of discordance between morphology and molecular data and the suitability of genetic markers used will help substantially towards resolving this question. Further studies are also needed to establish whether these species are host-specific, determine their habitats and lifestyles, the conditions under which they might switch lifestyle and their interactions with their plant hosts.

My fourth objective was to contribute to the fungal taxonomy and phylogeny by studying fungi in class Dothideomycetes and Sordariomycetes. Chapters 2–10 provide descriptions and illustrations of selected microfungal genera and evaluated fungal species in terms of morphological characters and multi-gene phylogenies. The study revealed forty-one species, consisting of one new family (Lamproconiaceae), three new host records, three species were assigned as epitype and reference specimens, one species was recombined (*Melomastia maolanensis*), and one herbarium specimen study (*Hercospora tiliae*). The newly described species are *Cytospora ampulliformis*, *C. curvata*, *C. donetzica*, *C. erumpens*, *C. longiostiolata*, *C. lumnitzericola*, *C. melnikii*, *C. parakantschavelii*, *C. paratranslucens*, *C. rusanovii*, *C. salicacearum*, *C. salicina*, *C. sorbi*, *C. sorbicola*, *C.*

thailandica, *C. ulmi*, *C. xylocarpi* (Cytosporaceae), *Melomastia italica* (Pleurotremaceae), *Neopestalotiopsis acrostichi*, *N. brachiate*, *N. petila*, *N. rhizophorae*, *N. sonneratae*, *N. thailandica* (Sporocadaceae), *Pestalotiopsis rhizophorae*, *P. thailandica* (Sporocadaceae), *Pseudopestalotiopsis avucenniae*, *Ps. curvatispora*, *Ps. rhizophorae*, *Ps. thailandica* (Sporocadaceae), *Phyllosticta rhizophorae* (Botryosphaeriaceae), and *Seimatosporium physocarpi* (Amphisphaeriaceae),. The new host records are *Alternaria gaisen* (Pleosporaceae), *C. nivea*, *C. parasitica*, and *C. salicicola* (Cytosporaceae). The species were designed as epitype and references specimens are *Seimatosporium rosae*, *S. lichenicola* (Amphisphaeriaceae), and *Lamproconium desmazieresi* (Lamproconiaceae). These chapters provide a fungal database for future studies and increase knowledge about the diversity of fungi as well as the discovery of new fungi. In particular, a possible reason for the high fungal diversity of selected host species can be the favorable climatic conditions for the fungal communities in the mangroves.

11.2 Research Advances

This dissertation implemented an interdisciplinary approach for fungal identification and encourages the combination of conventional and modern classification methods. A combined approach was applied based on morphological species concept, phylogenetic species concepts, and an integrated species concept with genealogical concordance phylogenetic species recognition (GCPSR) of high similarity in the morphology and molecular genetic strains. The knowledge of sexual-asexual relationships is vital in fungal identification. Moreover, revisions of *Phyllosticta* and *Diaporthe* complex genera were provided.

This research has contributed one new family, 11 genera and 33 novel taxa to science with illustrations and molecular data. This study also provides revisions for several families (Cytosporaceae, Diaporthaceae, Lamproconiaceae, Pleurotremaceae) and genera (*Phyllosticta*, *Diaporthe*), with updated multi-gene phylogenies and provided better resolution for complex genera based on combined gene trees and single-locus trees of each genus.

11.3 Future work

From the knowledge accomplished in this study, future research should be carried out based on several points:

11.3.1 Thailand is a hotspot for fungal biodiversity as most of the collections from Thailand are new to science. Therefore, further investigation would potentially increase the diversity of fungi.

11.3.2 Although several fungal taxa have now been documented from mangroves and marine vegetations, notably most of the taxa reported are saprobes. However, the endophytic, pathogenic and neotropic fungi are also important and more studies are needed on this subject. This is because mangrove forests are adapted to extreme salinity and temperature fluctuations, swampy sediments with low oxygen conditions, and several other interesting ecological adaptations. Thus, there is a high possibility that the plant could be the carrier of fungal species that were introduced in different countries. The study of fungus-host coevolution in mangroves will be useful for the detection of pathogens. It is also recommended to compare the fungal communities in different seasons or locations.

11.3.3 Fungal evolutionary approaches can serve as evidence for the migration of fungi and mangroves based on ecological fluctuations. Therefore, the preserved strains can be used for fungal genomics.

11.3.4 Several fungal strains have not been well-investigated for secondary metabolite production. In the future, secondary metabolites need to be investigated together with their biosynthesis pathways. In the future, these strains should be investigated to be used for producing antibiotics, agrochemicals, biological control, biodegradation, and industrial enzyme production.

11.4 Publications

As a result of this thesis and other activities during my PhD project, I have published nine papers as first author in SCI journals. Furthermore, I have also co-authored 34 other SCI publications. Those are listed below and appended to the thesis.

11.4.1 First Author

1. Norphanphoun, C., Maharachchikumbura, S. S. N., Daranagama, D. A., Bulgakov, T. S., Bhat, D. J., Bahkali, A. H., & Hyde, K. D. (2015). Towards a backbone tree for *Seimatosporium*, with *S. physocarpi* sp. nov. *Mycosphere, 6*, 385–400.
2. Norphanphoun, C., Hongsanan, S., Doilom, M., Bhat, D. J., Wen, T. C., Senanayake, I. C., . . . Hyde, K. D. (2016). Lamproconiaceae fam. nov. to accommodate *Lamproconium desmazieri*. *Phytotaxa, 270*, 089–102.
3. Norphanphoun, C., Jeewon, R., Mckenzie, E. H. C., Wen, T. C., Camporesi, E., & Hyde, K. D. (2017). Taxonomic position of *Melomastia italica* sp. nov. and phylogenetic reappraisal of *Dyfrolomyces*. *Cryptogamie Mycologie*, *38*, 507–525.
4. Norphanphoun, C., Doilom, M., Daranagama, D. A., Phookamsak, R., Wen, T. C., Bulgakov, T. S., & Hyde, K. D. (2017). Revisiting the genus *Cytospora* and allied species. *Mycosphere, 8*, 51–97.
5. Norphanphoun, C., Raspé, O., Jeewon, R., Wen, T. C., & Hyde, K. D. (2018). Morphological and phylogenetic characterisation of novel *Cytospora* species associated with mangroves. *MycoKeys, 38*, 93–120.
6. Norphanphoun, C., Jayawardena, R. S., Chen, Y., Wen, T. C., Meepol, W., & Hyde, K. D. (2019). Morphological and phylogenetic characterization of novel Pestalotioid species associated with mangroves in Thailand. *Mycosphere, 10*, 531–578.
7. Norphanphoun, C., Hongsanan, S., Gentekaki, E., Chen, Y. J., Kuo, C. H., & Hyde, K. D. (2020). Differentiation of species complexes in *Phyllosticta* enables better species resolution. *Mycosphere, 11*(1), 2542–2628.

8. Norphanphoun, C., Hongsanan, S., Bhat, J. D., 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 Science*, *48*(6), 1478−1499.
9. Norphanphoun, C., Gentekaki, E., Hongsanan, S., Jayawardena, R., Senanayake, C., Manawasinghe, I., . . . Hyde, K. D. (2022). The sections of *Diaporthe*: formalizing species-group concept. *Mycosphere* (accepted).
10. Norphanphoun, C., Gentekaki, E., Hongsanan, S., Jayawardena, R., Senanayake, C., Manawasinghe, I., . . . Hyde, K. D. (2022) Annotated species of *Diaporthe*. *Mycosphere* (inprep).

11.4.2 Co-Author

1. Ariyawansa, H. A., Hyde, K. D., Jayasiri, S. C., Buyck, B., Chethana, K. W. T., Dai, D. Q., Dai, Y. C., Daranagama, D. A., Jayawardena, R. S., Luecking, R., Ghobad-Nejhad, M., Niskanen, T., Thambugala, K. M., Voigt, K., Zhao, R. L., Li, G-J., Doilom, M., Boonmee, S., Yang, Z. L., . . . Hernawati (2015). Fungal diversity notes 111–252—taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *75*, 27−274.
2. Chaiwan, N., Wanasinghe, D. N., Mapook, A., Jayawardena, R. J., Norphanphoun, C., & Hyde, K. D. (2020). Novel species of *Pestalotiopsis* fungi on *Dracaena* from Thailand. *Mycology*, *11*(4), 306−315.
3. Chethana, K. W. T., Niranjan, M., Dong, W., Samarakoon, M. C., Bao, D. F., Calabon, M. S., Chaiwan, N., Chuankid, B., Dayarathne, M. C., de Silva, N. I., Devadatha, B., Dissanayake, A. J., Goonasekara, I. D., Huanraluek, N., Jayawardena, R. S., Karunarathna, A., Luo, Z. L., Marasinghe, D. S., Ma, X. Y., . . . Hyde, K. D. (2021). AJOM new records and collections of fungi: 101-150. *Asian Journal of Mycology*, *4*(1), 113–260.

4. Doilom, M., Hyde, K. D., Phookamsak, R., Dai, D. Q., Tang, L. Z., Hongsanan, S., Chomnunti, P., Boonmee, S., Dayarathne, M. C., Li, W., Thambugala, K. M., Perera, R. H., Daranagama, D. A., Norphanphoun, C., Konta, S., Dong, W., Ertz, D., Phillips, A. J., McKenzie, E. H., . . . Promputtha, I. (2018). Mycosphere Notes 225–274: types and other specimens of some genera of Ascomycota. *Mycosphere*, *9*, 647–754.
5. Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C. Sarma, V. V., Boonmee, S., Lücking, R., Bhat, D. J., Liu, N. G., Tennakoon, D. S., Pem, D., Karunarathna, A., Jiang, S. H., Jones, E. B. G., Phillips, A. J. L., Manawasinghe, I. S., Tibpromma, S., Jayasiri, S. C., . . . Xie, N. (2020a). Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. *Mycosphere, 11*(1), 1553–2107.
6. Hongsanan, S., Norphanphoun, C., Thambugala, K. M., Boonyuen, N., Huanraluek, N., & Cheewangkoon, R. (2020). Taxonomy and phylogeny of *Muyocopron thailandica* sp. nov. *Phytotaxa, 456*(2), 195–202.
7. Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C., Sarma, V. V., Lücking, R., Boonmee, S., Bhat, J. D., Liu, N.-G., Tennakoon, D. S., Pem, D., Karunarathna, A., Jiang, S.-H., Jones, G. E. B., Phillips, A. J. L., Manawasinghe, I. S., Tibpromma, S., Jayasiri, S. C., . . . Xie, N. (2020b). Refined families of Dothideomycetes: orders and families incertae sedis in Dothideomycetes. *Fungal Diversity, 105*, 17–318.
8. Huanraluek, N., Padaruth, O. D., Jayawardena, R. S., Li, W. J., Hongsanan, S., Jeewon, R., . . . Hyde, K. D. (2021). https://www.coelomycetes.org: Databank that contributes for the classification, identification, and nomenclature of Coelomycetes. *Asian Journal of Mycology, 4*(2), 114–122.

9. Hyde, K. D., Chaiwan, N., Norphanphoun, C., Boonmee, S., Camporesi, E., Chethana, K. W. T., Dayarathne, M. C., De Silva, N. I., Dissanayake, A. J., Ekanayaka, A. H., Hongsanan, S., Huang, S., Jayasiri, S. C., Jayawardena, R. S., Jiang, H., Karunarathna, A., Lin, C., Liu, J., Liu, N., . . . Zhao, Q. (2018). Mycosphere notes 169–224. *Mycosphere*, *9*(2), 271−430.
10. Hyde, K. D., Hongsanan, S., Jeewon, R., Bhat, D. J., McKenzie, E. H. C., Jones, E. B. G., Phookamsak, R., Ariyawansa, H. A., Boonmee, S., Zhao, Q., Abdel-Aziz, F. A., Abdel-Wahab, M. A., Banmai, S., Chomnunti, P., Cui, B., Daranagama, D. A., Das, K., Dayarathne, M. C., Silva, N. I., . . . Zhu, L. (2016). Fungal Diversity Notes 367–490: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *80*, 1–270.
11. Hyde, K. D., Norphanphoun, C., Abreu, V. P., Bazzicalupo, A., Chethana, K. W. T., Clericuzio, M., Dayarathne, M. C., Dissanayake, A. J., Ekanayaka, A. H., He, M. Q., Hongsanan, S., Huang, S. K., Jayasiri, S. C., Jayawardena, R. S., Karunarathna, A., Konta, S., Kušan, I., Lee, H., Li, J., . . . Mortimer, P. E. (2017). Fungal Diversity Notes 603–708: taxonomic and phylogenetic notes on genera and species. *Fungal Diversity*, *87*, 1−235.
12. 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.
13. Hyde, K. D., Norphanphoun, C., Maharachchikumbura, S. S. N., Bhat, D. J., Jones, E. B. G., Bundhun, D., Chen, Y. J., Bao, D. F., Boonmee, S., Calabon, M. S., Chaiwan, N., Chethana, K. W. T., Dai, D. Q., Dayarathne, M. C., Devadatha, B., Dissanayake, A. J., Dissanayake, L. S., Doilom, M., Dong, W., . . . Xiang, M. M. (2020c). Refined families of Sordariomycetes. *Mycosphere*, *11*, 305−1059.

14. Hyde, K. D., Tennakoon, D. S., Jeewon, R., Bhat, D. J., Maharachchikumbura, S. S. N., Rossi, W., Leonardi, M., Lee, H. B., Mun, H. Y., Houbraken, J., Nguyen, T. T., Jeon, S. J., Frisvad, J. C., Wanasinghe, D. N., Lücking, R., Aptroot, A., Cáceres, M. E., Karunarathna, S. C., Hongsanan, S., . . . Doilom, M. (2019). Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity*, *96*, 1–242.
15. Hyde, K. D., de Silva, N. I., Jeewon, R., Bhat, D. J., Phookamsak, R., Doilom, M., Boonmee, S., Jayawardena, R. S., Maharachchikumbura, S. S. N., Senanayake, I. C., Manawasinghe, I. S., Liu, N. G., Abeywickrama, P. D., Chaiwan, N., Karunarathna, A., Pem, D., Lin, C. G., Sysouphanthong, P., Luo, Z. L., . . . Bulgakov, T. S. (2020). AJOM new records and collections of fungi: 1–100. *Asian Journal of Mycology*, *3*(1), 22–294.
16. Hyde, K. D., Jeewon, R., Chen, Y. J., Bhunjun, C. S., Calabon, M. S., Jiang, H. B., . . . Lumyong, S. (2020). The numbers of fungi: Is the descriptive curve flattening?. *Fungal Diversity*, *103*, 219–271.
17. Jayawardena, R. S., Hyde, K. D., McKenzie, E. H. C., Jeewon, R., Phillips, A. J. L., Perera, R. H., De Silva, N. I., Maharachchikumburua, S.S., Samarakoon, M. C., Ekanayake, A. H., Tennakoon, D. S., Dissanayake, A. J., Norphanphoun, C., Lin, C., Manawasinghe, I. S., Tian, Q., Brahmanage, R. S., Chomnunti, P., Hongsanan, S., . . . Wan, Y. (2019). One stop shop III: taxonomic update with molecular phylogeny for important phytopathogenic genera: 51–75. *Fungal Diversity*, *98*, 77–160.
18. Jayawardena, R. S., McKenzie, E. H. C., Chen, Y. J., Phillips, A. J. L., Hongsanan, S., Norphanphoun, C., . . . Hyde, K. D. (2019). https://onestopshopfungi.org/, a database to enhance identification of phytopathogenic genera. *Asian Journal of Mycology*, *2*(1), 281–286.
19. Jones, G., Pang, K. L., Abdel Wahab, M. A., Scholz, B., Hyde, K. D., Boekhout, T., . . . Norphanphoun, C. (2019). An online resource for marine fungi. *Fungal Diversity*, *96*, 347–433.

20. Krisai-Greilhuber, I., Chen, Y., Jabeen, S., Madrid, H., Marincowitz, S., Razaq, A., Ševčíková, H., Voglmayr, H., Yazici, K., Aptroot, A., Aslan, A., Boekhout, T., Borovička, J., Crous, P. W., Ilyas, S., Jami, F., Jiang, Y. L., Khalid, A. N., Kolecka, A., . . . Yu, J. Y. (2017). Fungal Systematics and Evolution: FUSE 3. *Sydowia*, *69*, 229–264.
21. Li, G. J., Hyde, K. D., Zhao, R. N., Hongsanan, S., Abdel-Aziz, F. A., Abdel-Wahab, M. A., Mohamed A., Alvarado, P., Alves-Silva, G., Ammirati, J. F., Ariyawansa, H. A., Baghela, A., Bahkali, A. H., Beug, M., Bhat, D. J., Bojantchev, D., Boonpratuang, T., Bulgakov, T. S., Camporesi, E., Boro, M. C., . . . Maharachchikumbura, S. S. N. (2016). Fungal Divers notes 253–366: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *78*, 1–237.
22. Liu, J. K., Hyde, K. D., Jones, E. B. G., Ariyawansa, H. A., Bhat, D. J., Boonmee, S., Maharachchikumbura, S. S. N., McKenzie, E. C., Phookamsak, R., Phukhamsakda, C., Shenoy, B., Abdel-Wahab, M., Buyck, B., Chen, J., Chethana, K., Thilini, W., Singtripop, C., Dai, D., Dai, Y., . . . Camporesi, E. (2015). Fungal Diversity Notes 1–100: Taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity*, *72*, 1–197.
23. Maharachchikumbura, S. S. N., Hyde, K. D., Jones, E. B. G., McKenzie, E. H. C., Bhat, J. D., Dayarathne, M. C., Huang, S. K., Norphanphoun, C., Senanayake, I. C., Perera, R. H., Shang, Q. J., Xiao, Y., D'souza, M. J., Hongsanan, S., Jayawardena, R. S., Daranagama, D. A., Konta, S., Goonasekara, I. D., Zhuang, W. Y., . . . Wijayawardene, N. N. (2016b). Families of *Sordariomycetes*. *Fungal Diversity*, *79*(1), 1–317.
24. Maharachchikumbura, S. S. N., Hyde, K. D., Jones, E. B. G., McKenzie, E. H. C., Huang, S. K., Abdel-Wahab, M. A., Daranagama, D. A., Dayarathne, M., D'souza, M. J., Goonasekara, I. D., Hongsanan, S., Jayawardena, R. S., Kirk, P. M., Konta, S., Liu, J. K., Liu, Z.-Y., Norphanphoun, C., Pang, K. L., Perera, R. H., . . . Xu, J. (2015). Towards a natural classification and backbone tree for *Sordariomycetes*. *Fungal Diversity*, *72*, 199–301.

25. Monkai, J., McKenzie, E. H. C., Phillips, A. J. L., Hongsanan, S., Pem, D., Liu, J. K., Chethana, K. W. T., Tian, Q., Ekanayaka, A. H., Lestari, A. S., Zeng, M., Zhao, Q., Norphanphoun, C., Abeywikrama, P. D., Maharachchikumbura, S. S. N., Jayawardena, R. S., Chen, Y. J., Zhao, R. L., He, M. Q., . . . Hyde, K. D. (2019). https://fungalgenera.org/: a comprehensive database providing webbased information for all fungal genera. *Asian Journal of Mycology, 2*(1), 298–305.
26. Monkai, J., Tibpromma, S., Manowong, A., Mapook, A., Norphanphoun, C., Hyde, K. D., & Promputtha, I. (2021). Discovery of Three Novel *Cytospora* Species in Thailand and Their *Antagonistic Potential*, *13*(10), 488.
27. Phookamsak, R., Boonmee, S., Norphanphoun, C., Wanasinghe, D. N., de Silva N. I., Dayarathne, M. C., . . . Hyde, K. D. (2016). Schizothyriaceae. *Mycosphere*, *7*, 154–189.
28. Phookamsak, R., Wanasinghe, D. N., Hongsanan, S., Phukhamsakda, C., Huang, S. K., Tennakoon, D. S., . . . Hyde, K. D. (2017). Towards a natural classification of *Ophiobolus* and ophiobolus-like taxa; introducing three novel genera *Ophiobolopsis*, *Paraophiobolus* and *Pseudoophiobolus* in Phaeosphaeriaceae (Pleosporales). *Fungal Diversity*, *87*, 299–339.
29. Phookamsak, R., Hyde, K. D., Jeewon, R., Bhat, J. D., Jones, E. B. G., Maharachchikumbura, S. S. N., Raspé, O., Karunarathna, S. C., Wanasinghe, D. N., Hongsanan, S., Doilom, M., Tennakoon, D. S., Machado, A. R., Firmino, A. L., Ghosh, A., Karunarathna, A., Mešić, A., Dutta, A. K., Thongbai, B., . . . Xu, J. (2019). Fungal diversity notes 933–1040: taxonomic and phylogenetic contributions on genera and species of fungal taxa. *Fungal Diversity*, *95*, 1–273.
30. Senanayake, I. C., Crous, P. W., Groenewald, J. Z., Maharachchikumbura, S. S. N., Jeewon, R., Phillips, A. J. L., . . . Hyde, K. D. (2017). Families of Diaporthales based on morphological and phylogenetic evidence. *Studies in Mycology*, *86*, 217–296.

31. Senanayake, I. C., Jeewon, R., Chomnunti, P., Wanasinghe, D. N., Norphanphoun, C., Karunarathna, A., . . . Karunarathna, S. C. (2018). Taxonomic circumscription of Diaporthales based on multigene phylogeny and morphology. *Fungal Diversity*, *93*, 241–443.
32. Senanayake, I. C., Maharachchikumbura, S. S. N., Hyde, K. D., Bhat, J. D., Jones, E. B. G., McKenzie, E. H. C., Dai, D. Q., Daranagama, D. A., Dayarathne, M. C., Goonasekara, I. D., Konta, S., Li, W. J., Shang, Q. J., Stadler, M., Wijayawardene, N. N., Xiao, Y. P., Norphanphoun, C., Li, Q., Liu, X. Z., . . . Camporesi, E (2015). Towards unravelling relationships in Xylariomycetidae (Sordariomycetes). *Fungal Diversity 73*, 73–144.
33. Tibpromma, S., Hyde, K. D., Jeewon, R., Maharachchikumbura, S. S. N., Liu, J. K., Bhat, J. D., Jones, E. B. G., McKenzie, E. H. C., Camporesi, E., Bulgakov, T. S., Doilom, M., de Azevedo Santiago, A. L. C. M., Das, K., Manimohan, P., Gibertoni, T. B., Lim, Y. W., Ekanayaka, A. H., Thongbai, B., Lee, H. B., . . . Karunarathna, S. C. (2017). Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *83*, 1–261.
34. Wanasinghe, D. N., Phukhamsakda, C., Hyde, K. D., Jeewon, R., Lee, H. B., Jones, E. B. G., Tibpromma, S., Tennakoon, D. S., Dissanayake, A. J., Jayasiri, S. C., Gafforov, Y., Camporesi, E., Bulgakov, T. S., Ekanayake, A. H., Perera, R. H., Samarakoon, M. C., Goonasekara, I. D., Mapook, A., Li, W., . . . Karunarathna, S. C. (2018). Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. *Fungal Diversity*, *89*, 1–236.

REFERENCES

REFERENCES

Ariyawansa, H. A., Hawksworth, D. L., Hyde, K. D., Jones, E. B. G., Maharachchikumbura, S. S. N., Manamgoda, D. S., . . . Xu, J. C. (2014). Epitypification and neotypification: Guidelines with appropriate and inappropriate examples. *Fungal Diversity*, *69*, 57–91.

Abraham, S., Basukriadi, A., Pawiroharsono, S., & Sjamsuridzal, W. (2015). Insecticidal activity of ethyl acetate extracts from culture filtrates of mangrove fungal endophytes. *Mycobiology*, *43*, 137–149.

Adams, G. C., Roux, J., & Wingfield, M. J. (2006). *Cytospora* species (Ascomycota, Diaporthales, Valsaceae): Introduced and native pathogens of trees in South Africa. *Australasian Plant Pathology*, *35*, 521–548.

Adams, G. C., Surve-Iyer, R. S., & Iezzoni, A. (2002). Ribosomal DNA sequence divergence and group I introns within the *Leucostoma* species, *L. cinctum*, *L. persoonii*, and *L. parapersoonii* sp. nov., ascomycetes that cause *Cytospora* canker of fruit trees. *Mycologia*, *94*, 947–967.

Adams, G. C., Wingfield, M. J., Common, R., & Roux, J. (2005). Phylogenetic relationships and morphology of *Cytospora* species and related teleomorphs (Ascomycota, Diaporthales, Valsaceae) from *Eucalyptus*. *Studies in Mycology*, *52*, 1–144.

Adamska, I. (2001). Microscopic fungus-like organisms and fungi of the Słowiński National Park. II. (NW Poland). *Acta Mycologica*, *36*, 31–65.

Adesemoye, A. O., Mayorquin, J. S., Wang, D. H., Twizeyimana, M., Lynch, S. C., & Eskalen, A. (2014). Identification of species of Botryosphaeriaceae causing bot gummosis in citrus in California. *Plant Disease*, *98*, 55–61.

Ahmad, S. (1969). Fungi of West Pakistan. *Biological Society of Pakistan Monograph*, *5*(1), 1–110.

Ahmad, S., Iqbal, S. H., & Khalid, A. N. (1997). *Fungi of Pakistan*. Sultan Ahmad Mycological Society of Pakistan, Pakistan.

Akhtar, N., Hafeez, R., & Awan, Z. A. (2014). First report of rice leaf spot by *Alternaria gaisen* from Pakistan. *Plant Disease, 98*, 1440.

Al Ghafri, A., Maharachchikumbura, S. S. N., Hyde, K. D., Al-Saady, N. A., & Al-Sadi, A. M. (2019). A new section and a new species of *Alternaria* encountered from Oman. *Phytotaxa, 405*, 279–289.

Alfieri, Jr S. A., Langdon, K. R., Wehlburg, C., & Kimbrough, J. W. (1984). Index of plant diseases in Florida (Revised). *Florida Department of Agriculture and Consumer Services, Division of Plant Industry Bull, 11*, 1–389.

Al-Hatmi, A. M. S., Meis, J. F., & de Hoog, G. S. (2016). *Fusarium*: Molecular diversity and intrinsic drug resistance. *PLOS Pathogens 12*, e1005464.

Ali, M. S., & Saikia, U. N. (1997). Coelomycetes of Assam–I. *Indian Phytopathology, 50*, 200–205.

Alias, S. A. (1996). *Ecological and taxonomic studies of lignicolous marine fungi in Malaysian mangroves* (doctoral dissertation). University of Portsmouth, UK.

Alias, S. A., & Jones, E. B. G. (2000a). Colonization of Mangrove wood by marine fungi at Kuala Selangor mangrove stand. *Fungal Diversity, 5*, 9–21.

Alias, S. A., & Jones, E. B. G. (2000b). Vertical distribution of marine fungi in *Rhizophora apiculata* at Morib mangrove, Selangor, Malaysia. *Mycoscience, 41*, 431–436.

Alias, S. A., & Jones, E. B. G. (2009). *Marine fungi from mangroves of Malaysia*. Institute Ocean and Earth Sciences, University of Malaya, Kuala Lumpur, Malaysia.

Alias, S. A., Zainuddin, N., & Jones, E. B. G. (2010). Biodiversity of marine fungi in Malaysian mangroves. *Botanica Marina, 53*, 545–554.

Allen, J. (1998). Mangroves as alien species: The case of Hawaii. *Global Ecology & Biogeography Letters, 7*(1), 61–71.

Alvarez, M. G. (1976). Primer catalogo de enfermedades de plantas Mexicanas. *Fitofilo, 71*, 1–169.

Ananda, K., & Sridhar, K. R. (2002). Diversity of endophytic fungi in the roots of mangrove species on the west of India. *Canadian Journal of Microbiology, 48*, 871–878.

Anderson, P. J. (1919). Index to American species of *Phyllosticta*. *Mycologia, 11*, 66–79.

Ando, Y., Motohashi, K., & Yaguchi, Y. (2013). Taxonomic re-examination of *Cryptomeria* gall disease causing fungus. *Japanese Journal of Mycology, 54*, 15–26.

Andrew, M., Peever, T. L., & Pryor, B. M. (2009). An expanded multilocus phylogeny does not resolve morphological species among the small-spored *Alternaria* species complex. *Mycologia, 101*, 95–109.

Anonymous. (1928). The Marlborough Foray. *Transactions of the British Mycological Society, 13*, 145–150.

Anonymous. (1960). Index of plant diseases in the United States. *USDA Agriculture handbook, 165*, 1–531.

Anonymous. (1979). *List of plant diseases in Taiwan*. Plant Protection Society, Republic of China.

Arciuolo, R., Santos, C., Soares, C., Castello, G., Spigolon, N., Chiusa, G., . . . Battilani, P. (2020). Molecular characterization of *Diaporthe* species associated with hazelnut defects. *Frontiers in Plant Science, 11*(611655), 33362837.

Arfi, Y., Buee, M., Marchand, C., Levasseur, A., & Record, E. (2012). Multiple markers pyrosequencing reveals highly diverse and host-specific fungal communities on the mangrove trees *Avicennia marina* and *Rhizophora stylosa*. *FEMS Microbiology Ecology, 79*(2), 433–444.

Ariyawansa, H. A., & Hyde, K. D. (2018). Additions to *Pestalotiopsis* in Taiwan. *Mycosphere*, *9*, 999–1013.

Ariyawansa, H. A., Hyde, K. D., Jayasiri, S. C., Buyck, B., Chethana, K. W. T., Dai, D. Q., Dai, Y. C., Daranagama, D. A., Jayawardena, R. S., Lücking, R., Ghobad-Nejhad, M., Niskanen, T., Thambugala, K. M., Voigt, K., Zhao, R. L., Li, G. J., Doilom, M., Boonmee, S., Yang, Z. L., . . . Hernawati. (2015). Fungal diversity notes 111–252 taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *75*, 27–274.

Ariyawansa, H. A., Thambugala, K. M., Manamgoda, D. S., Jayawardena, R., Camporesi, E., Boonmee, S., . . . Hyde, K. D. (2015). Towards a natural classification and backbone tree for Pleosporaceae. *Fungal Diversity*, *71*, 85–139.

Arzanlou, M., & Torbati, M. (2013). Phenotypic and molecular characterisation of Colletotrichum acutatum, the causal agent of anthracnose disease on *Cornus mas* in Iran. *Archiv für Phytopathologie und Pflanzenschutz, 46*, 518–525.

Baayen, R. P., Bonants, P., Verkley, G., Carroll, G. C., van der Aa, H. A., de Weerdt, M., . . . Azevedo, J. L. (2002). Nonpathogenic isolates of the citrus black spot fungus, *Guignardia citricarpa*, identified as a cosmopolitan endophyte of woody plants, *G. mangiferae* (*Phyllosticta capitalensis*). *Phytopathology*, *92*, 464–77.

Bai, J. K. (2000). *Flora fungorum sinicorum. Vol. 15. Sphaeropsidales, Phoma, Phyllosticta*. Science Press, Beijing, China.

Bai, J. K. (2003). *Flora fungorum sinicorum. Vol. 17. Sphaeropsidales, Ascochyta, Septoria*. Science Press, Beijing, China.

Barber, P. A., Crous, P. W., Groenewald, J. Z., Pascoe, I. G., & Keane, P. (2011). Reassessing *Vermisporium* (Amphisphaeriaceae), a genus of foliar pathogens of eucalypts. *Persoonia, 27,* 90–118.

