Diaporthe is paraphyletic

Yahui Gao1,2*, Fang Liu*, Weijun Duan3, Pedro W. Crous4,5, and Lei Cai1,2

1State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, P.R. China
2University of Chinese Academy of Sciences, Beijing 100049, P.R. China; corresponding author e-mail: cail@im.ac.cn
3Ningbo Academy of Inspection and Quarantine, Zhejiang 315012, P.R. China
4Westerdijk Fungal Biodiversity Institute, Uppsalalaan 8, 3584CT Utrecht, The Netherlands
5Department of Microbiology and Plant Pathology, Tree Protection Co-operative Programme, Forestry and Agricultural Biotechnology Institute, University of Pretoria, Pretoria 0002, South Africa

*These authors contributed equally to this work.

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, Postulomyces, Phaeocystostroma, 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.

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. stenlis (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
(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, Melanoconis, 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), Phaeocytostroma (Lamprecht et al. 2011), Ophiidiaporthe (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 nRNA, the first internal transcribed spacer region, the 5.8S nRNA gene; the second internal transcribed spacer region and the 5’ end of the 28S nRNA 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 *Diaporthaceae*.

| Species names* | Culture collection no. | Isolation sources | Country | GenBank Accession Numbers | References |
|----------------|------------------------|-------------------|---------|--------------------------|------------|
| *D. acaciigena* | CBS 129521 (ex-type)   | Acacia retinodes  | Australia | KC343005 - KC343731     | Gomes et al. (2013) |
| *D. ampelina*   | FAU 586                | Vitis sp.         | USA: New York | - AF439635 - - - | -          |
| *D. angelicae*  | CBS 111592             | Heracleum spondylium | Austria | KC343027 - KC343753     | Gomes et al. (2013) |
|                 | AR 3724                | Heracleum spondylium | Austria | KC343026 - KC343752     | Gomes et al. (2013) |
| *D. apiculata*  | LC 3418 (ex-type)      | Camellia sinensis | China   | KP267896 KY011852 KP267970 | This study |
| *D. arecae complex* | LC 3452          | Camellia sinensis | China   | KP267850 KY011839 KP267924 | This study |
|                 | LC 4155               | Rhododendron sp.  | China   | KY011895 KY011879 KY011906 | This study |
|                 | LC 4159               | Rhododendron sp.  | China   | KY011896 KY011880 KY011907 | This study |
| *D. biguttus*   | LC 4164               | Unknown host      | China   | KY011897 KY011881 KY011908 | This study |
| *D. compacta*   | LC 1106 (ex-type)     | Lithocarpus glaber | China   | KB576262 KB576285       | This study |
| *D. discoidispora* | LC 3503          | Camellia sinensis | China   | KY011887 KY011854 KY011898 | This study |
| *D. ellipicola* | LC 3198 (ex-type)     | Lithocarpus glaber | China   | KB576270 KB576245       | This study |
| *D. ellipicola* | LC 3205               | Camellia sinensis | China   | KB714499 KB714511       | This study |
| *D. ellipicola* | LC 3206               | Camellia sinensis | China   | KB714500 KB714512       | This study |
|                 | CBS 109767            | Acer campestre    | Austria  | KC343075 - KC343801    | Gomes et al. (2013) |
| *D. fusicola*   | LC 1126               | Lithocarpus glaber | China   | KB576281 KB576256       | This study |
| *D. hongkongensis* | LC 0778          | Lithocarpus glaber | China   | KB576263 KB576238       | This study |
| *D. incompleta* | LC 0784               | Lithocarpus glaber | China   | KB576210 KB576245       | This study |
| *D. liriodendri* | LC 0812              | Smilax china      | China   | KB576207 KB576237       | This study |
| *D. lucida*     | LC 6706              | Camellia sinensis | China   | KB576287 KB576242       | This study |
| *D. mahothocarpi* | LC 0732             | Mahonia bealei    | China   | KB576297 KB576242       | This study |
| *D. masirevicii* | LC 0763 (ex-type)     | Lithocarpus glaber | China   | KB576297 KB576242       | This study |
| *D. neoarctii*  | CBS 109490           | Ambrosia trifida  | USA: New Jersey | KC343145 - KC343871     | Gomes et al. (2013) |
| *D. oncostoma* | CBS 109741           | Robinia pseudoacacia | Russia  | KC343161 - KC343887     | Gomes et al. (2013) |
| *D. oraccinii*  | LC 3166 (ex-type)     | Camellia sinensis | China   | KB576263 KB576238       | This study |
| *D. ovoicicola* | LC 1128 (ex-type)     | Lithocarpus glaber | China   | KB576287 KB576242       | This study |
| *D. penetriteum* | LC 3215             | Camellia sinensis | China   | KB576287 KB576242       | This study |
| *D. perjuncta*  | LC 3353 (ex-type)     | Camellia sinensis | China   | KB576297 KB576242       | This study |
| *D. perjuncta*  | LC 3394               | Camellia sinensis | China   | KB576297 KB576242       | This study |

