

Diaporthe is paraphyletic

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Abstract: Previous studies have shown that our understanding of species diversity within *Diaporthe* (syn. *Phomopsis*) is limited. In this study, 49 strains obtained from different countries were subjected to DNA sequence analysis. Based on these results, eight new species names are introduced for lineages represented by multiple strains and distinct morphology. Twelve *Phomopsis* species previously described from China were subjected to DNA sequence analysis, and confirmed to belong to *Diaporthe*. The genus *Diaporthe* is shown to be paraphyletic based on multi-locus (LSU, ITS and *TEF1*) phylogenetic analysis. Several morphologically distinct genera, namely *Mazzantia*, *Ophiodiaporthe*, *Pustulomyces*, *Phaeocystroma*, and *Stenocarpella*, are embedded within *Diaporthe s. lat.*, indicating divergent morphological evolution. However, splitting *Diaporthe* into many smaller genera to achieve monophyly is still premature, and further collections and phylogenetic datasets need to be obtained to address this situation.

Key words:
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Phomopsis
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INTRODUCTION

Species of *Diaporthe* are known as important plant pathogens, endophytes or saprobes (Udayanga *et al.* 2011, Gomes *et al.* 2013). They have broad host ranges, and occur on many plant hosts, including cultivated crops, trees, and ornamentals (Diogo *et al.* 2010, Thompson *et al.* 2011, Gomes *et al.* 2013, Huang *et al.* 2015). Some *Diaporthe* species are responsible for severe diebacks, cankers, leaf-spots, blights, decay or wilts on different plant hosts, several of which are economically important (Mostert *et al.* 2001, Van Rensburg *et al.* 2006, Thompson *et al.* 2011, Gomes *et al.* 2013), leading to serious diseases and significant yield losses (Santos *et al.* 2011). For example, *Diaporthe helianthi* is the cause of one of the most important diseases of sunflower (*Helianthus annuus*) worldwide, and has reduced production by up to 40 % in Europe (Masirevic & Gulya 1992, Thompson *et al.* 2011). *Diaporthe neoviticola* and *D. vitimegaspora*, the causal agents of leaf-spot and swelling arm, are known as severe pathogens of grapevines (*Vitis vinifera*) (Van Niekerk *et al.* 2005). Úrbez-Torres *et al.* (2013) indicated that *D. neoviticola* was one of the most prevalent fungi isolated from grapevine perennial cankers in declining vines. *Diaporthe scabra* has been reported causing cankers and dieback on London plane (*Platanus acerifolia*) in Italy (Grasso *et al.* 2012). Symptoms of umbel browning and necrosis caused by *D. angeliace*

have been regularly observed on carrots in France, resulting in seed production losses since 2007 (Ménard *et al.* 2014). Avocado (*Persea americana*), cultivated worldwide in tropical and subtropical regions, is threatened by branch cankers and fruit stem-end rot diseases caused by *D. foeniculina* and *D. sterilis* (Guarnaccia *et al.* 2016). Furthermore, species of *Diaporthe* are commonly introduced into new areas as endophytes or latent pathogens along with plant produce. For instance, Torres *et al.* (2016) reported *D. rudis* causing stem-end rot in avocados in Chile, which was imported *via* avocado fruit from California (USA). Some endophytes have been shown to act as opportunistic plant pathogens. *Diaporthe foeniculina* (syn. *P. theicola*), which is a common endophyte, has been shown to cause stem and shoot cankers on sweet chestnut (*Castanea sativa*) in Italy (Annesi *et al.* 2015, Huang *et al.* 2015). Because of this unique ecology and potential role as plant pathogens, it is of paramount importance to accurately identify species of *Diaporthe* to facilitate disease surveillance, control, and trade.

The initial species concept of *Diaporthe* based on the assumption of host-specificity, resulted in the introduction of more than 1000 names (<http://www.indexfungorum.org/Names/Names.asp>); (Gomes *et al.* 2013, Gao *et al.* 2016). In recent years, however, a polyphasic approach employing multi-locus DNA data together with morphology and ecology has been employed for species delimitation in the genus

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(Udayanga *et al.* 2011, Gomes *et al.* 2013). The nuclear ribosomal internal transcribed spacer (ITS), the translation elongation factor 1- α (*TEF1*), β -tubulin (*TUB*), histone H3 (*HIS*), and calmodulin (*CAL*) genes are the most commonly used molecular loci for the identification of *Diaporthe* spp. (Dissanayake *et al.* 2015, Udayanga *et al.* 2015, Huang *et al.* 2015, Santos *et al.* 2017). Furthermore, molecular marker aids are being used to rapidly identify *Diaporthe* species which tend to be morphologically conserved (Udayanga *et al.* 2012, Tan *et al.* 2013, Lombard *et al.* 2014, Thompson *et al.* 2015, Huang *et al.* 2015). However, defining species boundaries remains a major challenge in *Diaporthe* (Huang *et al.* 2015), which may be a consequence of limited sampling or the use of DNA loci with insufficient phylogenetic resolution (Liu *et al.* 2016). It has therefore been proposed that new species in the genus should be introduced with caution, and that multiple strains from different origins should be subjected to a multi-gene phylogenetic analysis to determine intraspecific variation (Liu *et al.* 2016).

The generic relationships of *Diaporthe* with other genera in *Diaporthaceae* remain unclear. The family name *Diaporthaceae* was established by Wehmeyer (1926) to accommodate *Diaporthe*, *Mazzantia*, *Melanconis*, and some other genera, mainly based on morphological characters such as the position, structure, and arrangement of ascomata, stroma, and spore shapes. Castlebury *et al.* (2002) reported that *Diaporthaceae* comprised *Diaporthe* and *Mazzantia* based on LSU DNA sequence data, removing other genera to different families in *Diaporthales*. Additional genera subsequently placed in the *Diaporthaceae* include *Leucodiaporthe* (Vasilyeva *et al.* 2007), *Stenocarpella* (Crous *et al.* 2006), *Phaeocystostroma* (Lamprecht *et al.* 2011), *Ophiodiaporthe* (Fu *et al.* 2013), and *Pustulomyces* (Dai *et al.* 2014). All the above genera were represented by a few species or are monotypic. Although they appeared to be morphologically divergent from *Diaporthe*, their phylogenetic relationships remain unclear.

About 991 names of *Diaporthe* and 979 of *Phomopsis* have been established to date (<http://www.indexfungorum.org/Names/Names.asp>). Among them, many old epithets lack molecular data, and few morphological characters can be used in species delimitation, making it difficult to merge these names to advance to the one name scenario (Rossman *et al.* 2014, 2015). In China, more than 50 plant pathogenic *Phomopsis* species have been published to date (Chi *et al.* 2007). In order to stabilize these species names in the genus *Diaporthe*, here we introduce 12 new combinations for *Phomopsis* species that have been subjected to DNA sequencing, and whose phylogenetic position has been resolved in *Diaporthe* in the present study.

The objectives of this study were: (1) to examine the phylogenetic relationships of *Diaporthe* with other closely related genera in *Diaporthaceae*; (2) to introduce new species in *Diaporthe*; and (3) to transfer *Phomopsis* species described from China to *Diaporthe* based on morphological and newly generated molecular data.

MATERIAL AND METHODS

Isolates

Strains were isolated from leaves of both symptomatic and healthy plant tissues from Yunnan, Zhejiang, and Jiangxi Provinces in China. A few other strains were obtained *via* the Ningbo Entry-Exit Inspection and Quarantine Bureau, which were isolated from imported plants from other countries. Single spore isolations were conducted from diseased leaves with visible fungal sporulation following the protocol of Zhang *et al.* (2013), and isolation from surface sterilized leaf tissues was conducted following the protocol of Gao *et al.* (2014). Fungal endophytes were isolated according to the method described by Liu *et al.* (2015). The *Diaporthe* strains were primarily identified from the other fungal species based on cultural characteristics on PDA, spore morphology, and ITS sequence data. Type specimens of new species were deposited in the Mycological Herbarium, Microbiology Institute, Chinese Academy of Sciences, Beijing, China (HMAS), with ex-type living cultures deposited in the China General Microbiological Culture Collection Center (CGMCC).

Morphological analysis

Cultures were incubated on PDA at 25 °C under ambient daylight and growth rates were measured daily for 7 d. To induce sporulation, isolates were inoculated on PNA (pine needle agar; Smith *et al.* 1996) containing double-autoclaved (30 min, 121°C, 1 bar) healthy pine needles and incubated at a room temperature of ca. 25 °C (Su *et al.* 2012). Cultures were examined periodically for the development of conidiomata and perithecia. Conidia were taken from pycnidia and mounted in sterilized water. The shape and size of microscopic structures were observed and noted using a light microscope (Nikon Eclipse 80i) with differential interference contrast (DIC). At least 10 conidiomata, 30 conidiophores, alpha and beta conidia were measured to calculate the mean size and standard deviation (SD).

DNA extraction, PCR amplification and sequencing

Isolates were grown on PDA and incubated at 25 °C for 7 d. Genomic DNA was extracted following the protocol of Cubero *et al.* (1999). The quality and quantity of DNA was estimated visually by staining with GelRed after 1 % agarose gel electrophoresis. The primers ITS5 and ITS4 (White *et al.* 1990) were used to amplify the internal transcribed spacer region (ITS) of the nuclear ribosomal RNA gene operon, including the 3' end of the 18S nrRNA, the first internal transcribed spacer region, the 5.8S nrRNA gene; the second internal transcribed spacer region and the 5' end of the 28S nrRNA gene. The primers EF1-728F and EF1-986R (Carbone & Kohn 1999) were used to amplify part of the translation elongation factor 1- α gene (*TEF1*), and the primers CYLH3F (Crous *et al.* 2004) and H3-1b (Glass & Donaldson 1995) were used to amplify part of the histone H3 (*HIS*) gene. The primers T1 (O'Donnell & Cigelnik 1997) and Bt2b (Glass & Donaldson 1995) were used to amplify the beta-tubulin gene (*TUB*); the additional combination of Bt2a/Bt2b (Glass & Donaldson 1995) was used in case of amplification failure of the T1/Bt2b primer pair. The primer pair CAL228F/CAL737R

Table 1. Sources of isolates and GenBank accession numbers used in the phylogenetic analyses of *Diaportheaceae*.

Species names [*]	Culture collection no.	Isolation sources	Country	GenBank Accession Numbers			References
				ITS	LSU	TEF1	
<i>D. acaciigena</i>	CBS 129521 (ex-type)	<i>Acacia retinodes</i>	Australia	KC343005	-	KC343731	Gomes <i>et al.</i> (2013)
<i>D. ampelina</i>	FAU 586	<i>Vitis</i> sp.	USA: New York	-	AF439635	-	-
<i>D. angelicae</i>	CBS 111592	<i>Heracleum sphondylium</i>	Austria	KC343027	-	KC343753	Gomes <i>et al.</i> (2013)
	AR 3724	<i>Heracleum sphondylium</i>	Austria	KC343026	-	KC343752	Gomes <i>et al.</i> (2013)
<i>D. apiculata</i>	LC 3418 (ex-type)	<i>Camellia sinensis</i>	China	KP267896	KY011852	KP267970	This study
	LC 3452	<i>Camellia sinensis</i>	China	KP267901	KY011853	KP267975	This study
<i>D. arecae complex</i>	LC 4155	<i>Rhododendron</i> sp.	China	KY011895	KY011879	KY011906	This study
	LC 4159	<i>Rhododendron</i> sp.	China	KY011896	KY011880	KY011907	This study
	LC 4164	Unknown host	China	KY011897	KY011881	KY011908	This study
<i>D. biguttusis</i>	LC 1106 (ex-type)	<i>Lithocarpus glaber</i>	China	KF576282	KY011878	KF576257	This study
<i>D. compacta</i>	LC 3078	<i>Camellia sinensis</i>	China	KP267850	KY011839	KP267924	This study
	LC 3083 (ex-type)	<i>Camellia sinensis</i>	China	KP267854	KY011840	KP267928	This study
	LC 3084	<i>Camellia sinensis</i>	China	KP267855	KY011841	KP267929	This study
<i>D. decedens</i>	CBS 109772	<i>Corylus avellana</i>	Austria	KC343059	-	KC343785	Gomes <i>et al.</i> (2013)
<i>D. detrusa</i>	CBS 109770	<i>Berberis vulgaris</i>	Austria	KC343061	-	KC343787	Gomes <i>et al.</i> (2013)
<i>D. discoidispora</i>	LC 3503	<i>Camellia sinensis</i>	China	KY011887	KY011854	KY011898	This study
<i>D. elaeagni-glabrae</i>	LC 4802 (ex-type)	<i>Elaeagnus glabra</i>	China	KX986779	KY011885	KX999171	This study
	LC 4806	<i>Elaeagnus glabra</i>	China	KX986780	KY011886	KX999172	This study
<i>D. ellipicola</i>	LC 0810 (ex-type)	<i>Lithocarpus glaber</i>	China	KF576270	KY011873	KF576245	This study
<i>D. eres</i>	LC 3198	<i>Camellia sinensis</i>	China	KP267873	KY011845	KP267947	This study
	LC 3205	<i>Camellia sinensis</i>	China	KP714499	KY011846	KP714511	This study
	LC 3206	<i>Camellia sinensis</i>	China	KP714500	KY011847	KP714512	This study
	CBS 109767	<i>Acer campestre</i>	Austria	KC343075	-	KC343801	Gomes <i>et al.</i> (2013)
<i>D. fusicola</i>	LC 1126	<i>Lithocarpus glaber</i>	China	KF576281	KY011836	KF576256	This study
	LC 0778 (ex-type)	<i>Lithocarpus glaber</i>	China	KF576263	KY011877	KF576238	This study
<i>D. hongkongensis</i>	LC 0784	<i>Lithocarpus glaber</i>	China	KC153104	KY011876	KC153095	This study
	LC 0812	<i>Smilax china</i>	China	KC153103	KY011875	KC153094	This study
<i>D. incompleta</i>	LC 6706	<i>Camellia sinensis</i>	China	KX986793	KY011859	KX999185	This study
	LC 1127 (ex-type)	<i>Lithocarpus glaber</i>	China	KF576267	KY011837	KF576242	This study
<i>D. mahothocarpi</i>	LC 0732	<i>Mahonia bealei</i>	China	KC153097	KY011872	KC153088	This study
	LC 0763 (ex-type)	<i>Lithocarpus glaber</i>	China	KC153096	KY011871	KC153087	This study
<i>D. masirevicii</i>	<i>Diaporthe</i> sp.	<i>Camellia sinensis</i>	China	KY011888	KY011861	KY011899	This study
<i>D. neoarctii</i>	CBS 109490	<i>Ambrosia trifida</i>	USA: New Jersey	KC343145	-	KC343871	Gomes <i>et al.</i> (2013)
<i>D. oncostoma</i>	CBS 109741	<i>Robinia pseudoacacia</i>	Russia	KC343161	-	KC343887	Gomes <i>et al.</i> (2013)
<i>D. oraccinii</i>	LC 3166 (ex-type)	<i>Camellia sinensis</i>	China	KP267863	KY011843	KP267937	This study
	LC 3172	<i>Camellia sinensis</i>	China	KP267864	KY011844	KP267938	This study
	LC 3296	<i>Camellia sinensis</i>	China	KP267884	KY011849	KP267958	This study
<i>D. ovoicicola</i>	LC 1128 (ex-type)	<i>Lithocarpus glaber</i>	China	KF576264	KY011838	KF576239	This study
<i>D. penetriteum</i>	LC 3215	<i>Camellia sinensis</i>	China	KP267879	KY011848	KP267953	This study
	LC 3353 (ex-type)	<i>Camellia sinensis</i>	China	KP714505	KY011850	KP714517	This study
	LC 3394	<i>Camellia sinensis</i>	China	KP267893	KY011851	KP267967	This study
<i>D. perijuncta</i>	CBS 109745	<i>Ulmus glabra</i>	Austria	KC343172	-	KC343898	Gomes <i>et al.</i> (2013)

Table 1. (Continued).

Species names [*]	Culture collection no.	Isolation sources	Country	GenBank Accession Numbers			References
				ITS	LSU	TEF1	
<i>D. pseudophoenicicola</i>	LC 6150	<i>Phoenix canariensis</i>	China	KY011891	KY011865	KY011902	This study
	LC 6151	<i>Phoenix canariensis</i>	China	KY011892	KY011866	KY011903	This study
<i>D. pustulata</i>	CBS 109742	<i>Acer pseudoplatanus</i>	Austria	KC343185	-	KC343911	Gomes et al. (2013)
	CBS 109760	<i>Acer pseudoplatanus</i>	Austria	KC343186	-	KC343912	Gomes et al. (2013)
	CBS 109784	<i>Prunus padus</i>	Austria	KC343187	-	KC343913	Gomes et al. (2013)
<i>D. rudis</i>	LC 6147	<i>Dendrobenthamia japonica</i>	USA	KY011890	KY011864	KY011901	This study
	LC 6145	<i>Ilex aquifolium</i>	China	KY011889	KY011863	KY011900	This study
<i>D. saccharata</i>	CBS 116311	<i>Protea repens</i> , cankers	South Africa	KC343190	-	KC34391	Gomes et al. (2013)
<i>D. sclerotioides</i>	CBS 296.67	<i>Cucumis sativus</i>	Netherlands	KC343193	-	KC343919	Gomes et al. (2013)
<i>D. tectonendophytica</i>	LC 6623	Unknown host	China	KX986795	KY011857	KX999187	This study
<i>D. tectonigena</i>	LC 6512	<i>Camellia sinensis</i>	China	KX986782	KY011856	KX999174	This study
<i>D. ternstroemiae</i>	LC 0777 (ex-type)	<i>Ternstroemia gymnanthera</i>	China	KC153098	KY011874	KC153089	This study
<i>D. ueckerae</i>	LC 3564	<i>Camellia sinensis</i>	China	KP267912	KY011855	KP267986	This study
<i>D. undulata</i>	LC 6624	Unknown host	China	KX986798	KY011858	KX999190	This study
<i>D. velutina</i>	LC 4414	<i>Lithocapus</i> sp.	China	KX986788	KY011882	KX999180	This study
	LC 4419	<i>Neolitsea</i> sp.	China	KX986789	KY011883	KX999181	This study
	LC 4421 (ex-type)	<i>Neolitsea</i> sp.	China	KX986790	KY011884	KX999182	This study
<i>D. xishuangbanica</i>	LC 6707	<i>Camellia sinensis</i>	China	KX986783	KY011860	KX999175	This study
	LC 6744	<i>Camellia sinensis</i>	China	KX986784	KY011862	KX999176	This study
<i>D. yunnanensis</i>	LC 6168	<i>Coffea</i> sp.	China	KX986796	KY011867	KX999188	This study
<i>Diaporthe</i> sp.	LC 3156	<i>Camellia sinensis</i>	China	KP267861	KY011842	KP267935	This study
	LC 6170	<i>Coffea</i> sp.	China	KY011893	KY011869	KY011904	This study
	LC 6171	<i>Solanum melongena</i>	China	KY011894	KY011870	KY011905	This study
	LC 6232	<i>Theobroma cacao</i>	China	KX986797	KY011868	KX999189	This study
<i>Mazzantia napelli</i>	AR 3498	<i>Aconitum vulparia</i>	Austria	-	AF408368	EU222017	Castlebury et al. (2002)
<i>Ophiodiaporthe cyatheae</i>	BCRC 34961	<i>Cyathea lepifera</i>	Taiwan	JX570889	JX570891	KC465406	Fu et al. (2013)
<i>Phaeocystostroma ambiguum</i>	CPC 17071	<i>Zea mays</i>	South Africa	FR748036	-	FR748068	Lamprecht et al. (2011)
	CPC 17072	<i>Zea mays</i>	South Africa	FR748037	FR748096	FR748069	Lamprecht et al. (2011)
<i>Ph. plurivorum</i>	CBS 113835	<i>Helianthus annuus</i>	Portugal	FR748046	FR748104	FR748078	Lamprecht et al. (2011)
<i>Ph. sacchari</i>	CBS 275.34	-	Japan	FR748047	FR748105	FR748079	Lamprecht et al. (2011)
<i>Ph. megalosporum</i>	CBS 284.65	Rice-field soil	India	FR748045	FR748103	FR748077	Lamprecht et al. (2011)
<i>Pustulomyces bambusicola</i>	MFLUCC 11-0436	on dead culm of bamboo	Thailand	-	KF806753	KF806755	Dai et al. (2014)
<i>Stenocarpella macrospora</i>	CBS 117560	Rain damaged Bt maize hybrid, 2003-04 season	South Africa	FR748048	DQ377934	-	Lamprecht et al. (2011)
<i>S. maydis</i>	CBS 117558	Traditional/landrace maize from 2003/04 season	South Africa	FR748051	DQ377936	FR748080	Lamprecht et al. (2011)
<i>Valsa ambiens</i>	CFCC 89894	<i>Pyrus bretschneideri</i>	China	KR045617	KR045699	KU710912	Fan et al. (2014)

*New species described in this paper are shown in bold.