Barber, P. A., Smith, I. W., & Keane, P. J. (2003). Foliar diseases of *Eucalyptus* spp. grown for ornamental cut foliage. *Australasian Plant Pathology, 32*, 109–111.

Barnard, E. L. (2000). *Inonotus root and butt rot of pines in Florida*. Plant Pathology Circular No. 403, Florida Department of Agriculture and Consumer Services, Division of Plant Industry.

Barr, M. E. (1970). Some amerosporous ascomycetes on Ericaceae and Empetraceae. *Mycologia*, *62*, 377–394.

Barr, M. E. (1975a). The genus *Ostreichnion*. *Mycotaxon*, *3*, 81–88.

Barr, M. E. (1975b). *Pestalosphaeria*, a new genus in the Amphisphaeriaceae. *Mycologia*, *67*, 187–194.

Barr, M. E. (1978). The Diaporthales in North America with emphasis on *Gnomonia* and its segregates. *Mycologia Memoir*, *7*, 1–232.

Barr, M. E. (1989). The genus *Dothidotthia* (Botryosphaeriaceae) in North America. *Mycotaxon*, *34*(2), 517–526.

Barr, M. E. (1990). Prodromus to nonlichenized, pyrenomycetous members of class Hymenoascomycetes. *Mycotaxon*, *39*, 43–184.

Barr, M. E. (1994). Note on Amphisphaeriaceae and related families. *Mycotaxon*, *51*, 191–224.

Bassimba, D. D. M., Nzambi, N., Paixao, M. I. S., Katula, I. G., & Vicent, A. (2018). First report of citrus black spot caused by *Phyllosticta citricarpa* in Angola. *Plant Disease*, *102*, 683.

Baudry, A., Morzieres, J. P., & Larue, P. (1993). First report of Japanese pear black spot caused by *Alternaria kikuchiana* in France. *Plant Disease*, *77*, 428.

Beger, M., Grantham, H. S., Pressey, R. L., Wilson, K. A., Peterson, E. L., Dorfman, D., . . . Possingham, H. P. (2010). Conservation planning for connectivity across marine, freshwater, and terrestrial realms. *Biological Conservation*, *143*, 565–575.

Begoude, B. A. D., Slippers, B., Wingfeld, M. J., & Roux, J. (2010). Botryosphaeriaceae associated with *Terminalia catappa* in Cameroon, South Africa and Madagascar. *Mycological Progress*, *9*, 101–123.

Bengtsson-Palme, J., Ryberg, M., Hartmann, M., Branco, S., Wang, Z., Godhe, A., Wit, P. D., Sánchez-García, M., Ebersberger, I., Sousa, F., Amend, A. S., Jumpponen, A., Unterseher, M., Kristiansson, E., Abarenkov, K., Bertrand, Y. J., Sanli, K., Eriksson, K. M., Vik, U., . . . Nilsson, R. H. (2013). Improved software detection and extraction of ITS1 and ITS2 from ribosomal ITS sequences of fungi and other eukaryotes for analysis of environmental sequencing data. *Methods in Ecology and Evolution*, *4*, 914–919.

Benjamin, C. R., & Slot, A. (1969). Fungi of Haiti. *Sydowia*, *23*, 125–163.

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.

Berkeley, M. J., & Broome, C. E. (1850). Notices of British fungi (380–437). *Annals and Magazine of Natural History*, *5*, 365–380.

Bharathidasan, R., & Panneerselvam, A. (2011). Isolation and identification of endophytic fungi from *Avicennia marina* in Ramanathapuram District, Karankadu, Tamilnadu, India. *European Journal of Experimental Biology*, *1*, 31–36.

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.

Bhunjun, C. S., Niskanen, T., Suwannarach, N., Wannathes, N., Chen, Y. J., McKenzie, E. H. C., Maharachchikumbura, S. S. N., Buyck, B., Zhao, C., Fan, Y., Zhang, J., Dissanayake, A. J., Marasinghe, D. S., Jayawardena, R. S., Kumla, J., Padamsee, M., Chen, Y., Liimatainen, K., Ammirati, J. F., . . . Lumyong, S. (2022). The numbers of fungi: Are the most speciose genera truly diverse?. *Fungal Diversity*, *114*, 387–462.

Bhunjun, C. S., Phukhamsakda, C., Jayawardena, R. S., Jeewon, R., Promputtha, I., & Hyde, K. D. (2021). Investigating species boundaries in *Colletotrichum*. *Fungal Diversity*, *107*, 107–127.

Bissett, J., & Darbyshire, S. J. (1984a). *Phyllosticta gaultheriae*. *Fungi Canadenses, 275*, 1–2.

Bissett, J., & Darbyshire, S. J. (1984b). *Phyllosticta hamamelidis*. *Fungi Canadenses*, *276*, 1–2.

Bissett, J., & Darbyshire, S. J. (1984c). *Phyllosticta minima*. *Fungi Canadenses*, *277*, 1–2.

Bissett, J., & Darbyshire, S. J. (1984d). *Phyllosticta pyrolae*. *Fungi Canadenses*, *279*, 1–2.

Blain, W. L. (1931). A list of diseases of economic plants in Alabama. *Mycologia*, *23*, 300–304.

Boa, E., & Lenné, J. (1994). *Diseases of Nitrogen fixing trees in developing countries: An annotated list*. Natural Resources Institute, Kent, UK.

Bobev, S. (2009). *Reference guide for the diseases of cultivated plants*. N.P.

Boewe, G. H. (1964). Some plant diseases new to Illinois. *Plant Disease Reporter*, *48*, 866–870.

Boonmee, S., Zhang, Y., Chomnunti, P., Chukeatirote, E., Tsui, C. K. M., Bahkali, A. H., & Hyde, K. D. (2012). Revision of lignicolous Tubeufiaceae based on morphological reexamination and phylogenetic analysis. *Fungal Diversity*, *51*(1), 63–102.

Bose, S. K., Roy, A. J., & Jain, V. B. (1970). A new leaf-spot diease of ivy (*Hedera helix* Linn.) caused by *Phyllostictina hederae Bose*, *Roy* and *Jain* sp. nov. *Progressive Horticulture, 2*, 75–77.

Boughalleb-M'Hamdi, N., Fathallah, A., Benfradj, N., Ben Mahmoud, S., Bel Hadj Ali, A., Medhioub, L., . . . Ioos, R. (2020). First report of citrus black spot disease caused by *Phyllosticta citricarpa* on *Citrus limon* and *C. sinensis* in Tunisia. *New Disease Reports*, *41*, 8.

Brenckle, J. F. (1918). (North Dakota fungi). II. *Mycologia*, *10*, 199–221.

Brittingham, R. L., & O'Brien, M. J. (1978). Occurrence of *Phyllosticta cryptomeriae* on *Cryptomeria japonica* in the United States. *Plant Disease Reporter*, *62*, 152–153.

Brockmann, I. (1976). Untersuchungen über die Gattung *Discostroma* Clements (Ascomycetes). *Sydowia*, *28*, 275–338.

Brunaud, P. (1890). Sphaeropsidées récoltées jusqu'a ce jour dans la Charente-Inférieure. *Annales de la Société royale des sciences médicales et naturelles*, *26*, 51–140.

Bulgakov, T. S. (2010). *Microfungi of Leucostoma and Valsa genera and their Cytospora anamorphs on arboreal plants in the steppe zone of Southern Russia*. Actual problems of ecology: Mater. IV All-Russian Science Conference in Vladikavkaz, North Ossetian State University.

Bull, J. J., Huelsenbeck, J. P., Cunningham, C. W., Swofford, D. L., & Waddell, P. J. (1993). Partitioning and combining data in phylogenetic analysis. *Systematic Biology*, *42*, 384–397.

Cai, L., Hyde, K. D., Taylor, P. W. J., Weir, B. S., Waller, J. M., Abang, M. M., . . . Johnston, P. R. (2009a). A polyphasic approach for studying *Colletotrichum*. *Fungal Diversity*, *39*, 183–204.

Cai, L., Jeewon, R., & Hyde, K. D. (2005). Phylogenetic evaluation and taxonomic revision of *Schizothecium* based on ribosomal DNA and protein coding genes. *Fungal Diversity*, *19*, 1–17.

Cai, L., Udayanga, D., Manamgoda, D. S., Maharachchikumbura, S. S. N., McKenzie, E. H. C., Guo, L. D., . . . Hyde, K. D. (2011). The need to carry out re-inventory of plant pathogenic fungi. *Tropical Plant Pathology, 36*(4), 205–213.

Cai, L., Wu, W. P., & Hyde, K. D. (2009b). Phylogenetic relationships of *Chalara* and allied species inferred from ribosomal DNA sequences. *Mycological Progress, 8*, 133–143.

Caio, G., Lungaro, L., Caputo, F., Zoli, E., Giancola, F., Chiarioni, G., . . . Zoli, G. (2021). Nutritional Treatment in Crohn's Disease. *Nutrients, 13*(5), 1628.

Camara, M. S. (1930). Contributiones ad mycofloram Lusitaniae. *Anais Instituto Superior de Agronomia, 3*, 59–141.

Cannon, P. F., & Minter, D. W. (2014). *Lamproconium desmazieresii*. IMI Descriptions of Fungi & Bacteria.

Cannon, P. F., Damm, U., Johnston, P. R., & Weir, B. S. (2012). *Colletotrichum* - current status and future directions. *Studies in Mycology, 73*, 181–213.

Cannon, P. F., Hawksworth, D. L., & Sherwood-Pike, M. A. (1985). *The British Ascomycotina: An annotated checklist*. Commonwealth Mycological Institute, Kew, Surrey, UK.

Carbone, I., & Kohn, L. M. (1999). A method for designing primer sets for speciation studies in filamentous ascomycetes. *Mycologia, 91,* 553–556.

Cash, E. K. (1953). A record of the fungi named by J.B. Ellis (Part 2). U.S.D.A. Special Publication, *2*, 167–345.

Cash, E. K., & Watson, A. J. (1955). Some fungi on Orchidaceae. *Mycologia, 47*, 729–747.

Castlebury, L. A., Rossman, A. Y., Jaklitsch, W. J., & Vasilyeva, L. N. (2002). A preliminary overview of the Diaporthales based on large subunit nuclear ribosomal DNA sequences. *Mycologia, 94*, 1017–1031.

Castresana, J. (2000). Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Molecular Biology and Evolution*, *17*, 540–552.

Chacón, S., & Carrion, G. (1984). New records of phytopathogenic ascomycetes in Mexico. *Boletin de la Sociedad Mexicana de Micologia*, *19*, 193–199.

Chaeprasert, S., Piapukiew, J., Whalley, A. J., & Sihanonth, P. (2010). Endophytic fungi from mangrove plant species of Thailand: Their antimicrobial and anticancer potentials. *Botanica Marina*, *53*, 555–564.

Chaisiri, C., Liu, X., Lin, Y., Fu, Y., Zhu, F., & Luo, C. (2021). Phylogenetic and Haplotype Network Analyses of *Diaporthe eres* Species in China Based on Sequences of Multiple Loci. *Biology*, *10*, 179.

Chen, C. C. (1967). *Phyllosticta eugeniae. Botanical Bulletin- Academia Sinica Taipei, 8*, 142.

Chen, M. M. (2002). *Forest fungi phytogeography, forest fungi phytogeography of China, North America, and Siberia and international quarantine of tree pathogens*. Pacific Mushroom Research and Education Center, Sacramento, California.

Chen, S. F., Morgan, D. P., & Michailides, T. J. (2014). *Botryosphaeriaceae* and *Diaporthaceae* associated with panicle and shoot blight of pistachio in California, USA. *Fungal Diversity*, *67*, 157–179.

Cheng, L. L., Thangaraj, K., Deng, C., Deng, W. W., & Zhang, Z. Z. (2019). *Phyllosticta capitalensis* causes leaf spot on tea plant (*Camellia sinensis*) in China. *Plant Disease*, *103*, 2964–2965.

Cho, W. D., & Shin, H. D. (2004). *List of plant diseases in Korea*. Korean Society of Plant Pathology.

Chomnunti, P., Hongsanan, S., Hudson, B. A., Tian, Q., Peršoh, D., Dhami, M. K., . . . Hyde, K. D. (2014). The sooty molds. *Fungal Diversity*, *66*, 1–36.

Chomnunti, P., Ko Ko, T. W., Chukeatirote, E., Hyde, K. D., Cai, L., Jones, E. B. G., . . . Chen, H. (2012). Phylogeny of Chaetothyriaceae in northern Thailand including three new species. *Mycologia*, *104*(2), 382–395.

Chomnunti, P., Schoch, C. L., Aguirre-Hudson, B., Ko Ko, T. W., Hongsanan, S., Jones, E. B. G., . . . Hyde, K. D. (2011). Capnodiaceae. *Fungal Diversity*, *51*(1), 103–134.

Ciferri, R. (1929). La esterilización de los semilleros de tabaco con los compuestos mercuroorganicos Bayer. *Review of Agricultural Santo Domingo, 30*, 4–5.

Ciferri, R. (1961). Mycoflora domingensis integrata. *Quaderno, 19*, 1–539.

Clinton, G. P. (1908). Report of the Botanist 1908. *Connecticut Agricultural Experiment Station, 12*, 849–907.

Clinton, G. P. (1934). Plant pest handbook for connecticut II. Diseases and injuries. *Storrs Agricultural Experiment Station, 358*, 149–329.

Conners, I. L. (1967). An annotated index of plant diseases in Canada and fungi recorded on plants in Alaska, Canada and Greenland. *Research Branch of Canadian Department of Agriculture*, *1251*, 1–381.

Cooke, W. B. (1969). The 1965 Illinois foray. *Mycologia, 61*, 817–822.

Cooke, W. B. (1978). The 1973 Massachusetts foray. *Mycologia, 69*, 1226–1231.

Costa, M. E. A., & Camara, M. S. (1952). Species aliquae mycologicae Lusitaniae. *Portugaliae Acta Biologica (B), 3*, 294–307.

Cribb, A. B., Cribb, J. W. (1955). Marine fungi from Queensland-I. Papers of the University of Queensland. *Department of Botany*, *3*, 78–81.

Crous, P. W., Denman, S., Taylor, J. E., Swart, L., & Palm, M. E. (2004). *Cultivation and diseases of Proteaceae, Leucadendron*: *Leucospermum and Protea.* Centraalbureau voor Schimmelcultures, Utrecht, Netherlands.

Crous, P. W., Denman, S., Taylor, J. E., Swart, L., Bezuidenhout, C. M., Hoffman, L., . . . Groenewald, J. Z. (2013). Cultivation and disease of Proteaceae, *Leucadendron*, *Leucospermum*, and *Protea*, Second edition. *CBS Biodiversity*, *13*, 360.

Crous, P. W., Knox-Davies, P. S., & Wingfield, M. J. (1989). A list of Eucalyptus leaf fungi and their potential importance to South African forestry. *South African Forestry Journal*, *149*, 17–29.

Crous, P. W., Phillips, A. J. L., & Baxter, A. P. (2000). *Phytopathogenic fungi from South Africa*. Department of Plant Pathology Press, University of Stellenbosch.

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.

Crous, P. W., Schumacher, R. K., Wingfield, M. J., Akulov, A., Denman, S., Roux, J., . . . Groenewald, J. Z. (2018). New and interesting fungi. 1. *Fungal systematics and evolution*, *1*, 169–215.

Crous, P. W., Shivas, R. G., Quaedvlieg, W., van der Bank, M., Zhang, Y., Summerell, B. A, Guarro, J., Wingfield, M. J., Wood, A. R., Alfenas, A. C., Braun, U., Cano-Lira, J. F., García, D., Marin-Felix, Y., Alvarado, P., Andrade, J. P., Armengol, J., Assefa, A., den Breeÿen, A., . . . Groenewald, J. Z. (2014). Fungal planet description sheets, 214–280. *Persoonia*, *32*, 184–306.

Crous, P. W., Shivas, R. G., Wingfield, M. J., Summerell, B. A., Rossman, A. Y., Alves, J. L., Adams, G. C., Barreto, R. W., Bell, A., Coutinho, M. L., Flory, S. L., Gates, G. K. R., Hardy, G. E. St. J., Kleczewski, N. M., Lombard, L., Longa, C. M. O., Louis-Seize, G., Macedo, F., Mahoney, D. P., . . . Groenewald, J. Z. (2012a). Fungal planet description sheets, 128–153. *Persoonia*, *29*, 146–201.

Crous, P. W., Summerell, B. A., & Swart, L. (2011). Fungal pathogens of *Proteaceae*. *Persoonia*, *27*, 20–45.

Crous, P. W., Summerell, B. A., Shivas, R. G., Burgess, T. I., Decock, C. A., Dreyer, L. L., Granke, L., Guest, D., Hardy, G., Hausbeck, M., Hüberli, D., Jung, T., Koukol, O., Lennox, C., Liew, E., Lombard, L., McTaggart, A., Pryke, J., Roets, F., . . . Groenewald, J. Z. (2012b). Fungal planet description sheets, 107–127. *Persoonia*, *28*, 138–182.

Crous, P. W., Summerell, B. A., Shivas, R. G., Romberg, M., Mel'nik, V. A., Verkley, G. J. M., & Groenewald, J. Z. (2011). Fungal planet description sheets, 92–106. *Persoonia*, *27*, 130–162.

Crous, P. W., Wingfield, M. J., Burgess, T. I., Carnegie, A. J., Hardy, G., Smith, D., Summerell, B. A., Cano-Lira, J. F., Guarro, J., Houbraken, J., Lombard, L., Martin, M., Sandoval-Denis, M., Alexandrova, A. V., Barnes, C., Baseia, I. G., Bezerra, J. D., Guarnaccia, V., May, T. W., . . . Groenewald, J. Z. (2017). Fungal planet description sheets, 625–715. *Persoonia*, *39*, 270–467.

Crous, P. W., Wingfield, M. J., Burgess, T. I., St J Hardy, G. E., Crane, C., Barrett, S., Cano-Lira, J. F., Le Roux, J. J., Thangavel, R., Guarro, J., Stchigel, A. M., Martín, M. P., Alfredo, D. S., Barber, P. A., Barreto, R. W., Baseia, I. G., Cano-Canals, J., Cheewangkoon, R., Ferreira, R. J., . . . Groenewald, J. Z. (2016). Fungal planet description sheets, 469–557. *Persoonia*, *37*, 218–403.

Crous, P. W., Wingfield, M. J., Le Roux, J. J., Richardson, D. M., Strasberg, D., Shivas, R. G., Alvarado, P., Edwards, J., Moreno, G., Sharma, R., Sonawane, M. S., Tan, Y. P., Altés, A., Barasubiye, T., Barnes, C. W., Blanchette, R. A., Boertmann, D., Bogo, A., Carlavilla, J. R., . . . Groenewald, J. Z. (2015). Fungal planet description sheets, 371–399. *Persoonia*, *35*, 264–327.

Crous, P. W., Wingfield, M. J., Schumacher, R. K., Summerell, B. A., Giraldo, A., Gené, J., Guarro, J., Wanasinghe, D. N., Hyde, K. D., Camporesi, E., Gareth Jones, E. B., Thambugala, K. M., Malysheva, E. F., Malysheva, V. F., Acharya, K., Álvarez, J., Alvarado, P., Assefa, A., Barnes, C. W., Bartlett, J. S., . . . Groenewald, J. Z. (2014). Fungal planet description sheets, 281–319. *Persoonia*, *33*, 212–289.

Cunningham, C. W. (1997). Can three incongruence tests predict when data should be combined?. *Molecular Biology and Evolution*, *14*, 733–740.

Cunnington, J. (2003). *Pathogenic fungi on introduced plants in Victoria. A host list and literature guide for their identification.* Department of Primary Industries, Research Victoria.

da Silva, L. L., Moreno, H., Correia, H., Santana, M. F., & de Queiroz, M. V. (2020). *Colletotrichum*: Species complexes, lifestyle, and peculiarities of some sources of genetic variability. *Applied Microbiology and Biotechnology*, *104*, 1891–1904.

da Silva, M., Barreto, R. W., & Pereira, O. L. (2012). Fungal pathogens of 'cat's claws' from Brazil for biocontrol of *Macfadyena unguiscati*. *Mycotaxon*, *119*, 181–195.

Damm, U., Cannon, P. F., Woudenberg, J. H. C., Johnston, P. R., Weir, B. S., Tan, Y. P., . . . Crous, P. W. (2012). The *Colletotrichum boninense* species complex. *Studies in Mycology*, *73*, 1–36.

Damm, U., Sato, T., Alizadeh, A., Groenewald, J. Z., & Crous, P. W. (2019). The *Colletotrichum dracaenophilum, C. magnum* and *C. orchidearum* species complexes. *Studies in Mycology*, *92*, 1–46.

Das, A. K., Nerkar, S., & Kumar, A. (2018). First report of P*hyllosticta citricarpa* causing citrus black spot on citrus sinensis and *C. reticulate* in India. *Plant Disease*, *102*, 1661–1662.

Davis, B. H. (1946). *Guignardia rhodorae,* the perfect stage of *Phyllosticta maxima* of Rhododendron. *Mycologia*, *38*, 40–51.

Dayarathne, M. C., Boonmee, S., Braun, U., Crous, P. W., Daranagama, D. A., Dissanayake, A. J., . . . Jeewon, R. (2016). Taxonomic utility of old names in current fungal classification and nomenclature: Conflicts, confusion & clarifications. *Mycosphere*, *7*, 1622–1648.

de Sousa Dias, M. R., Lucas, M. T., & Lopes, M. C. (1987). Fungi Lusitaniae XXX. *Agronomia Lusitana*, *42*, 179–188.

Défago, G. (1942). Seconde contributionále connaissance des Valśeesv. *H. Phytopathologische Zeitschrift*, *14*, 103–147.

Delsuc, F., Brinkmann, H., & Philippe, H. (2005). Phylogenomics and the reconstruction of the tree of life. *Nature Reviews Genetics*, *6*, 361–375.

Dennis, R. W. G. (1978). *British Ascomycetes*. J. Cramer, Vaduz.

Dennis, R. W. G. (1986). *Fungi of the Hebrides*. Royal Botanic Gardens, Kew.

Dennis, R. W. G., & Foister, C. E. (1942). List of diseases of economic plants recorded in Scotland. *Transactions of the British Mycological Society*, *25*, 266–306.

Devadatha. B., Sarma, V. V., Jeewon, R., Wanasinghe, D. N., Hyde, K. D., & Jones, E. B. G. (2018). *Thyridariella*, a novel marine fungal genus from India: Morphological characterization and phylogeny inferred from multigene DNA sequence analyses. *Mycological Progress*, *17*, 791–804.

Dingley, J. M., Fullerton, R. A., & McKenzie, E. H. C. (1981). *Survey of agricultural pests and diseases. Technical Report Volume 2. Records of Fungi, Bacteria, Algae, and Angiosperms Pathogenic on Plants in Cook Islands, Fiji, Kiribati, Niue, Tonga, Tuvalu, and Western Samoa*. F.A.O.

Diogo, E. L. F., Santos, J. M., & Phillips, A. J. L. (2010). Phylogeny, morphology and pathogenicity of *Diaporthe* and *Phomopsis* species on almond in Portugal. *Fungal Diversity*, *44*, 107–115.

Dissanayake, A. J., Camporesi, E., Hyde, K. D., Wei, Z., Yan, J. Y., & Li, X. H. (2017b). Molecular phylogenetic analysis reveals seven new *Diaporthe* species from Italy. *Mycosphere*, *8*, 853–877.

Dissanayake, A. J., Phillips, A. J. L., Hyde, K. D., Yan, J. Y., & Li, X. H. (2017c). The current status of species in *Diaporthe*. *Mycosphere*, *8*, 1106–1156.

Dissanayake, A. J., Zhang, W., Liu, M., Hyde, K. D., Zhao, W. S., Li, X. H., & Yan, J. Y. (2017a). *Diaporthe* species associated with peach tree dieback in Hubei, China. *Mycosphere, 8*, 533–549.

Doidge, E. M. (1950). The South African fungi and lichens to the end of 1945. *Bothalia, 5*, 1–1094.

Doilom, M., Dissanayake, A. J., Wanasinghe, D. N., Boonmee, S., Liu, J. K., Bhat, D. J., . . . Hyde, K. D. (2017). Microfungi on *Tectona grandis* (teak) in Northern Thailand. *Fungal Diversity, 82*, 107–182.

Doilom, M., Manawasinghe, I. S., Jeewon, R., Jayawardena, R. S., Tibpromma, S., Hongsanan, S., . . . Hyde, K. D. (2017). Can ITS sequence data identify fungal endophytes from cultures? A case study from *Rhizophora apiculata*. *Mycosphere, 8*, 1869–1892.

Driver, C. H. (1952). *Physalospora ilicis* on rotundifolia holly in Georgia. *Plant Disease Reporter, 36*, 355.

Duan, C. H., Chang, C. M., Su, C. C., Pan, H. R., & Wang, C. C. (2017). *Phyllosticta capitalensis* causes black spot of persimmon (Diospyros kaki) fruit in Taiwan. *Australasian Plant Disease Notes, 12*, 36.

Dudka, I. O., Heluta, V. P., Tykhonenko, Y. Y., Andrianova, T. V., Hayova, V. P., Prydiuk, M. P., . . . Isikov, V. P. (2004). *Fungi of the Crimean Peninsula*. M.G. Kholodny Institute of Botany, National Academy of Sciences of Ukraine.

Dzhalagonia, K. T. (1965). *Parasitic fungi of the main Abkhazian subtropical ornamental plants*. Izd–vo Metsniereba, Tbilisi.

Earle, F. S. (1897). New species of fungi imperfecti from Alabama. *Bulletin of the Torrey Botanical Club, 24*, 28–32.

Ebbels, D. L., & Allen, D. J. (1979). A supplementary and annotated list of plant diseases, pathogens and associated fungi in Tanzania. *Phytopathological Papers, 22*, 1–89.

Eglitis, M., Goul, C. J., & Johnson, F. (1966). Fungi found on Ericaceae in the Pacific coastal area. *Washington State University Agricultural Experiment Station Bulletin, 675,* 1–21.

Ehrenberg, C. G. (1818). *Sylvae Mycologicae Berolinenses*. Formis Theophili Bruschcke, Berlin, Germany.

Elliott, J. A. (1917). Taxonomic characters of the genera *Alternaria* and *Macrosporium*. *American Journal of Botany, 4*, 439–476.

Ellis, J. B., & Everhart, B. M. (1878–1898). *North American fungi*. Exsiccati set Center.

Ellis, J. B., & Everhart, B. M. (1888). New species of fungi from various localities. *Journal of Mycology, 4*, 97–107.

Ellis, J. B., & Everhart, B. M. (1889). New and rare species of North American fungi. *Journal of Mycology, 5*, 145–157.

Eriksson, O. E. (2001). Outline of Ascomycota. *Myconet, 6,* 1–27.

Eriksson, O. E. (2014). Checklist of the non–lichenized ascomycetes of Sweden. *Acta Universitatis Upsaliensis, Symbolae Botanicae Upsaliensis, 36,* 499.

Esfandiari, E., & Petrak, F. (1950). Pilze aus Iran. *Sydowia, 4,* 11–38.

Esmaeilzadeh, A., Zafari, D., & Bagherabadi, S. (2020). First report of *Phyllosticta capitalensis* causing leaf spots on ornamental Magnolia grandiflora and Syringa reticulate in Iran. *New Disease Reports, 41,* 7.

Everett, K. R., & Rees-George, J. (2006). Reclassification of an isolate of *Guignardia citricarpa* from New Zealand as *Guignardia mangiferae* by sequence analysis. *Plant Pathology, 55,* 194–199.

Fan, K. C. (2002). La mangrove de Taiwan. *Bois et Forêts des Tropiques, 273,* 43–54.

Fan, X. L., Hyde, K. D., Liu, M., Liang, Y. M., & Tian, C. M. (2015a). *Cytospora* species associated with walnut canker disease in China, with description of a new species *C. gigalocus*. *Fungal Biology, 119,* 310–319.

Fan, X. L., Hyde, K. D., Yang, Q., Liang, Y. M., Ma, R., & Tian, C. (2015b). *Cytospora* species associated with canker disease of three antidesertification plants in northwestern China. *Phytotaxa, 197*, 227–244.

Fan, X. L., Liang, Y. M., Ma, R., & Tian, C. M. (2014). Morphological and phylogenetic studies of *Cytospora* (Valsaceae, Diaporthales) isolates from Chinese scholar tree, with description of a new species. *Mycoscience, 55*, 252–259.

Farr, D. F. (1991). *Septoria* species on *Cornus*. *Mycologia, 83*, 611–623.

Farr, M. L. (1973). An annotated list of *Spegazzini*'s fungus taxa, Vol. 1. *Bibliotheca Mycologica, 35*, 1–823.

Farris, J. S., Källersjö, M., Kluge, A. G., & Bult, C. (1995a). Constructing a significance test for incongruence. *Systematic Biology, 44*, 570–572.

Farris, J. S., Källersjö, M., Kluge, A. G., & Bult, C. (1995b). Testing significance of incongruence. *Cladistics, 10*, 315–319.

Feau, N., Weiland, J. E., Stanosz, G. R., & Bernier, L. (2005). Specific and sensitive PCR–based detection of *Septoria musiva*, *S. populicola* and *S. populi*, the causes of leaf spot and stem canker on poplars. *Mycological Research, 109*, 1015–1028.

Felsenstein, J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution, 39*, 783–791.

Fergus, C. L. (1954). An epiphytotic of *Phyllosticta* leaf spot of maple. *Plant Disease Reporter, 38*, 678–679.

Ferreira, M. C., Vieira, M. de L. A., Zani, C. L., Alves, T. M. de A., Junior, P. A. S., Murta., S. M. F., . . . Rosa, H. (2015). Molecular phylogeny, diversity, symbiosis and discover of bioactive compounds of endophytic fungi associated with the medicinal Amazonian plant *Carapa guianensis* Aublet (Meliaceae). *Biochemical Systematics and Ecology, 59*, 36–44.

Ferrer-Gallego, P. P., & Boisset, F. (2017). Typification of the Indo-Australasian Malay Banyan *Ficus microcarpa* L. f. (Moraceae). *Annales Botanici Fennici, 54*, 145–151.

Firman, I. D. (1972). A list of fungi and plant parasitic bacteria, viruses and nematodes in Fiji. *Phytopathological Paper, 15*, 1–36.

Fisher, P., & Spalding, M. (1993). *Protected areas with mangrove habitat*. World Conservation Centre, Cambridge, UK.

Foister, C. E. (1961). The economic plant diseases of Scotland. *Technology Bulletin Department of Agriculture and Fishery Scotland, 1*, 1–210.

Food and Agriculture Organization of the United Nations. (2007). *The world's mangroves 1980–2005. FAO Forestry Paper, 53*. FAO, Rome, Italy.

Fotouhifar, K. B., Hedjaroude, G. A., & Leuchtmann, A. (2010). ITS rDNA phylogeny of Iranian strains of *Cytospora* and associated teleomorphs. *Mycologia, 102*, 1369–1382.

Fox, R. T. V. (2001). Fungal foes in your garden 51 Butt rot. *Mycologist, 15*, 184–185.

Franceschini, A., Marras, F., & Sutton, B. C. (1995). Notes of fungi of cork oak (*Quercus suber* L.) in Sardinia (Italy). IV *Vermisporium quercinum* sp. nov. *Bulletin OILB/SROP, 18*, 14–17.

French, A. M. (1987). *California plant disease host index. Part 1, Fruit and nuts*. California Department of Food and Agriculture, Sacramento.

