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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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Introduction

One stop shop (OSS) is a series of papers focused on providing a stable platform for the taxonomy of plant pathogenic fungi and organisms. Genera included in these paper series are associated with plant diseases. However, some may not be well-known plant pathogens and Kochs' postulates might have not been conducted in order to establish their pathogenicity. When this series was launched in 2014, its specific aims were mentioned (Hyde et al. 2014). Two issues of OSS have been published in which 50 genera were treated (Hyde et al. 2014; Jayawardena et al. 2019). In this study we treat 25 genera of plant pathogens as well as establish a new website, www.onestopshopfungi.org, to host a database for plant pathogenic fungi and organisms. This fungal database allows mycologists and plant pathologists to understand disease symptoms, host distribution, classification, morphology and provides an updated phylogeny which will enhance current understanding of plant pathogens and gain better insights into the current fungal classification system. The Onestopshopfungi webpage is an output funded by the Mushroom Research Foundation, Thailand, which is a non-government and non-profit organization. We invite all mycologists to contribute to make this a success. The outcome of this series provides a stable taxonomy and phylogeny for plant pathogens that can provide a reliable platform for mycologists and plant pathologists to accurately identify causal organisms.

Material and methods

Photo plates of the symptoms of the disease and morphological characters are given, when available. Classification follows Wijayawardene et al. (2018).

Sequence data from ex-type, ex-epitype or authentic strains for each species were retrieved from GenBank. Sequence data from single gene regions were aligned using Clustal X1.81 (Thompson et al. 1997) and further alignment of the sequences were carried out by using the default settings of MAFFT v.7 (Katoh and Toh 2008; http://mafft.cbrc.jp/alignment/server/), and manual adjustment was conducted using BioEdit where necessary. Gene regions were also combined using BioEdit v.7.0.9.0 (Hall 1999). Primers for each gene locus can be found in the bibliography related to the phylogeny presented for each genus. Phylogenetic analyses consisted of maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BYPP). Maximum parsimony analysis was performed using PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford 2002) to obtain the most parsimonious trees. Maximum likelihood analyses were also performed in raxmlGUIv.0.9b2 (Silvestro and Michalak 2012) or RAxML-HPC2 on XSEDE (8.2.8) in the CIPRES science gateway platform (Miller et al. 2010) using GTR+I+G model of evolution. Bayesian inference was used to construct the phylogenies using Mr. Bayes v.3.1.2 (Ronquist and Huelsenbeck 2003). MrModeltest v. 2.3 (Nylander et al. 2008) was used for statistical selection of best-fit model of nucleotide substitution and was incorporated into the analyses.

Results

Capnodium Mont., Annls Sci. Nat., Bot, sér. 3, 11: 233 (1849)

The genus *Capnodium* was introduced by Montagne (1849) to accommodate *C. salicinum*. *Capnodium* is one of the most commonly found sooty moulds in gardens and landscapes (Laemmlen 2011). *Capnodium* has a saprobic association with sap-feeding insects in the Order Homoptera, which includes aphids, whiteflies, soft scale, mealy bugs, leafhoppers and psyllids (Barr 1987). Gavrilov-Zimin (2017) reported that the larvae and female of a new species and a new monotypic genus of legless mealybug, *Orbuspedum machinator*, from bamboo twigs in southern Thailand are covered with densely packed fungal hyphae of the sooty mould *Capnodium* sp. Herath et al. (2012) reported that a tropical sooty mould (*Capnodium* sp.) is known to produce antibiotics such as tetramic acid, methiosetin and epicorazin A.

Capnodium species grow on honeydew, gradually covering the surface of the plant part affected by insects, colouring it with various shades of black. These fungi do not colonize the plant tissues or trigger symptoms. However, they alter the ability of the plant to perform photosynthesis and exchange of gases with the atmosphere. Severely affected leaves may die and fall, thereby affecting plant growth and survival. Therefore, we treat *Capnodium* as a main plant pathogenic group.

Classification—Dothideomycetes, *Dothideomycetidae*, *Capnodiales*, *Capnodiaceae*
Type species—***Capnodium salicinum*** Mont., Annls Sci. Nat., Bot, sér. 3 11:234 (1849)
Distribution—Species of *Capnodium* have a wide distribution but are most common in tropical and subtropical regions (Chomnunti et al. 2014). They can be found on plants that have been previously fed upon by insects.
Disease symptoms—Dark mycelium coating surface of host can cause chlorosis and reduce photosynthetic ability of plants, which effects plant growth, reduces yield, and leading to marketability problems (Chomnunti et al. 2014; Fig 1). In higher latitudes, *Capnodium* spp. are scarce during the winter; the most common being *C. salicinum* in the UK (Cannon et al. 1985; Royal Botanic Gardens, Kew, UK National Collection of Dried Fungi, unpublished data). Warm-temperate climates in Australia and the Mediterranean countries provide an abundance of perennial foliage on which sooty moulds are able to establish themselves during the winter, and so persist from one season to the next (Fraser 1935; Reynolds and Gilbert 2005). In northern Thailand, most of the sooty mould infections are caused by *Capnodium* species (Chomnunti et al. 2014).

Hosts—Many plants when colonised by insects that produce honeydew. Species of *Annona*, *Camellia*, *Citrus*, *Coffea*, *Chrysophyllum*, *Ficus*, *Malus*, *Mangifera*, *Olea*, *Populus*, *Prunus*, *Psidium*, *Rhododendron* and *Salix* (Farr and Rossman 2019)

Morphological based identification and diversity

The asexual morph forms elongated pycnidia that develop from a superficial mycelium on living plant surfaces and produce tiny, hyaline conidia on top of the pycnidia (Chomnunti et al. 2011). Persoon (1822) mention that *Fumago citri* is the sooty mould but it was not well described and completed; therefore it was transferred to genus *Polychaeton* by Léveillé (1847). Later, Berkeley-

Fig. 1 Sooty moulds on various host plants associated with insects. **a** On a hardwood tree, **b** on guava, **c** on coffee, **d–f** on mango

Desmazieres (1849) transferred all species once known in the genus *Fumago* to *Capnodium*. Molecular evidence revealed that *Polychaeton* is an asexual stage of *Capnodium*, therefore, both are the same organism. According to "one fungus one name" and the Melbourne Code under Art. 57.2, *Capnodium* was considered for conservation as it has a larger number of epithets and is more widely used in this group of fungi, even though *Polychaeton* is the older name (Chomnunti et al 2011, 2014; McNeill et al. 2012; Hyde et al. 2013; Wijayawardene et al. 2014, 2017, 2018; Liu et al. 2015; Hongsanan et al. 2015).

The morphology of *Capnodium* species can be recognised by black mycelial growth spreading on the host surface, which produces superficial colonies with septate, dark brown hyphae and cylindrical and bitunicate asci. On host surface *Capnodium* species share the same ecological niche and are similar in appearance to other genera and families of sooty moulds; often found with sexual and asexual states growing together and living in complex communities (Faull et al. 2002; Hughes 2003; Hughes and Seifert 2012; Chomnunti et al. 2014; Hongsanan et al. 2015).

Molecular based identification and diversity

DNA sequencing data of *Capnodium coffeae, C. coartatum, C. salicinum, C. coffeicola* and *C. dematum* and eleven unidentified *Capnodium* spp. are available in GenBank, including sequence data for LSU, SSU and ITS (4/7/2019). Hongsanan et al. (2015) introduced a new species *Capnodium coffeicola*. It differs from other *Capnodium* species in having pycnidia with short and black stalks at the base and is swollen at the central part, and it has cylindrical to oblong conidia, but its placement is supported with phylogenetic analysis using LSU and ITS sequence data.

Sooty moulds often grow in colonies of more than one species, and taxonomic descriptions thus often unknowingly combine elements of different genera and species. Identification based on morphology only is difficult as there are overlapping morphological characters among many taxa (Chomnunti et al. 2011, 2014). To achieve accurate generic and species identification and taxonomic placements, phylogenetic studies using large subunit ribosomal RNA (LSU rRNA) gene sequences and the internal transcribed spacer regions and 5.8S nrDNA gene (ITS) were performed (Crous et al. 2009; Chomnunti et al. 2011, 2014; Liu et al. 2015; Hongsanan et al. 2015).

This study reconstructs the phylogeny of *Capnodium* based on analyses of ITS sequence data (Table 1, Fig. 2) and corresponds with previous studies (Chomnunti et al. 2011, 2014; Hongsanan et al. 2015). This can be used as a backbone tree in the identification of *Capnodium* species (Fig. 3).

Table 1 Details of *Capnodium* isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS
C. coffeae	AFTOL-ID 939	DQ491515
C. coffeae	CBS 147.52	AJ244239
Capnodium coffeae	CTQE057	KX893384
Capnodium coffeicola	**MFLUCC 15-0206***	KU358921
Capnodium salicinum	CBS 131.34	AJ244240
Capnodium sp.	SZ-F22	KT443921
Capnodium sp.	S80	MH633887
Capnodium sp.	CP1	MH629975
Capnodium sp.	OUCMBI101100	HQ914834
Capnodium sp.	ELM115	KU556052
Capnodium sp.	GPO-CO-02	KC180729
Capnodium sp.	agrFF1633	HE584839
Capnodium sp.	agrFF1683	HE584838
Capnodium sp.	agrFF1681	HE584837
Capnodium sp.	agrFF1679	HE584836
Capnodium sp.	agrFF1678	HE584835
Capnodium sp.	agrFF1639	HE584834
***Capnodium* sp.**	**agrFF1638**	**HE584833**
Capnodium sp.	agrFF1614	HE584832
Capnodium sp.	agrFF1613	HE584831
Capnodium sp.	agrFF0153	HE584830
Capnodium sp.	agrFF1634	HE584829
Capnodium sp.	agrFF1631	HE584828
Capnodium sp.	agrFF0180	HE584822
Capnodium sp.	agrFF1690	HE584823
Species	**Isolate/Voucher no**	**ITS**
Capnodium sp.	agrFF0045	HE584825
Capnodium sp.	agrFF0207	HE584826
Capnodium sp.	TMS-2011	HQ631045
Capnodium sp.	TTI-247	KU985278
Conidiocarpus plumeriae	**MFLUCC 15-0205**	**KU358919**
Conidiocarpus siamensis	MFLUCC 10-0053	KU358922
Co. siamensis	MFLUCC 10-0061	KU358923
Co. siamensis	MFLUCC 10-0062	KU358924
Co. siamensis	**MFLUCC 10-0063**	**KU358925**
Co. siamensis	MFLUCC 10-0064	KU358926
Co. siamensis	MFLUCC 10-0065	KU358927
Co. siamensis	MFLUCC 10-0074	KU358928
Scoria leucadendri	CBS 131318	JQ044437

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

Recommended genetic marker (genus level)—LSU
Recommended genetic markers (species level)—LSU, ITS

Sequence data of LSU, SSU and ITS are available for five species of *Capnodium* in GenBank but none of them has complete sequence data. LSU is useful for preliminary

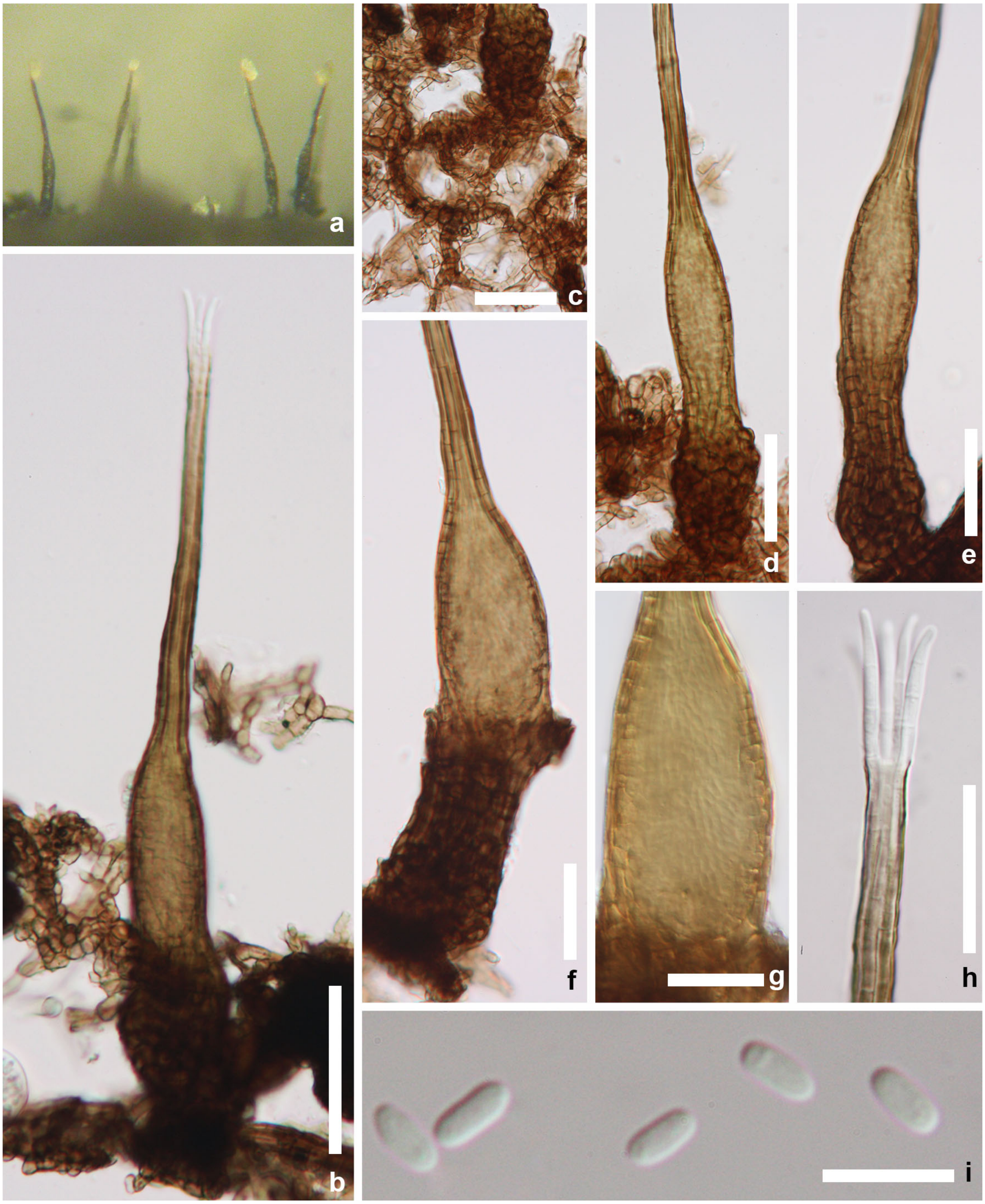


Fig. 2 Morphology of *Capnodium* sp. **a** pycnidia on the host. **b, d, e, f** stalked pycnidia **c** mycelium network, **g** conical pycnidium and pycnidial wall, **h** ostiole surrounded by hyaline hyphae, **i** conidia. Scale bars: **b**, **d**–**f** = 100 µm, **c**, **g** = 50 µm, **h**, = 20 µm, **i** = 10 µm

identification at the generic level (Chomnunti et al 2011, 2014; Quaedvlieg et al 2014). Hongsanan et al. (2015) recommended the use of combined LSU and ITS sequence data to identify the species. More protein-coding gene loci should be sequenced to clarify the taxonomic problems in this genus. In the current analyses, *C. cortatum* was not included due to lack of ITS sequences in GenBank. A revision of this genus is needed as it may reveal many new species. Re-sequencing of species as well as designating epitypes or representative species is also important.

Accepted number of species: There are 140 epithets in Index Fungorum (2019), however only **four** species have DNA sequence data.

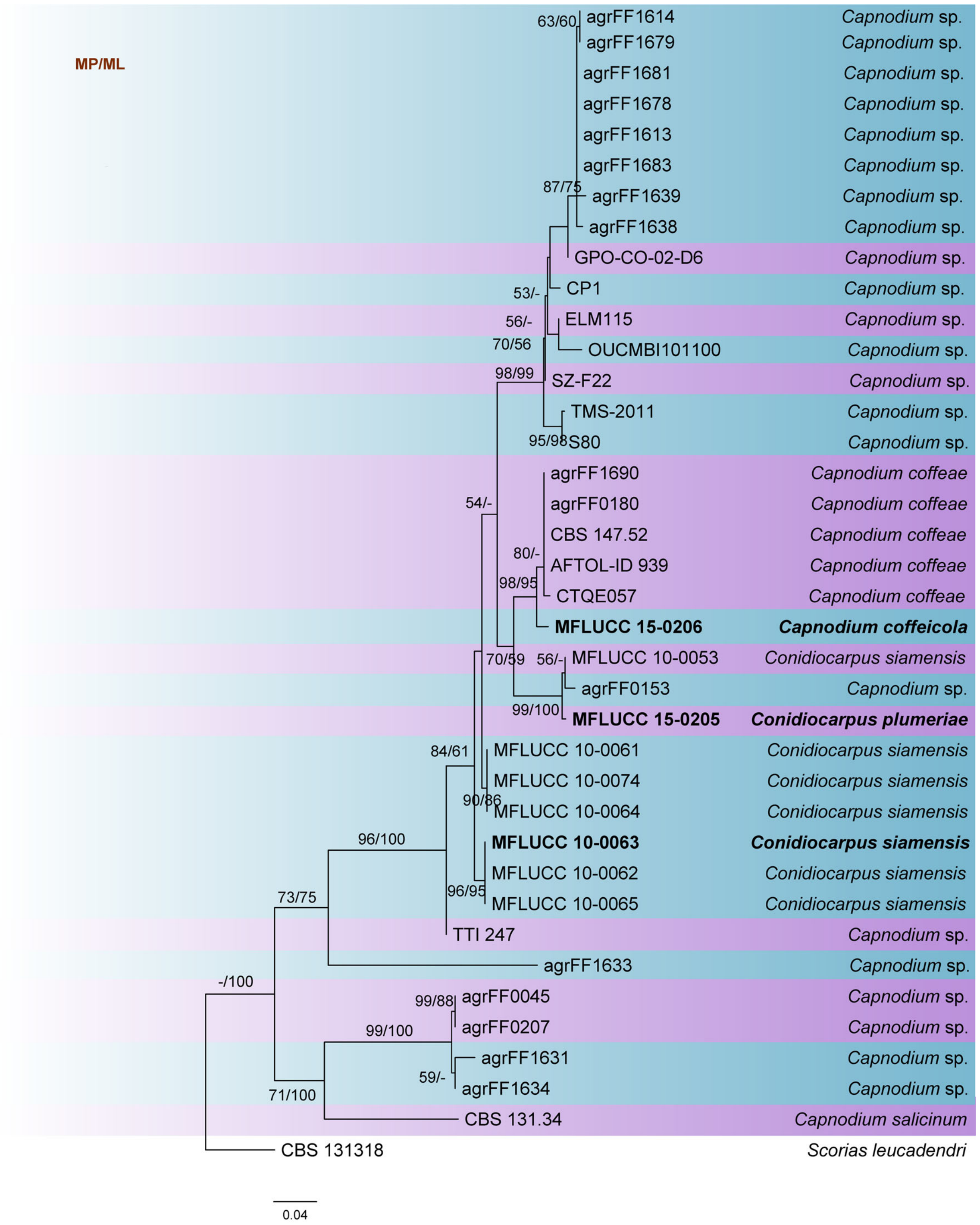


Fig. 3 Phylogenetic tree generated by maximum likelihood analysis of ITS sequence data of *Capnodium* species. Related sequences were obtained from GenBank. Thirty-eight strains are included in the analyses, which comprise 512 characters including gaps. The tree was rooted with *Scoria leucadendri* (CBS 131318). Tree topology of the ML analysis was similar to the MP analysis. The best scoring RAxML tree with a final likelihood value of -2398.970137 is presented. The matrix had 236 distinct alignment patterns, with 16.01% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.285338, C = 0.285338, G = 0.241464, T = 0.238894; substitution rates AC = 1.204962, AG = 1.857184, AT = 2.642904, CG = 1.319860, CT = 4.051266, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.287147$. The maximum parsimonious dataset consisted of constant 327, 125 parsimony-informative and 60 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 358 steps (CI = 0.735, RI = 0.875, RC = 0.630, HI = 0.265) in the first tree. RAxML and maximum parsimony bootstrap support value $\geq$ 50% are shown, respectively, near the nodes. Ex-type strains are in bold

References: Chomnunti et al 2011, 2014; Quaedvlieg et al 2014; Hongsanan et al. 2015 (morphology, phylogeny).

Chaetothyrina Theiss., Annls mycol. 11(6):495 (1913)

The genus *Chaetothyrina* was established by Theissen (1913), with *C. musarum* (Speg.) Theiss as the type species. *Chaetothyrina* was placed in *Micropeltidaceae* based on its superficial, flattened base, poorly developed thyriothecium and irregular meandering arrangement of compact hyphae of walled cells. Singtripop et al. (2016) provided molecular data of one reference specimen and one new species. Hongsanan et al. (2017) established a new species of *Chaetothyrina* and introduced a new family *Phaeothecoidiellaceae* to accommodate species of *Chaetothyrina*, *Houjia* and *Phaeothecoidiella* in Capnodiales. Based on its placement in phylogenetic trees and the morphological uniqueness, *Micropeltidaceae* was excluded from Microthyriales and treated as family *incertae sedis* in Lecanoromycetes (Hongsanan et al. 2017; Zeng et al. 2019) (Fig. 4).

Classification—Dothideomycetes, incertae sedis, Capnodiales, Phaeothecoidiellaceae

*Type species—**Chaetothyrina musarum*** (Speg.) Theiss., Annls mycol. 11(6):495 (1913)

Distribution—Known from Brazil, Cook Islands, Dominican Republic, India, Mexico, Pakistan, Panama, Thailand, US

Disease symptoms—Sooty blotch and flyspeck

Species in this genus cause flyspeck disease on various plants, such as *C. musarum* on *Musa* sp. and *C. panamensis* (F. Stevens & Dorman) Arx on *Oncoba laurina*. Sooty blotch and flyspeck (SBFS) is a disease complex caused by nearly 80 fungal species (Singtripop et al. 2016) that are epiphytes which blemish the epicuticular wax layer of several fruit crops, such as apple, pear, orange, persimmon, banana and grape worldwide (Gleason et al. 2011; Gao et al. 2014), cutting sale price and limiting the growth rate of fruit production (Williamson and Sutton 2000; Gao et al. 2014). 'Sooty blotch' is characterized by colonies produced on host tissues from superficial, spreading, dark irregular blotches of mycelium with or without sclerotium-like structures or fruiting bodies. On the other hand, 'flyspeck' defines clusters of shiny, small, black sclerotium-like structures or fruiting bodies, lacking visible intercalary mycelium (Gleason et al. 2011; Mayfield et al. 2012; Singtripop et al. 2016).

Hosts—Species of *Anacardium*, *Anodendron*, *Anogeissus*, *Carallia*, *Cassia*, *Chonemorpha*, *Dalbergia*, *Dianella*, *Euonymus*, *Hevea*, *Iiana*, *Magnifera*, *Magnolia*, *Mammea*, *Maytenus*, *Memecylon*, *Mitragyna*, *Musa*, *Myrcia*, *Ochrocarpos*, *Olea*, *Oncoba*, *Phoebe*, *Similax*, *Streblus* and *Vochysia*.

Morphological based identification and diversity

Chaetothyrina is characterized by superficial, flattened thyriothecia, with base poorly developed, with thyriothecial setae and 1-septate ascospores (Reynolds and Gilbert 2005; Singtripop et al. 2016; Hongsanan et al. 2017). *Chaetothyrina* can be distinguished from other species in *Micropeltidaceae* on the basis of thyriothecial setae appearance, shape and septation of the ascospores (Singtripop et al. 2016; Hongsanan et al. 2017). Twenty-three species of *Chaetothyrina* epithets are listed in Index Fungorum (2019), but sequence data are available for only two species (4/7/2019). *Chaetothyrina* is a poorly studied genus. Fresh collections and sequence data are needed for this genus. The disease cycle of this genus is yet to be established (Fig. 5).

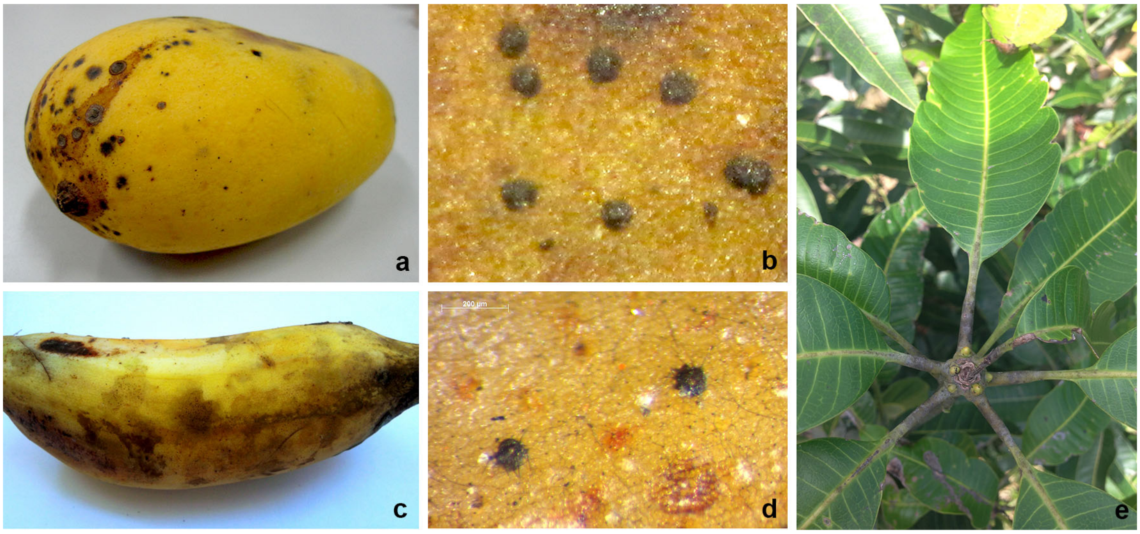


Fig. 4 Disease symptoms caused by *Chaetothyrina* spp. **a** on mango, **b**, **d** appearance of thyriothecia on hosts, **c** on a banana, **e** on mango leaves

Molecular based identification and diversity

Singtripop et al. (2016) provided a reference type specimen of *C. musarum* with sequence data. Using combined LSU, SSU and ITS sequence data, *Chaetothyrina* clustered as a sister genus to *Houjia* and *Phaeothecoidiella* within Capnodiales (Hongsanan et al. 2017; Table 2, Fig. 6).

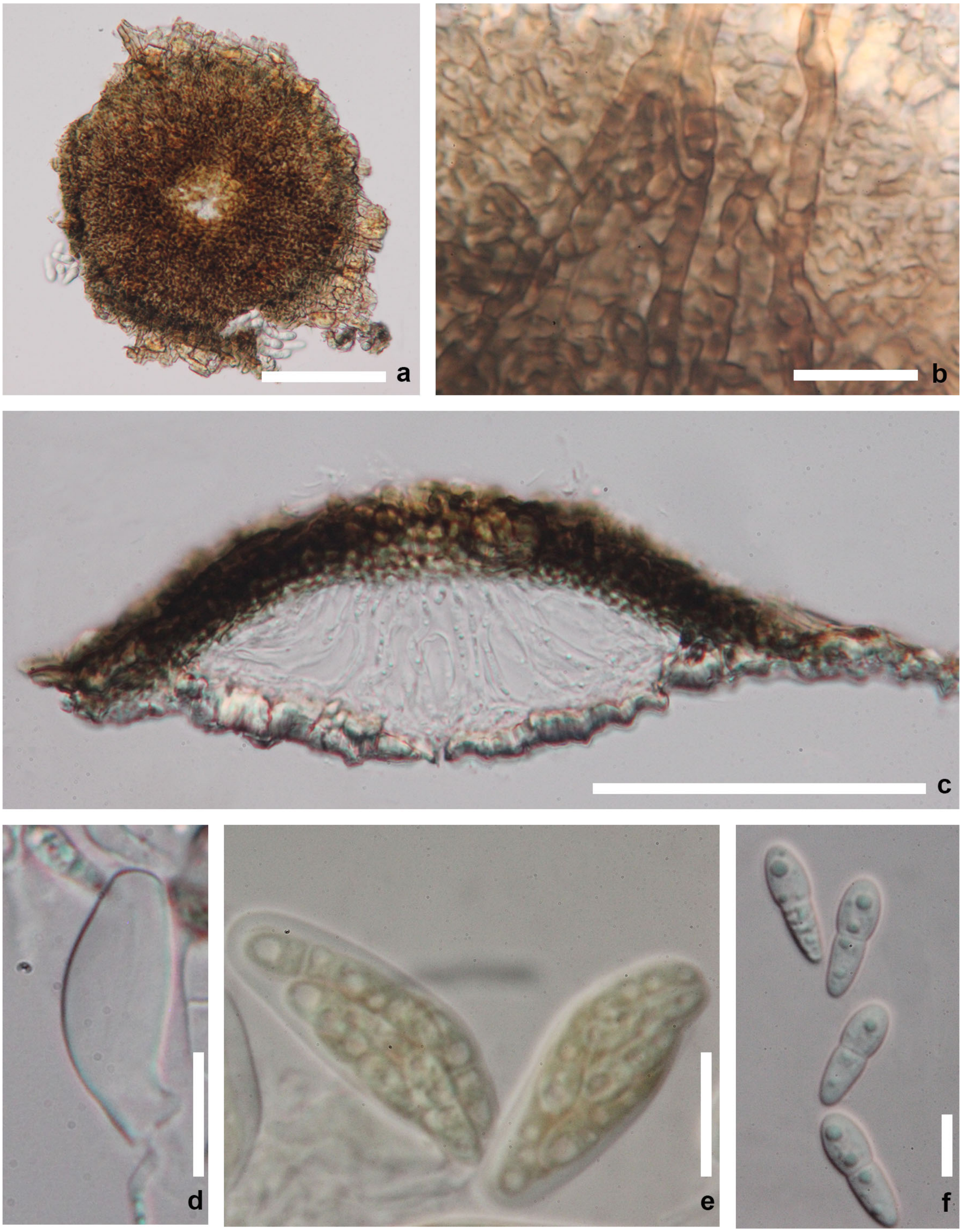


Fig. 5 *Chaetothyrina guttulata* **a** Thyriothecium when viewed in squash mount. **b** Surface of thyriothecium. **c** Section through thyriothecium. **d** Ascus when immature. **e** Asci at maturity. **f** Ascospores. Scale bars: **a** = 50 µm, **b**, **d**, **e** = 10 µm, **c** = 100 µm, **f** = 5 µm

Recommended genetic markers (genus level)—LSU and SSU

Recommended genetic markers (species level)—ITS and RPB2

Accepted number of species: There are 23 epithets in Index Fungorum (2019). However, only two species have molecular data.

References: Reynolds and Gilbert 2005; Singtripop et al. 2016; Hongsanan et al. 2017 (morphology, phylogeny)

Cytospora Ehrenb., Sylv. mycol. berol.: 28 (1818)

Cytospora was introduced by Ehrenberg (1818) as the type genus of the family *Cytosporaceae* in Diaporthales (Wehmeyer 1975; Barr 1978; Eriksson et al. 2001; Castlebury et al. 2002). The genus is an important

Table 2 Details of ***Chaetothyrina*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	LSU	SSU	ITS
Austroafricana associata	CBS 120732	KF901829	–	KF901512
Capnobotryella renispora	CBS 215.90	GU214399	AY220613	AY220613
Capnodium coffeae	CBS 147.52	GU214400	DQ247808	AJ244239
Chaetothyrina guttulata	MFLUCC15-1080	KU358917	KU358916	KX372277
C. guttulata	**MFLUCC15-1081***	KU358914	KU358915	KX372276
C. musarum	MFLUCC15-0383	KU710171	KU710174	KX372275
C. musarum	MFLUCC15-0383	KU710171	KU710174	KX372275
Devriesia strelitziae	CBS 122379	GU301810	GU296146	EU436763
Dissoconium aciculare	CBS 204.89	GU214419	GU214523	AY725520
D. dekkeri	CBS 342.86	JN232431	–	–
Dothistroma septosporum	CBS:112498	GQ852597	JX901744	JX901744
Hortaea werneckii	4263	JX141471	JX141470	DQ336709
Houjia yanglingensis	YHLB20	GQ433630	–	GQ433629
H. yanglingensis	**YHJN13***	GQ433631	–	GQ433628
Leptoxyphium cacuminum	**MFLUCC10-0049***	JN832602	JN832587	
Mycosphaerella ellipsoidea	**CBS:110843***	GQ852602	AY725545	AY725545
M. endophytica	**CBS:114662***	GQ852603	DQ302953	DQ302953
M. keniensis	**CBS:111001***	GQ852610	–	–
Myriangium duriaei	CBS 260.36	NG027579	AF242266	–
M. hispanicum	CBS 247.33	GU301854	GU296180	–
Phaeothecoidiella illinoisensis	CBS:125223	GU117901	–	GU117897
P. missouriensis	CBS:118959	GU117903	–	GU117899
Phragmocapnias asiticus	MFLUCC10-0062	JN832612	JN832597	–
P. betle	MFLUCC10-0053	JN832606	JN832591	–
P. betle	MFLUCC10-0050	JN832605	JN832590	–
Pseudoveronaea ellipsoidea	**MI3 34F1a***	JQ622103	–	FJ425205
P. obclavata	UIF3	AY598916	–	AY598877
Ramichloridium apiculatum	CBS 400.76	EU041851	EU041794	EU041794
Rasutoria pseudotsugae	rapssd	EF114704	EF114729	EF114687
R. tsugae	ratstk	EF114705	EF114730	EF114688
Schizothyrium pomi	CUA1a	AY598895	–	EF164898
S. pomi	Flyspeck1924-Zj001	AY598894	–	AY598848
Scorias spongiosa	MFLUCC10-0084	JN832586	JN832601	–
S. spongiosa	AFTOL-ID 1594	DQ678075	DQ678024	–
Stomiopeltis versicolor	GA3 23C2b	FJ147163	–	FJ438375
Zygophiala cryptogama	**KY1 1.2A1c***	EF164902	–	EF164900
Z. tardicrescens	**MWA1a***	EF164901	–	AY598856
Z. wisconsinensis	**MSTA8a***	AY598897	–	AY598853

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

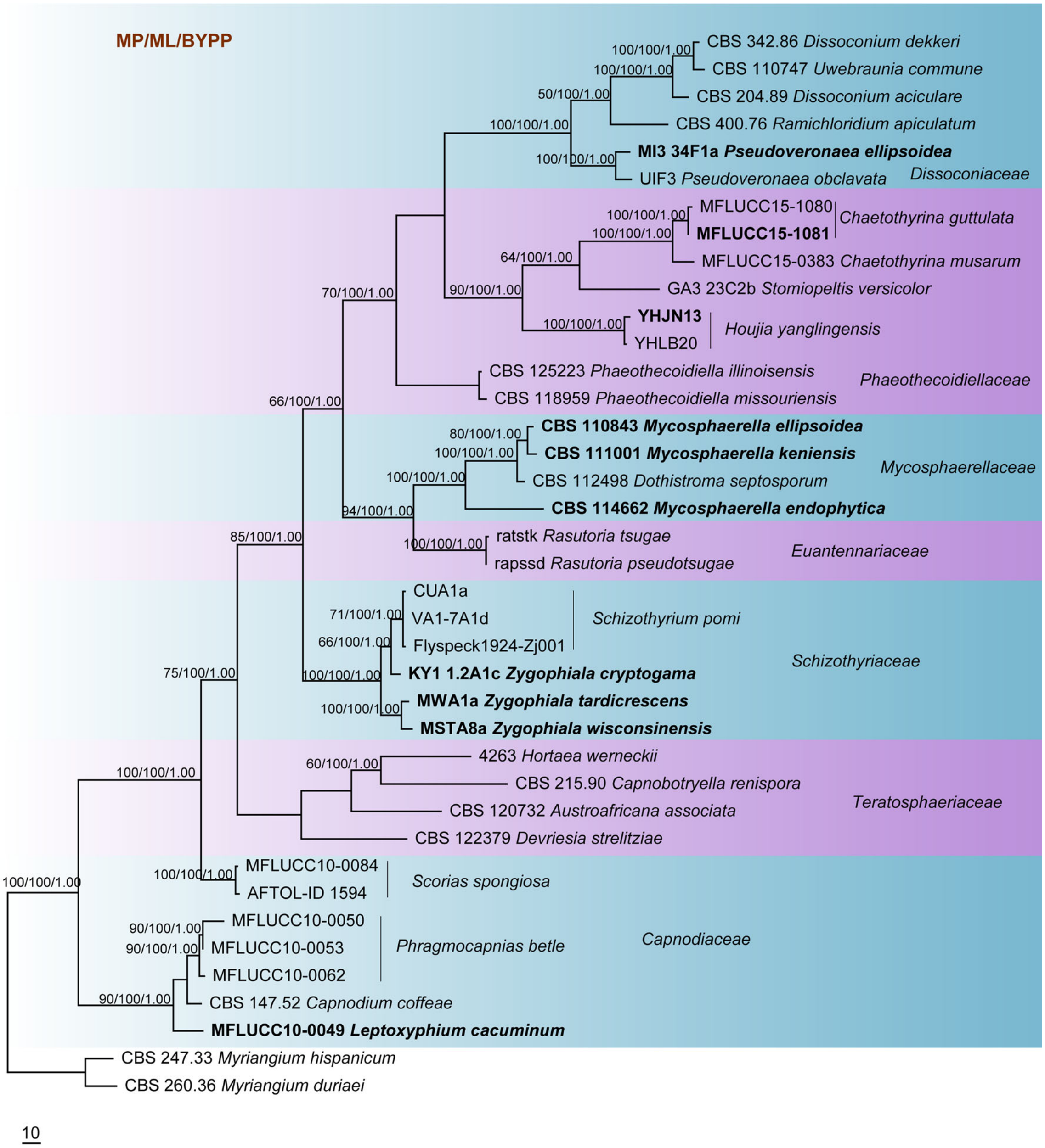


Fig. 6 Phylogenetic tree generated by maximum parsimony analysis of combined LSU, SSU and ITS sequence data. Thirty-nine strains are included in the analyses, which comprised 2225 characters including gaps. The tree was rooted with *Myriangium duriaei* (CBS 260.36) and *M. hispanicum* (CBS 247.33). The maximum parsimonious dataset consisted of 1645 constant, 461 parsimony-informative and 119 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of ten equally most parsimonious trees with a length of 1637 steps (CI = 0.549, RI 0.736, RC = 0.404, HI = 0.451) in the first tree. MP and ML bootstrap values ≥ 50% and bayesian posterior probabilities ≥ 0.90 (BYPP) are shown respectively near the nodes. Ex-type strains are in bold

pathogenic fungus, causing canker and dieback on branches of a wide range of hosts with a wide distribution (Adams et al. 2005, 2006; Hyde et al. 2017, 2018; Norphanphoun et al. 2017, 2018).

Classification—*Sordariomycetes*, *Diaporthomycetidae*, *Diaporthales*, *Valsaceae*

Type species—***Cytospora chrysosperma*** (Pers.) Fr. 1823

Distribution—Worldwide

Disease symptoms—Canker and dieback disease on branches

Hosts—Species of *Abies*, *Acer*, *Berberis*, *Betula*, *Ceratonia*, *Cornus*, *Cotinus*, *Crataegus*, *Elaeagnus*, *Eriobotrya*, *Eucalyptus*, *Juniperus*, *Lumnitzera*, *Malus*, *Picea*, *Pinus*, *Platanus*, *Platycladus*, *Populus*, *Prunus*, *Pyrus*, *Quercus*, *Rosa*, *Salix*, *Sequoia*, *Sibiraea*, *Sorbaronia*, *Sorbus*, *Spiraea*, *Styphnolobium*, *Syringa*, *Syzygium*, *Tibouchina*, *Ulmus*, *Vitis* and *Xylocarpus* (Norphanphoun et al. 2018).

Morphological based identification and diversity

Cytospora is characterized by multi-loculate conidiomata with ostiolar necks and unicellular, elongate-allantoid to subcylindrical, hyaline conidia (Fan et al. 2015a, b; Norphanphoun et al. 2017, 2018; Fig. 7). The genus which was reported as causing canker diseases in many woody plants was established in 1818 and studied in detail by taxonomists (Fries 1823; Saccardo 1884). *Valsa* Fr. was reported as the sexual stage of this genus and therefore, *Valsa* was treated as a synonym of *Cytospora* (1818) based on The International Code of Nomenclature for Algae, Fungi, and Plants (ICN, McNeill et al. 2012), with *Cytospora* being the oldest and most widely used name (Adams et al. 2005; Fotouhifar et al. 2010; Fan et al. 2014; Rossman et al. 2015). Previously, the conventional identification of species in *Cytospora* was based on their host association, often with vague morphological descriptions. Mycologists began to elucidate the relationships between *Cytospora* species and their hosts, with morphological observations combined with phylogenetic analyses using internal transcribed spacer (ITS) regions as an effective fungal DNA barcode (Adams et al. 2005, 2006; Fotouhifar et al. 2010; Schoch et al. 2012). The establishment of multi-gene analyses using ITS, LSU, ACT, RPB2, TUB2 has proved comprehensive for the species level (Fan et al. 2015a, b, 2020; Liu et al. 2015; Yang et al. 2015; Hyde et al. 2016; Li et al. 2016; Norphanphoun et al. 2017, 2018; Phookamsak et al. 2019).

Molecular based identification and diversity

Comprehensive multigene phylogenetic analyses for this genus were performed by Fan et al. (2015a, b, 2020) and Norphanphoun et al. (2017, 2018).

This study reconstructs the phylogeny of *Cytospora* based on analyses of a combined ITS, LSU, ACT and RPB2 sequence data (Table 3, Fig 8). The phylogenetic tree is updated with recently introduced *Cytospora* species and corresponds to previous studies (Norphanphoun et al. 2018).

Recommended genetic markers (genus level)—LSU, ITS

Recommended genetic markers (species level)—ITS, ACT and RPB2

Accepted number of species: There are 630 species in Index Fungorum (2019) and 110 species have molecular data.

References: Fan et al. 2015a, b, Lawrence et al. 2016, Senanayake et al. 2017, 2018 (morphology), Norphanphoun et al. 2017, 2018 (morphology, phylogeny).

Cyphellophora G.A. de Vries, Mycopath. Mycol. appl. 16(1):47(1962)

Cyphellophora is cosmopolitan, comprising species distributed from a broad range of environmental sources as human and animal disease, saprobes, epiphytes and plant pathogens (de Hoog et al. 1999, 2000; Jacob and Bhat 2000; Decock et al. 2003; Crous et al. 2007; Zhuang et al. 2010; Feng et al. 2014; Mayfield et al. 2012; Gao et al. 2014; Phookamsak et al. 2019). Most species, including the type species, *C. laciniata*, were isolated from nails or skin of humans, resulting in clinical symptoms (Feng et al. 2014). Phylogenetically, *C. phyllostachysdis* clustered with *C. europaea*, a human or mammal infection of hyperkeratosis (de Hoog et al. 2000). In contrast, *C. phyllostachysdis* causes sooty blotch and flyspeck (SBFS) of bamboo and is not found on humans (Gao et al. 2014). The sooty mould species *C. jingdongensis* was introduced with a sexual morph; it reduces plant photosynthesis but does not damage or cause disease of the plant (Chomnunti et al. 2014; Yang et al. 2018).