(Carbone & Kohn 1999) and LR0R/LR5 primer pair (Rytas & Mark 1990) were used to amplify the calmodulin gene (*CAL*) and the LSU rDNA, respectively. Amplification reactions of 25 μ L were composed of 10 \times EasyTaq buffer (MgCl²⁺ included; Transgen, Beijing), 50 μ M dNTPs, 0.2 μ M of each forward and reverse primers (Transgen), 0.5 U EasyTaq DNA polymerase (Transgen) and 1–10 ng of genomic DNA. PCR parameters were as follows: 94 °C for 5 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at a suitable temperature for 30 s (52 °C for ITS and LSU, 56 °C for *CAL*, *HIS*, *TEF1* and *TUB*), extension at 72 °C for 30 s and a final elongation step at 72 °C for 10 min. DNA sequencing was performed by Omegagenetics Company, Beijing.

Phylogenetic analyses

The DNA sequences generated with forward and reverse primers were used to obtain consensus sequences using MEGA v. 5.1 (Tamura *et al.* 2011), and subsequently aligned using MAFFT v. 6 (Kato & Toh 2010); alignments were manually edited using MEGA v. 5.1 when necessary. Two datasets were employed in the phylogenetic analyses. LSU, ITS and *TEF1* loci were selected to infer the generic relationships within *Diaportheaceae* (Table 1), with *Valsa ambiens* as outgroup. All available sequences of *Diaporthe* species were included in the dataset of combined ITS, *HIS*, *TEF1*, *TUB*, and *CAL* regions to infer the interspecific relationships within *Diaporthe* (Table 2) with *Diaporthe corylina* as outgroup. Maximum likelihood (ML) gene trees were estimated using the software RAxML v. 7.4.2 Black Box (Stamatakis 2006, Stamatakis *et al.* 2008). The RAxML software selected the GTR model of nucleotide substitution with the additional options of modelling rate heterogeneity (Γ) and proportion invariable sites (I). Bayesian analyses (critical value for the topological convergence diagnostic set to 0.01) were performed on the concatenated loci using MrBayes v. 3.2.2 (Ronquist *et al.* 2012) as described by (Crous *et al.* 2006) using nucleotide substitution models for each data partition selected by jModeltest (Darriba *et al.* 2012) and MrModeltest v. 2.3 (Nylander 2004). Bayesian analyses were launched with random starting trees for 10 000 000 generations, and Markov chains were sampled every 1000 generations. The first 25 % resulting trees were discarded as burn-in. The remaining trees were summarized to calculate the posterior probabilities (PP) of each clade being monophyletic. Trees were visualized in FigTree v. 1.1.2 (<http://tree.bio.ed.ac.uk/software/>). New sequences generated in this study were deposited in NCBI's GenBank nucleotide database (www.ncbi.nlm.nih.gov; Table 1).

RESULTS

Collection of *Diaporthe* strains

Twenty-one *Diaporthe* strains including presumed plant pathogens and endophytes were isolated from 11 different host plant species (Table 2) collected from three provinces

(Jiangxi, Yunnan, Zhejiang) in the northern part of China. In addition, 28 strains were isolated from the plant samples inspected by Jiangsu Entry-Exit Inspection and Quarantine Bureau.

The paraphyly of *Diaporthe*

Phylogenetic analysis was conducted with 224 sequences derived from 76 ingroup taxa from *Diaportheaceae* with *Valsa ambiens* as the outgroup (Table 1). The combined alignment comprised 1 817 characters including gaps (795 for LSU, 558 for ITS, 464 for *TEF1*). Based on the results of the Mrmodeltest, the following priors were set in MrBayes for the different data partitions: GTR+G models with gamma-distributed rates were implemented for LSU and ITS, HKY+I+G model with invgamma-distributed rates were implemented for *TEF1*. The Bayesian analysis lasted 7×10^8 generations and the consensus trees and posterior probabilities were calculated from the trees left after discarding the first 25 % generations for burn-in (Fig. 1).

The generic relationships of *Mazzantia*, *Ophiodiaporthe*, *Phaeocytostroma*, *Pustulomyces*, and *Stenocarpella* with *Diaporthe* from this analysis are shown in Fig. 1. The topology and branching order of the phylogenetic trees inferred from ML and Bayesian methods were essentially similar. Five genera from *Diaportheaceae* did not form discrete clades from *Diaporthe* species but are scattered in the latter, although the family remains monophyletic. The paraphyletic nature of *Diaporthe*, however, is demonstrated (Fig. 1). *Ophiodiaporthe* formed a well resolved and distinct clade represented by strain YMJ 1364, and clustered together with the ex-type culture of *D. sclerotioides* (CBS 296.67) (BPP 0.99, MLBS: 90). *Stenocarpella*, represented by *S. maydis* and *S. macrospora*, was well supported (BPP 1, MLBS = 96) and closely related to several species of *Phaeocytostroma*. *Mazzantia*, however, was poorly supported for its phylogenetic position in *Diaportheaceae* (Fig. 1).

Phylogenetic analyses of the combined datasets of *Diaporthe* species

In total, 1089 sequences derived from 273 ingroup taxa were combined and *Diaporthe corylina* was used as outgroup. A total of 2783 characters including gaps (568 for *CAL*, 554 for *HIS*, 523 for ITS, 636 for *TEF1* and 456 for *TUB*) were included in the multi-locus dataset, comprising sequences generated from this study and others downloaded from GenBank (Table 2). For the Bayesian inference, GTR+I+G model was selected for *CAL*, *HIS* and ITS, HKY+I+G for *TEF1* and *TUB* through the analysis of Mrmodeltest. The maximum likelihood tree conducted by the GTR model confirmed the tree topology and posterior probabilities of the Bayesian consensus tree.

The topology and branching order for the phylogenetic trees inferred from ML and Bayesian methods were essentially similar (Fig. 2). Based on the multi-locus phylogeny and morphology, 49 strains were assigned to 13 species, including eight taxa which we describe here as new (Fig. 2).

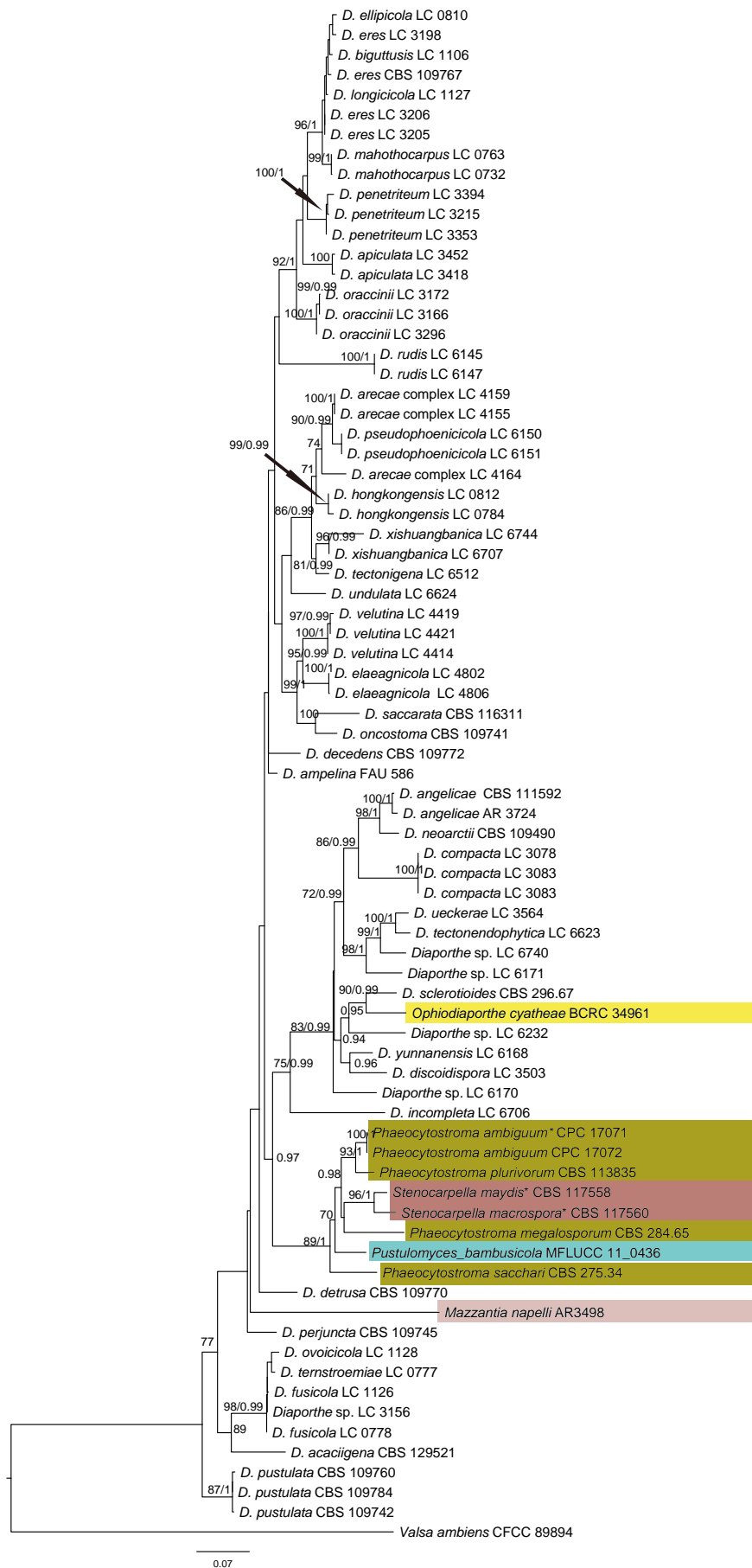


Fig. 1. Phylogenetic tree of the family *Diaporthaceae* from a maximum likelihood analysis based on the combined multi-locus dataset (ITS, LSU, *TEF1*). The ML bootstrap values $\geq 70\%$, bayesian probabilities BPP ≥ 0.90 are marked above the branches. The tree is rooted with *Valsa ambiens*.

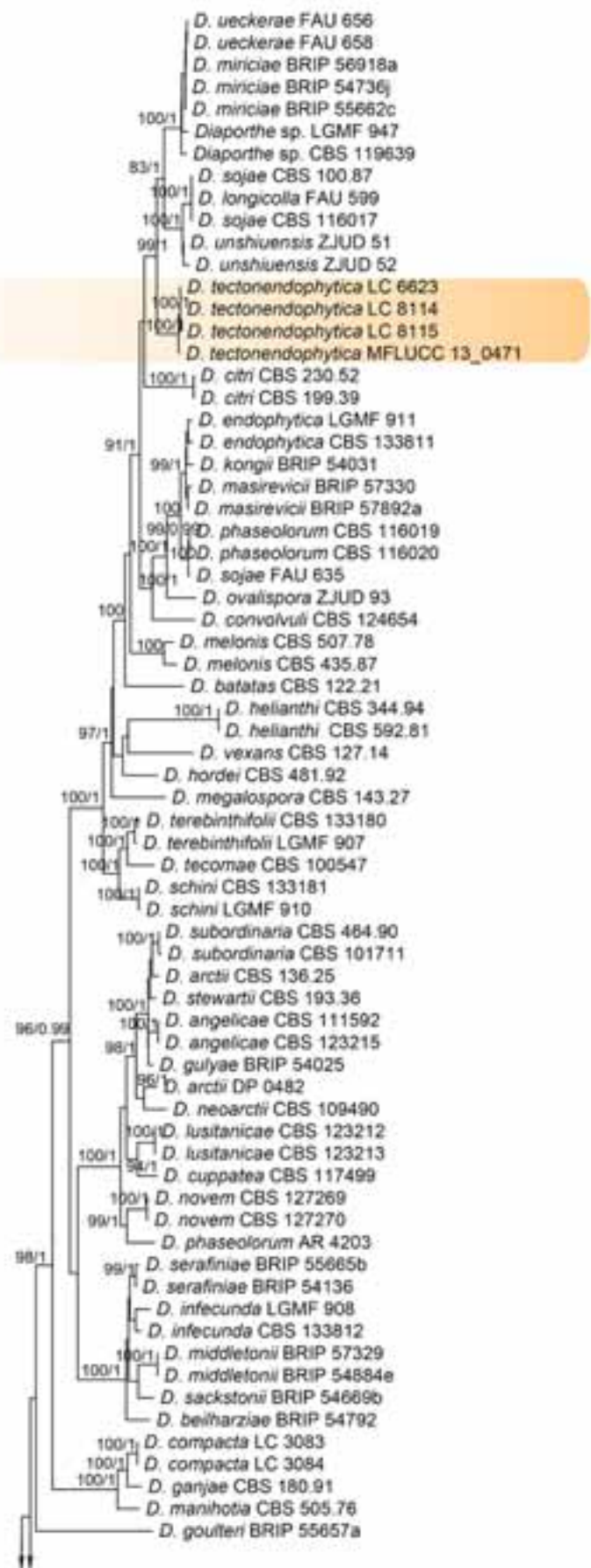


Fig. 2. Phylogenetic tree of the genus *Diaporthe* from a maximum likelihood analysis based on the combined multi-locus dataset (*CAL*, *HIS*, *ITS*, *TEF1*, *TUB*). The ML bootstrap values $\geq 70\%$, bayesian probabilities BPP ≥ 0.90 are marked above the branches. The tree is rooted with *Diaporthella corylina*. The novel species are highlighted.

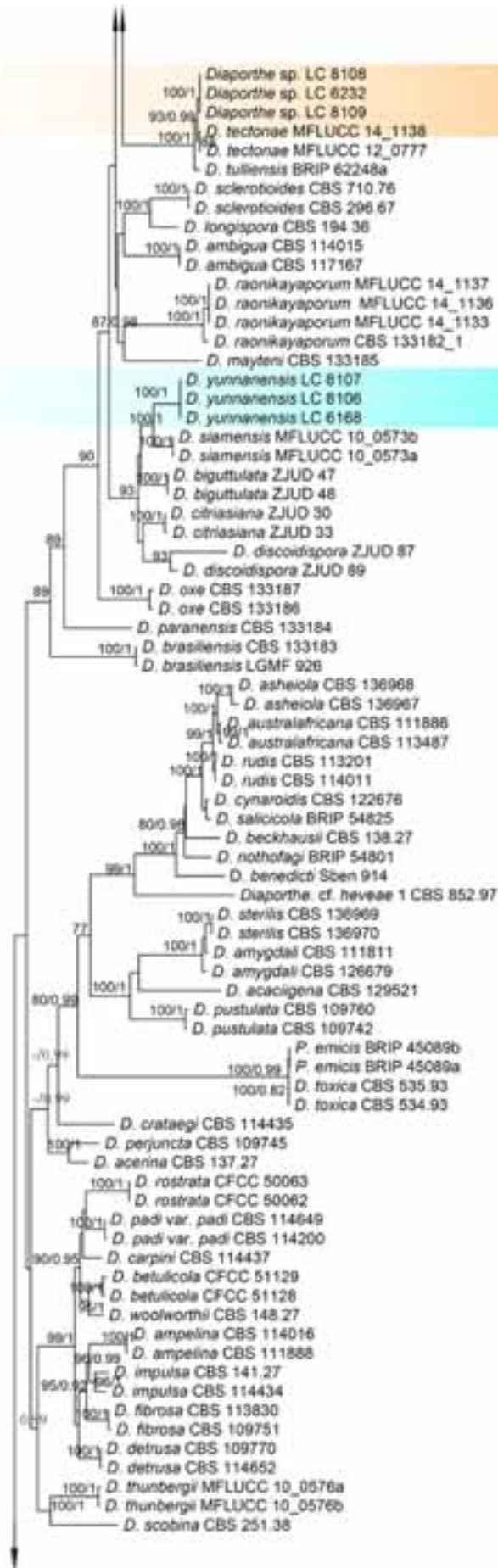


Fig. 2. (Continued).

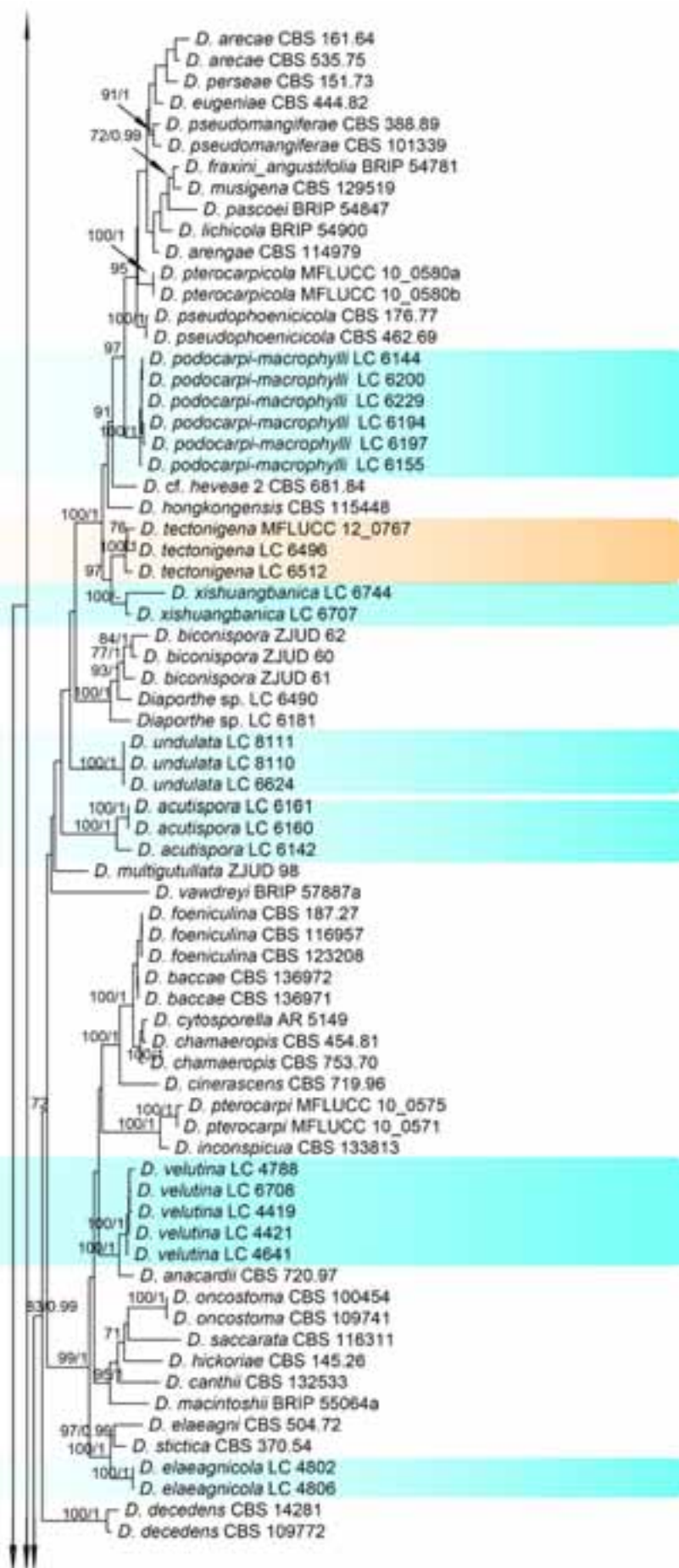


Fig. 2. (Continued).