French, A. M. (1989). *California plant disease host index*. California Department of Food and Agriculture, Sacramento.

Fries, E. M. (1823). *Systema mycologicum vol 2*. Greifswald, Germany.

Friess, D. A., Rogers, K., Lovelock, C. E., Krauss, K. W., Hamilton, S. E., Lee, S. Y., . . . Shi, S. (2019). The State of the World's Mangrove Forests: Past, Present, and Future. *Annual Review of Environment and Resources, 44*, 89–115.

Fu, C. H., Hsieh, H. M., Chen, C. Y., Chang, T. T., Huang, Y. M., & Ju, Y. M. (2013). *Ophiodiaporthe cyatheae* gen. et sp. nov., a diaporthalean pathogen causing a devastating wilt disease of *Cyathea lepifera* in Taiwan. *Mycologia*, *105*, 861–72.

Gadgil, P. D. (2005). *Fungi on trees and shrubs in New Zealand*. *Fungi of New Zealand (Volume 4)*. Fungal Diversity Press, Hong Kong.

Gafforov, Y. S. (2017). A preliminary checklist of ascomycetous microfungi from southern Uzbekistan. *Mycosphere*, *8*, 660–696.

Gao, Y., Liu, F., Duan, W., Crous, P. W., & Cai, L. (2017). *Diaporthe* is paraphyletic. *IMA Fungus*, *8*, 153–187.

Garcia-Reyne, A., Lopez-Medrano, F., Morales, J. M., Garcia Esteban, C., Martín, I., Eraña, I., . . . Aguado, J. M. (2011). Cutaneous infection by *Phomopsis longicolla* in a renal transplant recipient from Guinea: First report of human infection by this fungus. *Transplant Infectious Disease*, *13*, 204–207.

Garibaldi, A., Bertetti, D., & Gullino, M. L. (2003). First report of Septoria leaf spot on *Cornus sericea* in Italy. *Plant Disease*, *87*, 204.

Gasich, E. L., Titova, Y. A., & Berestetsky, A. O. (1999). The herbaceous wild plants mycobiota of the Valaam Island. *Mikologiya i Fitopatologiya, 33*, 392–401.

Ge, X., Zhou, R., Yuan, Y., Xu, H., Fu, J., & Li, H. (2016). Identification and characterization of *Paraphoma chrysanthemicola* causing leaf spot disease on *Atractylodes japonica* in China. *Journal of Phytopathology*, *164*, 372–377.

Giatgong, P. (1980). *Host index of plant diseases in Thailand* (2nd ed.). Mycology Branch, Plant Pathology and Microbiology Division, Department of Agriculture and Cooperatives, Bangkok, Thailand.

Gilbert, G. S., & Sousam, W. P. (2002). Host specialization among wood-decay polypore fungi in a Caribbean mangrove forest. *Biotropica, 34*, 396–404.

Gilman, J. C., & Archer, W. A. (1929). The fungi of Iowa parasitic on plants. *Iowa State College Journal of Science*, *3*, 299–507.

Ginns, J. H. (1986). Compendium of plant disease and decay fungi in Canada 1960–1980. *Canadian Government Publishing Centre, 1813*, 416.

Giri, C., Ochieng, E., Tieszen, L. L., Zhu, Z., Singh, A., Loveland, T., . . . Duke, N. (2011). Status and distribution of mangrove forests of the world using earth observation satellite data. *Global Ecology and Biogeography*, *20*(1), 154–159.

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*, 1323–30.

Glienke, C., Pereira, O. L., Stringari, D., Fabris, J., Kava-Cordeiro, V., Galli-Terasawa, L., . . . Crous, P. W. (2011). Endophytic and pathogenic *Phyllosticta* species, with reference to those associated with *Citrus* black spot. *Persoonia*, *26*, 47–56.

Glienke-Blanco, C., Aguilar-Vildoso, C. I., Vieira, M. L. C., Barroso, P. A. V., & Azevedo, J. L. (2002). Genetic variability in the endophytic fungus *Guignardia citricarpa* isolated from *Citrus* plants. *Genetic and Molecular Biology*, *25*, 251–255.

Gobashy, S. F. El, Mikhail, W. Z. A., Ismail, A. M., Zekry, A., Moretti, A., Susca, A., & Soliman, A. S. (2018). Morphological and Molecular Characterization of Large-spored *Alternaria* Species Associated with Potato and Tomato Early Blight in Egypt. *Mycological Progress*, *17*, 1269–1282.

Gomes, R. R., Glienke, C., Videira, S. I., Lombard, L., Groenewald, J. Z., & Crous, P. W. (2013). *Diaporthe*: A genus of endophytic, saprobic and plant pathogenic fungi. *Persoonia*, *31*, 1–41.

Gonzalez Fragoso, R. (1917). *Introduccion al Estudio de la Florula de micromicetos de Cataluna*. Junta de Ciències Naturals de Barcelona, Série Botánica.

Gonzalez, M. S., & Rondon, A. (2005). First report of *Guignardia psidii*, an ascigerous state of *Phyllosticta psidiicola*, causing fruit rot on guava in Venezuela. *Plant Disease*, *89*, 773.

Goos, R. D. (2010). *The mycota of Rhode Island, a checklist of the fungi recorded in Rhode Island (including lichens and myxomycetes) Vol. 4*. Rhode Island Natural History Survey.

Goos, R. D., & Gowing, D. P. (1992). Type specimens of fungi maintained at herbarium pacificum, Bernice P. Bishop Museum, Honolulu. *Mycotaxon, 43*, 177–198.

Gopal, K., Lakshmi, M. L., Sarada, G., Nagalakshmi, T., Gouri Sankar, T., Gopi, V., & Ramana, K. T. V. (2014). *Citrus melanose* (*Diaporthe citri* Wolf): A review. *International Journal of Current Microbiology and Applied Sciences, 3*, 113–124.

Gorter, G. J. M. A. (1977). Index of plant pathogens and the diseases they cause in cultivated plants in South Africa. *Republic of South Africa, Dept. of Agricultural Technical Services, 392*, 1–177.

Gostinčar, C., Zajc, J., Lenassi, M., Ana Plemenitaš, A., de Hoog, S., Al-Hatmi, A., & Gunde-Cimerman, N. (2018). Fungi between extremotolerance and opportunistic pathogenicity on humans. *Fungal Diversity, 93*, 195–213.

Grand, L. F. (1985). North Carolina plant disease index. *North Carolina Agricultural Research Service: Technology Bulletin, 240*, 1–157.

Grand, L. F., Menge, J. A., & Bond, J. J. (1975). Partial checklist of fungi from highlands, North Carolina and vicinity. *Journal of the Elisha Mitchell Scientific Society, 91*, 221–229.

Greene, H. C. (1942). Notes on Wisconsin parasitic fungi. II. *Transactions of the Wisconsin Academy of Sciences, 34*, 83–98.

Greene, H. C. (1949). Notes on Wisconsin parasitic fungi. XIII. *The American Midland Naturalist Journa*l, *41*, 740–758.

Greene, H. C. (1958). Notes on Wisconsin parasitic fungi. XXIV. *Transactions of the Wisconsin Academy of Sciences, 47*, 99–117.

Greene, H. C. (1962). Notes on Wisconsin parasitic fungi. XXVIII. *Transactions of the Wisconsin Academy of Sciences*, *51*, 57–78.

Greene, H. C. (1966). Notes on Wisconsin parasitic fungi. XXXII. *Transactions of the Wisconsin Academy of Sciences*, *55*, 147–166.

Greuter, W., Poelt, J., & Raimondo, F. M. (1991). A checklist of Sicillian fungi. *Bocconea*, *2*, 222.

Grove, W. B. (1918). The British species of *Melanconium*. *Bulletin of Miscellaneous Information (Royal Botanic Gardens, Kew)*, *1918*(5), 161–178.

Grove, W. B. (1937). *British stem and leaf-fungi (Coelomycetes) (Volume 2)*. Cambridge University Press.

Guarnaccia, V., Gehrmann, T., Silva-Junior, G. J., Fourie, P. H., Haridas, S., Vu, D., . . . Crous, P. W. (2019). *Phyllosticta citricarp*a and sister species of global importance to Citrus. *Molecular Plant Pathology*, *20*, 1619–1635.

Guarnaccia, V., Groenewald, J. Z., Li, H., Glienke, C., Carstens, E., Hattingh, V., . . . Crous, P. W. (2017). First report of *Phyllosticta citricarpa* and description of two new species, *P. paracapitalensis* and *P. paracitricarpa*, from citrus in Europe. *Studies in Mycology*, *87*, 161–185.

Guarnaccia, V., Vitale, A., Cirvilleri, G., Aiello, D., Susca, A., Epifani, F., . . . Polizzi, G. (2016). Characterisation and pathogenicity of fungal species associated with branch cankers and stem-end rot of avocado in Italy. *European Journal of Plant Pathology*, *146*, 963–976.

Guba, E. F. (1961). *Monograph of Pestalotia and Monochaetia*. Harvard University Press, Cambridge.

Guo, Y. L. (1997). Fungal flora of the Daba Mountains, Imperfect fungi. *Mycotaxon*, *61*, 13–33.

Gvritishvili, M. N. (1973). *Cytospora kantschavelii* Gvrit. *Mikologia Fitopatologia*, *7*, 547.

Gvritishvili, M. N. (1982). *The fungal genus Cytospora in the USSR*. Sabchota Sakarstvelo, Tbilisi.

Hall, T. A. (1999). BioEdit: A user-friendly biological sequence alignment editor and analysis pro- gram for Windows 95/98/NT. *Nucleic Acids Symposium Series*, *41*, 95–98.

Hamilton, S. E., & Casey, D. (2016). Creation of a high spatio-temporal resolution global database of continuous mangrove forest cover for the 21st century (CGMFC-21). *Global Ecology and Biogeography*, *25*(6), 729–738.

Harman, G. E., Howell, C. R., Viterbo, A., Chet, I., & Lorito, M. (2004). *Trichoderma* species-opportunistic, avirulent pant symbionts. *Nature Reviews Microbiology*, *2*, 43–56.

Harun, A., James, R. M., Lim, S. M., Abdul Majeed, A. B., Cole, A. L., & Ramasamy, K. (2011). BACE1 Inhibitory Activity of Fungal Endophytes from Malaysian Medicinal Plants. *BMC Complementary and Alternative Medicine, 11*, 79.

Hassan, M. K., Jintana, V., Kuittinen, S., & Pappinen, A. (2018). Management Practices and Aboveground Biomass Production Patterns of *Rhizophora apiculata* Plantation: Study from a Mangrove Area in Samut Songkram Province, Thailand. *BioResources*, *13*, 7826–7850.

Hawksworth, D. L. (1991). The fungal dimension of biodiversity–magnitude, significance, and conservation. *Mycological Research*, *95*, 641–655.

Hawksworth, D. L. (2001). The Magnitude of Fungal Diversity: The 1.5 Million Species Estimate Revisited. *Mycological Research, 105*, 1422–1432.

Hawksworth, D. L., Kirk, P. M., Sutton, B. C., & Pegler, D. N. (1995). *Dictionary of the Fungi* (8th Edn.). Oxford University Press.

He, H., Janso, J. E., Williamson, R. T., Yang, H. Y., & Carter, G. T. (2003). Cytosporacin, a highly unsatu- rated polyketide: Application of the ACCORD-ADEQUATE experiment to the structural determination of natural products. *The Journal of Organic Chemistry*, *68*(16), 6079–82.

Hennings, P. (1905). Fungi japonici VI. *Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie*, *37*, 156–166.

Hennings, P. (1908). Fungi S. paulenses IV a cl. Puttmans collecti. *Hedwigia*, *48*, 13.

Hernandez-Restrepo, M., Schumacher, R. K., Wingfield, M. J., Ahmad, I., Cai, L., Duong, T. A., Edwards J., Gené J., Groenewald J. Z., Jabeen S., Khalid A. N., Lombard L., Madrid H., Marin-Felix Y., Marincowitz S., Miller A. N., Rajeshkumar K. C., Rashid A., Sarwar S., . . . Crous, P. W. (2016). Fungal systematics and evolution, FUSE 2. *Sydowia*, *68*, 193–230.

Hong, S. G., Cramer, R. A., Lawrence, C. B., & Pryor, B. M. (2005). *Alt a 1* allergen homologs from *Alternaria* and related taxa: Analysis of phylogenetic content and secondary structure. *Fungal Genetics and Biology*, *42*, 119e129.

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C. Sarma, V. V., Boonmee, S., Lücking, R., Bhat, D. J., Liu, N. G., Tennakoon, D. S., Pem, D., Karunarathna, A., Jiang, S. H., Jones, E. B. G., Phillips, A. J. L., Manawasinghe, I. S., Tibpromma, S., Jayasiri, S. C., . . . Xie, N. (2020a). Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae. *Mycosphere*, *11*(1), 1553–2107.

Hongsanan, S., Hyde, K. D., Phookamsak, R., Wanasinghe, D. N., McKenzie, E. H. C. Sarma, V. V., Lücking, R., Boonmee, S., Bhat, J. D., Liu, N.-G., Tennakoon, D. S., Pem, D., Karunarathna, A., Jiang, S.-H., Jones, G. E. B., Phillips, A. J. L., Manawasinghe, I. S., Tibpromma, S., Jayasiri, S. C., . . . Xie, N. (2020b). Refined families of Dothideomycetes: Orders and families incertae sedis in Dothideomycetes. *Fungal Diversity*, *105*, 17–318.

Hongsanan, S., Maharachchikumbura, S. S. N., Hyde, K. D., Samarakoon, M. C., Jeewon, R., Zhao, Q., . . . Bahkali, A. H. (2017). An updated phylogeny of Sordariomycetes based on phylogenetic and molecular clock evidence. *Fungal Diversity*, *84*, 25–41.

Hsueh, M. L. (1995). *Decreasing wetland forest, about Taiwan mangroves*. Taiwan Endemic Species Research Institute, Taiwan.

Hu, H. L., Jeewon, R., Zhou, D. Q., Zhou, T. X., & Hyde, K. D. (2007). Phylogenetic diversity of endophytic *Pestalotiopsis* species in *Pinus armandii* and *Ribes* spp.: Evidence from rDNA and beta- tubulin gene phylogenies. *Fungal Diversity*, *24*, 1–22.

Huang, F., Chen, G. Q., Hou, X., Fu, Y. S., Cai, L., Hyde, K. D., & Li, H. Y. (2013). *Colletotrichum* species associated with cultivated citrus in China. *Fungal Diversity*, *61*, 61–74.

Huang, F., Udayanga, D., Wang, X. H., Hou, X., Mei, X., Fu, Y., . . . Li, H. (2015). Endophytic *Diaporthe* associated with *Citrus*: A phylogenetic reassessment with seven new species from China. *Fungal Biology*, *119*, 331–347.

Huang, S., Xia, J., Zhang, X., & Sun, W. (2021). Morphological and phylogenetic analyses reveal three new species of *Diaporthe* from Yunnan, China. *MycoKeys*, *78*, 49–77.

Huguenin, B. (1966). Micromycetes de Nouvelle-Caledonie. *Cahiers ORSTOM, Série Biologie*, *1*, 61–91.

Huseyinov, E., & Selcuk, F. (2001). Contribution to study of mycoflora of Turkey I. Coelomycetes of orders Melanconiales and Sphaeropsidales on forest trees and shrubs in the Black Sea coast (Rize and Trabzon Provinces). *Mikologiia i Fitopatologiia*, *35*, 28–33.

Hutchison, J., Manica, A., Swetnam, R., Balmford, A., & Spalding, M. (2014). Predicting global patterns in mangrove forest biomass. *Conservation Letters*, *7*, 233–240.

Hyde, K. D. (1992). The genus *Saccardoella* from intertidal mangrove wood. *Mycologia*, *84*, 803–810.

Hyde, K. D., & Alcorn, J. L. (1993). Some disease–associated microorganisms on plants of Cape York Peninsula and Torres Strait Islands. *Australasian Plant Pathology*, *22*, 73–83.

Hyde, K. D., & Cannon, P. F. (1992). *Polystigma sonneratiae* causing leaf spots on the mangrove genus Sonneratia. *Australian Systematic Botany*, *5*, 415–420.

Hyde, K. D., & Jones, E. B. G. (1988). Marine Mangrove Fungi. *Marine Ecology*, *9*, 15–33.

Hyde, K. D., & Lee, S. Y. (1995). Ecology of mangrove fungi and their role in nutrient cycling: What gaps occur in our knowledge?. *Hydrobiologia*, *295*, 107–118.

Hyde, K. D., Abd-Elsalam, K., & Cai, L. (2010). Morphology: Still essential in a molecular world. *Mycotaxon*, *114*, 439–451.

Hyde, K. D., Cai, L., Cannon, P. F., Crouch, J. A., Crous, P. W., Damm, U., Goodwin, P. H., Chen, H., Johnston, P. R., Jones, E. B., Liu, Z., McKenzie, E. H., Moriwaki, J., Noireung, P., Pennycook, S. R., Pfenning, L. H., Prihastuti, H., Sato, T., Shivas, R. G., . . . Zhang, J. Z. (2009). *Colletotrichum–names in current use*. *Fungal Diversity*, *39*, 147–183.

Hyde, K. D., Chaiwan, N., Norphanphoun, C., Boonmee, S., Camporesi, E., Chethana, K. W. T., Dayarathne, M. C., De Silva, N. I., Dissanayake, A. J., Ekanayaka, A. H., Hongsanan, S., Huang, S., Jayasiri, S. C., Jayawardena, R. S., Jiang, H., Karunarathna, A., Lin, C., Liu, J., Liu, N., . . . Zhao, Q. (2018). Mycosphere notes 169–224. *Mycosphere*, *9*, 271–430.

Hyde, K. D., de Silva, N. I., Jeewon, R., Bhat, D. J., Phookamsak, R., Doilom, M., Boonmee, S., Jayawardena, R. S., Maharachchikumbura, S. S. N., Senanayake, I. C., Manawasinghe, I. S., Liu, N. G., Abeywickrama, P. D., Chaiwan, N., Karunarathna, A., Pem, D., Lin, C. G., Sysouphanthong, P., Luo, Z. L., . . . Bulgakov, T. S. (2020a). AJOM new records and collections of fungi, 1–100. *Asian Journal of Mycology*, *3*, 22–294.

Hyde, K. D., Hongsanan, S., Jeewon, R., Bhat, D. J., McKenzie, E. H. C., Jones, E. B. G., Phookamsak, R., Ariyawansa, H. A., Boonmee, S., Zhao, Q., Abdel-Aziz, F. A., Abdel-Wahab, M. A., Banmai, S., Chomnunti, P., Cui, B., Daranagama, D. A., Das, K., Dayarathne, M. C., Silva, N. I., . . . Zhu, L. (2016). Fungal diversity notes 367–490: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *80*, 1–270.

Hyde, K. D., Jeewon, R., Chen, Y. J., Bhunjun, C., Calabon, M. S., Jiang, H. B., . . . Lumyong, S. (2020b). The numbers of fungi, is the descriptive curve flattening? *Funga Diversity*, *103*, 219–271.

Hyde, K. D., Jones, E. B. G., LeañoStephen, E., Pointing, B., Poonyth, A. D., & Vrijmoed, L. L. P. (1998). Role of fungi in marine ecosystems. *Biodiversity and Conservation*, *7*, 1147–1161.

Hyde, K. D., Jones, E. B. G., Liu, J. K., Ariyawansa, H., Boehm, E., Boonmee, S., Braun, U., Chomnunti, P., Crous, P. W., Dai, D. Q., Diederich, P., Dissanayake, A., Doilom, M., Doveri, F., Hongsanan, S., Jayawardena, R., Lawrey, J. D., Li, Y. M., Liu, Y. X., . . . Zhang, M. (2013). Families of Dothideomycetes. *Fungal Diversity*, *63*, 1–313.

Hyde, K. D., McKenzie, E. H. C., & KoKo, T. W. (2011). Towards incorporating anamorphic fungi in a natural classification - checklist and notes for 2010. *Mycosphere*, *2*(1), 1–88.

Hyde, K. D., Nilsson, R. H., Alias, S. A., Ariyawansa, H. A., Blair, J. E., Cai, L., de Cock, A. W. A. M., Dissanayake, A. J., Glockling, S. L., Goonasekara, I. D., Gorczak, M., Hahn, M., Jayawardena, R. S., van Kan, J. A. L., Laurence, M. H., Levesque, C. A., Li, X., Liu, J-K., Maharachchikumbura, S. S. N., . . . Zhou, N. (2014). One stop shop: Backbones trees for important phytopathogenic genera: I. *Fungal Diversity*, *67*, 21–125.

Hyde, K. D., Norphanphoun, C., Abreu, V. P., Bazzicalupo, A., Chethana, K. W. T., Clericuzio, M., Dayarathne, M. C., Dissanayake, A. J., Ekanayaka, A. H., He, M. Q., Hongsanan, S., Huang, S. K., Jayasiri, S. C., Jayawardena, R. S., Karunarathna, A., Konta, S., Kušan, I., Lee, H., Li, J., . . . Mortimer, P. E. (2017). Fungal diversity notes 603–708: Taxonomic and phylogenetic notes on genera and species. *Fungal Diversity*, *87*, 1–235.

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, K. D., Norphanphoun, C., Maharachchikumbura, S. S. N., Bhat, D. J., Jones, E. B. G., Bundhun, D., Chen, Y. J., Bao, D. F., Boonmee, S., Calabon, M. S., Chaiwan, N., Chethana, K. W. T., Dai, D. Q., Dayarathne, M. C., Devadatha, B., Dissanayake, A. J., Dissanayake, L. S., Doilom, M., Dong, W., . . . Xiang, M. M. (2020c). Refined families of Sordariomycetes. *Mycosphere*, *11*, 305−1059.

Hyde, K. D., Xu, J., Rapior, S., Jeewon, Lumyong, S., Niego, A. G. T., Abeywickrama, P. D., Aluthmuhandiram, J. V. S., Brahamanage, R. S., Brooks, S., Chaiyasen, A., Chethana, K. W. T., Chomnunti, P., Chepkirui, C., Chuankid, B., de Silva, N. I., Doilom, M., Faulds, C., Gentekaki, E., . . . Chaiyasen, A. (2019). The amazing potential of fungi: 50 ways we can exploit fungi industrially. *Fungal Diversity*, *97*, 1–136.

Index Fungorum. (2015). www.indexfungorum.org

Index Fungorum. (2016). www.indexfungorum.org

Index Fungorum. (2017). www.indexfungorum.org

Index Fungorum. (2018). www.indexfungorum.org

Index Fungorum. (2019). www.indexfungorum.org

Index Fungorum. (2020). www.indexfungorum.org

Index Fungorum. (2021). www.indexfungorum.org

Index Fungorum. (2022). www.indexfungorum.org

Iriart, X., Binois, R., For, A., Blanchet, D., Berry, A., Cassaing, S., . . . Couppié, P. (2011). Eumycetoma caused by *Diaporthe phaseolorum* (*Phomopsis phaseoli*): A case report and a mini-review of *Diaporthe*/*Phomopsis* spp. invasive infections in humans. *Clinical Microbiology and Infection, 17*, 1492–4.

Ismail, A. M., Cirvilleri, G., Lombard, L., Crous, P. W., Groenewald, J. Z., & Polizzi, G. (2013). Characterisation of *Neofusicoccum* species causing mango dieback in Italy. *Journal of Plant Pathology*, *95*, 549–557.

Ismail, A. M., Cirvilleri, G., Polizzi, G., Crous, P. W., Groenewald, J. Z., & Lombard, L. (2012). *Lasiodiplodia* species associated with dieback disease of mango (*Mangifera indica*) in Egypt. *Australasian Plant Pathology*, *41*, 649–660.

Jaczewski, A. A. (1915). *Materials for mycology and phytopathology in Russia (Vol. 1)*. Bureau of Mycology and Phytopathology, Petrograd.

Jaklitsch, W. A., & Voglmayr, H. (2014). Biodiversity of *Trichoderma* (*Hypocreaceae*) in Southern Europe and *Macaronesia. Studies in Mycology*, *80*, 1–87.

Jayasiri, S. C., Hyde, K. D., Ariyawansa, H. A., Bhat, J., Buyck, B., Cai, L., Dai, Y. C., Abd-Elsalam, K. A., Ertz, D., Hidayat, I., Jeewon, R., Jones, E. B. G., Bahkali, A. H., Karunarathna, S. C., Liu, J. K., Luangsa-ard, J. J., Lumbsch, H. T., Maharachchikumbura, S. S. N., McKenzie, E. H. C., . . . Promputtha, I. (2015). The faces of fungi database: Fungal names linked with morphology, phylogeny and human attributes. *Fungal Diversity*, *74*, 3–18.

Jayawardena, R. S., Hyde, K. D., Damm, U., Cai, L., Liu, M., Li, X. H., . . . Yan, J. Y. (2016). Notes on currently accepted species of *Colletotrichum*. *Mycosphere, 7,* 1192–1260.

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., Liew, E. C. Y., & Hyde, K. D. (2002). Phylogenetic relationships of *Pestalotiopsis* and allied genera inferred from ribosomal DNA sequences and morphological characters. *Molecular Phylogenetics and Evolution, 25*, 378–392.

Jeewon, R., Liew, E. C. Y., Simpson, J. A., Hodgkiss, I. J., & Hyde, K. D. (2003). Phylogenetic significance of morphological characters in the taxonomy of *Pestalotiopsis* species. *Molecular Phylogenetics and Evolution, 27*, 372–383.

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.

Jiang, N., Bonthond, G., Fan, X. L., & Tian, C. M. (2018). *Neopestalotiopsis* rosicola sp. nov. causing stem canker of *Rosa chinensis* in China. *Mycotaxon, 133,* 271–283.

Jin, J. (2011). Conidial morphology changes in four *Phyllosticta* species. *Mycotaxon, 115,* 401–406.

Johnston, A. (1960). *A preliminary plant disease survey in Sarawak.* Plant Protection Division, FAO, Rome, Italy.

Jones, E. B. G., & Kuthubutheen, A. J. (1989). 'Malaysian mangrove fungi'. *Sydowia, 41*, 160–169.

Jones, E. B. G., & Pang, K. L. (2012). Tropical aquatic fungi. *Biodiversity and Conservation*, *21*(9), 2403–2423.

Jones, E. B. G., Pang, K. L., Abdel-Wahab, M. A., Scholz, B., Hyde, K. D., Boekhout, T., . . . Norphanphoun, C. (2019). An online resource for marine fungi. *Fungal Diversity*, *96*, 347–433.

Jones, E. B. G., Suetrong, S., Sakayaroj, J., Bahkali, A. H., . . . Pang, K. L. (2015). Classification of marine Ascomycota, Basidiomycota, Blastocladiomycota and Chytridiomycota. *Fungal Diversity*, *73*, 1–72.

Jones, E. B. G., Zuccaro, A., Mitchell, J., Nakagiri, A., Chatmala, I., & Pang. K. L. (2009). Phylogenetic position of freshwater and marine *Sigmoidea* species: Introducing a marine hyphomycete *Halosigmoidea* gen. nov. (Halosphaeriales). *Botanica Marina*, *52*, 349–359.

Jorstad, I. (1960). Iranian plants collected by Per Wendelbo in 1959. II. Uredinales and some other parasitic fungi. Årbok for Universitetet i Bergen. *Matematisk-naturvitenskapelig Serie*, *11*, 1–33.

Jorstad, I. (1962). Investigations on the Uredinales and other parasitic fungi in Mallorca and Menorca. Skrifter utgitt av Det Norske Videnskaps-Akademi i Oslo. *Matematisk- Naturvidenskapelig Klasse*, *2*, 1–73.

Kamal. (2010). *Cercosporoid fungi of India*. Bishen Singh Mahendra Pal Singh, Dehra Dun, India.

Kang, J. C., Hyde, K. D., & Kong, R. Y. C. (1999). Studies on Amphisphaeriales: The genera excluded from the Amphisphaeriaceae, Cainiaceae and Clypeosphaeriaceae. *Fungal Diversity*, *2*, 135–151.

Katoh, K., & Standley, D. M. (2013). MAFFT multiple sequence alignment Software Version 7: Improvements in performance and usability. *Molecular Biology and Evolution*, *30*, 772–780.

Kinge, T. R., & Mih, A. M. (2011). *Ganoderma ryvardense* sp. nov. associated with basal stem rot (BSR) disease of oil palm in Cameroon. *Mycosphere*, *2*, 179–188.

Kirk, P. M., Cannon, P. F., David, J. C., & Stalpers, J. A. (2001). *Ainsworth & Bisby's Dictionary of the Fungi* (8th edn.). CABI Publishing, London.

Kirk, P. M., Cannon, P. F., Minter, D. W., & Stalpers, J. A. (2008). *Ainsworth & Bisby's dictionary of the fungi* (10th edn.). CABI, Wallingford.

Kirschner, R. (2018). *Phyllosticta capitalensis* sporulating on ginkgo leaves in Taiwan. *Plant Pathology and Quarantine*, *8*, 10–13.

Kishino, H., & Hasegawa, M. (1989). Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in *Hominoidea*. *Journal of Molecular Evolution*, *29*, 170–179.

Ko Ko, T. W., McKenzie, E. H. C., Bahkali, A. H., To-anun, C., Chukeatirote, E., Promputtha, I., . . . Hyde, K. D. (2011). The need for re-inventory of Thai phytopathogens. *Chiang Mai Journal of Science*, *38*(4), 001–013.

Kobayashi, T. (2007). *Index of fungi inhabiting woody plants in Japan. Host, distribution and literature*. Zenkoku–Noson–Kyoiku Kyokai Publishing Co., Ltd.

Kobayashi, T., & Sasaki, K. (1975). Notes on new or little–known fungi inhabiting woody plants in Japan VII. *Transactions of the Mycological Society of Japan, 16*, 230–244.

Kohlmeyer, J. (1969). Marine fungi of Hawaii including the new genus *Helicascus*. *Canadian Journal of Botany*, *47*, 1469–1487.

Kohlmeyer, J., & Kohlmeyer, E. (1971). Marine fungi from tropical America and Africa. *Mycologia*, *63*, 831–861.

Kohlmeyer, J., & Kohlmeyer, E. (1979). *Marine mycology. The higher fungi*. Academic Press, New York, USA.

Kumar, S., Stecher, G., & Tamura, K. (2015). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0. *Molecular Biology and Evolution*, *33*(7), 1870–1874.

Kumar, S., Stecher, G., Li, M, Knyaz, C., & Tamura, K. (2018). MEGA X, Molecular Evolutionary Genetics Analysis Across Computing Platforms. *Molecular Biology and Evolution*, *35*, 1547–1549.

Kumar, S., Stecher, G., Li, M., Knyaz, C., & Tamura, K. (2018). MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution*, *35*, 1547–1549.

Kumar, V., Cheewangkoon, R., Gentekaki, E., Maharachchikumbura, S., Brahmanage, R. S., & Hyde, K. D. (2019). *Neopestalotiopsis alpapicalis* sp. nov. a new endophyte from tropical mangrove trees in Krabi Province (Thailand). *Phytotaxa*, *393*, 251–262.

Kwon, J. H., Choi, O., Kang, D. W., Kim, W. I., & Kim, J. (2015). The occurence of leaf blight on *Ophiopogon japonicas* caused by *Phyllosticta ophiopogonis* in Korea. *Australasian Plant Disease Notes*, *10*, 22.

Lambe, R. C. (1960). Diseases of cut greenery in Oregon. *Plant Disease Reporter*, *44*, 718–720.