*Species names* include *Diaporthe* and *Spicaria*.
| Species names* | Culture collection no. | Isolation sources | Country | GenBank Accession Numbers | References |
|---------------|------------------------|-------------------|---------|---------------------------|------------|
| **D. pseudophoenicicola** | LC 6150 | Phoenix canariensis | China | KY011891 KY011865 KY011902 | This study |
| | LC 6151 | Phoenix canariensis | China | KY011892 KY011866 KY011903 | This study |
| **D. pseudophoenicicola** | CBS 109742 | Acer pseudoplatanus | Austria | KC343185 - KC343911 | Gomes et al. (2013) |
| | CBS 109760 | Acer pseudoplatanus | Austria | KC343186 - KC343912 | Gomes et al. (2013) |
| | CBS 109784 | Prunus padus | Austria | KC343187 - KC343913 | Gomes et al. (2013) |
| **D. rudis** | LC 6147 | Dendrobenthamia japonica | USA | KY011890 KY011864 KY011901 | This study |
| **D. undulata** | LC 6145 | Ilex aquifolium | China | KY011889 KY011863 KY011900 | This study |
| **D. velutina** | LC 4414 | Lithocapussp. | China | KX986789 KY011882 KY999180 | This study |
| | LC 4419 | Neolitsea sp. | China | KX986789 KY011883 KY999181 | This study |
| **D. xishuangbanica** | LC 6707 | Camellia sinensis | China | KX986783 KY011860 KY999175 | This study |
| | LC 6744 | Camellia sinensis | China | KX986784 KY011862 KY999176 | This study |
| **D. yunnanensis** | LC 6168 | Coffea sp. | China | KX986796 KY011867 KY999188 | This study |
| **Diaportha sp.** | LC 3156 | Camellia sinensis | China | KP267912 KY011855 KP267986 | This study |
| | LC 6170 | Coffea sp. | China | KX986786 KY011856 KY999174 | This study |
| | LC 6171 | Solanum melongena | China | KX986788 KY011882 KY999180 | This study |
| | LC 6232 | Theobroma cacao | China | KX986797 KY011868 KY999189 | This study |
| **Mazzantia napelli** | AR 3498 | Aconitum vulparia | Austria | - | AF408368 EJ222017 Castlebury et al. (2002) |
| **OphiodyaORTH Sp.** | BCRC 34961 | Cyathea lepifera | Taiwan | JX570889 JX570891 | KC65406 Fu et al. (2013) |
| **Phaeocytostroma ambiguum** | CPC 17071 | Zea mays | South Africa | FR748036 - FR748068 | Lamprecht et al. (2011) |
| | CPC 17072 | Zea mays | South Africa | FR748037 FR748096 FR748069 | Lamprecht et al. (2011) |
| **Ph. plurivorum** | CBS 113835 | Helianthus annuus | Portugal | FR748046 FR748104 FR748078 | Lamprecht et al. (2011) |
| **Ph. sacchari** | CBS 275.34 | - | Japan | FR748047 FR748105 FR748079 | Lamprecht et al. (2011) |
| **Ph. megalosporum** | CBS 284.65 | Rice-field soil | India | FR748045 FR748103 FR748077 | Lamprecht et al. (2011) |
| **Pustulomyces bambusicola** | MFLUCC 11-0436 | on dead culm of bamboo | Thailand | - | KF806753 KF806755 Dai et al. (2014) |
| **Stenocarpella macrospora** | CBS 117560 | Rain damaged Bt maize hybrid, 2003-04 season | South Africa | FR748048 DQ377934 - | Lamprecht et al. (2011) |
| **S. maydis** | CBS 117558 | Traditional/landrace maize from 2003/04 season | South Africa | FR748051 DQ377936 FR748080 | Lamprecht et al. (2011) |
| **Valsa ambiens** | CFCC 89894 | Pyrus bretschneideri | China | KR045617 KR045699 KU710912 | Fan et al. (2014) |