Classification—*Eurotiomycetes*, *Chaetothyriomycetidae*, *Chaetothyriales*, *Cyphellophoraceae*

Type species—***Cyphellophora laciniata*** G.A. de Vries, Mycopath. Mycol. appl. 16(1):47(1962)

Distribution—Australia, Brazil, China, Germany, India, Israel, Korea, Taiwan

Disease symptoms—Sooty blotch and flyspeck (main symptoms of this disease are given under *Chaetothyrina*).

To date, *C. artocarpi*, *C. guyanensis*, *C. jingdongensis*, *C. musae*, *C. olivacea*, *C. oxyspora*, *C. phyllostachydis* and *C. sessilis* have been isolated from plant materials (Gams and Holubová-Jechová 1976; de Hoog et al. 1999; Decock et al. 2003; Gao et al. 2014; Yang et al. 2018). *Cyphellophora artocarpi*, *C. musae*, *C. phyllostachydis* and *C. sessilis* were reported to cause sooty blotch and flyspeck from apple, jackfruit (*Artocarpus heterophyllus*) and bamboo (*Phyllostachys heterocycla*, *Sinobambusa tootsik*), resulting in significant economic damage (Zhuang et al. 2010; Mayfield et al. 2012; Gao et al. 2014).

Hosts—*Artocarpus heterophyllus*, *Dendrocalamus strictus*, *Eucalyptus* sp., *Helomeco velane*, *Hylomecon verlance*, *Malus domestica*, *Musa* sp., *Phyllostachys* sp., *Sinobasmbusa tootsik* and *Stenocalyx uniflorus.*

Morphological based identification and diversity

It is difficult to identify this black yeast-like genus based solely on morphological characters since the characters are very similar to those of other black yeast-like fungi, such as *Phialophora* and *Pseudomicrodochium*. Species of *Cyphellophora* resemble those of *Phialophora* in having melanized thalli with intercalary or terminal phialides bearing collarettes, but *Phialophora* has aseptate conidia whereas *Cyphellophora* produces larger, fusiform to

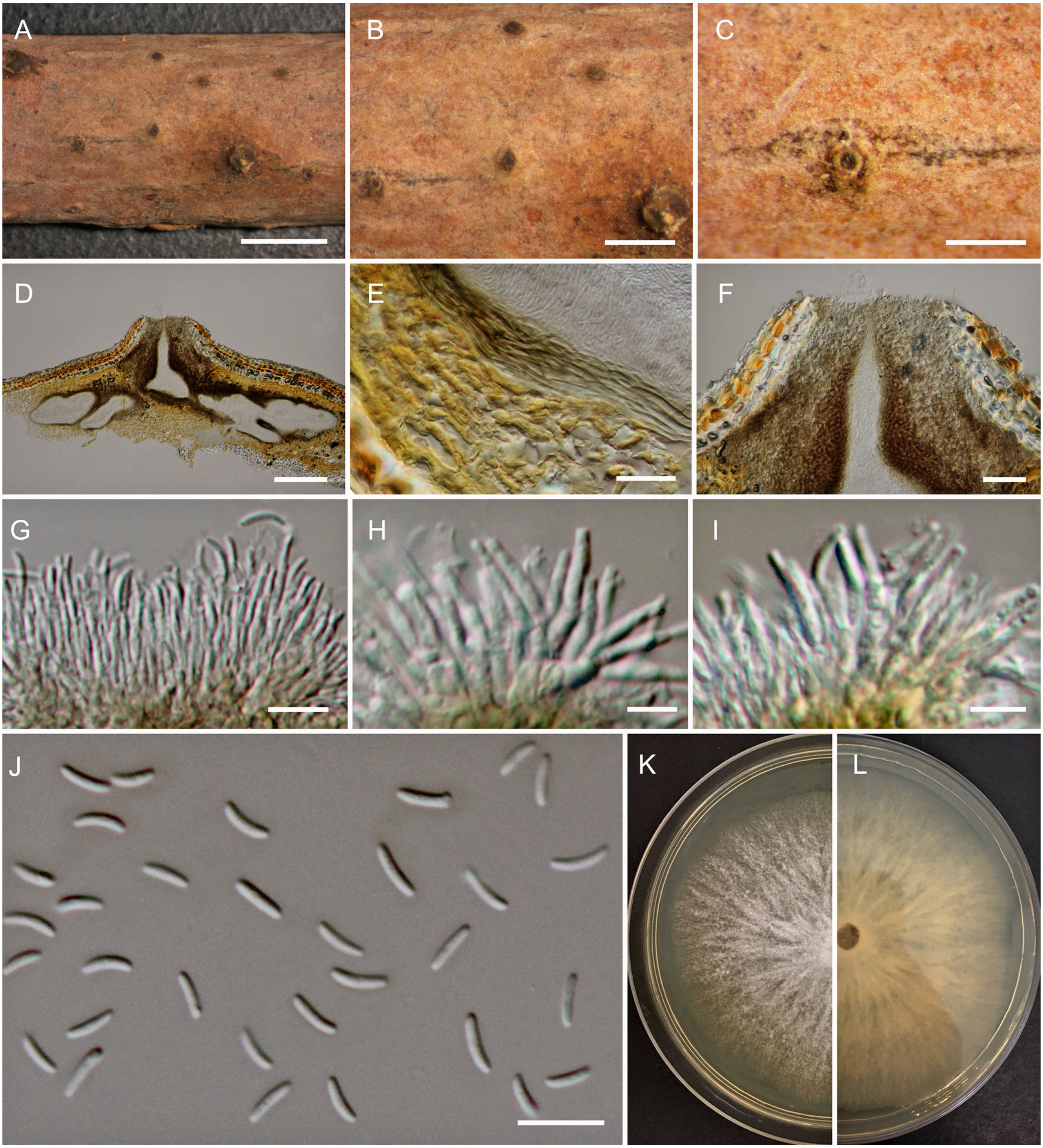


Fig. 7 *Cytospora ampulliformis* **a** stromatal habit in wood. **b** fruiting bodies on the substrate. **c** Surface of fruiting bodies. **d** Cross-section of the stroma showing conidiomata. **e** Peridium, **f** ostiolar neck. **g–i** Conidiogenous cells with attached conidia. **j** Mature conidia. **k**, **l** Colonies on MEA (**k**-from above, **l**-from below). Scale bars: **a** = 2 mm, **b** = 1 mm, **c** = 500 µm, **d**, **f** = 200 µm, **e** = 50 µm, **g**, **h** = 10 µm, **i**, **j** = 5 µm

sigmoid, aseptate to multi-septate conidia (Réblová et al. 2013). *Cyphellophora* can also be compared to *Pseudomicrodochium*, the former having melanized thalli while they are hyaline in *Pseudomicrodochium* (Decock et al. 2003; de Hoog et al. 2000, 2011). Yang et al. (2018) introduced *C. jingdongensis* as the first sexual morph, which is characterized by subglobose to globose, non-ostiolate ascomata, ellipsoidal to cylindrical asci and fusoid, 1–3 septate ascospores. However, the asexual morph of *C. jingdongensis* was difficult to observe in culture to

Table 3 Details of *Cytospora* isolates used in the phylogenetic analyses

Species	Isolate no	GenBank accession numbers					
		ITS	LSU	ACT	RPB2	*tef1*	TUB2
Cytospora acacia	CBS 468.69	DQ243804	–	–	–	–	–
C. ailanthicola	**CFCC 89970***	MH933618	MH933653	MH933526	MH933592	MH933494	MH933565
C. abyssinica	**CMW 10181***	AY347353	–	–	–	–	–
C. ampulliformis	**MFLUCC 16-0583***	KY417726	KY417760	KY417692	KY417794	–	–
C. amygdali	**CBS 144233***	MG971853	–	MG972002	–	–	–
C. atrocirrhata	CFCC 89615	KR045618	KR045700	KF498673	KU710946	KP310858	KR045659
C. austromontana	**CMW 6735***	AY347361	–	–	–	–	–
C. beilinensis	**CFCC 50493***	MH933619	MH933654	MH933527	–	MH933495	MH933561
C. berberidis	**CFCC 89927***	KR045620	KR045702	KU710990	KU710948	KU710913	KR045661
C. berkeleyi	**StanfordT3***	AY347350	–	–	–	–	–
C. brevispora	**CBS 116811***	AF192315	–	–	–	–	–
C. bungeanae	**CFCC 50495***	MH933621	MH933656	MH933529	MH933593	MH933497	MH933563
C. californica	**CBS 144234***	MG971935	-	MG972083	–	MG971645	–
C. carbonacea	CFCC 89947	MH933622	MH933657	MH933530	MH933594	MH933498	MH933564
C. carpobroti	**CMW 48981***	MH382812	MH411216	–	–	MH411212	MH411207
C. cedri	CBS 196.50	AF192311	–	–	–	–	–
C. celtidicola	**CFCC 50497***	MH933623	MH933658	MH933531	MH933595	MH933499	MH933566
C. centravillosa	**MFLUCC 16-1206***	MF190122	MF190068	–	MF377600	–	–
C. ceratosperma	CBS 116.21	AY347335	–	–	–	–	–
C. ceratospermopsis	**CFCC 89626***	KR045647	KR045726	KU711011	KU710978	KU710934	KR045688
C. chrysosperma	CFCC 89981	MH933625	MH933660	MH933533	MH933597	MH933501	MH933568
C. cinereostroma	**CMW 5700***	AY347377	–	–	–	–	–
C. cotini	**MFLUCC 14-1050***	KX430142	KX430143	–	KX430144	–	–
C. curvata	**MFLUCC 15-0865***	KY417728	KY417762	KY417694	KY417796	–	–
C. davidiana	**CXY 1350***	KM034870	–	–	–	–	–
C. diatrypelloidea	**CMW 8549***	AY347368	–	–	–	–	–
C. elaeagni	CFCC 89632	KR045626	KR045706	KU710995	KF765708	KU710918	KR045667
C. eriobotryae	**IMI 136523***	AY347327	–	–	–	–	–
C. erumpens	**MFLUCC 16-0580***	KY417733	KY417767	KY417699	KY417801	–	–
C. eucalypti	LSEQ	AY347340	–	–	–	–	–
C. eucalypticola	**ATCC 96150***	AY347358	–	–	–	–	–
C. eucalyptina	CMW 5882	AY347375	–	–	–	–	–
C. eugeniae	CMW 7029	AY347364	–	–	–	–	–
C. euonymicola	**CFCC 50499***	MH933628	MH933662	MH933535	MH933598	MH933503	MH933570
C. euonymina	**CFCC 89993***	MH933630	MH933664	MH933537	MH933600	MH933505	MH933590
C. fraxinigena	**MFLUCC 14-0868***	MF190133	MF190078	–	–	–	–
C. friesii	CBS 194.42	AY347328	–	–	–	–	–
C. fugax	CBS 203.42	AY347323	–	–	–	–	–
C. germanica	CXY 1322	JQ086563	JX524617	–	–	–	–
C. gigalocus	**CFCC 89620***	KR045628	KR045708	KU710997	KU710957	KU710920	KR045669
C. granati	**CBS 144237***	MG971799	–	MG971949	–	MG971514	MG971664
C. hippophaës	CFCC 89639	KR045632	KR045712	KU711001	KU710961	KU710924	KR045673
C. japonica	CBS 375.29	AF191185	–	–	–	–	–
C. joaquinensis	**CBS 144235***	MG971895	–	MG972044	–	MG971605	MG971761
C. junipericola	**MFLU 17-0882***	MF190125	MF190072	–	–	MF377580	–
C. juniperina	**CFCC 50501***	MH933632	MH933666	MH933539	MH933602	MH933507	–
C. kantschavelii	CXY 1383	KM034867	–	–	–	–	–

Table 3 (continued)

Species	Isolate no	GenBank accession numbers					
		ITS	LSU	ACT	RPB2	*tef1*	TUB2
C. kunzei	CBS 118556	DQ243791	–	–	–	–	–
C. leucosperma	CFCC 89622	KR045616	KR045698	KU710988	KU710944	KU710911	KR045657
C. longiostiolata	**MFLUCC 16-0628***	KY417734	KY417768	KY417700	KY417802	–	–
C. longispora	**CBS 144236***	MG971905	–	MG972054	–	MG971615	MG971764
C. lumnitzericola	**MFLUCC 17-0508***	MG975778	MH253453	MH253457	MH253461	–	–
C. mali	CFCC 50028	MH933641	MH933675	MH933548	MH933606	MH933513	MH933577
C. melnikii	**MFLUCC 15-0851***	KY417735	KY417769	KY417701	KY417803	–	–
C. mougeotii	ATCC 44994	AY347329	–	–	–	–	–
C. multicollis	**CBS 105.89***	DQ243803	–	–	–	–	–
C. myrtagena	**CBS 116843***	AY347363	–	–	–	–	–
C. nitschkii	**CMW 10180***	AY347356	–	–	–	–	–
C. nivea	MFLUCC 15-0860	KY417737	KY417771	KY417703	KY417805	–	–
C. oleicola	**CBS 144248***	MG971944	–	MG972098	–	MG971660	MG971752
C. palm	**CXY 1280***	JN411939	–	–	–	KJ781297	–
C. parakantschavelii	**MFLUCC 15-0857***	KY417738	KY417772	KY417704	KY417806	–	–
C. parapersoonii	**T28.1***	AF191181	–	–	–	–	–
C. parapistaciae	**CBS 144506***	MG971804	–	MG971954	–	MG971519	MG971669
C. paratranslucens	**MFLUCC 16-0506***	KY417741	KY417775	KY417707	KY417809	–	–
C. pini	**CBS 224.52***	AY347316	–	–	–	–	–
C. pistaciae	**CBS 144238***	MG971802	–	MG971952	–	MG971517	MG971667
C. platanicola	**MFLU 17-0327***	MH253451	MH253452	MH253449	MH253450	–	–
C. platycladi	**CFCC 50504***	MH933645	MH933679	MH933552	MH933610	MH933516	MH933581
C. platycladicola	**CFCC 50038***	KT222840	MH933682	MH933555	MH933613	MH933519	MH933584
C. plurivora	**CBS 144239***	MG971861	–	MG972010	–	MG971572	MG971726
C. populicola	**CBS 144240***	MG971891	–	MG972040	–	MG971601	MG971757
C. populina	CFCC 89644	KF765686	KF765702	KU711007	KU710969	KU710930	KR045681
C. predappioensis	**MFLUCC 17-2458***	MG873484	MG873480	–	–	–	–
C. predappioensis	MFLU 17-0327	MH253451	MH253452	MH253449	MH253450	–	–
C. prunicola	**MFLU 17-0995***	MG742350	MG742351	MG742353	MG742352	–	–
C. pruinopsis	**CFCC 50034***	KP281259	KP310806	KP310836	KU710970	KP310849	KP310819
C. pruinosa	CBS 201.42	DQ243801	–	–	–	–	–
C. punicae	CBS 144244	MG971943	–	MG972091	–	MG971654	MG971798
C. quercicola	**MFLUCC 14-0867***	MF190129	MF190073	–	–	–	–
C. rhizophorae	MUCC302	EU301057	–	–	–	–	–
C. ribis	CBS 187.36	DQ243810	–	–	–	–	–
C. rosae	**MFLUCC 14-0845***	MF190131	MF190075	–	–	–	–
C. rostrata	**CFCC 89909***	KR045643	KR045722	KU711009	KU710974	KU710932	KR045684
C. rusanovii	**MFLUCC 15-0854***	KY417744	KY417778	KY417710	KY417812	–	–
C. salicacearum	**MFLUCC 16-0509***	KY417746	KY417780	KY417712	KY417814	–	–
C. salicicola	**MFLUCC 14-1052***	KU982636	KU982635	KU982637	–	–	–
C. salicina	**MFLUCC 15-0862***	KY417750	KY417784	KY417716	KY417818	–	–
C. salicina	**MFLUCC 15-0862***	KY417750	KY417784	KY417716	KY417818	–	–
C. schulzeri	CFCC 50040	KR045649	KR045728	KU711013	KU710980	KU710936	KR045690
C. sibiraeae	**CFCC 50045***	KR045651	KR045730	KU711015	KU710982	KU710938	KR045692
C. sophorae	CFCC 89598	KR045654	KR045733	KU711018	KU710985	KU710941	KR045695
C. sophoricola	**CFCC 89595***	KR045655	KR045734	KU711019	KU710986	KU710942	KR045696
C. sophoriopsis	**CFCC 89600***	KR045623	KP310804	KU710992	KU710951	KU710915	KP310817

Table 3 (continued)

Species	Isolate no	GenBank accession numbers					
		ITS	LSU	ACT	RPB2	*tef1*	TUB2
C. sorbi	**MFLUCC 16-0631***	KY417752	KY417786	KY417718	KY417820	–	–
C. sorbicola	**MFLUCC 16-0584***	KY417755	KY417789	KY417721	KY417823	–	–
C. spiraeae	**CFCC 50049***	MG707859	MG707643	MG708196	MG708199	–	–
C. tamaricicola	**CFCC 50508***	MH933652	MH933687	MH933560	MH933617	MH933523	MH933588
C. tanaitica	**MFLUCC 14-1057***	KT459411	KT459412	KT459413	–	–	–
C. thailandica	**MFLUCC 17-0262***	MG975776	MH253455	MH253459	MH253463	–	–
C. tibouchinae	**CPC 26333***	KX228284	KX228335	–	–	–	–
C. translucens	CXY 1351	KM034874	–	–	–	–	KM034895
C. ulmi	**MFLUCC 15-0863***	KY417759	–	–	–	–	–
C. valsoidea	**CMW 4309***	AF192312	–	–	–	–	–
C. variostromatica	**CMW 6766***	AY347366	–	–	–	–	–
C. vinacea	**CBS 141585***	KX256256	–	–	–	KX256277	KX256235
C. viticola	**CBS 141586***	KX256239	–	–	–	KX256260	KX256218
C. xylocarpi	**MFLUCC 17-0251***	MG975775	MH253462	MH253462	MH253462	–	–

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

compare with other species in *Cyphellophora* (Yang et al. 2018). There are 26 epithets of *Cyphellophora* in Index Fungorum (2019). Yang et al. (2018) clarified 23 species in this genus. To properly delineate these species, phylogenetic studies using multi-loci sequences (ITS, LSU, RPB1 and TUB2) and the secondary structures of ITS analyses are needed (Réblová et al. 2013; Feng et al. 2014; Gao et al. 2014; Yang et al. 2018).

Molecular based identification and diversity

Based on SSU and LSU sequence data, *Cyphellophora* clustered in a well-supported clade within the Chaetothyriales (Feng et al. 2014). Generic and species delimitation with morphological characters, ecological traits, host distribution and phylogenetic analyses using the internal transcribed spacer region (ITS), the partial β-tubulin gene (TUB2), the nuclear large subunit rDNA gene (LSU) and the DNA dependent RNA polymerase II largest subunit (RPB1) were recently performed (Feng et al. 2014; Gao et al. 2014). The present study reconstructs the phylogeny of *Cyphellophora* based on analyses of a combined ITS, TUB2, LSU and RPB1 sequence data (Table 4, Fig. 9). The phylogenetic tree in this study is updated with recently introduced *Cyphellophora* species and corresponds to previous studies (Feng et al. 2014; Gao et al. 2014). *Cyphellophoroa indica* and *C. taiwanensis* lack sequences in GenBank (4/7/2019). *Cyphellophoroa hylomeconis* was synonymized as *Camptophora hylomeconis* and *C. eugeniae* was synonymized as *Aphanophora eugeniae* (Réblová et al. 2013). *Cyphellophoroa eucalypti* were synonymized as *C. guyanensis* (Feng et al. 2014). Therefore, these species were not included in the present phylogenetic analyses (Fig. 9).

Recommended genetic markers (genus level)—LSU and SSU

Recommended genetic markers (species level)—ITS, LSU, TUB2, RPB1 and secondary (2D) structure of ITS analyses

LSU is useful for preliminary identification at the generic level (Feng et al. 2014). Réblová et al. (2013) resolved *Cyphellophora* and *Phialophora* as close relatives within the Chaetothyriales, although both genera were paraphyletic based on analysis of ITS, TUB2 and nuc28S rDNA sequence data. It is recommended to use a combination of ITS, LSU, TUB2, RPB1 and secondary (2D) structure of ITS analyses (Réblová et al. 2013; Feng et al. 2014; Gao et al. 2014) in order to identify to the species level.

Accepted number of species: **24 species**

References: Vries 1962, 1986; Matsushima 1987; Walz and de Hoog 1987; Decock et al. 2003; Crous et al. 2013, 2016; Réblová et al. 2013; Feng et al. 2014; Gao et al. 2014; Madrid et al. 2016; Yang et al. 2018 (morphology, phylogeny)

Cyttaria Berk., Trans. Linn. Soc. London 19:40 (1842)

This genus is geographically restricted to South America (Argentina and Chile) and Southeastern Australasia (including Tasmania, and New Zealand) (Peterson and Pfister 2010). *Cyttaria* species are found in the secondary phloem and xylem, cambium and cortex of the hosts. They produce

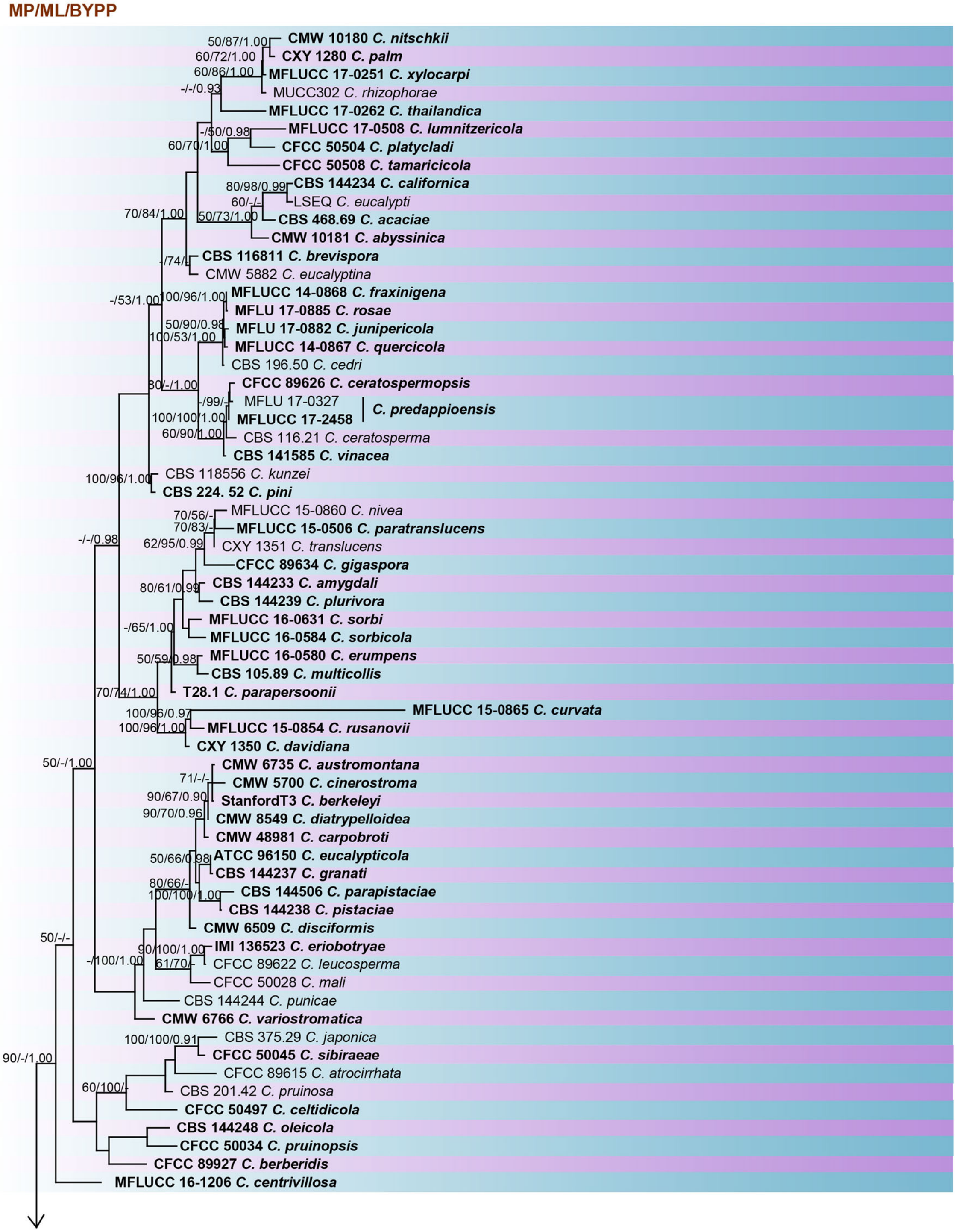


Fig. 8 Phylogenetic tree generated by maximum parsimony analysis of combined ITS, LSU, ACT and RPB2 sequence data of *Cytospora* species. Related sequences were obtained from GenBank. One hundred and eleven strains are included in the analyses, which comprised 2266 characters including gaps. The tree was rooted with *Diaporthe vaccinii* (CBS 160.32). The maximum parsimonious dataset consisted of 1358 constant, 596 parsimony-informative and 312 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of ten equally most parsimonious trees with a length of 3836 steps (CI = 0.364, RI 0.649, RC = 0.236, HI = 0.636) in the first tree. MP and ML bootstrap values ≥ 50% and Bayesian posterior probabilities ≥ 0.90 are shown respectively near the nodes. The scale bar indicates 10 changes per site. Ex-type strains are in bold

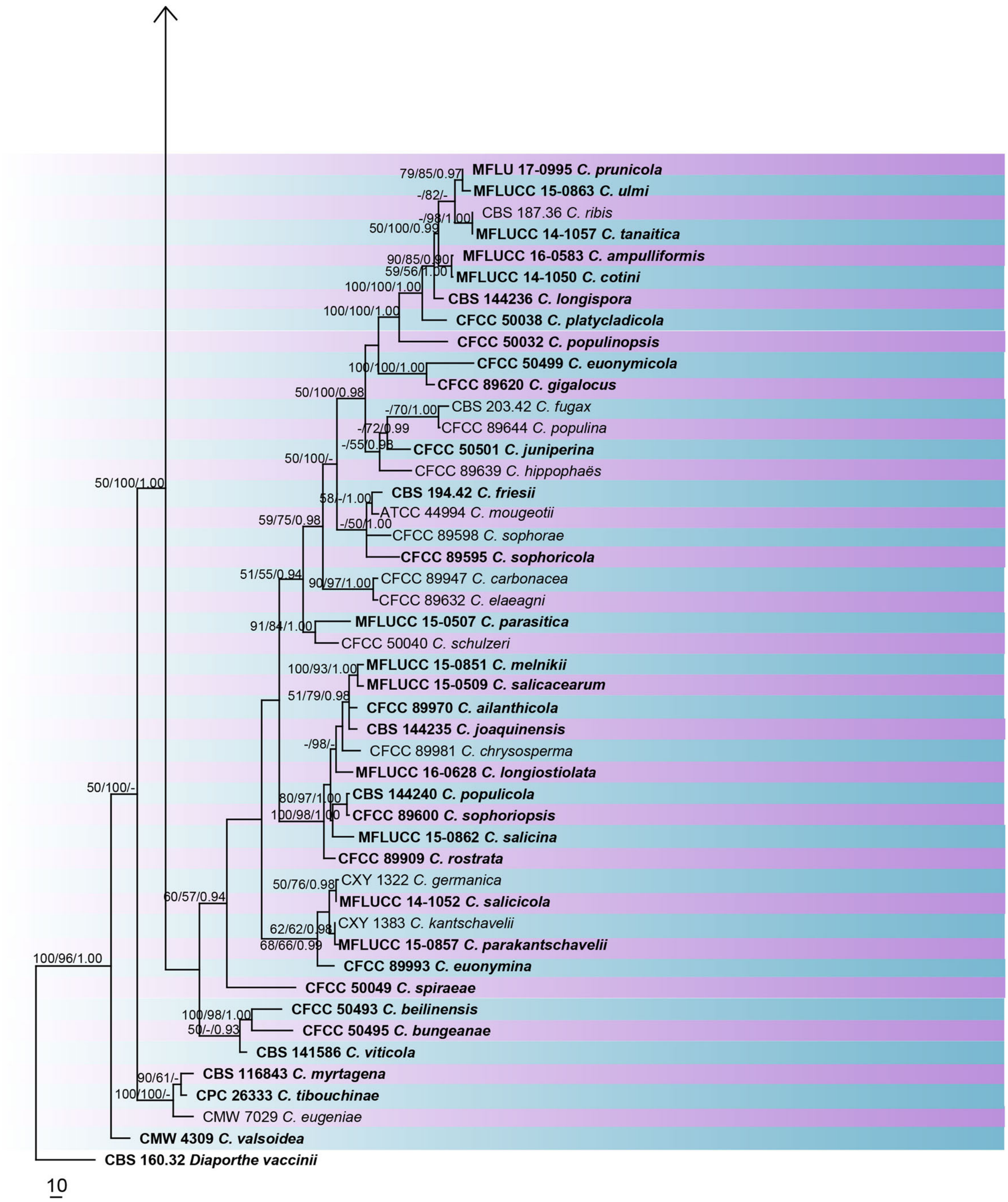


Fig. 8 continued

trunk and branch cankers that arise due to localized, stimulated cambial activity attributed to the presence of hyphae of *Cyttaria* (Wilson 1907; Gutierrez de Sanguinetti 1988). *Cyttaria* species are considered as weak parasites (Gamundí and De Lederkremer 1989).

Classification—*Leotiomycetes*, *Leotiomycetidae*, *Cyttariales*, *Cyttariaceae*

Type species—***Cyttaria darwinii*** Berk., Trans. Linn. Soc. London 19:40 (1842)

Distribution—Argentina, Australia, Chile, New Zealand, Tasmania.

Disease symptoms—Canker, galls

These species are known to cause two types of cankers: globose and longitudinal. Globose cankers arise from

Table 4 Details of the ***Cyphellophora*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	LSU	RPB1	TUB2
Cyphellophora ambigua	**CBS 235.93***	JQ766431	JQ766480	JQ766386	JQ766340
C. artocarpi	**CGMCC3.17496***	KP010367	KP122930	KP122920	KP122925
C. catalaunica	**CPC 22929***	HG003670	HG003673	–	–
C. chlamydospora	**CBS 127581 (= FMR 10878) ***	HG003674	HG003675	–	–
C. europaea	**CBS 101466***	JQ766443	KC455259	JQ766395	JQ766365
C. europaea	CBS 218.78	JQ766441	JQ766488	JQ766393	JQ766366
C. europaea	CBS 129.96	JQ766440	JQ766487	JQ766392	JQ766364
C. filicis	KUMCC 18-0144	MK404056	MK404052	–	–
C. fusarioides	**CBS 130291***	JQ766439	KC455252	JQ766391	JQ766363
C. gamsii	**CPC 25867***	KX228255	KX228307	–	KX228381
C. guyanensis	**MUCL 43737***	KC455240	KC455253	–	KC455223
C. guyanensis	CBS 124764	GQ303274	GQ303305	–	–
C. guyanensis	CBS 126014	JQ766434	JQ766483	JQ766389	JQ766339
C. jingdongensis	**IFRDCC 2659***	MF285234	MF285236	–	–
C. laciniata	**CBS 190.61***	JQ766423	JQ766472	JQ766378	JQ766329
C. laciniata	CBS 174.79	JQ766422	JQ766471	JQ766377	JQ766328
C. laciniata	CBS 239.91	JQ766424	JQ766473	JQ766379	JQ766330
C. livistonae	CPC19433	KC005774	KC005796	–	–
C. musae	**CGMCC3.17497***	KP010370	KP122932	KP122922	KP122927
C. musae	GLGZXJ9B	KP010368	KP122931	KP122923	KP122926
C. musae	GLMMZZ4	KP010369	KP122934	KP122921	KP122928
C. olivacea	**CBS 123.74***	KC455248	KC455261	–	KC455231
C. olivacea	CBS 122.74	KC455247	KC455260	–	KC455230
C. oxyspora	**CBS 698.73***	JQ766450	KC455262	JQ766402	KC455232
C. oxyspora	CBS 416.89	JQ766449	JQ766497	JQ766401	JQ766374
C. pauciseptata	**CBS 284.85***	JQ766466	JQ766515	JQ766415	JQ766360
C. phyllostachidis	**CGMCC3.17495***	KP010371	KP122933	KP122924	KP122929
C. pluriseptata	**CBS 286.85***	JQ766429	KC455255	JQ766384	JQ766335
C. pluriseptata	CBS 109633	JQ766430	JQ766479	JQ766385	JQ766336
C. reptans	**CBS 113.85***	JQ766445	JQ766493	JQ766397	JQ766370
C. reptans	CBS 152.90	JQ766446	JQ766494	JQ766398	JQ766371
C. reptans	CBS 458.92	JQ766447	JQ766495	JQ766399	JQ766372
C. reptans	CBS120903	JQ766448	JQ766496	JQ766400	JQ766373
C. sessilis	**CBS 243.85***	EU514700	EU514700	–	KC455234
C. sessilis	CBS 238.93	AY857541	KF928523	–	KF928587
C. suttonii	**CBS 449.91***	JQ766459	KC455256	–	KC455226
C. suttonii	FMR 10589	KU705828	KU705845	–	–
C. vermispora	**CBS 228.86***	KC455244	KC455257	JQ766381	JQ766332
C. vermispora	CBS 122852	JQ766427	JQ766476	JQ766382	JQ766333
C. vermispora	CBS 227.86	JQ766425	JQ766474	JQ766380	JQ766331
Cladophialophora immunda	CBS 834.96	EU137318	KC809990	–	EU137203

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

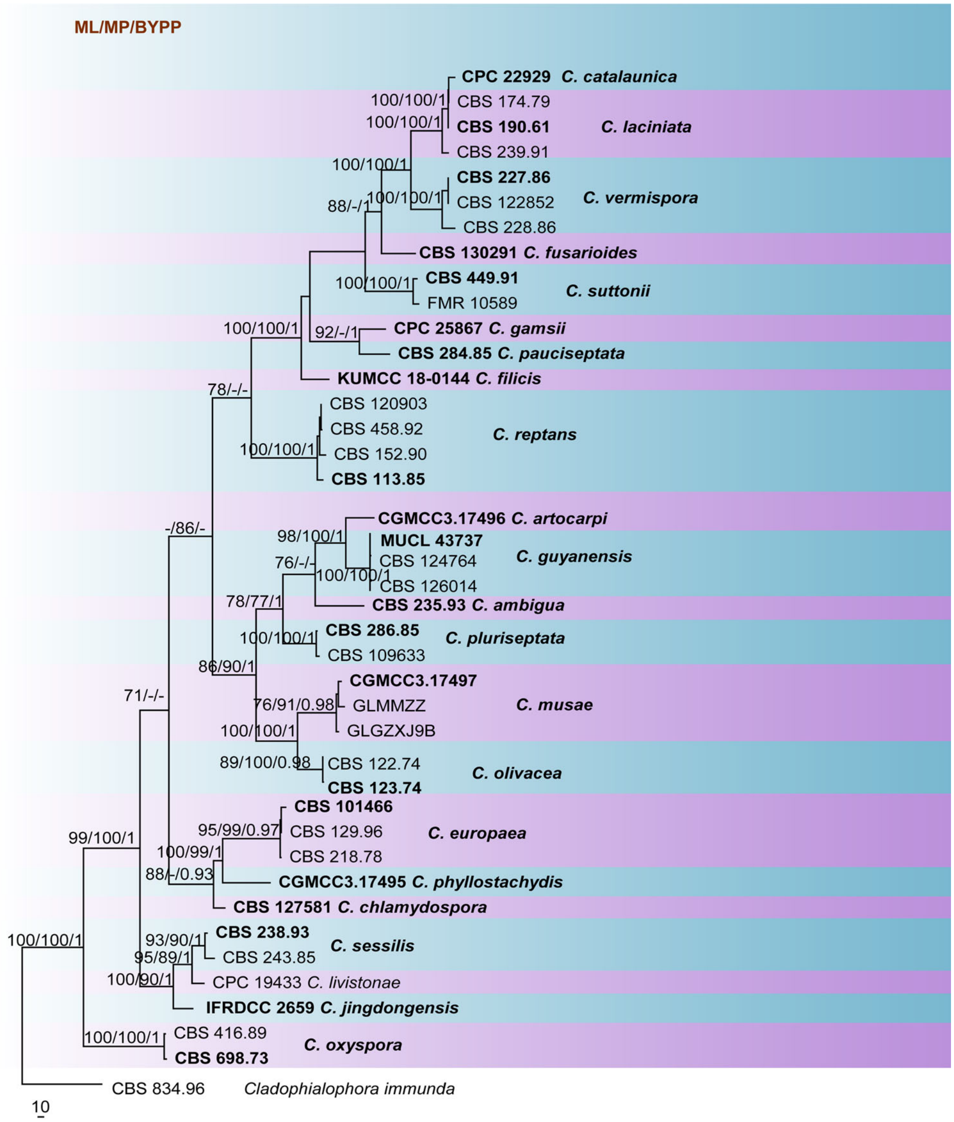


Fig. 9 Phylogram generated from RAxML analysis based on combined sequences of ITS, LSU, RPB1 and TUB2 sequences of all accepted species of *Cyphellophora*. Forty-one strains are included in the analyses, which comprise 2514 characters including gaps. The tree was rooted with *Cladophialophora immunda* (CBS 834.96). Tree topology of the ML analysis was similar to the MP and BYPP analyses. The best scoring RAxML tree with a final likelihood value of − 5928.387430 is presented. The matrix had 337 distinct alignment patterns, with 12.44% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.234866, C = 0.250597, G = 0.284325, T = 0.230211; substitution rates AC = 1.492532, AG = 2.025910, AT = 2.769660, CG = 1.674732, CT = 8.545312, GT = 1.000000; gamma distribution shape parameter α = 0.136482. RAxML and maximum parsimony bootstrap support value ≥ 50% are shown respectively near the nodes. Bayesian posterior probabilities ≥ 0.95 (BYPP) indicated as thickened black branches. Ex-type strains are in bold

growth mainly in the transverse axis of the branch while longitudinal cankers arise from growth mainly along the long axis (Rawlings 1956; Gamundi 1971). Development of perennial galls on branches and stems may lead to malformation and occasional death of branches (Gadgil 1985).

Hosts—*Nothofagus* spp.

Morphological based identification and diversity

Ascomata of *Cyttaria* species are orange, pitted apothecia similar to deeply dimpled golf balls. Each fruiting body is composed of 1–200 apothecia immersed in a sterile fleshy-gelatinous stroma. Asci are 8-spored, inoperculate and amyloid. Ascospores are uninucleate, subglobose to ovoid, smooth to rugulose, at first hyaline to yellowish but later becoming pigmented (Mengoni 1986; Peterson et al 2010).

Molecular based identification and diversity

The first phylogenetic analysis which included *Cyttaria* was done by Gargas and Taylor (1995) showing its relationship with other discomycetes. Wang et al. (2006) showed its placement within Leotiomycetes using combined analysis of SSU, LSU and 5.8S rDNA gene sequence data and then confirmed by Ekanayaka et al. (2017). Peterson and Pfister (2010) did large scale phylogeny for *Cyttaria* including all accepted 12 species in the genus using sequence data of partial nucSSU, nucLSU and mtSSU rRNA, as well as *tef1*. They found *Cyttaria* to be a strongly supported clade and suggested a close relationship between *Cyttaria* and some members of the Helotiales (*Cordierites*, *Encoelia*, *Ionomidotis* and *Chlorociboria*) (Peterson and Pfister 2010). The present study reconstructs the phylogeny of *Cyttaria* based on analyses of a combined

Table 5 Details of ***Cyttaria*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	LSU	SSU	mtSSU
C. berteroi	Isolate 16	EU107205	EU107178	EU10723
C. darwinii	Isolate 40	EU107207	EU107180	EU107236
C. darwinii	Isolate 14	EU107208	EU107181	–
C. darwinii	Isolate 57	EU107206	EU107179	EU107235
C. darwinii	Isolate 45	EU107209	–	–
C. darwinii	Isolate 50	EU107211	–	–
C. darwinii	Isolate 49	EU107210	–	–
C. espinosae	Isolate 187	–	EU107183	EU107238
C. espinosae	Isolate 92	EU107212	EU107182	EU107237
C. exigua	Isolate 77	EU107214	EU107185	EU107240
C. exigua	Isolate 76	EU107213	EU107184	EU107239
C. gunnii	Isolate 138	–	EU107189	EU107242
C. gunnii	Isolate 127	EU107215	EU107186	EU107241
C. gunnii	Isolate 136	–	EU107188	–
C. gunnii	Isolate 132	–	EU107187	–
C. hariotii	Isolate 44	EU107217	EU107194	EU107245
C. hariotii	Isolate 55	EU107218	EU107195	EU107246
C. hariotii	Isolate 65	EU107223	–	–
C. hariotii	Isolate 64	EU107222	–	–
C. hariotii	Isolate 63	EU107221	–	–
C. hariotii	Isolate 62	EU107220	–	–
C. hariotii	Isolate 51	EU107219	–	–
C. hookeri	Isolate 60	EU107227	–	–
C. hookeri	Isolate 59	EU107226	–	–
C. hookeri	Isolate 80	EU107228	–	–
C. hookeri	Isolate 61	EU107225	EU107197	–
C. hookeri	Isolate 58	EU107224	EU107196	–
C. johowii	Isolate 73	EU107229	EU107198	–
C. johowii	Isolate 74	EU107230	EU107199	–
C. nigra	Isolate 100	EU107232	EU107201	EU107248
C. nigra	Isolate 97	EU107231	EU107200	EU107247
C. septentrionalis	Isolate 199	–	EU107203	EU107249
C. septentrionalis	Isolate 85	–	EU107202	–

LSU, SSU and mtSSU sequence data (Table 5, Fig. 10). The phylogenetic tree is updated with recently introduced *Cyttaria* species and corresponds to previous studies (Feng et al. 2014; Gao et al. 2014).

Recommended genetic markers (genus level)—ITS, LSU
Recommended genetic markers (species level)—nucSSU, nucLSU, mitSSU rRNA, and *tef1*

Combined nucSSU, nucLSU, mitSSU rRNA, and *tef1* can resolve almost all species of *Cyttaria* currently known from sequence data (Peterson et al 2010).

Accepted number of species: There are 21 epithets in Index Fungorum (2019). However, **12 species have molecular data and are treated as accepted.**

References: Mengoni 1986, Peterson et al 2010 (morphology); Peterson and Pfister (2010), Ekanayaka et al. 2017 (morphology, phylogeny).