Larkin, M. A., Blackshields, G., Brown, N. P., Chenna, R., McGettigan, P. A., McWilliam, H., . . . Higgins, D. G. (2007). Clustal W and Clustal X version 2.0. *Bioinformatics*, *23*, 2947–2948.

Lateef, A. A., Sepiah, M., & Bolhassan, M. H. (2015). Description of *Pseudopestalotiopsis kubahensis* sp. nov., a new species of microfungi from Kubah National Park, Sarawak, Malaysia. *Current Research in Environmental & Applied Mycology*, *5*, 376–381.

Lawrence, D. P., Gannibal, P. B., Dugan, F. M., & Pryor, B. M. (2014). Characterization of *Alternaria* isolates from the infectoria species group and a new taxon from *Arrhenatherum*, *Pseudoalternaria arrhenatheria* sp. nov. *Mycological Progress*, *13*, 257–276.

Lawrence, D. P., Gannibal, P. B., Peever, T. L., & Pryor, B. M. (2013). The sections of *Alternaria*: Formalizing species-group concepts. *Mycologia*, *105*, 530–546.

Lawrence, D. P., Rotondo, F., & Gannibal, P. B. (2016). Biodiversity and taxonomy of the pleomorphic genus *Alternaria*. *Mycological Progress*, *15*, 1–22.

Lawrence, D. P., Travadon, R., Pouzoulet, J., Rolshausen, P. E., Wilcox, W. F., & Baumgartner, K. (2017). Characterization of *Cytospora* isolates from wood cankers of declining grapevine in North America, with the descriptions of two new *Cytospora* species. *Plant Pathology*, *66*, 713–725.

Lenne, J. M. (1990). World list of fungal diseases of tropical pasture species. *Phytopathological Paper*, *31*, 1–162.

Leuchtmann, A., Petrini, O., Petrini, L. E., & Carroll, G. C. (1992). Isozyme polymorphism in six endophytic *Phyllosticta* species. *Mycological Research*, *96*, 287–294.

Li Hu, H., Fournier, J., Jeewon, R., Bahkali, A. H., & Hyde, K. D. (2010). Revisiting the taxonomy of *Daruvedia bacillata*. *Mycotaxon*, *114*, 135–144.

Li, G. J., Hyde, K. D., Zhao, R. N., Hongsanan, S., Abdel-Aziz, F. A., Abdel-Wahab, M. A., Mohamed A., Alvarado, P., Alves-Silva, G., Ammirati, J. F., Ariyawansa, H. A., Baghela, A., Bahkali, A. H., Beug, M., Bhat, D. J., Bojantchev, D., Boonpratuang, T., Bulgakov, T. S., Camporesi, E., Boro, M. C., . . . Maharachchikumbura, S. S. N. (2016). Fungal Divers notes 253–366: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *78*, 1–237.

Li, J., Jeewon, R., Phookamsak, R., Bhat, D. J., Mapook, A., Chukeatirote, E., . . . McKenzie, E. H. C. (2018). *Marinophialophora garethjonesii* gen. et sp. nov.: A new hyphomy- cete associated with *Halocyphina* from marine habitats in Thailand. *Phytotaxa, 345*, 1–12.

Lin, S., Sun, X., He, W., & Zhang, Y. (2017). Two new endophytic species of *Phyllosticta* (Phyllostictaceae, Botryosphaeriales) from Southern China. *Mycosphere, 8*, 1273–1288.

Lind, J. (1913). *Danish fungi as represented in the herbarium of E. Rostrup*. Copenhagen, Gyldendalske boghandel.

Lisboa, D. O., Silva, M. A., Machado, A. R., Pinho, D. B., Borges, L. S., Pereira, O. L., & Furtado, G. Q. (2016). First report of Botryosphaeriaceous fungi causing canker on *Cedrela fissilis* and leaf spots on *Cariniana estrellensis* in forest nursery in Brazil. *Forest Pathology*, *46*, 362–365.

Liu, A. R., Chen, S. C., Jin, W. J., Zhao, P. Y., Jeewon, R., & Xu, T. (2012). Host specificity of endophytic *Pestalotiopsis* populations in mangrove plant species of South China. *African Journal of Microbiology Research, 6*, 6262–6269.

Liu, F., Hou, L. W., Raza, M., & Cai, L. (2017). *Pestalotiopsis* and allied genera from *Camellia*, with description of 11 new species from China. *Scientific Reports, 7*, 1–19.

Liu, J. K., Hyde, K. D., Jones, E. B. G., Ariyawansa, H. A., Bhat, D. J., Boonmee, S., Maharachchikumbura, S. S. N., McKenzie, E. C., Phookamsak, R., Phukhamsakda, C., Shenoy, B., Abdel-Wahab, M., Buyck, B., Chen, J., Chethana, K., Thilini, W., Singtripop, C., Dai, D., Dai, Y., . . . Camporesi, E. (2015). Fungal Diversity Notes 1–100: Taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity, 72*, 1–197.

Liu, J. K., Phookamsak, R., Doilom, M., Wikee, S., Li, Y. M., Ariyawansha, H., . . . Hyde, K. D. (2012). Toward a natural classification of Botryosphaeriales. *Fungal Diversity, 57*, 149–210.

Liu, P. S. W. (1977). A supplement to a host list of plant diseases in Sabah, Malaysia. *Phytopathological Paper*, *21*, 1–49.

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.

Lotz-Winter, H., Hofmann, T., Kirschner, R., Kursawe, M., Trampe, T., Piepenbring, M., . . . Piepenbring, M. (2011). Fungi in the botanical garden of the University of Frankfurt. *Zeitschrift für Mykologie*, *77*, 89–122.

Lou, B. G., Xu, Y. D., Sun, C., & Lou, X. M. (2009). First report of leaf blight on duying caused by *Phyllosticta anacardiacearum* in China. *Plant Disease*, *93*, 546.

Lu, B., Hyde, K. D., Ho, W. H., Tsui, K. M., Taylor, J. E., Wong, M. K. M., . . . Zhou, D. Q. (2000). *Checklist of Hong Kong Fungi*. Fungal Diversity Press, Hong Kong.

Luginbuehl, M., & Mueller, E. (1980). Studies on endophytic fungi. I. Infection patterns of endophytes on *Hedera helix* L. *Berichte der Deutschen Botanischen Gesellschaft*, *90*, 244–250.

Lumbsch, H. T., & Huhndorf, S. M. (2010). Myconet volume 14 Part One. Outline of Ascomycota-2009. *Fieldiana Life and Earth Sciences*, *1*, 1–922.

Luongo, L., Santori, A., Riccioni, L., & Belisario, A. (2011). *Phomopsis* sp. Associated with post-harvest fruit rots of kiwifruit in Italy. *Journal of Plant Pathology*, *93*, 205–209.

Lynch, S. C., Eskalen, A., Zambino, P. J., Mayorquin, J. S., & Wang, D. H. (2013). Identification and pathogenicity of Botryosphaeriaceae species associated with coast live oak (*Quercus agrifolia*) decline in southern California. *Mycologia*, *105*, 125–140.

Maharachchikumbura, S. S. N., Guo, L. D., Cai, L., Chukeatirote, E., Wu, W. P., Sun, X., . . . Hyde, K. D. (2012). A multi−locus backbone tree for *Pestalotiopsis*, with a polyphasic characterization of 14 new species. *Fungal Diversity*, *56*, 95–129.

Maharachchikumbura, S. S. N., Guo, L. D., Chukeatirote, E., & Hyde, K. D. (2013a). Improving the backbone tree for the genus *Pestalotiopsis*; addition of *P. steyaertii* and *P. magna* sp. nov. *Mycological Progress*, *13*, 617–624.

Maharachchikumbura, S. S. N., Guo, L. D., Chukeatirote, E., Bahkali, A. H., & Hyde, K. D. (2011). *Pestalotiopsis*–morphology, phylogeny, biochemistry and diversity. *Fungal Diversity*, *50*, 167–187.

Maharachchikumbura, S. S. N., Guo, L. D., Chukeatirote, E., McKenzie, E. H. C., & Hyde, K. D. (2013b). A destructive new disease of *Syzygium samarangense* in Thailand caused by the new species *Pestalotiopsis samarangensis*. *Tropical Plant Pathology*, *38*, 227–235.

Maharachchikumbura, S. S. N., Guo, L. D., Liu, Z. Y., & Hyde, K. D. (2016a). *Pseudopestalotiopsis ignota* and *Ps. camelliae* spp. nov. associated with grey blight disease of tea in China. *Mycological Progress*, *15*, 22.

Maharachchikumbura, S. S. N., Hyde, K. D., Groenewald, J. Z., Xu, J., & Crous, P. W. (2014). *Pestalotiopsis* revisited. *Studies Mycology*, *79*, 121–186.

Maharachchikumbura, S. S. N., Hyde, K. D., Jones, E. B. G., McKenzie, E. H. C., Bhat, J. D., Dayarathne, M. C., Huang, S. K., Norphanphoun, C., Senanayake, I. C., Perera, R. H., Shang, Q. J., Xiao, Y., D'souza, M. J., Hongsanan, S., Jayawardena, R. S., Daranagama, D. A., Konta, S., Goonasekara, I. D., Zhuang, W. Y., . . . Wijayawardene, N. N. (2016b). Families of *Sordariomycetes*. *Fungal Diversity*, *79*(1), 1–317.

Maharachchikumbura, S. S. N., Hyde, K. D., Jones, E. B. G., McKenzie, E. H. C., Huang, S. K., Abdel-Wahab, M. A., Daranagama, D. A., Dayarathne, M., D'souza, M. J., Goonasekara, I. D., Hongsanan, S., Jayawardena, R. S., Kirk, P. M., Konta, S., Liu, J. K., Liu, Z.-Y., Norphanphoun, C., Pang, K. L., Perera, R. H., . . . Xu, J. (2015). Towards a natural classification and backbone tree for *Sordariomycetes*. *Fungal Diversity*, *72*, 199–301.

Manamgoda, D. S., Cai, L., McKenzie, E. H. C., Crous, P. W., & Madrid, H. (2012). A phylogenetic and taxonomic re-evaluation of the *Bipolaris-Cochliobolus-Curvularia* complex. *Fungal Diversity*, *56*, 31–144.

Manawasinghe, I. S., Dissanayake, A. J., Li, X., Liu, M., Wanasinghe, D. N., Xu, J., . . . Yan, J. (2019). High genetic diversity and species complexity of *Diaporthe* associated with grapevine dieback in China. *Frontiers in Microbiology*, *10*, 1936.

Maneval, W. E. (1937). A list of the Missouri fungi. *University of Missouri Studies*, *12*(3), 150.

Mankin, C. J. (1969). Fungous diseases on non–grass plants in South Dakota. Agricultural Experiment Station, South Dakota State University. *Technology Bulletin*, *36*, 1–28.

Mapook, A., Boonmee, S., Ariyawansa, H. A., Tibpromma, S., Campesori, E., Jones, E. B. G., . . . Hyde, K. D. (2016). Taxonomic and phylogenetic placement of *Nodulosphaeria*. *Mycological Progress*, *15*, 34.

Marin-Felix, Y., Hernandez-Restrepo, M., Wingfield, M. J., Akulov, A., Carnegie, A. J., Cheewangkoon, R., Gramaje, D., Groenewald, J. Z., Guarnaccia, V., Halleen, F., Lombard, L., Luangsa-Ard, J., Marincowitz, S., Moslemi, A., Mostert, L., Quaedvlieg, W., Schumacher, R. K., Spies, C., Thangavel, R., . . . Crous, P. W. (2019). Genera of phytopathogenic fungi: GOPHY 2. *Study in Mycolology*, *92*, 47–133.

Martin, W. H. (1931). Miscellaneous diseases of *Rhododendron*. New Jersey Agricultural College Experiment Station. *Nursery Disease Notes*, *4*, 1–4.

Matheny, P. B. (2005). Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (Inocybe; Agaricales). *Molecular Phylogenetics and Evolution, 35*, 1–20.

Mathur, R. S. (1979). *The coelomycetes of India*. Bishen Singh Mahendra Pal Singh, Delhi, India.

Mattei, A. S., Severo, C. B., Guazzelli, L. S., Oliveira, F. M., Gené, J., Guarro, J., . . . Severo, L. C. (2013). Cutaneous infection by *Diaporthe phaseolorum* in Brazil. *Medical Mycology Case Reports, 2*, 85–7.

Mayorquin, J. S., Wang, D. H., Twizeyimana, M., & Eskalen, A. (2016). Identification, distribution, and pathogenicity of Diatrypaceae and Botryosphaeriaceae associated with citrus branch canker in the Southern California desert. *Plant Disease, 100*, 2402–2413.

McDonald, V., & Eskalen, A. (2011). Botrysphaeriaceae species associated with avocado branch cankers in California. *Plant Disease, 95*, 1465–1473.

McGuire, Jr J. U., & Crandall, B. S. (1967). *Survey of insect pests and plant diseases of selected food crops of Mexico, Central America and Panama.* International Agricultural Development Service, U.S. Department of Agriculture.

McKenzie, E. H. C. (1996). *Fungi, bacteria and pathogenic algae on plants in American Samoa, Technical paper No. 206*. South Pacific Commission Information Doc.

McManus, P. S. (1998). First report of early rot of cranberry caused by *Phyllosticta vaccinii* in Wisconsin. *Plant Disease, 82*, 350.

McMillan, Jr R. T. (1964). Studies of a recently described *Cercospora* on *Rhizophora mangle*. *Plant Disease Reporter, 48*, 909–911.

McMillan, Jr R. T. (1986). *Guignardia citricarpa* a cause of black spot on mango foliage in Florida. *Journal of Phytopathology, 117*, 260–264.

McMillan, R. T. Jr. (1964). Studies of a recently described *Cercospora* on *Rhizophora mangle*. *Plant Disease Report, 48*, 909–911.

McNeill, J., Turland, N. J., Barrie, F. R., Buck, W. R., Demoulin, V., Greuter, W., . . . Wiersema, J. H. (2012). *International code of nomenclature for Algae, Fungi, and Plants (Melbourne Code)*. The 8th International Botanical Congress Melbourne, Australia.

Mehrabi, M., Mohammadi Goltapeh, E., & Fotouhifar, K. B. (2011). Studies on *Cytospora* canker disease of apple trees in Semirom region of Iran. *Journal of Agricultural Technology*, *7*, 967–982.

Melnik, V. A. (1997). *Class Coelomycetes. Rare and little-known genera.* Nauka, St.-Petersburg.

Mendes, M. A. S., da Silva, V. L., Dianese, J. C., Ferreira, M. A. S. V., Santos, C. E. N., Gomez Neto, E., . . . Castro, C. (1998). *Fungos em plants no Brasil.* Embrapa–SPI/Embrapa–Cenargen, Brasilia.

Meredith, D. S. (1969). Fungal diseases of bananas in Hawaii. *Plant Disease Reporter*, *53*, 63–66.

Meyer, L., Sanders, G. M., Jacobs, R., & Korsten, L. (2006). A one-day sensitive method to detect and distinguish between the citrus black spot pathogen *Guignardia citricarpa* and the endophyte *Guignardia mangiferae*. *Plant Disease*, *90*, 97–101.

Meyer, L., Slippers, B., Korsten, L., Kotze, J. M., & Wingfeld, M. J. (2001). Two distinct *Guignardia* species associated with citrus in South Africa. *South African Journal of Science*, *97*, 191–194.

Mildred, E. (2012). *Mangal (Mangrove), World Vegetation*. Mathias Botanical Garden, University of California at Los Angeles.

Miles, A. K., Tan, Y. P., Tan, M. K., Donovan, N. J., Ghalayini, A., & Drenth, A. (2013). *Phyllosticta* spp. on cultivated citrus in Australia. *Australasian Plant Pathology*, *42*, 461–467.

Miller, J. H., Campbell, W. A., & Thompson, G. E. (1954). Diseases and insects affecting the commonly planted trees and shrubs in Georgia. *Plant Disease Reporter, 38*, 362–369.

Miller, J. W. (1990). Bureau of plant pathology. *Tri-ology Technical Report. Division of Plant Industry, Florida, 29*, 1.

Miller, J. W. (1991). Bureau of plant pathology. *Tri-ology Technical Report. Division of Plant Industry, Florida, 30*, 1–3.

Miller, J. W. (1997). Plant pathology. *Tri-ology Technical Report. Division of Plant Industry, Florida, 36*, 14–16.

Miller, M. A., Pfeiffer, W., & Schwartz, T. (2010). *Creating the CIPRES Science Gateway for inference of large phylogenetic trees*. Proceedings of the Gateway Computing Environments Workshop (GCE), 14 Nov. 2010, New Orleans, LA.

Minnis, A. M., Kennedy, A. H., Grenier, D. B., Palm, M. E., & Rossman, A. Y. (2012). Phylogeny and taxonomic revision of the. Planistromellaceae. including its coelomycetous anamorphs, contributions towards a monograph of the genus *Kellermania*. *Persoonia, 29*, 11–28.

Minter, D. W., Rodriguez Hernandez, M., & Mena Portales, J. (2001). *Fungi of the Caribbean, an annotated checklist*. PDMS Publishing.

Mix, A. J. (1954). Report of the 1952 foray. *Mycologia, 46*, 112–123.

Mordue, J. E. M. (1985). An unusual species of *Pestalotiopsis*: *P. steyaertii* sp. nov. *Transactions of the British Mycological Society, 85*, 378–380.

Mordue, J. E. M. (1986). Another unusual species of *Pestalotiopsis*: *P. montellicoides* sp. nov. *Transactions of the British Mycological Society, 86*, 665–668.

Moslemi, A., Ades, P. K., Groom, T., Nicolas, M. E., & Taylor, P. W. J. (2017). *Alternaria infectoria* and *Stemphylium herbarum*, two new pathogens of pyrethrum (*Tanacetum cinerariifolium*) in Australia. *Australasian Plant Pathology, 46*, 91–101.

Mostert, L., Crous, P. W., Kang, J. C., & Alan, J. L. (2001). Species of *Phomopsis* and a *Libertella* sp. occurring on Grapevines with specific reference to South Africa: Morphological, cultural, molecular and pathological characterization. *Mycologia*, *93*, 146–167.

Motohashi, K., Araki, I., & Nakashima, C. (2008). Four new species of *Phyllosticta*, one new species of *Pseudocercospora*, and one new combination in *Passalora* from Japan. *Mycoscience*, *49*, 138–146.

Motohashi, K., Inaba, S., Anzai, K., Takamatsu, S., & Nakashima, C. (2009). Phylogenetic analyses of Japanese species of *Phyllosticta* sensu stricto. *Mycoscience*, *50*, 291–302.

Mulenko, W., Majewski, T., & Ruszkiewicz-Michalska, M. (2008). *A preliminary checklist of micromycetes in Poland*. W. Szafer Institute of Botany, Polish Academy of Sciences.

Murali, T. S., Suryanarayanan, T. S., & Venkatesan, G. (2007). Fungal endophyte communities in two tropical forests of southern India, diversity and host affiliation. *Mycological Progress*, *6*, 191–199.

Myllys, L., Stenroos, S., & Thell, A. (2002). New genes for phylogenetic studies of lichenized fungi, glyceraldehyde-3-phosphate dehydrogenase and beta-tubulin genes. *Lichenologist*, *34*, 237–246.

Nag Raj, T. R. (1985). Redisposals and redescriptions in the *Monchaetia-Seiridium*, *Pestalotia-Pestalotiopsis* complexes I. The correct name for the type species of *Pestalotiopsis*. *Mycotaxon*, *22*, 43–51.

Nag Raj, T. R. (1986). Redisposals and redescriptions in the *Monchaetia-Seiridium*, *Pestalotia-Pestalotiopsis* complexes. VII. *Pestalotia citrini*, *P. maura* and *Pestalotia uvicola*. *Mycotaxon*, *26*, 211–222.

Nag Raj, T. R. (1993). *Coelomycetous anamorphs with appendage-bearing conidia*. Mycologue publications, Waterloo, Ontario, Canada.

Nasehi, A., Sathyapriya, H., & Wong, M. Y. (2020). First report of leaf spot on oil palm caused by *Phyllosticta capitalensis* in Malaysia. *Plant Disease, 104*, 288.

Neely, D. (1959). New and unusual leaf disease fungi for Illinois. *Plant Disease Reporter, 43*, 498–499.

Nees von Esenbeck, C. G. (1816). *Das system der pilze und schwämme*. Wurzburg, Germany.

Nelsen, M. P., Lücking, R., Grube, M., Mbatchou, J. S., Muggia, L., Plata, E. R., & Lumbsch, H. T. (2009). Unravelling the phylogenetic relationships of lichenised fungi in Dothideomyceta. *Studies in Mycology, 64*, 135–144.

Nelsen, M. P., Lücking, R., Mbatchou, J. S., Andrew, C. J., Spielmann, A. A., & Lumbsch, H. T. (2011). New insights into relationships of lichen-forming Dothideomycetes. *Fungal Diversity, 51*, 155–162.

Nishikawa, J., & Nakashima, C. (2019). Morphological and molecular characterization of the strawberry black leaf spot pathogen referred to as the strawberry pathotype of *Alternaria alternata*. *Mycoscience, 60*, 1–9.

Nishikawa, J., & Nakashima, C. (2020). Japanese species of *Alternaria* and their species boundaries based on host range. *Fungal Systematics and Evolution, 5*, 197–281.

Nitschke, T. (1867). *Pyrenomycetes Germanici*. Die Kernpilze Deutschlands, Breslau.

Nogueira Junior, A. F., Fischer, I. H., Braganca, C. A. D., Massola, Jr N. S., & Amorim, L. (2016). Identification of Botryosphaeriaceae species that cause stylar–end rot of guavas and characterisation of the disease monocycle. *European Journal of Plant Pathology, 144*, 271–287.

Norphanphoun, C., Doilom, M., Daranagama, D. A., Phookamsak, R., Wen, T. C., Bulgakov, T. S., & Hyde, K. D. (2017). Revisiting the genus *Cytospora* and allied species. *Mycosphere, 8*, 51–97.

Norphanphoun, C., Hongsanan, S., Bhat, D. J., Kuo, C. H., & Hyde, K. D. (2020). *Ficus microcarpa* (Moraceae) and *Kandelia candel* (Rhizophoraceae), Two New Host Records for *Alternaria gaisen* from Taiwan. *Chiang Mai Journal Science 48*(6), 1478−1499.

Norphanphoun, C., Hongsanan, S., Doilom, M., Bhat, D. J., Wen, T. C., Senanayake, I. C., . . . Hyde, K. D. (2016). Lamproconiaceae fam. nov. to accommodate *Lamproconium desmazieri*. *Phytotaxa*, *270*, 089–102.

Norphanphoun, C., Hongsanan, S., Gentekaki, E., Chen, Y. J., Kuo, C. H., & Hyde, K. D. (2020). Differentiation of species complexes in *Phyllosticta* enables better species resolution. *Mycosphere*, *11*, 2542–2628.

Norphanphoun, C., Jayawardena, R. S., Chen, Y., Wen, T. C., Meepol, W., & Hyde, K. D. (2019). Morphological and phylogenetic characterization of novel pestalotioid species associated with mangroves in Thailand. *Mycosphere*, *10*, 531–578.

Norphanphoun, C., Maharachchikumbura, S. S. N., Daranagama, D. A., Bulgakov, T. S., Bhat, D. J., Bahkali, A. H., & Hyde, K. D. (2015). Towards a backbone tree for *Seimatosporium*, with *S. physocarpi* sp. nov. *Mycosphere*, *6*(3), 385–400.

Norphanphoun, C., Raspé O., Jeewon, R., Wen, T. C., & Hyde, K. D. (2018). Morphological and phylogenetic characterisation of novel *Cytospora* species associated with mangroves. *MycoKeys*, *38*, 93–120.

Nouri, M. T., Lawrence, D. P., Yaghmour, M. A., Michailides, T. J., & Trouillas, F. P. (2018). *Neoscytalidium dimidiatum* causing canker, shoot blight and fruit rot of almond in California. *Plant Disease*, *102*, 1638–1647.

Nozawa, S., Ando, K., Phay, N., & Watanabe, K. (2018). *Pseudopestalotiopsis dawaina* sp. nov. and *Ps. kawthaungina* sp. nov.: Two new species from Myanmar. *Mycological Progress*, *17*, 865–870.

Nozawa, S., Yamaguchi, K., Van Hop, D., Phay, N., Ando, K., & Watanabe, K. (2017). Identification of two new species and asexual morph from the genus *Pseudopestalotiopsis*. *Mycoscience*, *58*, 328–337.

Nylander, J. A. A. (2004). *MrModeltest 2.0. Program distributed by the author*. Evolutionary Biology Centre, Uppsala University.

Nylander, J. A. A., Wilgenbusch, J. C., Warren, D. L., & Swofford, D. L. (2008). AWTY (are we there yet?): A system for graphical exploration of MCMC convergence in Bayesian phylogenetics. *Bioinformatics*, *24*, 581–583.

O'Donnell, K. (1993). Fusarium and Its Near Relatives. In: D. R. Reynolds & J. W. Taylor (Eds) *The Fungal Holomarph: Mititic, Meiotic and Pleomorpic Speciation in Fungal Systematic*. CAB International, Wallingford.

O'Donnell, K., & Cigelnik, E. (1997). Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. *Molecular Phylogenetics and Evolution*, *7*, 103–116.

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 of the United States of America 95*, 2044–2049.

O'Donnell, K., Rooney, A. P., Proctor, R. H., Brown, D. W., McCormick, S. P., Ward, T. J., . . . Geiser, D. M. (2013). Phylogenetic analyses of *rpb1* and *rpb2* support a middle Cretaceous origin for a clade comprising all agriculturally and medically important fusaria. *Fungal Genetics and Biology*, *52*, 20–31.

O'Donnell, K., Ward, T. J., Robert, V. A. R. G., Crous, P. W., Geiser, D. M., & Kang, S. (2015). DNA sequence-based identification of *Fusarium*: Current status and future directions. *Phytoparasitica*, *43*, 583–595.

Okane, I., Lumyong, S., Ito, T., & Nakagiri, A. (2003). Extensive host range of an endophytic fungus, *Guignardia endophyllicola* (anamorph, *Phyllosticta capitalensis*). *Mycoscience*, *44*, 353–363.

Olatinwo, R. O., Hanson, E. J., & Schilder, A. M. (2003). A first assessment of the cranberry fruit rot complex in Michigan. *Plant Disease*, *87*, 550–556.

Overholts, L. O. (1938). Notes on fungi from the lower Mississippi Valley. *Bulletin Torrey Botanical Club*, *65*, 167–180.

Ozawa, K., Mochizuki, K., Takagi, D., Ishida, K., Sunada, A., Ohkusu, K., . . . Tanaka, K. (2019). Identification and antifungal sensitivity of two new species of *Diaporthe* isolated. *Journal of Infection and Chemotherapy*, *25*, 9–103.

Page, R. D. M. (1996). Tree View: An application to display phylogenetic trees on personal computers. *Computer Applications in the Biosciences*, *12*, 357−358.

Palomares-Rius, J. E., Hirooka, Y., Tsai, I. J., Masuya, H., Hino, A., Kanzaki, N., . . . Kikuchi, T. (2014). Distribution and evolution of glycoside hydrolase family 45 cellulases in nematodes and fungi. *BMC Evolutionary Biology*, *14*, 69.

Pande, A. (2008). *Ascomycetes of Peninsular India*. Scientific Publishers (India), Jodhpur.

Pang, K. L. (2009). *Inventory of marine mangrove fungi in Taiwan*. National Science Council Report, Taiwan (R.O.C.).

Pang, K. L., Alias, S. A., Chiang, M. W. L., & Vrijmoed, L. L. P. (2010). '*Sedecimiella taiwanensis* gen. et sp. nov., a marine mangrove fungus in the Hypocreales (Hypocreomycetidae, Ascomycota)'. *Botanica Marina*, *53*(6), 493–498.

Pang, K. L., Alias, SA, Chiang, M. W. L., & Vrijmoed, L. L. P. (2010). '*Sedecimiella taiwanensis* gen. et sp. nov., a marine mangrove fungus in the Hypocreales (Hypocreomycetidae, Ascomycota)'. *Botanica Marina*, *53*, 493–498.

Pang, K. L., Hyde, K. D., Alias, S. A., Suetrong, S., & Jones, E. B. G. (2013). Dyfrolomycetaceae, a new family in the Dothideomycetes, Ascomycota. *Cryptogamie Mycologie*, *34*(1), 223–232.

Pang, K. L., Jheng, J. S., & Jones, E. B. G. (2011). *Marine mangrove fungi of Taiwan.* National Taiwan Ocean University Press. Keelung, Taiwan.

Pantidou, M. E. (1973). *Fungus–host index for Greece*. Benaki Phytopathology Inst., Kiphissia, Athens.

Parmelee, J. A. (1958). Some foliicolous fungi of the Pyrolaceae. *Canadian Journal of Botany*, *38*, 865–881.

Parmelee, J. A. (1988). Parasitic fungi of new found land based on specimens from Gros Morne National Park. *Canadian Field–Naturalist, 102*, 442–464.

Parris, G. K. (1959). *A revised host index of Mississippi plant diseases*. Mississippi State University, Botany Department.

Patriarca, A., & Pinto, V. F. (2018). *Alternaria*. *Encyclopedia of Food Microbiology*, *1*, 54–60.

Paul, A. R., & Blackburn, M. D. (1986). *Phyllosticta beaumarisii* sp. nov., a cause of leafspot on *Muehlenbeckia adpressa*. *Australasian Plant Pathology*, *15*, 40–41.

Paulus, B. C., Gadek, P. A., & Hyde, K. D. (2006). *Discostroma ficicola* sp. nov. (Amphisphaeriaceae) and a key to species of *Discostroma*. *Sydowia*, *58,* 76–90.

Pennycook, S. R. (1989). *Plant diseases recorded in New Zealand*. *Volume 3*. Plant Diseases Division, D.S.I.R., Auckland New Zealand.

Peregrine, W. T. H., & Ahmad, K. B. (1982). Brunei, A first annotated list of plant diseases and associated organisms. *Phytopathological Paper*, *27*, 1–87.

Peres, N. A., Harakava, R., Carroll, G. C., Adaskaveg, J. E., & Timmer, L. W. (2007). Comparison of molecular procedures for detection and identification of *Guignardia citricarpa* and *G. mangiferae*. *Plant Disease*, *91*, 525–531.

Persoon, C. H. (1818). *Traité sur les champignons comestibles, contenant l'indication des espèces nuisibles; précédé d'une introduction a l'histoire des champignons, avec quatre planches coloriées*. Paris, Belin-Leprieur.

Petrak, F. (1921). Mykologische Beitr€age I. *Hedwigia*, *62*, 282–319.

Petrak, F. (1934). Mykologische beitrage zur flora von sibirien II. *Hedwigia, 74*, 30–78.

Petrak, F. (1938). Beiträge zur Kenntnis der Gattung *Hercospora* mit besonderer Berücksichtigung ihrer Typusart *Hercospora tiliae* (Pers.) Fr. *Annales Mycologici, 36*(1), 44−60.

Petrak, F. (1953). Ein beitrag zur pilzflora Florida. *Sydowia, 7*, 103–116.

Petrak, F. (1963). Kleine Beiträge zur südamerikanischen Pilzflora. *Sydowia, 16*, 155–198.

Petrak, F., & Sydow, H. (1931). *Mycromycetes philippinenses*. Series secunda. *Annales Mycologici, 29*, 145–279.