*New species described in this paper are shown in bold.
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(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 μL were composed of 10 × EasyTaq buffer (MgCl$_2$ included; Transgen, Beijing), 50 μM dNTPs, 0.2 μM 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 Omogenetics 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 (Katoh & 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 Diaporthaceae (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 Diaporthella 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 invariant 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 Diaporthaceae 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+Γ model with gamma-distributed rates were implemented for LSU and ITS, HKY+Γ model with invariable-distributed rates were implemented for TEF1. The Bayesian analysis lasted 7 × 10$^6$ generations and the consensus tress 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, Ophiidiaporthe, 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 Diaporthaceae 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). Ophidiaporthe 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 Diaporthaceae (Fig. 1).

Phylogenetic analyses of the combined datasets of Diaporthe species

In total, 1089 sequences derived from 273 ingroup taxa were combined and Diaporthella 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+Γ model was selected for CAL, HIS and ITS, HKY+Γ 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 ≥ 70 %, bayesian probabilities BPP ≥ 0.90 are marked above the branches. The tree is rooted with Valsa ambiens.
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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 ≥ 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).
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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 |
|---------------|------------------------|-------------------|-------------|---------------------------|------------|
| *D. acaciigena* | CBS 129521 (ex-type)   | Acacia retinodes   | Mimosaceae  | KC343005 KC343731 KC343973 KC343489 KC343247 | Gomes et al. (2013) |
| *D. acerina*   | CBS 137.27             | Acer saccharum     | Aceraceae   | KC343006 KC343732 KC343974 KC343490 KC343248 | Gomes et al. (2013) |
| *D. acutispora* | CGMCC 3.18285 = LC 6160| Coffea sp., endophyte | Rubiaceae  | XXXX XXXX XXXX XXXX XXXX | This study |
| *D. alleghaniensis* | CBS 495.72 (ex-type)   | Betula alleghaniensis, branches | Betulaceae | XXXX XXXX XXXX XXXX XXXX | Gomes et al. (2013) |
| *D. alnea*     | CBS 137.46 (ex-type)   | Alnus sp.          | Betulaceae  | XXXX XXXX XXXX XXXX XXXX | Gomes et al. (2013) |
| *D. amelia*    | CBS 114015             | Pyrus communis     | Rosaceae    | XXXX XXXX XXXX XXXX XXXX | Gomes et al. (2013) |
| *D. amelina*   | CBS 111458             | Vitis vinifera     | Vitaceae    | AF230751 AY753006 JX270542 | Gomes et al. (2013) |
| *D. amygdali*  | CBS 126679 (ex-type)   | Prunus dulcis      | Rosaceae    | XXXX XXXX XXXX XXXX XXXX | Gomes et al. (2013) |
| *D. anacardi*  | CBS 123979 (ex-epitype)| Anacardium occidentale | Anacardiaceae | XXXX XXXX XXXX XXXX XXXX | Gomes et al. (2013) |
| *D. angelicae* | CBS 111592 (ex-epitype)| Heracleum spathylodium | Apiaceae    | XXXX XXXX XXXX XXXX XXXX | Gomes et al. (2013) |
| *D. apiculata* | LC 4152                | Camellia, leaf     | Theaceae    | XXXX XXXX XXXX XXXX XXXX | Gao et al. (2016) |
| *D. arctii*    | CBS 136.25             | Arctic sp.         | Arecaceae   | XXXX XXXX XXXX XXXX XXXX | Lombard et al. (2014) |
| *D. areca*     | CBS 553.75             | Citrus sp., fruit  | Rutaceae    | XXXX XXXX XXXX XXXX XXXX | Lombard et al. (2014) |
| *D. arengae*   | CBS 114979 (ex-type)   | Areca catechu, fruit | Arecaceae   | XXXX XXXX XXXX XXXX XXXX | Lombard et al. (2014) |
| *D. asheiola*  | CBS 136967, CPC 15608, (ex-type) | Vaccinium ashei | Ericaceae  | KJ160562 KJ160594 KJ160518 | Lombard et al. (2014) |
| *D. aspalathi* | CBS 136968, CPC 16611  | Vaccinium ashei    | Ericaceae   | KJ160563 KJ160595 KJ160519 | Lombard et al. (2014) |
| *D. australafricana* | CBS 11186             | Vitis vinifera     | Vitaceae    | XXXX XXXX XXXX XXXX XXXX | Lombard et al. (2014) |
| *D. baccae*    | CBS 136971             | Vaccinium corimbosum | Ericaceae  | KJ160564 KJ160596 | Lombard et al. (2014) |
| *D. clavata*   | CBS 136972 (ex-type)   | Vaccinium corimbosum | Ericaceae  | KJ160565 KJ160597 | Lombard et al. (2014) |
| Species name | Culture collection no. | GenBank Accession Numbers | ITS | TEF1 | TUB | HIS | CAL | References |
|--------------|------------------------|---------------------------|-----|-----|-----|-----|-----|------------|
| D. batatas   | CBS 122.27              | KC343716                   |     |     |     |     |     | Gao et al. (2013) |
| D. becerru | CBS 652.97              | KC343733                   |     |     |     |     |     | Gomes et al. (2013) |
| D. betulae   | CBS 133.183 (ex-type)   | KC343729                   |     |     |     |     |     | Gomes et al. (2013) |
| D. biguttus  | CBS 114.347             | KC343731                   |     |     |     |     |     | Gomes et al. (2013) |
| D. biguttus  | CBS 133.183 (ex-type)   | KC343732                   |     |     |     |     |     | Gomes et al. (2013) |
| D. brasilensis| CBS 176.55              | KC343738                   |     |     |     |     |     | Gomes et al. (2013) |
| D. caldarii  | CBS 122.27              | KC343716                   |     |     |     |     |     | Gao et al. (2013) |
| D. cauliflora| CBS 652.97              | KC343733                   |     |     |     |     |     | Gomes et al. (2013) |
| D. chlorosticta| CBS 133.183 (ex-type)  | KC343729                   |     |     |     |     |     | Gomes et al. (2013) |
| D. clavata   | CBS 114.347             | KC343731                   |     |     |     |     |     | Gomes et al. (2013) |
| D. clavata   | CBS 133.183 (ex-type)   | KC343732                   |     |     |     |     |     | Gomes et al. (2013) |
| D. clavata   | CBS 176.55              | KC343738                   |     |     |     |     |     | Gomes et al. (2013) |
| D. chlorosticta| CBS 652.97              | KC343733                   |     |     |     |     |     | Gomes et al. (2013) |
| D. chlorosticta| CBS 133.183 (ex-type)  | KC343729                   |     |     |     |     |     | Gomes et al. (2013) |
| D. chlorosticta| CBS 176.55              | KC343738                   |     |     |     |     |     | Gomes et al. (2013) |
| D. chlorosticta| CBS 652.97              | KC343733                   |     |     |     |     |     | Gomes et al. (2013) |
Table 2. (Continued).