Dactylonectria L. Lombard & Crous, in Lombard et al., Phytopath. Mediterr. 53(3): 523 (2014)

The genus *Dactylonectria* was introduced by Lombard et al. (2014) for a group of species which were previously treated in *Ilyonectria* (Chaverri et al. 2011; Cabral et al. 2012a, b, c). In morphology, *Dactylonectria* resembles *Ilyonectria* and *Neonectria* but can be distinguished by their characteristic ovoid to obpyriform, smooth to finely warted, dark-red ascomata with a papillate ostiolar region at the apex (Lombard et al. 2014; Gordillo and Decock

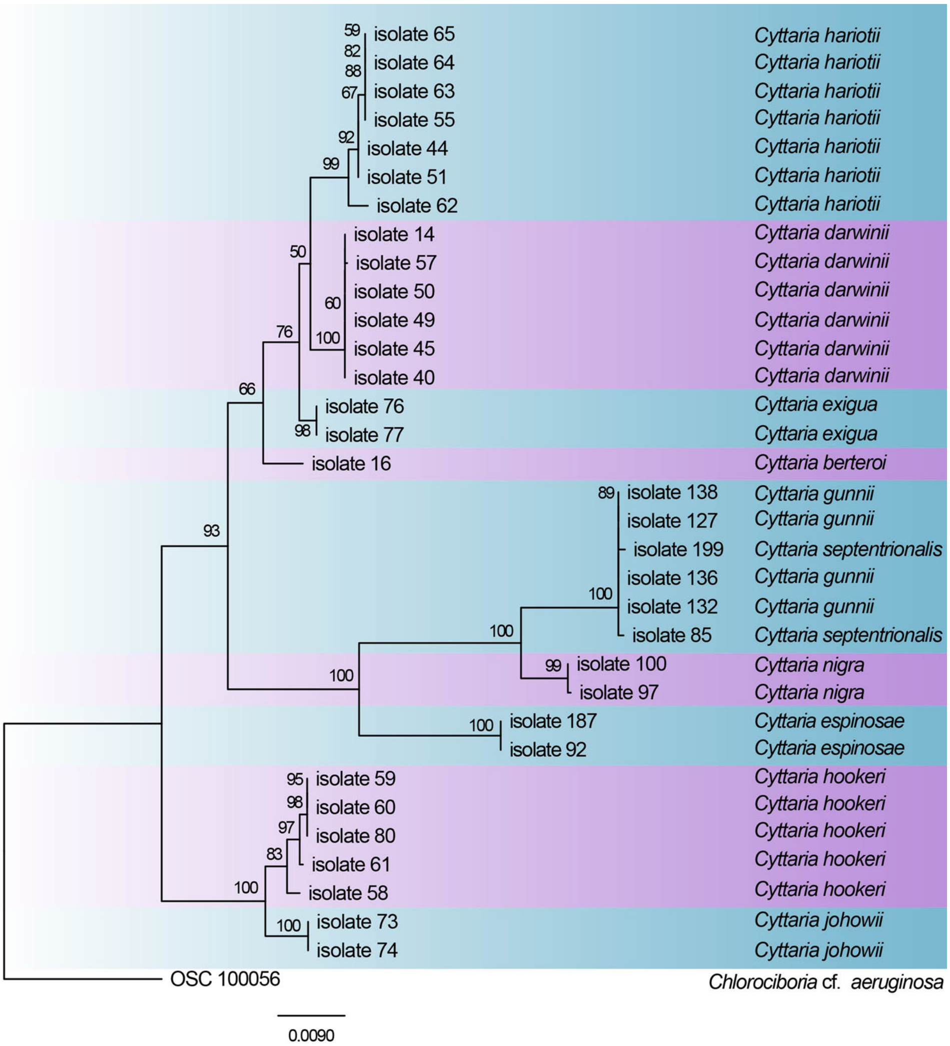


Fig. 10 Phylogram generated from RAxML analysis based on combined sequences of LSU, SSU and mtSSU sequences of all the accepted species of *Cyttaria*. Related sequences were obtained from GenBank. Thirty-four strains are included in the analyses, which comprise 3480 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree was rooted with *Chlorociboria cf. aeruginosa* (OSC 100056). The best scoring RAxML tree with a final likelihood value of − 7505.900855 is presented. The matrix had 360 distinct alignment patterns, with 39.17% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.256, C = 0.214, G = 0.280, T = 0.250; substitution rates AC = 1.190197, AG = 1.207782, AT = 0.373130, CG = 0.681125, CT = 3.724394, GT = 1.000000; gamma distribution shape parameter α = 0.020000. RAxML and maximum parsimony bootstrap support value ≥ 50% (BT) are shown respectively near the nodes

2018). Species of this genus are mostly associated with *Vitis* sp., while some species are also recorded from other hosts (Farr and Rossman 2019).

Classification—Sordariomycetes, *Hypocreomycetidae*, *Hypocreales*, *Nectriaceae*

*Type species—**Dactylonectria macrodidyma*** (Hallen, Schroers & Crous) L. Lombard & Crous, in Lombard et al., Phytopath. Mediterr. 53(3): 527 (2014)

Distribution—Worldwide

Disease symptoms—Black foot disease, black root rot

Characteristic symptoms of black foot disease include a reduction in root biomass and root hairs with sunken and necrotic lesions (Halleen et al. 2006). Severe necrosis of the root system results in stunting, wilting, leaf chlorosis, browning and leaf drop prior to death (Parkinson et al. 2017). *Dactylonectria alcacerensis*, *D. estremocensis*, *D. macrodidyma*, *D. novozelandica*, *D. pauciseptata*, *D. pinicola*, *D. torresensis* and *D. vitis* are associated with black foot disease of grapevine (Cabral et al. 2012a; Lombard et al. 2014) (Fig. 11).

Hosts—*Abies* sp., *Annona cherimola*, *Anthrium* sp., *Arbutus unedo*, *Cistus albidus*, *Crataegus azalous*, *Erica melanthera*, *Eriobotrya japonica*, *Ficus* sp., *Fragaria* sp., *Hordeum vulgare*, *Ilex aquifolium*, *Juglans regia*, *Juniperus phoenicea*, *Lonicera* sp., *Myrtus communis*, *Persea americana*, *Picea glauca*, *Pinus* sp., *Pistacia lentiscus*,

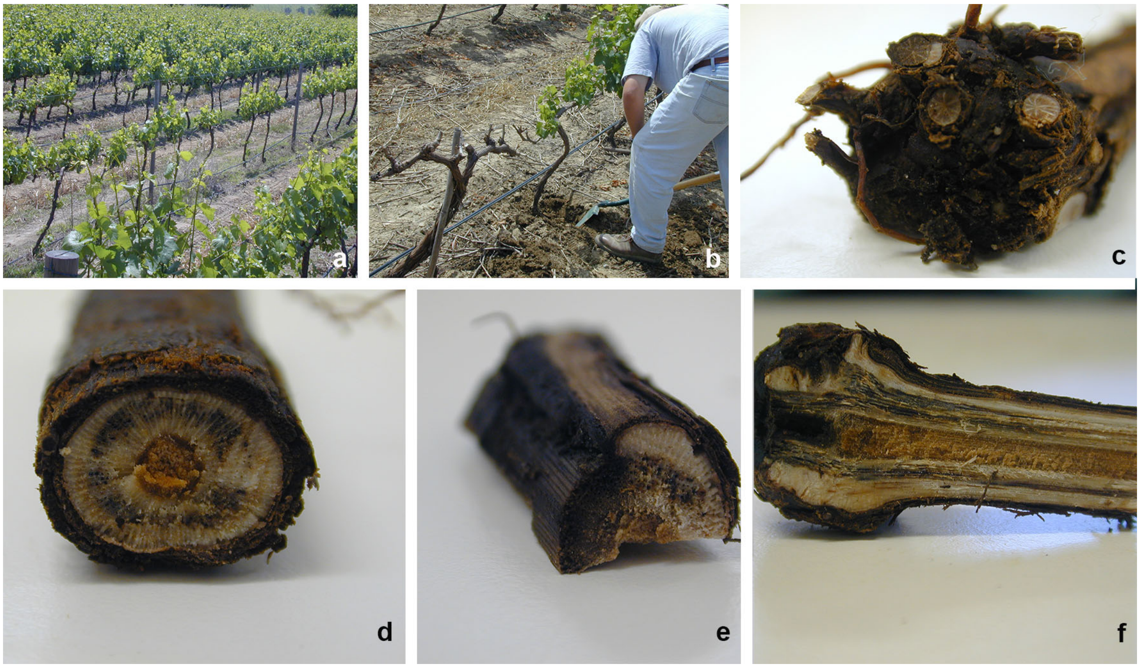


Fig. 11 Symptoms of black foot disease on *Vitis* spp. **a**, **b** dead plants and stunted growth of grapevine. **c**, **e** Infection of rootstock. **d** Blocked xylem vessels. **f** Black streak (Courtesy of Halleen)

Prunus domestica, *Pyracantha* sp., *Quercus* sp., *Rosmarinus officinalis*, *Santolina chamaecyparissus* and *Vitis* sp.

Morphological based identification and diversity

Lombard et al. (2014) accepted ten species in *Dactylonectria* based on ITS, LSU, TUB2 and *tef1* sequence data and morphological characters. Later, Gordillo and Decock (2018) introduced another four species to the genus based on morphology and sequence data.

Fourteen *Dactylonectria* species have been described with DNA sequence data in GenBank. *Dactylonectria* species produce cylindrocarpon-like asexual morphs, several of which were previously treated in *Ilyonectria* (Lombard et al. 2014). *Dactylonectria* species were distinguished mainly by phylogenetic inference and using unique fixed single nucleotide polymorphisms (SNP's) rather than morphological characters (Lombard et al. 2014; Gordillo and Decock 2018).

Molecular based identification and diversity

Lombard et al. (2014) re-evaluated genera with cylindrocarpon-like asexual morphs based on multi-gene phylogeny of ITS, LSU, TUB2 and *tef1* genes. Gordillo and Decock (2018) analysed His3 together with latter gene regions, for delimiting the species in *Dactylonectria*. Lombard et al. (2015) also supported the fact that *Dactylonectria* is monophyletic and distinct from *Ilyonectria*. In this study, we reconstruct the phylogeny of *Dactylonectria* based on analyses of a combined ITS, LSU, TUB2 and *tef1* sequence data (Table 6, Fig. 12). The phylogenetic tree is updated with recently introduced *Dactylonectria* species and corresponds to previous studies (Lombard et al. 2014, 2015; Gordillo and Decock 2018).

Recommended genetic markers (genus level)—ITS, LSU, TUB2, *tef1*
Recommended genetic markers (species level)—TUB, *tef1*
Accepted number of species: **14 species**
References: Cabral et al. 2012a, b; Halleen et al. 2004, Schroers et al. 2008; Lombard et al. 2014; Gordillo and Decock 2018 (morphology, phylogeny).

Entoleuca Syd., Annls mycol. 20(3/4):186 (1922)

The genus *Entoleuca* Syd. (*Xylariaceae*) consists of saprobic and plant pathogenic species distributed in Europe. *Entoleuca mammata* causes canker diseases (commonly known as Hypoxylon canker) on *Malus* sp. (*Rosaceae*), *Populus* sp., *Salix* sp. (*Salicaceae*) and *Sorbus* sp. (*Rosaceae*) (Shaw 1973; Callan 1998; Kasanen et al. 2004; Eriksson 2014) and also occurs as a saprobe on decaying tree trunks. The species are distributed in terrestrial habitats in temperate regions. The genus is characterized by its known sexual morph. It is characterized by partially embedded solitary or aggregated orbicular stroma, that has a whitish surface when young and dark surface at maturity, papillate ostiole; multiple, monostichous and embedded ascomata in stromata; 8-spored, unitunicate asci that are cylindrical, long pedicellate, with J+ apical ring bluing in Melzer's reagent and uniseriate, unicellular,

Table 6 Details of the ***Dactylonectria*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	LSU	TUB2	*tef1*
Campylocarpon fasciculare	**CBS 112613***	AY677301	HM364313	AY677221	JF735691
Dactylonectria alcacerensis	**CBS 129087***	JF735333	KM231629	AM419111	JF735819
D. anthuriicola	**CBS 564.95***	JF735302	KM515897	JF735430	JF735768
D. amazonica	**MUCL55433***	MF683707	MF683727	MF683644	MF683665
D. ecuadoriense	**MUCL55424***	MF683704	MF683724	MF683641	MF683662
D. estremocencis	**CBS 129085***	JF735320	KM231630	JF735448	JF735806
D. hordeicola	**CBS 162.89***	AM41906	KM515898	AM419084	JF735799
D. macrodidyma	**CBS 112615***	AY677290	KM515900	AY677233	JF735836
D. novozelandica	**CBS 112608***	AY677288	KM515901	AY677235	JF735821
D. palmicola	**MUCL55426***	MF683708	MF683728	MF683645	MF683666
D. pauciseptata	**CBS 120171***	EF607089	KM515903	EF607066	JF735776
D. pinicola	**CBS 173.37***	JF735319	KM515905	JF735447	JF735803
D. polyphaga	**MUCL55209***	MF683689	MF683710	MF683626	MF683647
D. torresensis	**CBS 129086***	JF735362	KM231631	JF735492	JF735870
D. vitis	**CBS 129082***	JF735303	KM515907	JF735431	JF735769

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

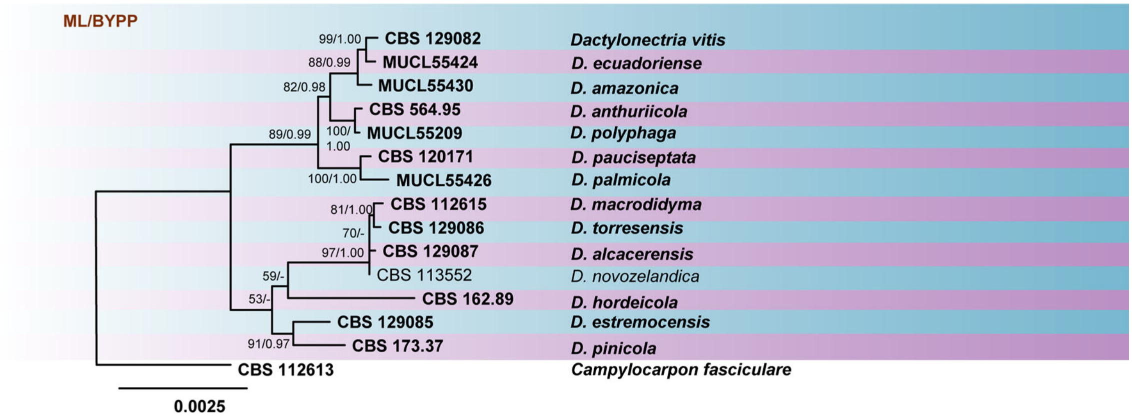


Fig. 12 Phylogram generated from RAxML analysis based on combined sequences of ITS, LSU, TUB and *tef1* sequences of all the accepted species of *Dactylonectria*. Related sequences were obtained from GenBank. Fifteen taxa are included in the analyses, which comprise 2460 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree was rooted with *Campylocarpon fasciculare* (CBS 112613). Tree topology of the ML analysis was similar to the BI. The best scoring RAxML tree with a final likelihood value of − 6772.195394 is presented. The matrix had 261 distinct alignment patterns, with 0.96% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.230657, C = 0.279364, G = 0.252128, T = 0.237852; substitution rates AC = 1.388608, AG = 2.845402, AT = 2.389715, CG = 0.838197, CT = 7.220493, GT = 1.000000; gamma distribution shape parameter α = 0.650385. RAxML and maximum parsimony bootstrap support value ≥ 50% are shown respectively near the nodes. Bayesian posterior probabilities ≥ 0.95 (BYPP) indicated as thickened black branches. Ex-type strains are in bold

ellipsoidal inequilateral, brown, with straight to oblique germ slit ascospores (Rogers and Ju 1996; Daranagama et al. 2018). Daranagama et al. (2018) provided an identification key with emphasis on the coarsely papillate ostiole in *Entoleuca*.

Sydow and Petrak (1922) introduced the genus with *E. callimorpha* as the type species. Until 1994, *Hypoxylon mammatum* was considered a similar taxon to *E. callimorpha*. However, Læssøe and Spooner (1994) and Læssøe (1994) treated *H. mammatum* as a separate, synonym to *Rosellinia*. Based on these taxonomic confusions, Rogers and Ju (1996) revised the type, authentic and other specimens and re-established the genus *Entoleuca*.

Classification—Sordariomycetes, *Xylariomycetidae*, *Xylariales*, *Xylariaceae*

Type species—***Entoleuca callimorpha*** Syd., in Sydow & Petrak, Annls mycol. 20(3/4):186 (1922)

Distribution—Austria, Canada, Poland, Sweden, USA

Disease symptoms—Canker

Symptoms may vary on the stage of disease development. Young cankers appear as slightly sunken, yellowish orange areas with irregular margins. Later, the outer-most bark within the canker breaks out in blisters exposing a powdery grey mat of fungal tissue and conidia. Then the patches of bark start to flake off making the canker rough and black in the centre. Advancing margins of the enlarging cankers become yellowish orange (Ostry 2013).

Hosts—Known from *Malus sylvestris*, *Populus* sp., *Salix* sp. and *Sorbus aucuparia*.

Morphological based identification and diversity

Currently, the genus comprises three species: *E. callimorpha*, *E. ellisii* and *E. mammata* (Sydow and Petrak 1922; Rogers and Ju 1996; Ju et al. 2004; Index Fungorum 2019). Due to the presence of clear papillate ostioles, they have been distinguished from closely related genera such as *Amphirosellinia*, *Nemania*, and *Rosellinia*. Molecular data are only available for *E. mammata*, which is the most important species in the genus as a pathogen. Rogers and Ju (1996) observed that there are no distinguishing morphological differences among *E. mammata* isolates from different hosts. However, there is a high polymorphism, but no major phylogenetic differences among the isolates from Europe (Kasanen et al. 2004). Ju et al. (2004) introduced *E. ellisii* based on characterizations of ascospore and germ slit. Therefore, a combination of morphological and phylogenetic analyses are needed for species delimitation of *Entoleuca*.

Molecular based identification and diversity

Several recent studies have focused on the molecular phylogeny of *Entoleuca*, especially *E. mammata*. Phylogenetic based population studies revealed that higher polymorphism occurs in North American than in Europe (Kasanen et al. 2004). The sterile mycelia associated with *Pinus tabulaeformis* and its ITS-based phylogenetic analyses revealed that the genus *Entoleuca* clusters in *Xylariaceae* and is closely related to *Nemania* (Guo et al. 2003). Daranagama et al. (2018) revisited the family *Xylariaceae* and due to the morphological differences and conidial state characters, they suggested that it is useful to maintain the taxa as distinct genera. Daranagama et al. (2018) and Wendt et al. (2018) conducted multi-gene phylogenetic analyses using ITS, LSU, RPB2 and TUB2 and revealed that *E. mammata* clusters with *Rosellinia corticium* with high support. Due to the lack of molecular data from other species and other gene regions, it is difficult to place *Entoleuca* in an appropriate family.

In this study, we included the available sequences of *Entoleuca* in the analysis done for *Rosellinia* (Table 7, Fig 13).

Recommended genetic markers (genus level)—LSU and ITS

Recommended genetic markers (species level)—RPB2 and TUB2

Combined LSU, ITS, RPB2 and TUB2 provide a satisfactory resolution for resolving species.

Accepted number of species: **Three species**

References: Sydow and Petrak 1922; Rogers and Ju 1996; Ju et al. 2004 (morphology), Daranagama et al. 2018 (morphology, phylogeny).

Eutiarosporella Crous, in Crous et al., Phytotaxa 202(2): 85 (2015)

Eutiarosporella was introduced by Crous et al. (2015) and is typified by *Eutiarosporella tritici* (B. Sutton & Marasas) Crous on *Triticum aestivum* from South Africa. The genus was named on account of its similarity to *Tiarosporella* Höhn. (Crous et al. 2006). *Eutiarosporella* species are coelomycetes that are saprobes or pathogens which occur in terrestrial habitats (Crous et al. 2015; Thynne et al. 2015; Li et al. 2016). *Eutiarosporella* species have been reported from *Celtis africana* (Rosales), *Triticum aestivum* (Poales), *Acacia karroo* (Fabales) and *Dactylis glomerata* (Poales) (Thambugala et al. 2014; Crous et al. 2015). On wheat, it causes the economically important disease known as white grain disorder (Thynne et al. 2015). Several studies have reported this genus on woody hosts as a saprobe (Jami et al. 2012, 2014; Dissanayake et al. 2016).

Classification—Dothideomycetes, *incertae sedis*, *Botryosphaeriales*, *Botryosphaeriaceae*

Type species—***Eutiarosporella tritici*** (B. Sutton & Marasas) Crous, in Crous et al., Phytotaxa 202(2):85 (2015)

Distribution—Worldwide

Disease symptoms—White grain disorder of wheats

White grain disorder shrivels and discolours (white to light grey) wheat grain (Thynne et al. 2015). Affected grains are more brittle and can break during harvesting. Infected spikelets of green heads may show bleaching appreance or grey discolouration. At first, the bleached florets may show blue-gray ‘highlights’. Rachis of affected heads and the upper peduncle may show a brownish discolouration (Thynne et al. 2015).

Even though species of this genus have been found to be associated with several hosts other than wheat, their diseases have not been described.

Hosts—Acacia karroo, *Arrhenatherum elatius*, *Avenella flexuosa*, *Celtis africana*, *Dactylis glomerata*, *Triticum aestivum* and *Vachelloa karroo* (Farr and Rossman 2019).

Morphological based identification and diversity

Eutiarosporella is characterized by hairy conidiomata with long necks, and holoblastic conidiogenesis, features which

Table 7 Details of the ***Entoleuca* and *Rosellinia*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	LSU	RPB2
Coniolariella gamsii	**CBS 114379***	GU553325	GU553329	N/A
C. hispanica	**ATCC MYA4453***	GU553323	GU553353	N/A
C. limonispora	CBS 382.86	KF719199	KF719211	N/A
C. limonispora var. *australis*	AV1L2-3	KP101193	N/A	N/A
C. limonispora var. *australis*	AH24323	AY908997	N/A	N/A
Entoleuca mammata	JDR 100	GU300072	N/A	GQ844782
E. mammata	ATCC 58108	AF201713	N/A	N/A
E. mammata	Osterby 1	AF176983	N/A	N/A
Rosellinia abscondita	CBS 447.89	FJ175180	KF719208	N/A
R. aquila	MUCL 51703	KY610392	KY610460	KY624285
R. arcuate	CBS347.29	AB017660	N/A	N/A
R. asperata* var. *minor	**CBS 138641***	KY941107	N/A	N/A
R. australiensis	**CBS 142160***	KY979742	KY979797	N/A
R. britannica	CBS 446.89	FJ175182	KF719209	N/A
R. bunodes	CBS 347.36	AB609598	KF719205	N/A
R. buxi	JDR 99	GU300070	N/A	GQ844780
R. buxi	ATCC 32869	AY909000	EF489467	N/A
R. capetribulensis	**HKU(M) 17499***	AY862570	N/A	N/A
R. acutispora	CBS 138730	KY941108	N/A	N/A
R. chiangmaiensis	**MFLU 15-3524***	KU246226	KU246227	N/A
R. compacta	**NIAES:20565***	AB430457	N/A	N/A
R. convexa	**GZUCC 13005***	KF614036	N/A	KP876561
R. convexa	ZG-1-2-1	KR822145	N/A	N/A
R. corticium	MUCL 51693	KC477236	KY610461	KY624229
R. desmazieri	olrim153	AY805591	N/A	N/A
R. lamprostoma	HAST 89112602	EF026118	N/A	GQ844778
R. mammiformis	CBS 445.89	KF719200	KF719212	N/A
R. mearnsii	**MFLU 16-1382***	KY514059	KY514060	KY514061
R. merrillii	**HAST 89112601***	GU300071	N/A	GQ844781
R. necatrix	HAST 89062904	EF026117	AY083824	GQ844779
R. necatrix	CBS 349.36	AY909001	KF719204	N/A
R. nectrioides	CBS 449.89	FJ175181	KF719213	N/A
R. quercina	ATCC 36702	AB017661	N/A	N/A
R. sanctaecruciana	HAST 90072903	GU292824	N/A	GQ844777
R. subiculata	ATCC 58850	AY909002	EF489468	N/A
R. thelena	CBS 400.61	KF719202	KF719215	N/A
R. truncatispora	**CBS 138732***	KY941109	N/A	N/A
Xylaria bambusicola	**WSP 205***	EF026123	AB376825	GQ844802
X. grammica	HAST 479	GU300097	N/A	GQ844813
X. hypoxylon	**CBS 122620***	AM993141	KM186301	KM186302

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

are clearly distinguishable from *Tiarosporella* (Höhnel 1919; Crous et al. 2015). This genus is morphologically similar to *Marasasiomyces* (long-necked, hairy conidiomata, and holoblastic conidiogenesis), except that it forms conidiomata in clusters, which are not found in *Marasasiomyces* (Crous et al. 2015). Li et al. (2016) reported the sexual morph of *Eutiarosporella* in *E. dactylidis* for the first time from *Avenella flexuosa* (Poales). The sexual morph is characterised by globose ascomata, with a central ostiole, a two-layered peridium, hyphae-like pseudoparaphyses and hyaline, aseptate, fusoid to ovoid ascospores, with a mucilaginous sheath (Thambugala et al. 2014).

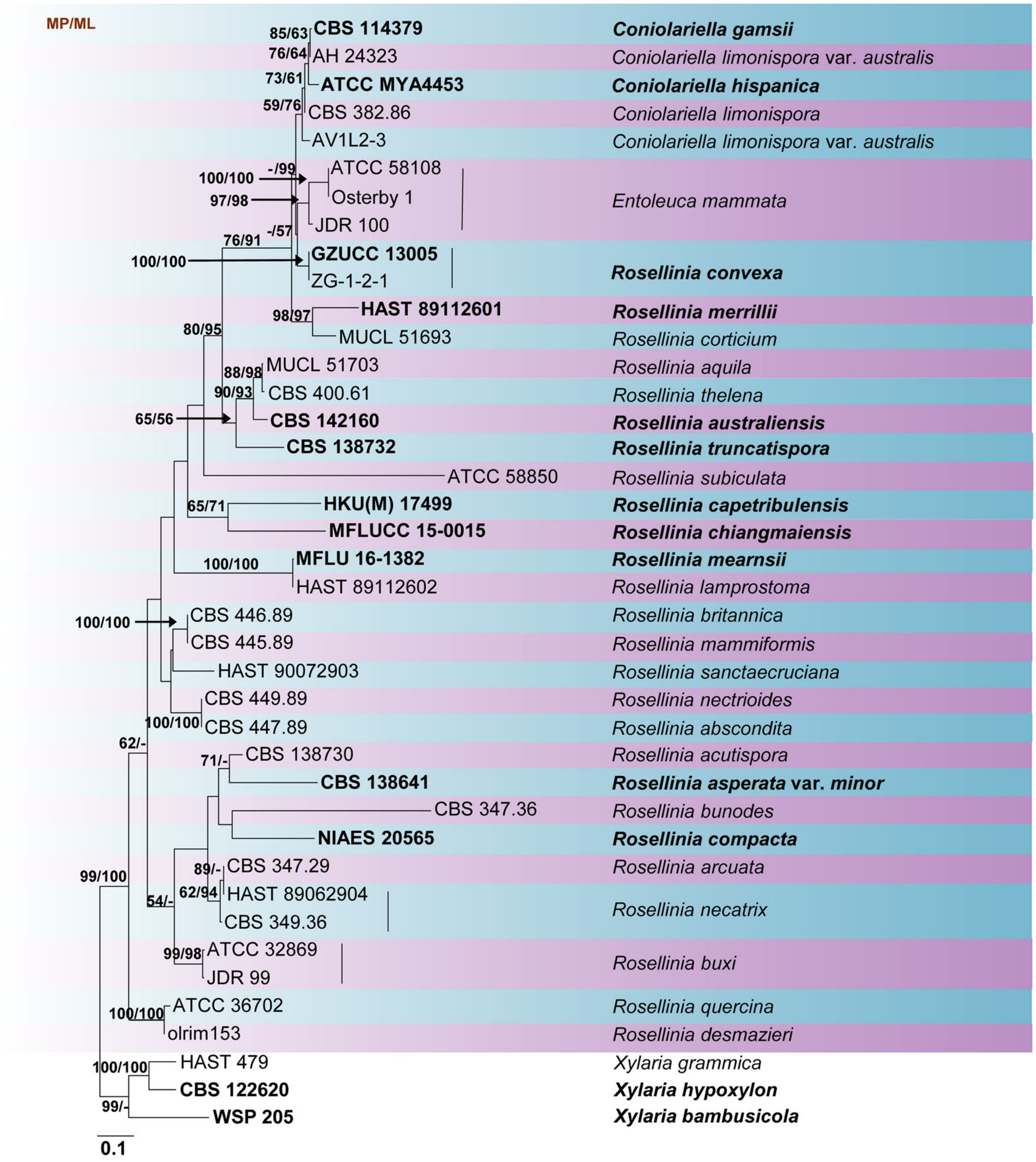


Fig. 13 Phylogenetic tree generated by maximum likelihood analysis of combined ITS, LSU and RPB2 sequence data of *Entoleuca* and *Rosellinia* species. Related sequences were obtained from GenBank. Forty strains are included in the analyses, which comprise 2336 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree was rooted with *Xylaria bambusicola* (WSP 205), *X. grammica* (HAST 479) and *X. hypoxylon* (CBS 122620). Tree topology of the ML analysis was similar to the MP. The best scoring RAxML tree with a final likelihood value of − 12521.202450 is presented. The matrix had 793 distinct alignment patterns, with 51.67% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.241655, C = 0.263843, G = 0.260086, T = 0.234416; substitution rates AC = 1.764265, AG = 4.237635, AT = 0.953946, CG = 1.541272, CT = 8.643978, GT = 1.000000; gamma distribution shape parameter α = 1.105097. The maximum parsimonious dataset consisted of constant 1567, 629 parsimony-informative and 140 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 2112 steps (CI = 0.545, RI = 0.668, RC = 0.364, HI = 0.455) in the first tree. RAxML and maximum parsimony bootstrap support value ≥ 50% are shown respectively near the nodes. Ex-type strains are in bold

Based on ITS and LSU sequence data, three species were initially included in this genus, *E. africana* (Jami et al.) Crous, *E. tritici* (B. Sutton & Marasas) Crous and *E. urbis-rosarum* (Jami et al.) Crous by Crous et al. (2015). Subsequently, *E. darliae* E. Thynne et al., *E. tritici-australis* E. Thynne, et al. and *E. dactylidis* (Thambug., Camporesi & K.D. Hyde) Dissan., Camporesi & K.D. Hyde were accommodated in the genus (Crous et al. 2015; Thynne et al. 2015; Li et al. 2016), which now comprises seven species (Dissanayake et al. 2016; Wijayawardene et al. 2017).

Colony and conidial morphology are the primary characters to identify species within this genus. Colonies on nutrient-rich media (PDA or V8-OMA) grow rapidly (Thynne et al. 2015). However, we consider morphological characters alone are inadequate to identify species due to plasticity and overlapping of conidial dimensions. Therefore, incorporation of molecular data together with morphology is recommended.

Molecular based identification and diversity

Taxonomy of *Eutiarosporella* is largely based on DNA sequence data to reveal the phylogenetic relationships between the species (Crous et al. 2015; Thynne et al. 2015; Dissanayake et al. 2016; Li et al. 2016). According to studies by Crous et al. (2015), Thynne et al. (2015) and Li et al. (2016), ITS and LSU are the most suitable loci for delineation of species within the genus. The phylogram generated with sequences available in GenBank including ex-epitype sequences is provided in Fig. 14 (Table 8). Our phylogenetic analyses are in accordance with previous studies by Crous et al. (2015), Thynne et al. (2015), Dissanayake et al. (2016) and Li et al. (2016).

Recommended genetic markers (genus level)—LSU and SSU
Recommended genetic markers (species level)—ITS and LSU
Accepted number of species: **Seven species**.
References: Crous et al. (2015), Thynne et al. (2015), Dissanayake et al. (2016), Li et al. 2016 (morphology, phylogeny).

Ilyonectria P. Chaverri & Salgado, in Chaverri et al., Stud. Mycol. 68:69 (2011)

Species of *Ilyonectria* (*Nectriaceae*, Hypocreales) are important soil-borne pathogens of various woody and herbaceous plant hosts. *Ilyonectria* species are cosmopolitan and are found on a wide range of hosts (Chaverri et al. 2011). They are mostly associated with root diseases and stem cankers (Seifert et al. 2003; Halleen et al. 2004, 2006; Chaverri et al. 2011; Cabral et al. 2012a, b, c; Vitale et al. 2012; Lombard et al. 2013; Aiello et al. 2014). There are 23 species of *Ilyonectria*, all associated with disease symptoms of their original plant hosts (Chaverri et al. 2011; Cabral et al. 2012a,c; Lombard et al. 2013, 2014; Aiello et al. 2014). *Ilyonectria* is a well-known genus causing black foot rot of grapevines in various countries (Halleen et al. 2003, 2004, 2006; Chaverri et al. 2011; Cabral et al. 2012a, b, c; Lombard et al. 2014).
Classification—*Sordariomycetes*, *Hypocreomycetidae*, *Hypocreales*, *Nectriaceae*
Type species—***Ilonectria radicicola*** (Gerlach & L. Nilsson) P. Chaverri & Salgado, in Chaverri et al., Stud. Mycol. 68:71 (2011)
Distribution—Worldwide
Disease symptoms—Black foot disease, black root rot

Symptoms are given under the genus *Dactylonectria*
Hosts—Wide host range including plant genera in *Amaryllidaceae*, *Aracaceae*, *Araliaceae*, *Cupressaceae*, *Fagaceae*, *Liliaceae*, *Myrtaceae*, *Pinaceae*, *Proteaceae*, *Rosaceae*, *Strelitziaceae* and *Vitaceae* (Farr and Rossman 2019).

Morphological based identification and diversity

The genus *Ilyonectria* was introduced based on *I. radicicola* as the type species, to accommodate *Neonectria* species belonging to the "*N. radicicola*" group (Booth 1959). This genus has asexual morphs and belonged to Booth's Group 3 (chlamydospores and microconidia present, Booth 1966; Chaverri et al. 2011; Lombard et al. 2014). Molecular phylogenetic studies revealed that *Ilyonectria*, as originally conceived, was paraphyletic (Cabral et al. 2012a, c; Lombard et al. 2013, 2014). Conidial size, culture characters and molecular data enabled the separation of *Ilyonectria* species (Cabral et al. 2012a, c; Lombard et al. 2013, 2014).

Molecular based identification and diversity

Delineating between species of *Ilyonectria* can be achieved with histone (His3) gene region. The topologies of the phylogenetic tree (Fig. 15, Table 9) is similar to previous studies done on this genus (Cabral et al. 2012a; Lombard et al. 2014).

Recommended genetic markers (genus level)—ITS, LSU, *tef1*, TUB2
Recommended genetic markers (species level)—*tef1*, TUB2, His3
Accepted number of species: **23** species
References: Booth 1959, 1966 (morphology), Cabral et al. 2012a, b, c; Lombard et al. 2013, 2014 (morphology, phylogeny).

Macrophomina Petr., Annls mycol. 21: 314 (1923)

Species of *Macrophomina* are mostly pathogens that cause damping-off, seedling blight, collar rot, stem rot, charcoal rot, basal stem rot and root rot in many plant species (Arora et al. 2001; Pal et al. 2001; Gupta et al. 2002; Sarr et al. 2014; Wijayawardene et al. 2017). The type species, *Macrophomina phaseolina* (Tassi) Goid., is a seed-borne polyphagous pathogen that affects more than 500 crop and non-crop species, including economically important crops, such as soybean, sunflower, common bean, peanut, corn, sorghum, cowpea and cotton (Gupta et al. 2002; Ndiaye et al. 2010; Sarr et al. 2014).

Classification—Dothideomycetes, *incertae sedis*, *Botryosphaeriales*, *Botryosphaeriaceae*

*Type species—**Macrophomina phaseolina*** (Tassi) Goid., Annali Sper. agr., N.S. 1(3): 457 (1947)

Distribution—Worldwide

Disease symptoms—Charcoal rot, collar rot, damping off, root rot, seedling blight, stem rot, wilt

Seedling damage can occur when infected seeds are planted. Infected plants may produce slightly smaller leaflets than healthy plants and have reduced vigour. As the disease advances, leaflets turn yellow, wilt and turn brown (Adorada et al. 2018). A grey/silver discolouration can be observed in the roots and lower stem when the plants split open (Romero Luna et al. 2017; Koehler and Shew 2018; Meena et al. 2018). In charcoal rot, the abundant production of minute black sclerotia by the fungus causes the rotted tissues to become blackened. Infections on soybean lead to early maturation and incomplete pod filling (ElAraby et al. 2003; Yang and Navi 2005; Sarr et al. 2014). In peanut, it causes seed and seedling rots, wilt, root and stem rots, leaf spot and rotting of developing pods and seeds (Gupta et al. 2002; Deshwal et al. 2003).

Hosts—This soil-borne fungus can infect more than 500 agricultural crops and weed species including, *Fragaria*, *Glycine*, *Helianthus*, *Sorghum* and *Zea*.

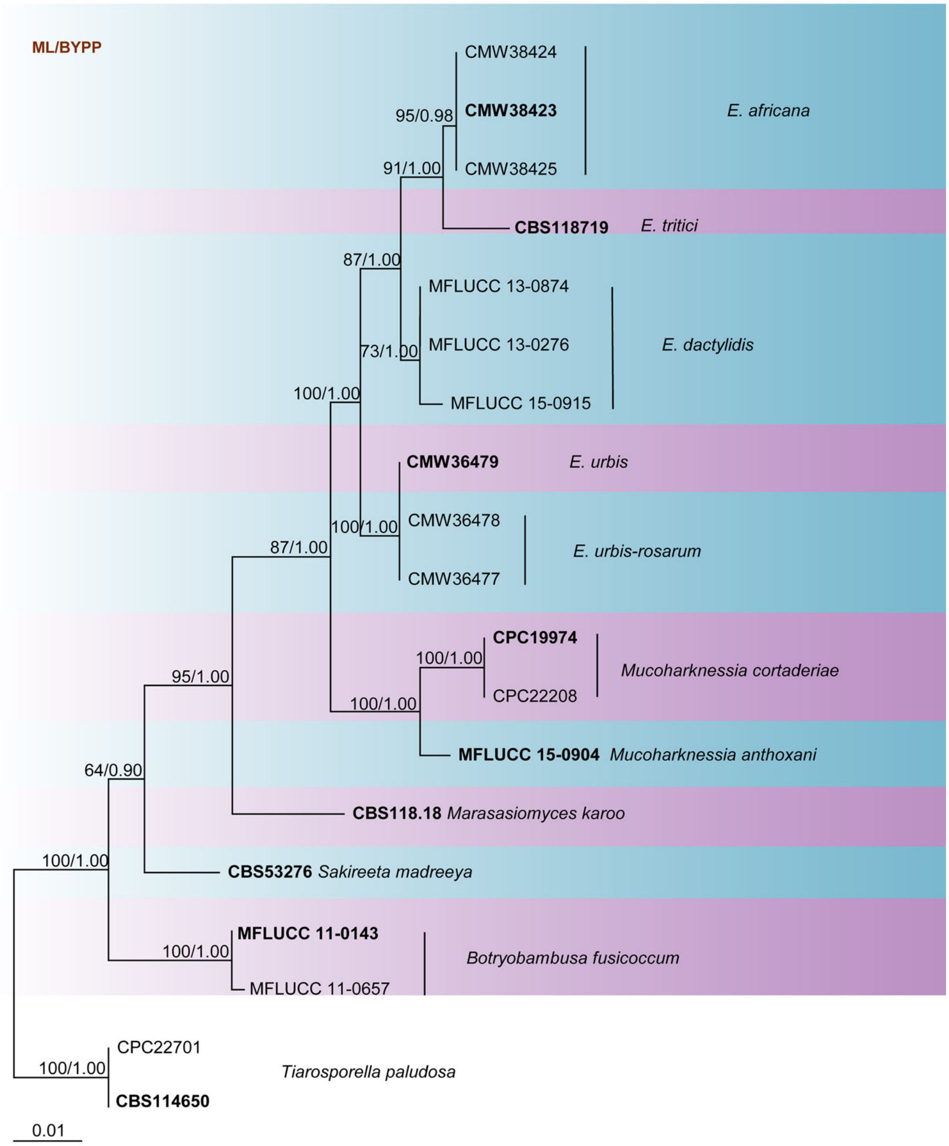


Fig. 14 Phylogram generated from maximum likelihood analysis based on combined LSU and ITS sequence data retrieved from GenBank. The tree is rooted in *Tiarosporella paludosa* (CPC 22701 and CBS 114650). Tree topology of the ML analysis was similar to the Bayesian analysis. The best scoring RAxML tree with a final likelihood value of − 7055.996836 is presented. The matrix had 380 distinct alignment patterns, with 40.12% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.229604, C = 0.264209, G = 0.282595, T = 0.223593; substitution rates AC = 1.357965, AG = 1.612491, AT = 0.913118, CG = 2.194420, CT = 5.121479, GT = 1.000000; gamma distribution shape parameter α = 0.137391. Maximum likelihood bootstrap support values greater than 60% are indicated above the nodes. Ex-type (ex-epitype) and voucher strains are in bold

Table 8 Details of the ***Eutiarosporella*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	LSU	ITS
Botryobambusa fusicoccum	MFLUCC 11-0657	JX646810	JX646793
B. fusicoccum	**MFLUCC 11-0143***	**JX646809**	**NR111793**
Eutiarosporella africana	**CMW 38423***	**KC769990**	**KC769956**
E. dactylidis	MFLUCC 15-0915	KU246380	NR148093
Eutiarosporella dactylidis	MFLUCC 13-0874	KM978948	KM978945
E. dactylidis	**MFLUCC 13-0276***	**KM978949**	**KM978944**
E. urbis	**CMW 36477***	**JQ239420**	**NR111705**
E. urbis-rosarum	CMW 36479	JQ239422	JQ239409
E. urbis-rosarum	CMW 36478	JQ239421	JQ239408
Marasasiomyces karoo	**CBS 1187.18***	**DQ377939**	**KF531828**
Mucoharknessia anthoxanthi	**MFLUCC 15-0904***	**KU246379**	**NR148092**
M. cortaderiae	CPC 22208	KM108402	KM108375
M. cortaderiae	**CPC 19974***	**KM108401**	**NR148075**
Sakireeta madreeya	**CBS 532.76***	**DQ377940**	**KC769960**
Tiarosporella africana	CMW 38425	KC769992	KC769958
T. africana	CMW 38424	KC769991	KC769957
T. paludosa	CPC 22701	KM108404	NR132907
T. paludosa	**CBS 114650***	**KM108403**	**KM108377**
T. tritici	**CBS 118719***	**DQ377941**	**KC769961**

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

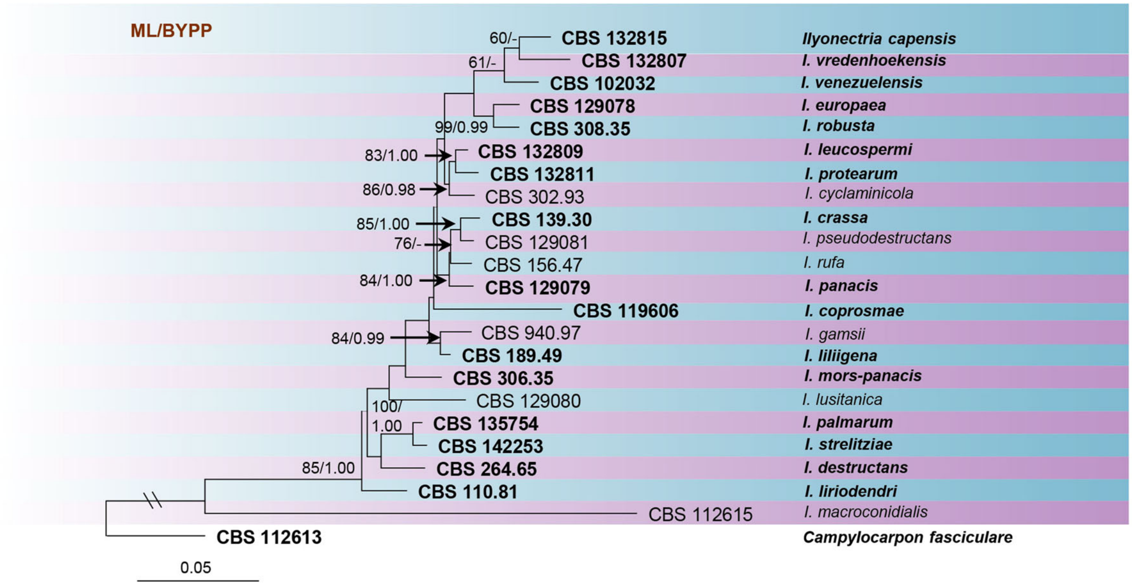


Fig. 15 Phylogenetic tree generated by maximum likelihood analysis of combined ITS, TEF, TUB, and His3 sequence data of *Ilyonectria* species. Twenty-three strains are included in the analyses, which comprise 2242 characters including gaps. The tree is rooted in *Campylocarpon fasciculare*. Tree topology of the ML analysis was similar to the one generated from BI (Figure not shown). The best scoring RAxML tree with a final likelihood value of − 9669.617830 is presented. The matrix had 507 distinct alignment patterns, with 5.11% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.219321, C = 0.325516, G = 0.222910, T = 0.230587; substitution rates AC = 0.215721, AG = 0.328038, AT = 0.225653, CG = 0.615208, CT = 5.798530, GT = 1.000000; gamma distribution shape parameter α = 0.518017. Maximum likelihood bootstrap support values ≥ 60% and bayesian posterior probabilities ≥ 95 (BYPP) are indicated above or near the nodes. Ex-type strains are in bold

Morphological based identification and diversity

Eight species names are recorded in Index Fungorum (2019), however, sequences are available for only two species *Macrophomina phaseolina* and *M. pseudophaseolina* (Sarr et al. 2014). Morphological characteristics of *M.*

phaseolina are mostly similar to *M. pseudophaseolina*, except that conidia of the latter are shorter.