Petrini, L. E., Petrini, O., Leuchtmann, A, & Carroll, G. C. (1991). Conifer inhabiting species of *Phyllosticta*. *Sydowia, 43*, 148–169.

Petrović, L. T., Milovanović, D., & Desbordes, M. (2015). Emerging technologies and sports events: Innovative information and communication solutions. *Sport, Business and Management: An international Journal, 5*(2), 175–190.

Phillips, A. J. L., & Alves, A. (2009). Taxonomy, phylogeny, and epitypification of *Melanops tulasnei*, the type species of *Melanops*. *Fungal Diversity, 38*, 155–166.

Phillips, A., Alves, A., Correia, A., & Luque, J. (2005). Two new species of Botryosphaeria with brown, 1–septate ascospores and *Dothiorella* anamorphs. *Mycologia, 97*, 513–529.

Photita, W., Lumyong, S., Lumyong, P., Hyde, K. D., & McKenzie, E. H. C. (2002). Index of fungi described from the Musaceae. *Mycotaxon, 81*, 491–503.

Piepenbring, M. (2006). Checklist of fungi in Panama. Preliminary version. *Puente Biologica, 1*, 1–190.

Pirone, P. P. (1939). Diseases of ornamental plants. *New Jersey Agricultural College Experiment Station: Circular, 385*, 1–80.

Pirozynski, K. A. (1974). *Botryosphaeria rhodorae*. *Fungi Canadenses, 21*, 1–2.

Polashock, J. J., Caruso, F. L., Oudemans, P. V., McManus, P. S., & Crouch, J. A. (2009). The North American cranberry fruit rot fungal community, a systematic overview using morphological and phylogenetic affinities. *Plant Pathology, 58*, 1116–1127.

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.

Preston, D. A. (1945). *Host index of Oklahoma plant diseases*. Oklahoma Agricultural and Mechanical College, Agricultural Experiment Station.

Preston, D. A. (1947). *Host index of Oklahoma plant diseases*. Oklahoma Agricultural and Mechanical College, Agricultural Experiment Station.

Raabe, R. D., Conners, I. L., & Martinez, A. P. (1981). *Checklist of plant diseases in Hawaii. College of Tropical Agriculture and Human Resources, University of Hawaii. Information Text Series No. 22*. Hawaii Institute of Tropical Agriculture and Human Resources.

Raghukumar, S. (2017). *Fungi in coastal and oceanic marine ecosystems*. Springer.

Rambaut, A. (2012). *FigTree. Tree Figure Drawing Tool* (Version 1.4.0) [computer program] http://treebio.ed.ac.uk/software/ figtree/

Rambaut, A. (2014). *FigTree v1.4: Tree figure drawing tool.* http://treebio.ed.ac.uk/software/ figtree/

Rambaut, A., & Drummond, A. J. (2009). *Tracer* (Version 1.5) [computer program] http://tree.bio.ed.ac.uk/software/tracer/

Rambaut, A., Suchard, M. A., Xie, D., & Drummond, A. J. (2013). *Tracer* (Version 1.6) [computer program] http://beast.bio.ed.ac.uk/ software/tracer/

Rampadarath, S., Puchooa, D., Jeewon, R., & Bandhoa, K. (2018). Diversity, seasonal variation and antibacterial activity of endophytic fungi associated with the genus *Jatropha* in Mauritius. *Journal of Biotechnology and Biomaterials, 8*, 1.

Rao, V. G., Mani, & Varghese, K. I. (1988). Forest micro–fungi. V. Some new records of ascomycetes from India. *International Journal of Mycology and Lichenology*, *3*, 287–293.

Rashmi, M., Kushveer, J. S., & Sarma, V. V. (2019). A worldwide list of endophytic fungi with notes on ecology and diversity. *Mycosphere*, *10*, 798–1079.

Reeder, R., Kelly, P. L., & Harling, R. (2008). First confirmed report of citrus black spot caused by *Guignardia citricarpa* on sweet oranges (*Citrus sinensis*) in Uganda. *New Disease Reports*, *17*, 33.

Rehner, S. A., & Uecker, F. A. (1994). Nuclear ribosomal internal transcribed spacer phylogeny and host diversity in the coelomycete Phomopsis. *Canadian Journal of Botany*, *72*, 1666–1674.

Reinking, O. A. (1918). Philippine economic plant diseases. *Philippine Journal of Science*, *13*, 165–274.

Reinking, O. A. (1919). Host index of diseases of economic plants in the Philippines. *Philippine Agricultural Scientist*, *8*, 38–54.

Reinking, O. A. (1921). Citrus diseases of the Philippines, southern China, Indo–China and Siam. *Philippine Agricultural Scientist*, *9*, 121–179.

Rodrigues, K. F., Sieber, T. N., Grunig, C. R., & Holdenrieder, O. (2004). Characterization of *Guignardia mangiferae* isolated from tropical plants based on morphology, ISSC-PCR amplifications and ITS1-5.8S-ITS2 sequences. *Mycological Research*, *108*, 45–52.

Rogerson, C. T. (1953). Kansas mycological notes, 1951. *Transactions of the Kansas Academy of Science*, *56*, 53–57.

Rokas, A., & Carroll, S. B. (2005). More genes or more taxa? The relative contribution of gene number and taxon number to phylogenetic accuracy. *Molecular Biology and Evolution*, *22*, 1337–1344.

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*, 539–542.

Rossman, A. (2014). Lessons learned from moving to one scientific name for fungi. *International Mycological Association Fungus*, *5*, 81–89.

Rossman, A. Y. (2009). The impact of invasive fungi on agricultural ecosystems in the United States. *Biological Invasions*, *11*, 97–107.

Rossman, A. Y. (2014). Lessons learned from moving to one scientific name for fungi. *International Mycological Association Fungus*, *5*, 81–89.

Rossman, A. Y., Adams, G. C., Cannon, P. F., Castlebury, L. A., Crous, P. W., Gryzenhout, M., . . . Walker, D. M. (2015). Recommendations of generic names in Diaporthales competing for protection or use. *International Mycological Association Fungus*, *6*, 145–154.

Rossman, A. Y., Farr, D. F., & Castlebury, L. A. (2007). Review of the phylogeny and biology of the Diaporthales. *Mycoscience*, *48*, 135–144.

Roy, A. J. (1967). Some fungi from *Almora*. *Indian Phytopathology*, *20*, 340–348.

Ruszkiewicz-Michalska, M., Tkaczuk, C., Dynowska, M., Sucharzewska, E., Szkodzik, J., Tkaczuk, C., . . . Wrzosek, M. (2012). Preliminary studies of fungi in the Biebrza National Park (NE Poland). I. Micromycetes. *Acta Mycologica*, *47*, 213–234.

Ryvarden, L. (2000). Studies in Neotropical Polypores 2: A Preliminary Key to Neotropical Species of Ganoderma with a Laccate Pileus. *Mycologia*, *92*, 180–191.

Saccardo, P. A, & Roumeguère, C. (1884). Reliquiae mycologicae Libertianae. IV. Revue Mycologique, *Toulouse*, *6*, 26–39.

Saccardo, P. A. (1875). Conspectus generum pyrenomycetum italicorum additis speciebus fungorum Venetorum novis vel criticis, systemate carpologico dispositorum. *Atti della Società Veneziana-Trentina-Istriana di Scienze Naturali, 4*, 77–100.

Saccardo, P. A. (1884). *Sylloge Fungorum vol 3*. Typis Seminarii, Italy.

Saenger, P. (2002). *Mangrove ecology, silviculture and conservation*. Dordrecht, Kluwer Academic Publishers.

Sakayaroj, J., Pang, K. L., & Jones, E. B. G. (2012). Multigene phylogeny of the Halosphaeriaceae, Its ordinal status, relationships between genera and morphological character evolution. *Fungal Diversity*, *46*, 87–109.

Sampson, P. J., & Walker, J. (1982). *An annotated list of plant diseases in Tasmania*. Department of Agriculture Tasmania.

Sánchez, R., Serra, F., Tárraga, J., Medina, I., Carbonell, J., Pulido, L., . . . Dopazo, H. (2011). Phylemon 2.0: A suite of web-tools for molecular evolution, phylogenetics, phylogenomics and hypotheses testing. *Nucleic Acids Research*, *39*, W470–W474.

Santos, J. M., & Phillips, A. J. L. (2009). Resolving the complex of *Diaporthe* (*Phomopsis*) species occurring on *Foeniculum vulgare* in Portugal. *Fungal Diversity*, *34*, 111–125.

Santos, J. M., Correia, V. G., & Phillips, A. J. L. (2010). Primers for mating-type diagnosis in *Diaporthe* and *Phomopsis*, their use in teleomorph induction in vitro and biological species definition. *Fungal Biology*, *114*, 255–270.

Sarbhoy, A. K., Lal, G., & Varshney, J. L. (1971). *Fungi of India (1967–71)*. Navyug Traders, New Delhi.

Sarma, V. V., & Hyde, K. D. (2001). A review on frequently occurring fungi in mangroves. *Fungal Diversity*, *8*, 1–34.

Schröter, J. (1894). [1835-1894]: *Die Pilze Schlesiens*. Breslau: J. U. Kern Verlag (M. Müller).

Schubert, T. S, Peres, N. A., Palm, M. E., Jeyaprakash, A., Sutton, B., Mondal, S. N., . . . Picton, D. D. (2012). First report of *Guignardia citricarpa* associated with citrus black spot-on sweet orange (*Citrus sinensis*) in North America. *Plant Disease*, *96*, 1225.

Schubert, T. S. (1991). Bureau of plant pathology. *Triology Technical Report. Division of Plant Industry, Florida*, *30*, 5–6.

Seaver, F. J. (1922). Phyllostictales, Phyllostictaceae (Pars). *North American Flora, 6,* 1–84.

Senanayake, I. C., Al-Sadi, A. M., Bhat, J. D., Camporesi, E., Dissanayake, A. J., Lumyong, S., . . . Hyde, K. D. (2016). Phomatosporales ord. nov. and Phomatosporaceae fam. nov., to accommodate *Lanspora*, *Phomatospora* and *Tenuimurus*, gen. nov. *Mycosphere*, *7*(5), 628–641.

Senanayake, I. C., Crous, P. W., Groenewald, J. Z., Maharachchikumbura, S. S. N., Jeewon, R., Phillips, A., . . . Tangthirasunun, N. (2017). Families of Diaporthales based on morphological and phylogenetic evidence. *Studies in Mycology*, *86*, 217–296.

Senanayake, I. C., Maharachchikumbura, S. S. N., Hyde, K. D., Bhat, J. D., Jones, E. B. G., McKenzie, E. H. C., Dai, D. Q., Daranagama, D. A., Dayarathne, M. C., Goonasekara, I. D., Konta, S., Li, W. J., Shang, Q. J., Stadler, M., Wijayawardene, N. N., Xiao, Y. P., Norphanphoun, C., Li, Q., Liu, X. Z., . . . Camporesi, E. (2015). Towards unraveling relationships in *Xylariomycetidae* (*Sordariomycetes*). *Fungal Diversity*, *73*, 73–144.

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.

Shaw, B. D., Carroll, G. C., & Hoch, H. C. (2006). Generality of the prerequisite of conidium attachment to a hydrophobic substratum as a signal for germination among *Phyllosticta* species. *Mycologia*, *98*, 186–194.

Shaw, C. G. (1973). *Host fungus index for the Pacific Northwest-I. Hosts*. College of Agriculture, Washington State University.

Shaw, D. E. (1984). Microorganisms in Papua New Guinea. *Department of Primary Industries, Research Bulletin, 33*, 1–344.

Sheue, C. R., Liu, H. Y., & Yong, J. W. H. (2003). *Kandelia obovata* (Rhizophoraceae), a New Mangrove Species from Eastern Asia. *Taxon, 52*, 287–294.

Shivas, R. G. (1989). Fungal and bacterial diseases of plants in Western Australia. *Journal of the Royal Society of Western Australia, 72*, 1–62.

Shivas, R. G., Young, A. J., & Crous, P. W. (2009). *Pseudocercospora avicenniae*. Fungal Planet 40. *Persoonia, 23*, 192–193.

Shoemaker, R. A., & Müller, E. (1964). Generic correlations and concepts: *Clathridium* (= *Griphosphaeria*) and *Seimatosporium* (= *Sporocadus*). *Canadian Journal of Botany, 42*, 403–410.

Silva, M., & Pereira, O. L. (2007). First report of *Guignardia endophyllicola* leaf blight on *Cymbidium* (Orchidaceae) in Brazil. *Australasian Plant Disease Notes, 2*, 31–32.

Silva, M., Pereira, O. L., Braga, I. F., & Leli, S. M. (2008). Leaf and pseudobulb diseases on *Bifrenaria harrisoniae* (Orchidaceae) caused by *Phyllosticta capitalensis* in Brazil. *Australasian Plant Disease Notes, 3*, 53–56.

Silvestro, D., & Michalak, I. (2012). RAxMLGUI: A graphical front-end for RAxML. *Organisms Diversity & Evolution, 12*, 335–337.

Simmonds, J. H. (1966). *Host index of plant diseases in Queensland*. Queensland Department of Primary Industries, Brisbane.

Simmons, E. G. (1995). *Alternaria* themes and variations (112–144). *Mycotaxon, 55*, 55–163.

Simmons, E. G. (1999). *Alternaria* themes and variations (236–243). Host-specific toxin producers. *Mycotaxon, 70*, 325–369.

Simmons, E. G. (2007). *Alternaria an identification manual*. CBS Fungal Biodiversity Centre, Utrecht.

Simon, U. K., Groenewald, J. Z., & Crous, P. W. (2009). *Cymadothea trifolii*, an obligate biotrophic leaf parasite of *Trifolium*, belongs to Mycosphaerellaceae as shown by nuclear ribosomal DNA analyses. *Persoonia*, *22*, 49–55.

Simonyan, S. A. (1981). *Mycoflora of Botanical gardens and arboretums of the Armenian S.S.R.* Hayka Armenian SSR USSR.

Singh, M. P., Janso, J. E., & Brady, S. F. (2007). *Cytoskyrins* and *Cytosporones* produced by *Cytospora* sp. CR200: Taxonomy, Fermentation, and Biological activities. *Marine Drugs*, *5*, 71–84.

Sivanesan, A. (1984). *The bitunicate ascomycetes and their anamorphs*. J. Cramer, Vaduz.

Sivanesan, A., & Holliday, P. (1970). *Valsa eugeniae. CMI Descriptions of Pathogenic Fungi and Bacteria*, *230*, 1–2.

Sivanesan, A., & Hsieh, W. H. (1989). New species and new records of ascomycetes from Taiwan. *Mycological Research*, *93*, 340–351.

Sivestro, D., & Michalak, I. (2012). RAxMlGUI: A graphical front-end for RAxML. *Organisms Diversity & Evolution*, *12*(4), 335–337.

Slippers, B., Crous, P. W., Denman, S., Coutinho, T. A., Wingfield, B. D., & Wingfield, M. J. (2004). Combined multiple gene genealogies and phenotypic characters differentiate several species previously identified as *Botryosphaeria dothidea*. *Mycologia*, *96*, 83–101.

Smith, H., Wingfield, M. J., & Petrini, O. (1996). *Botryosphaeria dothidea* endophytic in *Eucalyptus grandis* and *Eucalyptus nitens* in South Africa. *Forest Ecology and Management*, *89*, 189–195.

Song, Y., Geng, K., Zhang, B., Hyde, K. D., Zhao, W. S., Wei, J. G., . . . Wang, Y. (2013). Two new species of *Pestalotiopsis* from Southern China. *Phytotaxa*, *126*, 22–30.

Song, Y., Tangthirasunun, N., Maharachchikumbura, S. S. N., Jiang, Y., Xu, J. J., Hyde, K. D., & Wang, Y. (2014). Novel *Pestalotiopsis* species from Thailand point to the rich undiscovered diversity of this chemically creative genus. *Cryptogamie Mycologie*, *35*, 139–149.

Spatafora, J. W., Sung, G. H., Johnson, D., Hesse, C., O'Rourke, B., Serdani, M., Spotts, R., Lutzoni, F., Hofstetter, V., Miadlikowska, J., Reeb, V., Gueidan, C., Fraker, E., Lumbsch, T., Lücking, R., Schmitt, I., Hosaka, K., Aptroot, A., Roux, C., . . . Schoch, C. L. (2006). A five-gene phylogeny of Pezizomycotina. *Mycologia, 98*, 1018–1028.

Spaulding, P. (1961). Foreign diseases of forest trees of the world. *USDA Agriculture handbook, 197*, 1–361.

Spegazzini, C. (1879). Nova addenda ad Mycologiam Venetam. *Michelia 1*(5), 453–487.

Spegazzini, C. (1887). [1888] Boln Acad. nac. Cienc. *Córdoba, 11*(2), 216.

Spielman, L. J. (1983). *Taxonomy and Biology of Valsa Species on Hardwoods in North America, with Special Reference to Species on Maples*. Cornell University, NY, USA.

Spielman, L. J. (1985). A monograph of Valsa on hardwoods in North America. *Canadian Journal of Botany, 63*, 1355–1378.

Stamatakis, A. (2006). RAxML-VI-HPC: Maximum likelihood - based phylogenetic analyses with thousands of taxa and mixed models. *Bioinformatics, 22*, 2688–2690.

Stamatakis, A. (2014). RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics (Oxford, England), 30*, 1312–1313.

Stevens, F. L. (1920). New or noteworthy Puerto Rican fungi. *Botanical Gazette, 70*, 399–402.

Stevens, F. L. (1925). Hawaiian fungi. *Bulletin of the Bernice P. Bishop Museum, 19*, 1–189.

Stevenson, J. A. (1975). Fungi of Puerto Rico and the American Virgin Islands. *Contribution of Reed Herbarium, 23*, 743.

Su, Y. Y., & Cai, L. (2012). Polyphasic charcterization of three new *Phyllosticta* spp. *Persoonia, 28*, 76–84.

Suetrong, S., Schoch, C. L., Spatafora, J. W., Kohlmeyer, J., Volkmann-Kohlmeyer, B., Sakayaroj, J., . . . Jones, E. B. G. (2009). Molecular systematics of the marine Dothideomycetes. *Studies in Mycology, 64*, 155–173.

Sultan, A., Johnston, P. R., Park, D., & Robertson, A. W. (2011). Two new pathogenic ascomycetes in *Guignardia* and *Rosenscheldiella* on New Zealand's pygmy mistletoes (*Korthalsella*, Viscaceae). *Study in Mycology, 68*, 237–247.

Sun, J. M., Zhang, Y., Zhang, J. Z., Lan, X., & Lu, J. (2016). First report of freckle disease of banana caused by *Phyllosticta capitalensis* in Guangxi, Southwest China. *Journal of Plant Pathology*, *98*, 175.

Sun, J. Z., Liu, X. Z., McKenzie, E. H., Jeewon, R., Liu, J. K., Zhang, X. L., . . . Hyde, K. D. (2019). Fungicolous fungi: Terminology, diversity, distribution, evolution and species checklist. *Fungal Diversity*, *95*(12), 337–430.

Sun, J., Wang, D. M., Huang, X. Y., & Liu, Z. H. (2013). First report of a leaf spot on Hazel leaves caused by *Phyllosticta coryli* in Liaoning Province of China. *Plant Disease*, *97*, 1254.

Sun, X., & Zhang, T. Y. (2008). Morphological and molecular characterization of *Alternaria* isolates on fruits of *Pyrus bretschneideri* Rehd Ya Li. *Mycosystema*, *27*, 105–117.

Sun, X., Guo, L. D., & Hyde, K. D. (2011). Community composition of endophytic fungi in *Acer truncatum* and their role in decomposition. *Fungal Diversity*, *47*, 85–95.

Sutton, B. C. (1980). *The coelomycetes*: *Fungi imperfecti with pycnidia, acervular and stromata*. Commonwealth Mycological Institute, Kew.

Swart, H. J., & Williamson, M. A. (1983). Australian leaf-inhabiting fungi XVI. *Vermisporium*, a new genus of coelomycetes on *Eucalyptus* leaves. *Transactions of the British Mycological Society, 81*, 491–502.

Swart, L., Crous, P. W., Denman, S., & Palm, M. E. (1998). Fungi occurring on Proteaceae. I. *South African Journal of Botany, 64*, 137–146.

Swe, A., Jeewon, R., & Hyde, K. D. (2008b). Nematode-trapping fungi from mangrove habitats. *Cryptogamie Mycologie, 29*, 333–354.

Swe, A., Jeewon, R., Pointing, S. B., & Hyde, K. D. (2008a). Taxonomy and phylogeny of *Arthrobotrys mangrovispora*, a new marine nematode-trapping fungal species. *Botanica Marina, 51*, 331–338.

Swofford, D. L. (2002). *PAUP: Phylogenetic analysis using parsimony* (Version 4.0 b10). Sinauer Associates, Sunderland, MA, USA.

Swofford, D. L. (2003). *PAUP: Phylogenetic analysis using parsimony (*and other methods)* (Version 4.0 b10). Sinauer Associates, Sunderland MA, USA.

Tai, F. L. (1979). *Sylloge Fungorum Sinicorum*. Science Press, Academia Sinica. Peking, China.

Takeda, I., Guerrero, R., & Bettucci, L. (2003). Endophytic fungi of twigs and leaves from *Ilex paraguariensis* in Brazil. *Sydowia, 55*, 372–380.

Talavera, G., & Castresana, J. (2007). Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. *Systematic Biology, 56*, 564–577.

Tanaka, K., Endo, M., Hirayama, K., Okane, I., Hosoya, T., & Sato, T. (2011). Phylogeny of *Discosia* and *Seimatosporium*, and introduction of *Adisciso* and *Immersidiscosia* genera nova. *Persoonia, 26*, 85–98.

Tang, J. R., Li, Y. L., Yin, X. G., Lu, J. N., & Zhou, Y. H. (2020). First report of castor dark leaf spot caused by *Phyllosticta capitalensis* in Zhanjiang, China. *Plant Disease, 104*, 1856.

Tassi, F. (1902). I generi *Phyllosticta* Pers., *Phoma* Fr., *Macrophoma* (Sacc.) Berl. et Vogl. e i loro generi analoghi, giusta la legge d'analogia. *Universita Di Siena Istituto Botanico, 5*, 133–672.

Taylor, J. W. (2011). One Fungus = One Name: DNA and fungal nomenclature twenty years after PCR. *International Mycological Association Fungus, 2*, 113–120.

Telle, S., & Thines, M. (2011). Reclassification of an enigmatic downy mildew species on lovegrass (*Eragrostis*) to the new genus *Eraphthora*, with a key to the genera of the Peronosporaceae. *Mycological Progress, 11*, 121–129.

Teng, S. C. (1996). *Fungi of China*. Mycotaxon, Ltd., Ithaca, NY.

Tengwall, T. A. (1924). Ueber einige parasitische pilze auf kultivierten *Rhododendren*. Meded. Phytopathology Lab. *Willie Commelin Scholten, 6*, 58–61.

Teodoro, N. G. (1937). An enumeration of Philippine fungi. *Technical bulletin Philippines Department of Agriculture and Commerce, 4*, 1–585.

Than, P. P., Jeewon, R., Hyde, K. D., Pongsupasamit, S., Mongkolpornd, O., & Taylor, P. W. J. (2008). Characterisation and pathogenicity of *Colletotrichum* species asscoaited with anthracnose on Chili (*Capsicum* spp.) in Thailand. *Plant Pathology, 57*, 562–572.

Thanoi, H., Behera, B. C., Mishra, R. R., & Dutta, S. K. (2012). Biodiversity and biotechnological potential of microorganisms from mangrove ecosystems: A review. *Annals of Microbiology, 63*, 1–19.

Thatoi, H. N., Behera, B. C., Danger, T. K., & Mishra, R. R. (2012). Microbial biodiversity in mangrove soil of Bhitarkanika, Odisha, India. *International Journal of Environmental Biology, 2*, 50–58.

Thatoi, H., Behera, B. C., & Mishra, R. R. (2013). Ecological role and biotechnological potential of mangrove fungi, a review. *Mycology*, *4*, 54–71.

Thatoi, H., Behera, B. C., Mishra, R. R., & Dutta, S. K. (2013). Biodiversity and biotechnological potential of microorganisms from mangrove ecosystems: A review. *Annals of Microbiology*, *63*, 1–19.

Thaung, M. M. (2008a). Biodiversity survey of coelomycetes in Burma. *Australasian Mycologist*, *27*, 74–110.

Thaung, M. M. (2008b). Pathologic and taxonomic analysis of leaf spot and tar spot diseases in a tropical dry to wet monsoon ecosystem of lowland Burma. *Australasian Plant Pathology*, *37*, 180–197.

Thomas, S. A. L., Fleming, R., Shaw, L. N., & Baker, B. J. (2016). Isolation of bioactive secondary metabolites from mangrove fungal endophytes using epigenetic regulation. *Planta Medica, 82,* S1–S381.

Thomidis, T., Exadaktylou, E., & Chen, S. (2013). *Diaporthe neotheicola*, a new threat for kiwi fruit in Greece. *Crop Protection*, *47*, 35–40.

Thompson, S. M., Tan, Y. P., Young, A. J., Neate, S. M., Aitken, E. A., & Shivas, R. G. (2011). Stem cankers on sunflower (*Helianthus annuus*) in Australia reveal a complex of pathogenic *Diaporthe* (*Phomopsis*) species. *Persoonia*, *27*, 80–89.

Tian, Y., Qiu, C. D., Zhang, Y. Y., & Liu, Z. Y. (2020). First report of *Alternaria gaisen* causing leaf blight on wintersweet (*Chimonanthus praecox*) in China. *Plant Disease*, *104*, 977.

Tibpromma, S., Hyde, K. D., Jeewon, R., Maharachchikumbura, S. S. N., Liu, J. K., Bhat, D. J., Jones, E. B. G., McKenzie, E. H. C., Camporesi, E., Bulgakov, T. S., Doilom, M., de Azevedo Santiago, A. L. C. M., Das, K., Manimohan, P., Gibertoni, T. B., Lim, Y. W., Ekanayaka, A. H., Thongbai, B., Lee, H. B., . . . Karunarathna, S. C. (2017). Fungal diversity notes 491–602: Taxonomic and phylogenetic contributions to fungal taxa. *Fungal Diversity*, *83*, 1–261.

Tibpromma, S., Hyde, K. D., McKenzie, E. H. C., Bhat, D. J., Phillips, A. J. L., Wanasinghe, D. N., . . . Karunarathna, S. C. (2018). Fungal diversity notes 840–928: Micro-fungi associated with Pandanaceae. *Fungal Diversity*, *92*, 1–160.

Timmwemans, A. (1957). A attack of Rhododendron-leaves by *Chaetapiospora rhododendri* (Tengw.) v. Arx. *Tijdschr Over Planteziekten, 63*, 191–192.

Tomoshevich, M. A. (2012). *Atlas of plant-pathogenic fungi on arboreal plants in Siberia*. Novosibirsk, publishing house 'Geo'.

Tracy, S. M., & Earle, F. S. (1895). New species of parasitic fungi. *Bulletin of the Torrey Botanical Club*, *22*, 174–179.

Trakunyingcharoen, T., Lombard, L., Groenewald, J. Z., Cheewangkoon, R., To-Anun, C., & Crous, P. W. (2015). Caulicolous Botryosphaeriales from Thailand. *Persoonia, 34*, 87–99.

Tran, N. T., Miles, A. K., Dietzgen, R. G., & Drenth, A. (2019). *Phyllosticta capitalensis* and *P. paracapitalensis* are endophytic fungi that show potential to inhibit pathogenic *P. citricarpa* on citrus. *Australasian Plant Pathology, 48*, 281–296.

Treigiene, A. (2006). Species of *Phyllosticta* and their teleomorphs from *Lithuania*. *Mikologiya i Fitopatologiya, 40*, 426–432.

Tsai, I., Maharachchikumbura, S. S. N., Hyde, K. D., & Ariyawansa, H. A. (2018). Molecular phylogeny, morphology and pathogenicity of *Pseudopestalotiopsis* species of *Ixora* in Taiwan. *Mycological Progress, 17*, 941–952.

Tsui, K. M., Hyde, K. D., Hodgkiss, I. J., & Goh, T. K. (1998). A new freshwater species of *Saccardoella* from Hong Kong and South Africa. *Mycologia, 90*, 701–704.

Tulasne, L. R., & Tulasne, C. (1863). *Selecta Fungorum Carpologia (Volume 2)*. The Imperial Press.

Turner, P. D. (1971). Microorganisms associated with oil palm (*Elaeis guineensis* Jacq.). *Phytopathological Paper*, *14*, 1–58.

Udayanga, D., Castkebury, L. A., Rossman, A. Y., Cukeatirote, E., & Hyde, K. D. (2014b). Insights into the genus *Diaporthe*: Phylogenetic species delimitation in the *D. eres* species complex. *Fungal Diversity*, *67*, 203–229.

Udayanga, D., Castlebury, L. A., Rossman, A. Y., & Hyde, K. D. (2014a). Species limits in *Diaporthe*: Molecular re-assessment of *D. citri*, *D. cytosporella*, *D. foeniculina* and *D. rudis*. *Persoonia*, *32*, 83–101.

Udayanga, D., Castlebury, L. A., Rossman, A. Y., Chukeatirote, E., & Hyde, K. D. (2015). The *Diaporthe sojae* species complex: Phylogenetic reassessment of pathogens associated with soybean, cucurbits and other field crops. *Fungal Biology*, *119*, 383–407.

Udayanga, D., Liu, X. Z., Crous, P. W., McKenzie, E. H. C., Chukeatirote, E., & Hyde, K. D. (2012b). Multilocus phylogeny of *Diaporthe* reveals three new cryptic species from Thailand. *Cryptogamie Mycologie*, *33*, 295–309.

Udayanga, D., Liu, X. Z., Crous, P. W., McKenzie, E. H., Chukeatirote, E., & Hyde, K. D. (2012a). A multi-locus phylogenetic evaluation of *Diaporthe* (*Phomopsis*). *Fungal Diversity*, *56*(1), 157–171.

Udayanga, D., Liu, X. Z., McKenzie, E. H. C., Chukeatirote, E., Bahkali, A. H. A., & Hyde, K. D. (2011). The genus *Phomopsis*: Biology, applications, species concepts and names of common phytopathogens. *Fungal Diversity*, *50*, 189–225.

Udayanga, D., Manamgoda, D. S., Liu, X., Chukeatirote, E., & Hyde, K. D. (2013). What are the common anthracnose pathogens of tropical fruits?. *Fungal Diversity*, *61*, 165–179.

Uecker, F. A. (1988). *A World List of Phomopsis Names with Notes on Nomenclature, Morphology and Biology*. Cramer Publisher, Berlin.

Unamuno, P. L. M. (1941). Enumeracion y distribucion geografica de los ascomicetos de la Peninsula Iberica y de las Islas Baleares. *Memorias Real Academia de Ciencias Exactas Madrid, 8*, 1–403.

Urtiaga, R. (1986). *Indice de enfermedades en plantas de Venezuela y Cuba*. Impresos Nuevo Siglo Barquisimeto, Edo Venezuela.

Urtiaga, R. (2004). *Indice de enfermedades en plantas de Venezuela y Cuba, Second edition*. N.P.

van der Aa, H. A. (1973). Studies in Phyllosticta. I. *Study in Mycology, 5*, 1–110.

van der Aa, H. A., & Vanev, S. (2002). *A revision of the species described in Phyllosticta*. Centraalbureau voor Schimmelcutures.

van Niekerk, J. M., Groenewald, J. Z., Farr, D. F., Fourie, P. H., Halleer, F., & Crous, P. W. (2005). Reassessment of *Phomopsis* species on grapevines. *Australasian Plant Pathology, 34*, 27–39.