| Species names | Culture collection no. | Isolation sources | Host family | GenBank Accession Numbers | References |
|---------------|------------------------|-------------------|-------------|---------------------------|------------|
| *D. citriasiana* | ZJUD 30 (ex-type) | Citrus unshiu, dead wood | Rutaceae | JQ954645 | Huang et al. (2015) |
| | ZJUD 33 | Citrus paradise, stem-end rot fruit | Rutaceae | JQ954658 | Huang et al. (2015) |
| | ZJUD 34 | Citrus sp. | Rutaceae | JQ954648 | Huang et al. (2015) |
| | ZJUD 35 | Citrus unshiu, dead wood | Rutaceae | JQ954649 | Huang et al. (2015) |
| | ZJUD 36 | Citrus unshiu, dead wood | Rutaceae | JQ954649 | Huang et al. (2015) |
| | LC3083 (ex-type) | Camellia sinensis, leaf, endophyte | Theaceae | KP267854 | Gao et al. (2016) |
| | LC3084 | Camellia sinensis, leaf, endophyte | Theaceae | KP267855 | Gao et al. (2016) |
| *D. convolvuli* | CBS 124654 | Convolvulus arvensis | Convolvulaceae | KC343054 | Huang et al. (2015) |
| *D. crataegi* | CBS 114435 | Crataegus oxyacantha | Rosaceae | KC343055 | Gomes et al. (2013) |
| *D. crotalariae* | CBS 162.33 (ex-type) | Crotalaria spectabilis | Fabaceae | KC343056 | Gomes et al. (2013) |
| *D. cuppatae* | CBS 117499 | Aspalathus linearis | Fabaceae | KC343057 | Gomes et al. (2013) |
| *D. cynaroidis* | CBS 122676 | Protea cynaroides | Proteaceae | KC343058 | Gomes et al. (2013) |
| *D. cytosporella* | AR 5149 | Citrus sinensis | Rutaceae | KC843309 | Udayanga et al. (2014b) |
| *D. decedens* | CBS 114281 | Corylus avellana | Corylaceae | KC343060 | Gomes et al. (2013) |
| | CBS 109772 | Corylus avellana | Corylaceae | KC343061 | Gomes et al. (2013) |
| *D. detrusa* | CBS 109770 | Berberis vulgaris | Berberidaceae | KC343062 | Gomes et al. (2013) |
| | CBS 114652 | Berberis vulgaris | Berberidaceae | KC343063 | Gomes et al. (2013) |
| *D. discoidispora* | ZJUD 87, CGMCC 3.17254 | Citrus sinensis | Rutaceae | KJ490622 | Huang et al. (2015) |
| | ZJUD 89, CGMCC 3.17255 | Citrus sinensis | Rutaceae | KJ490624 | Huang et al. (2015) |
| *D. ellipicola* | CGMCC 3.18287 = LC 4802 | Elaeagnus glabra, pathogen | Elaeagnaceae | KX999779 | This study |
| | LC 4806 | Elaeagnus glabra, pathogen | Elaeagnaceae | KX999780 | This study |
| *D. eugeniae* | CBS 133811 (ex-type) | Schinus terebinthifolius | Anacardiaceae | KC343065 | Gomes et al. (2013) |
| | LGMF 911 | Schinus terebinthifolius | Anacardiaceae | KC343066 | Gomes et al. (2013) |
| *D. eres* | ARS193, CBS 13859 (ex-epitype) | Ulmus laevis | Ulmaceae | KJ210529 | Udayanga et al. (2014a) |
| | CBS 113470 | Castanea sativa | Fagaceae | KJ210530 | Udayanga et al. (2014a) |
| *D. fibrosa* | CBS 444.82 | Eugenia aromatica, leaf | Myrtaceae | KC343084 | Gomes et al. (2013) |
| | CBS 109751 | Rhamnus cathartica | Rhamnaceae | KC343099 | Gomes et al. (2013) |
| | CBS 113830 | Rhamnus cathartica | Rhamnaceae | KC343100 | Gomes et al. (2013) |
Table 2. (Continued).