Colony and conidial morphology are the primary characters used to identify species within this genus (Ellis 1971, 1976; Simmons 1992). However, the connectivity of sexual and asexual morphs is not proven, as no sexual morph has been obtained from nature or culture (Crous et al. 2006; Wijayawardene et al. 2017, 2018). According to the morphological identifications, *Macrophomina phaseolina* has conidia with apical mucoid appendages as found in *Tiarosporella* (Sutton and Marasas 1976). Nevertheless, it can be distinguished from *Tiarosporella* in having conidia with apical mucoid appendages, per currently proliferating conidiogenous cells and dark brown (at maturity) conidia (Crous et al. 2006; Phillips et al. 2013). Morphologically *M. phaseolina* is similar to *M. pseudophaseolina*, except that conidia of the latter are shorter.

Molecular based identification and diversity

Phillips et al. (2013) suggested that phylogenetic analysis of a combined SSU, LSU, ITS, *tef1* and TUB2 genes provide better resolution. Sarr et al. (2014) used ITS, *tef1*, ACT, CAL and TUB2 sequence data representing a large sample of *Macrophomina* isolates from many hosts. According to the multi-gene analysis of SSU, LSU, ITS, *tef1* and TUB2 genes in this study (Fig. 16, Table 10), the two species cluster in a well-supported clade with high bootstrap values (100% ML, 1.00 BYPP). The overall topology of our phylogeny tree is similar to previous studies.

*Recommended genetic markers (genus level)*cosmopolitan genus, and—LSU and SSU
Recommended genetic markers (species level)—ITS, *tef1*, ACT, CAL and TUB2

Accepted number of species: There are eight epithets in Index Fungorum (2019) However, **two** species have molecular data.

References: Crous et al. 2006; Phillips et al. 2013; Sarr et al. 2014, Wijayawardene et al. 2017 (morphology, phylogeny).

Medeolaria Thaxt., Proc. Amer. Acad. Arts & Sci. 57(17): 432 (1922)

The genus *Medeolaria* belongs to the family *Medeolariaceae* (Medeolariales, Leotiomycetes, Ascomycota).

Table 9 Details of the ***Ilyonectria*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	tef1	tub2	His3
Campylocarpon fasciculare	CBS 112613	AY677301	JF735691	AY677221	JF735502
Ilyonectria capensis	**CBS 132815***	JX231151	JX231119	JX231103	JX231135
I. coprosmae	**CBS 119606***	JF735260	JF735694	JF735373	JF735505
I. crassa	**CBS 139.30***	JF735275	JF735723	JF735393	JF735534
I. cyclaminicola	**CBS 302.93***	JF735304	JF735770	JF735432	JF735581
I. destructans	**CBS 264.65***	AY677273	JF735695	AY677256	JF735506
I. europaea	**CBS 129078***	JF735294	JF735756	JF735421	JF735567
I. gamsii	CBS 940.97	AM419065	JF735766	AM419089	JF735577
I. leucospermi	**CBS 132809***	JX231161	JX231129	JX231113	JX231145
I. liliigena	**CBS 189.49***	JF735297	JF735762	JF735425	JF735573
I. liriodendri	**CBS 110.81***	DQ178163	JF735696	DQ178170	JF735507
I. lusitanica	CBS 129080	JF735296	JF735759	JF735423	JF735570
I. macroconidialis	CBS 112615	AY677290	JF735836	AY677233	JF735647
I. mors-panacis	**CBS 306.35***	JF735288	JF735746	JF735414	JF735557
I. palmarum	**CBS 135754***	HF937431	HF922614	HF922608	HF922620
I. panacis	**CBS 129079***	AY295316	JF735761	JF735424	JF735572
I. protearum	**CBS 132811***	JX231157	JX231125	JX231109	JX231141
I. pseudodestructans	CBS 129081	AJ875330	JF735752	AM419091	JF735563
I. robusta	**CBS 308.35***	JF735264	JF735707	JF735377	JF735518
I. rufa	CBS 156.47	AY677272	JF735730	AY677252	JF735541
I. strelitziae	**CBS 142253 ***	KY304649	KY304727	KY304755	KY304621
I. venezuelensis	**CBS 102032 ***	AM419059	JF735760	AY677255	JF735571
I. vredenhoekensis	**CBS 132807***	JX231155	JX231123	JX231107	JX231139

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

Medeolaria was introduced by Thaxter (1922) and typified with *Medeolaria farlowii*. *Medeolaria* species are pathogens of *Medeola virginiana* (*Liliaceae*). Currently, the known distribution of this genus is only from America.

Classification—Leotiomycetes, *Medeolariales*, *Medeolariaceae*

Type species—***Medeolaria farlowii*** Thaxt., Proc. Amer. Acad. Arts & Sci. 57(17): 432 (1922)

Distribution—America

Disease symptoms—This fungus causes gall-like deformations on thickened, hypertrophic 9 parts below leaf whorls of herbaceous stems of the host tissue, in autumn. However, they are present not only in stem lesions of the host plant but in uninfected leaves, stems and rhizomes (Pfister et al 2013). Pfister et al. (2013) also showed the long-term perpetuation of the fungus in populations of the plant. They suggested the fungus remains as a systemic infection of vegetative plant parts and when the plant reproduces clonally, this infection is carried in populations of the host plant (Pfister et al 2013).

Hosts—*Magnolia* spp.

Morphological based identification and diversity

This genus contains only a single species, *Medeolaria farlowii* Thaxter (1922), described from material collected from *Magnolia*. It produces erumpent, indefinite apothecia with a palisade layer of asci and paraphyses. An excipulum is absent or is a very thin layer. The hymenium layer forms fusiform swellings below and/or between the shortened internodes of the host plant. Ascospores are large, fusiform to naviculate, with a dark, striate outer wall. The asexual morph of this fungus is unknown (Korf 1973; Pfister and LoBuglio 2009; Ekanayaka et al 2017).

Molecular based identification and diversity

The first stable taxonomic placement for this genus was provided by Korf (1973) under the family *Medeolariaceae*, order Medeolariales within Leotiomycetes, according to its morphology. Recent phylogenetic studies (LoBuglio and Pfister 2010; Pfister et al 2013; Ekanayaka et al. 2017) confirmed its phylogenetic relationship with Leotiomycetes (Fig. 10), but the phylogenetic position within the class is unresolved.

Recommended genetic marker (genus level)—ITS

Recommended genetic marker (species level)—ITS

ITS is the best single genetic marker for the genus *Medeolaria* (Pfister et al 2013). Pfister et al. (2013) provided primers, designed to specifically amplify ITS rDNA regions of *Medeolaria farlowii*.

Accepted number of species: **One species**

References: Korf 1973; LoBuglio and Pfister 2010; Pfister et al. 2013(morphology, phylogeny).

Neonectria Wollenw., Annls mycol. 15(1/2):52 (1917)

Neonectria is a cosmopolitan genus, and their asexual morphs are common in tropical and temperate regions (Chaverri et al. 2011). *Neonectria* species can be found on the bark of recently dead woody plants and sometimes on decaying herbaceous material (Samuels and Brayford 1990; Samuels and Brayford 1990, 1993, 1994; Rossman et al. 1999; Castlebury et al. 2006; Chaverri et al. 2011). Some species of *Neonectria* are plant pathogens causing cankers and other diseases on hardwood and coniferous trees (Castlebury et al. 2006; Rossman and Palm-Hernández 2008; Crane et al. 2009; Chaverri et al. 2011; Schmitz et al. 2017; Wenneker et al. 2017). *Neonectria neomacrospora* has been added to the European and Mediterranean Plant Protection Organization (EPPO) alert list (EPPO, 2019).

Classification—Sordariomycetes, *Hypocreomycetidae*, *Hypocreales*, *Nectriaceae*

Type species—***Neonectria ramulariae*** Wollenw., Annls mycol. 15(1/2):52 (1917)

Distribution—Worldwide

Disease symptoms—Canker

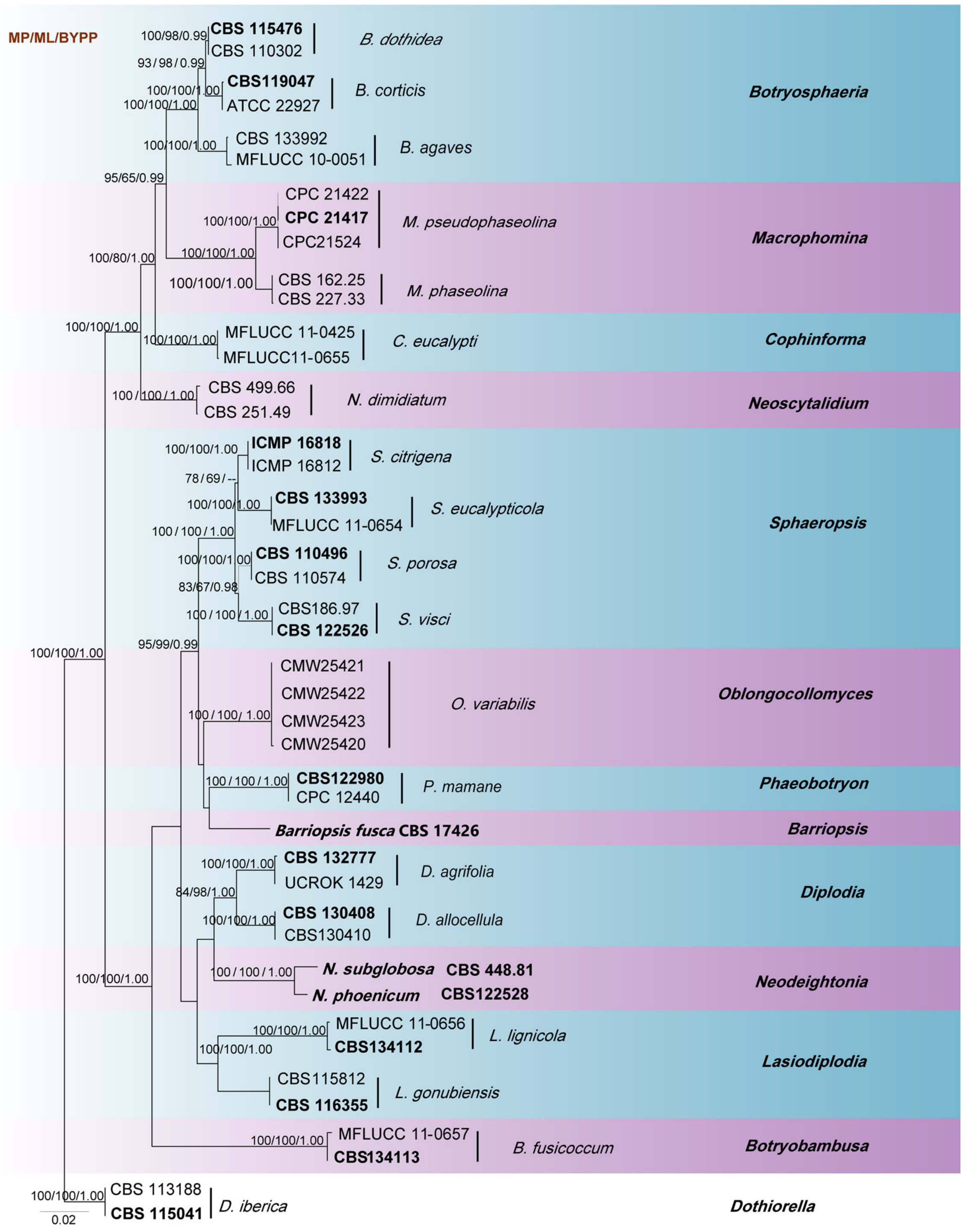
Dead shoots can be observed in the lower branches or all over the affected tree. Affected branches or trunks show canker and some may have abundant resin flow. When the canker girdles the affected area, part of the tree above the canker dies. Under humid conditions characteristic small, red fruiting bodies will be formed. Badly affected trees will eventually die (Castlebury et al. 2006).

Beech (*Fagus*) bark disease is caused by *N. coccinea*, *N. ditissima*, *N. fuckeliana* and *N. faginata*. Cankers of fruit trees are caused by *N. rugulosa* and *N. ditissima*. Shoot dieback of *Abies* species are caused by *N. neomacrospora* (Castlebury et al. 2006; Rossman et al. 2008; Crane et al. 2009; Chaverri et al. 2011; Schmitz et al. 2017; Wenneker et al. 2017).

Hosts—Wide host range including plant genera in *Amaryllidaceae*, *Aracaceae*, *Araliaceae*, *Betulaceae*, *Ericaceae*, *Fagaceae*, *Lauraceae*, *Myrtaceae*, *Pinaceae*, *Proteaceae*, *Rosaceae*, *Sapindaceae* and *Vitaceae* (Farr and Rossman 2019).

Morphological based identification and diversity

The genus *Neonectria* was established by Wollenweber (1917). The generic concept of *Neonectria* has been revised by different authors (Booth 1959; Samuels and Brayford 1994; Rossman et al. 1999). Rossman et al. (1999) accepted only three species (*N. coccinia*, *N. galligena* and *N. ramulariae*) in *Neonectria*. Subsequently, species were added to the genus based on morphology and/or phylogeny (Hirooka et al. 2005; Castlebury et al. 2006; Luo and Zhuang 2010a, b; Zhao et al. 2011; Lombard et al. 2014, 2015). However, some unrelated species were transferred to other genera based on molecular analyses


MP/ML/BYPP
100/98/0.99
CBS 115476
CBS 110302
B. dothidea
93/98/0.99
100/100/1.00
CBS119047
100/100/1.00
ATCC 22927
B. corticis
Botryosphaeria
100/100/1.00
CBS 133992
MFLUCC 10-0051
B. agaves
95/65/0.99
CPC 21422
100/100/1.00
CPC 21417
CPC21524
M. pseudophaseolina
Macrophomina
100/100/1.00
100/80/1.00
100/100/1.00
CBS 162.25
CBS 227.33
M. phaseolina
100/100/1.00
MFLUCC 11-0425
100/100/1.00
MFLUCC11-0655
C. eucalypti
Cophinforma
100 /100 / 1.00
CBS 499.66
CBS 251.49
N. dimidiatum
Neoscytalidium
100/100/1.00
ICMP 16818
ICMP 16812
S. citrigena
78/69/--
100/100/1.00
CBS 133993
MFLUCC 11-0654
S. eucalypticola
100 / 100 / 1.00
Sphaeropsis
100/100/1.00
CBS 110496
CBS 110574
S. porosa
83/67/0.98
100 / 100 / 1.00
CBS186.97
CBS 122526
S. visci
100/100/1.00
95/99/0.99
CMW25421
CMW25422
O. variabilis
Oblongocollomyces
100 / 100 / 1.00
CMW25423
CMW25420
100 / 100 / 1.00
CBS122980
CPC 12440
P. mamane
Phaeobotryon
Barriopsis fusca CBS 17426
Barriopsis
100/100/1.00
CBS 132777
UCROK 1429
D. agrifolia
84/98/1.00
Diplodia
100/100/1.00
CBS 130408
CBS130410
D. allocellula
100/100/1.00
100 / 100 / 1.00
N. subglobosa CBS 448.81
N. phoenicum CBS122528
Neodeightonia
100/100/1.00
MFLUCC 11-0656
CBS134112
L. lignicola
100/100/1.00
Lasiodiplodia
CBS115812
CBS 116355
L. gonubiensis
100/100/1.00
MFLUCC 11-0657
CBS134113
B. fusicoccum
Botryobambusa
100/100/1.00
CBS 113188
CBS 115041
D. iberica
Dothiorella
0.02

◀ **Fig. 16** Phylogenetic tree generated by maximum likelihood analysis of combined ITS, LSU, SSU, *tef1* and TUB2 sequences. Related sequences were obtained from GenBank. Forty-four strains are included in the analyses, which comprise 3477 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree was rooted with *Dothiorella iberica* (CBS 113188 and CBS 115041). Tree topology of the ML analysis was similar to the MP and BI. The best scoring RAxML tree with a final likelihood value of − 12764.659013 is presented. The matrix had 898 distinct alignment patterns, with 28.31% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.238049, C = 0.253522, G = 0.272022, T = 0.236408; substitution rates AC = 1.121500, AG = 2.393284, AT = 1.053637, CG = 1.711098, CT = 4.682724, GT = 1.000000; gamma distribution shape parameter α = 0.545763. The maximum parsimonious dataset consisted of constant 2820, 575 parsimony-informative and 82 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 1490 steps (CI = 0.626, RI = 0.861, RC = 0.539, HI = 0.374) in the first tree. RAxML, maximum parsimony bootstrap support values $\geq$ 65% and Bayesian posterior probabilities $\geq$ 0.95 (BYPP) are shown respectively near the nodes. Ex-type strains are in bold

and morphological data (Lombard et al. 2014, 2015). There are 31 species recognised in the genus, while 23 species have sequence data in GenBank (4/7/2019). Morphological characters (perithecial morphology, ascospore size, macroconidial morphology, presence or absence of microconidia and chlamydospores) along with DNA sequence analysis are appropriate for identification of *Neonectria* species (Brayford et al. 2004).

Molecular based identification and diversity

Since 2001, DNA sequence analysis has been used to clarify the taxonomy of *Neonectria* (Mantiri et al. 2001; Brayford et al. 2004; Halleen et al. 2004; Hirooka et al. 2005; Chaverri et al. 2011). Mantiri et al. (2001) and Brayford et al. (2004) used mtSSU rDNA sequence data to infer intrageneric relationships of some *Neonectria* and *Cylindrocarpon* species. Later, Halleen et al. (2004) used mtLSU rDNA, TUB2 and nrDNA ITS regions to separate some *Cylindrocarpon* species included in the *N. mammoidea* group. Chaverri et al. (2011) approached a comprehensive treatment of *Cylindrocarpon* and *Neonectria* based on combined loci analyses and morphological data. Chaverri et al. (2011) defined *Neonectria sensu stricto* within *Nectriaceae* with *Cylindrocarpon sensu stricto* based on multi-gene phylogeny of ITS, LSU, *tef1*, TUB2, ACT, and RPB1. The ITS, *tef1* and TUB2 loci possess highly variable regions (Chaverri et al. 2011) and are important in species delimitation of *Neonectria*. Rossman et al. (2013) proposed to protect generic name *Neonectria* over *Cylindrocarpon*. Maharachchikumbura et al. (2015) considered *Cylindrodendrum* not to be congeneric with *Neonectria* and accepted *Neonectria* over *Cylindrocarpon*.

This study reconstructs the phylogeny of *Neonectria* based on analyses of a combined ITS, LSU, *tef1* and TUB2 sequence data (Table 11, Fig. 17). The phylogenetic tree is updated with recently introduced *Neonectria* species and corresponds to previous studies (Chaverri et al. 2011; Lombard et al. 2014; Mantiri et al. 2001).

Recommended genetic markers (genus level)—LSU, ITS, *tef1* and TUB2

Recommended genetic markers (species level)—ITS, *tef1* and TUB2

Accepted number of species: **28 species**

References: Rossman et al. 1999 (morphology), Brayford et al. 2004; Hirooka and Kobayashi 2007; Chaverri et al. 2011; Lombard et al. 2014 (morphology, phylogeny).

Neopestalotiopsis Maharachch., K.D. Hyde & Crous (2014), in Maharachchikumbura et al., Stud. Mycol. 79:147 (2014a)

Neopestalotiopsis is an important plant pathogenic, saprobic and endophytic genus commonly present in tropical and subtropical ecosystems. The genus was introduced by Maharachchikumbura et al. (2014b). Species of *Neopestalotiopsis* are appendage-bearing asexual coelomycetes in the family *Sporocadaceae* (Jayawardena et al. 2016).

Classification—Sordariomycetes, *Xylariomycetidae*, *Amphisphaeriales*, *Sporocadaceae*

*Type species—**Neopestalotiopsis protearum*** (Crous & L. Swart) Maharachch. et al., in Maharachchikumbura et al., Stud. Mycol. 79:147 (2014a)

Distribution—Worldwide

Disease symptoms—Canker, dieback, fruit rots, leaf spot

Pathogenic *Neopestalotiopsis* are recorded in post-harvest fruit rots of grapes, trunk diseases in grapevine in China, India and France, leaf spot disease of grapevine in China and leaf blights in many plant species worldwide (Hyde et al. 2014; Jayawardena et al. 2015, 2016; Maharachchikumbura et al. 2017).

Neopestalotiopsis species infect a variety of grapevine cultivars, causing diseases including grapevine dieback, fruit rot, postharvest disease and severe defoliation. Initial symptoms of fruit rot disease are mostly observed at the splits between the pedicel and the berry and at the wounds of the fruits and severely infected fruits become rotten and separate completely from the pedicel (Jayawardena et al. 2015). *Neopestalotiopsis asiatica* and *N. javaensis* are associated with grapevine trunk disease (Maharachchikumbura et al. 2017). Grapevine trunk diseases reduce the yield and quality of grapes, even leading to partial or total death of individual plants.

Neopestalotiopsis clavispora and *N. surinamensis* cause guava scab (Solarte et al. 2018). *Neopestalotiopsis ellipsospora* causes leaf spot on sweet potatoes

Table 10 Details of ***Macrophomina*** and ***Sphaeropsis*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	SSU	ITS	LSU	tef1	TUB2
Barriopsis fusca	**CBS 174.26***	EU673182	EU673330	DQ377857	EU673296	EU673109
Botryobambusa fusicoccum	**CBS 134113***	JX646826	JX646792	JX646809	JX646857	N/A
	MFLUCC 11-0657	JX646827	JX646793	JX646810	JX646858	N/A
Botryosphaeria agaves	**CBS 133992***	JX646825	JX646791	JX646808	JX646856	JX646841
	MFLUCC 10-0051	JX646824	JX646790	JX646807	JX646855	JX646840
B. corticis	**CBS 119047***	EU673175	DQ299245	EU673244	EU017539	EU673107
	ATCC 22927	EU673176	DQ299247	EU673245	EU673291	EU673108
B. dothidea	**CBS 115476** *	EU673173	AY236949	AY928047	AY236898	AY236927
	CBS 110302	EU673174	AY259092	EU673243	AY573218	EU673106
Cophinforma atrovirens	**MFLUCC 11-0425***	JX646833	JX646800	JX646817	JX646865	JX646848
	MFLUCC 11-0655	JX646834	JX646801	JX646818	JX646866	JX646849
Dothiorella iberica	**CBS 115041***	EU673155	AY573202	AY928053	AY573222	EU673096
	CBS 113188	EU673156	AY573198	EU673230	EU673278	EU673097
Diplodia allocellula	**CBS 130408***	N/A	JQ239397	JQ239410	JQ239384	JQ239378
	CBS 130410	N/A	JQ239399	JQ239412	JQ239386	JQ239380
D. agrifolia	**CBS 132777***	N/A	JN693507	N/A	JQ517317	JQ411459
	UCROK 1429	N/A	JQ411412	N/A	JQ512121	JQ411443
Lasiodiplodia gonubiensis	**CBS 115812***	EU673193	AY639595	DQ377902	DQ103566	DQ458860
	CBS 116355	EU673194	AY639594	EU673252	DQ103567	EU673126
L. lignicola	**CBS 134112***	JX646830	JX646797	JX646814	JX646862	JX646845
	MFLUCC 11-0656	JX646831	JX646798	JX646815	JX646863	JX646846
Neoscytalidium hyalinum	CBS 499.66	KF531818	KF531820	DQ377925	KF531798	KF531800
	CBS 251.49	KF531817	KF531819	DQ377923	KF531797	KF531799
Neodeightonia subglobosa	**CBS 448.81***	EU673202	EU673337	DQ377866	EU673306	EU673137
N. phoenicum	**CBS 122528***	EU673205	EU673340	EU673261	EU673309	EU673116
Macrophomina phaseolina	CBS 227.33	KF531823	KF531825	DQ377906	KF531804	KF531806
	CBS 162.25	KF531824	KF531826	DQ377905	KF951996	KF531805
M. pseudophaseolina	CPC 21422	N/A	KF951792	N/A	KF952154	KF952234
	CPC 21417*	N/A	KF951791	N/A	KF952153	KF952233
	CPC 21524	N/A	KF951799	N/A	KF952161	KF952240
Phaeobotryon mamane	**CBS 122980***	EU673184	EU673332	EU673248	EU673298	EU673121
	CPC 12442	EU673185	EU673333	DQ377899	EU673299	EU673124
Oblongocollomyces variabilis	CMW 25420	N/A	EU101313	N/A	EU101358	N/A
	CMW 25421, CBS 121775	N/A	EU101314	N/A	EU101359	N/A
	CMW 25422, CBS 121776	N/A	EU101326	N/A	EU101371	N/A
	CMW 25423	N/A	EU101327	N/A	EU101372	N/A
Sphaeropsis citrigena	**ICMP 16812***	EU673180	EU673328	EU673246	EU673294	EU673140
	ICMP 16818	EU673181	EU673329	EU673247	EU673295	EU673141
S. eucalypticola	**CBS 133993***	JX646835	JX646802	JX646819	JX646867	JX646850
	MFLUCC 11-0654	JX646836	JX646803	JX646820	JX646868	JX646851
S. porosa	**CBS 110496***	EU673179	AY343379	DQ377894	AY343340	EU673130
	CBS 110574	N/A	AY343378	N/A	AY343339	N/A
S. visci	**CBS 122526** *	N/A	EU673324	N/A	EU673292	N/A
	CBS 186.97	EU673178	EU673325	DQ377868	EU673293	EU673128

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

Table 11 Details of the ***Neonectria*** isolates used in the phylogenetic analyses

Species	Isolates/voucher no	ITS	LSU	TUB	*tef1*
Neonectria austroradicicola	PDD 46334 G.J.S. 83-154	EF607077	–	–	–
N candida	CBS 151 29 IMI 113894/MUCL 28083	AY677291	AY677333	DQ789863	DQ789723
N. coccinea	CBS 119158/GJS 98-114	JF268759	KC660620	KC660727	JF268734
N. confusa	**CBS 127485/HMAS 99197***	**FJ560437**	**KM515934**	**FJ860054**	–
N. confusa	CBS 127484/HMAS 99198	KM515889	KM515933	KM515886	–
N. ditissima	CBS 100318	KM515890	KM515935	DQ789858	KM515944
N. ditissima	CBS 100317	KM515891	KM515936	KM515887	KM515945
N. ditissimopsis	**HMAS 98329***	**JF268764**	–	**JF268729**	**JF268745**
N. faginata	**CBS 217.67/IMI 105738/ATCC 16547***	**HQ840385**	**HQ840382**	**JF268730**	**JF268746**
N. faginata	CBS 119160/GJS 04-159	HQ840384	HQ840383	DQ789883	DQ789740
N. fuckeliana	CBS 239.29/IMI 039700	HQ840386	HQ840377	DQ789871	JF268748
N. hederae	**IMI 058770a/ATCC 16543***	–	**KC660617**	**DQ789895**	**DQ789752**
N. hederae	CBS 714.97/PD 97/1932	–	KC660616	DQ789878	KC660461
N. lugdunensis	CBS 125485/DAOM 235831/TG 2008-07	KM231762	KM231625	KM232019	KM231887
N. major	**CBS 240.29/IMI 113909***	**JF735308**	**KM515942**	**DQ789872**	**JF735782**
N. microconidia	HMAS 98294	KC660530	KC660587	–	–
N. neomacrospora	CBS 198.62/BBA 9628/IMI 113890	AJ009255	HM364316	HM352865	HM364351
N. neomacrospora	CBS 324.61/DSM 62489/IMB 9628	JF735312	HM364318	DQ789875	–
N. obtusispora	CBS 183.36/IMI 113895	AM419061	KM515943	AM419085	JF735796
N. punicea	CBS 242.29	KC660522	KC660565	DQ789873	DQ789730
N. shennongjiana	HMAS 183185	FJ560440	–	FJ860057	–
N. tsugae	**CBS 788.69***	**KM231763**	**HQ232146**	**KM232020**	–
Thelonectria gongylodes	**CBS 12511/GJS 90-48**	**JQ403330**	**JQ403369**	**HM352870**	**HM364357**

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

(Maharachchikumbura et al. 2016). *Neopestalotiopsis clavispora* causes crown and root rot of strawberry worldwide while *N. iranensis* infects leaves and fruits of strawberry (Ayoubi and Soleimani 2016), with the pathogen initially developing circular, black, and slightly sunken spots that expand outwards on the surface. Droplets of spores are scattered over the white aerial mycelial area and later cause soft decay of the fruit flesh (Ayoubi and Soleimani 2016). Canker and dieback on blueberry in Chile and Uruguay are also caused by *N. clavispora* (Espinoza et al. 2008; González et al. 2012; Chamorro et al. 2016). *Neopestalotiopsis samarangensis* has been described from wax apple fruit rot in Thailand (Maharachchikumbura et al. 2013a, b). In fruit rots, the initial symptom is small, circular, black, slightly sunken spots on fruits. Later, the spots enlarged rapidly, become sunken and result in a soft decay of the fruit flesh (Maharachchikumbura et al. 2013a, b). *Hosts*—Species of *Fragaria* × *ananassa*, *Ipomoea*, *Malus*, *Psidium*, *Vaccinium* and *Vitis*

Morphological based identification and diversity

Neopestalotiopsis species can be differentiated using morphology and molecular phylogeny (Maharachchikumbura et al. 2014b). There are 36 species epithets listed in Index Fungorum (2019). *Neopestalotiopsis* species differ from *Pestalotiopsis* and *Pseudopestalotiopsis* in having somewhat versicolorous median cells (Maharachchikumbura et al. 2014b) whereas both *Pestalotiopsis* and *Pseudopestalotiopsis* have concolourous median cells (Maharachchikumbura et al. 2014b) as well as its conidiophores which are indistinct and often reduced to conidiogenous cells (Maharachchikumbura et al. 2014b).

Conidial morphology is widely used in taxonomy in pestalotioid fungi (Steyaert 1949; Guba 1961; Nag Raj 1993; Maharachchikumbura et al. 2012, 2014b). Species delimitation based on morphological characters is limited as these characters are plastic and vary between hosts and environments (Maharachchikumbura et al. 2011, 2016). Therefore, phylogenetic species recognition is an effective method to identify different pestalotioid species (Maharachchikumbura et al. 2016).

Molecular based identification and diversity

Neopestalotiopsis species can be roughly separated from *Pestalotiopsis* and *Pseudopestalotiopsis* based on the total number of base pairs in the ITS region

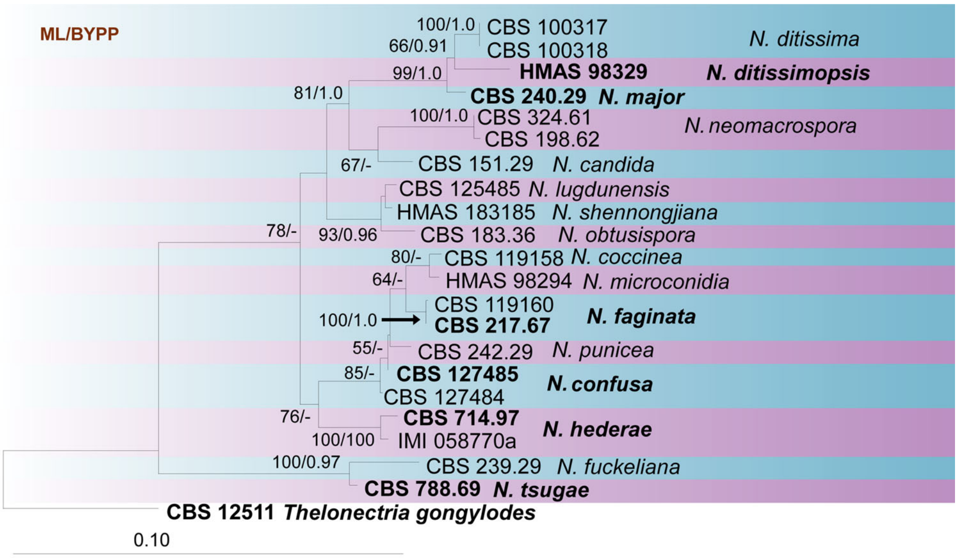


Fig. 17 Phylogenetic tree generated by maximum likelihood analysis of combined ITS, LSU, *tef1* and TUB sequence data of *Neonectria* species. Related sequences were obtained from GenBank. Twenty-three strains are included in the analyses, which comprise 2336 characters including gaps. Tree topology of the ML analysis was similar to the one generated from BI (figure not shown). The best scoring RAxML tree with a final likelihood value of − 7942.756270 is presented. The matrix had 525 distinct alignment patterns, with 18.13% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.223071, C = 0.285136, G = 0.261197, T = 0.230596; substitution rates AC = 1.213729, AG = 2.500008, AT = 1.727890, CG = 0.720430, CT = 6.191594, GT = 1.000000; gamma distribution shape parameter α = 0.749195. Maximum likelihood bootstrap support (≥ 55%) and posterior probabilities (BYPP ≥ 0.90) from Bayesian inference analysis are indicated respectively near the nodes. Ex-type strains are in bold. The tree is rooted in *Thelonectria gongylodes*

(Maharachchikumbura et al. 2014b). However, the use of ITS sequences alone does not resolve *Neopestalotiopsis* species (Maharachchikumbura et al. 2012). Therefore, Maharachchikumbura et al. (2014b) suggested using combined ITS, TUB2 and *tef1* genes to provide a better resolution in phylogenetic analyses. This study reconstructs the phylogeny of *Neopestalotiopsis* based on a combined ITS, TUB2 and *tef1* sequence data (Fig 18, Table 12) and reveals similar phylogenetic relationships to previous studies by Maharachchikumbura et al. (2014b, 2016).

Recommended genetic marker (genus level)—LSU
Recommended genetic markers (Species level)—ITS, TUB2 and *tef1*
Accepted number of species: **41 species**.
References: Maharachchukumbura 2012, 2014b (morphology, phylogeny); Maharachchukumbura et al. 2016 (morphology, phylogeny); Jayawardena et al. 2015, 2016 (morphology, phylogeny, pathogenicity)

Plasmopara J. Schröt., in Cohn, Krypt.-Fl. Schlesien 3.1(9–16): 236 (1886) [1889]

The genus *Plasmopara* belongs to the family *Peronosporaceae* of the Peronosporales in Oomycetes (Riethmüller et al. 2002; Görg et al. 2017). This genus is included in this study as it is an important plant pathogen on many economically important crops. *Plasmopara* was introduced by Schröter (1886), but no species was assigned as a type for the genus (Constantinescu et al. 2005). *Plasmopara nivea* is considered as the type species of this genus (Constantinescu et al. 2005). *Plasmopara* species are commonly known as downy mildew pathogens. There are 2064 records in USDA fungal database under genus *Plasmopara* (Farr and Rosman 2019). Downy mildew has become one of the most troublesome diseases in agriculture including *P. viticola* on grape, *P. geranii* on geranium and *P. halstedii* on sunflower (McTaggart et al. 2015). Kamoun et al. (2015) categorized *P. viticola* among the top ten Oomycetes pathogens in plant pathology. Current interest in this genus is to understand the co-evolution with the host and effective disease management (Thines and Kamoun 2010). Taxonomically useful morphological or ecological characters are few for the downy mildews and this makes identification of synapomorphic states impossible (Göker et al. 2003).

Classification—*Oomycota incertae sedis*, *Peronosporea*, *Peronosporidae*, *Peronosporales*, *Peronosporaceae*
Type species—***Plasmopara nivea*** (Unger) J. Schröt.
Distribution—Worldwide
Disease symptoms—Downy mildew
Hosts—Species belonging to this genus are obligate biotrophs on a wide range of hosts including *Acanthaceae*, *Asteraceae*, *Balsaminaceae*, *Geraniaceae*, *Malvaceae*, *Onagraceae*, *Orobanchaceae*, *Violaceae* and *Vitaceae*

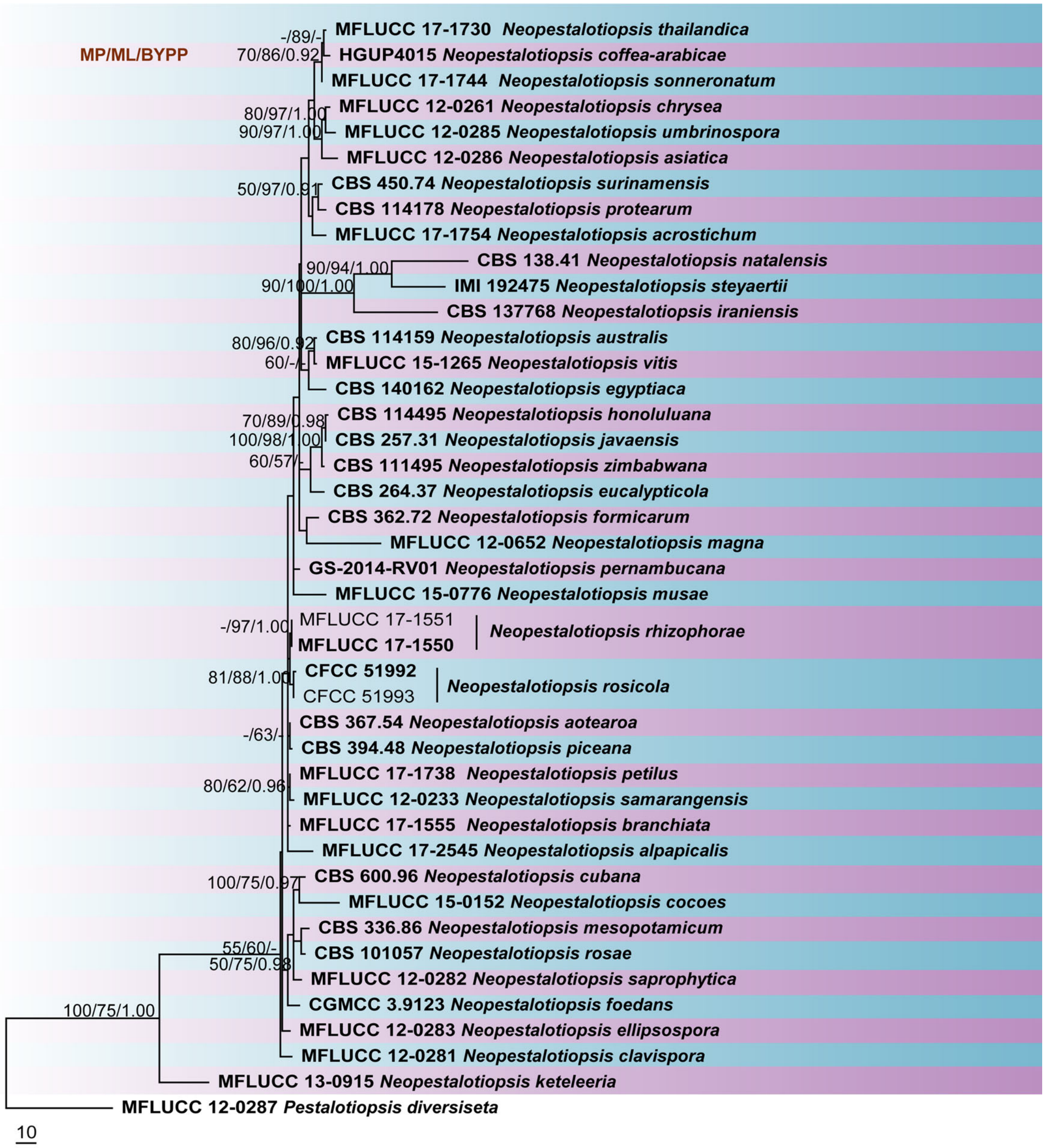


Fig. 18 Phylogram generated from maximum likelihood analysis based on combined ITS, TUB2 and *tef1* sequence data of *Neopestalotiopsis* species. Related sequences were obtained from GenBank. Forty-three strains are included in the combined sequence analyses, which comprise 1391 characters with gaps. *Pestalotiopsis diversiseta* (MFLUCC 12-0287) is used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of -5457.035085 is presented. The matrix had 409 distinct alignment patterns, with 6.30% of undetermined characters or gaps. Estimated base frequencies were as follows; $A = 0.231067$, $C = 0.270889$, $G = 0.213946$, $T = 0.284098$; substitution rates $AC = 0.847461$, $AG = 2.876343$, $AT = 1.282349$, $CG = 0.723831$, $CT = 3.850003$, $GT = 1.000000$; gamma distribution shape parameter $\alpha = 0.235476$. The maximum parsimonious dataset consisted of 1026 constant, 177 parsimony-informative and 188 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of ten equally most parsimonious trees with a length of 650 steps ($CI = 0.688$, $RI = 0.609$, $RC = 0.419$, $HI = 0.312$) in the first tree. RAxML and maximum parsimony bootstrap support value $\geq 50\%$ and posterior probabilities BYPP ≥ 0.90 from Bayesian inference analysis are indicated respectively near the nodes, are shown respectively near the nodes. Ex-type strains are in bold

(Voglmayr et al. 2004; Thines and Kamoun 2010; McTaggart et al. 2015).