Vanev, S. G., & van der Aa, H. A. (1998). An annotated list of the published names in *Asteromella*. *Persoonia, 17*, 47–67.

Vanev, S. G., Sameva, E. F., & Bakalova, G. G. (1997). Order Sphaeropsidales. *Fungi Bulgaricae, 3*, 1–335.

Venkatasubbaiah, P., Grand, L. F., & Dyke, C. G. V. (1991). A new species of *Pestalotiopsis* on *Oenothera*. *Mycologia, 83*(4), 511–513.

Verkley, G. J. M., Quaedvlieg, W., Shin, H. D., & Crous, P. W. (2013). A new approach to species delimitation in Septoria. *Study in Mycology, 75*, 213–305.

Viala, P., & Ravaz, L. (1892). Sur la dénomination botanique (*Guignardia bidwellii*) du black-rot. *Bulletin de la Société Mycologique de France, 8*, 63.

Vilgalys, R., & Hester, M. (1990). Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology, 172*(8), 4238–4246.

Voglmayr, H., & Jaklitsch, W. M. (2014). Stilbosporaceae resurrected: Generic reclassification and speciation. *Persoonia*, *33*, 61–82.

Voglmayr, H., Rossman, A. Y., Castlebury, L. A., & Jaklitsch, W. (2012). Multigene phylogeny and taxonomy of the genus *Melanconiella* (Diaporthales). *Fungal Diversity*, *57*, 1–44.

Vollbrecht, G., Johansson, U., Eriksson, H., & Stenlid, J. (1995). Butt rot inci-dence, yield and growth pattern in a tree species experiment in southwest-ern Sweden. *Forest Ecology and Management*, *76*(1–3), 87–93.

von Arx, J. A., & Mueller, E. (1954). Die Gattungen der amerosporen Pyrenomyceten. *Beiträge zur Kryptogamenflora der Schweiz*, *11*, 1–434.

von Hoehnel, F. (1931). Mykologische Beitrage Mitt. *Mitteilung Botanical Laboratory*, *8*, 33–40.

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. *Study in Mycology*, *92*, 135–154.

Waller, T. J., Gager, J., Constantelos, C., & Oudemans, P. V. (2020). The role of flowers in the disease cycle of *Colletotrichum fioriniae* and other cranberry fruit rot fungi. *Phytopathology*, *110*, 1270–1279.

Wang, H. K., & Zhang, T. Y. (2003). RAPD analysis on small-spored *Alternaria* species. *Mycosystema*, *22*, 35–41.

Wang, X. H., Chen, G., Huang, F., Zhang, J., Hyde, K. D., & Li, H. (2012). *Phyllosticta* species associated with citrus diseases in China. *Fungal Diversity*, *52*, 209–224.

Wang, X. L., Kang, Z. S., Huang, L. L., & Wei, J. (2011). Re-evaluation of pathogens causing *Valsa* canker on apple in China. *Mycologia*, *103*, 317–324.

Wang, Y. L., Lu, Q., Decock, C., Li, Y. X., & Zhang, X. Y. (2015). *Cytospora* species from *Populus* and *Salix* in China with *C. davidiana* sp. nov. *Fungal Biology, 119*, 420–432.

Watanabe, K., Nozawa, S., Hsiang, T., & Callan, B. (2018). The cup fungus *Pestalopezia brunneopruinosa* is *Pestalotiopsis gibbosa* and belongs to Sordariomycetes. *PLoS ONE, 13*, e0197025.

Watson, A. J. (1971). *Foreign bacterial and fungus diseases of food, forage, and fiber crops: An annotated list*. U.S.D.A. Agricultural Research Service.

Wehmeyer, L. E. (1975). The pyrenomycetous fungi. *Mycologia Memoir, 6*, 1–250.

Wei, J. G., Phan, C. K., Wang, L., Xu, T., Luo, J. T., Sun, X., & Guo, L. D. (2013). *Pestalotiopsis yunnanensis* sp. nov., an endophyte from *Podocarpus macrophyllus* (Podocarpaceae) based on morphology and ITS sequence data. *Mycological Progress, 12*, 563–568.

Weidemann, G. J., & Boone, D. M. (1983). Incidence and pathogenicity of *Phyllosticta vaccinii* and *Botryosphaeria vaccinii* on cranberry. *Plant Disease, 67*, 1090–1093.

Weidemann, G. J., Boone, D. M., & Burdsall, Jr H. H. (1982). Taxonomy of *Phyllosticta vaccinii* (Coelomycetes) and a new name for the true anamorph of *Botryosphaeria vaccinii* (Dothideales, Dothioraceae). *Mycologia, 74*, 59–65.

Weir, B., Johnston, P. R., & Damm, U. (2012). The *Colletotrichum gloeosporioides* species complex. *Studies in Mycology, 73*, 115–180.

White, R. P. (1933). The insects and diseases of *Rhododendron* and *Azalea*. *Journal of Economic Entomology, 26*, 631–640.

White, R. P., & Hamilton, C. C. (1935). Diseases and insect pests of *Rhododendron* and *Azalea*. *New Jersey Agricultural Experiment Station; Circular, 350*, 1–22.

White, T., Bruns, T., Lee, S., & Taylor, J. (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.* Academic Press, Inc., New York.

Whiteside, J. O. (1966). A revised list of plant diseases in *Rhodesia*. *Kirkia*, *5*, 87–196.

Wiehe, P. O. (1953). The plant diseases of Nyasaland. *Mycological Paper, 53*, 1–39.

Wier, A. M., Tattar, T. A., & Klekowski, E. J. (2000). Disease of red mangrove (*Rhizophora mangle*) in southwest Puerto Rico caused by *Cytospora rhizophorae*. *Biotropica*, *32*, 299–306.

Wijayawardene, N. N., Hyde, K. D., Al-Ani, L. K. T., Tedersoo, L., Haelewaters, D., Rajeshkumar, K. C., Zhao, R. L., Aptroot, A., Leontyev, D. V., Saxena, R. K., Tokarev, Y. S., Dai, D. Q., Letcher, P. M., Stephenson, S. L., Ertz, D., Lumbsch, H. T., Kukwa, M., Issi, I. V., Madrid, H., . . . Thines, M. (2020). Outline of Fungi and fungus-like taxa. *Mycosphere*, *11*, 1060–1456.

Wijayawardene, N. N., Hyde, K. D., Lumbsch, T., Liu, J. K., Maharachchikumbura, S. S. N., Ekanayaka, A. H., . . . Phookamsak, R. (2018). Outline of Ascomycota-2017. *Fungal Diversity*, *88*, 167–263.

Wijayawardene, N. N., Hyde, K. D., Rajeshkumar, K. C., Hawksworth, D. L., Madrid, H., Kirk, P. M., Braun, U., Singh, R. V., Crous, P. W., Kukwa, M., Lücking, R., Kurtzman, C. P., Yurkov, A., Haelewaters, D., Aptroot, A., Lumbsch, H. T., Timdal, E., Ertz, D., Etayo, J., . . . Karunarathna, S. C. (2017). Notes for genera-Ascomycota. *Fungal Diversity*, *86*(1), 1–594.

Wikee, S., Lombard, L., Crous, P. W., Nakashima, C., Motohashi, K., Chukeatirote, E., . . . Hyde, K. D. (2013a). *Phyllosticta capitalensis*, a widespread endophyte of plants. *Fungal Diversity*, *60*, 91–105.

Wikee, S., Lombard, L., Nakashima, C., Motohashi, K., Chukeatirote, E., Cheewangkoon, R., . . . Crous, P. W. (2013b). A phylogenetic re-evaluation of *Phyllosticta* (Botryosphaeriales). *Study in Mycology*, *76*, 1–29.

Wikee, S., Udayanga, D., Crous, P. W., Chukeatirote, E., McKenzie, E. H. C., Bahkali, A. H., . . . Hyde, K. D. (2011). *Phyllosticta*—an overview of current status of species recognition. *Fungal Diversity, 51*, 43–61.

Wikee, S., Wulandari, N. F., McKenzie, E. H. C., & Hyde, K. D. (2012). *Phyllosticta ophiopogonis* sp. nov. from *Ophiopogon japonicas* (Liliaceae). *Saudi Journal of Biological Sciences, 19*, 13–16.

Williams, L., & Hayne, S. C. (1982). *Index of plant diseases in West Virginia*. West Virginia Department of Agriculture, Plant Pest Control Division.

Williams, T. H., & Liu, P. S. W. (1976). A host list of plant diseases in Sabah, Malaysia. *Phytopathological Paper, 19*, 1–67.

Williamson, P. M., Highet, A. S., Gams, W., Sivasithamparam, K., & Cowling, W. A. (1994). *Diaporthe toxica* sp. nov, the cause of lupinosis in sheep. *Mycological Research, 98*, 1364–1368.

Winter, G. (1885). Exotische Pilze II. *Hedwigia*, *24*, 21–35.

Winter, G. (1887). II. Abtheilung: Ascomyceten: Gymnoasceen und Pyrenomyceten. In G. Winter, Pilze. In A. Grunow, F. Hauck, G. Limpricht, Ch. Luerssen, P. Richter, G. Winter et al., *Rabenhorst's Kryptogamen-Flora von Deutschland, Oesterreich und der Schweiz, Zweite Auflage 1*. Verlag von Eduard Kummer, Leipzig.

Wolf, F. A., Garren, K. H., & Miller, J. K. (1938). Fungi of the Duke Forest and their relation to forest pathology. *Bulletin of Duke University, the School of Forestry, 2*, 1–122.

Wong, M. H., Crous, P. W., Henderson, J., Groenewald, J. Z., & Drenth, A. (2012). *Phyllosticta* species associated with freckle disease of banana. *Fungal Diversity*, *56*, 173–187.

Wong, M. H., Henderson, J., & Drenth, A. (2013). Identification and differentiation of *Phyllosticta* species causing freckle disease of banana using high resolution melting (HRM) analysis. *Plant Pathology, 62*, 1285–1293.

Woudenberg, J. H. C., Groenewald, J. Z., Binder, M., & Crous, P. W. (2013). *Alternaria* redefined. *Studies in Mycology*, *75*, 171–212.

Woudenberg, J. H., Seidl, M. F., Groenewald, J. Z., de Vries, M., Stielow, J. B., Thomma, B. P., & Crous, P. W. (2015). *Alternaria* section *Alternaria*: Species, formae speciales or pathotypes?. *Studies in Mycology, 82*, 1–21.

Wu, S., Liu, Y., Yuan, J., Wang, Y., Hyde, K. D., & Liu, Z. Y. (2014). *Phyllosticta* species from banana (*Musa* sp.) in Chongqing and Guizhou Provinces. China. *Phytotaxa*, *188*, 135–44.

Wu, W. P., & Sutton, B. C. (1996). A reassessment of some *Discosia* species. *Mycological Research*, *100*, 287–290.

Wulandari, N. F., Bhat, D. J., & To-anun, C. (2013). A modern account of the genus *Phyllosticta*. *Plant Pathology & Quarantine*, *3*, 145–159.

Wulandari, N. F., To-anun, C., Cai, L., Abd-Elsalam, K. A., & Hyde, K. D. (2010). *Guignardia/ Phyllosticta* species on banana. *Cryptogamic Mycology*, *31*, 403–418.

Wulandari, N. F., To-anun, C., Hyde, K. D., Duong, L. M., De Gruyter, J., Meffert, J. P., . . . Crous, P. W. (2009). *Phyllosticta citriasiana* sp. nov., the cause of *Citrus* tan spot of *Citrus maxima* in Asia. *Fungal Diversity*, *34*, 23–39.

Xu, J., Kjer, J., Sendker, J., Wray, V., Guan, H., Edrada, R., . . . Chaidir, C. (2009). Chromones from the endophytic fungus *Pestalotiopsis* sp. isolated from the Chinese mangrove plant *Rhizophora mucronata*. *Journal of Natural Products*, *72*, 662–5.

Xu, J., Kjer, J., Sendker, J., Wray, V., Guan, H., Edrada, R., . . . Proksch, P. (2009). Cytosporones, coumarins, and an alkaloid from the endophytic fungus *Pestalotiopsis* sp. isolated from the Chinese mangrove plant *Rhizophora mucronata*. *Bioorganic & Medicinal Chemistry*, *17*, 7362–7367.

Yang, Q., Fan, Z. L., Crous, P. W., Liang, Y. M., & Tian, C. M. (2015). *Cytospora* from *Ulmus pumila* in North- ern China. *Mycological Progress*, *14*, 74.

Yen, J. M. (1972). Etude sur les champignons parasites du sud-est asiatique XVIII. Maladies des taches foliaires des bananiers provoquees, a Formose, par deux nouveaux champignons. III. *Bulletin Société mycologique de France, 88,* 221–225.

Yu, J., Wu, Y., He, Z., Li, M., Zhu, K., & Gao, B. (2018). Diversity and antifungal activity of endophytic fungi associated with *Camellia oleifera*. *Mycobiology*, *46*, 85–91.

Yu, S. H. (2001). *Korea species of Alternaria and Stemphylium*. National Institute of Agricultural Science and Technology, Suwon, Korea.

Zapata, M., Palma, M. A., Aninat, M. J., & Piontelli, E. (2020). Polyphasic studies of new species of *Diaporthe* from native forest in Chile, with descriptions of *Diaporthe araucanorum* sp. nov., *Diaporthe foikelawen* sp. nov. and *Diaporthe patagonica* sp. nov. *International Journal of Systematic and Evolutionary Microbiology*, *70*, 3379–3390.

Zeller, S. M. (1934). Some new or noteworthy fungi on ericaceous hosts in the Pacific Northwest. *Mycologia, 26,* 291–304.

Zhang, J., Liu, J., Hyde, K. D., Chen, Y., Liu, Y., & Liu, Z. (2017). Two new species of *Dyfrolomyces* (Dyfrolomycetaceae, Dothideomycetes) from karst landforms. *Phytotaxa*, *313*, 267–277.

Zhang, K., Su, Y. Y., & Cai, L. (2013a). Morphological and phylogenetic characterization of two new species of *Phyllosticta* from China. *Mycolgical Progress*, *12*, 547–556.

Zhang, K., Zhang, N., & Cai, L. (2013b). Typification and phylogenetic study of *Phyllosticta ampelicida* and *P. vaccinii*. *Mycologia, 105,* 1030–1042.

Zhang, Q. T., He, M., Lu, Q., Liang, J., & Zhang, X. Y. (2013). Morphological and molecular identification of *Cytospora germanica* causing canker on *Populus* spp. in China. *Plant Disease*, *97*, 846.

Zhang, Q. T., Lu, Q., He, M., Decock, C., & Zhang, X. Y. (2014). *Cytospora palm* sp. nov. (Diaporthales, Ascomycota), a canker agent on *Cotinus coggygria* (Anacardiaceae) in Northern China. *Cryptogamie Mycologie*, *35*, 211–220.

Zhang, T. Y. (2003). *Flora Fungorum Sinicorum, Volume 16: Alternaria*. Science Press, Beijing, China.

Zhang, X., & Wang, W. (2015). Control of climate and litter quality on leaf litter decomposition in different climatic zones. *Journal of Plant Research*, *128*(5), 791–802.

Zhou, J., Diao, X., Wang, T., Chen, G., Lin, Q., Yang, X., & Xu, J. (2018). Phylogenetic diversity and antioxidant activities of culturable fungal endophytes associated with the mangrove species *Rhizophora stylosa* and *R. mucronata* in the South China Sea. *PLoS ONE*, *13*, e0197359.

Zhou, N., Chen, Q., Carroll, G., Zhang, N., Shivas, R. G., & Cai, L. (2015). Polyphasic characterization of four new plant pathogenic *Phyllosticta* species from China, Japan, and the United States. *Fungal Biology*, *119*, 433–446.

Zhu, H. Y., Tian, C. M., & Fan, X. L. (2018). Studies of botryosphaerialean fungi associated with canker and dieback of tree hosts in Dongling Mountain of China. *Phytotaxa*, *348*, 63–76.

Zhuang, W. Y. (2001). *Higher fungi of tropical China*. Mycotaxon, Ltd. Ithaca, NY.

Zhuang, W. Y. (2005). *Fungi of Northwestern China*. Mycotaxon, Ltd. Ithaca, NY.

APPENDICES

APPENDIX A

PUBLICATIONS

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RESEARCH ARTICLE

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Morphological and phylogenetic characterisation of novel *Cytospora* species associated with mangroves

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Abstract

Mangroves are relatively unexplored habitats and have been shown to harbour a number of novel species of fungi. In this study, samples of microfungi were collected from symptomatic branches, stem and leaves of the mangrove species *Xylocarpus granatum*, *X. moluccensis* and *Lumnitzera racemosa* and examined morphologically. The phylogeny recovered supports our morphological data to introduce three new species, *Cytospora lumnitzericola*, *C. thailandica* and *C. xylocarpi*. In addition, a combined multi-gene DNA sequence dataset (ITS, LSU, ACT and RPB2) was analysed to investigate phylogenetic relationships of isolates and help in a more reliable species identification.

Keywords

3 new species, Cytosporaceae, *Lumnitzera racemosa*, Mangroves, Phylogeny, Taxonomy, *Xylocarpus granatum*, *Xylocarpus moluccensis*

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Morphological and phylogenetic characterization of novel pestalotioid species associated with mangroves in Thailand

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Abstract

Pestalotioid fungi are associated with a wide variety of plants worldwide and are endophytes, pathogens and saprobes. The present study provides an updated phylogenetic placement of *Neopestalotiopsis*, *Pestalotiopsis* and *Pseudopestalotiopsis* using fresh collections from mangrove plants in Thailand. Twelve novel species are characterized based on combined sequence data analyses of internal transcribed spacer (ITS), beta tubulin (β-tubulin) and translation elongation factor 1-alpha (EF1α) coupled with morphological characters. The taxonomy and phylogenetic relationships of pestalotioid-fungi are reappraised with suggestions for future work.

Keywords – 12 new species – Asymptomatic leaves – *Acrostichum aureum* – *Avicenia marina* – Leaf spots – Mangroves – *Neopestalotiopsis* – *Pestalotiopsis* – pestalotiopsis-like – Phylogeny – *Pseudopestalotiopsis* – *Rhizophora* sp. – *Sonneronata alba* – Taxonomy

Introduction

Mangrove forests are one of the most productive ecosystems which play a major role in the ecological communities in coastal tropical and subtropical waters (Hyde & Lee 1995). They serve as hatcheries and nursery habitats for marine organisms and protect coastlines from catastrophic events such as storms and tidal surges (Hyde & Jones 1988, Fisher & Spalding 1993, Hyde & Lee 1995, Hyde et al. 1998). The greatest diversity of mangrove species occurs in Indonesia, Malaysia and Thailand, which also harbour a great diversity of micro-organisms especially fungi (Alias & Jones 2009, Alias et al. 2010). However, the phylogenetic and functional description of microbial diversity in mangrove ecosystems has not been addressed to the same extent as for other environments. Even though mangrove ecosystems are very rich in microbial diversity, less than 5% of species are believed to have been described (Thatoi et al. 2012). Recently developed technologies in molecular biology and genetics offer a great promise to explore the potential of microbial diversity. Hence, the present paper makes an effort to identify the species of fungi in

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Contributed Paper

Ficus microcarpa (Moraceae) and *Kandelia candel* (Rhizophoraceae), Two New Host Records for *Alternaria gaisen* from Taiwan

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ABSTRACT

Mangroves grow adjacent to estuarine regions of the tropics and subtropics. Fungi cause diseases in mangroves; however, it is not clear if the diseases are unique to mangrove species or ubiquitous. In this study, we identified a species of *Alternaria*, a genus comprising with saprobic and pathogenic species of a large number of plants. The genus is currently divided into 28 sections based on phylogenetic and morphological evidence. *Alternaria* is characterized by macronematous conidiophores, sympodial, polytretic conidiogenous cells, and obclavate to obovoid, muriform conidia gradually tapering towards beaked apex. We found *A. gaisen* associated with leaf blight of *Ficus microcarpa* and leaf spots of *Kandelia candel* from Taiwan. Phylogenetic analysis of combined SSU, LSU, ITS, *gapdh*, *rpb2*, *ef1a*, *Alta1*, *endoPG* and OPA10-2 sequence data supports positioning of our isolates as *A. gaisen* in section *Alternaria*. This species was first reported from Japanese pear causing black spot disease. This is also a new host record of *A. gaisen* from mangroves in Taiwan.

Keywords: new host record, mangroves, microfungi, phylogenetic analyses, pleosporaceae, *Alternaria gaisen*

1. INTRODUCTION

Alternaria Nees is a genus composed of many important plant pathogens as well as endophytic and saprobic species with a worldwide distribution [5], [59]. Species of *Alternaria* mainly inflict damage to pre- and post-harvest agricultural products [37]. Some *Alternaria* species produce secondary metabolites considered as phytotoxins (harmful to plants), and mycotoxins (harmful to humans and animals) [37].

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Differentiation of species complexes in *Phyllosticta* enables better species resolution

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Abstract

Phyllosticta species have worldwide distribution and are pathogens, endophytes, and saprobes. Taxa have also been isolated from leaf spots and black spots of fruits. Taxonomic identification of *Phyllosticta* species is challenging due to overlapping morphological traits and host associations. Herein, we have assembled a comprehensive dataset and reconstructed a phylogenetic tree. We introduce six species complexes of *Phyllosticta* to aid the future resolution of species. We also introduce a new species, *Phyllosticta rhizophorae* isolated from spotted leaves of *Rhizophora stylosa* in mangrove forests of Taiwan. Phylogenetic analysis based on combined sequence data of ITS, LSU, *ef1α*, *actin* and *gapdh* loci coupled with morphological evidence support the establishment of the new species. We synonymize strains of *P. capitalensis* (CPC 20508 and CPC20509) under the new species. Six strains (CBS 173.77, CBS 119720, CPC 17748, CPC 20252, CPC 20269, and CBS 123404) are unnamed species based on phylogenetic analyses and nucleotide polymorphisms and probably represent new species. The phylogenetic relationships of *Phyllosticta* species are reappraised and suggestions are given for future work.

Key words – 1 New Species – Microfungi – Morphology – Phylogenetic Analysis – Phyllostictaceae – Rhizophoraceae – Synonym – Taxonomy

Introduction

Mangroves are forests situated in intertidal zones in tropical and subtropical backwaters, estuaries, deltas, and lagoons. They are important for wetland ecosystems providing numerous valuable services to the marine environment. Mangroves provide protection to coastal communities against natural hazards such as cyclones, tsunamis, and shoreline erosion (Saenger 2002, FAO 2007). Mangroves are found in Africa, North and Central America and Asia, including Taiwan (Alias & Jones 2009, Alias et al. 2010). The fungi in mangoves are important in nutrient cycling helping to provide detritus and nutrients for mangrove inhabitants (Hyde & Jones 1988, Hyde &

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Diaporthe: Formalizing species-group concepts

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Norphanphoun C, Gentekaki E, Hongsanan S, Jayawardena R, Senanayake C, Manawasinghe I, Abeywickrama P, Bhunjun CS, Hyde KD 2022 – *Diaporthe*: Formalizing species-group concepts. Mycosphere X(X), X–X, Doi 10.5943/mycosphere/X/X/X

Abstract

Diaporthe species have a worldwide distribution and are associated with economically important hosts as pathogens, endophytes, and saprobes. Taxonomic identification of *Diaporthe* species is challenging due to overlapping morphological traits and host associations. Herein, we have assembled a comprehensive dataset and inferred a phylogenetic tree of Diaporthaceae using combined sequence data of ITS, *ef1α*, *β-tubulin*, *cal* and *his3*. *Diaporthe* is not monophyletic and splits into several phylogenetically distinct clades. We introduce 13 species complexes of *Diaporthe* to aid identification of species in the genus and to make communication easier. Nine species were kept as singletons. Two taxa of Diaporthaceae, *Ophiodiaporthe cyatheae* and *Chiangraiomyces bauhiniae*, are synonymized under *D. cyatheae* (≡ *O. cyatheae*) and *D. pseudobauhiniae* (≡ *C. bauhiniae*), respectively based on phylogenetic analyses and morphological characters. The phylogenetic relationships of Diaporthaceae are reappraised, and suggestions are given for future work.

Key words – Diaporthaceae – Morphology – Phylogeny – Plant disease – Species complexes

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Towards a backbone tree for *Seimatosporium*, with *S. physocarpi* sp. nov.

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Norphanphoun C, Maharachchikumbura SSN, Daranagama A, Bulgakov TS, Bhat DJ, Bahkali AH, Hyde KD 2015 – Towards a backbone tree for *Seimatosporium*, with *S. physocarpi* sp. nov. Mycosphere 6(3), 385–400, doi 10.5943/mycosphere/6/3/12

Abstract

The genus *Seimatosporium* is saprobic or pathogenic on plants, and are 'pestalotioid fungi'. The genus presently belongs in *Discosiaceae* (*Amphisphaeriales*) and includes 78 species epithets. In this study, we observed three specimens of *Seimatosporium* from Russia and they are characterized by morphological and sequence data. We analyzed combined ITS and LSU gene sequence data of 42 species representing the genera *Discostroma* (7), *Sarcostroma* (2) and *Seimatosporium* (32, including the three new strains) with *Pseudopestalotiopsis theae* as the outgroup taxon. One isolate from dead branches of *Physocarpus opulifolius* is unique and is introduced as *Seimatosporium physocarpi* sp. nov., in this paper. It can be distinguished from similar and related species by phenotypic conidial characters and phylogenetic analyses. A specimen from *Rosa kalmiussica* Chrshan. & Lasebna (often included in *Rosa canina sensu lato*) is designated as an epitype for *S. rosae*, the type of the genus. In addition, a collection of *S. lichenicola* is described, illustrated and compared with other species in the genus.

Key words – *Discosiaceae* – new species – phylogeny – epitype – combine gene – taxonomy.

Introduction

The genus *Seimatosporium* was introduced by Corda (1833), with *S. rosae* Corda as the type species. This genus is presently placed in the family the *Discosiaceae*, *Amphisphaeriales* (Senanayake et al. 2015). The sexual morph of *Seimatosporium* has been identified as *Discostroma*

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Lamproconiaceae *fam. nov.* to accommodate *Lamproconium desmazieri*

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Abstract

The genus *Lamproconium* comprises species that are endophytes, saprobes and pathogens on a wide variety of plants. This genus is currently placed in Diaporthales genera *incertae sedis*. Fresh specimens of *Lamproconium* were collected in Russia and studied to provide morphological and phylogenetic data. Phylogenetic analyses of single spore isolates generated from maximum likelihood, maximum parsimony and Bayesian inference analyses using combined ITS and LSU sequence data, place *L. desmazieri* in the order Diaporthales. *Melanconis desmazieri* is synonymized under *Lamproconium desmazieri*, and Lamproconiaceae is introduced as a new family to accommodate *L. desmazieri* and *Hercospora tiliae*, based on morphology and phylogenetic analyses.

Key words: Foliar pathogens, genera *incertae sedis*, morphological data, phylogenetic analyses, synonym

Introduction

Lamproconium (Grove) Grove was introduced as a monotypic genus by Grove (1937) to accommodate *L. desmazieri* (Berk. & Broome) Grove, and was placed in genera *incertae sedis* in the order Diaporthales by Cannon & Minter (2014). This genus is apparently a saprobe with an endophytic life style, or vice versa. Some authors, however, have considered a few species in this genus to be plant pathogens (Grove 1937, Cannon & Minter 2014, Sutton 1980).

The type species of *Lamproconium*, originally described as *Discella desmazieri* Berk. & Broome, was collected from twigs of lime (*Citrus aurantiifolia*) in the UK (Berkeley & Broome 1850). Grove (1918) transferred the species to *Melanconium* in the subgenus *Lamproconium* as *Melanconium desmazieri* (Berk. & Broome) Sacc. Subsequently, Grove (1937) found that *M. desmazieri* differed from the type species of *Melanconium* (*M. atrum* Link) in having bluish to glistening or dark blue, but not brownish black, 1-septate conidia and accordingly re-circumscribed the species. *Melanconium desmazieri* differed from species of *Discella* by the absence of a true peridium, whereas *Discella* species have a proliferous stratum at the base. Grove (1937) therefore considered *Discella desmazieri* and *Melanconium desmazieri* as conspecific and introduced a new genus *Lamproconium* to accommodate this taxon (Grove 1937, Sutton 1980).

Melanconium has been reported as the asexual morph of *Melanconis* Tul. & C. Tul. (Sutton 1980). The genus *Melanconis* belongs in the family Melanconidaceae in Diaporthales, Sordariomycetes (Maharachchikumbura *et al.* 2015, 2016). Castlebury *et al.* (2002) used LSU sequence data from *M. stilbostoma* (Fr.) Tul. & C. Tul., the type species of *Melanconis*, plus *M. alni* Tul. & C. Tul. and *M. marginalis* (Peck) Wehm. in a phylogenetic analysis and showed that *Melanconis desmazieri* Petr. clustered with *Hercospora tiliae* Tul. & C. Tul. However, the group clustered distantly from the family Melanconidaceae. Thus, Castlebury *et al.* (2002) placed *Melanconis desmazieri* and *Hercospora tiliae* in *Melanconis sensu lato* as genera *incertae sedis* in Diaporthales. This taxonomic treatment was followed by Voglmayr *et al.* (2012), Voglmayr & Jaklitsch (2014) and Maharachchikumbura *et al.* (2015, 2016).

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Revisiting the genus *Cytospora* and allied species

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Abstract

Cytospora species are important plant pathogens causing dieback and canker diseases on a wide range of hosts, worldwide. However, species level identification is difficult due to poor phylogenetic understanding and lack of sequenced type species. ITS sequence data are only available for most *Cytospora* strains in GenBank. In this study, samples of *Cytospora* were collected from symptomatic twigs and branches in European Russia. A combination of morphological characters and multi-gene phylogenetic analysis (ITS, LSU, RPB2, ACT) were used to identify taxa. A total of 34 collections, representing 17 fungal species of *Cytospora* were studied. Of these, 14 new species are described and illustrated. Three species were known taxa and identified as *C. nivea*, *C. parasitica*, and *C. salicicola*. Newly introduced species are *C. ampulliformis*, *C. curvata*, *C. donetzica*, *C. erumpens*, *C. longiostiolata*, *C. melnikii*, *C. parakantschavelii*, *C. paratranslucens*, *C. rusanovii*, *C. salicacearum*, *C. salicina*, *C. sorbi*, *C. sorbicola* and *C. ulmi*. Descriptions, illustrations and notes are provided for all studied taxa in this study. The distribution patterns of *Cytospora* species on different hosts are discussed. The study represents a preliminary study of *Cytospora* species from a small region and provides an initial contribution to the understanding of the genus.