| Species names* | Culture collection no. | Isolation sources | Host family | GenBank Accession Numbers | References |
|----------------|------------------------|-------------------|-------------|---------------------------|------------|
| D. foeniculina  | CBS 116957             | Pyrus pyrifolia   | Rosaceae    | KC343103 KC343829 KC344071 KC343587 KC343345 | Gomes et al. (2013) |
|                 | CBS 187.27 (ex-type of P. theicola) | Camellia sinensis, leaves and branches | Theaceae | KC343107 KC343833 KC344075 KC343591 KC343349 | Gomes et al. (2013) |
|                 | CBS 123208             | Foeniculum vulgare | Apiaceae    | KC343104 KC343830 KC344072 KC343588 KC343346 | Gomes et al. (2013) |
| D. fraxiniangustifolia | BRIP 54781 (ex-epitype) | Fraxinus-angustifolia subsp. oxycapa | Oleaceae | JX862528 JX852534 KF170920 | Tan et al. (2013) |
| D. ganjae       | CBS 180.91 (ex-type)   | Cannabis sativa, dead leaf | Cannabaceae | KC343112 KC343838 KC344075 KC343596 KC343349 | Gomes et al. (2013) |
| D. gardeniae    | CBS 288.56             | Gardenia florid, stem | Rubiaceae   | KC343113 KC343839 KC344076 KC343597 KC343355 | Gomes et al. (2013) |
| D. gulyae       | BRIP 55657a (ex-type)  | Helianthus annusus | Asteraceae  | JF431299 JN645603 KJ197271 | Thompson et al. (2015) |
| D. helianthi    | CBS 344.94             | Helianthus annusus | Asteraceae  | KC343114 KC343840 KC344082 KC343598 KC343356 | Gomes et al. (2013) |
| D. helicis      | AR 5211                | Hedera helix      | Araliaceae  | KC343115 KC343841 KC344083 KC343599 KC343357 | Gomes et al. (2013) |
| D. hickoriae    | CBS 145.26 (ex-epitype) | Carya glabra | Juglandaceae | KC343116 KC343844 KC344086 KC343602 | Gomes et al. (2013) |
| D. hongkongensis| CBS 114434             | Dichroa febrifuga, fruit | Hydrangeaceae | KC343119 KC343845 KC344087 KC343603 KC343356 | Gomes et al. (2013) |
| D. hordei       | CBS 481.92             | Hordeum vulgare   | Poaceae     | KC343120 KC343846 KC344088 KC343604 KC343357 | Gomes et al. (2013) |
| D. impulsa      | CBS 141.27             | Sorbus aucuparia  | Rosaceae    | KC343121 KC343847 KC344089 KC343605 KC343358 | Gomes et al. (2013) |
| D. incompleta   | CGMCC 3.18288 = LC 6754 | Camellia sinensis, pathogen | Theaceae | KC986794 KC999186 KC999226 KC999265 KC999289 | This study |
|                 | LC 6706                | Camellia sinensis, pathogen | Theaceae | KC986793 KC999185 KC999264 KC999288 | This study |
| D. inconspicua  | CBS 133813 (ex-type)   | Maytenus ilicifolia, endophytic in petiole | Celastraceae | KC343123 KC343849 KC344091 KC343607 KC343365 | Gomes et al. (2013) |
| D. infecunda    | CBS 133812 (ex-type)   | Schinus terebinthifolius | Anacardaceae | KC343126 KC343852 KC344094 KC343610 KC343368 | Gomes et al. (2013) |
|                 | LGMF 908               | Schinus terebinthifolius | Anacardaceae | KC343127 KC343853 KC344095 KC343611 KC343369 | Gomes et al. (2013) |
| D. kongii       | BRIP 54031 (ex-type)   | Helianthus annusus | Asteraceae  | JF431301 JN645797 KJ197272 | Thompson et al. (2011) |
| D. lichicola    | BRIP 54900 (ex-type)   | Litchi chinensis  | Sapindaceae | JX862533 JX862539 KF170925 | Tan et al. (2013) |