Morphological based identification and diversity

Wilson (1907) was the first to consider *P. pygmaea* as the type of *Plasmopara*. However, even after a century of discussion of nomenclatural and taxonomic problems of this genus, *Plasmopara* was segregated in two different groups by morphology and phylogeny (Constantinescu et al. 2005). Constantinescu et al. (2005) proposed to introduce a new generic name for *P. pygmaea* and for six

Table 12 Details of the ***Neopestalotiopsis*** isolates used in the phylogenetic analyses

Species	Isolate no	ITS	TUB2	*tef1*
Neopestalotiopsis acrostichum	**MFLUCC 17-1754***	MK764272	MK764338	MK764316
N. alapicalis	**MFLUCC 17-2544***	MK357772	MK463545	MK463547
N. aotearoa	**MFLUCC 17-1754**	MK764272	MK764338	MK764316
N. asiatica	**MFLUCC12-0286***	JX398983	JX399018	JX399049
N. australis	**CBS 114159***	KM199348	KM199432	KM199537
N. brachiata	**MFLUCC 17-1555***	MK764274	MK764340	MK764318
N. chrysea	**MFLUCC12-0261***	JX398985	JX399020	JX399051
N. clavispora	**MFLUCC 12-0281***	JX398979	JX399014	JX399045
N. cocoes	**MFLUCC 15-0152***	KX789687	–	KX789689
N. coffeae-arabicae	**HGUP 4019***	KF412647	–	–
N. cubana	**CBS 600 96***	KM199347	KM199438	KM199521
N. egyptiaca	**CBS 140162***	KP943747	KP943746	KP943748
N. ellipsospora	**MFLUCC 12-0283***	JX398980	JX399016	JX399047
N. eucalypticola	**CBS 264 37***	KM199376	KM199431	KM199551
N. foedans	**CGMCC3 9123***	JX398987	JX399022	JX399053
N. formicarum	**CBS 362 72***	KM199358	KM199455	KM199517
N. honoluluana	**CBS 114495***	KM199364	KM199457	KM199548
N. iraniensis	**CBS 137768***	KM074048	KM074057	KM074051
N. javaensis	**CBS 257 31***	KM199357	KM199437	KM199543
N. keteleeria	**MFLUCC 13-0915***	KJ503820	KJ503821	KJ503822
N. macadamiae	**BRIP 63738B***	KX186604	KX186654	KX186627‘
N. magna	**MFLUCC12-652***	KF582795	KF582793	KF582791
N. mesopotamica	**CBS 336 86***	KM199362	KM199441	KM199555
N. musae	**MFLUCC 15-0776***	KX789683	KX789686	KX789685
N. natalensis	**CBS 138 41***	KM199377	KM199466	KM199552
N. pernambucana	**GS-2014 strain RV01***	KJ792466	–	KU306739
N. petila	**MFLUCC 17-1738***	MK764275	MK764341	MK764319
N. piceana	**CBS 394 48***	KM199368	KM199453	KM199527
N. protearum	**CBS 114178***	JN712498	KM199463	KM199542
N. rhisophorae	**MFLUCC 17-1550***	MK764277	MK764343	MK764321
N. rosae	**CBS 101057***	KM199359	KM199429	KM199523
N. rosicola	**CFCC 51992**	KY885239	KY885245	KY885243
N. samarangensis	**MFLUCC 12-0233***	JQ968609	JQ968610	JQ968611
N. saprophytica	**MFLUCC 12-0282***	KM199345	KM199433	KM199538
N. sonneratae	**MLFUCC 17-1745***	MK764279	MK264345	MK264323
N. steyaertii	**IMI192475***	KF582796	KF582794	KF582792
N. surinamensis	**CBS 450.74***	KM199351	KM199465	KM199518
N. thailandica	**MFLUCC 17-1730***	MK764281	MK764347	MK754325
N. umbrinospora	**MFLUCC 12-0285***	JX398984	JX399019	JX399050
N. vitis	**MFLUCC 15-1265***	KU140694	KU140685	KU140676
N. zimbabwana	**CBS 111495***	–	KM199456	KM199545

Ex-type (or ex-epitype) strains are in bold and marked with an asterisk* and voucher strains are in bold

other related species and they have established the current classification for *Plasmopara*.

Species belonging to *Plasmopara* have the following characters. Hyphae are intercellular, haustoria are intracellular, as obpyriform, globose, or slightly elongated vesicles (Göker et al. 2003; Voglmayr et al. 2004; Constantinescu et al. 2005). A callose sheath often surrounds haustoria. Sporangiophores are mostly present on the under leaf surface of the host, but sometimes also on other parts of the plant (eg. *P. viticola* produces sporangiophores on inflorescences and young berries, Zhang et al. 2017). Sporangiophores are colourless, branched in the upper part. They branch monopodially, in two to more orders (Göker et al. 2003; Constantinescu et al. 2005). Branches are more or less divergent, ending in a number of elongated ultimate branchlets. The newly formed wall closing the tip after sporangium discharge (Constantinescu et al. 2005). Callose plugs usually present in trunk and/or branches. Sporangiogenesis is holoblastic. These species produce sporangia synchronously, which vary in shape, sporangia wall is colourless, appearing smooth in light microscopy but showing various types of ornamentations in the electron microscope (Constantinescu et al. 2005). There are 199 epithets listed in Index Fungorum (2019), however, 40 of them do not belong to *Plasmopara* based on phylogenetic evidence (Figs. 19, 20).

Oospores develop a single germ tube, terminating with sporangium, once a sporangium disseminated, by rain flash or wind, it releases zoospores (Ash 2000; Rossi et al. 2008; Carisse 2016; Kamoun et al. 2015; Wilcox et al. 2015).

Molecular based identification and diversity

Molecular and phylogenetic studies have shown that *Plasmopara* is polyphyletic (Riethmüller et al. 2002; Göker et al. 2003, 2007; Voglmayr et al. 2004; Voglmayr and Constantinescu 2008). Even though Wilson (1907) proposed *P. pygmaea* as the type species of the genus *Plasmopara*, it has a close relationship with *Bremia*, *Paraperonospora* and *Basidiophora* (Göker et al. 2003). With these morphological and phylogenetic aspects, many species that are traditionally included in *Plasmopara* have moved into new genera. The newly introduced genera are *Viennotia* (Göker et al. 2003), *Protobremia* (Voglmayr et al. 2004), and *Plasmoverna* (Constantinescu et al. 2005). Constantinescu et al. (2005) resolved *Plasmopara* phylogeny, introducing *Plasmoverna* as a new genus to accommodate the morphologically dissimilar and polyphyletic taxa belonging to previous classifications. Voglmayr and Constantinescu (2008) re-classified three species of *Plasmopara* into new genus *Novotelnova* Voglmayr & Constant. The species belonging to *Novotelnova* were identical in the analyses of the nuLSU and nuSSU-ITS1-5.8S datasets. Therefore, in the present study, we follow Voglmayr and Constantinescu (2008) to provide a backbone tree for *Plasmopara* using combined nuLSU sequence data (Fig. 21, Table 13).

The downy mildew pathogens have been studied extensively to understand their host specificity and co-evolution with the host plants. The grape downy mildew has been identified as a host-specific cryptic species (Rouxel et al 2013; Zhang et al. 2017). Rouxel et al. (2013) considered the cryptic species as formae speciales: *P. viticola* f. sp. *riparia* (lineage A occurring on *V. riparia* and some hybrids); *P. viticola* f. sp. *aestivalis* (lineage B found on *V. aestivalis*, *V. labrusca*, *V. vinifera* and some hybrids); *P. viticola* f. sp. *vinifera* (lineage C occurring on *V. vinifera* and some hybrids); *P. viticola* f. sp. *quinquefolia* (lineage D found on *V. quinquefolia*). To understand the cryptic lineages genealogical concordance phylogenetic species recognition (GCPSR) approach is currently accepted (Taylor et al. 2000; Rouxel et al. 2013). GCPSR facilitate the most convenient analysis for species that cannot be cultivated or mate in control conditions (O'Donnell et al. 2000; Steenkamp et al. 2002; Rouxel et al. 2013).

Recommended genetic marker (genus level)—LSU

Recommended genetic marker (species level)—LSU

The universal barcode for the Oomycetes, the cytochrome oxidase subunit 1 and 2 genes (cox 1 and cox 2) are used. However Choi et al. (2015) suggested cox2 is better suited to this because of its ease of amplification among oomycete lineages, better performance on herbarium specimens, higher discriminatory power at the species level and the availability of a large taxonomically diverse database that already includes many species of oomycetes, especially the downy mildew. In previous studies, nuLSU gene regions (D1–D3 and D7–D8 sequences) were widely used (Riethmüller et al. 2002; Göker et al. 2003, 2007; Voglmayr et al. 2004; Voglmayr and Constantinescu 2008). Branch supports of the backbone tree was often higher in the nuLSU data, which resulted in a larger data matrix and a higher number of parsimony-informative characters than when ITS was used (Voglmayr and Constantinescu 2008). No study has combined these gene regions or any other gene regions as the marker to understand the phylogenetic relationship within the genus.

Accepted number of species: There are 199 species in Index Fungorum (2019) and only **19** species have molecular data in this genus.

References: Riethmüller et al. 2002; Göker et al. 2003; 2007; Voglmayr et al. 2004; Voglmayr and Constantinescu 2008; Rouxel et al 2013; Zhang et al. 2017 (morphology, phylogeny).

Pseudopestalotiopsis Maharachch., K.D. Hyde & Crous (2014), in Marachchikumbura et al., in Maharachchikumbura et al., Stud. Mycol. 79:180 (2014a)

The genus was introduced by Maharachchikumbura et al. (2014b) with *Pseudopestalotiopsis theae* (Sawada) Maharachch., K.D. Hyde & Crous as the type species. Species of *Pseudopestalotiopsis* are appendage-bearing phenotypically diverse coelomycetes in the family

Fig. 19 Grape downy mildew disease symptoms. **a** Infected grapevines, **b–c** appearance of oil spot on the upper leaf surface. **d** Sporulation on the lower leaf surface. **e** Young infected berries with sporulation. **f** Infection on fruits

Sporocadaceae and are commonly found in tropical and subtropical ecosystems (Jaklitsch et al. 2016; Maharachchikumbura et al. 2016). *Pseudopestalotiopsis* is characterized by brown to dark brown or olivaceous median cells and knobbed or not knobbed apical appendages (Maharachchikumbura et al. 2014b, 2016). The epitype of *Pseudopestalotiopsis theae* (Sawada) Steyaert was designated from fresh leaves of *Camellia sinensis* collected in Thailand (Maharachchikumbura et al. 2013a, b). *Pseudopestalotiopsis* has been studied for the production of various secondary metabolites with diverse structural features, with antitumour, antifungal, antimicrobial and other activities (Ding et al. 2008; Maharachchikumbura et al. 2011, 2016).

Pseudopestalotiopsis theae is economically significant as it has been identified as a pathogen in major tea-growing areas in the world (Maharachchikumbura et al. 2016). *Pseudopestalotiopsis theae* causes grey blight of tea and reduces yield (Maharachchikumbura et al. 2011, 2013a, b, 2016). *Pseudopestalotiopsis theae* was also isolated as an endophyte from different hosts (*Camellia nitidissima*, *C. sinensis*, *Holarrhena antidysenterica*, *Podocarpus macrophyllus*, *Terminalia arjuna*) or as a saprobe (seeds of *Diospyros crassiflora*) (Maharachchikumbura et al. 2011, 2013a, b, 2016).

Classification—Sordariomycetes, *Xylariomycetidae*, *Amphisphaeriales*, *Sporocadaceae*
Type species—***Pseudopestalotiopsis theae*** (Sawada) Maharachch., in Maharachchikumbura et al., Stud. Mycol. 79:183 (2014a)
Distribution—China, India, Indonesia, Malaysia, Thailand (Maharachchikumbura et al. 2016)
Disease symptoms—*Pseudopestalotiopsis theae* causes grey blight in major tea growing areas in the world (Horikawa 1986, Maharachchikumbura et al. 2013a, b, 2016). The pathogen develops circular to irregular leaf spots initially and grey, brown margins when mature, covering up to half of the leaf with acervuli (Maharachchikumbura et al. 2016). *Pseudopestalotiopsis ixorae* and *P. taiwanensis* cause a leaf spot which initially develops small, circular, ash-coloured spots which later turn into brown spots (Tsai et al. 2018).
Hosts—*Averrhoa carambola*, *Camellia* sp., *Cinnamomum* sp., *Cocos nucifera*, *Diospyros crassiflora*, *Fragaria* sp., *Hibiscus rosa-sinensis*, *Holarrhena antidysenterica*, *Ixora* sp., *Kandelia obovate*, *Macaranga* sp., *Pandanus odoratissimus*, *Podocarpus macrophyllus*, *Prunus* sp., *Terminalia arjuna* and *Thea sinensis*

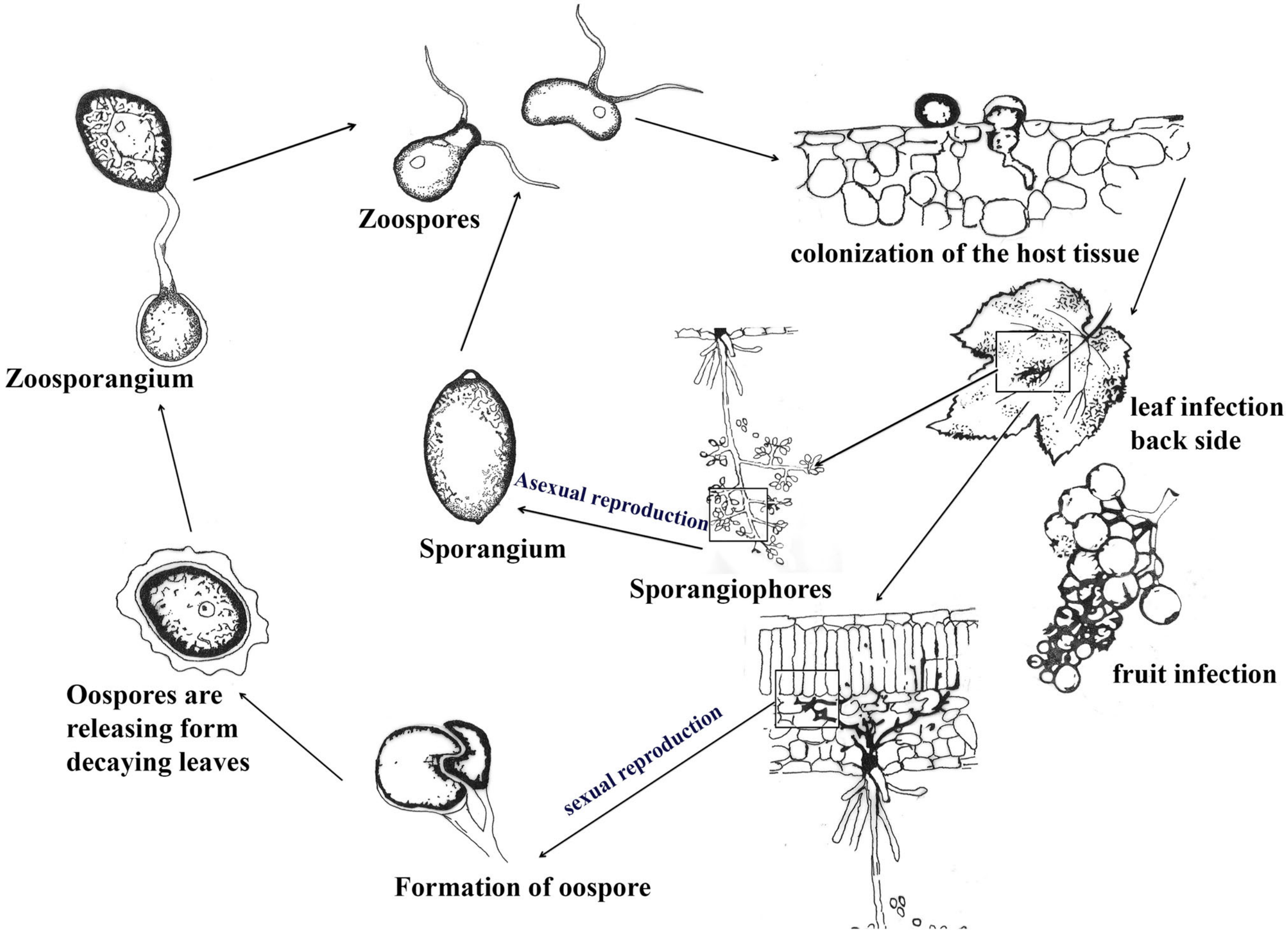


Fig. 20 Disease cycle of grape downy mildew. Redrawn from Kassemeyer (2017)

Morphological based identification and diversity

Pseudopestalotiopsis can be distinguished from *Neopestalotiopsis* and *Pestalotiopsis* by dark concolourous median cells with indistinct conidiophores (Maharachchikumbura et al. 2014b, 2016). However, there could be a wide host range for *Pseudopestalotiopsis* species and the actual number of species could be much higher than presently known (Maharachchikumbura et al. 2011, 2016).

Conidial morphology is widely used in taxonomy in pestalotioid fungi (Steyaert 1949; Guba 1961; Nag Raj 1993; Maharachchikumbura et al. 2011, 2012, 2014b). Species delimitation based on morphological characters is limited as these characters are plastic and vary between hosts and environments (Maharachchikumbura et al. 2011, 2016). Therefore, phylogenetic species recognition is an effective method to identify different pestalotioid species (Maharachchikumbura et al. 2016).

Molecular based identification and diversity

ITS sequence data alone is not sufficient for species delimitation of *Pseudopestalotiopsis*. Therefore, Maharachchikumbura et al. (2012) suggested a phylogenetic analysis of combined ITS, TUB2 and *tef1* genes provide better resolution as compared to single gene phylogeny (Fig. 22, Table 14).

Recommended genetic markers (genus level)—LSU (as outlined in Maharachchikumbura et al. 2012)
Recommended genetic markers (species level)—ITS, TUB2 and *tef1* (as outlined in Maharachchikumbura et al. 2012)
Accepted number of species: **20 species**
References: Maharachchukumbura 2013a, b, 2014b, 2016b (morphology, phylogeny)

Rosellinia De Not., G. bot. ital.1 (1): 334(1844)

Rosellinia (*Xylariaceae*) species are characterized mainly as saprobes, some endophytes and occasionally as pathogens. They have a worldwide distribution and common in both temperate and tropical regions (Petrini

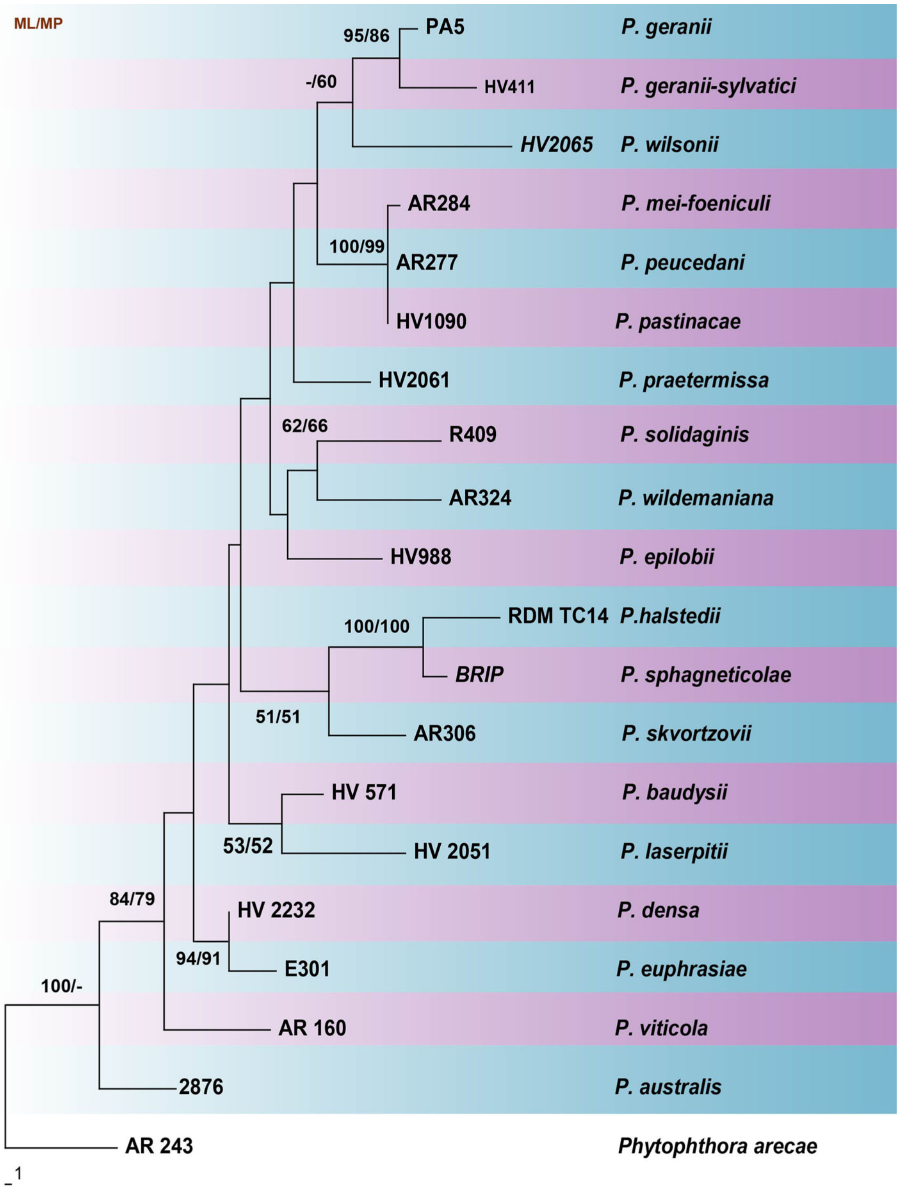


Fig. 21 Phylogenetic tree generated by maximum parsimony analysis of LSU sequence data of *Plasmopara* species. Related sequences were obtained from GenBank. Nineteen strains are included in the analyses, which comprise 1263 characters including gaps. The tree was rooted with *Phytophthora arece* (AR 234). Tree topology of the MP analysis was similar to the ML. The maximum parsimonious dataset consisted of constant 1053, 110 parsimony-informative and 100 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of two equally most parsimonious trees with a length of 365 steps (CI = 0.641, RI = 0.539, RC = 0.345, HI = 0.359) in the first tree. The best scoring RAxML tree with a final likelihood value of − 3660.849005 is presented. The matrix had 254 distinct alignment patterns, with 30.91% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.229156, C = 0.177763, G = 0.308486, T = 0.284595; substitution rates AC = 0.706031, AG = 4.368078, AT = 1.048734, CG = 0.141039, CT = 7.063364, GT = 1.000000; gamma distribution shape parameter α = 0.163551. RAxML and maximum parsimony bootstrap support value ≥ 50% (BT) are shown respectively near the nodes

1993, 2013; ten Hoopen and Krauss 2006). Plant pathogenic *Rosellinia* species play a vital role in economically important crops, trees and ornamental plants. *Rosellinia desmazieresii* and *R. necatrix* are mostly known from temperate regions, while *R. bunodes* is known only from the tropics causing root rot on fruit trees and vines (Agrios 2005; ten Hoopen and Krauss 2006). Among the root diseases cause by *Rosellinia* species, *R. bunodes* is responsible for black root rot, *R. necatrix* for white root rot and *R. pepo* for stellate root rot (Castro et al. 2013). Species of this genus can survive as microslerotia in wood, roots and soil and the infection spreads through feeder roots when they contact hyphae or microsclerotia (Ploetz et al. 2003).

Table 13 Details of the ***Plasmopara*** isolates used in the phylogenetic tree

Species	Isolate/voucher no	Host	LSU
Plasmopara australis	HV 2867	*Luffa cylindrica*	KT159461
P. baudysii	HV 571	*Berula erecta*	AY035517
P. densa	HV 2232	*Rhinanthus minor*	EF553463
P. epilobii	HV988	*Epilobium parviflorum*	AY250178
P. euphrasiae	EV 301	*Euphrasia rostkoviana*	EF553467
P. geranii	PA5	*Geranium maculatum*	DQ148397
P. geranii-sylvatici	HV411	*Geranium sylvaticum*	DQ148398
P. halstedii	RDM TC14	*Rudbeckia fulgida*	KP164999
P. laserpitii	HV2051	*Laserpitium latifolium*	KC495034
P. mei-foeniculi	AR284	*Meum athamanticum*	AY250160
P. pastinacae	HV1090	*Pastinaca sativa*	AY250157
P. peucedani	AR277	*Peucedanum palustre*	AY250154
P. praetermissa	HV2061	*Geranium sylvaticum*	DQ148396
P. skvortzovii	AR306	*Abutilon theophrasti*	AY250179
P. solidaginis	R409	*Solidago virgaurea*	AY250144
P. sphagneticolae	BRIP	*Sphagneticola trilobata*	KM085176
P. viticola	AR 160	*Vitis vinifera*	AY035524
P. wildemaniana	AR324	*Hypoestes* sp.	AY250180
P. wilsonii	HV2065	*Geranium nepalense*	DQ148408
Phytophthora arecae	AR 243	Unknown	AY035530

Rosellinia was introduced to accommodate species which are characterized by uniascomatal and carbonaceous stromata that develop within a subiculum. There have been different contradiction placements of *Rosellinia.* Miller (1928) placed it in the family *Xylariaceae* and this was confirmed in morphology and phylogeny-based studies later (Hsieh et al. 2010; Daranagama et al. 2015). Daranagama et al. (2018) and Wendt et al. (2018) revealed that *Rosellinia* is closely related to *Entoleuca* and *Nemania.*
Classification—*Sordariomycetes*, *Xylariomycetidae*, *Xylariales*, *Xylariaceae*
Type species—***Rosellinia aquila*** (Fr.) Ces. & De Not., G. bot. ital.1 (1): 334(1844)
Distribution—Worldwide
Disease symptoms—Root rots

Black root rot is characterized by the occurrence in patches that extend in a circular pattern. *Rosellinia bunodes* the main causal agent of black root rot typically shows black branching strands that are firmly attached to the roots and may form condensed irregular knots and chlorotic leaves may shed gradually (Sivanesan and Holiday 1972; Oliverira et al. 2008).

The symptoms of white root rot caused by *R. necatrix* in the upper parts of the plants (such as yellow foliage, shrivelled fruits, no new growth) cannot be recognized in early stages of root infection. Cottony, white mycelia cover feeder roots of a tree and decay sets in. Mycelia grow into the soil and upward in the tree forming small, pale patches under or in the bark of major roots, root crown and lower trunk which eventually decay. A purple canker in wood at the root crown of young trees can also be caused by the fungus. Diseased trees will defoliate and premature death may occur (Pérez-Jiménez 2006; Pasini et al. 2016).
Hosts—This genus has a wide range of hosts including *Adoxaceae*, *Annonaceae*, *Apiaceae*, *Asteraceae*, *Betulaceae*, *Celastraceae*, *Convolvulaceae*, *Euphorbiaceae*, *Fabaceae*, *Fagaceae*, *Grossulariaceae*, *Juglandaceae*, *Lauraceae*, *Moraceae*, *Myrtaceae*, *Oleaceae*, *Pinaceae*, *Poaceae*, *Rosaceae*, *Rutaceae*, *Salicaceae*, *Sapindaceae*, *Scrophulariaceae*, *Tamaricaceae*, *Verbenaceae*, *Vitaceae* and *Zingiberaceae*.

Morphological based identification and diversity

The genus is characterized by globose-subglobose, uni- to multiloculate, often collapsed ascomata, mostly detached from the stroma wall,; septate, hyaline paraphyses, asci that are 8-spored, unitunicate, cylindrical to clavate, long pedicellate, rounded at the apex, with J + apical ring bluing in Melzer's reagent, massive barrel-shaped with distinctive rings ascospores that are uniseriate, unicellular, elongated ellipsoidal-fusiform, light to dark brown, with germ slits, cellular appendages and/or may be slimy sheaths or caps and a dematophora-like or geniculosporium-like asexual morphs (Daranagama et al. 2018).

Rosellinia is a large genus with 483 epithets in Mycobank, 517 in Index Fungorum and 311 in Global Biodiversity Information Facility (GBIF); there are currently 158 accepted species (Petrini 2013; Li and Guo 2015; Li et al.

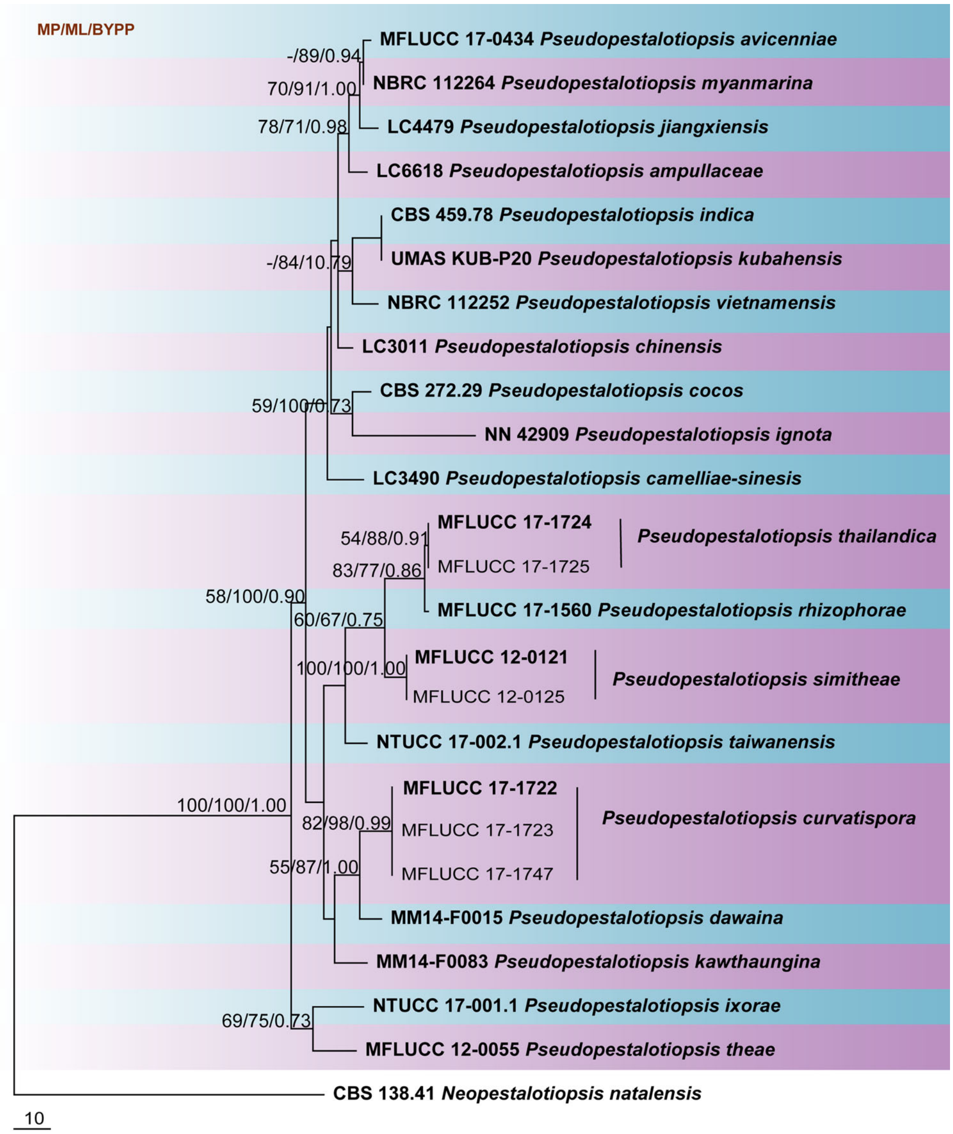


Fig. 22 Phylogram generated from maximum likelihood analysis based on combined ITS, TUB2 and *tef1* sequence data of *Pseudopestalotiopsis* species. Related sequences were obtained from GenBank. Twenty-five strains are included in the combined sequence analyses, which comprise 1404 characters with gaps. *Neopestalotiopsis natalensis* (CBS 138.41) was used as the outgroup taxa. The best scoring RAxML tree with a final likelihood value of − 4028.799660 is presented. The matrix had 274 distinct alignment patterns, with 6.34% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.235765, C = 0.270775, G = 0.213073, T = 0.280387; substitution rates AC = 1.242401, AG = 3.217138, AT = 1.272343, CG = 0.837226, CT = 4.463116, GT = 1.000000; gamma distribution shape parameter α = 0.229606. The maximum parsimonious dataset consisted of 1122 constant, 79 parsimony-informative and 203 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of four equally most parsimonious trees with a length of 386 steps (CI = 0.832, RI = 0.737, RC = 0.613, HI = 0.168) in the first tree. RAxML and maximum parsimony bootstrap support value ≥ 50% are shown respectively near the nodes. Bayesian posterior probabilities ≥ 0.95 (BYPP) indicated as thickened black branches. Ex-type strains are in bold

2015, 2016; Su et al. 2016; Crous et al. 2017; Fournier et al. 2017a, b; Tibpromma et al. 2017). Petrini (2013) found seven morphologically distinct groups with distinguishing morphological characters associated with the shape, size and orientations of stroma, ostiole, ascospores and germ slit, which can be used for species delimitation (Fig. 23).

Molecular based identification and diversity

Protein coding gene sequences are available for nine species of *Rosellinia*, mostly with only ITS and LSU sequence data. However, with the limited data, Daranagama et al. (2018) provided an updated backbone tree for genera in *Xylariaceae*, and *Rossellinia* clustered with *Nemania* and *Entoleuca*. Several phylogenetic studies have focused on

Table 14 Details of the ***Pseudopestalotiopsis*** isolates used in the phylogenetic analyses

Species	Isolates	ITS	TUB2	*tef1*
Pseudopestalotiopsis ampullacea	**LC6618***	KX895025	KX895358	KX895244
P. avucenniae	**MFLUCC 17-0434***	MK764287	MK764353	MK764331
P. camelliae-sinensis	**LC3490***	KX894985	KX895316	KX895202
P. chinensis	**LC3011***	KX894937	KX895269	KX895154
P. cocos	**CBS 272.29***	KM199378	KM199467	KM199553
P. dawaina	**MM14-F0015***	LC324750	LC324751	LC324752
P. curvatispora	**MFLUCC 17-1722***	MK764288	MK764354	MK764332
P. ignota	**NN 42909***	KU500020	–	KU500016
P. indica	**CBS 459.78***	KM199381	KM199470	KM199560
P. ixorae	**NTUCC 17-001.1***	MG816316	MG816326	MG816336.
P. jiangxiensis	**LC 4479***	KX895034	KX895343	KX895229
P. kawthaungina	**MM14-F0083**	LC324753	LC324754	LC324755
P. kubahensis	**UMAS KUB-P20***	KT006749	–	–
P. myanmarina	**NBRC 112264***	LC114025	LC114045	LC114065
P. rhizophorae	**MFLUCC 17-1560***	MK764291	MK764357	MK764335
P. smitheae	**MFLUCC 12-0121***	KJ503812	KJ503815	KJ503818
P. thailandica	**MFLUCC 17-1724***	MK764292	MK764358	MK764336
P. taiwanensis	**NTUCC 17-002.1***	MG816319	MG816329	MG816339
P. theae	**MFLUCC 12-0055***	JQ683727	JQ683711	JQ683743
P. vietnamensis	**NBRC 112252***	LC114034	LC114054	LC114074

Ex-type (ex-epitype) strains are in bold and marked with an asterisk* and voucher stains are in bold

pathogenic species such as *R. bunodes* and *R. pepo*. Castro et al. (2013) investigated *R. bunodes* and *R. pepo* isolated from *Coffea arabica* (*Rubiaceae*), *Hevea brasiliensis* (*Euphorbiaceae*), *Macadamia integrifolia* (*Proteaceae*), *Psidium guajava* (*Myrtaceae*) and *Theobroma cacao* (*Malvaceae*) using ITS based phylogenetic analyses from Colombia. Another ITS-based phylogenetic study identified *R. necatrix*, the pathogen responsible for white root disease on *Aronia melanocarpa* (*Rosaceae*) in Korea (Choi et al. 2017).

This study reconstructs the phylogeny of *Rosellinia* based on analyses of combined ITS, LSU and RPB2 sequence data (Table 7, Fig. 13). The phylogenetic tree is updated with recently introduced *Rosellinia* species and corresponds to previous studies (Li et al. 2015, 2016; Su et al. 2016; Crous et al. 2017; Fournier et al. 2017a, b; Tibpromma et al. 2017).

Recommended genetic markers (genus level)—LSU, ITS
Recommended genetic marker (species level)—ITS

Based on several studies and the availability of sequence data, ITS based phylogenetic studies are sufficient to identify *Rosellinia* to species level. There are few other studies carried out using LSU, ITS and RPB2 sequences. With a lack of sequence data for most species, there are some contradictions for the species and generic delimitat ion.

Accepted number of species: 158 with only **26 species with molecular data**

References: Petrini 2013; Li and Guo 2015; (morphology), Castro et al. 2013; Li et al. 2015, 2016; Crous et al. 2017; Fournier et al. 2017a, b; Tibpromma et al. 2017, Daranagama et al. 2018 (morphology, phylogeny), Shimizu et al. 2012; dos Santos et al. 2017; Arjona-Girona and López-Herrera 2018; Kleina et al. 2018 (pathogenicity).

Sphaeropsis Sacc., Michelia 2: 105. 1880.

The genus *Sphaeropsis* was introduced by Saccardo (1880) (for species of *Diplodia* with brown, aseptate conidia), with *S. visci* as the type species. *Sphaeropsis* is the asexual morph of *Phaeobotryosphaeria* (Phillips et al. 2008, 2013; Wijayawardene et al. 2017). Species in *Sphaeropsis* seem to be cosmopolitan in distribution since they have been recorded from both temperate and tropical countries (i.e. Germany, New Zealand, South Africa, Thailand (Phillips et al. 2013; Slippers et al. 2014; Farr and Rossman 2019). Host specificity of *Sphaeropsis* has not yet been clarified and species have been recorded from various plant families.

Classification—Dothideomycetes, *incertae sedis*, *Botryosphaeriales*, *Botryosphaeriaceae*
*Type species—****Sphaeropsis visci*** (Alb. & Schwein.) Sacc.
Distribution—Worldwide
Disease symptoms—calyx-end rot, stem end rot

The decayed tissues in rot diseases are firm or spongy and brown in colour. The skin of decayed areas generally remains brown or dark brown but may appear dark in aged areas (Kim et al. 2005).

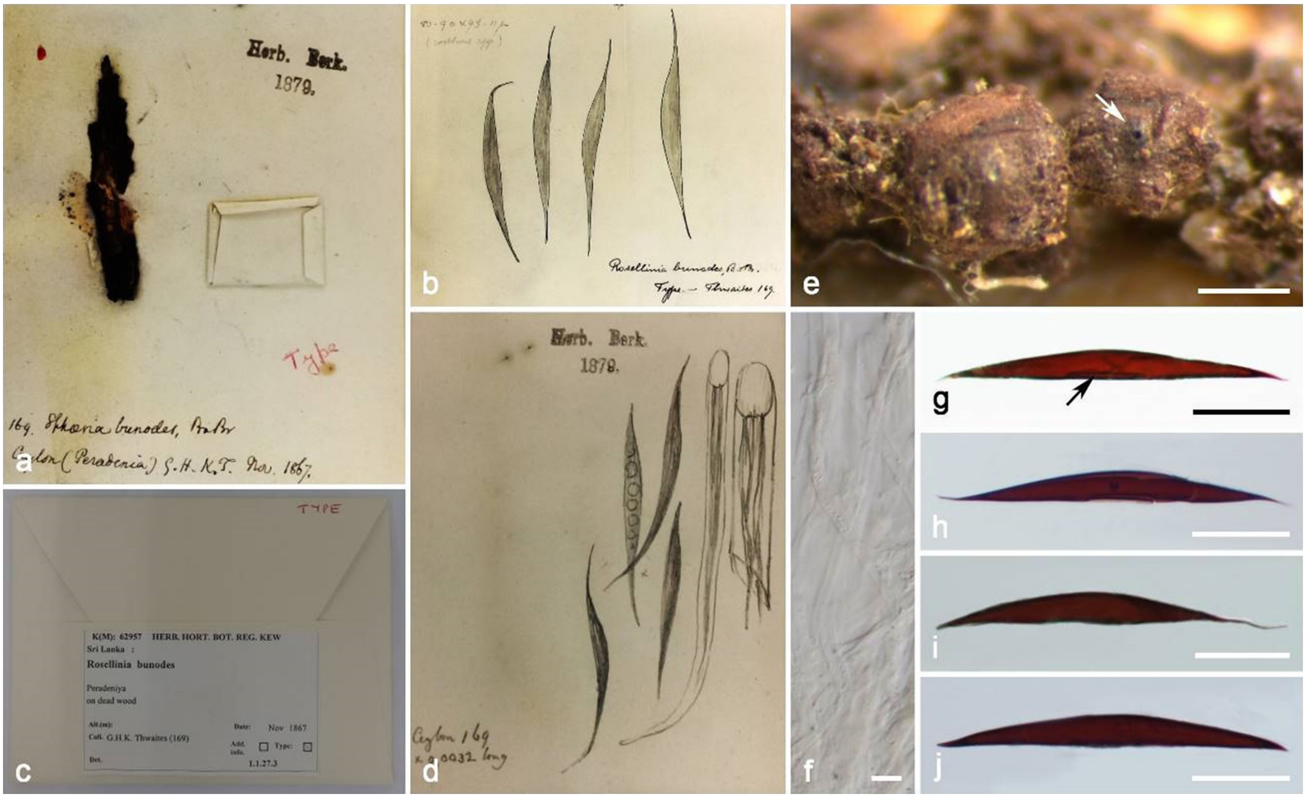


Fig. 23 *Rosellinia bunodes* (holotype, K(M) 62957, Sri Lanka, Peradeniya, on dead wood, November 1867, G.H.K. Thwaites) **a**, **e** Stromata (e ostiole white arrow). **b–d** Herbarium details. **f** Paraphyses. **g–j** Ascospores (**g** germ slit black arrow). Scale bars: **e** = 500 µm, **g–j** = 20 µm, **f** = 5 µm

Hosts—Broad range of hosts, including *Myrtaceae*, *Rutaceae*, *Santalaceae* and *Vitaceae*.

Morphological based identification and diversity

Over 600 species names are listed in Index Fungorum (2019), but few of them are currently in use and for most species cultures are not available except for *S. citrigena* (A.J.L. Phillips et al.) A.J.L. Phillips & A. Alves, *S. eucalypti* Berk. & Broome, *S. porosa* (Van Niekerk & Crous) A.J.L. Phillips & A. Alves, and *S. visci* (Alb. & Schwein.) Sacc. Pycnidial paraphyses in *Sphaeropsis* species distinguish this genus from *Diplodia* species, which do not have paraphyses. The aseptate, smooth-walled conidia of *Sphaeropsis* species differentiate them from *Lasiodiplodia* species, which have 1-septate, striate conidia. Recently, *S. variabilis* was transferred to a separate genus, *Oblongocollomyces* due to distinct morphological differences (Yang et al. 2017).

Colony and conidial morphology are the primary characters to identify species within this genus (Ellis 1971, 1976; Simmons 1992). The sexual and asexual morphs connection of *Sphaeropsis* was established by Phillips et al. (2008) who obtained coelomycetes with large, brown, aseptate conidia typical of *Sphaeropsis* from *Phaeobotryosphaeria* culture. Four *Sphaeropsis* species have been identified from culture. *Sphaeropsis porosa* differs from other species in having distinct pitted conidial walls. *Sphaeropsis visci* and *S. citrigena* can be distinguished from each other with their conidial pigmentation and swollen paraphyses tips (Phillips et al. 2013).

Molecular based identification and diversity

Phillips et al. (2013) suggested that phylogenetic analysis of combined SSU, LSU, ITS, *tef1* and TUB2 genes provide better resolution compared to ITS alone. This study provides the phylogenetic analyses of combined ITS, LSU, SSU, *tef1* and TUB2 sequence data (Table 10, Fig. 16). The topology of the *Sphaeropsis* species tree is identical to the phylogeny tree of Phillips et al. (2013).

Recommended genetic markers (genus level)—LSU and SSU
Recommended genetic markers (species level)—ITS, *tef1* and TUB2

Accepted number of species: There are 624 species epithets in Index Fungorum (2019) under this genus. However, only **four** species have sequence data.
References: Phillips et al. 2013; Yang et al. 2017 (morphology, phylogeny).