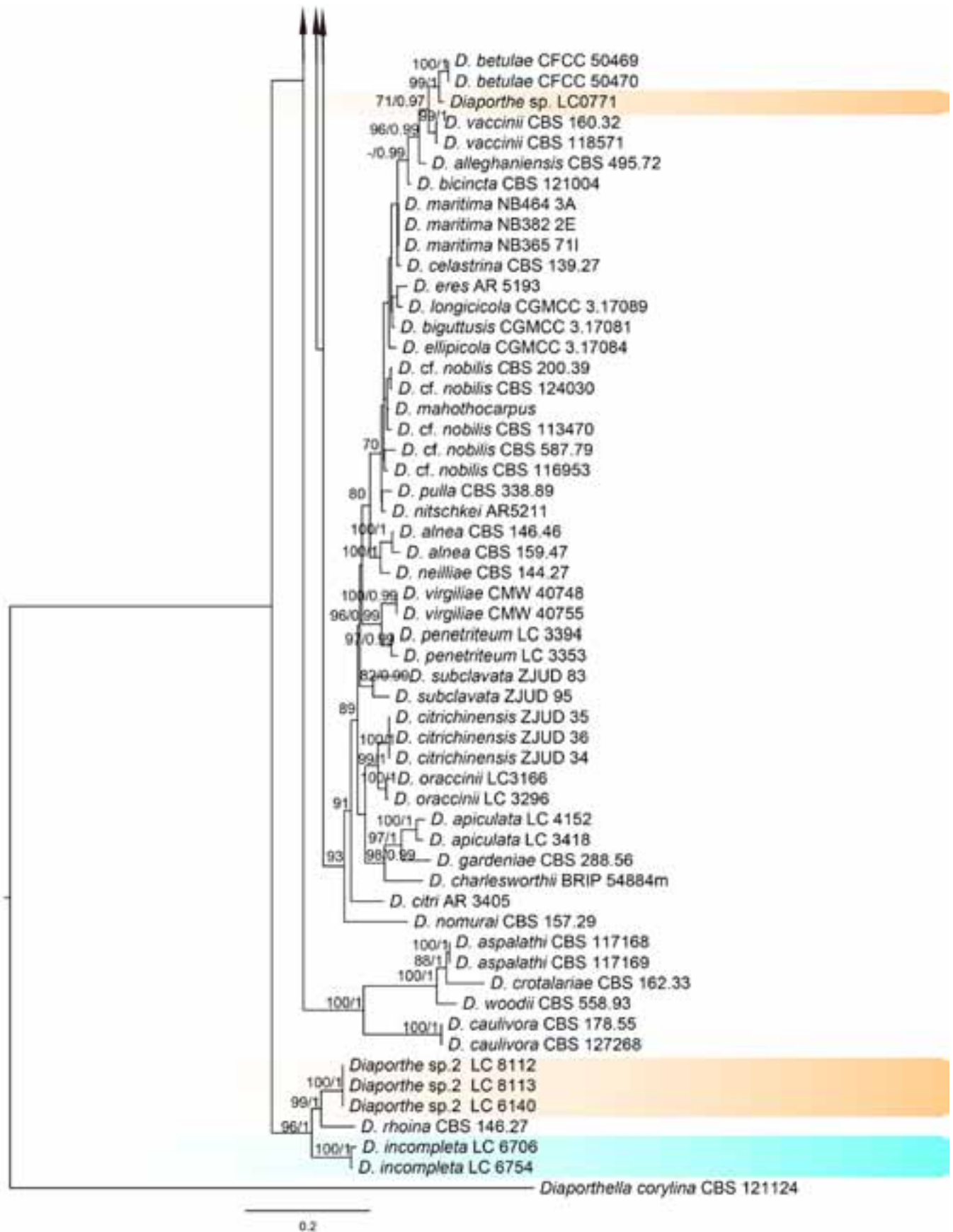


Fig. 2. (Continued).

Table 2. Sources of isolates and GenBank accession numbers used in the phylogenetic analyses of *Diaporthe*. Newly sequenced material is indicated in bold type.

Species names*	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers							References
				ITS	TEF1	TUB	HIS	CAL			
<i>D. acaciigena</i>	CBS 129521 (ex-type)	<i>Acacia retinodes</i>	Mimosaceae	KC343005	KC343731	KC343973	KC343489	KC343247	KC343489	Gomes et al. (2013)	
<i>D. acerina</i>	CBS 137.27	<i>Acer saccharum</i>	Aceraceae	KC343006	KC343732	KC343974	KC343490	KC343248	KC343490	Gomes et al. (2013)	
<i>D. acutispora</i>	CGMCC 3.18285 = LC 6161	<i>Coffea</i> sp., endophyte	Rubiaceae	KX986764	KX999155	KX999195	KX999235	KX999274	KX999235	This study	
	LC 6142	<i>Camellia sasanqua</i>, endophyte	Theaceae	KX986762	KX999153	KX999193	KX999233	KX999272	KX999233	This study	
	LC 6160	<i>Camellia sasanqua</i>, endophyte	Theaceae	KX986800	KX999192	KX999232	KX999271	KX999293	KX999271	This study	
<i>D. alleghaniensis</i>	CBS 495.72 (ex-type)	<i>Betula alleghaniensis</i> , branches	Betulaceae	KC343007	KC343733	KC343975	KC343491	KC343249	KC343491	Gomes et al. (2013)	
<i>D. alnea</i>	CBS 146.46 (ex-type)	<i>Alnus</i> sp.	Betulaceae	KC343008	KC343734	KC343976	KC343492	KC343250	KC343492	Gomes et al. (2013)	
	CBS 159.47	<i>Alnus</i> sp.	Betulaceae	KC343009	KC343735	KC343977	KC343493	KC343251	KC343493	Gomes et al. (2013)	
<i>D. ambigua</i>	CBS 114015	<i>Pyrus communis</i>	Rosaceae	KC343010	KC343736	KC343978	KC343494	KC343252	KC343494	Gomes et al. (2013)	
	CBS 117176	<i>Aspalathus linearis</i> , crown	Fabaceae	KC343011	KC343737	KC343979	KC343495	KC343253	KC343495	Gomes et al. (2013)	
<i>D. ampelina</i>	CBS 114016	<i>Vitis vinifera</i>	Vitaceae	AF230751	AY745056	JX275452	-	AY745026	AY745026	Gomes et al. (2013)	
	CBS 111888	<i>Vitis vinifera</i>	Vitaceae	KC343016	KC343742	KC343984	KC343500	KC343258	KC343500	Gomes et al. (2013)	
<i>D. amygdali</i>	CBS 126679 (ex-type)	<i>Prunus dulcis</i>	Rosaceae	KC343022	KC343748	KC343990	KC343506	KC343264	KC343506	Gomes et al. (2013)	
	CBS 111811	<i>Vitis vinifera</i>	Vitaceae	KC343019	KC343745	KC343987	KC343503	KC343261	KC343503	Gomes et al. (2013)	
<i>D. anacardii</i>	CBS 720.97 (ex-epitype)	<i>Anacardium occidentale</i>	Anacardiaceae	KC343024	KC343750	KC343992	KC343508	KC343266	KC343508	Gomes et al. (2013)	
<i>D. angelicae</i>	CBS 111592 (ex-epitype)	<i>Heracleum sphondylium</i>	Apiaceae	KC343027	KC343743	KC343995	KC343511	KC343269	KC343511	Gomes et al. (2013)	
	CBS 123215	<i>Foeniculum vulgare</i>	Apiaceae	KC343028	KC353754	KC343996	KC343512	KC343270	KC343512	Gomes et al. (2013)	
<i>D. apiculata</i>	LC 4152	<i>Camellia</i> , leaf	Theaceae	KP267915	KP267989	KP293495	KP293562	-	-	Gao et al. (2016)	
	LC 3418, (ex-type)	<i>Camellia sinensis</i> , leaf, endophyte	Theaceae	KP267896	KP267970	KP293476	KP293550	-	-	Gao et al. (2016)	
<i>D. arctii</i>	CBS 136.25	<i>Arctium</i> sp.	Arecaceae	KC343032	KC343758	KC344000	KC343516	KC343273	KC343516	Gomes et al. (2013)	
<i>D. arecae</i>	CBS 535.75	<i>Citrus</i> sp., fruit	Rutaceae	KC343033	KC343759	KC344001	KC343517	KC343275	KC343517	Gomes et al. (2013)	
	CBS 161.64 (ex-isotype)	<i>Areca catechu</i> , fruit	Arecaceae	KC343032	KC343758	KC344000	KC343516	KC343274	KC343516	Gomes et al. (2013)	
<i>D. arengae</i>	CBS 114979 (ex-type)	<i>Arenga engleri</i>	Arecaceae	KC343034	KC343760	KC344002	KC343518	KC343276	KC343518	Gomes et al. (2013)	
<i>D. asheiola</i>	CBS 136967, CPC 16508, (ex-type)	<i>Vaccinium ashei</i>	Ericaceae	KJ160562	KJ160594	KJ160518	-	KJ160542	-	Lombard et al. (2014)	
	CBS 136968, CPC 16511	<i>Vaccinium ashei</i>	Ericaceae	KJ160563	KJ160595	KJ160519	-	KJ160543	-	Lombard et al. (2014)	
<i>D. aspalathi</i>	CBS 117168	<i>Aspalathus linearis</i>	Fabaceae	KC343035	KC343761	KC344003	KC343519	KC343277	KC343519	Gomes et al. (2013)	
	CBS 117169, (ex-type)	<i>Aspalathus linearis</i>	Fabaceae	KC343036	KC343762	KC344004	KC343520	KC343278	KC343520	Gomes et al. (2013)	
<i>D. australafricana</i>	CBS 111886	<i>Vitis vinifera</i>	Vitaceae	KC343038	KC343764	KC344006	KC343522	KC343280	KC343522	Gomes et al. (2013)	
	CBS 113487	<i>Vitis vinifera</i>	Vitaceae	KC343039	KC343765	KC344007	KC343523	KC343281	KC343523	Gomes et al. (2013)	
<i>D. baccae</i>	CBS 136971	<i>Vaccinium corymbosum</i>	Ericaceae	KJ160564	KJ160596	-	-	-	-	Lombard et al. (2014)	
	CBS 136972 (ex-type)	<i>Vaccinium corymbosum</i>	Ericaceae	KJ160565	KJ160597	-	-	-	-	Lombard et al. (2014)	

Table 2. (Continued).

Species names*	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers							References
				ITS	TEF1	TUB	HIS	CAL			
<i>D. batatas</i>	CBS 122.21	<i>Ipomoea batatas</i>	Convolvulaceae	KC343040	KC343766	KC344008	KC343524	KC343282	KC343282	Gomes et al. (2013)	
<i>D. beckhausii</i>	CBS 138.27	<i>Viburnum</i> sp.	Caprifoliaceae	KC343041	KC343767	KC344009	KC343525	KC343283	KC343283	Gomes et al. (2013)	
<i>D. beilharziae</i>	BRIP 54792 (ex-type)	<i>Indigofera australis</i>	Papilionaceae	JX862529	JX862535	KF170921	-	-	-	Thompson et al. (2015)	
<i>D. benedicti</i>	CFCC 50062 (ex-type)	<i>Juglans mandshurica</i>	Juglandaceae	KP208847	KP208853	KP208855	KP208851	KP208849	KP208849	Fan et al. (2015)	
	CFCC 50063	<i>Juglans mandshurica</i>	Juglandaceae	KP208848	KP208854	KP208856	KP208852	KP208850	KP208850	Fan et al. (2015)	
<i>D. betulae</i>	CFCC 50469 (ex-type)	<i>Betula platyphylla</i>	Betulaceae	KT732950	KT733016	KT733020	KT732999	KT732997	KT732997	Du et al. (2016)	
	CFCC 50470	<i>Betula platyphylla</i>	Betulaceae	KT732951	KT733017	KT733021	KT733000	KT732998	KT732998	Du et al. (2016)	
<i>D. betulicola</i>	CFCC 51128 (ex-type)	<i>Betula albosinensis</i>	Betulaceae	KX024653	KX024655	KX024657	KX024661	KX024659	KX024659	Du et al. (2016)	
	CFCC 51129	<i>Betula albosinensis</i>	Betulaceae	KX024654	KX024656	KX024658	KX024662	KX024660	KX024660	Du et al. (2016)	
<i>D. bichincta</i>	DP0659, CBS 121004	<i>Juglans</i> sp., dead wood	Juglandaceae	KC343134	KC343860	KC344102	KC343618	-	-	Udayanga et al. (2014a)	
<i>D. biconisporea</i>	ZJUD 60, CGMCC 3.17250	<i>Citrus sinensis</i>	Rutaceae	KJ490595	KJ490474	KJ490416	KJ490537	-	-	Huang et al. (2015)	
	ZJUD 61, CGMCC 3.17251	<i>Fortunella margarita</i>	Rutaceae	KJ490596	KJ490475	KJ490417	KJ490538	-	-	Huang et al. (2015)	
	ZJUD 62, CGMCC 3.17252	<i>Citrus grandis</i>	Rutaceae	KJ490597	KJ490476	KJ490418	KJ490539	-	-	Huang et al. (2015)	
<i>D. biguttulata</i>	ZJUD 47, CGMCC 3.17248 (ex-type)	<i>Citrus limon</i>	Rutaceae	KJ490582	KJ490461	KJ490403	KJ490524	-	-	Huang et al. (2015)	
	ZJUD 48, CGMCC 3.17249	<i>Citrus limon</i>	Rutaceae	KJ490583	KJ490462	KJ490403	KJ490525	-	-	Huang et al. (2015)	
<i>D. biguttusis</i>	CGMCC 3.17081 (ex-type)	<i>Lithocarpus glabra</i>	Fagaceae	KF576282	KF576257	KF576306	-	-	-	Gao et al. (2015)	
<i>D. brasiliensis</i>	CBS 133183 (ex-type)	<i>Aspidosperma tomentosus</i>	Apocynaceae	KC343042	KC343768	KC344010	KC343526	KC343284	KC343284	Gomes et al., 2013	
	LGMF 926	<i>Aspidosperma tomentosus</i>	Apocynaceae	KC343043	KC343769	KC344011	KC343527	KC343285	KC343285	Gomes et al., 2013	
<i>D. canthii</i>	CBS 132533 (ex-type)	<i>Canthium inerme</i>	Rubiaceae	JX069864	KC843120	KC843230	-	KC843174	KC843174	Du et al. (2016)	
<i>D. carpini</i>	CBS 114437	<i>Carpinus betulus</i>	Corylaceae	KC343044	KC343770	KC344012	KC343528	KC343286	KC343286	Gomes et al. (2013)	
<i>D. caulivora</i>	CBS 127268 (ex-neotype)	<i>Glycine max</i>	Fabaceae	KC343045	KC343771	KC344013	KC343529	KC343287	KC343287	Gomes et al. (2013)	
	CBS 178.55	<i>Glycine soja</i>	Fabaceae	KC343046	KC343772	KC344014	KC343530	KC343288	KC343288	Gomes et al. (2013)	
<i>D. celastrina</i>	CBS 139.27	<i>Celastrus scandens</i>	Celastraceae	KC343047	KC343773	KC344015	KC343531	-	-	Gomes et al. (2013)	
<i>D. cf. heveae 1</i>	CBS 852.97	<i>Hevea brasiliensis</i>	Euphorbiaceae	KC343116	KC343842	KC344084	KC343600	KC343358	KC343358	Gomes et al. (2013)	
<i>D. cf. heveae 2</i>	CBS 681.84	<i>Hevea brasiliensis</i> , leaf	Euphorbiaceae	KC343117	KC343843	KC344085	KC343601	KC343359	KC343359	Gomes et al. (2013)	
<i>D. chamaeropsis</i>	CBS 454.81	<i>Chamaerops humilis</i> , dead part of leaf	Areaceae	KC343048	KC343774	KC344016	KC343532	KC343290	KC343290	Gomes et al. (2013)	
	CBS 753.70	<i>Spartium junceum</i> , dead branch	Fabaceae	KC343049	KC343775	KC344017	KC343533	KC343291	KC343291	Gomes et al. (2013)	
<i>D. charlesworthii</i>	BRIP 4884m (ex-type)	<i>Rapistrum rugostrum</i>	Brassicaceae	KJ197288	KJ197250	KJ197268	-	-	-	Thompson et al. (2015)	
<i>D. cinerascens</i>	CBS 719.96	<i>Ficus carica</i>	Moraceae	KC343050	KC343776	KC344018	KC343534	KC343292	KC343292	Gomes et al. (2013)	
<i>D. citri</i>	CBS 230.52	<i>Citrus sinensis</i>	Rutaceae	KC343052	KC343778	KC344020	KC343536	KC343294	KC343294	Gomes et al. (2013)	
	CBS 199.39	-	-	KC343051	KC343777	KC344019	KC343535	KC343293	KC343293	Gomes et al. (2013)	
	AR 3405	<i>Citrus</i> sp.	Rutaceae	KC843311	KC843071	KC843187	KJ420881	-	-	Udayanga et al. (2014b)	

Table 2. (Continued).

Species names*	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers				References	
				ITS	TEF1	TUB	HIS		CAL
<i>D. citrifasiana</i>	ZJUD 30 (ex-type)	<i>Citrus unshiu</i> , dead wood	Rutaceae	JQ954645	JQ954663	KC357459	-	KC357491	Huang et al. (2015)
	ZJUD 33	<i>Citrus paradise</i> , stem-end rot fruit	Rutaceae	JQ954658	JQ972716	KC357460	-	KC357493	Huang et al. (2015)
<i>D. citrichinensis</i>	ZJUD 34	<i>Citrus</i> sp.	Rutaceae	JQ954648	JQ954666	-	-	KC357494	Huang et al. (2015)
	ZJUD 35	<i>Citrus unshiu</i> , dead wood	Rutaceae	JQ954649	JQ954667	KC357461	-	KC357495	Huang et al. (2015)
	ZJUD 36	<i>Citrus unshiu</i> , dead wood	Rutaceae	KC357556	KC357525	KC357462	-	KC357496	Huang et al. (2015)
	LC3083 (ex-type)	<i>Camellia sinensis</i> , leaf, endophyte	Theaceae	KP267854	KP267928	KP293434	KP293508	-	Gao et al. (2016)
<i>D. compacta</i>	LC3084	<i>Camellia sinensis</i> , leaf, endophyte	Theaceae	KP267855	KP267929	KP293435	KP293509	-	Gao et al. (2016)
	CBS 124654	<i>Convolvulus arvensis</i>	Convolvulaceae	KC343054	KC343780	KC344022	KC343538	KC343296	Huang et al. (2015)
<i>D. crataegi</i>	CBS 114435	<i>Crataegus oxyacantha</i>	Rosaceae	KC343055	KC343781	KC344023	KC343539	KC343297	Gomes et al. (2013)
<i>D. crotalariae</i>	CBS 162.33 (ex-type)	<i>Crotalaria spectabilis</i>	Fabaceae	KC343056	KC343782	KC344024	KC343540	KC343298	Gomes et al. (2013)
<i>D. cuppatae</i>	CBS 117499	<i>Aspalathus linearis</i>	Fabaceae	KC343057	KC343783	KC344025	KC343541	KC343299	Gomes et al. (2013)
<i>D. cynaroidis</i>	CBS 122676	<i>Protea cynaroides</i>	Proteaceae	KC343058	KC343784	KC344026	KC343542	KC343300	Gomes et al. (2013)
<i>D. cytosporella</i>	AR 5149	<i>Citrus sinensis</i>	Rutaceae	KC843309	KC843118	KC843222	-	KC843143	Udayanga et al. (2014b)
<i>D. decedens</i>	CBS 114281	<i>Corylus avellana</i>	Corylaceae	KC343060	KC343786	KC344028	KC343544	KC343302	Gomes et al. (2013)
<i>D. detrusa</i>	CBS 109772	<i>Corylus avellana</i>	Corylaceae	KC343059	KC343785	KC344027	KC343543	KC343301	Gomes et al. (2013)
	CBS 109770	<i>Berberis vulgaris</i>	Berberidaceae	KC343061	KC343787	KC344029	KC343545	KC343303	Gomes et al. (2013)
	CBS 114652	<i>Berberis vulgaris</i>	Berberidaceae	KC343062	KC343788	KC344030	KC343546	KC343304	Gomes et al. (2013)
	ZJUD 87, CGMCC 3.17254	<i>Citrus sinensis</i>	Rutaceae	KJ490622	KJ490501	KJ490443	KJ490564	-	Huang et al. (2015)
<i>D. discoidispora</i>	ZJUD 89, CGMCC 3.17255	<i>Citrus unshiu</i>	Rutaceae	KJ490624	KJ490503	KJ490445	KJ490566	-	Huang et al. (2015)
	CBS 504.72	<i>Elaeagnus</i> sp., twig	Elaeagnaceae	KC343064	KC343790	KC344032	KC343548	KC343306	Gomes et al. (2013)
<i>D. elaeagni-glabrae</i>	CGMCC 3.18287 = LC 4802	<i>Elaeagnus glabra</i>, pathogen	Elaeagnaceae	KX986779	KX999171	KX999212	KX999251	KX999281	This study
	LC 4806	<i>Elaeagnus glabra</i>, pathogen	Elaeagnaceae	KX986780	KX999172	KX999213	KX999252	KX999282	This study
<i>D. ellipicola</i>	CGMCC 3.17084 (ex-type)	<i>Lithocarpus glabra</i> , diseased leaves	Fagaceae	KF576270	KF576245	KF576291	-	-	Gao et al. (2015)
<i>D. endophytica</i>	CBS 133811 (ex-type)	<i>Schinus terebinthifolius</i>	Anacardiaceae	KC343065	KC343791	KC344033	KC343549	KC343307	Gomes et al. (2013)
	LGMF 911	<i>Schinus terebinthifolius</i>	Anacardiaceae	KC343066	KC343792	KC344034	KC343550	KC343308	Gomes et al. (2013)
<i>D. eres</i>	AR5193, CBS 13859 (ex-epitype)	<i>Ulmus laevis</i>	Ulmaceae	KJ210529	KJ210550	KJ420799	KJ420850	-	Udayanga et al. (2014a)
	CBS 113470	<i>Castanea sativa</i>	Fagaceae	KC343146	KC343872	KC344114	KC343630	-	Udayanga et al. (2014a)
<i>D. eugeniae</i>	CBS 444.82	<i>Eugenia aromatica</i> , leaf	Myrtaceae	KC343098	KC343824	KC344066	KC343582	KC343340	Gomes et al. (2013)
<i>D. fibrosa</i>	CBS 109751	<i>Rhamnus cathartica</i>	Rhamnaceae	KC343099	KC343825	KC344067	KC343583	KC343341	Gomes et al. (2013)
	CBS 113830	<i>Rhamnus cathartica</i>	Rhamnaceae	KC343100	KC343826	KC344068	KC343584	KC343342	Gomes et al. (2013)

Table 2. (Continued).