| D. longicicola  | CGMCC 3.17089 (ex-type) | Lithocarpus glabra | Fabaceae    | KF576267 KF576242 KF576291 | - Gao et al. (2015) |
| D. longicolla   | FAU 599                | Glycine max       | Fabaceae    | KJ509728 KJ590767 KJ610883 KJ659188 | - Udayanga et al. (2015) |
| D. longispora   | CBS 194.36 (ex-type)   | Ribes sp.         | Grossulariaceae | KC343135 KC343861 KC344103 KC343619 KC343377 | Gomes et al. (2013) |
| D. lusitanicae  | CBS 123212 (ex-type)   | Foeniculum vulgare | Apiceae    | KC343136 KC343862 KC344104 KC343620 | Gomes et al. (2013) |
| D. macintoshii  | BRIP 55604a            | Rapistrum rugosum | Brassicaceae | KJ197290 KJ197251 KJ197269 | Thompson et al. (2015) |
| D. mahothocarpus | CGMCC 3.15181         | Lithocarpus glabra | Fabaceae    | KC153096 KC153087 | - Gao et al. (2014) |
| D. manihotia    | CBS 505.76             | Manihot utilisima, 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 |
|----------------|------------------------|-------------------|-------------|---------------------------|------------|
| *D. maritima*  | NB 3657-71 (ex-type)   | Picea rubens needle Pinaceae |            | KU574614 - - Y. Tanney et al. (2016) |
| *D. masirevi- ci* | BRIP 57892a (ex-type) | Helianthus annuus Asteraceae |            | KJ197277 - - L. Huang et al. (2015) |
| *D. mayteni*  | CBS 133.22            | Maytenus ilicicolia Celastraceae |            | KC343139 KC343865 KC344107 KC343623 KC343381 Gomes et al. (2013) |
| *D. megalospo- ra* | CBS 143.27            | Sambucus canadensis Caprifoliaceae |            | KC343140 KC343866 KC344108 KC343624 KC343382 Gomes et al. (2013) |
| *D. melonis*  | CBS 507.18I (ex-type) | Glycine soja Fabaceae |            | KC343141 KC343867 KC344109 KC343625 KC343383 Gomes et al. (2013) |
| *D. middle- tonii* | BRIP 57329             | Chrysanthemoides monilifera subsp. rotundata Rosaceae |            | KJ197278 - - B. Thompson et al. (2015) |
| *D. miriciae* | BRIP 55662c (ex-type)  | Glycine max Fabaceae |            | KJ197277 - - L. Huang et al. (2015) |
| *D. musigena* | CBS 127.29             | Musa sp., leaves Musaceae |            | KC343143 KC343870 KC344111 KC343627 KC343384 Gomes et al. (2013) |
| *D. neilliae* | CBS 144.22             | Spiraea sp. Rosaceae |            | KC343144 KC343871 KC344112 KC343628 KC343385 Gomes et al. (2013) |
| *D. neoarctii* | CBS 109.29             | Ambrosia trifida Asteraceae |            | KC343145 KC343872 KC344113 KC343629 KC343386 Gomes et al. (2013) |
| *D. neoraoniko- yaporum* | MFLUCC 14-1136 | Tectona grandis Verbenaceae |            | JX862530 JX862536 KF170922 - KF170921 Doilom et al. (2017) |
| *D. nobilis*  | CBS 127.29             | Glycine max Fabaceae |            | KJ197278 - - L. Huang et al. (2015) |
| *D. nomurai*  | CBS 157.29             | Morus sp., leaves Moraceae |            | KC343145 KC343870 KC344111 KC343627 KC343384 Gomes et al. (2013) |
| *D. nothofagi* | BRIP 54801 (ex-type)   | Nothofagus cunninghamii Fagaceae |            | JX862530 JX862536 KF170922 - KF170921 Doilom et al. (2017) |
| *D. novem*    | CBS 127.29             | Glycine max Fabaceae |            | KJ197278 - - L. Huang et al. (2015) |
| *D. oraccini- ii* | LC 3186 (ex-type)     | Camellia sinensis Theaceae |            | KP267863 KP267856 KP267858 KP293464 Gao et al. (2016) |