Updates on important phytopathogens

Alternaria Nees, Syst. Pilze (Würzburg): 72 (1816)

Species of *Alternaria* are saprotrophs on dead vegetation and are frequently isolated from soil, air, dust and water-damaged buildings (Ellis 1971, 1976; De Hoog and Horré 2002; Runa et al. 2009; Woudenberg et al. 2013; Lawrence et al. 2016). The majority of species, however, are pathogens, infecting a vast array of host species (Jayawardena et al. 2019). A detailed background, diseases and the symptoms, morphological characters is discussed in Jayawardena et al. (2019). In this paper, we provide an update for the sections in *Alternaria* based on six gene combination analyses (Al Ghafri et al. 2019; Table 15, Fig. 24).

Diplodia Fr., in Montagne, Annls Sci. Nat., Bot., sér. 2 1: 302 (1834)

The genus *Diplodia* was introduced by Montagne (1834) and comprises species with hyaline or dark brown, aseptate or 1-septate, thick-walled conidia (Phillips et al. 2005). *Diplodia* is defined by having unilocular, solitary or aggregated conidiomata lined with conidiogenous cells that form conidia at their tips (Phillips et al. 2005). The type species of *Diplodia* is *Diplodia mutila* (Montagne 1834; Fries 1849), but there are no living cultures linked to the holotype of this species. As this has severely hampered studies on taxonomy and phylogeny of *Diplodia*, Alves et al. (2004) provided a detailed description of *D. mutila* based on an isolate from grapevines in Portugal (CBS 112553). Alves et al. (2014) designated an epitype for *Diplodia mutila*, with associated ex-epitype cultures. This epitype confirmed in all ways with the isotype of *D. mutila* and with the asexual morph on BPI 599153 as described by Alves et al. (2004). *Diplodia mutila* has hyaline conidia that become brown and one-septate after discharge from the pycnidia. Species of *Diplodia* can be differentiated on slight differences in conidial dimensions (Alves et al. 2014).

Classification—Dothideomycetes, *incertae sedis*, *Botryosphaeriales*, *Botryosphaeriaceae*
*Type species—**Diplodia mutila*** (Fr. : Fr.) Fr., Summa Veg. Scand. 2:417 (1849)
Distribution—Worldwide
Disease symptoms—Diebacks, cankers, fruit rots.
Hosts—Plurivorous on woody hosts.

Morphological based identification and diversity

Diplodia is a large genus and a search in MycoBank (2019) revealed 1398 names while Index Fungorum (2019) has 1268 names. Cryptic speciation is common in the genus, which makes species identification difficult if based only on morphological characters (Phillips et al. 2012, 2013). Dissanayake et al. (2016) included 26 *Diplodia* species in their phylogeny. Recently, a novel species *Diplodia eriobotryicola* on *Eriobotrya japonica* from Spain was introduced by González-Domínguez et al. (2016). Yang et al. (2017) introduced *D. pyri* on *Pyrus* sp., the Netherlands, *D. citricarpa* on *Citrus* sp., Iran, and *D. gallae* on galls of *Quercus* sp. However, the ITS and *tef1* of the novel species, *D. citricarpa* are not available in GenBank and hence we could not include this species in our phylogeny. The genus now comprises 30 species known from culture.

Molecular based identification and diversity

Earlier taxonomic studies on *Diplodia* using molecular data employed ITS rDNA, but this single marker can underestimate species diversity among closely related or cryptic species. Multiple gene sequence concordance phylogenies have therefore been applied to identify cryptic or previously overlooked species of *Diplodia* (Slippers et al. 2004a, b, c; Burgess et al. 2006; Phillips et al. 2005, 2012, 2013; Hyde et al. 2014; Dissanayake et al. 2016). As the *tef1* gene is considerably more variable than the ITS rDNA region in these taxa, data from *tef1* have been combined with ITS sequence data. Unfortunately, no single gene region is sufficient to distinguish all species in this genus. The present phylogenetic analysis was performed based on up to date ex-holotype or ex-epitype sequence data available in GenBank (Fig. 25, Table 16).

Recommended genetic markers (genus level)—SSU and LSU
Recommended genetic markers (species level)—ITS, *tef1*, TUB2
Accepted number of species: **30 species**
References: Phillips et al. 2013 (morphology, phylogeny, distribution, hosts); Dissanayake et al. 2016 (phylogeny).

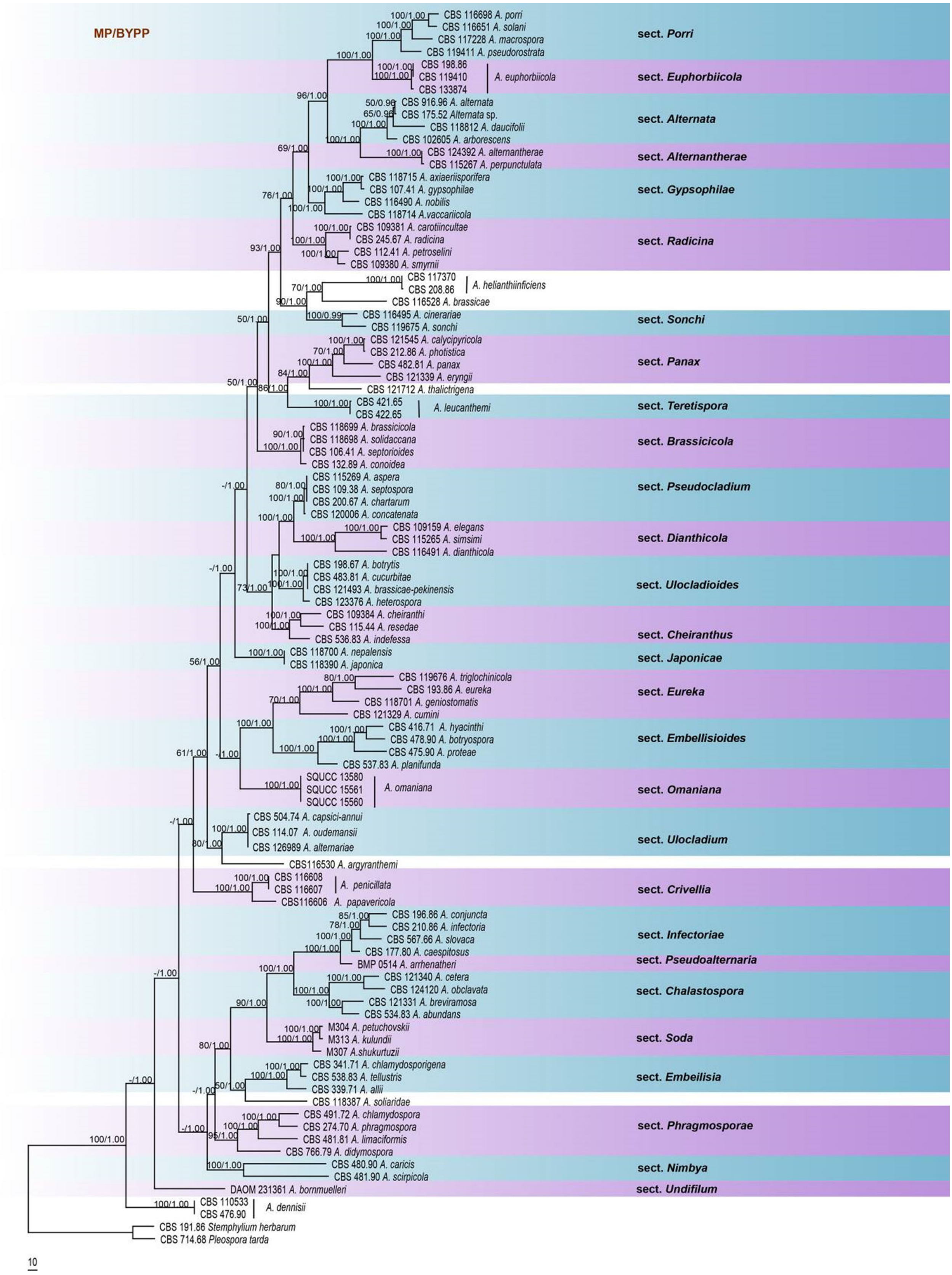
Dothiorella Sacc., Michelia 2(6): 5 (1880)
Dothiorella was proposed by Saccardo to accommodate *D. pyrenophora* (Hyde et al. 2014). Members of this genus are pathogens, endophytes and saprobes (Phillips et al. 2013; Dissanayake et al. 2016). Taxonomy of this genus has been in a state of flux for decades (Phillips et al. 2013). Sivanesan (1984) treated *D. pyrenophora* as a synonym of *Dothichiza sorbi* (asexual morph of *Dothiora pyrenophora*). However, Sivanesan (1984) was referring to *Dothiorella pyrenophora* Sacc. (1884) which, according to Sutton (1977), is a later homonym of *Dothiorella pyrenophora* Sacc. (1880). Crous and Palm (1999) studied the holotype of *D. pyrenophora* and considered it a synonym of *Diplodia*. However, Phillips et al. (2005) based on both morphological and molecular data revived the genus *Dothiorella* for species in which the conidia become brown and 1-septate while attached to the conidiogenous cells.

Table 15 Details of the ***Alternaria*** isolates used in the phylogenetic analyses

Species name	Strain number	GenBank accession numbers					
		SSU	LSU	RPB2	ITS	GPDH	*tef1*
Alternaria abundans	CBS 534.83	KC584581	KC584323	KC584448	JN383485	KC584154	KC584707
A. alternantherae	CBS 124392	KC584506	KC584251	KC584374	KC584179	KC584096	KC584633
A. alternariae	CBS 126989	KC584604	KC584346	KC584470	AF229485	AY278815	KC584730
A. alternate	CBS 916.96	KC584507	DQ678082	KC584375	AF347031	AY278808	KC584634
A. arborescens	CBS 102605	KC584509	KC584253	KC584377	AF347033	AY278810	KC584636
A. argyranthemi	CBS 116530	KC584510	KC584254	KC584378	KC584181	KC584098	KC584637
A. arrhenatheri	BMP 0514	–	–	–	JQ693680	JQ693629	–
A. aspera	CBS 115269	KC584607	KC584349	KC584474	KC584242	KC584166	KC584734
A. atra	CBS 195.67	KC584608	KC584350	KC584475	AF229486	KC584167	KC584735
A. axiaeriisporifera	CBS 118715	KC584513	KC584257	KC584381	KC584184	KC584101	KC584640
A. bornmueller	DAOM 231361	KC584624	KC584366	KC584491	FJ357317	FJ357305	KC584751
A. botryospora	CBS 478.90	KC584594	KC584336	KC584461	AY278844	AY278831	KC584720
A. botrytis	CBS 197.67	KC584609	KC584351	KC584476	KC584243	KC584168	KC584736
A. brassicae	CBS 116528	KC584514	KC584258	KC584382	KC584185	KC584102	KC584641
A. brassicae-pekinensis	CBS 121493	KC584611	KC584353	KC584478	KC584244	KC584170	KC584738
A. brassicicola	CBS 118699	KC584515	KC584259	KC584383	JX499031	KC584103	KC584642
A. breviramosa	CBS 121331	KC584574	KC584318	KC584442	FJ839608	KC584148	KC584700
A. calycipyricola	CBS 121545	KC584516	KC584260	KC584384	KC584186	KC584104	KC584643
A. capsici-annui	CBS 504.74	C584517	KC584261	KC584385	KC584187	KC584105	KC584644
A. caricis	CBS 480.90	KC584600	KC584342	KC584467	Y278839	AY278826	C584726
A. carotiincultae	CBS 109381	KC584518	KC584262	KC584386	KC584188	KC584106	KC584645
A. cetera	CBS 121340	KC584573	KC584317	KC584441	JN383482	AY562398	KC584699
A. chartarum	CBS 200.67	KC584614	KC584356	KC584481	AF229488	KC584172	KC584741
A. cheiranthi	CBS 109384	C584519	C584263	C584387	F229457	C584107	C584646
A. chlamydospora	CBS 491.72	KC584520	KC584264	KC584388	KC584189	KC584108	KC584647
A. chlamydosporigena	CBS 341.71	KC584584	KC584326	KC584451	KC584231	KC584156	KC584710
A. cinerariae	CBS 116495	KC584521	KC584265	KC584389	KC584190	KC584109	KC584648
A. concatenate	CBS 120006	KC584613	KC584355	KC584480	KC584246	AY762950	KC584740
A. conjuncta	CBS 196.86	KC584522	KC584266	KC584390	J266475	Y562401	KC584649
A. conoidea	CBS 132.89	KC584585	KC584327	KC584452	AF348226	FJ348227	KC584711
A. consortialis	CBS 104.31	KC584615	KC584357	KC584482	KC584247	KC584173	KC584742
A. cucurbitae	CBS 483.81	KC584616	KC584358	KC584483	FJ266483	AY562418	KC584743
A. cumini	CBS 121329	KC584523	KC584267	KC584391	KC584191	KC584110	KC584650
A. daucifolii	CBS 118812	KC584525	KC584269	KC584393	KC584193	KC584112	KC584652
A. dennisii	CBS 110533	KC584586	KC584328	KC584453	KC584232	KC584157	KC584712
A. dennisii	CBS 476.90	KC584587	KC584329	KC584454	JN383488	JN383469	KC584713
A. dianthicola	CBS 116491	KC584526	KC584270	KC584394	KC584194	KC584113	KC584653
A. didymospora	CBS 766.79	KC584588	KC584330	KC584455	FJ357312	FJ357300	KC584714
A. elegans	CBS 109159	KC584527	KC584271	KC584395	KC584195	KC584114	KC584654
A. embellisia	CBS 339.71	KC584582	KC584324	KC584449	KC584230	KC584155	KC584708
A. eryngii	CBS 121339	KC584529	KC584273	KC584397	Q693661	Y562416	KC584656
A. eureka	CBS 193.86	KC584589	KC584331	KC584456	JN383490	JN383471	KC584715
A. geniostomatis	CBS 118701	KC584532	KC584276	KC584400	KC584198	KC584117	KC584659
A. gypsophilae	CBS 107.41	KC584533	KC584277	KC584401	KC584199	KC584118	KC584660
A. helianthiinficiens	CBS 117370	KC584534	KC584278	KC584402	KC584200	KC584119	KC584661
A. helianthiinficiens	CBS 208.86	KC584535	KC584279	KC584403	JX101649	KC584120	EU130548
A. heterospora	CBS 123376	KC584621	KC584363	KC584488	KC584248	KC584176	KC584748

Table 15 (continued)

Species name	Strain number	GenBank accession numbers					
		SSU	LSU	RPB2	ITS	GPDH	*tef1*
A. hyacinthi	CBS 416.71	KC584590	KC584332	KC584457	KC584233	KC584158	KC584716
A. indefessa	CBS 536.83	KC584591	KC584333	KC584458	KC584234	KC584159	KC584717
A. infectoria	CBS 210.86	KC584536	KC584280	KC584404	DQ323697	AY278793	KC584662
A. japonica	CBS 118390	KC584537	KC584281	KC584405	KC584201	KC584121	KC584663
A. kulundii	M313	KJ443087	KJ443132	KJ443176	KJ443262	KJ649618	-
A. leucanthemi	CBS 421.65	KC584605	KC584347	KC584472	KC584240	KC584164	KC584732
A. leucanthemi	CBS 422.65	KC584606	KC584348	KC584473	KC584241	KC584165	KC584733
A. limaciformis	CBS 481.81	KC584539	KC584283	KC584407	KC584203	KC584123	KC584665
A. macrospora	CBS 117228	KC584542	KC584286	KC584410	KC584204	KC584124	KC584668
A. nepalensis	CBS 118700	KC584546	KC584290	KC584414	KC584207	KC584126	KC584672
A. nobilis	CBS 116490	KC584547	KC584291	KC584415	KC584208	KC584127	KC584673
A. obclavata	CBS 124120	KC584575	FJ839651	KC584443	KC584225	KC584149	KC584701
A. oudemansii	CBS 114.07	KC584619	KC584361	KC584486	FJ266488	KC584175	KC584746
A. omaniana	SQUCC 13580	MK878559	MK878556	MK880893	MK878562	MK880899	MK880896
A. omaniana	SQUCC 15560	MK878560	MK878557	MK880894	MK878563	MK880900	MK880897
A. omaniana	SQUCC 15561	MK878561	MK878558	MK880895	MK878564	MK880901	MK880898
A. panax	CBS 482.81	KC584549	KC584293	KC584417	KC584209	KC584128	KC584675
A. papavericola	CBS 116606	KC584579	KC584321	KC584446	FJ357310	FJ357298	KC584705
A. penicillata	CBS 116608	KC584572	KC584316	KC584440	FJ357311	FJ357299	KC584698
A. penicillata	116607	KC584580	KC584322	KC584447	KC584229	KC584153	KC584706
A. perpunctulata	CBS 115267	KC584550	KC584294	KC584418	KC584210	KC584129	KC584676
A. petroselini	CBS 112.41	KC584551	KC584295	KC584419	KC584211	KC584130	KC584677
A. petuchovskii	M304	KJ443079	KJ443124	KJ443170	KJ443254	KJ649616	–
A. photistica	CBS 212.86	KC584552	KC584296	KC584420	KC584212	KC584131	KC584678
A. phragmospora	CBS 274.70	KC584595	KC584337	KC584462	JN383493	JN383474	KC584721
A. porri	CBS 116698	KC584553	KC584297	KC584421	DQ323700	KC584132	KC584679
A. proteae	CBS 475.90	KC584597	KC584339	KC584464	AY278842	KC584161	KC584723
A. pseudorostrata	CBS 119411	KC584554	KC584298	KC584422	JN383483	AY562406	KC584680
A. radicina	CBS 245.67	KC584555	KC584299	KC584423	KC584213	KC584133	KC584681
A. scirpicola	CBS 481.90	KC584602	KC584344	KC584469	KC584237	KC584163	KC584728
A. septorioides	CBS 106.41	KC584559	KC584303	KC584427	KC584216	KC584136	KC584685
A. septospora	CBS 109.38	KC584620	KC584362	KC584487	FJ266489	FJ266500	KC584747
A. shukurtuzii	M307	KJ443082	KJ443127	KJ443172	KJ443257	KJ649620	-
A. simsimi	CBS 115265	KC584560	KC584304	KC584428	JF780937	KC584137	KC584686
A. slovaca	CBS 567.66	KC584576	KC584319	KC584444	KC584226	KC584150	KC584702
A. smyrnii	CBS 109380	KC584561	KC584305	KC584429	AF229456	KC584138	KC584687
A. solani	CBS 116651	KC584562	KC584306	KC584430	KC584217	KC584139	KC584688
A. soliaridae	CBS 118387	KC584563	KC584307	KC584431	KC584218	KC584140	KC584689
A. solidaccana	CBS 118698	KC584564	KC584308	KC584432	KC584219	KC584141	KC584690
A. sonchi	CBS 119675	KC584565	KC584309	KC584433	KC584220	KC584142	KC584691
Alternaria sp.	CBS 175.52	KC584577	KC584320	KC584445	KC584227	KC584151	KC584703
A. tagetica	CBS 479.81	KC584566	KC584310	KC584434	KC584221	KC584143	KC584692
A. tellustris	CBS 538.83	KC584598	KC584340	KC584465	FJ357316	AY562419	KC584724
A. thalictrigena	CBS 121712	KC584568	KC584312	KC584436	EU040211	KC584144	KC584694
A. triglochinicola	CBS 119676	KC584569	KC584313	KC584437	KC584222	KC584145	KC584695
A. vaccariae	CBS 116533	KC584570	KC584314	KC584438	KC584223	KC584146	KC584696
A. vaccariicola	CBS 118714	KC584571	KC584315	KC584439	KC584224	KC584147	KC584697


MP/BYPP
CBS 116698 A. porri
CBS 116651 A. solani
CBS 117228 A. macrospora
CBS 119411 A. pseudorostrata
sect. Porri
CBS 198.86
CBS 119410
CBS 133874
A. euphorbiicola
sect. Euphorbiicola
CBS 916.96 A. alternata
CBS 175.52 Alternata sp.
CBS 118812 A. daucifolii
CBS 102605 A. arborescens
sect. Alternata
CBS 124392 A. alternantherae
CBS 115267 A. perpunctulata
sect. Alternantherae
CBS 118715 A. axiaeriisporifera
CBS 107.41 A. gypsophilae
CBS 116490 A. nobilis
CBS 118714 A.vaccariicola
sect. Gypsophilae
CBS 109381 A. carotiincultae
CBS 245.67 A. radicina
CBS 112.41 A. petroselini
CBS 109380 A. smyrnii
sect. Radicina
CBS 117370
CBS 208.86
A. helianthiinficiens
CBS 116528 A. brassicae
CBS 116495 A. cinerariae
CBS 119675 A. sonchi
sect. Sonchi
CBS 121545 A. calycipyricola
CBS 212.86 A. photistica
CBS 482.81 A. panax
CBS 121339 A. eryngii
CBS 121712 A. thalictrigena
sect. Panax
CBS 421.65
CBS 422.65
A. leucanthemi
sect. Teretispora
CBS 118699 A. brassicicola
CBS 118698 A. solidaccana
CBS 106.41 A. septorioides
CBS 132.89 A. conoidea
sect. Brassicicola
CBS 115269 A. aspera
CBS 109.38 A. septospora
CBS 200.67 A. chartarum
CBS 120006 A. concatenata
sect. Pseudocladium
CBS 109159 A. elegans
CBS 115265 A. simsimi
CBS 116491 A. dianthicola
sect. Dianthicola
CBS 198.67 A. botrytis
CBS 483.81 A. cucurbitae
CBS 121493 A. brassicae-pekinensis
CBS 123376 A. heterospora
sect. Ulocladioides
CBS 109384 A. cheiranthi
CBS 115.44 A. resedae
CBS 536.83 A. indefessa
sect. Cheiranthus
CBS 118700 A. nepalensis
CBS 118390 A. japonica
sect. Japonicae
CBS 119676 A. triglochinicola
CBS 193.86 A. eureka
CBS 118701 A. geniostomatis
CBS 121329 A. cumini
sect. Eureka
CBS 416.71 A. hyacinthi
CBS 478.90 A. botryospora
CBS 475.90 A. proteae
CBS 537.83 A. planifunda
sect. Embellisioides
SQUCC 13580
SQUCC 15561
SQUCC 15560
A. omaniana
sect. Omaniana
CBS 504.74 A. capsici-annui
CBS 114.07 A. oudemansii
CBS 126989 A. alternariae
sect. Ulocladium
CBS116530 A. argyranthemi
CBS 116608
CBS 116607
A. penicillata
CBS116606 A. papavericola
sect. Crivellia
CBS 196.86 A. conjuncta
CBS 210.86 A. infectoria
CBS 567.66 A. slovaca
CBS 177.80 A. caespitosus
sect. Infectoriae
BMP 0514 A. arrhenatheri
sect. Pseudoalternaria
CBS 121340 A. cetera
CBS 124120 A. obclavata
CBS 121331 A. breviramosa
CBS 534.83 A. abundans
sect. Chalastospora
M304 A. petuchovskii
M313 A. kulundii
M307 A.shukurtuzii
sect. Soda
CBS 341.71 A. chlamydosporigena
CBS 538.83 A. tellustris
CBS 339.71 A. allii
sect. Embeilisia
CBS 118387 A. soliaridae
CBS 491.72 A. chlamydospora
CBS 274.70 A. phragmospora
CBS 481.81 A. limaciformis
CBS 766.79 A. didymospora
sect. Phragmosporae
CBS 480.90 A. caricis
CBS 481.90 A. scirpicola
sect. Nimbya
DAOM 231361 A. bornmuelleri
sect. Undifilum
CBS 110533
CBS 476.90
A. dennisii
CBS 191.86 Stemphylium herbarum
CBS 714.68 Pleospora tarda
10

◀**Fig. 24** Phylogenetic tree generated by maximum parsimony analysis of combined SSU, LSU, ITS, GPDH, *tef1* and RPB2 sequence data of *Alternaria* species. One hundred strains are included in the analyses, which comprised 4056 characters including gaps. The tree was rooted with *Stemphylium herbarium* (CBS 191.86) and *Pleospora tarda* (CBS 714.68). The maximum parsimonious dataset consisted of 3091 constant, 852 parsimony-informative and 113 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of ten equally most parsimonious trees with a length of 4520 steps (CI = 0.335, RI 0.708, RC = 0.237, HI = 0.665) in the first tree. MP and ML bootstrap values ≥ 50% and Bayesian posterior probabilities ≥ 0.90 are shown respectively near the nodes. Ex-type strains are in bold

Classification—Dothideomycetes, *incertae sedis*, *Botryosphaeriales*, *Botryosphaeriaceae*
*Type species—***Dothiorella pyrenophora** Berk. ex Sacc., Michelia 2 (6): 5 (1880) (1909)
Distribution—Worldwide
Disease symptoms—Diebacks, cankers, fruit rots.
Hosts—Plurivorous on woody hosts.

Morphological based identification and diversity

Species of this genus were mostly described based on host association, which has led to the introduction of many species names and currently there are 393 epithets in Index Fungorum (2019). Slippers et al. (2013) suggested that host association cannot be considered as an important factor in species delimitation, many names are likely to be synonyms. Phillips et al. (2008) introduced a new genus *Spencermartinsia* to accommodate dothiorella-like species with apiculate ascospores. However, Yang et al. (2017) based on six-gene phylogeny and a broad taxon sampling considered that *Spencermartinsia* should be treated as a synonym of *Dothiorella*. Phillips et al. (2013) listed all cultures available for this genus and provided a phylogenetic tree and a key to the species. In that study 13 species names and 16 unnamed lineages were listed. Hyde et al. (2014), Dissanayake et al. (2016) and Yang et al. (2017) provided updates for the genus. Hyde et al. (2014) accepted 19 species and Dissanayake et al. (2016) accepted 30 species in the genus. After making *Spencermartinsia* a synonym of *Dothiorella* Yang et al. (2017) accepted 36 species in this genus.

Phillips et al. (2013) differentiated 13 *Dothiorella* species on the basis of conidiomata and conidial dimensions. However, the dimensions of these characters overlap between species. Therefore, using morphology alone without molecular data is not suitable to define species.

Molecular based identification and diversity

Recent studies have re-evaluated this genus based on multi-gene phylogeny of ITS, TUB2 and *tef1* sequence data. We reconstruct the phylogeny of *Dothiorella* based on analyses of a combined ITS and *tef1* sequence data (Table 17, Fig. 26). The phylogenetic tree is updated with recently introduced *Dothiorella* species and corresponds to previous studies (Dissanayake et al. 2016; Yang et al. 2017; Hyde et al. 2018; Phookamsak et al. 2019). In the analyses, it appears that several species are synonyms, such as *D. parva*/*D. guttulata* and *D. rhamni*/*D. eriobotryae* and possibly others. Therefore, a thorough revision of the genus is recommended to clarify the status of these dubious species.

Recommended genetic markers (genus level)—SSU and LSU
Recommended genetic markers (species level)—ITS and *tef1*

Accepted number of species: Currently, 393 species names are listed for *Dothiorella* in Index Fungorum (2019). Cultures and DNA sequences are available for 46 species, therefore **46 species are currently accepted in *Dothiorella*.**

References: Phillips et al. 2013; Dissanayake et al. 2016 (morphology, phylogeny, distribution, hosts), Yang et al. 2017 (morphology and phylogeny)

Fusarium Link, Mag. Gesell. naturf. Freunde, Berlin 3(1-2): 10 (1809)

Fusarium is a genus with 20 monophyletic species complexes (Rana et al. 2017).

Species formely belonged to *F. solani* species complex were transferred to genus *Neocosmospora* based on sexual morph characters and molecular phylogeny (Lombard et al. 2015; Sandoval-Denis and Crous (2018). *Fusarium* species are saprobes, parasites, endophytes, soil-borne or isolated from water (Rana et al. 2017). Species of *Fusarium* are economically important fungi as they are responsible for blights, cankers, rots, and wilts of horticultural, ornamental and forest crops in both agricultural and natural ecosystems, worldwide, and also human infections (Rana et al. 2017; Varela et al. 2013; Peraldi et al. 2014; Al-Hatmi et al. 2019; Maryani et al. 2019a, b). In nature, sexual morphs of *Fusarium* occur less commonly than the asexual morphs (Gräfenhan et al. 2011; Rossman et al. 1999).
Classification—Sordariomycetes, *Hypocreomycetidae*, *Hypocreales*, *Nectriaceae*
*Type species—***Fusarium sambucinum** Fuckel, Hedwigia 2: 135.1863.
Distribution—Worldwide
Disease symptoms—blights, cankers, rots, and wilts

Plant pathogenic species of this genus have the capability to change their lifestyle to saprotrophic and can survive for long periods as chlamydospores in host tissues. *Fusarium* species damage their hosts by systemically colonizing and occluding the host xylem (Ploetz et al. 2003).
Hosts—Known from many host plant families.

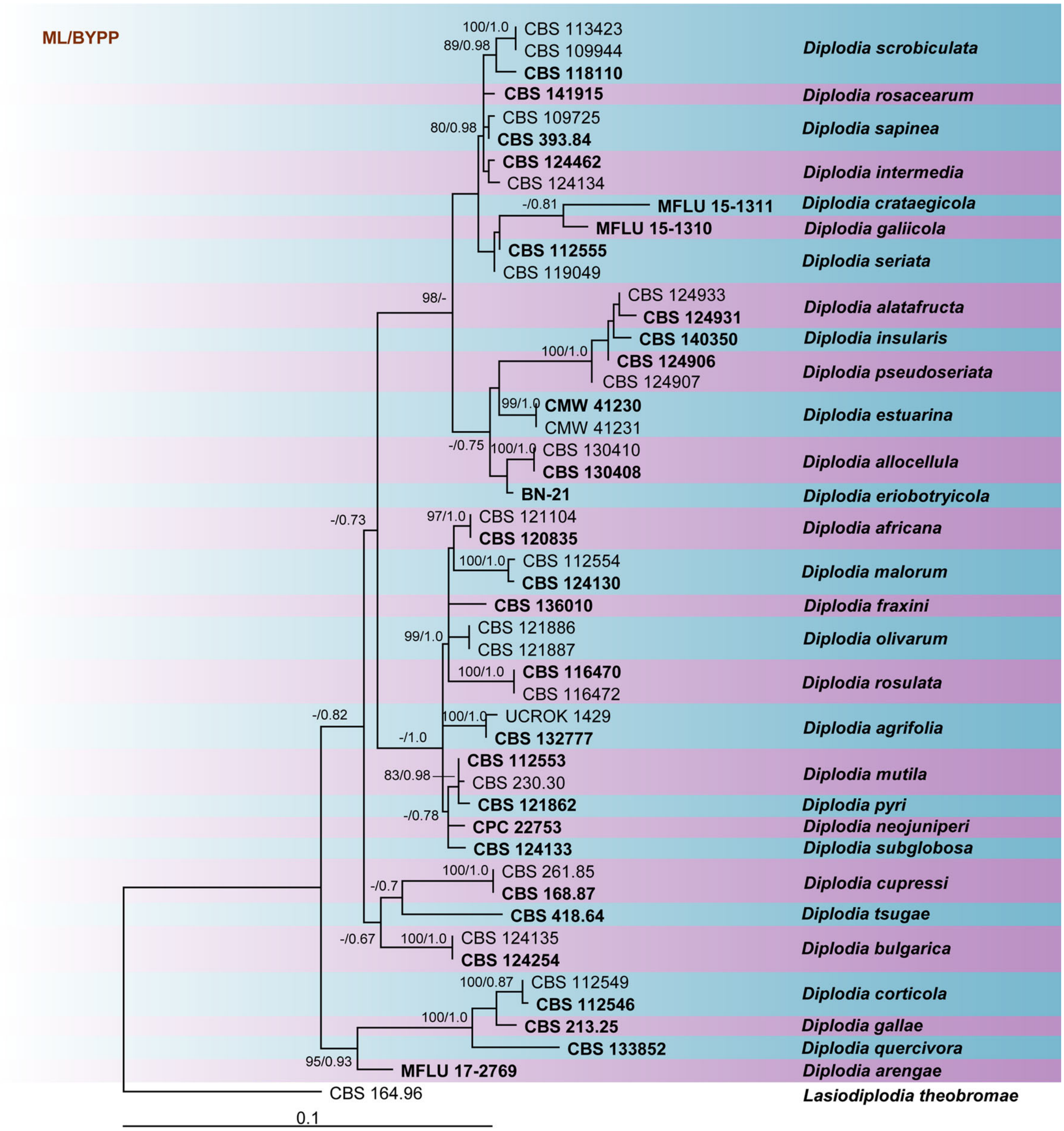


Fig. 25 Phylogenetic tree generated by maximum likelihood analysis of combined ITS and *tef1* sequence data of *Diplodia* species. Related sequences were obtained from GenBank. Forty nine strains are included in the analyses, which comprise 866 characters including gaps. The tree was rooted with *Lasiodiplodia theobromae* (CBS 164.96). Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 3342.903931 is presented. The matrix had 278 distinct alignment patterns, with 9.02%. % of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.207781, C = 0.297582, G = 0.261770, T = 0.232868; substitution rates AC = 0.993193, AG = 3.566477, AT = 0.787748, CG = 1.607220, CT = 4.471399, GT = 1.000000; gamma distribution shape parameter α = 1.224079. RAxML bootstrap support values ≥ 80% (BT) are shown respectively near the nodes. Bayesian posterior probabilities ≥ 0.5 (PP) indicated as thickened black branches. Ex-type strains are in bold

Morphological based identification and diversity

Fusarium was also known from the sexual morphic fungus name *Gibberella*, which was suppressed in favour of *Fusarium* by Rossman et al. (2013). Variation and mutation in culture and lack of clear morphological characters for separating species are the main problems which make the species concept of *Fusarium* much broader (Geiser et al. 2004). It leads to the incorrect and confusing application of species names to toxigenic and pathogenic isolates (Geiser et al. 2004). Species boundaries have been inferred using multi-gene phylogenetic methods, reflecting the species diversity more than morphological treatments (Aoki and O'Donnell 1999; Geiser et al. 2004; O'Donnell 2000;

Table 16 Details of the ***Diplodia*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	*tef1*
Diplodia africana	**CBS 120835***	**EF445343**	**EF445382**
Diplodia africana	CBS 121104	EF445344	EF445383
Diplodia agrifolia	**CBS 132777***	**JN693507**	**JQ517317**
Diplodia agrifolia	UCROK1429	JQ411412	JQ512121
Diplodia alatafructa	**CBS 124931***	**FJ888460**	**FJ888444**
Diplodia alatafructa	CBS 124933	FJ888478	FJ888446
Diplodia allocellula	**CBS 130408***	**JQ239397**	**JQ239384**
Diplodia allocellula	CBS 130410	JQ239399	JQ239386
Diplodia arengae	**MFLU 17-2769**	MG762771	MG762774
Diplodia bulgarica	**CBS 124254***	**GQ923853**	**GQ923821**
Diplodia bulgarica	CBS 124135	GQ923852	GQ923820
Diplodia corticola	**CBS 112549***	**AY259100**	**AY573227**
Diplodia corticola	CBS 112546	AY259110	DQ458872
Diplodia crataegicola	**MFLU 15-1311***	**KT290244**	**KT290248**
Diplodia cupressi	**CBS 168.87***	**DQ458893**	**DQ458878**
Diplodia cupressi	CBS 261.85	DQ458894	DQ458879
Diplodia estuarina	**CMW41231***	**KP860831**	**KP860676**
Diplodia estuarina	CMW41230	KP860830	KP860675
Diplodia fraxinii	**CBS 136010***	**KF307700**	**KF318747**
Diplodia galiicola	**MFLU 15-1310***	**KT290245**	**KT290249**
Diplodia insularis	**CBS 140350***	**KX833072**	**KX833073**
Diplodia intermedia	**CBS 124462***	**GQ923858**	**GQ923826**
Diplodia intermedia	CBS 124134	HM036528	GQ923851
Diplodia malorum	**CBS 124130***	**GQ923865**	**GQ923833**
Diplodia malorum	CBS 112554	AY259095	DQ458870
Diplodia mutila	**CBS 112553***	**AY259093**	**AY573219**
Diplodia mutila	CBS 230.30	DQ458886	DQ458869
Diplodia neojuniperi	**CPC 22753***	**KM006431**	**KM006462**
Diplodia olivarum	**CBS 121887***	**EU392302**	**EU392279**
Diplodia olivarum	CBS 121886	EU392297	EU392274
Diplodia pseudoseriata	**CBS 124906***	**EU080927**	**EU863181**
Diplodia pseudoseriata	CBS 124907	EU080922	EU863179
Diplodia quercivora	**CBS 133852***	**JX894205**	**JX894229**
Diplodia rosacearum	**CBS 141915***	**KT956270**	**KU378605**
Diplodia rosulata	**CBS 116470***	**EU430265**	**EU430267**
Diplodia rosulata	CBS 116472	EU430266	EU430268
Diplodia sapinea	**CBS 393.84***	**DQ458895**	**DQ458880**
Diplodia sapinea	CBS 109725	DQ458896	DQ458881
Diplodia scrobiculata	**CBS 118110***	**AY253292**	**AY624253**
Diplodia scrobiculata	CBS 109944	DQ458899	DQ458884
Diplodia scrobiculata	CBS 113423	DQ458900	DQ458885
Diplodia seriata	**CBS 112555***	**AY259094**	**AY573220**
Diplodia seriata	CBS 119049	DQ458889	DQ458874
Diplodia subglobosa	**CBS 124133***	**GQ923856**	**GQ923824**
Diplodia tsugae	**CBS 418.64***	**DQ458888**	**DQ458873**

Ex-type (ex-epitype) strains are in bold and marked with an asterisk* and voucher stains are in bold

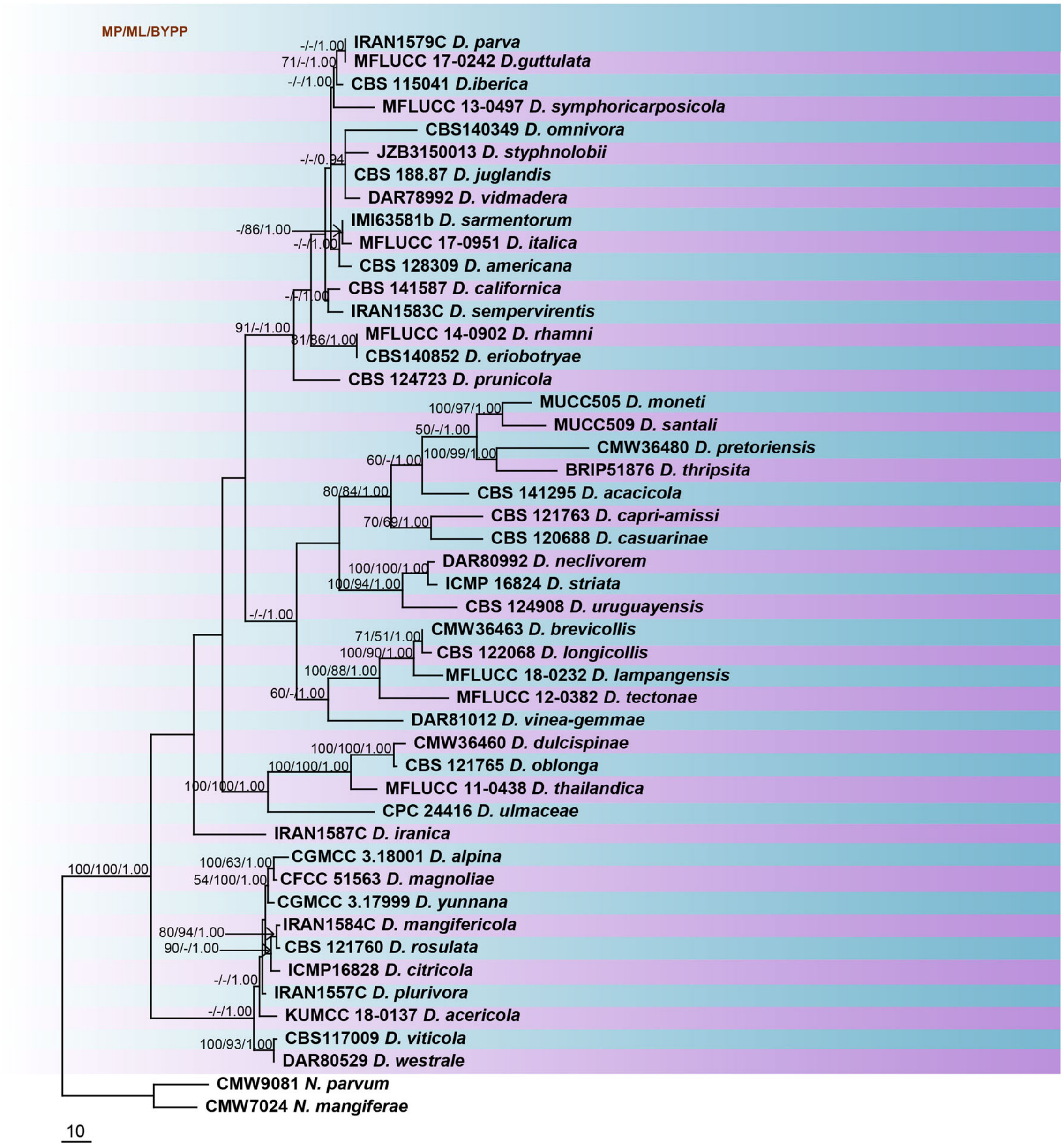


Fig. 26 Phylogenetic tree generated by maximum parsimony analysis of combined ITS and *tef1* sequence data of *Dothiorella* species. Related sequences were obtained from GenBank. Forty eight strains are included in the analyses, which comprised 873 characters including gaps. The tree was rooted with *Neofusicoccum parvum* (CMW9081) and *N. mangiferae* (CMW7024). The maximum parsimonious dataset consisted of 572 constant, 204 parsimony-informative and 97 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of ten equally most parsimonious trees with a length of 891 steps (CI = 0.532, RI 0.738, RC = 0.393, HI = 0.468) in the first tree. MP and ML bootstrap values ≥ 50% and Bayesian posterior probabilities ≥ 0.90 are shown respectively near the nodes. The scale bar indicates 10 changes per site. Ex-type strains are in bold

O'Donnell et al. 1998a, b; Ward et al. 2002). A combined phylogenetic analysis of LSU, ITS, RPB2 and new phylogenetic marker acl1 by Gräfenhan et al. (2011), revealed that the early concept of *Fusarium* is not monophyletic. *Fusarium sensu* Wollenweber divided into two large groups, basal '*Fusarium*-like clades', and the other one terminal '*Fusarium* clade' in the *Nectriaceae* (Gräfenhan et al. 2011) (Fig. 27).