Species names	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers						References
				ITS	TEF1	TUB	HIS	CAL		
<i>D. foeniculina</i>	CBS 116957	<i>Pyrus pyrifolia</i>	Rosaceae	KC343103	KC343829	KC344071	KC343587	KC343345	Gomes et al. (2013)	
	CBS 187.27 (ex-type of <i>P. theicola</i>)	<i>Camellia sinensis</i> , leaves and branches	Theaceae	KC343107	KC343833	KC344075	KC343591	KC343349	Gomes et al. (2013)	
	CBS 123208	<i>Foeniculum vulgare</i>	Apiaceae	KC343104	KC343830	KC344072	KC343588	KC343346	Gomes et al. (2013)	
<i>D. fraxini-angustifolia</i>	BRIP 54781 (ex-epitype)	<i>Fraxinus-angustifolia</i> subsp. <i>oxyca</i>	Oleaceae	JX862528	JX852534	KF170920	-	-	Tan et al. (2013)	
<i>D. ganjae</i>	CBS 180.91 (ex-type)	<i>Cannabis sativa</i> , dead leaf	Cannabaceae	KC343112	KC343838	KC344080	KC343596	KC343354	Gomes et al. (2013)	
<i>D. gardeniae</i>	CBS 288.56	<i>Gardenia florida</i> , stem	Rubiaceae	KC343113	KC343839	KC344081	KC343597	KC343355	Gomes et al. (2013)	
<i>D. goulteri</i>	BRIP 55657a (ex-type)	<i>Helianthus annuus</i>	Asteraceae	KJ197289	KJ197252	KJ197270	-	-	Thompson et al. (2015)	
<i>D. guiyae</i>	BRIP 54025 (ex-type)	<i>Helianthus annuus</i>	Asteraceae	JF431299	JN645803	KJ197271	-	-	Thompson et al. (2015)	
<i>D. helianthi</i>	CBS 344.94	<i>Helianthus annuus</i>	Asteraceae	KC343114	KC343840	KC344082	KC343598	KC343356	Gomes et al. (2013)	
	CBS 592.81 (ex-type)	<i>Helianthus annuus</i>	Asteraceae	KC343115	KC343841	KC344083	KC343599	KC343357	Gomes et al. (2013)	
<i>D. helicis</i>	AR 5211	<i>Hedera helix</i>	Araliaceae	KJ210538	KJ210559	KJ420828	KJ420875	KJ435043	Udayanga et al. (2014a)	
<i>D. hickoriae</i>	CBS 145.26 (ex-epitype)	<i>Carya glabra</i>	Juglandaceae	KC343118	KC343844	KC344086	KC343602	KC343360	Gomes et al. (2013)	
<i>D. hongkongensis</i>	CBS 115448 (ex-type)	<i>Dichroa febrifuga</i> , fruit	Hydrangeaceae	KC343119	KC343845	KC344087	KC343603	KC343361	Gomes et al. (2013)	
<i>D. hordei</i>	CBS 481.92	<i>Hordeum vulgare</i>	Poaceae	KC343120	KC343846	KC344088	KC343604	KC343362	Gomes et al. (2013)	
<i>D. impulsae</i>	CBS 114434	<i>Sorbus aucuparia</i>	Rosaceae	KC343121	KC343847	KC344089	KC343605	KC343363	Gomes et al. (2013)	
	CBS 141.27	<i>Sorbus americana</i>	Rosaceae	KC343122	KC343848	KC344090	KC343606	KC343364	Gomes et al. (2013)	
<i>D. incompleta</i>	CGMCC 3.18288 = LC 6754	<i>Camellia sinensis</i>, pathogen	Theaceae	KX996794	KX999186	KX999226	KX999265	KX999289	This study	
	LC 6706	<i>Camellia sinensis</i>, pathogen	Theaceae	KX996793	KX999185		KX999264	KX999288	This study	
<i>D. inconspicua</i>	CBS 133813 (ex-type)	<i>Maytenus ilicifolia</i> , endophytic in petiole	Celastraceae	KC343123	KC343849	KC344091	KC343607	KC343365	Gomes et al. (2013)	
<i>D. infecunda</i>	CBS 133812 (ex-type)	<i>Schinus terebinthifolius</i>	Anacardiaceae	KC343126	KC343852	KC344094	KC343610	KC343368	Gomes et al. (2013)	
	LGMF 908	<i>Schinus terebinthifolius</i>	Anacardiaceae	KC343127	KC343853	KC344095	KC343611	KC343369	Gomes et al. (2013)	
<i>D. kongii</i>	BRIP 54031 (ex-type)	<i>Helianthus annuus</i>	Asteraceae	JF431301	JN645797	KJ197272	-	-	Thompson et al. (2011)	
<i>D. lichicola</i>	BRIP 54900 (ex-type)	<i>Litchi chinensis</i>	Sapindaceae	JX862533	JX862539	KF170925	-	-	Tan et al. (2013)	
<i>D. longicicola</i>	CGMCC 3.17089 (ex-type)	<i>Lithocarpus glabra</i>	Fagaceae	KF576267	KF576242	KF576291	-	-	Gao et al. (2015)	
<i>D. longicolla</i>	FAU 599	<i>Glycine max</i>	Fabaceae	KJ590728	KJ590767	KJ610883	KJ659188	-	Udayanga et al. (2015)	
<i>D. longispora</i>	CBS 194.36 (ex-type)	<i>Ribes</i> sp.	Grossulariaceae	KC343135	KC343861	KC344103	KC343619	KC343377	Gomes et al. (2013)	
<i>D. lusitanicae</i>	CBS 123212 (ex-type)	<i>Foeniculum vulgare</i>	Apiaceae	KC343136	KC343862	KC344104	KC343620	-	Gomes et al. (2013)	
	CBS 123213	<i>Foeniculum vulgare</i>	Apiaceae	KC343137	KC343863	KC344105	KC343621	KC343379	Gomes et al. (2013)	
<i>D. macintoshii</i>	BRIP 55064a	<i>Rapistrum rugostrum</i>	Brassicaceae	KJ197290	KJ197251	KJ197269	-	-	Thompson et al. (2015)	
<i>D. mahothocarpus</i>	CGMCC 3.15181	<i>Lithocarpus glabra</i>	Fagaceae	KC153096	KC153087	-	-	-	Gao et al. (2014)	
<i>D. manihoti</i>	CBS 505.76	<i>Manihot utilissima</i> , leaves	Euphorbiaceae	KC343138	KC343864	KC344106	KC343622	KC343380	Gomes et al. (2013)	

Table 2. (Continued).

Species names	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers							References
				ITS	TEF1	TUB	HIS	CAL			
<i>D. maritima</i>	NB 382-2E	<i>Picea rubens</i> needle	Pinaceae	KU552026	KU552024	KU574614	-	-	-	Tanney et al. (2016)	
	NB 463-3A	<i>Picea rubens</i> needle	Pinaceae	KU552027	KU552022	KU574616	-	-	-	Tanney et al. (2016)	
	NB 365-711 (ex-type)	<i>Picea rubens</i> needle	Pinaceae	KU552025	KU552023	KU574615	-	-	-	Tanney et al. (2016)	
<i>D. masirevicii</i>	BRIP 57330	<i>Chrysanthemoides monilifera</i> subsp. <i>rotundata</i>	Rosaceae	KJ197275	KJ197237	KJ197255	-	-	-	Huang et al. (2015)	
	BRIP 57892a (ex-type)	<i>Helianthus annuus</i>	Asteraceae	KJ197277	KJ197239	KJ197257	-	-	-	Huang et al. (2015)	
<i>D. mayteni</i>	CBS 133185 (ex-type)	<i>Maytenus illicolia</i>	Celastraceae	KC343139	KC343865	KC344107	KC343623	KC343381	-	Gomes et al. (2013)	
<i>D. megalospora</i>	CBS 143.27	<i>Sambucus canadensis</i>	Caprifoliaceae	KC343140	KC343866	KC344108	KC343624	KC343382	-	Gomes et al. (2013)	
<i>D. melonis</i>	CBS 435.87	<i>Glycine soja</i>	Fabaceae	KC343141	KC343867	KC344109	KC343625	KC343383	-	Gomes et al. (2013)	
	CBS 507.78 (ex-isotype)	<i>Cucumis melo</i>	Cucurbitaceae	KC343142	KC343868	KC344110	KC343626	KC343384	-	Gomes et al. (2013)	
<i>D. middletonii</i>	BRIP 57329	<i>Chrysanthemoides monilifera</i> subsp. <i>rotundata</i>	Rosaceae	KJ197285	KJ197247	KJ197265	-	-	-	Thompson et al. (2015)	
	BRIP 54884e (ex-type)	<i>Rapistrum rugostrum</i>	Brassicaceae	KJ197286	KJ197248	KJ197266	-	-	-	Thompson et al. (2015)	
<i>D. miriciae</i>	BRIP 55662c	<i>Glycine max</i>	Fabaceae	KJ197283	KJ197245	KJ197263	-	-	-	Thompson et al. (2015)	
	BRIP 54736j (ex-type)	<i>Helianthus annuus</i>	Asteraceae	KJ197282	KJ197244	KJ197262	-	-	-	Thompson et al. (2015)	
	BRIP 56918a	<i>Vigna radiata</i>	Papilionaceae	KJ197284	KJ197246	KJ197264	-	-	-	Thompson et al. (2015)	
<i>D. multiguttulata</i>	ZJUD 98	<i>Citrus grandis</i>	Rosaceae	KJ490633	KJ490512	KJ490454	KJ490575	-	-	Huang et al. (2015)	
<i>D. musigena</i>	CBS 129519; CPC 17026 (ex-type)	<i>Musa</i> sp., leaves	Musaceae	KC343143	KC343869	KC344111	KC343627	KC343385	-	Gomes et al. (2013)	
<i>D. neilliae</i>	CBS 144.27	<i>Spiraea</i> sp.	Rosaceae	KC343144	KC343870	KC344112	KC343628	KC343386	-	Udayanga et al. (2014a)	
<i>D. neoarctii</i>	CBS 109490 (ex-type)	<i>Ambrosia trifida</i>	Asteraceae	KC343145	KC343871	KC344113	KC343629	KC343387	-	Gomes et al. (2013)	
<i>D. neoaraonikayapurum</i>	MFLUCC 14-1136	<i>Tectona grandis</i>	Verbenaceae	KU712449	KU749369	KU743988	-	-	-	Doilom et al. (2017)	
	MFLUCC 14-1137	<i>Tectona grandis</i>	Verbenaceae	KU712450	KU749370	KU743989	-	-	-	Doilom et al. (2017)	
	MFLUCC 14-1133	<i>Tectona grandis</i>	Verbenaceae	KU712448	KU749368	KU743987	-	-	-	Doilom et al. (2017)	
<i>D. nobilis</i>	CBS 200.39	<i>Laurus nobilis</i> , stem	Lauraceae	KC343151	KC343877	KC344119	KC343635	KC343393	-	Gomes et al. (2013)	
<i>D. nomurai</i>	CBS 157.29	<i>Morus</i> sp.	Moraceae	KC343154	KC343880	KC344122	KC343638	KC343396	-	Gomes et al. (2013)	
<i>D. nothofagi</i>	BRIP 54801 (ex-type)	<i>Nothofagus cunninghamii</i>	Fagaceae	JX862530	JX862536	KF170922	-	-	-	Tan et al. (2013)	
<i>D. novem</i>	CBS 127269	<i>Glycine max</i>	Fabaceae	KC343155	KC343881	KC344123	KC343639	KC343397	-	Gomes et al. (2013)	
	CBS 127270 (ex-type)	<i>Glycine max</i>	Fabaceae	KC343156	KC343882	KC344124	KC343640	KC343398	-	Gomes et al. (2013)	
<i>D. oncostoma</i>	CBS 100454	<i>Robinia pseudoacacia</i> , leaf spot	Fabaceae	KC343160	KC343886	KC344128	KC343644	KC343402	-	Gomes et al. (2013)	
	CBS 109741	<i>Robinia pseudoacacia</i>	Fabaceae	KC343161	KC343887	KC344129	KC343645	KC343403	-	Gomes et al. (2013)	
<i>D. oraccinii</i>	LC 3166 (ex-type)	<i>Camellia sinensis</i> , leaf, endophyte	Theaceae	KP267863	KP267937	KP293443	KP293517	-	-	Gao et al. (2016)	
	LC 3296	<i>Camellia sinensis</i> , leaf, endophyte	Theaceae	KP267884	KP267958	KP293464	KP293538	-	-	Gao et al. (2016)	

Table 2. (Continued).

Species names	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers					References
				ITS	TEF1	TUB	HIS	CAL	
<i>D. ovalispora</i>	ZJUD 93, CGMCC 3.17256	Citrus limon	Rosaceae	KJ490628	KJ490507	KJ490449	KJ490570	-	Huang et al. (2015)
<i>D. oxe</i>	CBS 133186 (ex-type)	Maytenus ilicifolia	Celastraceae	KC343164	KC343890	KC344132	KC343648	KC343406	Gomes et al. (2013)
	CBS 133187	Maytenus ilicifolia	Celastraceae	KC343165	KC343891	KC344133	KC343649	KC343407	Gomes et al. (2013)
<i>D. padi</i> var. <i>padi</i>	CBS 114200	Prunus padus	Rosaceae	KC343169	KC343895	KC344137	KC343653	KC343411	Gomes et al. (2013)
	CBS 114649	Alnus glutinosa	Betulaceae	KC343170	KC343896	KC344138	KC343654	KC343412	Gomes et al. (2013)
<i>D. paranensis</i>	CBS 133184 (ex-type)	Maytenus ilicifolia	Celastraceae	KC343171	KC343897	Kc344139	KC343655	KC343413	Gomes et al. (2013)
<i>D. pascoei</i>	BRIP 54847 (ex-type)	Persea americana	Lauraceae	JX862532	JX862538	KF170924	-	-	Tan et al. (2013)
<i>D. penetrifera</i>	LC 3353	Camellia sinensis, leaf	Theaceae	KP714505	KP714517	KP714529	KP714493	-	Gao et al. (2016)
	LC 3394	Camellia sinensis, leaf	Theaceae	KP267893	KP267967	KP293473	KP293547	-	Gao et al. (2016)
<i>D. perijuncta</i>	CBS 109745 (ex-type)	Ulmus glabra	Ulmaceae	KC343172	KC343898	KC344140	KC343656	KC343414	Gomes et al. (2013)
<i>D. perniciososa</i>	CBS 124030	Malus pumila, bark	Rosaceae	KC343149	KC343875	KC344117	KC343633	KC343391	Gomes et al. (2013)
<i>D. perseae</i>	CBS 151.73	Persea gratissima, young fruit	Lauraceae	KC343173	KC343899	KC344141	KC343657	KC343415	Gomes et al. (2013)
<i>D. phaseolorum</i>	AR 4203, CBS 139281	Phaseolus vulgaris	Fabaceae	KJ590738	KJ590739	KJ610893	KJ659220	-	Huang et al. (2015)
	CBS 116019	Caperonia palustris	Euphorbiaceae	KC343175	KC343901	KC344143	KC343659	KC343417	Gomes et al. (2013)
	CBS 116020	Aster exilis	Asteraceae	KC343176	KC343902	KC344144	KC343660	KC343418	Gomes et al. (2013)
<i>D. podocarpimacrophylli</i>	CGMCC 3.18281 = LC 6155	Podocarpus macrophyllus, endophyte	Podocarpaceae	KX986774	KX999167	KX999207	KX999246	KX999278	This study
	LC 6144	Podocarpus macrophyllus, endophyte	Podocarpaceae	KX986773	KX999166	KX999206	KX999245	-	This study
	LC 6194	Podocarpus macrophyllus, endophyte	Podocarpaceae	KX986765	KX999156	KX999196	KX999236	KX999275	This study
	LC 6197	Podocarpus macrophyllus, endophyte	Podocarpaceae	KX986777	KX999170	KX999210	KX999249	KX999279	This study
	LC 6200	Podocarpus macrophyllus, endophyte	Podocarpaceae	KX986769	KX999161	KX999201	KX999240	KX999276	This study
<i>D. pseudomangiferae</i>	LC 6229	Olea europaea, endophytes	Oleaceae	KX986771	KX999164	KX999204	KX999243	KX999277	This study
	CBS 101339 (ex-type)	Mangifera indica	Anacardiaceae	KC343181	KC343907	KC344149	KC343665	KC343423	Gomes et al. (2013)
	CBS 388.89	Mangifera indica, peel of fruit	Anacardiaceae	KC343182	KC343908	KC344150	KC343666	KC343424	Gomes et al. (2013)
<i>D. pseudophoenicola</i>	CBS 462.69 (ex-type)	Phoenix dactylifera, dead tops of green leaves	Anacardiaceae	KC343184	KC343910	KC344152	KC343668	KC343426	Gomes et al. (2013)
	CBS 176.77	Mangifera indica, showing dieback	Anacardiaceae	KC343183	KC343909	KC344151	KC343667	KC343425	Gomes et al. (2013)
<i>D. pterocarpi</i>	MFLUCC 10-0571	Pterocarous indicus	Papilionaceae	JQ619899	JX275416	JX275460	-	JX197451	Udayanga et al. (2012)
	MFLUCC 10-0575	Pterocarous indicus	Papilionaceae	JQ619901	JX275418	JX275462	-	JX197453	Udayanga et al. (2012)

Table 2. (Continued).