Key words – Diaporthales – Morphology – Phylogenetic analyses – Plant pathogenic fungi – Russia – *Valsaceae*

Introduction

Cytospora was introduced by Ehrenberg (1818) and is one of the most important forest pathogenic genera causing canker disease on branches of various tree species. The disease often leads to large areas of dieback on a wide range of plants (Adams et al. 2005, 2006). *Cytospora* is the asexual morph of *Valsa*, which is the type genus of *Valsaceae* Tul. & C. Tul. in Diaporthales Nannf. comprising the genera *Amphicytostroma*, *Chadefaudiomyces*, *Cryptascoma*, *Cytospora*,

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Taxonomic position of *Melomastia italica sp. nov.* and phylogenetic reappraisal of Dyfrolomycetales

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Abstract – *Melomastia* is a genus of saprobic fungal species found on wood, with 29 species epithets listed in Index Fungorum. The classification of species in the genus has been a challenge due to a high degree of morphological overlap and a lack of DNA based phylogenies. The present study clarifies the phylogenetic placement of the genus and with an additional new species based on a fresh collection from Italy. The new species, *Melomastia italica*, is described based on morphological and relationships inferred from phylogenetic analyses of SSU and LSU sequence data. *Melomastia* is accommodated within the family *Pleurotremaceae* in the class Dothideomycetes. The phylogenetic relationships and intergeneric taxonomy within the family *Pleurotremaceae* are revisited, while *Dyfrolomyces maolanensis* is transferred to the genus *Melomastia*.

Genera *incertae sedis* / Dothideomycetes / Molecular analyses/ Morphology / Saprobic fungi

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Fungal diversity notes 111–252—taxonomic and phylogenetic contributions to fungal taxa

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Novel species of *Pestalotiopsis* fungi on *Dracaena* from Thailand

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ABSTRACT

A survey of the diversity and distribution of microfungi on *Dracaena* leaf litter in Songkhla Province (Thailand) yielded two collections of pestalotiopsis-like fungi. Analyses of a combined ITS, TEF1-α and TUB2 sequence data matrix were applied to infer the phylogenetic position of these new isolates in *Pestalotiopsis*. The phylogenies indicated that these two isolates were monophyletic and constituted a distinct lineage that perceived a taxonomic novelty in *Pestalotiopsis*. This clade shared a close phylogenetic affinity with *P. adusta, P. krabiensis, P. pandanicola* and *P. papuana*. The comparison of morphological features with the phylogenetically closely related taxa are given and the new species is introduced as *Pestalotiopsis dracaenicola* sp. nov. with comprehensive descriptions and illustrations herein.

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1 new taxon; multigene; phylogeny; saprobe; taxonomy

Introduction

Dracaena is a monocotyledon belonging to the family *Agavaceae* that are used as ornamentals, herbs or medicinal plants (Pires et al. 2004). *Dracaena* consists of about 550–600 species in 18 genera including various shrubs and trees (Pires et al. 2004; Mabberley 2008). Species of *Dracaena* are widely distributed in the tropics and subtropical regions of the world. In Europe and Canada, most *Dracaena* plants are cultivated as ornamentals (Ilodibia et al. 2015). *Dracaena marginata* an important ornamental plant exported as a popular houseplant, has been shown to reduce the levels of formaldehyde in the air (Jaminson 2012). Robiansyah and Hajar (2017) have shown that there is a decline in the population of *D. ombet* throughout its native ranges due to overgrazing, disease by pathogens, human overexploitation, and climate change. The conservation actions for these species are hindered due to poor information about their natural enemies. The plant associated fungi which can be pathogens/opportunistic pathogens, may directly relevant with quarantine measures when the plant is exported as ornamentals to different regions. In contrast to the detailed studies on other hosts such as grasses, bamboo and palms in Thailand, information is still limited on *Dracaena* based fungi. Some taxa occurring on dead leaves of *Dracaena* are *Colletotrichum gloeosporioides* (*D. sanderiana*) (Stev enson 1975), *Gloeosporium* sp. (*D. reflexa*) (Giatgong 1980), *Ophioceras chiangdaoense* (*D. loureiroi*) (Thon gkantha et al. 2009), *Parapallidocercospora thailandica* (*D. loureiroi*) (Hyde et al. 2016) and *Phaeosphaeriopsis dracaenicola* (*Dracaena loureiroi*) (Phookamsak et al. 2014). There have been two *Pestalotiopsis* species reported on *Dracaena fragrans: P. affinis* Y.X. Chen & G. Wei and *P. dracaenea* Yong Wang bis, Yu Song, K. Geng & K.D. Hyde.

We are investigating the microfungi associated with monocotyledons in Thailand which has a high species diversity (Dai et al. 2017; Hyde et al. 2018; Tibpromma et al. 2018). In this paper we introduce a novel species in *Pestalotiopsis* from *Dracaena* based on morphology coupled with multigene phylogeny.

Materials and methods

Isolates and morphology

Dracaena leaf litter was collected from Songkhla Province in Thailand during May 2018. Collected samples were brought to the laboratory in plastic bags. Specimens were observed with a stereomicroscope

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Mycosphere Notes 225–274: types and other specimens of some genera of *Ascomycota*

Doilom M[1,2,3], Hyde KD[2,3,6], Phookamsak R[1,2,3], Dai DQ[4], Tang LZ[4,14], Hongsanan S[5], Chomnunti P[6], Boonmee S[6], Dayarathne MC[6], Li WJ[6], Thambugala KM[6], Perera RH [6], Daranagama DA[6,13], Norphanphoun C[6], Konta S[6], Dong W[6,7], Ertz D[8,9], Phillips AJL[10], McKenzie EHC[11], Vinit K[6,7], Ariyawansa HA[12], Jones EBG[7], Mortimer PE[2], Xu JC[2,3], Promputtha I[1]

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Abstract

This is the fifth in a series, *Mycosphere notes*, wherein 50 notes are provided on types of genera and other specimens with descriptions and illustrations. This includes one genus in *Arthoniomycetes*, one genus in *Eurotiomycetes*, 38 genera in *Dothideomycetes*, six genera in *Sordariomycetes*, two genera in *Ascomycota*, families *incertae sedis*, one genus in *Pezizomycotina*, and one taxon, *Angatia rondoniensis*, is treated as a doubtful species. *Pycnocarpon magnificum* is classified in *Asterinaceae*. We reinstate *Eopyrenula* in *Dacampiaceae* on the basis of its

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Refined families of Dothideomycetes: orders and families incertae sedis in Dothideomycetes

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Abstract

Numerous new taxa and classifications of Dothideomycetes have been published following the last monograph of families of Dothideomycetes in 2013. A recent publication by Honsanan et al. in 2020 expanded information of families in Dothideomycetidae and Pleosporomycetidae with modern classifications. In this paper, we provide a refined updated document on orders and families *incertae sedis* of Dothideomycetes. Each family is provided with an updated description, notes, including figures to represent the morphology, a list of accepted genera, and economic and ecological significances. We also provide phylogenetic trees for each order. In this study, 31 orders which consist 50 families are assigned as orders *incertae sedis* in Dothideomycetes, and 41 families are treated as families *incertae sedis* due to lack of molecular or morphological evidence. The new order, Catinellales, and four new families, *Catinellaceae*, *Morenoinaceae Neobuelliellaceae* and *Thyrinulaceae* are introduced. Seven genera (*Neobuelliella*, *Pseudomicrothyrium*, *Flagellostrigula*, *Swinscowia*, *Macroconstrictolumina*, *Pseudobogoriella*, and *Schummia*) are introduced. Seven new species (*Acrospermum urticae*, *Bogoriella complexoluminata*, *Dothiorella ostryae*, *Dyfrolomyces distoseptatus*, *Macroconstrictolumina megalateralis*, *Patellaria microspora*, and *Pseudomicrothyrium thailandicum*) are introduced base on morphology and phylogeny, together with two new records/reports and five new collections from different families. Ninety new combinations are also provided in this paper.

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Extended author information available on the last page of the article

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Refined families of Dothideomycetes: Dothideomycetidae and Pleosporomycetidae

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Taxonomy and phylogeny of *Muyocopron thailandica* sp. nov.

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Abstract

A new fungus, *Muyocopron thailandica*, collected from a dead plant sample in northern Thailand, is described and compared with other described species of *Muyocopron*. Multi-gene phylogenetic analyses based on LSU and ITS sequence data indicated that *M. thailandica* forms a distinct lineage within the genus *Muyocopron*, and is closely related to *M. castanopsis* and *M. lithocarpi*. *Muyocopron thailandica* differs from these two species in having ellipsoid to subcylindrical asci, with a very short and thin pedicel and oval to obovoid ascospores. Asci and ascospores of *M. thailandica* are larger than those of *M. castanopsis* and *M. lithocarpi*. Morphological description and a detailed illustration of the new species are provided.

Keywords: Ascomycota, Dothideomycetes, microfungi, morphology, molecular systematics, Thailand

Introduction

Muyocopronaceae K.D. Hyde was invalidly established by Luttrell (1951), with *Muyocopron* Speg. as the type genus. The family was validly introduced by Hyde *et al.* (2013). *Muyocopron* was introduced by Spegazzini (1881), with the type species *M. corrientinum* Speg. Saccardo (1883) re-described *Muyocopron* and placed it in *Microthyriaceae* Sacc. However, *Muyocopron* differs from the members of *Microthyriaceae* in having pseudothyriothecia which comprise two-layered peridial wall, pseudoparaphyses longer than that of the asci, and non-septate ascospores (Hyde *et al.* 2013). Furthermore, Hyde *et al.* (2013) formally introduced *Muyocopronaceae* as a family *incertae sedis* in Dothideomycetes O.E. Eriksss. & Winka. However, Mapook *et al.* (2016a) provided fresh collections of *Muyocopron* with sequence data to clarify its taxonomic placement. The phylogenetic analysis of combined dataset in Mapook *et al.* (2016a) showed that *Muyocopron* is distantly related to *Microthyriaceae* within Dothideomycetes, and clustered with *Dyfrolomycetaceae* K.D. Hyde *et al.* (Dyfrolomycetales K.L. Pang). Therefore, Mapook *et al.* (2016a) introduced Muyocopronales Mapook *et al.* to accommodate *Muyocopronaceae* which comprises a single genus *Muyocopron*. This was followed by Tibpromma *et al.* (2016), Wijayawardene *et al.* (2017), and Senwanna *et al.* (2019). Hernández-Restrepo *et al.* (2019) provided several new sequence data related to Muyocopronales and added more genera in *Muyocopronaceae* based

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https://www.coelomycetes.org: Databank that contributes for the classification, identification and nomenclature of Coelomycetes

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Abstract

Over the years, there have been continuous updates in the taxonomy of coelomycetes. In particular, traditional classification has been revised and updated based on extensive collections supplemented with morphological examinations and phylogenetic analyses. Most of the data available are scattered in the literature. In an attempt to ease the work of mycologists and bring all these data together, a website has been created, available at https://www.coelomycetes.org. Information provided on the webpage is in line with the current ranking and classification of taxa and will include photoplates, drawings, phylogenetic trees, notes and descriptions.

Keywords – asexual fungi – conidiogenesis – curators – database – website

Introduction

Coelomycetes is an artificial group known as imperfect fungi. It was introduced by Grove (1919) to accommodate the asexual morphs of fungi such as *Phomopsis*, *Phloeospora* and

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Fungal diversity notes 367–490: taxonomic and phylogenetic contributions to fungal taxa

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Fungal diversity notes 603–708: taxonomic and phylogenetic notes on genera and species

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Abstract
This is the sixth in a series of papers where we bring collaborating mycologists together to produce a set of notes of several taxa of fungi. In this study we introduce a new family *Fuscostagonosporaceae* in Dothideomycetes. We also introduce the new ascomycete genera *Acericola*, *Castellaniomyces*, *Dictyosporina* and *Longitudinalis* and new species *Acericola italica*, *Alternariaster trigonosporus*, *Amarenomyces dactylidis*, *Angustimassarina coryli*, *Astrocystis bambusicola*, *Castellaniomyces rosae*, *Chaetothyrina artocarpi*, *Chlamydotubeufia krabiensis*, *Colletotrichum lauri*, *Collodiscula chiangraiensis*, *Curvularia palmicola*, *Cytospora mali-sylvestris*, *Dictyocheirospora cheirospora*, *Dictyosporina ferruginea*, *Dothiora coronillae*, *Dothiora spartii*, *Dyfrolomyces phetchaburiensis*, *Epicoccum cedri*, *Epicoccum pruni*, *Fasciatispora calami*, *Fuscostagonospora cytisi*, *Grandibotrys hyalinus*, *Hermatomyces nabanheensis*, *Hongkongmyces thailandica*, *Hysterium rhizophorae*, *Jahnula guttulaspora*, *Kirschsteiniothelia rostrata*, *Koorchalomella salmonispora*, *Longitudinalis nabanheensis*, *Lophium zalerioides*, *Magnibotryascoma mali*, *Meliola clerodendri-infortunati*, *Microthyrium chinense*, *Neodidymelliopsis moricola*, *Neophaeocryptopus spartii*, *Nigrograna thymi*, *Ophiocordyceps cossidarum*, *Ophiocordyceps issidarum*, *Ophiosimulans plantaginis*, *Otidea pruinosa*, *Otidea stipitata*, *Paucispora kunmingense*, *Phaeoisaria microspora*, *Pleurothecium floriforme*, *Poaceascoma halophila*, *Periconia aquatica*, *Periconia submersa*, *Phaeosphaeria acaciae*, *Phaeopoacea muriformis*, *Pseudopithomyces kunmingnensis*, *Ramgea ozimecii*, *Sardiniella celtidis*, *Seimatosporium italicum*, *Setoseptoria scirpi*, *Torula gaodangensis* and *Vamsapriya breviconidiophora*. We also provide an amended account of *Rhytidhysteron* to include apothecial ascomata and a J+ hymenium. The type species of *Ascotrichella*

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Thailand's amazing diversity: up to 96% of fungi in northern Thailand may be novel

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Abstract
Fungi have been often neglected, despite the fact that they provided penicillin, lovastatin and many other important medicines. They are an understudied, but essential, fascinating and biotechnologically useful group of organisms. The study of fungi in northern Thailand has been carried out by us since 2005. These studies have been diverse, ranging from ecological aspects, phylogenetics with the incorportation of molecular dating, taxonomy (including morphology and chemotaxonomy) among a myriad of microfungi, to growing novel mushrooms, and DNA-based identification of plant pathogens. In this paper, advances in understanding the biodiversity of fungi in the region are discussed and compared with those further afield. Many new species have been inventoried for the region, but many unknown species remain to be described and/or catalogued. For example, in the edible genus *Agaricus*, over 35 new species have been introduced from northern Thailand, and numerous other taxa await description. In this relatively well known genus, 93% of species novelty is apparent. In the microfungi, which are relatively poorly studied, the percentage of novel species is, surprisingly, generally not as high (55–96%). As well as Thai fungi, fungi on several hosts from Europe have been also investigated. Even with the well studied European microfungi an astounding percentage of new taxa (32–76%) have been discovered. The work is just a beginning and it will be a daunting task to document this astonishingly high apparent novelty among fungi.

Keywords *Agaricus* · *Amanita* · *Colletotrichum* · *Cornus* · Fungal diversity · Pandanaceae · Rosaceae · *Rosa* · Teak fungi

Introduction

Fungi are an incredibly understudied, but an essential, fascinating and biotechnologically useful group of organisms. The fungi of northern Thailand have been studied by Hyde and coworkers since 2005. The studies have been diverse, ranging across ecology, traditional taxonomy, phylogenetics, evolution, microbial community and chemotaxonomy (Thongkantha et al. 2008; Pinnoi et al. 2010; Phookamsak et al. 2015; Wurzbacher et al. 2017; Norphanphoun et al. 2018; Tedersoo et al. 2018), to growing novel mushrooms (Thongklang et al. 2014), molecular identification of endophytes and plant pathogens (Jayawardena et al. 2016b; Doilom et al. 2017b), and identification of entomophagous fungi (Xiao et al. 2017, 2018).

Although there are many negative facets to fungi (see Hyde et al. 2018), they are an essential component of most ecosystems and without them there would be ecological imbalance, and possibly mankind would not survive on earth (Watkinson et al. 2015). They are major contributors to nutrient cycling, and the main organisms which can degrade lignocellulose in wood and leaves (Pointing et al. 2005; Bucher et al. 2004; Tang et al. 2005); without them we would live amongst mountains of dead trees (Gadd et al. 2007). Many species exist as symbionts with plants

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Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa

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Abstract
This article is the tenth series of the Fungal Diversity Notes, where 114 taxa distributed in three phyla, ten classes, 30 orders and 53 families are described and illustrated. Taxa described in the present study include one new family (viz. Pseudoberkleasmiaceae in Dothideomycetes), five new genera (*Caatingomyces*, *Cryptoschizotrema*, *Neoacladium*, *Paramassaria* and *Trochilispora*) and 71 new species, (viz. *Acrogenospora thailandica*, *Amniculicola aquatica*, *A. guttulata*, *Angustimassarina sylvatica*, *Blackwellomyces lateris*, *Boubovia gelatinosa*, *Buellia viridula*, *Caatingomyces brasiliensis*, *Calophoma humuli*, *Camarosporidiella mori*, *Canalisporium dehongense*, *Cantharellus brunneopallidus*, *C. griseotinctus*, *Castanediella meliponae*, *Coprinopsis psammophila*, *Cordyceps succavus*, *Cortinarius minusculus*, *C. subscotoides*, *Diaporthe italiana*, *D. rumicicola*, *Diatrypella delonicis*, *Dictyocheirospora aquadulcis*, *D. taiwanense*, *Digitodesmium chiangmaiense*, *Distoseptispora dehongensis*, *D. palmarum*, *Dothiorella styphnolobii*, *Ellisembia aurea*,

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AJOM new records and collections of fungi: 1–100

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Refined families of Sordariomycetes

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The numbers of fungi: is the descriptive curve flattening?

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Abstract
The recent realistic estimate of fungal numbers which used various algorithms was between 2.2 and 3.8 million. There are nearly 100,000 accepted species of Fungi and fungus-like taxa, which is between 2.6 and 4.5% of the estimated species. Several forums such as Botanica Marina series, Fungal Diversity notes, Fungal Biodiversity Profiles, Fungal Systematics and Evolution—New and Interesting Fungi, Mycosphere notes and Fungal Planet have enhanced the introduction of new taxa and nearly 2000 species have been introduced in these publications in the last decade. The need to define a fungal species more accurately has been recognized, but there is much research needed before this can be better clarified. We address the evidence that is needed to estimate the numbers of fungi and address the various advances that have been made towards its understanding. Some genera are barely known, whereas some plant pathogens comprise numerous species complexes and numbers are steadily increasing. In this paper, we examine ten genera as case studies to establish trends in fungal description and introduce new species in each genus. The genera are the ascomycetes *Colletotrichum* and *Pestalotiopsis* (with many species or complexes), *Atrocalyx*, *Dothiora*, *Lignosphaeria*, *Okeanomyces*, *Rhamphoriopsis*, *Thozetella*, *Thyrostroma* (relatively poorly studied genera) and the basidiomycete genus *Lepiota*. We provide examples where knowledge is incomplete or lacking and suggest areas needing further research. These include (1) the need to establish what is a species, (2) the need to establish how host-specific fungi are, not in highly disturbed urban areas, but in pristine or relatively undisturbed forests, and (3) the need to establish if species in different continents, islands, countries or regions are different, or if the same fungi occur worldwide? Finally, we conclude whether we are anywhere near to flattening the curve in new species description.

Keywords 11 new taxa · *Atrocalyx* · *Colletotrichum* · *Dothiora* · fungal numbers · Host-specificity · *Lepiota* · *Lignosphaeria* · *Okeanomyces* · *Pestalotiopsis* · *Rhamphoriopsis* · *Thozetella* · *Thyrostroma*

Introduction

The estimated numbers of fungi have always been a compelling topic with numerous discussion papers over time. Mycologists have always pondered over how many fungal species there are, as this has important implications for conservation practices. Fungi, including the seen mushrooms and unseen microorganisms are diverse and form an integral component of life's genetic diversity, but their actual numbers are poorly understood and the estimates available so far are debatable. Hawksworth (1991) provide a comprehensive account and argument for the numbers being 1.5 million. This was based on, amongst other metrics, there being circa six taxa as unique to each plant species. Since this critical paper, there have been several revisions (Table 1) with estimates ranging from 0.5 to 13.2 million, and the latest estimate being 11.7–13.2 million (Wu et al. 2019). Hawksworth and Lücking (2017) based their estimates (2.2–3.8 M), taking into account cryptic species, the rates and patterns at which new species are being described, unexplored niches and DNA based species from environmental DNA. New generation sequencing has also provided

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https://onestopshopfungi.org/, a database to enhance identification of phytopathogenic genera

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Abstract

Correct taxonomic identification of phytopathogens is essential as there is a need to gather precise stored information on different genera. It is important to scientifically document and records the diversity of fungal pathogens in order to collate information, as well as for utilizing the data efficiently. Fungal databases need to play an essential role in the documentation of fungal pathogens. There are numerous fungal databases which provide lists of fungal names, literature, DNA sequence and morphological data to facilitate morpho-molecular identification, however, few are dedicated to the identification of phytopathogens. For this reason, a web-based platform is established, namely https://www.onestopshopfungi.org to fill the void, as well to enhance the identification of phytopathogenic genera based on the *One Stop Shop* publication series. This paper introduces the database, explains its function, provides data on the information it includes and how to use it and invites plant pathologists to participate in building the database.

Keywords – One stop shop – Molecular phylogeny – Symptoms – Plant pathogens

Introduction

Fungi have their own unique cell biology and life cycle and also play critical roles in wider

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One stop shop III: taxonomic update with molecular phylogeny for important phytopathogenic genera: 51–75 (2019)

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Abstract
This is a continuation of a series focused on providing a stable platform for the taxonomy of phytopathogenic fungi and organisms. This paper focuses on 25 phytopathogenic genera: *Alternaria*, *Capnodium*, *Chaetothyrina*, *Cytospora*, *Cyphellophora*, *Cyttaria*, *Dactylonectria*, *Diplodia*, *Dothiorella*, *Entoleuca*, *Eutiarosporella*, *Fusarium*, *Ilyonectria*, *Lasiodiplodia*, *Macrophomina*, *Medeolaria*, *Neonectria*, *Neopestalotiopsis*, *Pestalotiopsis*, *Plasmopara*, *Pseudopestalotiopsis*, *Rosellinia*, *Sphaeropsis*, *Stagonosporopsis* and *Verticillium*. Each genus is provided with a taxonomic background, distribution, hosts, disease symptoms, and updated backbone trees. A new database (Onestopshopfungi) is established to enhance the current understanding of plant pathogenic genera among plant pathologists.

Keywords Classification · Database · Plant pathology · Phylogeny · Taxonomy · Symptoms · Systematics

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An online resource for marine fungi

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Abstract
Index Fungorum, Species Fungorum and MycoBank are the key fungal nomenclature and taxonomic databases that can be sourced to find taxonomic details concerning fungi, while DNA sequence data can be sourced from the NCBI, EBI and UNITE databases. Nomenclature and ecological data on freshwater fungi can be accessed on http://fungi.life.illinois.edu/, while http://www.marinespecies.org/provides a comprehensive list of names of marine organisms, including information on their synonymy. Previous websites however have little information on marine fungi and their ecology, beside articles that deal with marine fungi, especially those published in the nineteenth and early twentieth centuries may not be accessible to those working in third world countries. To address this problem, a new website www.marinefungi.org was set up and is introduced in this paper. This website provides a search facility to genera of marine fungi, full species descriptions, key to species and illustrations, an up to date classification of all recorded marine fungi which includes all fungal groups (Ascomycota, Basidiomycota, Blastocladiomycota, Chytridiomycota, Mucoromycota and fungus-like organisms e.g. Thraustochytriales), and listing recent publications. Currently, 1257 species are listed in the marine fungi website (www.marinefungi.org), in 539 genera, 74 orders, 168 families, 20 classes and five phyla, with new taxa continuing to be described. The website has curators with specialist mycological expertise who help to provide update data on the classification of marine fungi. This article also reviews knowledge of marine fungi covering a wide range of topics: their higher classification, ecology and world distribution, role in energy transfer in the oceans, origin and new chemical structures. An updated classification of marine fungi is also included. We would like to invite all mycologists to contribute to this innovative website.

Keywords Fungal classification · marine fungi website · High-throughput sequencing techniques · Fungal diversity · Origin of marine fungi

Introduction

Marine fungi have been studied since the first record of the species *Sphaeria posidoniae* (= *Halotthia posidoniae*) on the rhizome of the sea grass *Posidonia oceanica* in Algeria by Durieu and Montagne (in Montagne 1856), but as yet there has been no webpage to accommodate all of the information on these organisms. This review introduces the website, www.marinefungi.org which has been developed to provide an up-to-date compendium on marine fungi.

There have been various definitions as to what a marine fungus is, the generally quoted one is by Kohlmeyer and Kohlmeyer (1979): "obligate marine fungi are those that grow and sporulate exclusively in a marine or estuarine habitat". Jones et al. (2015) broadened this as they were of the opinion it was too narrow and they included marine derived fungi, as many are taxa isolated during bioprospecting for new secondary metabolites (Fenical and Jensen 1993; Fenical et al. 1998). Marine derived fungi are

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Fungal Systematics and Evolution: FUSE 3

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Krisai-Greilhuber I., Chen Y., Jabeen S., Madrid H., Marincowitz S., Razaq A., Ševčíková H., Voglmayr H., Yazici K., Aptroot A., Aslan A., Boekhout T., Borovička J., Crous P.W., Ilyas S., Jami F., Jiang Y.-L., Khalid A.N., Kolecka A., Konvalinková T., Norphanphoun C., Shaheen S., Wang Y., Wingfield M.J., Wu S.-P., Wu Y.-M. & Yu J.-Y. (2017): Fungal Systematics and Evolution: FUSE 3. – Sydowia 69: 229-264.

The present study introduces seven new species, one new combination, one new variety and several interesting taxonomical notes and/or geographical records. Most of the new taxa are Ascomycetes, but the study also includes a new variety of a Basidiomycete. Novel species include *Gyromitra khanspurensis* (Discinaceae, Pezizales, Pezizomycetes) from Pakistan growing near *Cedrus deoadara* and *Paramyrothecium guiyangense* and *Paramyrothecium verruridum* (Stachybotriaceae, Hypocreales, Sordariomycetes) both isolated from soil in China. New species from South Africa are *Sclerostagonospora elegiae* on culm litter of *Elegia equisetacea, Sclerostagonospora fusiformis* on culm litter of *Thamnochortus spicigerus, Sclerostagonospora pinguis* on culm litter of *Cannomois virgata* and *Sclerostagonospora sulcata* on culm litter of *Ischyrolepis subverticellata* (Phaeosphaeriaceae, Pleosporales, Dothideomycetes). *Hapalocystis berkeleyi* var. *kickxii* with its basionym *Hypoxylon kickxii* is shown to be a taxon on species level and thus recombined as *Hapalocystis kickxii* (Sydowiellaceae, Diaporthales, Sordariomycetes), and it is lecto- and epitypified. The new variety *Pluteus romellii* var. *luteoalbus* (Pluteaceae, Agaricales, Agaricomycetes) growing on a mossy fallen stem of a deciduous tree is described from Czech Republic. *Cortinarius scaurocaninus* (Cortinariaceae, Agaricales, Agaricomycetes) is new for Austria, *Humicola grisea* (Chaetomiaceae, Sordariales, Sordariomycetes) is an interesting new record for Chile. Two taxa are reported as new for Turkey: the lichenicolous fungus *Opegrapha parasitica* (Opegraphaceae, Arthoniales, Arthoniomycetes) growing partly immersed in the thallus of *Aspicilia* and the lichen *Rinodina zwackhiana* (Physciaceae, Teloschistales, Lecanoromycetes) from calcareous rock. Finally, *Xerula strigosa* (Physalacriaceae, Agaricales, Agaricomycetes), described from China, is confirmed to be present also in Pakistan.

Keywords: biodiversity, ITS barcodes, phylogeny, systematics.

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Fungal diversity notes 253–366: taxonomic and phylogenetic contributions to fungal taxa

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Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species

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Towards a natural classification and backbone tree for *Sordariomycetes*

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Abstract
Sordariomycetes is one of the largest classes of *Ascomycota* and is characterised by perithecial ascomata and inoperculate unitunicate asci. The class includes many important plant pathogens, as well as endophytes, saprobes, epiphytes, and fungicolous, lichenized or lichenicolous taxa. The class includes freshwater, marine and terrestrial taxa and has a worldwide distribution. This paper provides an updated outline of the *Sordariomycetes* and a backbone tree incorporating asexual and sexual genera in the class. Based on phylogeny and morphology we introduced three subclasses; *Diaporthomycetidae, Lulworthiomycetidae* and *Meliolomycetidae* and five orders; *Amplistromatales*, *Annulatascales*, *Falcocladiales*, *Jobellisiales* and

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Families of Sordariomycetes

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Abstract Sordariomycetes is one of the largest classes of Ascomycota that comprises a highly diverse range of fungi characterized mainly by perithecial ascomata and inoperculate unitunicate asci. The class includes many important plant pathogens, as well as endophytes, saprobes, epiphytes, coprophilous and fungicolous, lichenized or lichenicolous taxa. They occur in terrestrial, freshwater and marine habitats worldwide. This paper reviews the 107 families of the class

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https://fungalgenera.org/: a comprehensive database providing web-based information for all fungal genera

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Abstract

Maintaining and updating databases and checklists of genera of fungi is an essential task for most fungal research. Advances in molecular techniques in the last 20 years have greatly influenced the fungal taxonomy and classification. Consequently, it is important to have access to all existing data and for these data to be continuously updated with recent changes. To address this issue, a website: https://fungalgenera.org/, was established in 2017 and introduced in this paper. This website provides basic information and links to data for all fungal genera with easily accessible and searchable functions.

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Article

Discovery of Three Novel *Cytospora* Species in Thailand and Their Antagonistic Potential

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Abstract: During an ongoing research survey of saprobic fungi in Thailand, four coelomycetous strains were isolated from decaying leaves in Chiang Mai and Phitsanulok Provinces. Morphological characteristics demonstrated that these taxa are typical of *Cytospora* in forming multi-loculate, entostromatic conidiomata, branched or unbranched conidiophores, with enteroblastic, phialidic conidiogenous cells and hyaline, allantoid, aseptate conidia. Multiloci phylogeny of ITS, LSU, ACT, RPB2, TEF1-α and TUB2 confirmed these taxa are distinct new species in *Cytospora* in Cytosporaceae (Diaporthales, Sordariomycetes), viz., *Cytospora chiangmaiensis*, *C. phitsanulokensis* and *C. shoreae*. *Cytospora chiangmaiensis* has a close phylogenetic relationship with *C. shoreae*, while *C. phitsanulokensis* is sister to *C. acaciae*. These three novel species were also preliminary screened for their antagonistic activity against five plant pathogenic fungi: *Colletotrichum fructicola*, *Co. siamense*, *Co. artocarpicola*, *Co. viniferum* and *Fusarium sambucinum*. *Cytospora shoreae* and *C. phitsanulokensis* showed >60% inhibition against *Co. viniferum* and *F. sambucinum*, while *C. chiangmaiensis* had moderate inhibition activity against all pathogens.