Molecular based identification and diversity

ITS and LSU are least informative in species-level identification of *Fusarium* (O'Donnell et al. 1998a; Hyde et al. 2014). Moreover, non-orthologous copies of the ITS2, which can lead to wrong phylogenetic inferences, can be detected in many species of *Fusarium* (Geiser et al. 2004; O'Donnell et al. 1998a, b). Generally, for the species-level identification of fungi intron-rich regions of protein-coding

Table 17 Details of the ***Dothiorella*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	*tef1*
Dothiorella acacicola	**CBS 141295**	KX228269	KX228376
D. acericola	**KUMCC 18-0137***	MK359449	MK361182
D. alpina	**CGMCC 3.18001***	KX499645	KX499651
D. americana	**CBS 128309***	HQ288218	HQ288262
D. brevicollis	**CBS 130411***	JQ239403	JQ239390
D. californica	**CBS 141587***	KX357188	KX357211
D. capri-amissi	**CMW 25403***	EU101323	EU101368
D. casuarinae	**CBS 120688***	DQ846773	DQ875331
D. citricola	**ICMP16828***	EU673323	EU673290
D. dulcispinae	**CBS 130413***	JQ239400	JQ239387
D. eriobotryae	**CBS 140852***	KT240287	KT240262
D. guttulata	**MFLUCC 17-0242**	KY797637	–
D. iberica	**CBS 115041***	AY573202	AY573222
D. iranica	**IRAN1587C***	KC898231	KC898214
D. italica	**MFLUCC 17-0951**	MG828897	MG829267
D. juglandis	**CBS 188.87**	EU673316	EU673283
D. lampangensis	**MFLUCC 18-0232**	MK347758	MK340869
D. longicollis	**CBS 122068***	EU144054	EU144069
D. magnoliae	**CFCC 51563**	KY111247	KY213686
D. mangifericola	**IRAN1584C***	KC898221	KC898204
D. moneti	**MUCC505***	EF591920	EF591971
D. neclivorem	**DAR80992***	KJ573643	KJ573640
D. oblonga	**CMW 25407***	EU101300	EU101345
D. omnivora	**CBS 140349***	KP205497	KP205470
D. parva	**IRAN1579C***	KC898234	KC898217
D. plurivora	**IRAN1557C***	KC898225	KC898208
D. pretoriensis	**CBS 130404***	JQ239405	JQ239392
D. prunicola	**CBS 124723***	EU673313	EU673280
D. rhamni	**MFLUCC 14-0902***	KU246381	–
D. rosulata	**CBS 121760***	EU101290	EU101335
D. santali	**MUCC 509***	EF591924	EF591975
D. sarmentorum	**IMI63581b***	AY573212	AY573235
D. sempervirentis	**IRAN1583C***	KC898236	KC898219
D. striata	**ICMP16824***	EU673320	EU673287
D. styphnolobii	**JZB3150013***	MH880849	MK069594
D. symphoricarposicola	**MFULCC 13-0497***	KJ742378	KJ742381
D. tectonae	**MFLUCC12-0382***	KM396899	KM409637
D. thailandica	**CBS 133991***	JX646796	JX646861
D. thripsita	**BRIP 51876***	FJ824738	KJ573639
D. ulmacea	**CBS 138855***	KR611881	KR611910
D. uruguayensis	**CBS 124908***	EU080923	EU863180
D. vidmadera	**DAR78992***	EU768874	EU768881
D. vinea-gemmae	**DAR81012***	KJ573644	KJ573641
D. viticola	**CBS 117009***	AY905554	AY905559
D. westrale	**DAR80529***	HM009376	HM800511
D. yunnana	**CGMCC 3.17999***	KX499643	KX499649

Ex-type (ex-epitype) strains are in bold and marked with an asterisk* and voucher stains are in bold

[a] the *tef1* sequence of *D. guttulata* in GenBank is incorrect, therefore was not included in the analyses

genes are used as the markers (Geiser et al. 2004). The translation elongation factor 1-a (*tef1*), which lacks non-orthologous copies of the gene, is highly informative at the species level in *Fusarium* (Geiser et al. 2004). RPB1 and RPB2 are also very informative gene regions for species identification of *Fusarium* (O'Donnell et al. 2013; Hyde et al. 2014). Lombard et al. (2018) observed that tef1 and RPB2 genes provide better resolution of the species in the *F. oxysporum* complex than cmdA and tub2 (Fig. 28, Table 18).

Recommended genetic markers (genus level)—ATP citrate lyase (acl1), *tef1* and ITS
Recommended genetic markers (species level)—calmodulin-encoding gene (cmdA), tub2, *tef1*, RPB1 and RPB2

Accepted number of species: There are 1552 species epithets in Index Fungorum (2019) under this genus. More than 175 species have DNA sequence data.
References: Booth 1971, Rossman et al. 1999 (morphology), Rana et al. 2017, Gräfenhan et al. 2011; Laurence et al. 2014; Lombard et al. 2018, 2019; Maryani et al. 2019a, b; Wang et al. 2019; Nalim et al. 2011 (morphology, phylogeny).

Lasiodiplodia Ellis & Everh., Bot. Gaz. 21:92 (1896)

According to Clendenin (1896), a fungus causing rot of sweet potatoes imported from Java was identified by Ellis in 1894 as a new genus and he named the fungus *Lasiodiplodia tubericola*. However, Ellis (1894) did not describe the fungus or publish the new genus. Clendenin (1896) provided a description of the genus and the species, attributing both to Ellis and Everhardt. Griffin and Maublanc (1909) considered that on account of the pycnidial paraphyses, *Botryodiplodia theobromae*, described by Patouillard and de Lagerheim (1892), was more suitably accommodated in *Lasiodiplodia*. Since the epithet *theobromae* (1892) is older than *tubericola* (1896), *L. theobromae* should be regarded as the type species of *Lasiodiplodia*. Neither Patouillard and de Lagerheim (1892) nor Clendenin (1896) referred to any type or other specimens of the genus or species. Pavlic et al. (2004) could not locate the types, and they could not find any specimens from the original hosts or origins. Phillips et al. (2013) designated CBS H-21411 as neotype with CBS 164.96 as culture ex-neotype.

The sexual morph has been reported for *L. theobromae*, but the connection with the asexual morph has not been confirmed (Phillips et al. 2013). Sexual morphs have also been reported for *L. pseudotheobromae* (Tennakoon et al. 2016), *L. gonubiensis* (Trakunyingcharoen et al. 2015) and *L. lignicola* (Phillips et al. 2013) with clear evidence that connects sexual with asexual morphs.

Classification—Dothideomycetes, *incertae sedis*, *Botryosphaeriales*, *Botryosphaeriaceae*
*Type species—**Lasiodiplodia theobromae*** (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909)
Distribution—Worldwide, mostly confined to tropical and sub-tropical regions, but becoming increasingly more common in warm temperate regions.
Disease symptoms—Diebacks, cankers, fruit rots.
Hosts—Plurivorous on woody hosts

Morphological based identification and diversity

The pigmented, 1-septate conidia with longitudinal striations together with the pycnidial paraphyses distinguish *Lasiodiplodia* from all other genera in *Botryosphaeriaceae* (Phillips et al. 2013). Striations on the conidia distinguish it from *Diplodia*, the conidiomata paraphyses distinguish it from *Neodeightonia*, which also has striate conidia. Although *Barriopsis* has striate conidia and paraphyses, *Lasiodiplodia* is unique in the *Botryosphaeriaceae* because striations are visible on immature, hyaline conidia. Although Phillips et al. (2013) differentiated 18 species in *Lasiodiplodia* on the basis of conidial morphology (especially dimensions) and morphology of the paraphyses, in reality, species in *Lasiodiplodia* cannot be identified with any confidence from their morphology and molecular data are necessary for definitive identifications.

Molecular based identification and diversity

Denman et al. (2000) suggested that *Lasiodiplodia* could be a synonym of *Diplodia*. When Crous et al. (2006) re-organized *Botryosphaeria* on the basis of LSU phylogeny they split the genus into 10 genera, but could not resolve the position of *Lasiodiplodia* or separate it from *Diplodia*. Following a multi-locus approach (SSU, ITS, LSU, *tef1* and TUB2) Phillips et al. (2008) showed that *Lasiodiplodia* constitutes a clear phylogenetic lineage.

For many years, only the type species of *Lasiodiplodia* (*L. theobromae*) was mentioned in the phytopathological and mycological literature, and it was regarded as a cosmopolitan, plurivorous pathogen restricted mainly to tropical and sub-tropical regions (Punithalingam 1976, 1980). Soon after the widespread application of DNA-based phylogenies, Pavlic et al. (2004) introduced *L. gonubiensis* as a new species on the basis of conidial morphology and ITS sequence data. Soon after, Burgess et al. (2006) described three new species (*L. crassispora*, *L. venezuelensis* and *L. rubropurpurea*) from the tropics based on ITS and *tef1* sequence data and morphological characters. Alves et al. (2008) also used ITS and *tef1* sequence data to reveal two cryptic species in the *L. theobromae* complex. Over the years more species were introduced and Phillips et al. (2013) listed 18 species and Dissanayake et al. (2016) listed 31 species known from culture. Today

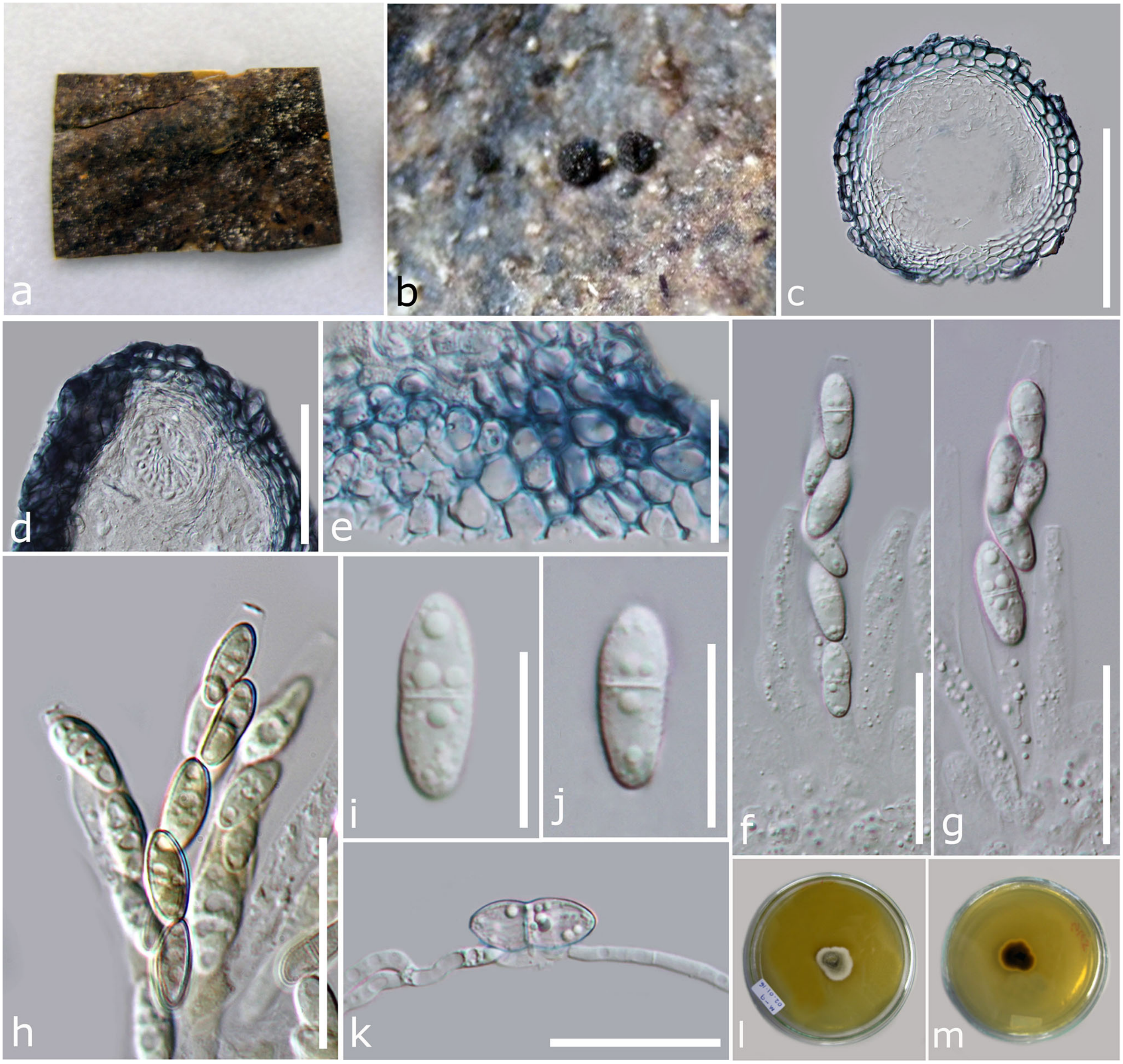
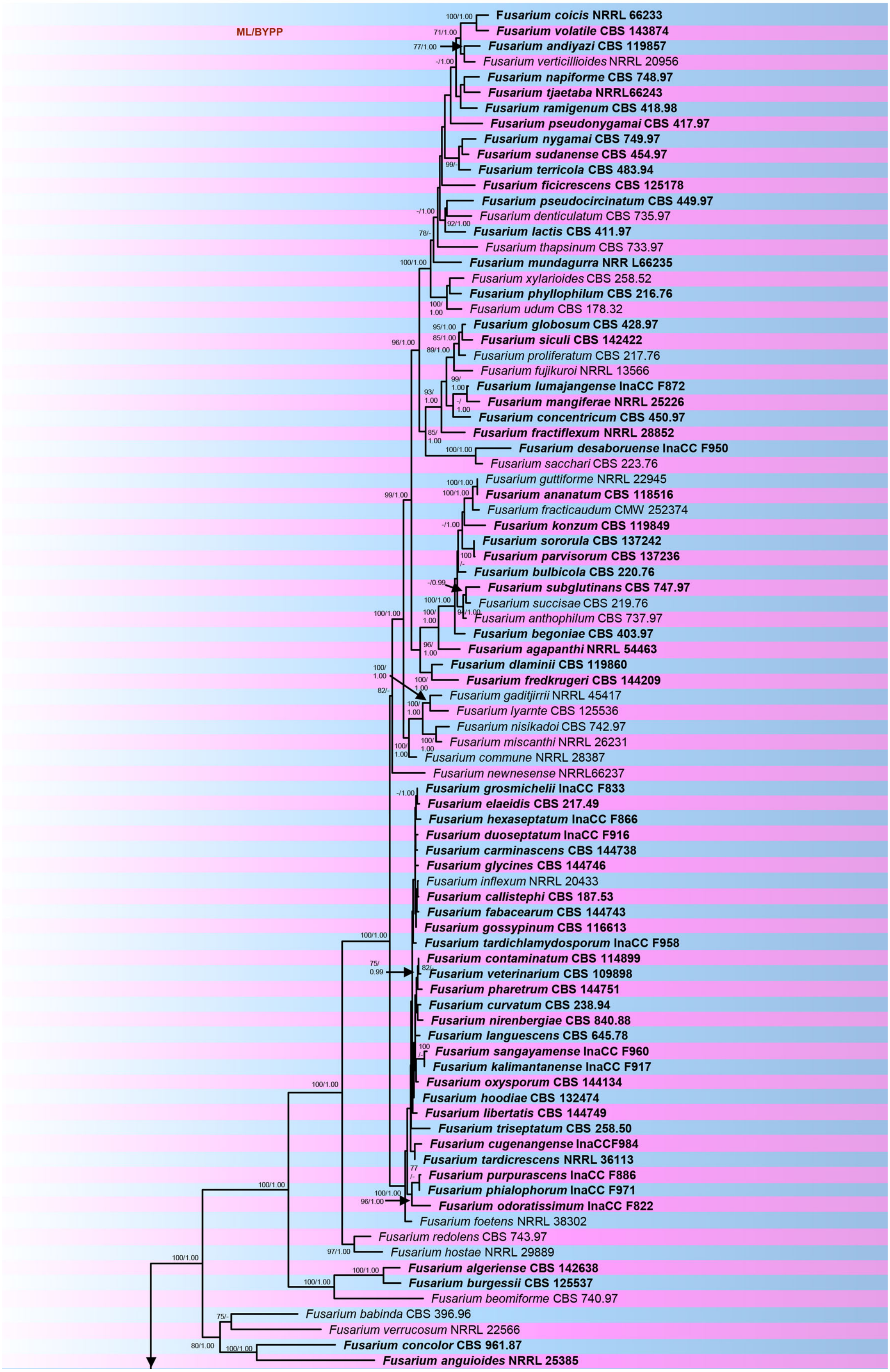


Fig. 27 Sexual morph of a *Fusarium* sp. **a** Herbarium material. **b** Ascomata on the host. **c** Section of ascomata. **d** Section of the ostiolar region. **e** Peridium in face view. **f–h** Asci (**h** in Melzer's reagent). **i, j** Ascospores. **k** Germinating ascospore. **l, m** Colony on MEA. Scale bars: **c** = 100 µm, **d** = 50 µm, **e–k** = 20 µm

the figure stands at 40 (Fig. 29). Apart from *L. theobromae*, all species have been introduced almost entirely on the basis of DNA sequence phylogenies. Although the phylogenies were derived from analysis of multiple loci (mostly ITS, *tef1* and TUB2 and sometimes RPB2) the genealogical concordance phylogenetic species recognition concept (Taylor et al. 2000) has not always been strictly applied and species have been introduced on the basis of minor differences in only one locus. The result is that some species are not well separated phylogenetically (Fig. 29, Table 19), such as *L. hyalina* and *L. thailandica*, *L. chinensis*, *L. sterculiae, L. pseudotheobromae*, *L. pyriformis* and *L. crassispora*. In a detailed study of five loci of 19 *Lasiodiplodia* species, Cruywagen et al. (2017) concluded that several accepted species (*L. viticola*, *L. missouriana*, *L. laeliocattleyae*, *L. brasiliense*) may, in fact, be hybrids. There has been no such study of the 16 species introduced after the work of Cruywagen et al. (2017). In view of the questionable status of several species in *Lasiodiplodia,* there is an urgent need to re-assess all of the species currently accepted in this genus.


ML/BYPP
100/1.00
Fusarium coicis NRRL 66233
71/1.00
Fusarium volatile CBS 143874
77/1.00
Fusarium andiyazi CBS 119857
-/1.00
Fusarium verticillioides NRRL 20956
Fusarium napiforme CBS 748.97
Fusarium tjaetaba NRRL66243
Fusarium ramigenum CBS 418.98
Fusarium pseudonygamai CBS 417.97
Fusarium nygamai CBS 749.97
Fusarium sudanense CBS 454.97
99/-
Fusarium terricola CBS 483.94
Fusarium ficicrescens CBS 125178
-/1.00
Fusarium pseudocircinatum CBS 449.97
Fusarium denticulatum CBS 735.97
92/1.00
78/-
Fusarium lactis CBS 411.97
Fusarium thapsinum CBS 733.97
100/1.00
Fusarium mundagurra NRR L66235
Fusarium xylarioides CBS 258.52
Fusarium phyllophilum CBS 216.76
100/1.00
Fusarium udum CBS 178.32
95/1.00
Fusarium globosum CBS 428.97
85/1.00
Fusarium siculi CBS 142422
96/1.00
89/1.00
Fusarium proliferatum CBS 217.76
Fusarium fujikuroi NRRL 13566
99/1.00
Fusarium lumajangense InaCC F872
93/1.00
-/1.00
Fusarium mangiferae NRRL 25226
Fusarium concentricum CBS 450.97
85/1.00
Fusarium fractiflexum NRRL 28852
100/1.00
Fusarium desaboruense InaCC F950
Fusarium sacchari CBS 223.76
100/1.00
Fusarium guttiforme NRRL 22945
99/1.00
100/1.00
Fusarium ananatum CBS 118516
Fusarium fracticaudum CMW 252374
-/1.00
Fusarium konzum CBS 119849
Fusarium sororula CBS 137242
100/-
Fusarium parvisorum CBS 137236
Fusarium bulbicola CBS 220.76
-/0.99
Fusarium subglutinans CBS 747.97
100/1.00
Fusarium succisae CBS 219.76
100/1.00
100/1.00
94/1.00
Fusarium anthophilum CBS 737.97
Fusarium begoniae CBS 403.97
96/1.00
Fusarium agapanthi NRRL 54463
100/1.00
Fusarium dlaminii CBS 119860
100/1.00
Fusarium fredkrugeri CBS 144209
82/-
Fusarium gaditjirrii NRRL 45417
100/1.00
Fusarium lyarnte CBS 125536
Fusarium nisikadoi CBS 742.97
100/1.00
100/1.00
Fusarium miscanthi NRRL 26231
Fusarium commune NRRL 28387
Fusarium newnesense NRRL66237
-/1.00
Fusarium grosmichelii InaCC F833
Fusarium elaeidis CBS 217.49
Fusarium hexaseptatum InaCC F866
Fusarium duoseptatum InaCC F916
Fusarium carminascens CBS 144738
Fusarium glycines CBS 144746
Fusarium inflexum NRRL 20433
Fusarium callistephi CBS 187.53
Fusarium fabacearum CBS 144743
Fusarium gossypinum CBS 116613
100/1.00
Fusarium tardichlamydosporum InaCC F958
Fusarium contaminatum CBS 114899
75/0.99
82/-
Fusarium veterinarium CBS 109898
Fusarium pharetrum CBS 144751
Fusarium curvatum CBS 238.94
Fusarium nirenbergiae CBS 840.88
Fusarium languescens CBS 645.78
100/-
Fusarium sangayamense InaCC F960
Fusarium kalimantanense InaCC F917
100/1.00
Fusarium oxysporum CBS 144134
Fusarium hoodiae CBS 132474
Fusarium libertatis CBS 144749
Fusarium triseptatum CBS 258.50
Fusarium cugenangense InaCCF984
Fusarium tardicrescens NRRL 36113
77/-
Fusarium purpurascens InaCC F886
100/1.00
Fusarium phialophorum InaCC F971
100/1.00
96/1.00
Fusarium odoratissimum InaCC F822
Fusarium foetens NRRL 38302
Fusarium redolens CBS 743.97
97/1.00
Fusarium hostae NRRL 29889
100/1.00
100/1.00
Fusarium algeriense CBS 142638
100/1.00
Fusarium burgessii CBS 125537
Fusarium beomiforme CBS 740.97
75/-
Fusarium babinda CBS 396.96
Fusarium verrucosum NRRL 22566
80/1.00
100/1.00
Fusarium concolor CBS 961.87
Fusarium anguioides NRRL 25385

◀**Fig. 28** Phylogram generated from RAxML analysis based on combined RPB1, RPB2 and *tef1* sequences of accepted species of *Fusarium*. Related sequences were obtained from GenBank. One hundred sixty-five taxa are included in the analyses, which comprise 3980 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree was rooted in *Fusicolla aquaeductuum* (NRRL 20696). Tree topology of the ML analysis was similar to the BYPP. The best scoring RAxML tree with a final likelihood value of − 63956.723151 is presented. The matrix had 2254 distinct alignment patterns, with 25.13% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.257298, C = 0.251723, G = 0.248896, T = 0.242083; substitution rates AC = 1.366599, AG = 4.760724, AT = 1.266971, CG = 0.903914, CT = 9.564945, GT = 1.000000; gamma distribution shape parameter α = 1.089091. Maximum likelihood bootstrap support values ≥70% (BT) and Bayesian posterior probabilities ≥ 0.99 (PP) are given near the nodes respectively

Recommended genetic markers (genus level)—SSU and LSU
Recommended genetic markers (species level)—ITS, *tef1*, TUB2

Accepted number of species: Currently, 51 species names are listed for *Lasiodiplodia* in MycoBank and Index Fungorum (2019). Cultures and DNA sequences are available for 43 species, three of which have been reduced to synonymy under existing names. **Thus, 40 species are currently recognised in *Lasiodiplodia*.**

References: Phillips et al. 2013 (morphology, phylogeny, distribution, hosts); Dissanayake et al. 2016 (species).

Pestalotiopsis Steyaert, Bull. Jard. bot. État Brux. 19: 300 (1949)

Pestalotiopsis is an appendage-bearing, 5-celled conidia (asexual coelomycetes) in the family *Sporocadaceae* (Maharachchikumbura et al. 2014a, b; Jayawardena et al. 2016). The genus was introduced by Steyaert (1949). *Pestalotiopsis* species are widely distributed throughout tropical and temperate regions (Guba 1961; Maharachchikumbura et al. 2012, 2014a). *Pestalotiopsis* species have been isolated from dead leaves, bark, twigs, soil, polluted stream water, wood, paper, fabrics, and wool (Guba 1961; Maharachchikumbura et al. 2012, 2014a). Some species have been associated with human and animal infections, and others (e.g. *P. guepinii* and *P. microspora*) have also been isolated from extreme environments (Maharachchikumbura et al. 2014b).
Classification—Sordariomycetes, *Xylariomycetidae*, *Amphisphaeriales*, *Sporocadaceae*
*Type species—**Pestalotiopsis guepinii*** (Desm.) Steyaert [as ‘guepini’], Bull. Jard. bot. État Brux. 19(3): 312 (1949)
Distribution—Worldwide
Disease symptoms—Species of *Pestalotiopsis* cause a variety of diseases in plants including canker lesions, shoot dieback, leaf spots, needle blight, tip blight, grey blight, scabby canker, severe chlorosis, fruit rots and various post-harvest diseases (Maharachchikumbura et al. 2013a, b, 2014a, b). These pathogens reduce production and cause economic loss in apple, blueberry, coconut, chestnut, ginger, grapevine, guava, hazelnut, lychee, mango, orchid, peach, rambutan, tea and wax apple due to diseases (Maharachchikumbura et al. 2013a, b, 2014a, b). Grapevine trunk diseases are the most destructive diseases of grapevines that impact the economic production and longevity of vineyards and even leading to partial or total death of individual plants. Therefore, the initial identification of the causal agent is essential for early control of these diseases (Jayawardene et al. 2015; Maharachchikumbura et al. 2017). Pestalotoid fungi have been reported as pathogens on a variety of grapevine cultivars, causing diseases including grapevine dieback, fruit rot, postharvest disease and severe defoliation and they infect all plant parts including leaves, canes, wood, berries and flowers (Jayawardene et al. 2015; Maharachchikumbura et al. 2017). *Pestalotiopsis menezesiana* (Bres. & Torr.) Bissett. and *P. uvicola* (Spegazzini) Bissett, are the most common species recorded from grapevine around the world and especially *P. biciliata* are associated with trunk grapevine disease (Jayawardene et al. 2015; Maharachchikumbura et al. 2017).
Hosts—Broad range of hosts including members of *Altingiaceae*, *Arecaceae*, *Bromeliaceae*, *Euphorbiaceae*, *Myrtaceae*, *Poaceae*, *Proteaceae*, *Rosaceae*, *Rutaceae*, *Theaceae* and *Vitaceae*.

Morphological based identification and diversity

There are around 250 species, most of which were named according to their host associations (Maharachchikumbura et al. 2014a, b). However, *Pestalotiopsis* species are not hosted specific and are found on a wide range of plants and substrates (Jeewon et al. 2003; Lee et al. 2006; Maharachchikumbura et al. 2014a, b). They exhibit considerable diversity in phenotype, and group together based on similarities in conidial morphology (Jeewon et al. 2003; Maharachchikumbura et al. 2012, 2013a, b, 2014a, b). Considering morphology, conidial length, width, median cell length, the colour of median cells and length of the apical appendages appear to be stable characters within *Pestalotiopsis* (Jeewon et al. 2003; Maharachchikumbura et al. 2014b).
Pestalotiopsis guepinii was considered to be the type species of the genus described from stems and leaves of *Camellia japonica* collected in France, and is characterised by 5-celled conidia with three concolourous median cells, hyaline terminal cells and simple or unbranched

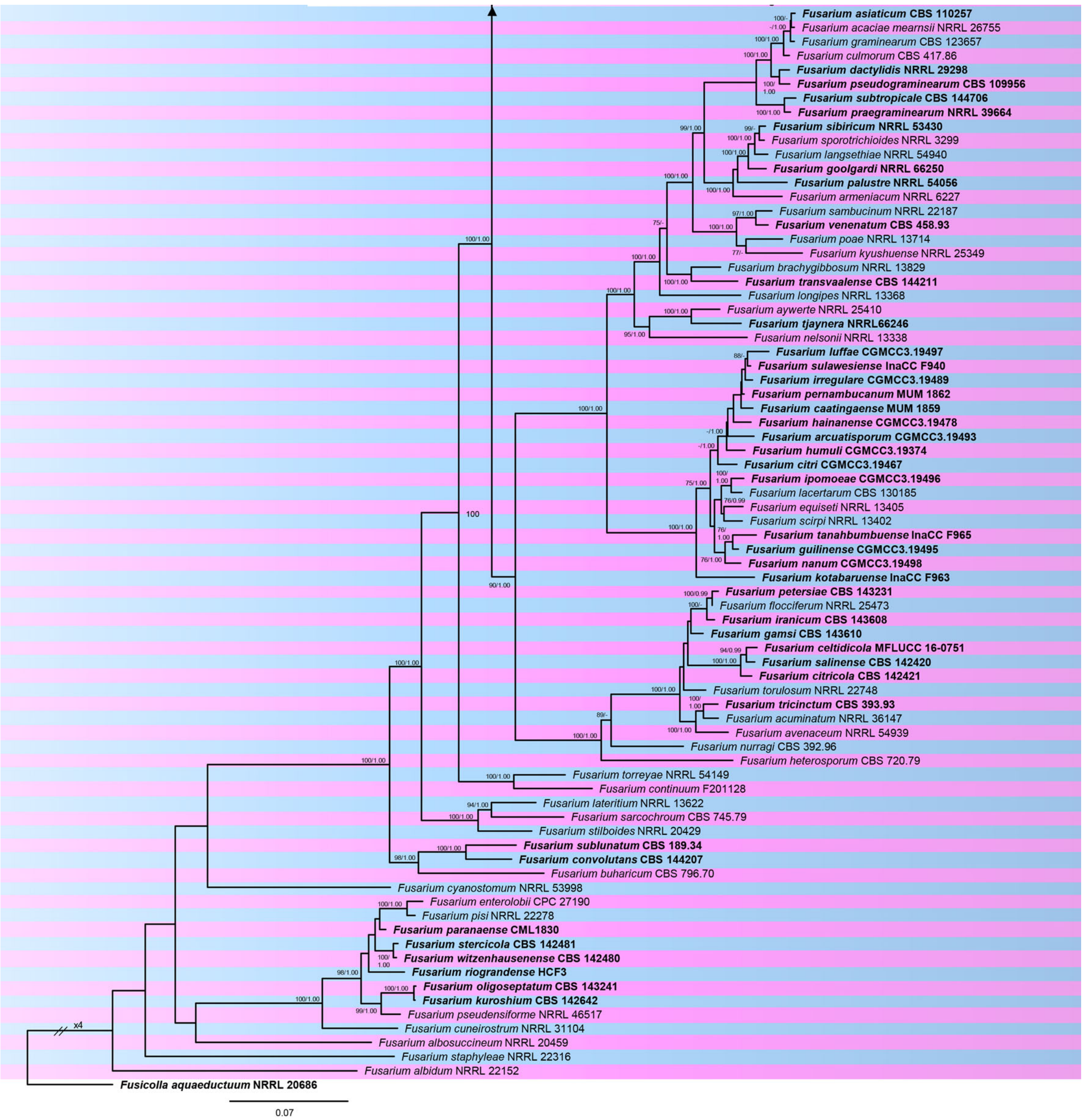


Fig. 28 continued

appendages arising from the apex of the apical cell (Steyaert 1949; Maharachchikumbura et al. 2014b). Nag Raj (1985) regarded *P. maculans* as the type species of *Pestalotiopsis* with *P. guepinii* as a synonym. Jeewon et al. (2003) also accepted *P. maculans* clusters with species having concolourous median cells based on phylogenetic analysis of ITS sequence data and that *P. karstenii* might be a synonym of *P. maculans* (Maharachchikumbura et al. 2014b).

Most *Pestalotiopsis* species lack sexual morphs. The sexual morph of *Pestalotiopsis* was treated as *Pestalosphaeria* Barr, with the type species *Pestalosphaeria concentrica* collected from grey-brown spots on living leaves of *Rhododendron maximum* in North Carolina, USA (Maharachchikumbura et al. 2014b). *Pestalosphaeria concentrica* is characterised by immersed, subglobose ascomata and unitunicate, cylindrical asci with a J + apical ring; ascospores uniseriate in the ascus, ellipsoid, pale dull brown and 2-septate (Maharachchikumbura et al. 2014b).

Pestalotiopsis species have the ability to switch life-modes as endophytes, pathogens and saprobes (Hu et al. 2007; Maharachchikumbura et al. 2012). Therefore, many endophytic and plant pathogenic *Pestalotiopsis* species persist as saprobes and have been isolated from dead leaves, bark and twigs (Maharachchikumbura et al. 2012, 2013a, b, 2014b).

Table 18 Details of the ***Fusarium*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	RPB1	RPB2	*tef1*
Fusarium anguioides	**NRRL 25385***; ATCC 66485	JX171511	JX171624	MH742689
F. acaciae-mearnsii	NRRL 26755	KM361640	KM361658	AF212449
F. acuminatum	NRRL 36147; CBS 109232	HM347174	GQ505484	GQ505420
F. agapanthi	**NRRL 54463***	KU900620	KU900625	KU900630
F. albidum	NRRL 22152	JX171492	JX171605	–
F. albosuccineum	NRRL 20459	JX171471	JX171585	–
F. algeriense	**NRRL 66647***; CBS 142638; IL-79	MF120488	MF120499	–
F. ananatum	**CBS 118516***	LT996188	LT996137	KU604416
F. andiyazi	NRRL 31727; CBS 119857	LT996189	LT996138	KP662901
F. anthophilum	NRRL 13602; CBS 737.97	LT996190	LT996139	KU711685
F. arcuatisporum	**CGMCC3.19493***; LC12147	MK289799	MK289739	MK289584
F. armeniacum	NRRL 6227	JX171446	JX171560	HM744692
F. asiaticum	**NRRL 13818***; CBS 110257	JX171459	JX171573	AF212451
F. avenaceum	NRRL 54939	JX171551	JX171663	MH582391
F. aywerte	NRRL 25410	JX171513	JX171626	KU171717
F. babinda	NRRL 25539; CBS 396.96	JX171519	JX171632	MH742712
F. begoniae	**CBS 403.97***; NRRL 25300	LT996191	LT996140	AF160293
F. beomiforme	NRRL 25174; CBS 740.97	–	JX171619	–
F. brachygibbosum	NRRL 13829	JX171460	JX171574	–
F. buharicum	NRRL 13371; CBS 796.70	JX171449	JX171563	–
F. bulbicola	**NRRL 13618***; CBS 220.76	KF466394	KF466404	KF466415
F. burgessii	**CBS 125537***; RBG 5319	KJ716217	HQ646393	HQ667149
F. callistephi	**CBS 187.53***	–	MH484905	MH484966
F. carminascens	**CBS 144738***; CPC 25800	–	MH484937	MH485028
F. celtidicola	**MFLUCC 16-0751***	–	MH576580	–
F. citri	**CGMCC3.19467***; LC6896	MK289828	MK289771	MK289617
F. citricola	**CBS 142421***; CPC 27805	LT746290	LT746310	LT746197
F. coicis	**NRRL 66233***; RBG5368	KP083269	KP083274	KP083251
F. commune	NRRL 28387	–	JX171638	KU171720
F. concentricum	**NRRL 25181***; CBS 450.97	LT996192	JF741086	AF160282
F. concolor	**NRRL 13459***; CBS 961.87	JX171455	JX171569	MH742681
F. contaminatum	**CBS 114899***	–	MH484901	MH484992
F. continuum	F201128	KM520389	KM236780	KM236720
F. convolutans	**CBS 144207***; CPC 33733	LT996193	LT996141	LT996094
F. cugenangense	**InaCCF984***	LS479560	LS479308	–
F. culmorum	NRRL 25475; CBS 417.86	JX171515	JX171628	KY873384
F. cuneirostrum	NRRL 31104	–	EU329558	EF408413
F. curvatum	CBS 238.94; NRRL 26422; PD 94/184	–	MH484893	MH484984
F. cyanostomum	NRRL 53998	JX171546	JX171658	–
F. dactylidis	**NRRL 29298***	KM361654	KM361672	DQ459748
F. denticulatum	NRRL 25302; CBS 735.97	LT996195	LT996143	AF160269
F. desaboruense	InaCC F950	LS479870	LS479852	–
F. dlaminii	**NRRL 13164***; CBS 119860	KU171681	KU171701	MK639039
F. duoseptatum	**InaCC F916***	LS479495	LS479239	–
F. elaeidis	**CBS 217.49***; NRRL 36358	–	MH484870	MH484961
F. enterolobii	CPC 27190	–	LT746312	LT746199
F. equiseti	NRRL 13405	–	GQ915491	GQ915507
F. fabacearum	**CBS 144743***; CPC 25802	–	MH484939	MH485030

Table 18 (continued)

Species	Isolate/voucher no	RPB1	RPB2	*tef1*
F. ficicrescens	**CBS 125178***	–	KT154002	KP662899
F. flocciferum	NRRL 25473	JX171514	JX171627	–
F. foetens	NRRL 38302	JX171540	JX171652	GU170559
F. fracticaudum	CMW 252374	LT996196	LT996144	KJ541059
F. fractiflexum	**NRRL 28852***	–	LT575064	AF160288
F. fredkrugeri	**CBS 144209***; CPC 33747	LT996199	LT996147	LT996097
F. fujikuroi	NRRL 13566	JX171456	JX171570	–
F. gaditjirrii	NRRL 45417	–	JX171654	KU171724
F. gamsi	**CBS 143610***; CPC 30862; OrSaAg4	–	LT970760	LT970788
F. globosum	**NRRL 26131***; CBS 428.97	KF466396	KF466406	KF466417
F. glycines	**CBS 144746***; CPC 25808	–	MH484942	MH485033
F. gossypinum	**CBS 116613***	–	MH484909	MH485000
F. graminearum	NRRL 31084; CBS 123657	JX171531	JX171644	HM744693
F. grosmichelii	**InaCC F833***	LS479548	LS479295	LS479744
F. guilinense	**CGMCC3.19495***; LC12160	MK289831	MK289747	MK289594
F. guttiforme	NRRL 22945	JX171505	JX171618	–
F. hainanense	**CGMCC3.19478***; LC11638	MK289833	MK289735	MK289581
F. heterosporum	NRRL 20693; CBS 720.79	JX171480	JX171594	–
F. hexaseptatum	**InaCC F866***	–	LS479359	LS479805
F. hoodiae	**CBS 132474***	–	MH484929	MH485020
F. hostae	NRRL 29889	JX171527	JX171640	AY329034
F. inflexum	NRRL 20433	–	JX171583	AF008479
F. ipomoeae	**CGMCC3.19496***; LC12165	MK289859	MK289752	MK289599
F. iranicum	**CBS 143608***; CPC 30860; OrSaAg2	–	LT970757	LT970785
F. irregulare	**CGMCC3.19489***; LC7188	MK289863	MK289783	MK289629
F. kalimantanense	**InaCC F917***	LS479497	LS479241	LS479690
F. konzum	**CBS 119849***	LT996200	LT996148	LT996098
F. kotabaruense	**InaCC F963***	LS479875	LS479859	LS479445
F. kuroshium	**CBS 142642***; UCR3641	KX262236	KX262256	KX262216
F. kyushuense	NRRL 25349	–	GQ915492	GQ915508
F. lacertarum	NRRL 20423; CBS 130185	HM347137	JX171581	GQ505593
F. lactis	**NRRL 25200***; CBS 411.97	LT996201	LT996149	AF160272
F. langsethiae	NRRL 54940	JX171550	JX171662	–
F. languescens	**CBS 645.78***; NRRL 36531	–	MH484880	MH484971
F. lateritium	NRRL 13622	JX171457	JX171571	AY707173
F. libertatis	**CBS 144749***; CPC 28465	–	MH484944	MH485035
F. longipes	NRRL 13368	JX171448	JX171562	–
F. luffae	**CGMCC3.19497***; LC12167	MK289869	MK289754	MK289601
F. lumajangense	**InaCC F872***	–	LS479850	LS479441
F. lyarnte	NRRL 54252; CBS 125536	JX171549	JX171661	–
F. mangiferae	**NRRL 25226***; BBA 69662	JX171509	JX171622	–
F. miscanthi	NRRL 26231	–	JX171634	KU171725
F. mundagurra	**NRR L66235***; RBG5717	KP083272	KP083276	MK639058
F. nanum	**CGMCC3.19498*;** LC12168	MK289871	MK289755	MK289602
F. napiforme	**CBS 748.97***; NRRL 13604	HM347136	EF470117	KU604409
F. nelsonii	NRRL 13338	JX171447	JX171561	GQ505402
F. newnesense	NRRL 66237; RBG5443	KP083271	KP083277	KJ397074
F. nirenbergiae	**CBS 840.88***	–	MH484887	MH484978

Table 18 (continued)

Species	Isolate/voucher no	RPB1	RPB2	*tef1*
F. nisikadoi	NRRL 25179; CBS 742.97	JX171507	JX171620	–
F. nurragi	NRRL 36452; CBS 392.96	JX171538	JX171650	–
F. nygamai	**NRRL 13448***; CBS 749.97	LT996202	EF470114	AF160273
F. odoratissimum	**InaCC F822***	LS479618	LS479386	–
F. oligoseptatum	**NRRL 62579***; FRC S- 2581; MAFF 246283; CBS 143241	KC691596	KC691656	KC691538
F. oxysporum	**CBS 144134***	–	MH484953	MH485044
F. palustre	**NRRL 54056***	KT597718	KT597731	–
F. paranaense	**CML1830***	–	KF680011	KF597797
F. parvisorum	**CBS 137236***; FCC 5407; CMW 25267	–	LT996150	KJ541060
F. pernambucanum	**MUM 1862***; URM 7559	MH668869	–	–
F. petersiae	**CBS 143231***	MG386139	MG386150	MG386159
F. pharetrum	**CBS 144751***; CPC 30824	–	MH484952	MH485042
F. phialophorum	**InaCC F971***	LS479545	LS479292	LS479741
F. phyllophilum	**NRRL 13617***; CBS 216.76	KF466399	KF466410	KF466421
F. pisi	NRRL 22278	–	EU329501	AF178337
F. poae	NRRL 13714	JX171458	JX171572	–
F. praegraminearum	**NRRL 39664***	KX260125	KX260126	KX260120
F. proliferatum	NRRL 22944; CBS 217.76	JX171504	JX171617	–
F. pseudensiforme	NRRL 46517	KC691615	KC691645	KC691555
F. pseudocircinatum	**NRRL 22946***; CBS 449.97	LT996204	LT996151	AF160271
F. pseudograminearum	**NRRL 28062***; CBS 109956	JX171524	JX171637	AF212468
F. pseudonygamai	**NRRL 13592***; CBS 417.97	LT996205	LT996152	AF160263
F. purpurascens	**InaCC F886***	–	LS479385	LS479827
F. ramigenum	**NRRL 25208***; CBS 418.98	KF466401	KF466412	KF466423
F. redolens	NRRL 22901; CBS 743.97	–	KU171708	KU171728
F. riograndense	**HCF3***	–	KX534003	KX534002
F. roseum	NRRL 22187	JX171493	JX171606	–
F. sacchari	NRRL 13999; CBS 223.76	JX171466	JX171580	KU711669
F. salinense	**CBS 142420***; CPC 26973	LT746286	LT746306	LT746193
F. sangayamense	**InaCC F960***	LS479537	LS479283	–
F. sarcochroum	NRRL 20472; CBS 745.79	JX171472	JX171586	–
F. scirpi	NRRL 13402	JX171452	JX171566	GQ505592
F. sibiricum	**NRRL 53430***	–	HQ154472	HM744684
F. siculi	**CBS 142422***; CPC 27188	LT746299	LT746327	LT746214
F. sororula	**CBS 137242***	LT996206	LT996153	–
F. sporotrichioides	NRRL 3299	JX171444	JX171558	HM744665
F. staphyleae	NRRL 22316	JX171496	JX171609	MH582426
F. stercicola	**CBS 142481***; DSM 106211	–	KY556552	KY556524
F. stilboides	NRRL 20429; ATCC 15662	JX171468	JX171582	–
F. subglutinans	**NRRL 22016***; CBS 747.97	JX171486	JX171599	HM057336
F. sublunatum	**NRRL 13384***; CBS 189.34	JX171451	JX171565	–
F. subtropicale	**NRRL 66764***; CBS 144706	MH706972	MH706973	MH706974
F. succisae	NRRL 13613; CBS 219.76	LT996207	LT996154	AF160289
F. sudanense	**CBS 454.97***; NRRL 25451	LT996208	LT996155	KU711697
F. sulawesiense	**InaCC F940***	–	LS479855	LS479443
F. tanahbumbuense	**InaCC F965***	LS479877	LS479863	LS479448
F. tardichlamydosporum	**InaCC F958***	–	LS479280	LS479729
F. tardicrescens	**NRRL 36113***	LS479474	LS479217	LS479665

Table 18 (continued)

Species	Isolate/voucher no	RPB1	RPB2	*tef1*
F. terricola	**CBS 483.94***	LT996209	LT996156	KU711698
F. thapsinum	NRRL 22045; CBS 733.97	JX171487	JX171600	AF160270
F. tjaetaba	**NRRL66243***; RBG5361	KP083267	KP083275	KP083263
F. tjaynera	**NRRL66246***; RBG5367	KP083268	KP083279	–
F. torreyae	NRRL 54149	JX171548	HM068359	HM068337
F. torulosum	NRRL 22748; NRRL 13919	JX171502	JX171615	–
F. transvaalense	**CBS 144211***; CPC 30923	LT996210	LT996157	LT996099
F. tricinctum	**NRRL 25481***; CBS 393.93	JX171516	HM068327	MH582379
F. triseptatum	**CBS 258.50*;** NRRL 36389	–	MH484873	MH484964
F. udum	NRRL 22949; CBS 178.32	LT996220	LT996172	AF160275
F. venenatum	**CBS 458.93***	–	KM232382	KM231942
F. verrucosum	NRRL 22566, BBA 64786	–	JX171613	–
F. verticillioides	NRRL 20956	JX171485	JX171598	–
F. veterinarium	**CBS 109898***; NRRL 36153	–	MH484899	MH484990
F. volatile	**CBS 143874***	–	LR596006	LR596007
F. witzenhausenense	**CBS 142480***	–	KY556553	KY556525
F. xylarioides	NRRL 25486; CBS 258.52	JX171517	JX171630	AY707136
F. caatingaense	**MUM 1859***; URM 6779	MH668845	LS398495	LS398466
F. goolgardi	**NRRL 66250***; RBG5411	KP083270	KP083280	KP101123
F. humuli	**CGMCC3.19374***; CQ1039	MK289840	MK289724	MK289570
Fusicolla aquaeductuum	**NRRL 20686***	JX171476	JX171590	–

Ex-type (ex-epitype) strains are in bold and marked with an asterisk* and voucher stains are in bold

Pestalotiopsis species that were isolated as endophytes are important in the discovery of novel compounds with medicinal, agricultural and industrial applications (Maharachchikumbura et al. 2014b; Xu et al. 2010, 2014). *Pestalotiopsis* species are a rich source for bioprospecting compared to other fungal genera, and more than 100 compounds have been isolated from *Pestalotiopsis* (Maharachchikumbura et al. 2014b; Xu et al. 2010, 2014).