Species names	Culture collection no.	Isolation sources	Host family	ITS	GenBank Accession Numbers				References
					TEF1	TUB	HIS	CAL	
<i>D. pterocarpicola</i>	MFLUCC 10-0580a (ex-type)	<i>Pterocarpus indicus</i>	Papilionaceae	JQ619887	JX275403	JX275441	-	JX197433	Udayanga et al. (2012)
	MFLUCC 10-0580b	<i>Pterocarpus indicus</i>	Papilionaceae	JQ619888	JX275404	JX275442	-	JX197434	Udayanga et al. (2012)
<i>D. pulla</i>	CBS 338.89	<i>Hedera helix</i>	Araliaceae	KC343152	KC343878	KC344120	KC343636	-	Udayanga et al. (2014a)
<i>D. pustulata</i>	CBS 109742	<i>Acer pseudoplatanus</i>	Aceraceae	KC343185	KC343911	KC344153	KC343669	KC343427	Gomes et al. (2013)
	CBS 109760	<i>Acer pseudoplatanus</i>	Aceraceae	KC343186	KC343912	KC344154	KC343670	KC343428	Gomes et al. (2013)
<i>D. raonikayaporum</i>	CBS 133182 (ex-type)	<i>Spondias mombin</i>	Anacardiaceae	KC343188	KC343914	KC344156	KC343672	KC343430	Gomes et al. (2013)
<i>D. rhoina</i>	CBS 146.27	<i>Rhus toxicodendron</i>	Anacardiaceae	KC343189	KC343915	KC344157	KC343673	KC343431	Gomes et al. (2013)
<i>D. rudis</i>	CBS 113201 (ex-type)	<i>Vitis vinifera</i>	Vitaceae	KC343234	KC343960	KC344202	KC343718	KC343476	Machingambi et al. (2015)
	CBS 114011	<i>Vitis vinifera</i>	Vitaceae	KC343235	KC343961	KC344203	KC343718	KC343477	Machingambi et al. (2015)
<i>D. saecarata</i>	CBS 116311 (ex-type)	<i>Protea repens</i> , cankers	Proteaceae	KC343190	KC343916	KC344158	KC343674	KC343432	Gomes et al. (2013)
<i>D. sackstonii</i>	BRIP 54669b (ex-type)	<i>Helianthus annuus</i>	Asteraceae	KJ197287	KJ197249	KJ197267	-	-	Gomes et al. (2013)
<i>D. salicicola</i>	BRIP 54825 (ex-type)	<i>Salix purpurea</i>	Salicaceae	JX862531	JX862537	KF170923	-	-	Gomes et al. (2013)
<i>D. schini</i>	LGMF 910, CPC 20286	<i>Schinus terebinthifolius</i> , endophytic in leaf	Anacardiaceae	KC343192	KC343918	KC344160	KC343676	KC343434	Thompson et al. (2015)
	CBS 133181 (ex-type)	<i>Schinus terebinthifolius</i> , endophytic in leaf	Anacardiaceae	KC343191	KC343917	KC344159	KC343675	KC343433	Tan et al. (2013)
<i>D. sclerotoides</i>	CBS 296.67 (ex-type)	<i>Cucumis sativus</i>	Cucurbitaceae	KC343193	KC343919	KC344161	KC343677	KC343435	Gomes et al. (2013)
	CBS 710.76	<i>Cucumis sativus</i>	Cucurbitaceae	KC343194	KC343920	KC344162	KC343678	KC343436	Gomes et al. (2013)
<i>D. scobina</i>	CBS 251.38	<i>Fraxinus Excelsior</i> , living and dead twig	Oleaceae	KC343195	KC343921	KC344163	KC343679	KC343437	Gomes et al. (2013)
<i>D. serafinae</i>	BRIP 55665a (ex-type)	<i>Helianthus annuus</i>	Asteraceae	KJ197274	KJ197236	KJ197254	-	-	Gomes et al. (2013)
	BRIP 54136	<i>Lupinus albus</i> "Rosetta"	Fabaceae	KJ197273	KJ197235	KJ197253	-	-	Gomes et al. (2013)
<i>D. siamensis</i>	MFLUCC 10_0573a	<i>Dasymaschalon</i> sp.	Annonaceae	JQ619879	JX275393	JX275429	-	-	Thompson et al. (2015)
	MFLUCC 10_0573b	<i>Dasymaschalon</i> sp.	Annonaceae	JQ619880	JX275395	JX275430	-	-	Thompson et al. (2015)
<i>D. sojae</i>	CBS 100.87	<i>Glycine soja</i>	Fabaceae	KC343196	KC343922	KC344164	KC343680	KC343438	Udayanga et al. (2012)
	CBS 116017	<i>Euphorbia nutans</i>	Euphorbiaceae	KC343197	KC343923	KC344165	KC343681	KC343439	Udayanga et al. (2012)
	FAU 635	<i>Glycine max</i>	Fabaceae	KJ590719	KJ590762	KJ610875	KJ659208	-	Gomes et al. (2013)
<i>D. sterilis</i>	CBS 136969 (ex-type)	<i>Vaccinium corymbosum</i>	Ericaceae	KJ160579	KJ160611	KJ160528	-	KJ160548	Gomes et al. (2013)
	CBS 136970	<i>Vaccinium corymbosum</i>	Ericaceae	KJ160580	KJ160612	KJ160529	-	KJ160549	Huang et al. (2015)
<i>D. stewartii</i>	CBS 193.36	-	-	FJ889448	GQ250324	-	-	-	Lombard et al. (2014)
<i>D. stfifica</i>	CBS 370.54	<i>Buxus sempervirens</i> , dead twig	Buxaceae	KC343212	KC343938	KC344180	KC343696	KC343454	Lombard et al. (2014)
<i>D. subclavata</i>	ZJUD 83, CGMCC 3.17253	<i>Citrus grandis</i> cv. <i>Shatianyou</i>	Rosaceae	KJ490618	KJ490497	KJ490439	KJ490560	-	Udayanga et al. (2011)

Table 2. (Continued).

Species names*	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers						References
				ITS	TEF1	TUB	HIS	CAL		
<i>D. subordinaria</i>	ZJUD 95, CGMCC 3.17257	<i>Citrus unshiu</i>	Rosaceae	KJ490630	KJ490509	KJ490451	KJ490572	-	Gomes et al. (2013)	
	CBS 101711	<i>Plantago lanceolata</i>	Plantaginaceae	KC343213	KC343939	KC344181	KC343697	KC343455	Huang et al. (2015)	
	CBS 464.90	<i>Plantago lanceolata</i>	Plantaginaceae	KC343214	KC343940	KC344182	KC343698	KC343456	Huang et al. (2015)	
<i>D. tecomae</i>	CBS 100547	<i>Tabebuia</i> sp.	Bignoniaceae	KC343215	KC343941	KC344183	KC343699	KC343457	Gomes et al. (2013)	
<i>D. tectonae</i>	MFLUCC 12-0777	<i>Tectona grandis</i>	Verbenaceae	KU712430	KU749359	KU743977	-	KU749345	Gomes et al. (2013)	
	MFLUCC 14-1138	<i>Tectona grandis</i>	Verbenaceae	KU712437	KU749365	KU743984	-	KU749352	Gomes et al. (2013)	
<i>D. tectonendophytica</i>	MFLUCC 13-0471	<i>Tectona grandis</i>	Verbenaceae	KU712439	KU749367	KU743986	-	KU749354	Doilom et al. (2017)	
<i>D. tectonigena</i>	MFLUCC 12-0767	<i>Tectona grandis</i>	Verbenaceae	KU712429	KU749371	KU743976	-	KU749358	Doilom et al. (2017)	
<i>D. terebinthifolii</i>	CBS 133180	<i>Schinus terebinthifolius</i>	Anacardiaceae	KC343216	KC343942	KC344184	KC343700	KC343458	Doilom et al. (2017)	
	LGMF 907	<i>Schinus terebinthifolius</i>	Anacardiaceae	KC343217	KC343943	KC344185	KC343701	KC343459	Doilom et al. (2017)	
<i>D. thunbergii</i>	MFLUCC 10_0756a	<i>Thunbergia laurifolia</i>	Acanthaceae	JQ619893	JX275409	JX275449	-	JX197440	Doilom et al. (2017)	
	MFLUCC 10_0756b	<i>Thunbergia laurifolia</i>	Acanthaceae	JQ619894	JX275410	JX275450	-	JX197441	Doilom et al. (2017)	
<i>D. toxica</i>	CBS 534.93 (ex-type)	<i>Lupinus angustifolius</i> , stem	Fabaceae	KC343220	KC343946	KC344188	KC343704	KC343462	Udayanga et al. (2012)	
	CBS 535.93	<i>Lupinus</i> sp.	Fabaceae	KC343221	KC343947	KC344189	KC343705	KC343463	Udayanga et al. (2012)	
<i>D. tulliensis</i>	BRIP 62248a	<i>Theobroma cacao</i>	Sterculiaceae	KR936130	KR936133	KR936132	-	-	Gomes et al. (2013)	
	FAU 656	<i>Cucumis melo</i>	Cucurbitaceae	KJ590726	KJ590747	KJ610881	KJ659215	-	Gomes et al. (2013)	
<i>D. ueckeriae</i>	FAU 658	<i>Cucumis melo</i>	Cucurbitaceae	KJ590725	KJ590746	KJ610880	KJ659214	-	Crous et al. (2015)	
<i>D. undulata</i>	CGMCC 3.18293 = LC 6624	Unknown host, pathogen	-	KX986798	KX999190	KX999230	KX999269	-	Huang et al. (2015)	
	LC 8110	Unknown host, pathogen	-	KY491545	KY491555	KY491565	-	-	Huang et al. (2015)	
	LC 8111	Unknown host, pathogen	-	KY491546	KY491556	KY491566	-	-	This study	
<i>D. unshiuensis</i>	ZJUD 51, CGMCC 3.17568	<i>Fortunella margarita</i>	Rutaceae	KJ490586	KJ490465	KJ490407	KJ490528	-	This study	
	ZJUD 52, CGMCC 3.17569	<i>Citrus unshiu</i>	Rosaceae	KJ490587	KJ490466	KJ490408	KJ490529	-	This study	
<i>D. vaccinii</i>	CBS 160.32 (ex-type)	<i>Oxyccoccus macrocarpos</i>	Ericaceae	KC343228	KC343954	KC344196	KC343712	KC343470	Huang et al. (2015)	
	CBS 118571	<i>Vaccinium corymbosum</i>	Ericaceae	KC343223	KC343949	KC344191	KC343707	KC343465	Huang et al. (2015)	
<i>D. vawdreyi</i>	BRIP 57887a	<i>Psidium guajava</i>	Sterculiaceae	KR936126	KR936129	KR936128	-	-	Gomes et al. (2013)	
<i>D. velutina</i>	CGMCC 3.18286 = LC 4421	Neofitsea sp., pathogen	Lauraceae	KX986790	KX999182	KX999223	KX999261	-	Gomes et al. (2013)	
	LC 4419	Neofitsea sp., pathogen	Lauraceae	KX986789	KX999181	KX999222	KX999260	KX999286	Crous et al. (2015)	
	LC 4641	Callerya cinerea, pathogen	Fabaceae	KX986792	KX999184	KX999225	KX999263	KX999287	This study	
	LC 4788	Unknown host, pathogen	-	KX986785	KX999177	KX999218	KX999256	KX999285	This study	
	LC 6708	Camellia sinensis, pathogen	Theaceae	KX986787	KX999179	KX999220	KX999258	-	This study	
<i>D. vexans</i>	CBS 127.14	<i>Solanum melongena</i>	Solanaceae	KC343229	KC343955	KC344197	KC343713	KC343471	This study	
<i>D. virgilia</i>	CMW 40755 (ex-type)	<i>Virgilia oroboides</i>	Unknown	KP247573	-	KP247582	-	-	This study	

Table 2. (Continued).

Species names*	Culture collection no.	Isolation sources	Host family	GenBank Accession Numbers							References
				ITS	TEF1	TUB	HIS	CAL			
	CMW 40748	<i>Virgilia oroboides</i>	Unknown	KP247566	-	KP247575	-	-	-	Gomes et al. (2013)	
<i>D. woodii</i>	CBS 558.93	<i>Lupinus</i> sp.	Fabaceae	KC343244	KC343970	KC344212	KC343728	KC343486	KC343486	Gomes et al. (2013)	
<i>D. woolworthii</i>	CBS 148.27	<i>Ulmus americana</i>	Ulmaceae	KC343245	KC343971	KC344213	KC343729	KC343487	KC343487	Gomes et al. (2013)	
<i>D. xishuangbanica</i>	CGMCC 3.18282 = LC 6707	<i>Camellia sinensis</i>, pathogen	Theaceae	KX986783	KX999175	KX999216	KX999255	-	-	This study	
	LC 6744	<i>Camellia sinensis</i>, pathogen	Theaceae	KX986784	KX999176	KX999217	-	-	-	This study	
<i>D. yunnanensis</i>	CGMCC 3.18289 = LC6168	<i>Coffea</i> sp., endophytes	Rubiaceae	KX986796	KX999188	KX999228	KX999267	KX999290	KX999290	This study	
	LC 8106	<i>Coffea</i> sp., endophytes	Rubiaceae	KY491541	KY491551	KY491561	-	KY491571	KY491571	This study	
	LC 8107	<i>Coffea</i> sp., endophytes	Rubiaceae	KY491542	KY491552	KY491562	-	KY491572	KY491572	This study	
<i>Diaporthe</i> sp.	LC 6496	<i>Camellia sinensis</i>, endophytes	Theaceae	KX986781	KX999173	KX999214	KX999253	KX999283	KX999283	This study	
	LC 6512	<i>Camellia sinensis</i>, endophyte	Theaceae	KX986782	KX999174	KX999215	KX999254	KX999284	KX999284	This study	
	LC 6232	<i>Theobroma cacao</i>, endophyte	Sterculiaceae	KX986797	KX999189	KX999229	KX999268	KX999291	KX999291	This study	
	LC 8108	<i>Theobroma cacao</i>, endophyte	Sterculiaceae	KY491543	KY491553	KY491563	-	KY491573	KY491573	This study	
	LC 8109	<i>Theobroma cacao</i>, endophyte	Sterculiaceae	KY491544	KY491554	KY491564	-	KY491574	KY491574	This study	
	LC 6623	Unknown host, pathogen	-	KX986795	KX999187	KX999227	KX999266	-	-	This study	
	LC 8114	Unknown host, pathogen	-	KY491549	KY491559	KY491569	-	-	-	This study	
	LC 8115	Unknown host, pathogen	-	KY491550	KY491560	KY491570	-	-	-	This study	
	LGMF 947	<i>Glycine max</i>, seed	Fabaceae	KC343203	KC343929	KC344171	KC343687	KC343445	KC343445	Gomes et al. (2013)	
	CBS 119639	Man, abscess	-	KC343202	KC343928	KC344170	KC343687	KC343444	KC343444	Gomes et al. (2013)	
<i>Diaporthe</i> sp. 1	CGMCC 3.18292 = LC 0771	<i>Alnus</i> sp., pathogen	Betulaceae	KX986799	KX999191	KX999231	KX999270	KX999292	KX999292	This study	
<i>Diaporthe</i> sp. 2	CGMCC 3.18291 = LC 6140	<i>Acer</i> sp., endophyte	Aceraceae	KX986799	KX999191	KX999231	KX999270	KX999292	KX999292	This study	
	LC8112	<i>Acer</i> sp., endophyte	Aceraceae	KY491547	KY491557	KY491567	-	KY491575	KY491575	This study	
	LC8113	<i>Acer</i> sp., endophyte	Aceraceae	KY491548	KY491558	KY491568	-	KY491576	KY491576	This study	
<i>Diaporthea corylina</i>	CBS 121124	<i>Corylus</i> sp., dying stems	Corylaceae	KC343004	KC343730	KC343972	KC343488	KC343246	KC343246	Gomes et al. (2013)	
<i>P. conorum</i>	CBS 587.79	<i>Penus pentaphylla</i>	Pinaceae	KC343153	KC343879	KC344121	KC343637	KC343395	KC343395	Gomes et al. (2013)	
<i>P. emicis</i>	BRIP 45089a (ex-type)	<i>Emex australis</i>	Polygonaceae	JF957784	JX275414	JX275458	-	JX197449	JX197449	Udayanga et al. (2012)	
<i>P. fukushii</i>	CBS 116953	<i>Pyrus pyrifolia</i>	Roseaceae	KC343147	KC343873	KC344115	KC343631	KC343389	KC343389	Gomes et al. (2013)	
	BRIP 45089b	<i>Emex australis</i>	Polygonaceae	JQ619898	JX275415	JX275459	-	JX197450	JX197450	Udayanga et al. (2012)	

-. not provided in literatures.



Fig. 3. *Diaporthe acutispora* (CGMCC 3.18285). **A–B.** 30-d-old culture on PNA medium. **C.** Conidiomata. **D–E.** Conidiophores. **F–G.** Alpha conidia. Bars: C = 100 μ m; D–G = 10 μ m.

TAXONOMY

Diaporthe acutispora Y.H. Gao & L. Cai, **sp. nov.**

Mycobank MB820679

(Fig. 3)

Etymology: Named after the acute spores.

Diagnosis: *Diaporthe acutispora* is phylogenetically distinct and morphologically differs from species reported from the host genera *Coffea* and *Camellia* in the larger conidiophores and alpha conidia (Table 3).

Type: **China:** *Yunnan Province:* Aini Farm, on healthy leaves of *Coffea* sp., 20 Sep. 2014, W.J. Duan (HMAS 247086 – holotype, dried culture; CGMCC 3.18285 = LC 6161 – ex-type culture).

Description: On PNA: *Conidiomata* pycnidial, globose, brownish, embedded in tissue, erumpent at maturity, 99–473 μ m diam, often with a yellowish conidial cirrus exuding from the ostioles. *Conidiophores* 10–34.5 \times 2–3 μ m, cylindrical, hyaline, septate, branched, straight or slightly curved, tapering towards the apex. *Alpha conidia* abundant in culture, 7–10.5 \times 2–3 μ m (\bar{x} = 8.4 \pm 0.7 \times 2.6 \pm 0.2, n = 30), aseptate, hyaline, ellipsoidal to fusoid, multi-guttulate. *Beta conidia* not observed.

Culture characters: Cultures incubated on PDA at 25 $^{\circ}$ C in darkness, growth rate 7.5 mm diam/d. Colony entirely white at surface, reverse with pale brown pigmentation, white, fluffy aerial mycelium.

Additional material examined: **China:** *Yunnan Province:* Xishuangbanna, on healthy leaves of *Camellia sasanqua*, 20 Sep. 2014, W.J. Duan, culture LC 6142; *ibid.* culture LC 6160.

Diaporthe elaeagni-glabrae Y.H. Gao & L. Cai, **sp. nov.**

Mycobank MB820680

(Fig. 4)

Etymology: Named after the host species *Elaeagnus glabra*.

Diagnosis: *Diaporthe elaeagni-glabrae* can be distinguished from the closely related species *D. elaeagni* (96 % in ITS, 93 % in *TEF1*, 94 % in *TUB*, 96 % in *HIS*, and 94 % in *CAL*) and *D. stictica* (96 % in ITS, 95 % in *TEF*, 97 % in *TUB*, 96 % in *HIS*, and 96 % in *CAL*) (Fig. 2). *Diaporthe elaeagni-glabrae* differs from other species recorded from *Elaeagnus* in the significantly longer alpha conidia (Table 3).

Type: **China:** *Jiangxi Province:* on diseased leaves of *Elaeagnus glabra*, 5 Sep. 2013, Y.H. Gao (HMAS 247089 – holotype, dried culture; CGMCC 3.18287 = LC 4802 – ex-type culture).

Table 3. Synoptic characters of *Diaporthe* spp. referred to in this study.