Keywords: antifungal activity; coelomycetous fungi; Cytosporaceae; multiloci phylogeny; saprobes; taxonomy

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1. Introduction

Cytospora Ehrenb. is mainly characterized by the coelomycetous asexual morph producing single or labyrinthine, loculate stromata, filamentous conidiophores, with enteroblastic, phialidic conidiogenous cells and hyaline, allantoid, aseptate conidia [1–3]. The sexual morph of *Cytospora* is characterized as solitary, immersed to erumpent ascostromata, composed of prosenchymatous or pseudoparenchymatous cells of valsoid or diatrypelloid configurations, embedded in ectostromatic disc, present or absent paraphyses, J-, ellipsoid to clavate asci with refractive apical ring, and hyaline, ellipsoid to allantoid, aseptate ascospores [1,4,5]. Ehrenberg [6] initially introduced the genus *Cytospora* to accommodate four species, *C. betulina*, *C. epimyces*, *C. resinae* and *C. ribis*. The type species, *C. chrysosperma*, was introduced by Donk [7] as the asexual morph of *Valsa sordida* [8]. *Cytospora* was previously treated as the asexual morph of *Valsa* and other related genera, *Leucocytospora*, *Leucostoma*, *Valsella* and *Valseutypella* [4,8,9]. Based on the International Code of Nomenclature for Algae, Fungi, and Plants (ICN) [10], Rossman et al. [8] recommended to use *Cytospora* instead of *Valsa* as *Cytospora* was prior introduced and thus *Valsa* was treated as

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Schizothyriaceae

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Abstract

Schizothyriaceae is a poorly understood family which was introduced to accommodate epiphytes belonging to the class Dothideomycetes. Sixteen sexual and asexual genera have at various times been accommodated in *Schizothyriaceae*. However, modern taxonomic descriptions, molecular data and phylogenetic investigation of the genera in this family are limited. We therefore revisit the genera in *Schizothyriaceae* by loaning and examining the type and other specimens from herbaria worldwide. Circumscriptions of the genera previously placed in *Schizothyriaceae* are provided with illustrations and their higher level placements are determined based on modern descriptions. Based on morphology, we currently accept *Hexagonella*, *Lecideopsella*, *Mycerema*, *Plochmopeltis* and *Schizothyrium* in *Schizothyriaceae*. *Kerniomyces*, *Metathyriella* and *Myriangiella* are treated in *Schizothyriaceae*, *genera incertae sedis*, while *Chaetoplaca* is transferred to Ascomycetes, *genera incertae sedis*. *Neopeltella* is excluded from *Schizothyriaceae*, based on its thyriothecial ascomata and tentatively placed in *Micropeltidaceae*. *Henningsiella* is placed in *Saccardiaceae* due to its discoid ascomata. *Linopeltis* and *Orthobellus* are tentatively treated in Dothideomycetes, *genera incertae sedis*. *Hysteropeltella* which has elongate apothecial or hypothecia-like ascomata, is placed in *Patellariaceae* due to its similar morphology with *Baggea*. *Mendogia* is transferred to the family *Myriangiaceae* based on a morphologically similar specimen which is phylogenetically placed in *Myriangiaceae*. The hyphomycetous, *Zygophiala* is reported as the asexual morph of *Schizothyrium*. Hence, the genus is currently treated as a synonym of *Schizothyrium*. Nevertheless, representative species of the genera in *Schizothyriaceae*, including the type species, need to be recollected and sequenced to clarify the natural placement in *Schizothyriaceae*.

Keywords – asexual morph – epifoliar fungi – epiphytic fungi – *Schizothyrium*– taxonomy

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Towards a natural classification of *Ophiobolus* and ophiobolus-like taxa; introducing three novel genera *Ophiobolopsis*, *Paraophiobolus* and *Pseudoophiobolus* in *Phaeosphaeriaceae* (Pleosporales)

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Abstract
Ophiobolus is a large genus of *Phaeosphaeriaceae* comprising more than 350 possible species, most of which are saprobes on herbaceous plants in Europe and North America. *Ophiobolus* species are polyphyletic and the type of *Ophiobolus* is not represented in GenBank. Therefore, an increased taxon sampling of ophiobolus-like taxa and epitypification of the type species, *O. disseminans* is reported. Multigene phylogenetic analyses of combined LSU, SSU, TEF1-α and ITS sequence data position *O. disseminans* in a sister clade with *O. ponticus* and several *Entodesmium* species in *Phaeosphaeriaceae* with high support. Therefore, *Entodesmium* is synonymized under *Ophiobolus*. *Premilcurensis* with it type species, *P. senecionis* also clusters within the *Ophiobolus* clade and is synonymized under *Ophiobolus*. *Ophiobolus rossicus* sp. nov. is introduced and a reference specimen is designated for *O. ponticus*. Other ophiobolus-like taxa (*Ophiobolus sensu lato*) can be distinguished as three main groups, which are introduced as new genera. *Ophiobolopsis* is introduced to accommodate the new species, *Ophiobolopsis italica*. The new genus *Paraophiobolus* is introduced to accommodate *P. arundinis* sp. nov. and *P. plantaginis* comb. nov. This genus is characterized by hyaline to pale yellowish ascospores, some green-yellowish at maturity, with a swollen cell, terminal appendages and ascospores not separating into part spores. *Pseudoophiobolus* gen. nov. is introduced to accommodate six new species and two new combinations, viz. *Ps. achilleae*, *Ps. erythrosporus*, *Ps. galii*, *Ps. italicus*, *Ps. mathieui*, *Ps. rosae*, *Ps. subhyalinisporus* and *Ps. urticicola*. *Pseudoophiobolus* is characterized by subhyaline to pale yellowish or yellowish ascospores, with a swollen cell, lack of terminal appendages and ascospores that do not separate into part spores and is related to *Nodulosphaeria*. An updated tree for *Phaeosphaeriaceae* based on multigene analysis is also provided.

Keywords 7 new combinations · 11 new taxa · Dothideomycetes · Epitypification

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Fungal diversity notes 929–1035: taxonomic and phylogenetic contributions on genera and species of fungi

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Abstract
This article is the ninth in the series of Fungal Diversity Notes, where 107 taxa distributed in three phyla, nine classes, 31 orders and 57 families are described and illustrated. Taxa described in the present study include 12 new genera, 74 new species, three new combinations, two reference specimens, a re-circumscription of the epitype, and 15 records of sexual-asexual morph connections, new hosts and new geographical distributions. Twelve new genera comprise *Brunneofusispora*, *Brunneomurispora*, *Liua*, *Lonicericola*, *Neoeutypella*, *Paratrimmatostroma*, *Parazalerion*, *Proliferophorum*, *Pseudoastrosphaeriellopsis*, *Septomelanconiella*, *Velebitea* and *Vicosamyces*. Seventy-four new species are *Agaricus memnonius*, *A. langensis*, *Aleurodiscus patagonicus*, *Amanita flavoalba*, *A. subtropicana*, *Amphisphaeria mangrovei*, *Baorangia major*, *Bartalinia kunmingensis*, *Brunneofusispora sinensis*, *Brunneomurispora lonicerae*, *Capronia camelliae-yunnanensis*, *Clavulina thindii*, *Coniochaeta simbalensis*, *Conlarium thailandense*, *Coprinus trigonosporus*, *Liua muriformis*, *Cyphellophora filicis*, *Cytospora ulmicola*, *Dacrymyces invisibilis*, *Dictyocheirospora metroxylonis*, *Distoseptispora thysanolaenae*, *Emericellopsis koreana*, *Galiicola baoshanensis*, *Hygrocybe lucida*, *Hypoxylon teeravasati*,

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Towards unraveling relationships in *Xylariomycetidae* (*Sordariomycetes*)

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Abstract The classification of subclass *Xylariomycetidae* is revisited with additional collections and phylogeny based on novel rDNA sequence data. Phylogenetic inferences are provided and are based on analysis of 115 sequence data, including new data for 27 strains. An updated outline to the subclass is presented based on the phylogenies and comprises two orders, 18 families and 222 genera. An account of each order, family and genus in the subclass is given. We accept the orders *Amphisphaeriales* and *Xylariales* based on morphological and phylogenetic evidence. *Amphisphaeriales* comprises *Amphisphaeriaceae*, *Bartaliniaceae* fam. nov., *Clypeosphaeriaceae*, *Discosiaceae* fam. nov., *Pestalotiopsidaceae* fam. nov. and *Phlogicylindriaceae* fam. nov. *Xylariales* comprises *Apiosporaceae*, *Cainiaceae*, *Coniocessiaceae*, *Diatrypaceae*, *Graphostromataceae* (doubtful), *Hyponectriaceae*, *Iodosphaeriaceae*, *Lopadostomaceae* fam. nov., *Melogrammataceae*, *Pseudomassariaceae* fam. nov., *Vialaeaceae* and *Xylariaceae*. The new genera and species introduced are *Arthrinium hyphopodii*, *A. subglobosa*, *Cainia anthoxanthis*, *Ciferriascosea* gen. nov., *C. fluctamurum*, *C. rectamurum*, *Discosia neofraxinea*, *D. pseudopleurochaeta*, *Hyalotiella rubi*, *Seimatosporium cornii*, *S. ficeae*, *S. vitis* and *Truncatella spartii*.

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Families of *Diaporthales* based on morphological and phylogenetic evidence

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Abstract: *Diaporthales* is an important ascomycetous order comprising phytopathogenic, saprobic, and endophytic fungi, but interfamilial taxonomic relationships are still ambiguous. Despite its cosmopolitan distribution and high diversity with distinctive morphologies, this order has received relativelyiaceae, *Macrohilaceae*, *Melanconidaceae*, *Pseudoplagiostomaceae*, *Schizoparmaceae*, *Stilbosporaceae* and *Sydowiellaceae*. Taxonomic uncertainties among genera are also clarified and recurrent discrepancies in the taxonomic position of families within the *Diaporthales* are discussed. An updated outline and key to families and genera of the order is presented.

Key words: Multi-gene DNA phylogeny, New taxonomic arrangement, Phytopathogenic fungi, Sordariomycetes, Systematics.

Taxonomic novelties: New families: *Apiosporopsidaceae* Senan. Maharachch. & K.D. Hyde, *Apoharknessiaceae* Senan. Maharachch. & K.D. Hyde, *Asterosporiaceae* Senan. Maharachch. & K.D. Hyde, *Auratiopycnidiellaceae* Senan. Maharachch. & K.D. Hyde, *Erythrogloeaceae* Senan. Maharachch. & K.D. Hyde, *Melanconiellaceae* Senan. Maharachch. & K.D. Hyde, *Prosopidicolaceae* Senan. & K.D. Hyde; **New genera:** *Marsupiomyces* Senan. & K.D. Hyde, *Microascospora* Senan., Camporesi & K.D. Hyde, *Phaeoappendicospora* Senan., Q.R. Li & K.D. Hyde, *Paradiaporthe* Senan., Camporesi, & K.D. Hyde, *Hyaliappendispora* Senan., Camporesi & K.D. Hyde, *Chiangraiomyces* Senan. & K.D. Hyde; **New species:** *Chiangraiomyces bauhiniae* Senan. & K.D. Hyde, *Coniella pseudokoreana* Senan., Tangthir. & K.D. Hyde, *Cytospora centrivillosa* Senan., Camporesi & K.D. Hyde, *Cytospora junipericola* Senan., Camporesi & K.D. Hyde, *Cytospora quercicola* Senan., Camporesi & K.D. Hyde, *Cytospora rosae* Senan., Camporesi & K.D. Hyde, *Cytospora fraxinigena* Senan., Camporesi & K.D. Hyde, *Diaporthe litoricola* Senan., E.B.G. Jones & K.D. Hyde, *Ditopella biseptata* R.H. Perera, Senan., Camporesi & K.D. Hyde, *Gnomoniopsis agrimoniae* Senan., Camporesi & K.D. Hyde, *Hyaliappendispora galii* Senan., Camporesi & K.D. Hyde, *Marsupiomyces epidermoidea* R.H. Perera, Senan., Bulgakov & K.D. Hyde, *Marsupiomyces quercina* Senan., Camporesi & K.D. Hyde, *Melanconis italica* Senan., Camporesi & K.D. Hyde, *Microascospora rubi* Senan., Camporesi & K.D. Hyde, *Paradiaporthe artemisiae* Senan., Camporesi & K.D. Hyde, *Phaeoappendicospora thailandensis* Senan., Q.R. Li & K.D. Hyde, *Plagiostoma jonesii* Senan., & K.D. Hyde, *Plagiostoma salicicola* Senan., Camporesi & K.D. Hyde, *Sydowiella urticicola* Senan., Camporesi & K.D. Hyde, *Tubakia thailandensis* Senan., Tangthir., K.D. Hyde; **New combinations:** *Coryneum arausiaca* (Fabre) Senan., Maharachch. & K.D. Hyde, *Microascospora fragariae* (F. Stevens & Peterson) Senan., Maharachch. & K.D. Hyde.

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INTRODUCTION

The *Diaporthales* is a distinct order in the subclass *Diaporthomycetidae* (*Sordariomycetes*) and it includes pathogens, saprobes and endophytes, with no known coprophilous, hypersaprobes or mycophylic species (Barr 1978, Rossman *et al.* 2007, Vasilyeva *et al.* 2007, Maharachchikumbura *et al.* 2015, 2016). Taxa of this order inhabit a wide diversity of hosts and substrates, including most economically and ecologically important trees and crops, soil and living animal and human tissues (Barr 1978, Gryzenhout *et al.* 2006c). Species in *Diaporthales* form solitary or aggregated, immersed to erumpent, rarely superficial, orange, brown to black perithecial ascomata, with short or long necks, that are located in stromatic tissues or substrates, with a centrum (or hamathecium) lacking or with few paraphyses (Alexopoulos & Mims 1978, Barr 1978, Castlebury *et al.* 2002). Asci are unitunicate with a conspicuous refractive ring (Hawksworth *et al.* 1995, Rossman *et al.* 2007). Ascospore morphology is diverse, ranging from short to elongate and aseptate or septate with hyaline or pigmented walls. The asexual morphs of *Diaporthales* are generally coelomycetous (Rossman *et al.* 2007), producing acervuli or pycnidial conidiomata, with or without a well-developed stroma. Conidiogenesis is phialidic or rarely annellidic and conidia are usually unicellular or 1-septate (Rossman *et al.* 2007).

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Taxonomic circumscription of *Diaporthales* based on multigene phylogeny and morphology

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Abstract
Demarcation of family, genus and species boundaries in the *Diaporthales* has been tentative due to uninformative illustrations and descriptions, overlapping morphological characteristics, misplacement or poor condition of type specimens and shortage of molecular data from ex-type cultures. In this study, we obtained the type specimens or other authentic specimens of diaporthalean taxa from worldwide fungaria. We examined, described and illustrated them. This study is based on morphological characters from type or authentic specimens, details from protologue and original illustrations and molecular data obtained from GenBank. Combined analyses of nrITS, nrLSU, RPB2 and TEF1-α sequence data were used to construct the molecular phylogeny. Additionally, we provided separate phylogenetic trees for families when necessary to show the generic distribution within these families based on suitable gene markers. Based on morphology and phylogeny, we treat 17 genera previously assigned to *Diaporthales* genera *incertae sedis* within several families. For some genera we have designated new generic types as they are lacking type species or type species have affiliations with other families. We exclude *Anisomycopsis* from *Diaporthales* and place it in *Xylariomycetidae* genera *incertae sedis*. *Tirisporellaceae*, which was previously placed in *Tirisporellales* is placed in *Diaporthales* based on phylogeny and morphology. A new combination, *Dendrostoma leiphaemia* propose for *Amphiporthe leiphaemia* (Fr.) Butin. Based on the morphological characters and molecular data we accept 27 families and 138 genera within *Diaporthales*, 24 genera in *Diaporthales* genera *incertae sedis* and one genus in *Xylariomycetidae* genera *incertae sedis*. We provide notes for genera in *Diaporthales* genera *incertae sedis*, and excluded and doubtful genera are listed with notes on their taxonomy and phylogeny.

Keywords Authentic specimens · *Dendrostoma leiphaemia* · Incertae sedis · Classification · Taxonomy · Families · Accepted genera

Introduction

History

Fries (1823) accommodated the composite genus *Sphaeria*, which comprises most diaporthoid taxa, within *Sphaeriaceae*. Fuckel (1870) placed non-stromatic forms under subfamily *Ceratostomeae*, while stromatic forms were distributed among subfamilies *Melanconideae*, *Valseae*, *Dothideae* and *Melogrammeae*. Karsten (1873) revised *Sphaeriaceae* and divided it into four subfamilies as *Bertieae* (*Linospora*, *Ceuthocarpon*), *Diaportheae* (*Diaporthe*, *Gnomonia*, *Hypospila*), *Melanconideae* (*Pseudovalsa*, *Melanconis*, *Hercospora*, *Cytospora*) and *Valseae* (*Valsa*). Saccardo (1883) used ascospore septation and pigmentation to classify ascomycetes and diaporthoid taxa were distributed within various sections of his classification. He divided *Sphaeriaceae* into several subfamilies, those having stromatic tissues in *Ceratostomeae*, *Clypeosphaerieae*, *Valseae*, *Melanconideae*, *Melogrammeae* and non-stromatic taxa *Gnomonieae*. Lindau (1897) resurrected *Sphaeriales* to accommodate *Clypeosphaeriaceae*,

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Fungal Diversity
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Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa

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Fungal Diversity
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Fungal diversity notes 709–839: taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on *Rosaceae*

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Abstract
This paper is the seventh in the Fungal Diversity Notes series, where 131 taxa accommodated in 28 families are mainly described from *Rosa* (*Rosaceae*) and a few other hosts. Novel fungal taxa are described in the present study, including 17 new genera, 93 new species, four combinations, a sexual record for a species and new host records for 16 species. *Bhatiellae*, *Cycasicola*, *Dactylidina*, *Embarria*, *Hawksworthiana*, *Italica*, *Melanocucurbitaria*, *Melanodiplodia*, *Monoseptella*, *Uzbekistanica*, *Neoconiothyrium*, *Neopaucispora*, *Pararoussoella*, *Paraxylaria*, *Marjia*, *Sporormurispora and Xenomassariosphaeria* are introduced as new ascomycete genera. We also introduce the new species *Absidia jindoensis*, *Alternaria doliconidium*, *A. hampshirensis*, *Angustimassarina rosarum*, *Astragalicola vasilyevae*, *Backusella locustae*, *Bartalinia rosicola*, *Bhatiellae rosae*, *Broomella rosae*, *Castanediella camelliae*, *Coelodictyosporium rosarum*, *Comoclathris rosae*, *C. rosarum*, *Comoclathris rosigena*, *Coniochaeta baysunika*, *C. rosae*, *Cycasicola goaensis*, *Dactylidina shoemakeri*, *Dematiopleospora donetzica*, *D. rosicola*, *D. salsolae*, *Diaporthe rosae*, *D. rosicola*, *Endoconidioma rosae-hissaricae*, *Epicoccum rosae*, *Hawksworthiana clematidicola*, *H. lonicerae*, *Italica achilleae*, *Keissleriella phragmiticola*, *K. rosacearum*, *K. rosae*, *K. rosarum*, *Lophiostoma rosae*, *Marjia tianschanica*, *M. uzbekistanica*, *Melanocucurbitaria uzbekistanica*, *Melanodiplodia tianschanica*, *Monoseptella rosae*, *Mucor fluvius*, *Muriformistrickeria rosae*, *Murilentithecium rosae*, *Neoascochyta rosicola*, *Neoconiothyrium rosae*, *Neopaucispora rosaecae*, *Neosetophoma rosarum*, *N. rosae*, *N. rosigena*, *Neostagonospora artemisiae*, *Ophiobolus artemisiicola*, *Paraconiothyrium rosae*, *Paraphaeosphaeria rosae*, *P. rosicola*, *Pararoussoella rosarum*, *Parathyridaria rosae*, *Paraxylaria rosacearum*, *Penicillium acidum*, *P. aquaticum*, *Phragmocamarosporium rosae*, *Pleospora rosae*, *P. rosae-caninae*, *Poaceicola agrostina*, *P. arundinicola*, *P. rosae*, *Populocrescentia ammophilae*, *P. rosae*, *Pseudocamarosporium pteleae*, *P. ulmi-minoris*, *Pseudocercospora rosae*, *Pseudopithomyces rosae*, *Pseudostrickeria rosae*, *Sclerostagonospora lathyri*, *S. rosae*, *S. rosicola*, *Seimatosporium rosigenum*, *S. rosicola*, *Seiridium rosarum*, *Setoseptoria arundelensis*, *S. englandensis*, *S. lulworthcovensis*, *Sigarispora agrostidis*, *S. caryophyllacearum*, *S. junci*, *S. medicaginicola*, *S. rosicola*, *S. scrophulariae*, *S. thymi*, *Sporormurispora atraphaxidis*, *S. pruni*, *Suttonomyces rosae*, *Umbelopsis sinsidoensis*, *Uzbekistanica rosae-hissaricae*, *U. yakutkhanika*, *Wojnowicia rosicola*, *Xenomassariosphaeria rosae*. New host records are provided for *Amandinea punctata*, *Angustimassarina quercicola*, *Diaporthe rhusicola*, *D. eres*, *D. foeniculina*, *D. rudis*, *Diplodia seriata*, *Dothiorella iberica*, *Lasiodiplodia theobromae*, *Lecidella elaeochroma*, *Muriformistrickeria rubi*, *Neofusicoccum australe*, *Paraphaeosphaeria michotii*, *Pleurophoma pleurospora*, *Sigarispora caulium* and *Teichospora rubriostiolata*. The new combinations are *Dactylidina dactylidis* (=*Allophaeosphaeria dactylidis*), *Embarria clematidis* (=*Allophaeosphaeria clematidis*), *Hawksworthiana alliariae* (=*Dematiopleospora alliariae*) and *Italica luzulae*

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APPENDIX B

CHEMICAL REAGENTS AND MEDIA

List of Media

1. Malt Extract Agar (MEA)

Agar	15 g/L
Malt Extract	30 g/L
Peptone	5 g/L

pH 5.4±0.2 (25 °C)

Combine malt extract agar in 1000 mL of distill water. Sterilization by autoclave at 121 °C for 15 minutes.

2. Potato-Carrot Agar (PCA)

Agar	15 g/L
Potatoes, infusion from	250 g/L
Carrot, infusion from	200 g/L

pH 6.5±0.2

Suspend all composition in 1000 ml distilled water. Heat to boiling to dissolve the medium completely. Sterilize by autoclaving at at 121 °C for 15 minutes.

3. Potato Dextrose Agar (PDA)

Agar	15 g/L
Dextrose	20 g/L
Potato extract	4 g/L

pH 5.6±0.2 (25 °C)

Combine malt extract agar in 1000 mL of distill water. Sterilization by autoclave at 121 °C for 15 minutes.

4. 2% Water Agar (WA)

Agar	20 g/L

Dissolve 20 g agar in distilled water then mixed and add volume to 1000 ml of water.

Heath until dissolved and autoclave at 121oC for 15 minutes

5. V-8 juice agar (V8)

V-8 juice (100 ml)	8.3 g/L
L-Asparagine	10 g/L
Yeast extract	2 g/L
Calcium carbonate	2 g/L
Glucose	2 g/L
Agar	20 g/L

pH (at 25°C) 5.7±0.2

Combine all composition (suspend 44.3 g) in 1000 ml of distilled water. Heat just to boiling. Sterilization by autoclave at 121 °C for 15 minutes.

Chemical Reagents

1. India ink

used for observing mucilaginous sheath or appendage of ascospores in some species

2. Potassium hydroxide (KOH)

used in the rehydration of dried specimens. 5% aqueous solution

3. Lactoglycerol

used for maintaining semipermanent slides

Lactic acid	10 ml
Glycerol	10 ml
Distilled water	10 ml

Mix 10 ml lactic acid, 10 ml glycerol, and add 10 ml distilled water

4. Lactophenol-Cotton Blue

used to highlight fungal structures for viewing with the compound light microscope. Cotton blue is the most popular stain for observe pseudoparaphyses, septate or ascus walled.

Phenol (crystals)	20 g
Lactic acid	16 ml
Glycerol	31 ml

Dissolve phenol in distilled water, add lactic acid, glycerol and 0.05 g of Poirrier's (cotton) blue or acid fuchsin

5. Melzer's Reagent

Chloral hydrate	100 g
Potassium iodide	5 g
Iodine	1.5 g
Distilled water	100 ml

APPENDIX C

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Chada Norphanphoun
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2) Norphanphoun, C., Doilom, M., Daranagama, D. A., Phookamsak, R., Wen, T. C., & Hyde, K. D. (2017). Revisiting the genus Cytospora and allied species. Mycosphere 8, 51–97.
3) Norphanphoun, C., Jayawardena, R. S., Chen, Y., Wen, T. C., & Hyde, K. D. (2019). Morphological and phylogenetic characterization of novel Pestalotioid species associated with mangroves in Thailand. Mycosphere 10, 531–578.
4) Norphanphoun, C., Hongsanan, S., Gentekaki, E., Chen, Y. J., Kuo, C. H., Hyde, K. D. (2020). Differentiation of species complexes in Phyllosticta enables better species resolution. Mycosphere 11(1), 2542–2628.

and one publication was accepted by journal:

1) Norphanphoun, C., Gentekaki, E., Hongsanan, S., Jayawardena, R., ..., Hyde, K.D. (2022) The sections of Diaporthe: formalizing species-group concepts. Mycosphere.

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Jayawardena

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APPENDIX D

MFLU/ MFLUCC COLLECTIONS

Table D1 MFLU/ MFLUCC collections that use in this study

Taxon	MFLU number	MFLUCC number	Comment
Alternaria gaisen	NCYUCC 19-0351	NCYUCC 19-0351	Chapter 4
	NCYUCC 19-0353	NCYUCC 19-0353	Chapter 4
Cytospora ampulliformis	MFLU 15-2187	MFLUCC 16-0583	Chapter 9
	MFLU 15-3756	MFLUCC 16-0629	Chapter 9
Cytospora curvata	MFLU 15-2229	MFLUCC 15-0865	Chapter 9
Cytospora donetzica	MFLU 15-2227	MFLUCC 15-0864	Chapter 9
	MFLU 15-3764	MFLUCC 16-0641	Chapter 9
	MFLU 15-2093	MFLUCC 16-0574	Chapter 9
	MFLU 15-2047	MFLUCC 16-0589	Chapter 9
Cytospora erumpens	MFLU 15-2165	MFLUCC 16-0580	Chapter 9
Cytospora longiostiolata	MFLU 15-3784	MFLUCC 16-0628	Chapter 9
Cytospora lumnitzericola	MFLU 18-1227	MFLUCC 17-0508	Chapter 2
Cytospora melnikii	MFLU 15-1910	MFLUCC 15-0851	Chapter 9
	MFLU 15-3766	MFLUCC 16-0635	Chapter 9
Cytospora nivea	MFLU 15-2210	MFLUCC 15-0860	Chapter 9
Cytospora parakantschavelii	MFLU 15-1953	MFLUCC 15-0857	Chapter 9
	MFLU 15-2094	MFLUCC 16-0575	Chapter 9
Cytospora parasitica	MFLU 15-1991	MFLUCC 16-0507	Chapter 9
Cytospora paratranslucens	MFLU 15-1986	MFLUCC 16-0506	Chapter 9
	MFLU 15-3678	MFLUCC 16-0627	Chapter 9
Cytospora rusanovii	MFLU 15-1929	MFLUCC 15-0853	Chapter 9

Table D1 (continued)

Taxon	MFLU number	MFLUCC number	Comment
	MFLU 15- 1931	MFLUCC 15-0854	Chapter 9
Cytospora salicacearum	MFLU 15-2213	MFLUCC 15-0861	Chapter 9
	MFLU 15-2061	MFLUCC 16-0509	Chapter 9
	MFLU 15-2097	MFLUCC 16-0576	Chapter 9
	MFLU 15-2207	MFLUCC 16-0587	Chapter 9
Cytospora salicicola	MFLU 15-2231	MFLUCC 15-0866	Chapter 9
Cytospora salicina	MFLU 15-2212	MFLUCC 15-0862	Chapter 9
	MFLU 15-3679	MFLUCC 16-0637	Chapter 9
Cytospora sorbi	MFLU 15-3781	MFLUCC 16-0631	Chapter 9
Cytospora sorbicola	MFLU 15-2176	MFLUCC 16-0581	Chapter 9
	MFLU 15-2180	MFLUCC 16-0582	Chapter 9
	MFLU 15-2203	MFLUCC 16-0584	Chapter 9
	MFLU 15-2205	MFLUCC 16-0585	Chapter 9
	MFLU 15-2206	MFLUCC 16-0586	Chapter 9
	MFLU 15-3768	MFLUCC 16-0633	Chapter 9
Cytospora thailandica	MFLU 17-0709	MFLUCC 17-0262	Chapter 2
		MFLUCC 17-0263	Chapter 2
Cytospora ulmi	MFLU 15-2225	MFLUCC 15-0863	Chapter 9
Cytospora xylocarpi	MFLU 17-0708	MFLUCC 17-0251	Chapter 2
Lamproconium desmazieri	MFLU 14-0780	MFLUCC 14-1047	Chapter 8
	MFLU 15-1940	MFLUCC 15-0870	Chapter 8
	MFLU 15-2037	MFLUCC 15-0871	Chapter 8
	MFLU 15-2111	MFLUCC 15-0872	Chapter 8
	MFLU 15-2192	MFLUCC 15-0873	Chapter 8
Melomastia italica	MFLU 15-0228	MFLUCC 15-0160	Chapter 10
Neopestalotiopsis acrostichi	MFLU 19-0774	MFLUCC 17-1754	Chapter 3
	MFLU 19-0775	MFLUCC 17-1755	Chapter 3

Table D1 (continued)

Taxon	MFLU number	MFLUCC number	Comment
Neopestalotiopsis brachiata	MFLU 19-0776	MFLUCC 17-1555	Chapter 3
Neopestalotiopsis petila	MFLU 19- 0778	MFLUCC 17-1738	Chapter 3
	MFLU 19-0777	MFLUCC 17-1737	Chapter 3
Neopestalotiopsis rhizophorae	MFLU 19-0779	MFLUCC 17-1550	Chapter 3
	MFLU 19-0780	MFLUCC 17-1551	Chapter 3
Neopestalotiopsis sonneratae	MFLU 19-0782	MFLUCC 17-1745	Chapter 3
	MFLU 19-0781	MFLUCC 17-1744	Chapter 3
Neopestalotiopsis thailandica	MFLU 19-0783	MFLUCC 17-1730	Chapter 3
	MFLU 19-0784	MFLUCC 17-1731	Chapter 3
Pestalotiopsis rhizophorae	MFLU 19-0785	MFLUCC 17-0416	Chapter 3
	MFLU 19-0786	MFLUCC 17-0417	Chapter 3
Pestalotiopsis thailandica	MFLU 19-0787	MFLUCC 17-1616	Chapter 3
	MFLU 19-0788	MFLUCC 17-1617	Chapter 3
Phyllosticta rhizophorae	NCYUCC 19-0352	NCYUCC 19-0352	Chapter 5
		NCYUCC 19-0358	Chapter 5
Pseudopestalotiopsis avucenniae	MFLU 19-0789	MFLUCC 17-0434	Chapter 3
Pseudopestalotiopsis curvatispora	MFLU 19-0791	MFLUCC 17-1722	Chapter 3
	MFLU 19-0792	MFLUCC 17-1723	Chapter 3
	MFLU 19-0790	MFLUCC 17-1747	Chapter 3
Pseudopestalotiopsis rhizophorae	MFLU 19-0793	MFLUCC 17-1560	Chapter 3

Table D1 (continued)

Taxon	MFLU number	MFLUCC number	Comment
Pseudopestalotiopsis thailandica	MFLU 19-0794	MFLUCC 17-1724	Chapter 3
	MFLU 19-0795	MFLUCC 17-1725	Chapter 3
Seimatosporium lichenicola	MFLU 14-0773	MFLUCC 14-0623	Chapter 7
Seimatosporium physocarpi	MFLU 14-0775	MFLUCC 14-0625	Chapter 7
Seimatosporium rosae	MFLU 14-0771	MFLUCC 14-0621	Chapter 7