Molecular based identification and diversity

Maharachchikumbura et al. (2012) tested with 10 gene regions to resolve species boundaries in *Pestalotiopsis* (actin, calmodulin, glutamine synthase, glyceraldehyde-3-phosphate dehydrogenase, ITS, LSU, 18S nrDNA, RNA polymerase II, *tef1* and TUB2). Maharachchikumbura et al. (2014b) used phylogenetic analysis of combined ITS, TUB2 and *tef1* genes to successfully resolve *Pestalotiopsis* species (Fig. 30, Table 20).

Recommended genetic marker (genus level)—LSU (as outlined in Maharachchikumbura et al. 2012)
Recommended genetic markers (species level)—ITS, TUB2 and *tef1* (as outlined in Maharachchikumbura et al. 2012)

Accepted number of species: There are 360 epithets in Index Fungorum in this genus, however, **75 species** with DNA sequence data are accepted.
References: Maharachchikumbura et al. 2013a, b, 2014b, 2016 (morphology, phylogeny)

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

Stagonosporopsis is a coelomycetous genus in the family *Didymellaceae* (de Gruyter et al. 2013), accommodating several important phytopathogenic species. Some of the species have described sexual forms in *Didymella* (Diedicke 1912; Aveskamp et al. 2010). Some *Stagonosporopsis* species have quarantine importance. *Stagonosporopsis andigena* is listed in Annex IAI by European Union (EU), meaning its introduction to EU is prohibited. This pathogen is also listed in the A1 list by the European and Mediterranean Plant Protection Organization (EPPO 2019). *Stagonosporopsis chrysanthemi* is another species listed in A2 list by EPPO (EPPO 2019).
Classification—Dothideomycetes, *Pleosporomycetidae*, *Pleosporales*, *Didymellaceae*
Type species—***Stagonosporopsis boltshauseri*** (Sacc.) Died. 1912
Distribution—Worldwide

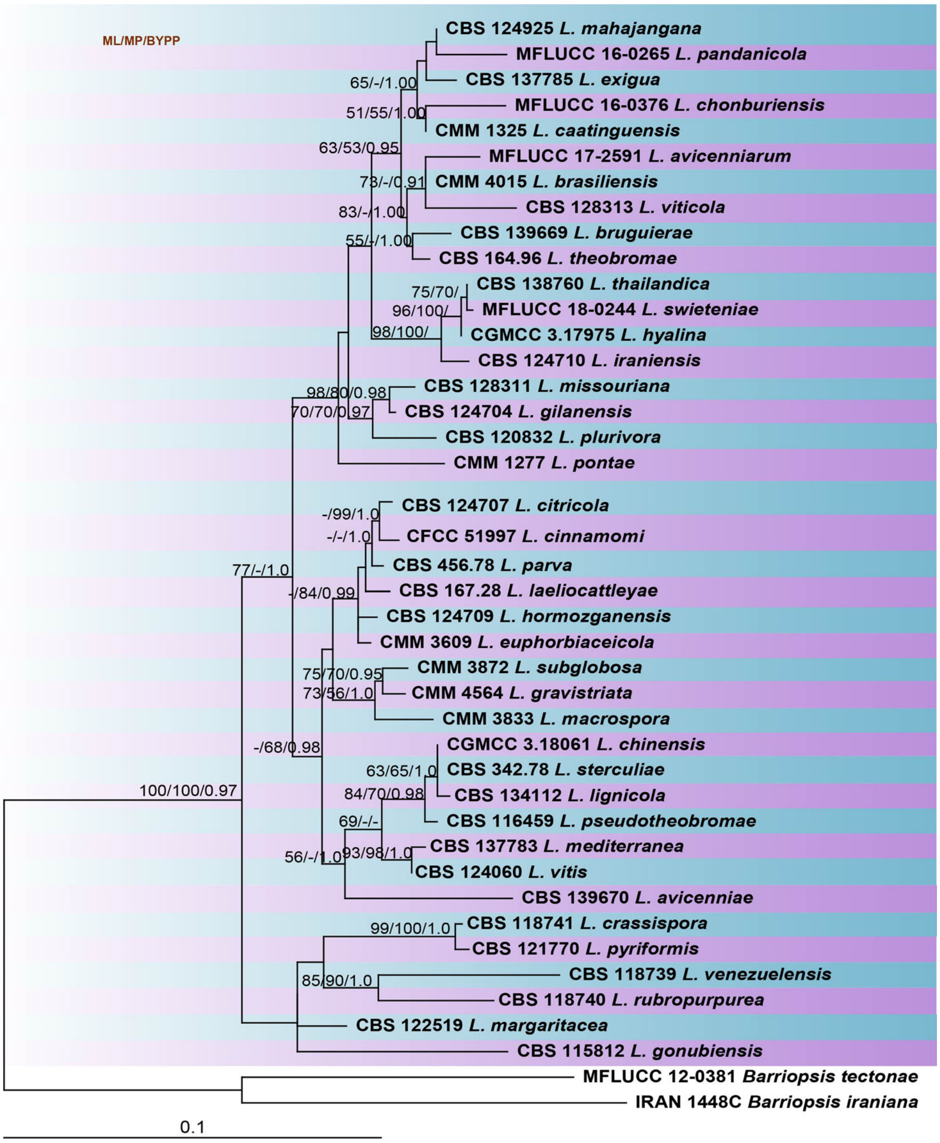


Fig. 29 Phylogenetic tree generated by maximum likelihood analysis of combined ITS and *tef1* sequence data of *Lasiodiplodia* species. Related sequences were obtained from GenBank. Forty nine strains are included in the analyses, which comprise 866 characters including gaps. The tree was rooted with *Barriopsis tectonae* and *B. iraniana*. Tree topology of the ML analysis was similar to MP and BYPP. The best scoring RAxML tree with a final likelihood value of − 3733.342990 is presented. The matrix had 253 distinct alignment patterns, with 4.41% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.211797, C = 0.285190, G = 0.260783, T = 0.242230; substitution rates AC = 0.983905, AG = 3.303939, AT = 1.281593, CG = 0.950258, CT = 5.553417, GT = 1.000000; gamma distribution shape parameter α = 0.221126. RAxML bootstrap support values ≥ 80% are shown respectively near the nodes. Bayesian posterior probabilities ≥ 0.5 (BYPP) indicated as thickened black branches. Ex-type strains are in bold

Disease symptoms—the Black blight of potato, gummy stem blight, ray blight

All plant parts may be attacked by *S. chrysanthemi* and *S. inoxydabilis,* however, flowers and cuttings are highly susceptible. Death of flowers and buds, a necrotic lesion on leaves and peduncles of unopened buds, soft rot of cortex of roots and discolouration of bark are the main symptom of the disease. Eventually, plant death occurs (Fox 1998; Pethybridge et al. 2008). In gummy stem blight of cucurbits, symptoms can be observed on all above ground and reproductive parts. Leaf spots are the main diagnostic character of this disease. Most of the circular or triangular shaped spots start at the margin of the leaf or extend towards the margin. The centre of the leaf spot is a lighter shade of brown than the surrounding portion. As leaf spots coalesce leaf blights occur. Actively expanding lesions on leaves, petioles, and pedicels often appear as water-soaked. Cankers may form on crowns, main stems and vines (Keinath 2013). *Stagonosporopsis andigena* the black blight of potato causal agent affects leaves, petioles and stems causing lesions and premature leaf drop, but does not infect the underground parts. On leaves, the pathogen causes small, blackish concentric lesions. The initial symptoms can be observed on the lower leaves, however, as the disease progresses lesions may also develop in upper leaves as well. Lesions may coalesce and severely affected leaves may turn blackish giving a scorched appearance (EFSA panel on plant health 2019).

Hosts—*Amaranthaceae*, *Asteraceae*, *Campanulaceae*, *Caryophyllaceae*, *Cucurbitaceae*, *Fabaceae*, *Lamiaceae, Pinaceae*, *Ranunculaceae*, *Solanaceae* and *Valerianaceae*.

Table 19 Details of the ***Lasiodiplodia*** isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	*tef1*
Lasiodiplodia avicenniae	**CBS 139670***	KP860835	KP860680
L. avicenniarum	**MFLUCC 17-2591***	MK347777	MK340867
L. brasiliense	**CMM 4015***	JX464063	JX464049
L. bruguierae	**CBS 139669***	KP860832	KP860677
L. caatinguensis	**CMM 1325***	KT154760	KT008006
L. chinensis	**CGMCC 3.18061***	KX499889	KX499927
L. chonburiensis	**MFLUCC 16-0376***	MH275066	MH412773
L. cinnamomi	**CFCC 51997***	MG866028	MH236799
L. citricola	**CBS 124707***	GU945354	GU945340
L. crassispora	**CBS 118741***	DQ103550	EU673303
L. euphorbiicola	**CMM 3609***	KF234543	KF226689
L. exigua	**CBS 137785***	KJ638317	KJ638336
L. gilanensis	**CBS 124704***	GU945351	GU945342
L. gonubiensis	**CBS 115812***	AY639595	DQ103566
L. gravistriata	**CMM 4564***	KT250949	KT250950
L. hormozganensis	**CBS 124709***	GU945355	GU945343
L. hyalina	**CGMCC 3.17975***	KX499879	KX499917
L. iraniensis	**CBS 124710***	GU945346	GU945334
L. laeliocattleyae	**CBS 167.28***	KU507487	KU507454
L. lignicola	**CBS 134112***	JX646797	KU887003
L. macrospora	**CMM 3833***	KF234557	KF226718
L. mahajangana	**CBS 124925***	FJ900595	FJ900641
L. margaritacea	**CBS 122519***	EU144050	EU144065
L. mediterranea	**CBS 137783***	KJ638312	KJ638331
L. missouriana	**CBS 128311***	HQ288225	HQ288267
L. pandanicola	**MFLUCC 16-0265***	MH275068	MH412774
L. parva	**CBS 456.78***	EF622083	EF622063
L. plurivora	**CBS 120832***	EF445362	EF445395
L. pontae	**CMM 1277***	KT151794	KT151791
L. pseudotheobromae	**CBS 116459***	EF622077	EF622057
L. pyriformis	**CBS 121770***	EU101307	EU101352
L. rubropurpurea	**CBS 118740***	DQ103553	EU673304
L. sterculiae	**CBS 342.78***	KX464140	KX464634
L. subglobosa	**CMM 3872***	KF234558	KF226721
L. swieteniae	**MFLUCC 18-0244***	MK347789	MK340870
L. thailandica	**CBS 138760***	KJ193637	KJ193681
L. theobromae	**CBS 164.96***	AY640255	AY640258
L. venezuelensis	**CBS 118739***	DQ103547	EU673305
L. viticola	**CBS 128313***	HQ288227	HQ288269
L. vitis	**CBS 124060***	KX464148	KX464642

Ex-type (ex-epitype) strains are in bold and marked with an asterisk* and voucher stains are in bold

Morphological based identification and diversity

Stagonosporopsis is characterized by ellipsoidal to subglobose, aseptate to 3 septate conidia and sexual morph with ellipsoidal, fusiform or obovoid, 1 septate ascospore (Aveskamp et al. 2010; Chen et al. 2015). *Stagonosporopsis* was originally separated from *Ascochyta* by Diedicke (1912) based on the occasional formation of multi-septate (Stagonospora-like) conidia. In the phylogenetic reassessment of *Didymellaceae* (Aveskamp et al. 2010) based on the sequences LSU and ITS of the nrDNA and TUB2 region, multiple *Phoma* species, including *P. ligulicola*, were recovered in a high supported clade with the interpretive types of the genus *Stagonosporopsis*; *S.*

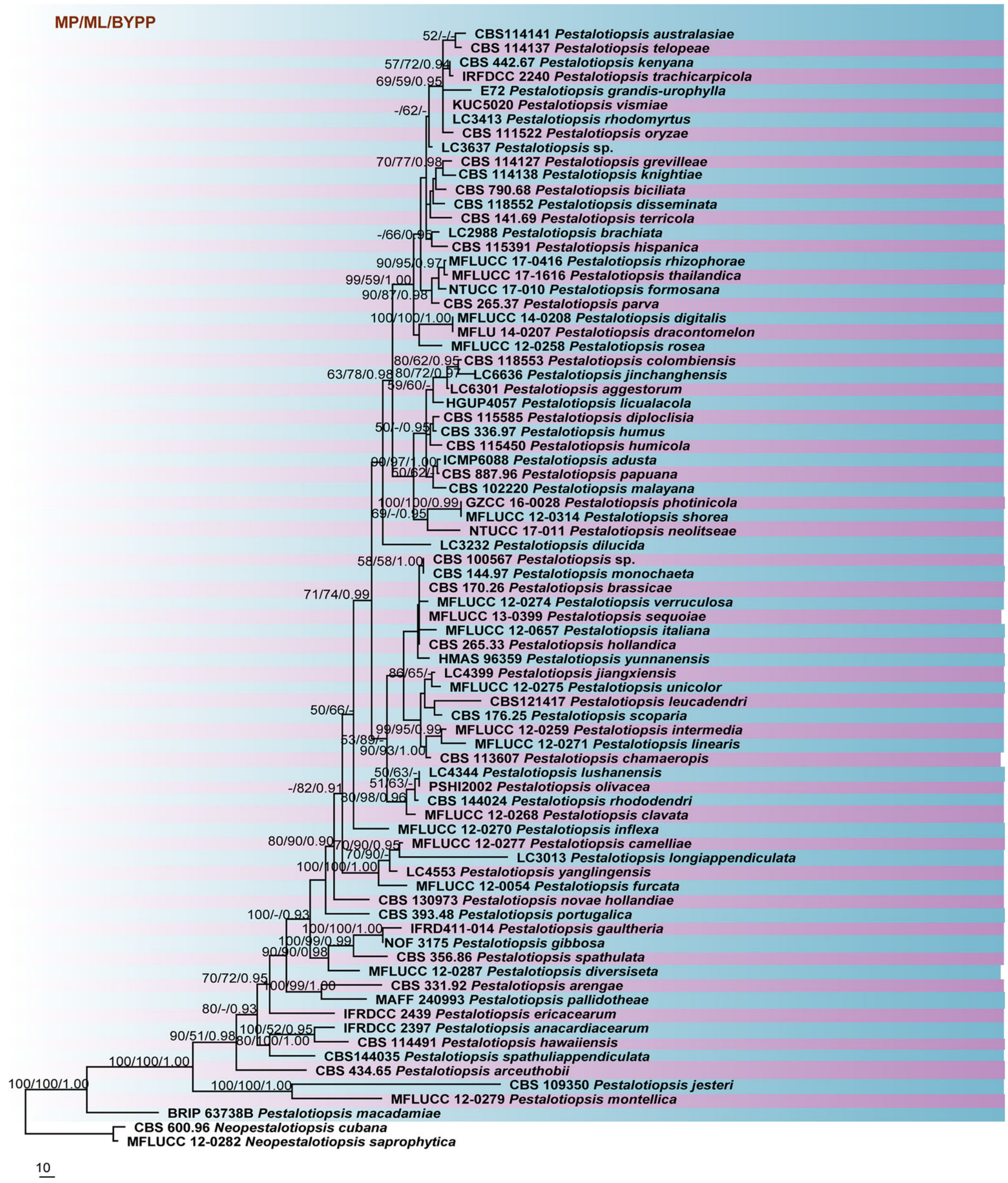


Fig. 30 Phylogram generated from RAxML analysis based on combined ITS, TUB2 and *tef1* sequences of all the accepted species of *Pestalotiopsis*. Related sequences were obtained from GenBank. Seventy-nine taxa are included in the analyses, which comprise 1581 characters including gaps. The tree was rooted in *Neopestalotiopsis cubana* (CBS 600.96) and *N. saprophytica* (MFLUCC 12-0282). Tree topology of the ML analysis was similar to the BYPP and MP. The best scoring RAxML tree with a final likelihood value of − 12269.881063 is presented. The matrix had 763 distinct alignment patterns, with 15.79% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.234129, C = 0.293516, G = 0.211518, T = 0.260837; substitution rates AC = 1.189917, AG = 3.402399, AT = 1.153875, CG = 1.001451, CT = 4.301074, GT = 1.000000; gamma distribution shape parameter α = 0.283001. The maximum parsimonious dataset consisted of 948 constant, 450 parsimony-informative and 183 parsimony-uninformative characters. The parsimony analysis of the data matrix resulted in the maximum of ten equally most parsimonious trees with a length of 1962 steps (CI = 0.498, RI = 0.697, RC = 0.347, HI = 0.502) in the first tree. RAxML and maximum parsimony bootstrap support value ≥ 50% and BYPP ≥ 0.90 values are shown near the nodes. The scale bar indicates 10 changes per site. The ex-type strains are in bold

actaeae (Boerema 1997, Boerema et al. 2004). In addition, *S. tanaceti* shows morphological similarity to *S. inoxydabilis* but can be differentiated by the faster growth rate, larger conidia, presence of chlamydospores, and lack of ascomata in culture (Vaghefi et al. 2012). Morphological characters overlap between the species in this genus and species are primarily separated based on molecular data.

Molecular based identification and diversity

Most comprehensive multigene phylogeny analyses for this genus were performed by Aveskamp et al. (2010), Vaghefi

Table 20 Details of ***Pestalotiopsis*** the isolates used in the phylogenetic analyses

Species	Isolate/voucher no	ITS	TUB2	*tef1*
Pestalotiopsis adusta	**ICMP 6088***	JX399006	JX399037	JX399070
P. aggestorum	**LC6301***	KX895015	KX895348	KX895234
P. anacardiacearum	**IFRDCC 2397***	NR120255.1	KC247155	KC247156
P. arceuthobii	**CBS 434.65***	NR147561	KM199427	KM199516
P. arengae	**CBS 331.92***	NR147560	KM199426	KM199515
P. australasiae	**CBS 114126***	NR147546	KM199409	KM199499
P. australis	**CBS 114193***	KM199332	KM199383	KM199475
P. biciliata	**CBS 124463***	KM199308	KM199399	KM199505
P. brachiata	**LC2988***	KX894933	KX895265	KX895150
P. brassicae	**CBS170.26***	NR147562	–	KM199558
P. camelliae	**MFLUCC12-0277***	NR120188	JX399041	JX399074
P. chamaeropis	**CBS 186.71***	KM199326	KM199391	KM199473
P. clavata	**MFLUCC12-0268***	JX398990	JX399025	JX399056
P. colombiensis	**CBS 118553***	NR147551	KM199421	KM199488
P. digitalis	**ICMP 5434***	KP781879	KP781883	–
P. dilucida	**LC3232***	KX894961	KX895293	KX895178
P. diploclisiae	**CBS 115587***	NR147552	KM199419	KM199486
P. diversiseta	**MFLUCC12-0287***	NR120187	JX399040	JX399073
P. dracontomelon	**MFUCC 10-0149***	KP781877	–	KP781880
P. ericacearum	**IFRDCC 2439***	KC537807	KC537821	KC537814
P. formosana	**NTUCC 17-009***	MH809381	MH809385	MH809389
P. furcata	**MFLUCC12-0054***	JQ683724	JQ683708	JQ683740
P. gaultheria	**IFRD 411-014***	KC537805	KC537819	KC537812
P. gibbosa	**NOF3175***	LC311589	LC311590	LC311591
P. grevilleae	**CBS 114127***	NR147548	KM199407	KM199504
P. hawaiiensis	**CBS 114491***	NR147559	KM199428	KM199514
P. hollandica	**CBS 265.33***	KM199328	KM199388	KM199481
P. humus	**CBS 336.97***	KM199317	KM199420	KM199484
P. inflexa	**MFLUCC12-0270***	JX399008	JX399039	JX399072
P. intermedia	**MFLUCC12-0259***	JX398993	JX399028	JX399059
P. italiana	**MFLUCC12-0657***	KP781878	KP781882	KP781881
P. jester	**CBS 109350***	KM199380	KM199468	KM199554
P. jiangxiensis	**LC4399***	KX895009	KX895341	KX895227
P. jinchanghensis	**LC6636***	KX895028	KX895361	KX895247
P. kenyana	**CBS 442.67***	KM199302	KM199395	KM199502
P. knightiae	**CBS 114138***	KM199310	KM199408	KM199497
P. licualacola	**HGUP 4057***	KC492509	KC481683	KC481684
P. linearis	**MFLUCC12-0271***	JX398992	JX399027	JX399058
P. longiappendiculata	**LC3013***	KX894939	KX895271	KX895156
P. lushanensis	**LC4344***	KX895005	KX895337	KX895223
P. macadamiae	**BRIP 63738b***	KX186588	KX186680	KX186621
P. malayana	**CBS 102220***	NR147550	KM199411	KM199482
P. monochaeta	**CBS 144.97***	KM199327	KM199386	KM199479
P. montellica	**MFLUCC12-0279***	JX399012	JX399043	JX399076
P. neolitseae	**NTUCC 17-011***	MH809383	MH809387	MH809391
P. novae-hollandiae	**CBS 130973***	NR147557	KM199425	KM199511
P. olivaceae	**PSHI2002***	AY687883	DQ333580	–
P. oryzae	**CBS 353.69***	KM199299	KM199398	KM199496
P. pallidotheae	**MAFF 240993***	NR111022	LC311584	LC311585
P. papuana	**CBS 887.96***	KM199318	KM199415	KM199492

Table 20 (continued)

Species	Isolate/voucher no	ITS	TUB2	*tef1*
P. parva	**CBS 265.37***	KM199312	KM199404	KM199508
P. photinicola	**GZCC 16-0028***	KY092404	KY047663	KY047662
P. portugalica	**CBS 393.48***	KM199335	KM199422	KM199510
P. rhizophorae	**MFLUCC17-0416***	MK764283	MK764349	MK764327
P. rhododendri	**IFRDCC 2399***	NR120265	KC537818	KC537811
P. rhodomyrtus	**HGUP 4230***	KF412648	KF412642	KF412645
P. rosea	**MFLUCC12-0258***	JX399005	JX399036	JX399069
P. scoparia	**CBS 176.25***	KM199330	KM199393	KM199478
P. shorea	**MFLUCC12-0314***	KJ503811	KJ503814	KJ503817
P. spathulata	**CBS 356.86***	NR147558	KM199423	KM199513
P. telopeae	**CBS 114161***	NR147545	KM199403	KM199500
P. thailandica	**MFLUCC17-1616***	MK764285	MK764351	MK764329
P. trachicarpicola	**IFRDCC 2440***	NR120109	JQ845945	JQ845946
P. unicolor	**MFLUCC12-0276***	JX398999	JX399030	–
P. verruculosa	**MFLUCC12-0274***	NR120185	–	JX399061
P. yanglingensis	**LC4553***	KX895012	KX895345	KX895231
P. yunnanensis	**HMAS 96359***	AY373375	–	–

Ex-type (ex-epitype) strains are in bold and marked with an asterisk* and voucher stains are in bold

et al. (2012), Hyde et al. (2014), Chen et al. (2015, 2017) and Jayasiri et al. (2019). Five-marker phylogeny of the *Stagonosporopsis* spp. for which these DNA sequence data are available is shown (Table 21).

Identification of *Stagonosporopsis* species associated with ray blight of *Asteraceae* can be achieved through multi-locus sequence typing (Aveskamp et al. 2010; Vaghefi et al. 2012) and also with a species-specific multiplex PCR assay developed by Vaghefi et al. (2016). This assay is based on a four-primer PCR that targets the intergenic spacer of the nrDNA of the ray blight pathogens, producing species-specific amplicons of ~ 560 in *S. chrysanthemi*, ~ 630 bp in *S. inoxydabilis* and ~ 400 bp in *S. tanaceti*, which can be easily differentiated on an agarose gel (Vaghefi et al. 2016).

This study reconstructs the phylogeny of *Stagonosporopsis* based on analyses of a combined ITS, LSU, RPB2 and TUB2 sequence data (Fig. 31). The phylogenetic tree is updated with recently introduced *Stagonosporopsis* species and corresponds to previous studies (Chen et al. 2017, Jayasiri et al. 2019).

Recommended genetic marker (genus level)—ITS
Recommended genetic markers (species level)—TUB2 and RPB2
Accepted number of species: There are 55 species in Index Fungorum (2019) and only 24 species are accepted/ have molecular data in this genus.
References: Chen et al. 2015, 2017, Jayasiri et al. 2019 (morphology, phylogeny).

Verticillium Nees, Syst. Pilze (Würzburg): 57 (1816) [1816-17]

The genus *Verticillium* Nees was introduced by Nees von Esenbeck (1816) for a single saprotrophic species, *V. tenerum* Nees, which was proposed as the type species. Zare et al. (2004) synonymized *V. tenerum* under *Acrostalagmus luteoalbus* (Link) Zare, W. Gams & Schroers, and Gams et al. (2005) proposed *V. dahliae* Kleb. as the conserved type of the genus *Verticillium*.

Verticillium includes several plant pathogenic species that infect trees, insects, mushrooms and, in particular, dicotyledonous plants: *V. dahliae* Kleb., *V. albo-atrum* Reinke et Berth., *V. nigrescens* Pethybr., *V. nubilum* Pethybr., *V. tricorpus* Isaac., *V. theobromae* (Turc.) Mas. & Hughes and *V. fungicola* (Preuss) Hassebrauk (Pegg and Brady 2002). Zare et al. (2007) assigned *V. nigrescens* to the genus *Gibellulopsis* and *V. theobromae* to *Musicillium*. Zare and Gams (2008) assigned *V. fungicola* to the genus *Lecanillium*. *Verticillium dahliae* and *V. albo-atrum* are the two most notorious species which cause *Verticillium* wilt diseases in a wide range of mainly dicotyledonous hosts and result in billions of dollars of damage annually in crop losses worldwide (Pegg and Brady 2002; Barbara and Clewes 2003; Inderbitzin et al. 2011).

Verticillium species, in particular, *V. dahliae* and *V. albo-atrum*, can infect a wide range of plant species. Many hosts of *Verticillium* species were given by different mycologists, e.g., Van der Meer (1925); Rudolph (1931); Engelhard and Carter (1956); Parker (1959); Stark (1961); Devaux and Sackston (1966); Himelick (1969), including high-value crop plants, e.g., cotton (Land et al. 2016), lettuce (Garibaldi et al. 2007; Powell et al. 2013), mango (Baeza-Montanez et al. 2010; Ahmed et al. 2014), gold kiwifruit (Auger et al. 2009), bean (Berbegal and Armengol 2009; Sun et al. 2016; Blomquist et al. 2017), watermelon (Bruton et al. 2007), olive tree (Lo Giudice et al. 2010; Kaliterna et al. 2016), potato (Pace-Lupi et al. 2006), pumpkin (Rampersad 2008). The most comprehensive hosts' list was provided by Pegg and Brady (2002).

Classification—Sordariomycetes, *Hypocreomycetidae*, *Glomerellales*, *Plectosphaerellaceae*

Type species—***Verticillium dahliae*** Kleb., Mykol. Zentbl. 3: 66 (1913)

Distribution—Worldwide

Disease symptoms—Wilt

Wilt caused by *Verticillium* species is a serious fungal disease that causes injury or death to many plant species. Symptoms of this disease vary according to the host species and to environmental conditions including sudden wilting of small branches, yellowing of foliage, stunt growth and premature defoliation. Olive- green to black streaks can be observed in the sapwood of infected branches. In cross sections, vascular tissue appears as a dark ring or pinpoint dark spots. Initial symptoms can occur on one side of the tree or the entire plant (Fradin and Thomma 2006; Blum et al. 2018).

Hosts—Species of this genus have a broad host range including members of *Amaranthaceae*, *Amaryllidaceae*, *Asteraceae*, *Brassicaceae*, *Musaceae*, *Pinaceae*, *Rosaceae*, *Rubiaceae*, *Sapindaceae*, *Solanaceae*, *Theaceae*, *Vitaceae* and *Zingiberaceae* (Farr and Rossman 2019).

Morphological based identification and diversity

There are 270 records in Index Fungorum (2019) and 288 records in MycoBank (Crous et al. 2004) in this genus. Most of the species have been transferred to other genera, e.g., *Gibellulopsis* (Zare et al. 2007), *Haptocillium* (Zare and Gams 2001b), *Lecanicillium* (Zare and Gams 2001a), *Musicillium* (Zare et al. 2007), *Pochonia* (Zare and Gams 2001a, b), *Simplicillium* (Zare and Gams 2001a). Only ten

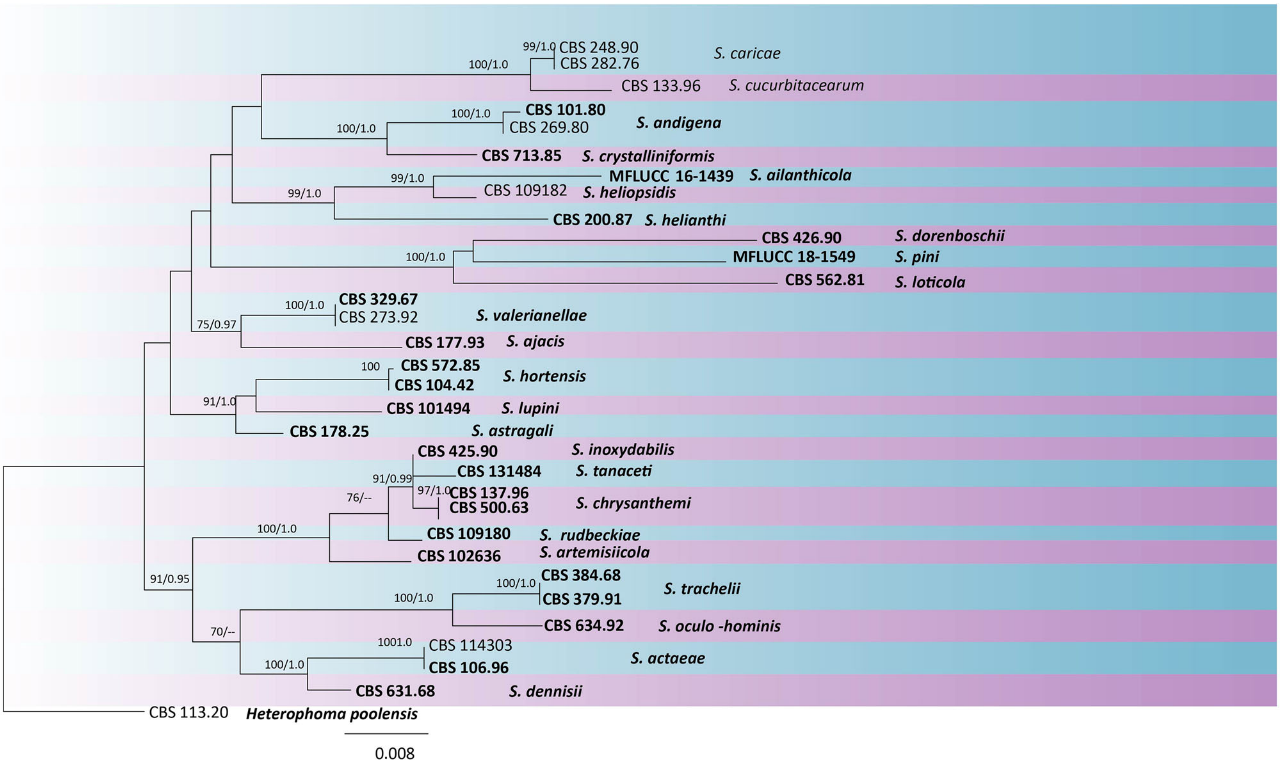


Fig. 31 Phylogenetic tree generated by maximum likelihood analysis of combined ITS, LSU, RPB2 and TUB2 sequence data of *Stagonosporopsis* species. Related sequences were obtained from GenBank. Thirty-two are included in the analyses, which comprise 2756 characters including gaps. Single gene analyses were carried out and compared with each species, to compare the topology of the tree and clade stability. The tree was rooted with *Heterophoma poolensis* (CBS 113.20). Tree topology of the ML analysis was similar to the MP. The best scoring RAxML tree with a final likelihood value of − 8386.622374 is presented. The matrix had 388 distinct alignment patterns, with 11.83% of undetermined characters or gaps. Estimated base frequencies were as follows; A = 0.245798, C = 0.237676, G = 0.273178, T = 0.243348; substitution rates AC = 1.882600, AG = 4.123164, AT = 2.015920, CG = 0.907833, CT = 12.626910, GT = 1.000000; gamma distribution shape parameter α = 1.105097. RAxML bootstrap support values ≥ 50% and Bayesian posterior probabilities ≥ 0.95 (BYPP) are shown respectively near the nodes. Ex-type strains are in bold

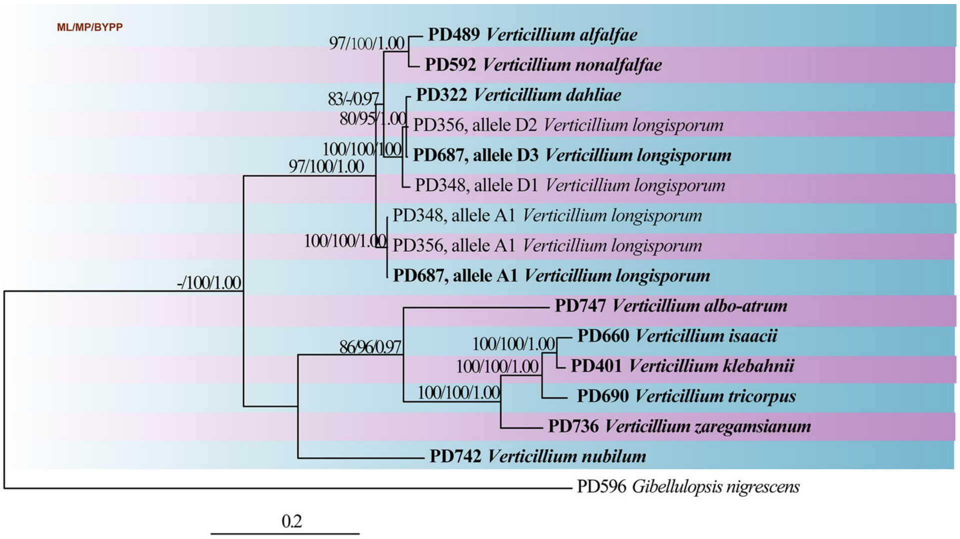


Fig. 32 Phylogenetic tree generated from Bayesian analysis based on combined ACT, *tef1*, GPD and TS sequence data for the genus *Verticillium*. Sixteen strains are included in the combined genes sequence analyses which comprise total of 2597 characters (609 characters for the ACT, 620 characters for *tef1*, 744 characters for GPD, 624 characters for TS) after alignment. For the Bayesian analysis, two parallel runs with six chains were run for 1,000,000 generations and trees were sampled every 100th generation, resulted in 20,002 trees from two runs of which 15,002 trees were used to calculate the posterior probabilities (each run resulted in 10,001 trees of which 7501 trees were sampled). Bootstrap support values for maximum likelihood (ML, first set) and maximum parsimony (MP, second set) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above or below the nodes. Ex-type strains are in bold. The tree is rooted with *Gibellulopsis nigrescens* (PD596)

species, *V. albo-atrum*, *V. alfalfae*, *V. dahliae*, *V. isaacii*, *V. klebahnii*, *V. longisporum*, *V. nonalfalfae*, *V. nubilum*, *V. tricorpus* and *V. zaregamsianum*, were accepted within *Verticillium sensu stricto* (Inderbitzin et al. 2011). No sexual states are known. Descriptions and a key to these ten species were provided by Inderbitzin et al. (2011).

Molecular based identification and diversity

The first phylogenetic analysis of *Verticillium* species was made by Morton et al. (1995) to analysis the relationship between *V. alboatrum* and *V. dahliae* based on the internal transcribed spacer regions and intervening 5.8S rDNA (ITS) sequences data (Fig. 32, Table 22). Subsequently, SSU, LSU, RNA polymerase II largest subunit gene (RPB1), the cytochrome oxidase subunit III gene (*cox3*), the small ribosomal rRNA subunit (*rns*), NADH dehydrogenase subunit genes (*nad1* and *nad3*) were used (Barbara and Clewes 2003; Pantou et al. 2005; Zare and Gams 2008, 2016).

Recommended genetic marker (genus level)—LSU
Recommended genetic marker (species level)—ITS
Accepted number of species: **10 species**.
References: Inderbitzin et al. 2011 (morphology and phylogeny); Barbara and Clewes 2003, Morton et al. 1995, Pantou et al. 2005, Zare and Gams 2008, 2016 (phylogeny); Fradin and Thomma 2006, Blum et al. 2018 (pathogenicity)

Table 21 Details of the ***Stagonosporopsis*** isolates used in the phylogenetic analyses

Species	Culture	LSU	GenBank Accession numbers		TUB2
			ITS	RPB2	
Stagonosporopsis actaeae	**CBS 106.96***	GU238166	GU237734	KT389672	GU237671
	CBS 114303	KT389760	KT389544	–	KT389847
S. ailanthicola	**MFLUCC 16-1439***	KY100874	KY100872	KY100876	KY100878
S. ajacis	**CBS 177.93***	GU238168	GU237791	KT389673	GU237673
S. andigena	CBS 269.80	GU238170	GU237817	–	GU237675
	CBS 101.80	GU238169	GU237714	–	GU237674
S. artemisiicola	**CBS 102636**	GU238171	GU237728	KT389674	GU237676
S. astragali	**CBS 178.25**	GU238172	GU237792	–	GU237677
S. caricae	CBS 248.90	GU238175	GU237807	–	GU237680
	CBS 282.76	GU238177	GU237821	–	GU237682
S. chrysanthemi	**CBS 500.63**	GU238190	GU237871	–	GU237695
	CBS 137.96	GU238191	GU237783	–	GU237696
S. crystalliniformis	**CBS 713.85***	GU238178	GU237903	KT389675	GU237683
S. cucurbitacearum	CBS 133.96	GU238181	GU237780	KT389676	GU237686
S. dennisii	**CBS 631.68***	GU238182	GU237899	KT389677	GU237687
S. dorenboschii	**CBS 426.90***	GU238185	GU237862	KT389678	GU237690
S. helianthi	**CBS 200.87***	KT389761	KT389545	KT389683	KT389848
S. heliopsidis	**CBS 109182**	GU238186	GU237747	KT389679	GU237691
S. hortensis	**CBS 104.42**	GU238198	GU237730	KT389680	GU237703
	CBS 572.85	GU238199	GU237893	KT389681	GU237704
S. inoxydabilis	**CBS 425.90***	GU238188	GU237861	KT389682	GU237693
S. loticola	**CBS 562.81***	GU238192	GU237890	KT389684	GU237697
S. lupini	**CBS 101494***	GU238194	GU237724	KT389685	GU237699
S. oculohominis	**CBS 634.92***	GU238196	GU237901	KT389686	GU237701
S. pini	**MFLUCC 18-1549***	MK348019	MK347800	MK434860	–
S. rudbeckiae	**CBS 109180**	GU238197	GU237745	–	GU237702
S. tanaceti	**CBS 131484***	JQ897461	NR_111724	–	JQ897496
S. trachelii	**CBS 379.71**	GU238173	GU237850	KT389687	GU237678
	CBS 384.68	GU238174	GU237856	–	GU237679
S. valerianellae	CBS 273.92	GU238200	GU237819	–	GU237705
	CBS 329.67*	GU238201	GU237832		GU237706

Table 22 GenBank accession numbers of ***Verticillium*** isolates included in this study

Taxa	Strains	Haplotype	ACT	*tef1*	GPD	TS
Verticillium albo-atrum	PD747		JN188144	JN188272	JN188208	JN188080
V. alfalfa	PD489		JN188097	JN188225	JN188161	JN188033
V. dahlia	PD322		HQ206921	HQ414624	HQ414719	HQ414909
V. isaacii	PD660		HQ206985	HQ414688	HQ414783	HQ414973
V. klebahnii	PD401		JN188093	JN188221	JN188157	JN188029
V. longisporum	PD348	a1	HQ206930	HQ414633	HQ414728	HQ414918
V. longisporum	PD348	d1	HQ206931	HQ414634	HQ414729	HQ414919
V. longisporum	PD356	a1	HQ206934	HQ414637	HQ414732	HQ414922
V. longisporum	PD356	d2	HQ206935	HQ414638	HQ414733	HQ414923
V. longisporum	PD687	a1	HQ206993	HQ414696	HQ414791	HQ414981
V. longisporum	PD687	d2	HQ206994	HQ414697	HQ414792	HQ414982
V. nonalfalfae	PD592		JN188099	JN188227	JN188163	JN188035
V. nubilum	PD742		JN188139	JN188267	JN188203	JN188075
V. tricorpus	PD690		JN188121	JN188249	JN188185	JN188057
V. zaregamsianum	PD736		JN188133	JN188261	JN188197	JN188069

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