Host genera	Species	Conidiomata (µm)	Conidiophores (µm)	Alpha conidia (µm)	Beta conidia (µm)	References
<i>Coffea</i>	<i>P. coffeae</i>	200–250	12–16 × 2	8–9 × 2.5	-	Uecker (1988)
<i>Camellia</i>	<i>D. acutispora</i>	99–473	10–34.5 × 2–3	6.9–10.4 × 2.1–3.1	-	This study
	<i>D. amygdali</i>	160–220 × 120–300	7.4–36.3 × 1.5–3.2	(4.18–)6.27–6.32(–9.64) × (1.63–)2.36–2.38(–3.31)	-	Diogo et al. (2010)
	<i>D. apiculata</i>	74–195 (–416)	9.0–12.5 × 1.5–2.5	6.5–10 × 2–3	(20.0–)25.0–39.0 × 1.0–1.5	Gao et al. (2016)
	<i>D. compacta</i>	237–350	6.0–12.5 × 1.5–2.5	6–7.5 × 2–3	20.0–24.5 × 1.0–1.5	Gao et al. (2016)
	<i>D. discoispora</i>	200 × 118	8.9–23.4 × 1.3–2.7	5.6–8 × 2.1–3.2	21.2–38.7 × 0.9–1.6	Huang et al. (2015)
	<i>D. eres</i>	200–250	10–15 × 2–3	(6–)6.5–8.5(–9) × 3–4	(18–)22–28(29) × 1–1.5	Udayanga et al. (2014b)
	<i>D. foeniculacea</i>	560 × 350	10–13 × 1.5–3	(5.4–)6.8–7(–9) × (2–)2.3–2.4(–3.1)	(16.8–)19.6–21(–24.2) × (1.1–)1.3–1.4(–1.7)	Phillips (2003)
	<i>D. foeniculina</i>	400–700	9–15(–18) × 1–2	(7.5–)8.5–9(–9.2) × (2–)2.3–2.5(–2.7)	(20–)22–28(–29) × (1.1–)1.4–1.6(–2)	Udayanga et al. (2014c)
	<i>D. hongkongensis</i>	to 200	5–12 × 2–4	(5–)6–7(–8) × (2–)2.5(–3)	18–22 × 1.5–2	Gomes et al. (2013)
	<i>D. oraccinii</i>	400	10.5–22.5 × 1–2	5.5–7.5 × 0.5–2	24.5–31.0 × 1.0–1.5	Gao et al. (2016)
	<i>D. penetriteum</i>	176–486	13–21.5 (–27) × 1–2	4.5–5.5 × 1.5–2.5	16.5–27.5 × 1.0–2.0	Gao et al. (2016)
	<i>D. ueckeræ</i>	150–200	(9–)12–28(–30) × 1.5–2.5	(6–)6.4–8.2(–8.6) × (2–)2.3–3	-	Udayanga et al. (2014a)
	<i>D. xishuangbanica</i>	180–310	13–34.5 × 1.5–3	7–9.5 × 2.5–3.5	-	This study
	<i>D. yunnanensis</i>	195–880	-	3–6.5 × 1–2.5	13.5–33.5 × 1–1.5	This study
	<i>P. acacicola</i>	-	-	7–9 × 3–3.5	-	Diedicke (1911)
	<i>P. theae</i>	40 × 25	-	6–8 × 1.5–2	18–24 × 0.75	Petch (1925)
<i>Elaeagnus</i>	<i>P. arnoldiae</i>	900 × 500	6–12 × 1–2	5.5–11 × 1.5–2	15–20	Uecker (1988)
	<i>P. elaeagni</i>	500–750	20–25 × 1–1.5	6–10 × 2–3	-	Uecker (1988)
	<i>P. elaeagnicola</i>	175–413 × 83–185	10.0–22.5 × 1.5–2.7	6.0–7.4 × 1.7–2.2	19–43 × 0.7–1.2	Chang et al. (2005)
	<i>D. elaeagni-glabrae</i>	330–1170	16–28 × 1.5–2.5	6–13 × 1.5–3	7.5–22.5 × 1–2	This study
	<i>D. incompleta</i>	207–650	8–22 × 1–2.5	-	19–44 × 0.5–1.5	This study
<i>Neolitsea</i>	<i>D. velutina</i>	69–428	10–23 × 1–2.5	5.5–10 × 2–2.5	11–27.5 × 0.5–1.5	This study

AR, DP, FAU: Isolates in culture collection of Systematic Mycology and Microbiology Laboratory, USDA-ARS, Beltsville, Maryland, USA; **BCRC:** Bioresource Collection and Research Center, Taiwan; **BRIP:** Australian plant pathogen culture collection, Queensland, Australia; **CBS:** Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; **CFCC:** China Forestry Culture Collection Center, China. **CGMCC:** China General Microbiological Culture Collection; **CMW:** culture collection (CMW) of the Forestry and Agricultural Biotechnology Institute; **CPC:** working collection of Pedro Crous maintained at the Westerdijk Institute; **LGMF:** Culture collection of Laboratory of Genetics of Microorganisms, Federal University of Paraná, Curitiba, Brazil; **LC:** Working collection of Lei Cai, housed at Institute of Microbiology, CAS, China; **MFLUCC:** Mae Fah Luang University Culture Collection; **ZJUD:** Zhe Jiang University, China.

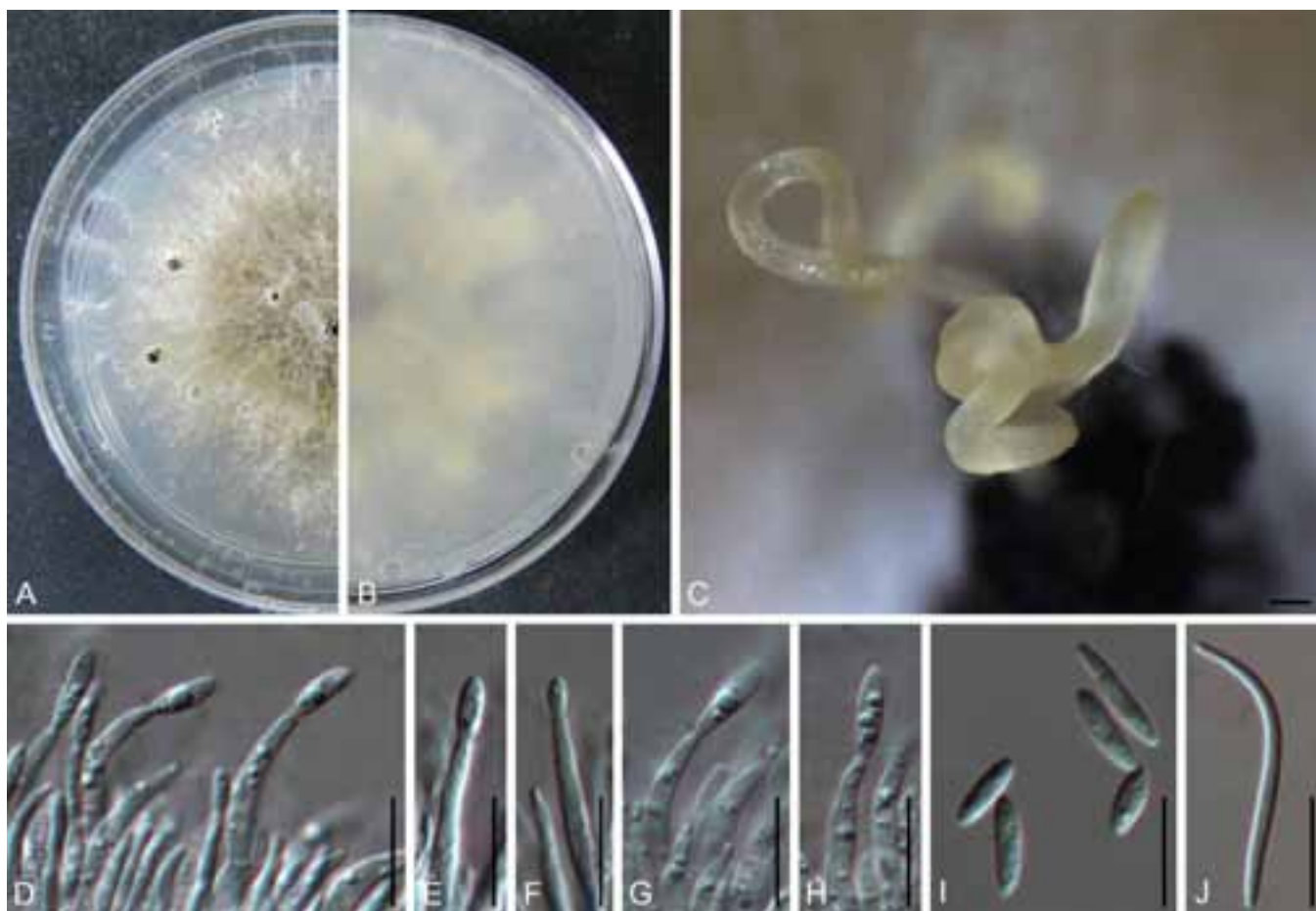


Fig. 4. *Diaporthe elaeagni-glabrae* (CGMCC 3.18287). **A–B.** 14-d-old culture on PDA; **C.** Conidiomata; **D–H.** Conidiophores; **I.** Alpha conidia; **J.** Beta conidia. Bars: C = 100 μ m; D–J = 10 μ m.

Description: On PDA: *Conidiomata* globose, to 330–1170 μ m, erumpent, with slightly elongated black necks, yellowish or dirty white, spiral conidial cirri extruding from ostioles. *Conidiophores* 16–28 \times 1.5–2.5 μ m, cylindrical, phialidic, septate, branched, sometimes inflated. *Alpha conidia* 6–13 \times 1.5–3 μ m (\bar{x} = 8.3 \pm 1.4 \times 2.2 \pm 0.3, n = 30), hyaline, fusiform or oval, usually biguttulate. *Beta conidia* 7.5–22.5 \times 1–2 μ m (\bar{x} = 15.1 \pm 3.5 \times 1.2 \pm 0.2, n = 40), hyaline, filiform, smooth, curved, base truncate.

Culture characters: Cultures incubated on PDA at 25 $^{\circ}$ C in darkness, growth rate 7 mm diam/d. Colony pale yellowish, greenish to brownish at the centre, reverse pale yellowish and brownish at the centre with age. Aerial mycelium white, sparse, fluffy, with irregular margin and visible conidiomata at maturity.

Additional material examined: **China:** Jiangxi Province: on diseased leaves of *Elaeagnus glabra*, 5 Sep. 2013, Y.H. Gao, culture LC 4806.

***Diaporthe helianthi* Munt.-Cvetk. et al., Nova Hedwigia 34: 433 (1981).**
(Fig. 5)

Description: Sexual morph not produced. *Conidiomata* pycnidial globose to subglobose, dark brownish to black,

erumpent or immersed in medium, translucent conidia exuded from the ostioles, 110–380 μ m diam. *Conidiophores* cylindrical, straight or sinuous, apical or base sometimes swelling, 11.5–23.5 \times 1.8–3.5 μ m (\bar{x} = 16 \pm 3 \times 2.5 \pm 0.5, n = 30). *Beta conidia* filiform, hamate or slightly curved, base truncate, tapering towards one apex, 11.5–32 \times 0.5–2 μ m (\bar{x} = 20 \pm 7.5 \times 1 \pm 0.4, n = 20). *Alpha conidia* not observed.

Culture characters: Cultures on PDA at 25 $^{\circ}$ C in dark, with 12/12 h alternation between daylight and darkness pure white (surface) and pale yellow to cream (reverse). Colony pellicular, forming less pigmented sectors, with concentric rings of gummy mycelium. Growth rate was 10.5 mm diam/d.

Material examined: **Ukraine:** from seeds of *Helianthus annuus*, 30 Oct. 2015, W.J. Duan culture LC 6173. – **Japan:** *Lagerstroemia indica*, 30 Oct. 2015, W.J. Duan, culture LC 6185.

Notes: *Diaporthe helianthi*, responsible for stem canker and grey spot disease of sunflower (*Helianthus annuus*) (Muntanola-Cvetkovic et al. 1981), has been listed in the Chinese quarantine directory. There is increasing evidence that this serious sunflower pathogen is being quickly and globally disseminated with international trade. The cases reported here were intercepted from imported sunflower seeds from Ukraine and *Lagerstroemia indica* from Japan.

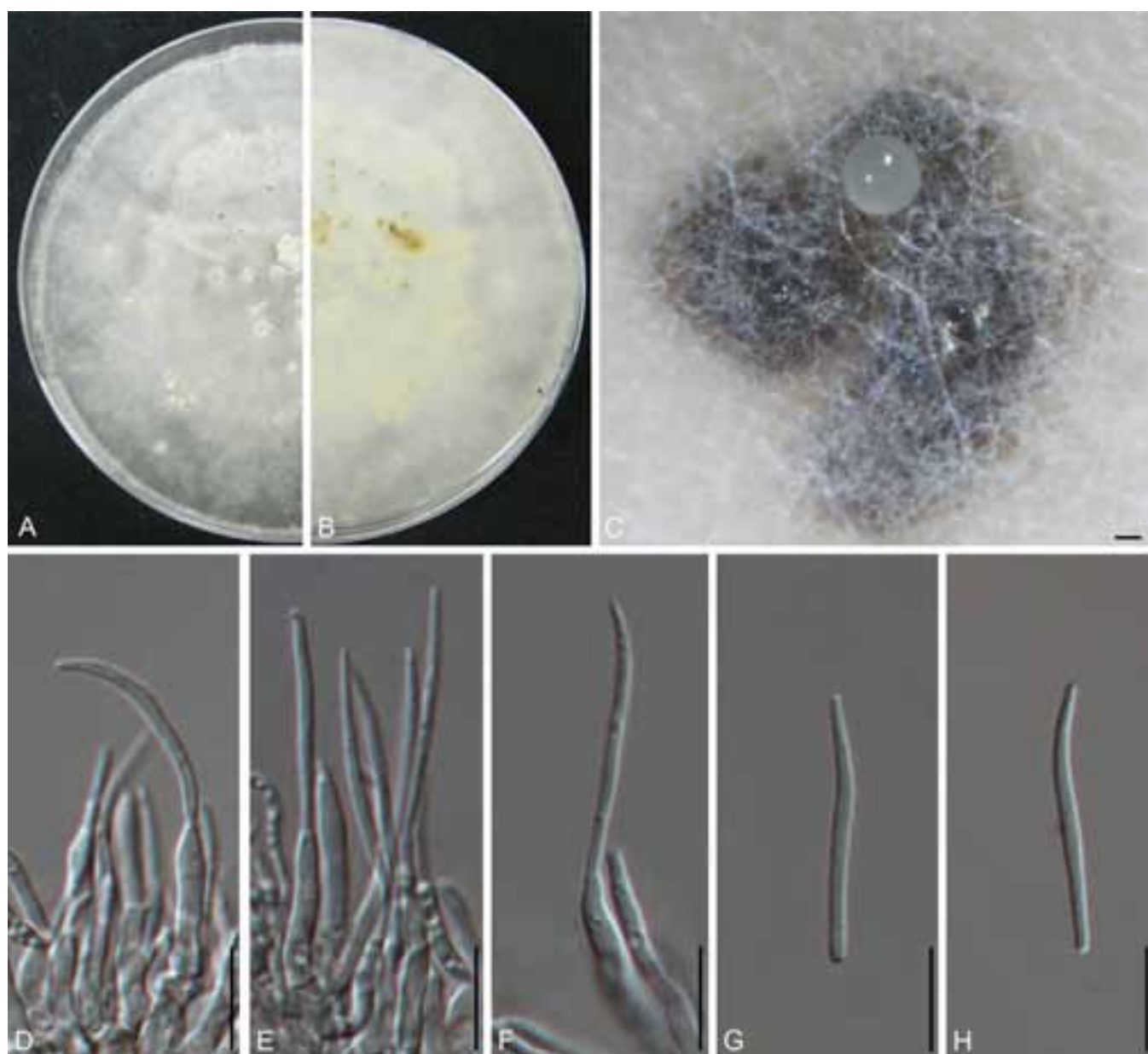


Fig. 5. *Diaporthe helianthi* (LC 6185). **A–B.** 7-d-old culture on PDA; **C.** Conidiomata; **D–F.** Conidiophores; **G–H.** Beta conidia. Bars: C = 100 μ m; D–H = 10 μ m.

Diaporthe incompleta Y.H. Gao & L. Cai, **sp. nov.**

Mycobank MB820681

(Fig. 6)

Etymology: Named after the absence of alpha conidia.

Diagnosis: *Diaporthe incompleta* is phylogenetically distinct and differs morphologically from other species recorded from *Elaeagnus* and *Camellia* in the much longer beta conidia (Table 3).

Type: China: Yunnan Province: Xishuangbanna, on diseased of *Elaeagnus glabra*, 19 Apr. 2015, F. Liu (HMAS 247088 – holotype, dried culture; CGMCC 3.18288 = LC 6754 – ex-type culture).

Description: Conidiomata pycnidial, subglobose to globose, brownish to black, 207–650 μ m diam, cream to pale luteous

conidial droplets exuding from the central ostioles. Conidiophores 8–22 \times 1–2.5 μ m, cylindrical, hyaline, septate, unbranched, smooth, slightly curved, tapering towards apex. Alpha conidia not observed. Beta conidia 19–44 \times 0.5–1.5 μ m (\bar{x} = 30.5 \pm 8.7 \times 1.1 \pm 0.4, n = 30), smooth, hyaline, filiform, base subtruncate, straight or curved.

Culture characters: Cultures incubated on PDA at 25 $^{\circ}$ C in darkness, growth rate 16.5 mm diam/d. Colony entirely white, flat, reverse pale yellowish, becoming brownish zoned at the centre with age. Aerial mycelium white, cottony, margin lobate, conidiomata visible at maturity.

Additional material examined: China: Yunnan Province: Xishuangbanna, on diseased leaves of *Camellia sinensis*, 19 Apr. 2015, F. Liu, culture LC 6706.



Fig. 6. *Diaporthe incompleta* (CGMCC 3.18288). **A.** Leaves of host plant; **B–C.** 7-d-old culture; **D.** Conidiomata; **E–F.** Conidiophores; **G.** Beta conidia. Bars: D = 100 μ m; E–G = 10 μ m.

***Diaporthe podocarpi-macrophylli* Y.H. Gao & L. Cai,
sp. nov.**

Mycobank MB820682
(Fig. 7)

Etymology. Named after the host plant *Podocarpus macrophyllus*.