*Diaporthe is paraphyletic*
### Table 2. (Continued).

| Species names* | Culture collection no. | Isolation sources | Host family | GenBank Accession Numbers | References |
|----------------|------------------------|-------------------|-------------|---------------------------|------------|
| D. ovalispora  | ZJUD 93, CGMCC 3.17256 | Citrus limon      | Rosaceae    | KJ490628 KJ490507 KJ490449 KJ490570 | Huang et al. (2015) |
| D. oxe        | CBS 133186 (ex-type)   | Maytenus ilicifolia | Celastraceae | KC343164 KC343890 KC344132 KC343648 KC343406 | Gomes et al. (2013) |
| D. ovifera     | CBS 133187             | Maytenus ilicifolia | Celastraceae | KC343165 KC343891 KC344133 KC343649 KC343407 | Gomes et al. (2013) |
| D. padi var. padi | CBS 114200         | Prunus padus      | Rosaceae    | KC343169 KC343895 KC344137 KC343653 KC343411 | Gomes et al. (2013) |
| D. oxe        | CBS 114649             | Alnus glutinosa   | Betulaceae  | KC343170 KC343896 KC344138 KC343654 KC343412 | Gomes et al. (2013) |
| D. paxensei    | CBS 133184 (ex-type)   | Maytenus ilicifolia | Celastraceae | KC343171 KC343897 KC344139 KC343655 KC343413 | Gomes et al. (2013) |
| D. pascoei     | BRIP 54847 (ex-type)   | Persica americana | Lauraceae   | JX862532 JX862538 KF170924 | - | Tan et al. (2013) |
| D. penetriteum | LC 3353                | Camellia sinensis, leaf | Theaceae | KP714505 KP714517 KP714529 KP714493 | - | Gao et al. (2016) |
| D. perjuncta   | LC 3394                | Camellia sinensis, leaf | Theaceae | KP267893 KP267967 KP293473 KP293547 | - | Gao et al. (2016) |
| D. perjuncta   | CBS 109745 (ex-type)   | Ulmus glabra      | Ulmaceae    | KC343172 KC343898 KC344140 KC343656 KC343414 | Gomes et al. (2013) |
| D. penicillata | CBS 124030             | Malus pumila, bark | Rosaceae    | KC343149 KC343875 KC344117 KC343633 KC343391 | Gomes et al. (2013) |
| D. perseae     | CBS 151.73             | Persea gratissima, young fruit | Lauraceae | KC343173 KC343899 KC344141 KC343657 KC343415 | Gomes et al. (2013) |
| D. phaseolorum | AR 4203, CBS 139281    | Phaseolus vulgaris | Fabaceae    | KJ590735 KJ590739 KJ610890 KJ659220 | - | Huang et al. (2015) |
| D. podocarpini | CGMCC 3.18281 = LC 6155 | Podocarpus macrophyllus, endophyte | Podocarpaceae | XX986774 XX999167 XX999207 XX999246 XX999278 | This study |
| D. podocarpini | LC 6144                | Podocarpus macrophyllus, endophyte | Podocarpaceae | XX986773 XX999166 XX999206 XX999245 | - | This study |
| D. podocarpini | LC 6194                | Podocarpus macrophyllus, endophyte | Podocarpaceae | XX986765 XX999156 XX999196 XX999236 XX999275 | - | This study |
| D. podocarpini | LC 6197                | Podocarpus macrophyllus, endophyte | Podocarpaceae | XX986777 XX999170 XX999210 XX999240 XX999279 | - | This study |
| D. podocarpini | LC 6200                | Podocarpus macrophyllus, endophyte | Podocarpaceae | XX986769 XX999161 XX999201 XX999240 XX999276 | - | This study |
| D. pseudomangiferae | CBS 101339 (ex-type) | Olea europaea, endophytes | Oleaceae | XX986771 XX999164 XX999204 XX999243 XX999277 | This study |
| D. pseudophoenicicolae | CBS 388.89 | Mangifera indica, peel of fruit | Anacardiaceae | KC343181 KC343907 KC344149 KC343665 KC343423 | Gomes et al. (2013) |
| D. pseudophoenicicolae | CBS 462.69 (ex-type) | Phoenix dactylifera, dead tops of green leaves | Anacardiaceae | KC343182 KC343908 KC344150 KC343666 KC343424 | Gomes et al. (2013) |
| D. pterocarpus | MFLUCC 10-0571         | Pterocarbus indicus | Papilionaceae | JQ619899 JX275416 JX275460 | - | Udayanga et al. (2012) |
| D. pterocarpus | MFLUCC 10-0575         | Pterocarbus indicus | Papilionaceae | JQ619901 JX275418 JX275462 | - | Udayanga et al. (2012) |
Diaporthe is paraphyletic