Diagnosis: *Diaporthe podocarpi-macrophylli* can be distinguished from the phylogenetically closely related species *D. pseudophoenicicola* (97 % identity in ITS, 90 % in *TEF1*, 98 % in *TUB*, 97 % in *HIS*, and 97 % in *CAL*). Morphologically, *D. podocarpi-macrophylli* differs from other species occurring on the host genera *Podocarpus* and *Olea*, i.e. *D. cinerascens* and *Phomopsis podocarpi* in its wider and shorter alpha co-

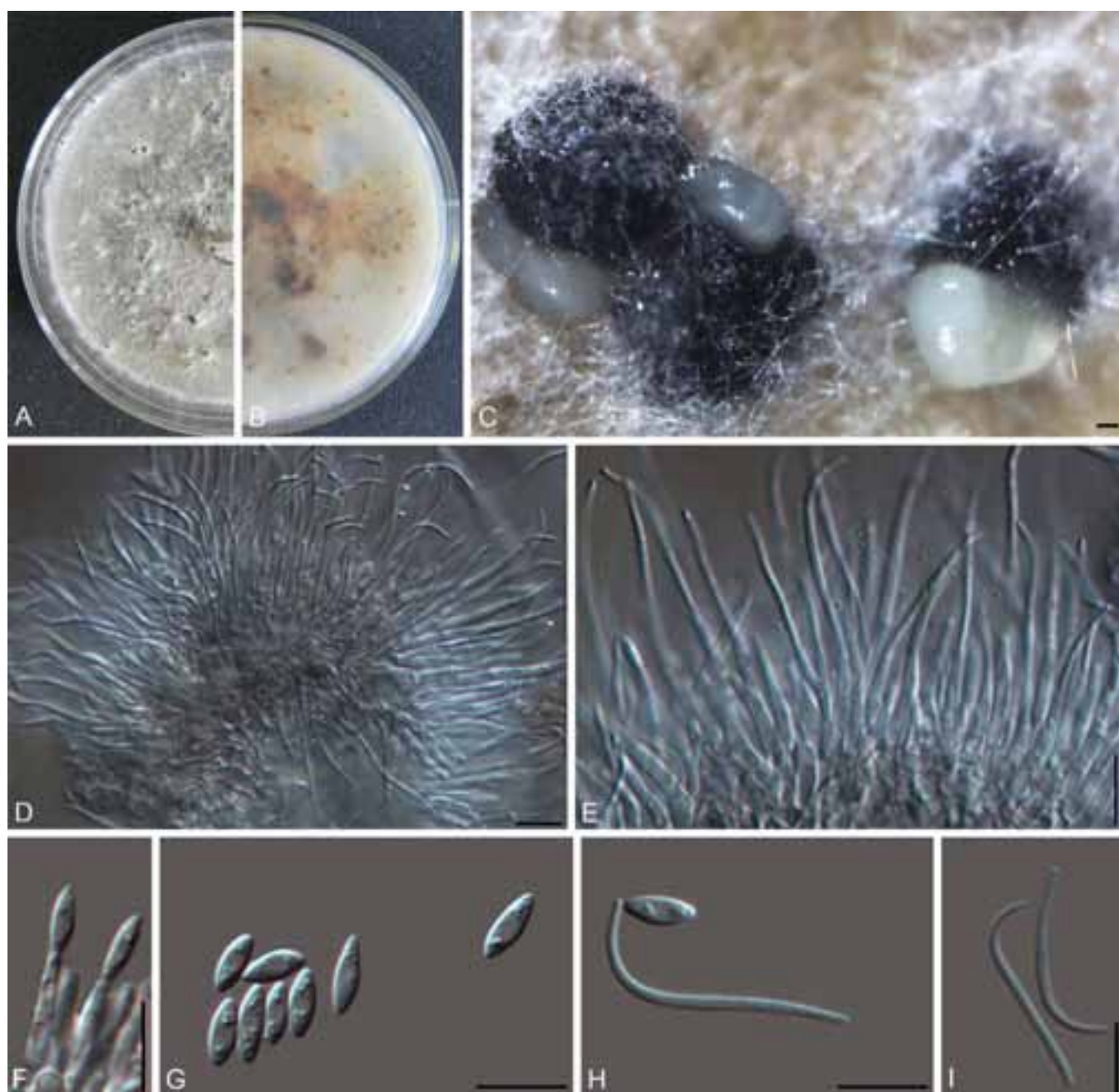


Fig. 7. *Diaporthe podocarpi-macrophylli* (CGMCC 3.18281). **A–B.** 30-d-old culture on PDA; **C.** Conidiomata; **D–F.** Conidiophores; **G–I.** Alpha and beta conidia. Bars: C = 100 μm ; D–I = 10 μm .

nidia and the presence of beta conidia (Chang *et al.* 2005, Gomes *et al.* 2013; <https://nt.ars-grin.gov/fungaldatabases/>).

Type: Japan: on healthy leaves of *Podocarpus macrophyllus*, 20 Sep. 2014, *W.J. Duan* (HMAS 247084 – holotype, dried culture; CGMCC 3.18281 = LC 6155 – ex-type culture).

Description: *Conidiomata* pycnidial in culture on PDA, solitary or aggregated, deeply embedded in the PDA, erumpent, dark brown to black, 222–699 μm diam, yellowish translucent conidial drops exuding from the ostioles. *Alpha conidiophores* 6–18 \times 1.5–3 μm (\bar{x} = 12.3 \pm 2.6 \times 2.1 \pm 0.3, n = 30), hyaline, septate, branched, cylindrical, straight to sinuous, sometimes inflated, occurring in dense clusters. *Beta conidiophores*

10.5–27 \times 1.5–2.5 μm (\bar{x} = 15.3 \pm 4.3 \times 2.1 \pm 0.3, n = 30), cylindrical to clavate, hyaline, septate, branched, smooth, straight. *Alpha conidia* 3.5–8.5 \times 1–3 μm (\bar{x} = 6.3 \pm 1.7 \times 2.1 \pm 0.7, n = 50), unicellular, aseptate, fusiform, hyaline, usually biguttulate and acute at both ends. *Beta conidia* 8.5–31.5 \times 0.5–2 μm (\bar{x} = 19.5 \pm 7.1 \times 1.1 \pm 0.4, n = 30), hyaline, aseptate, eguttulate, filiform, curved, tapering towards both ends, base truncate.

Culture characters: Cultures incubated on PDA at 25 $^{\circ}\text{C}$ in darkness, growth rate 12.5 mm diam/d. Colony at first white, becoming cream to yellowish, flat, with dense and felted mycelium, reverse pale brown with brownish dots with age, with visible solitary or aggregated conidiomata at maturity.

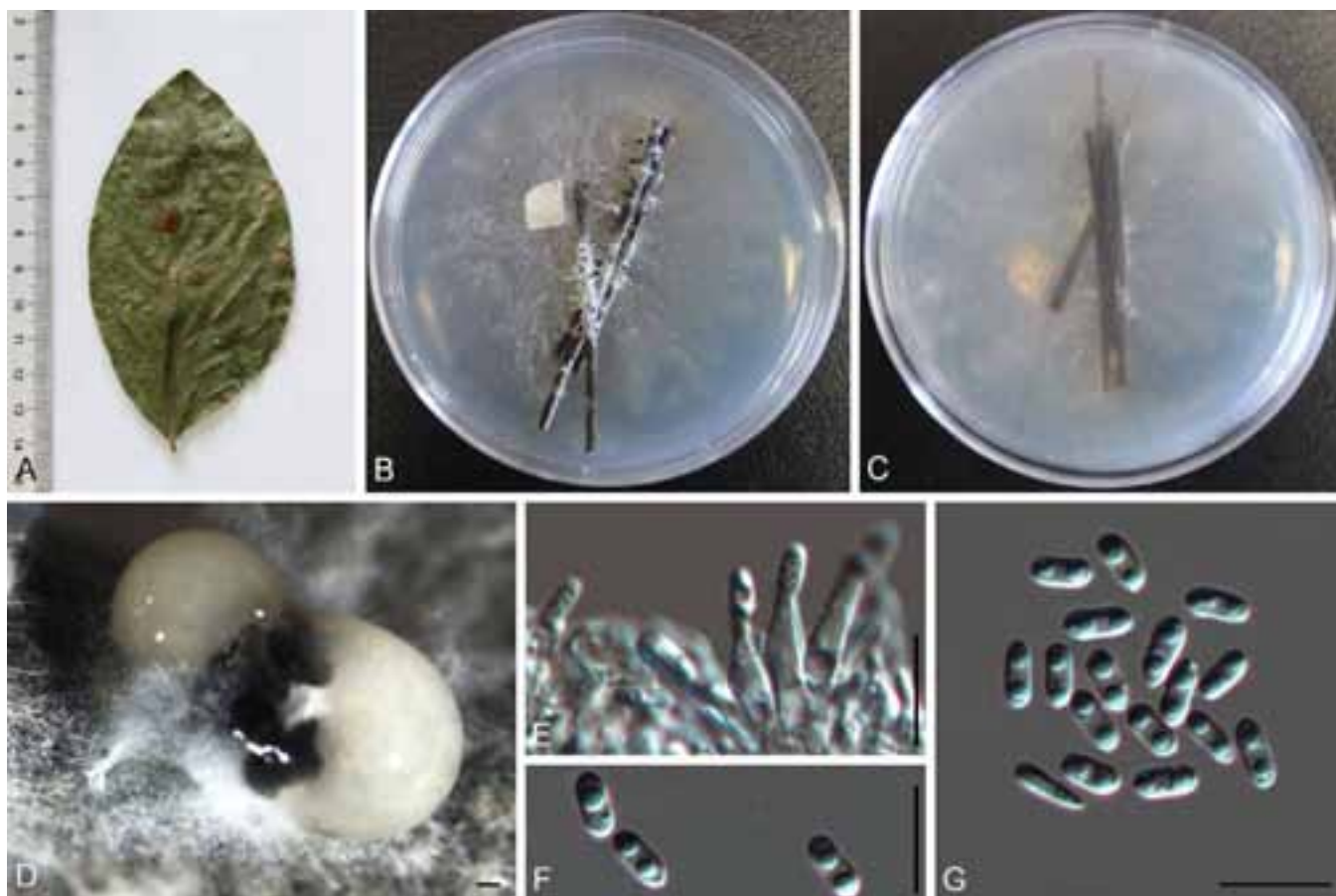


Fig. 8. *Diaporthe undulata* (CGMCC 3.18293). **A.** Leaves of host plant; **B–C.** 30-d-old culture on PNA medium; **D.** Conidiomata; **E.** Conidiophores; **F–G.** Alpha conidia. Bars: D = 100 μ m; E–G = 10 μ m.

Additional material examined: **Japan:** on healthy leaves of *Podocarpus macrophyllus*, 20 Sep. 2014, *W.J. Duan*, culture LC 6141; *ibid.* culture LC 6144; *ibid.* culture LC 6156; *ibid.* culture LC 6157. – **China:** Zhejiang Province: on healthy leaves of *P. macrophyllus*, 10 Jul. 2015, *W.J. Duan*, culture LC 6194; *ibid.* culture LC 6195; *ibid.* culture LC 6196; *ibid.* culture LC 6197; *ibid.* culture LC 6198; *ibid.* culture LC 6199; *ibid.* culture LC 6200; *ibid.* culture LC 6201; *ibid.* culture LC 6202; *ibid.* culture LC 6235. – **Italy:** on healthy leaves of *Olea europaea*, 20 Sep. 2014, *W.J. Duan*, culture LC 6229.

Diaporthe undulata Y.H. Gao & L. Cai, **sp. nov.**
Mycobank MB820683
(Fig. 8)

Etymology: Named after the colony's undulate margin.

Diagnosis: *Diaporthe undulata* differs from the most closely related species, *D. biconispora*, in several loci (94 % in ITS, 84 % in *TEF1*, and 93 % in *TUB*), and from other *Diaporthe* species in the obpyriform conidiophores and shorter and wider alpha conidia (Table 3).

Type: **China-Laos border:** on diseased leaves of unknown host, 19 Apr. 2014, *F. Liu* (HMAS 247091 – holotype, dried culture; CGMCC 3.18293 = LC 6624 – ex-type culture).

Description: *Conidiomata* pycnidial, irregular, embedded in the needle, erumpent, necks, hairy, 282–543 μ m long, coated with short hyphae, one to several necks forming from a single pycnidium. *Conidiophores* obpyriform, hyaline, phialidic, septate, branched, 5–17.5 \times 2–3 μ m (\bar{x} = 9.7 \pm 4.0 \times 2.4 \pm 0.5, n = 20). *Alpha conidia* ellipsoid, hyaline, biguttulate, rounded at both ends, 5–6.5 \times 2–3 (\bar{x} = 5.8 \pm 0.4 \times 2.3 \pm 0.3, n = 50). *Beta conidia* not observed.

Culture characters: Cultures incubated on PDA at 25 $^{\circ}$ C in darkness, growth rate 10.5 mm diam/d. Colony entirely white, reverse pale yellowish and dark brownish at the centre with age. Aerial mycelium white, cottony, dense, with undulate margin and visible conidiomata at maturity.

Additional material examined: **China-Laos border:** unknown host, 19 Apr. 2014, *F. Liu*, culture LC 8110; *ibid.* culture LC 8111.

Diaporthe velutina Y.H. Gao & L. Cai, **sp. nov.**
Mycobank MB820684
(Fig. 9)

Etymology: Named after the felted colony.

Diagnosis: *Diaporthe velutina* is distinguished from *D. anacardii* in the ITS, *TEF1*, *TUB* and *HIS* loci (99 % in ITS, 95 % in *TEF1*, 99 % in *TUB*, and 98 % in *HIS*), and from

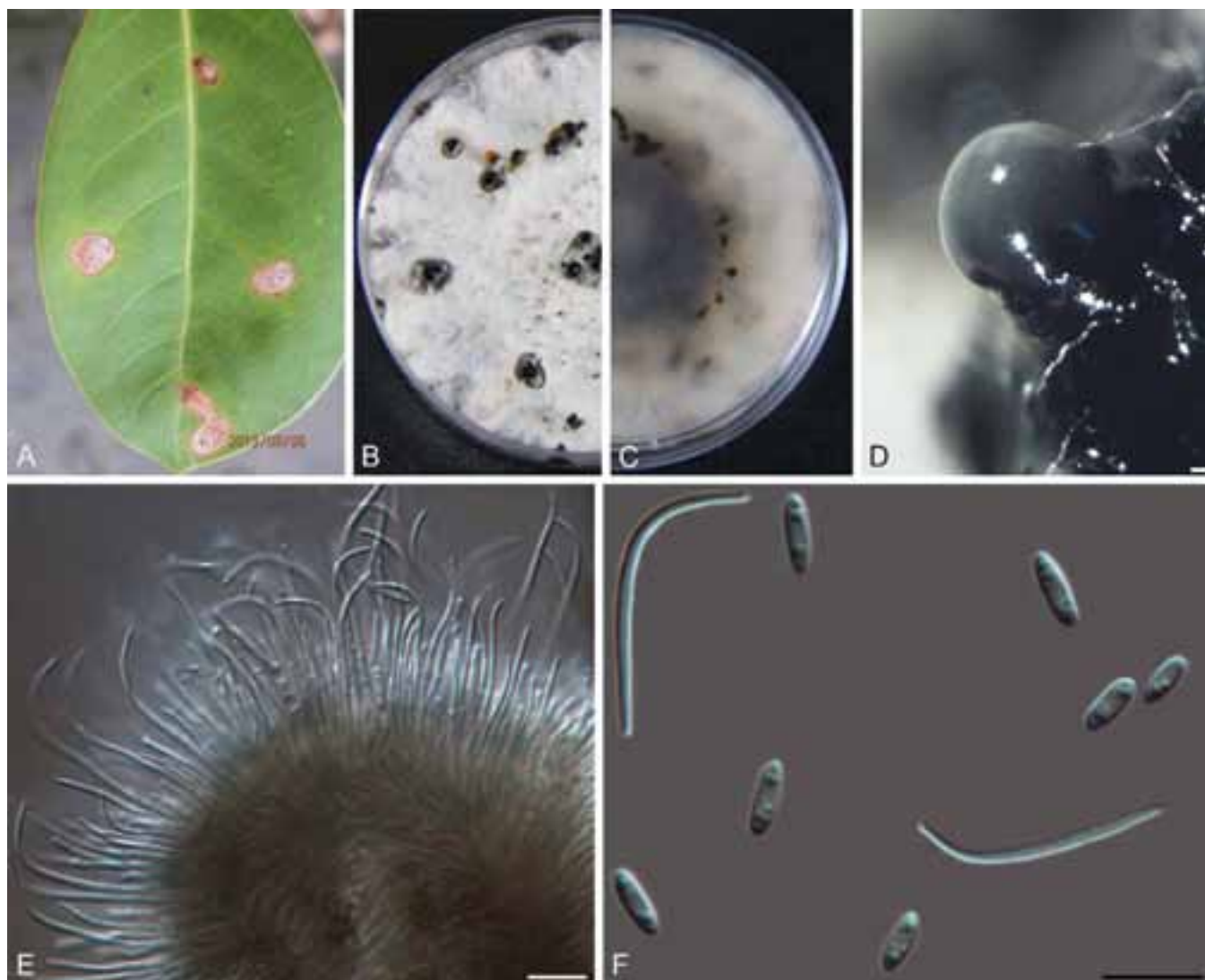


Fig. 9. *Diaporthe velutina* (CGMCC 3.18286). **A.** Diseased leaves; **B–C.** 30-d-old culture on PDA; **D.** Conidiomata; **E.** Conidiophores; **E.** Alpha and beta conidia. Bars: D = 100 μ m; E–F = 10 μ m.

other *Diaporthe* species reported from *Camellia sinensis* in the more variable size of the alpha conidia (Table 3).

Type: China: Jiangxi Province: on diseased leaves of *Neolitsea* sp., 5 Sep. 2013, Y.H. Gao (HMAS 247087 – holotype, dried culture; CGMCC 3.18286 = LC 4421 – ex-type culture).

Description: Conidiomata pycnidial, globose, black, embedded in PDA, aggregated in clusters, 69–428 μ m diam, cream translucent drop of conidia exuded from the central ostioles. Conidiophores 10–23 \times 1–2.5 μ m, cylindrical, hyaline, branched, densely aggregated, slightly tapering towards the apex, sometimes slightly curved. Alpha conidia 5.5–10 \times 2–2.5 μ m (\bar{x} = 6.9 \pm 0.9 \times 2.2 \pm 0.2, n = 50), unicellular, aseptate, hyaline, fusoid to ellipsoid or clavate, bi-guttulate or multi-guttulate. Beta conidia 11–27.5 \times 0.5–1.5 μ m (\bar{x} = 16.1 \pm 5.0 \times 0.8 \pm 0.4, n = 30), smooth, hyaline, apex acutely rounded, curved.

Culture characters: Cultures incubated on PDA at 25 $^{\circ}$ C in darkness, growth rate 18.75 mm diam/d. Colony entirely white, surface mycelium greyish to brownish at the centre,

dense, felted, conidiomata erumpent at maturity, reverse centre yellowish to brownish.

Additional material examined: China: Jiangxi Province: Yangling, on diseased leaves of *Neolitsea* sp., 5 Sep. 2013, Y.H. Gao, culture LC 4419; *ibid.* culture LC 4422; Gannan Normal University, unknown host, 23 Apr. 2013, Q. Chen, culture LC 4788; Fengshan, on diseased leaves of *Callerya cinerea*, 5 Sep. 2013, Y.H. Gao, culture LC 4641. **Yunnan Province:** Xishuangbanna, on diseased leaves of *Camellia sinensis*, 19 Apr. 2015, F. Liu, culture LC 6708; *loc. cit.*, on healthy leaves of *C. sinensis*, 21 Apr. 2015, F. Liu, culture LC 6519.

***Diaporthe xishuangbanica* Y.H. Gao & L. Cai, sp. nov.**

MycoBank MB820685
(Fig. 10)

Etymology: Named after the locality, Xishuangbanna.

Diagnosis: *Diaporthe xishuangbanica* can be distinguished from the phylogenetically closely related *D. tectorigena* in several loci (98 % in ITS, 90 % in *TEF1*, and 96 % in *TUB*)

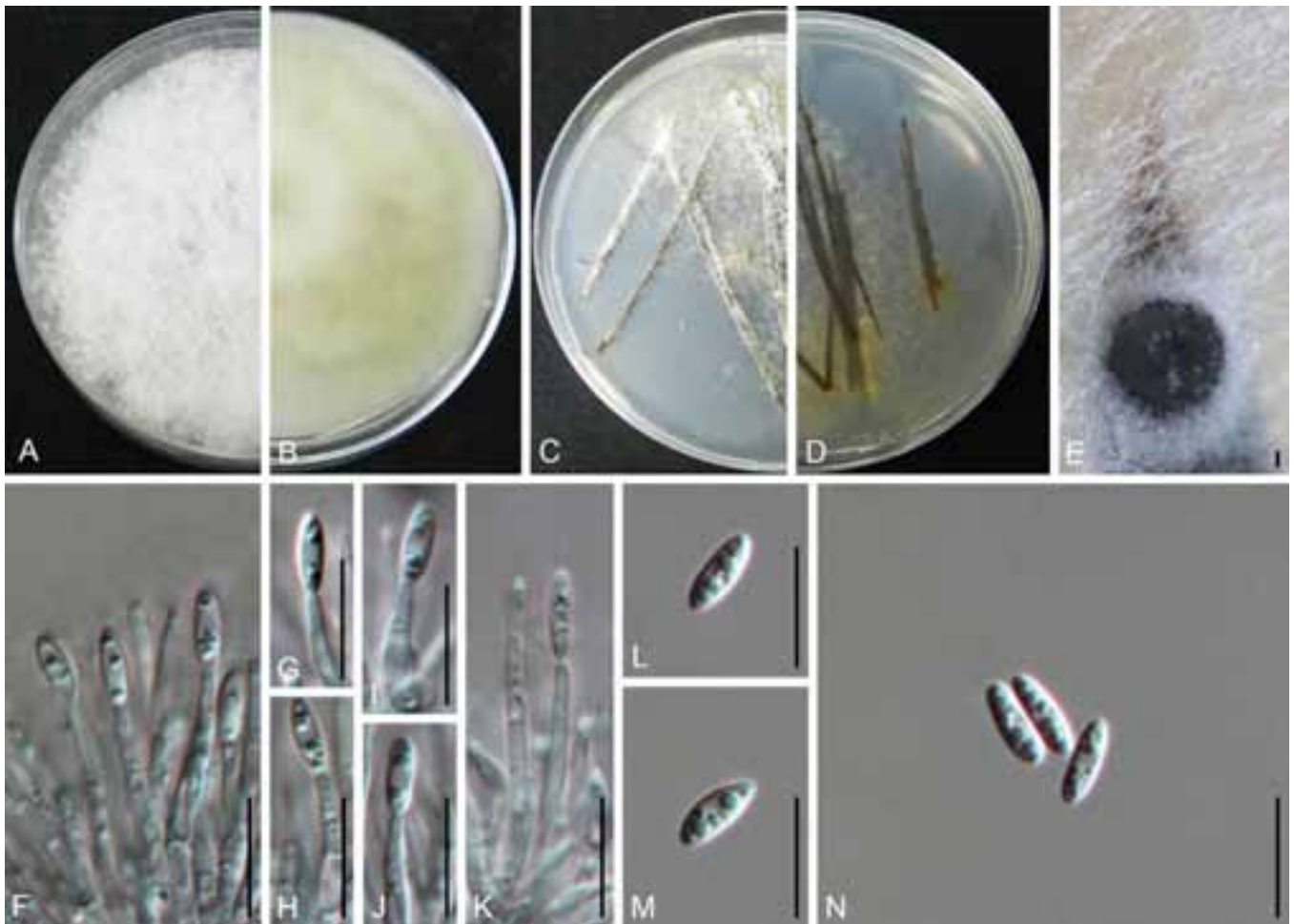


Fig. 10. *Diaporthe xishuangbanica* (CGMCC 3.18283). **A–B.** 7-d-old culture on PDA; **C–D.** 30-d-old culture on PNA medium; **E.** Conidiomata; **F–K.** Conidiophores; **L–N.** Alpha conidia. Bars: E = 100 μ m; F–N = 10 μ m.

(Fig. 2), and from other *Diaporthe* species reported from *Camellia* in the longer conidiophores and alpha conidia (Table 3).

Type: **China:** Yunnan Province: Xishuangbanna, on diseased leaves of *Camellia sinensis*, 19 Apr. 2015, *F. Liu* (HMAS 247083 – holotype, dried culture; CGMCC 3.18283 = LC 6744 – ex-type culture).

Description: Conidiomata pycnidial, globose, 180–310 μ m diam, scattered on the pine needle. Conidiophores cylindrical, 13–34.5 \times 1.5–3 μ m (\bar{x} = 20.9 \pm 5.2 \times 2.1 \pm 0.3, n = 40), branched, septate, straight, sometimes sinuous or lateral. Alpha conidia 7–9.5 \times 2.5–3.5 μ m (\bar{x} = 8.3 \pm 0.7 \times 2.8 \pm 0.3, n = 30), fusiform, hyaline, multi-guttulate. Beta conidia not observed.

Culture characters: Cultures incubated on PDA at 25 $^{\circ}$ C in darkness, growth rate 17.5 mm diam/d. Colony entirely white, reverse pale yellowish to greenish. Aerial mycelium white, velvety, margin well defined, with visible conidiomata at maturity.

Additional material examined: **China:** Yunnan Province: Xishuangbanna, on diseased leaves of *Camellia sinensis*, 19 Apr. 2015, *F. Liu*, culture LC 6707 (CGMCC 3.18282).

***Diaporthe yunnanensis* Y.H. Gao & L. Cai, sp. nov.**

Mycobank MB820686

(Fig. 11)

Etymology: Named after the location where the fungus was collected, Yunnan Province.

Diagnosis: *Diaporthe yunnanensis* can be distinguished from the phylogenetically closely related *D. siamensis* (96 % in ITS, 91 % in *TEF1*, and 94 % in *TUB*) (Fig. 2), and from other *Diaporthe* species reported on the genus *Camellia* in the smaller alpha conidia (Table 3).

Type: **China:** Yunnan Province: Xishuangbanna, on healthy leaves of *Coffea* sp., 20 Sep. 2014, *W.J. Duan* (HMAS 247096 – holotype, dried culture; CGMCC 3.18289 = LC 6168 – ex-type culture).

Description: Conidiomata pycnidial, 195–880 μ m diam, globose or irregular, erumpent, solitary or aggregated together, dark brown to black. Conidia exuding from the pycnidia in white to cream drops. Conidiophores cylindrical, straight or slightly curved. Alpha conidia 3–6.5 \times 1–2.5 μ m (\bar{x} = 5.5 \pm 1 \times 2 \pm 0.5, n = 30), fusiform, hyaline, biguttulate, with one end obtuse and the other acute. Beta conidia 13.5–33.5 \times 1–1.5 μ m (\bar{x} = 27.5 \pm 5.5 \times 1.5 \pm 0.3, n = 30), hyaline,



Fig. 11. *Diaporthe yunnanensis* (FCGMCC 3.18289). **A–B.** 7-d-old culture on PDA; **C.** Conidiomata; **D.** Conidiophores; **E.** Alpha and beta conidia; **F.** Beta conidia. Bars: C = 100 μ m; D–F = 10 μ m.

aseptate, hamate or curved, base truncate.

Culture characters: Colonies on PDA flat, with a moderate growth rate of 5.5 mm diam/d, with abundant dirty white and yellowish pigmented mycelium, dry, felted, extensive thin, and in reverse the centre cream, with zone rings of pale to dark brownish pigmentation.

Additional material examined: **China:** Yunnan Province: Xishuangbanna, on healthy leaves of *Coffea* sp., 20 Sep. 2014, W.J. Duan, culture LC 8106; *ibid.* culture LC 8107.

Diaporthe sp. 1 (Fig. 12)

Description: Conidiomata pycnidial, subglobose to globose, dark brown to black, deeply embedded in the substrate, scattered on the substrate surface, embedded in PDA, clusters in group of 2–7 pycnidia, 268–509 μ m, yellowish drop of conidia diffusing from the central ostioles. Conidiophores 6.5–19.5 \times 1–3 μ m, cylindrical, hyaline, septate, branched, straight to sinuous, base inflated, slightly tapering towards the apex. Alpha conidia 7.5–13.5 \times 2–3.5 μ m (\bar{x} = 9.9 \pm 1.4 \times 2.8 \pm 0.4, n = 30), unicellular, hyaline, fusoid to ellipsoid or clavate, two or several large guttulae

observed, base subtruncate. Beta conidia 15–40.5 \times 1–2.5 μ m (\bar{x} = 26.0 \pm 5.8 \times 1.8 \pm 0.5, n = 30), smooth, hyaline, curved, base subtruncate, tapering towards one apex.

Culture characters: Cultures incubated on PDA at 25 °C in darkness, growth rate 7.83 mm diam/day. Colony entire, white to dirty pink, cottony, sparse, brownish to black conidiomata erumpent at maturity, coated with white hypha, granular at margin, reverse pale brown, with brownish dots when maturity.

Material examined: **China:** Zhejiang Province: Gutianshan Nature Reserve (29°20' N 18°14' E), on leaves of *Alnus mill*, Jan. 2010, Y.Y. Su (culture CGMCC 3.18292 = LC 0771).

Notes: The present culture belongs to the *Diaporthe eres* complex, which is reported from a very wide range of host plants and includes mostly opportunistic pathogens or secondary invaders on saprobic host substrata (Udayanga *et al.* 2014a, Gao *et al.* 2016). Species delimitation in this complex is currently unclear. Udayanga *et al.* (2015) accepted nine phylogenetic species in the *D. eres* complex, including *D. alleghaniensis*, *D. alnea*, *D. bicincta*, *D. celsastrina*, *D. eres*, *D. helicis*, *D. neilliae*, *D. pulla*, and *D. vaccinia*. Gao *et al.* (2016) examined 17 isolates belonging to the *D. eres*



Fig. 12. *Diaporthe* sp. 1 (CGMCC 3.18292). **A.** Leaves of host plant; **B–C.** 30-d-old culture on PDA; **D.** Conidiomata; **E–F.** Conidiophores; **G.** Beta conidia; **H–I.** Alpha conidia. Bars: D = 100 μ m; E–I = 10 μ m.

complex, and reported that many presented intermediate morphology among “species” and the phylogenetic analyses often resulted in ambiguous clades with short branch and

moderate statistical support. The identification of taxa in this group remains unresolved.

Diaporthe sp. 2

Culture characters: Cultures incubated on PDA at 25 °C in darkness, growth rate, slow, 3.83 mm diam/d. Colony low, convex, entire white to yellowish, reverse brownish. Aerial mycelia white, dry, downy, with near-circular margin.

Material examined: **Japan:** on leaves of *Acer* sp., 20 Sep. 2014, W.J. Duan, culture CGMCC 3.18291 = LC 6140, culture LC 8112; *ibid.* culture LC 8113.

Notes: Although three isolates clustered in a clade distinctly different from known species in the genus included, they are not formally described because they were sterile. *Diaporthe* sp. 2 shares a low homology to the most closely related species, *D. rhoina* (95 % in ITS, 87 % in *TEF1*, 97 % in *TUB*, 94 % in *HIS*, and 95 % in *CAL*). Five *Diaporthe* species are so far only known from the sterile state, including *D. endophytica*, *D. inconspicua*, *D. infecunda*, *D. asheicola*, and *D. sterilis* (Gomes *et al.* 2013, Lombard *et al.* 2014).

Diaporthe averrhoae (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821437

Basionym: *Phomopsis averrhoae* C.Q. Chang *et al.*, *Mycosystema* **24**: 6 (2005).

Type: China: Fujian Province: on living branches of *Averrhoa carambola*, Y.H. Cheng (SCHM 3605 – holotype; AY618930, ITS sequence derived from the holotype SCHM 3605).

Diaporthe camptothecae (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821438

Basionym: *Phomopsis camptothecae* C.Q. Chang *et al.*, *Mycosystema* **24**: 145 (2005).

Type: China: Hunan Province: on living branches of *Campthotheca acuminata*, L.J. Luo (SCHM 3611 – holotype; AY622996, ITS sequence derived from the holotype SCHM 3611).

Diaporthe chimonanthi (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821439

Basionym: *Phomopsis chimonanthi* C.Q. Chang *et al.*, *Mycosystema* **24**: 146 (2005).

Type: China: Hunan Province: on living branches of *Chimonanthus praecox*, C.Q. Chang (SCHM 3614 – holotype; AY622993, ITS sequence derived from the holotype SCHM 3614).

Diaporthe eucommiae (F.X. Cao *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821440

Basionym: *Phomopsis eucommiae* F.X. Cao *et al.*, *J. Middle-South China Forestry Coll.* **10**: 34 (1990); as '*eucomm?*'.

Type: China: Guangdong Province: from leaves of *Eucommia ulmoides*, F.X. Cao (SCHM 0020 – holotype; AY601921, ITS sequence derived from the holotype SCHM 0020).

Diaporthe eucommicola (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821441

Basionym: *Phomopsis eucommicola* C.Q. Chang *et al.*, *Mycosystema* **24**: 147 (2005).

Type: China: Hunan Province: on living branches of *Eucommia ulmoides* and *Styrax hypoglauca*, L.J. Luo (SCHM 3607 – holotype; AY578071, ITS sequence derived from the holotype SCHM 3607).

Diaporthe glabrae (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821443

Basionym: *Phomopsis glabrae* C.Q. Chang *et al.*, *Mycosystema* **24**: 8 (2005).

Type: China: Fujian Province: on living branches of *Bougainvillea glabra*, Y.H. Cheng (SCHM 3622 – holotype; AY601918, ITS sequence derived from the holotype SCHM 3622).

Diaporthe lagerstroemiae (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821444

Basionym: *Phomopsis lagerstroemiae* C.Q. Chang *et al.*, *Mycosystema* **24**: 148 (2005).

Type: China: Hunan Province: on living branches of *Lagerstroemia indica*, C.Q. Chang (SCHM 3608 – holotype; AY622994, ITS sequence derived from the holotype SCHM 3608).

Diaporthe liquidambaris (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821446

Basionym: *Phomopsis liquidambaris* C.Q. Chang *et al.*, *Mycosystema* **24**: 9 (2005).

Type: China: Fujian Province: on living branches of *Liquidambar formosana*, Y.H. Cheng (SCHM 3621 – holotype; AY601919, ITS sequence derived from the holotype SCHM 3621).

Diaporthe loropetali (C.Q. Chang *et al.*) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821448

Basionym: *Phomopsis loropetali* C.Q. Chang *et al.*, *Mycosystema* **24**: 148 (2005).

Type: China: Hunan Province: on living branches of *Loropetalum chinense*, C.Q. Chang (SCHM 3615 – holotype; AY601917, ITS sequence derived from the holotype SCHM 3615).

Diaporthe magnoliicola Y.H. Gao & L. Cai, **nom. nov.**

MycoBank MB821459

Replaced name: *Phomopsis magnoliae* M.M. Xiang *et al.*, *Mycosystema* **21**: 501 (2002).

Type: China: Guangdong Province: on leaves of *Magnolia coco*, Z.D. Jiang (SCHM 3001 – holotype; AY622995, ITS sequence derived from the holotype SCHM 3001).

Note: The epithet *magnoliae* is occupied, so *Diaporthe magnolicola* is proposed as a replacement name.

Diaporthe michelina (C.Q. Chang et al.) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821460

Basionym: *Phomopsis michelina* C.Q. Chang et al., *Mycosystema* **24**: 9 (2005); as '*micheliae*'.

Type: China: Fujian Province: on living branches of *Michelia alba*, Y.H. Cheng (SCHM 3603 – holotype; AY620820, ITS sequence derived from the holotype SCHM 3603).

Diaporthe phyllanthicola (C.Q. Chang et al.) Y.H. Gao & L. Cai, **comb. nov.**

MycoBank MB821461

Basionym: *Phomopsis phyllanthicola* C.Q. Chang et al., *Mycosystema* **24**: 10 (2005).

Type: China: Fujian Province: on living branches of *Phyllanthus emblica*, Y.H. Cheng (SCHM 3680 – holotype; AY620819, ITS sequence derived from the holotype SCHM 3680).

DISCUSSION

In this study, eight new species of *Diaporthe* are introduced, having been isolated from various plant hosts collected in different countries. Twelve *Phomopsis* species described from China were subjected to molecular analysis, and transferred to *Diaporthe* to conform to the “one fungus one name” rule (Udayanga et al. 2011, Rossman et al. 2016). To address the taxonomy of the other *Phomopsis* species described from China, neo- or epitypes will need to be designated to resolve their position and confirm their placement in *Diaporthe*.

Previous taxonomic studies in *Diaporthe* (syn. *Phomopsis*) have been primarily based on morphology, which has been shown to be unnatural in reflecting evolutionary history due to the simple and plastic morphological characters (Gao et al. 2015). The same applies to many other genera of ascomycetes. For example, species referred to *Phoma* have been shown to be highly polyphyletic and scattered throughout at least six families within *Pleosporales* (Aveskamp et al. 2010, Chen et al. 2015). Although *Diaporthe* was previously thought to be monophyletic based on its typical and unique *Phomopsis* asexual morph and diaporthean sexual morph (Gomes et al. 2013), a paraphyletic nature is revealed in the present study (Fig. 1). Several genera, notably *Ophiodiaporthe* (Fu et al. 2013), *Pustulomyces* (Dai et al. 2014), *Phaeocystostroma*, and *Stenocarpella* (Lamprecht et al. 2011), are shown to be embedded in *Diaporthe* s. lat., none of which present an independent lineage from *Diaporthe* as currently circumscribed (Fig. 1). These genera were established based on their morphological characteristics (Vasilyeva et al. 2007, Lamprecht et al. 2011,

Fu et al. 2013, Dai et al. 2014). For example, *Ophiodiaporthe* produces only one type of globose or subglobose conidia that differs from the dimorphic (fusiform and filiform) conidia of *Diaporthe* (Fu et al. 2013); *Phaeocystostroma* and *Stenocarpella* produce pigmented alpha conidia which differ from the hyaline conidia of *Diaporthe* (Lamprecht et al. 2011); *Pustulomyces* produces larger, straight or sigmoid conidia (Dai et al. 2014). *Phaeocystostroma* and *Stenocarpella* were originally suspected to be members of *Botryosphaeriaceae* (*Botryosphaeriales*) because of their pigmented alpha conidia and diplo-dia-like morphology (Crous et al. 2006). However, they were subsequently allocated to *Diaportheales* based on phylogenetic analysis (Lamprecht et al. 2011), which is confirmed in this study.

The large “*Diaporthe*” clade embedded with the heterogeneous genera *Ophiodiaporthe*, *Pustulomyces*, *Phaeocystostroma*, and *Stenocarpella* is probably a typical example of divergent evolution in morphological characters. Such an evolution could have been driven by host and/or environmental adaptations. For example, the monotypic *Ophiodiaporthe* is associated with *Cyathea lepifera* (a fern), while *Pustulomyces* is bambusicolous (Dai et al. 2014). On the contrary, none of the previously named over 1 900 *Diaporthe* / *Phomopsis* species was recorded from a fern or *Bambusaceae* (<https://nt.ars-grin.gov/fungal-databases/>). It is therefore reasonable to speculate that the speciation of *Ophiodiaporthe* and *Pustulomyces*, as well as the distinctly different morphologies from their close *Diaporthe* allies, are the consequences of evolutionary adaptation to new hosts. Similarly, *Phaeocystostroma* and *Stenocarpella* are mainly restricted to maize (*Zea mays*), causing root stalk and cob rot (Stovold et al. 1996, Lamprecht et al. 2011).

Splitting *Diaporthe* into many smaller genera would achieve monophyletic groupings, but would also create many additional problems. The “new genera” split from *Diaporthe* would have no recognisable morphological distinctions in either sexual or asexual morphs. In addition, splitting *Diaporthe* into many smaller genera will result in numerous name changes, which is certainly an unfavourable option for both mycologists and plant pathologists.

Diaporthe has long been well-known to include plant pathogens, some on economically important hosts, such as *Helianthus annuus* (sunflower; Thompson et al. 2011) and *Glycine max* (soybean; Santos et al. 2011). However, the number of known endophytic *Diaporthe* species has increased rapidly in recent years (Huang et al. 2015, Gao et al. 2016). Wang et al. (2013) concluded that our current knowledge of the ecology and biology of endophytic *Diaporthe* species is just the “tip of the iceberg”. In 2013, a new sterile endophytic species, *Diaporthe endophytica*, was formally named (Gomes et al. 2013). The research on *Citrus* conducted by Huang et al. (2015) recorded seven apparently undescribed endophytic *Diaporthe* species. Inspection of *Diaporthe* species on *Camellia sinensis* resulted in the description of four new and five known species, all occurring as endophytes (Gao et al. 2016). Because many of these plant pathogenic *Diaporthe* species are commonly encountered as sterile endophytes, a multigene DNA database will be essential to aid in their future identification.

Accurate identification of fungal pathogens is the basis of quarantine and disease control (Udayanga et al. 2011).

Thompson *et al.* (2011) reported significant damage to sunflower in Australia caused by *Diaporthe helianthi* which was originally only known from Europe (former Yugoslavia), and is apparently an invasive species in Australia. *Diaporthe helianthi* is listed in the Chinese quarantine directory, and has long been considered a predominant disease limiting production in Europe (Desanlis *et al.* 2013). Duan *et al.* (2016) reported this pathogen on sunflower seeds imported from Ukraine into China. Here, we report another interception of *D. helianthi* from *Lagerstroemia indica* imported from Japan to China. This serves as additional evidence of how quickly serious pathogens such as *Diaporthe* species can be distributed as endophytes or latent pathogens with global trade.

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