| Species names* | Culture collection no. | Isolation sources | Host family | GenBank Accession Numbers | References |
|----------------|------------------------|-------------------|-------------|---------------------------|------------|
| **D. pterocarpica** | MFLUCC 10-0580a (ex-type) | *Pterocarpus indicus* | Papilionaceae | JQ619887 JX275403 JX275441 - JX197433 | Udayanga et al. (2012) |
| **D. pterocarpica** | MFLUCC 10-0580b | *Pterocarpus indicus* | Papilionaceae | JQ619888 JX275404 JX275442 - JX197434 | Udayanga et al. (2012) |
| **D. pulla** | CBS 338.89 | *Hedera helix* | Araliaceae | KC343152 KC343878 KC344120 KC343636 - | Udayanga et al. (2014a) |
| **D. pulla** | CBS 109742 | *Acer pseudoaplatanus* | Aceraceae | KC343185 KC343911 KC344153 KC343669 KC343427 | Gomes et al. (2013) |
| **D. pulla** | CBS 109760 | *Acer pseudoaplatanus* | Aceraceae | KC343186 KC343912 KC344154 KC343670 KC343428 | Gomes et al. (2013) |
| **D. raonikayaporum** | CBS 133182 (ex-type) | *Spondias mombin* | Anacardiaceae | KC343188 KC343914 KC344156 KC343672 KC343430 | Gomes et al. (2013) |
| **D. rhoina** | CBS 146.27 | *Rhus toxicodendron* | Anacardiaceae | KC343189 KC343915 KC344157 KC343673 KC343431 | Gomes et al. (2013) |
| **D. rudis** | CBS 113201 (ex-type) | *Vitis vinifera* | Vitaceae | KC343234 KC343960 KC344202 KC343718 KC343476 | Machingambi et al. (2015) |
| **D. rudis** | CBS 114011 | *Vitis Vinifera* | Vitaceae | KC343235 KC343961 KC344203 KC343718 KC343477 | Machingambi et al. (2015) |
| **D. saccarata** | CBS 116311 (ex-type) | *Protea repens, cankers* | Proteaceae | KC343190 KC343916 KC344158 KC343674 KC343435 | Gomes et al. (2013) |
| **D. sackstonii** | BRIP 54669b (ex-type) | *Helianthus annuus* | Asteraceae | KJ197287 KJ197249 KJ197267 - | - | Gomes et al. (2013) |
| **D. salicicola** | BRIP 54825 (ex-type) | *Salix purpurea* | Salicaceae | JX862531 JX862537 KF170923 - | - | Gomes et al. (2013) |
| **D. scobina** | CBS 133181 (ex-type) | *Schinus terebinthifolius*, endophytic in leaf | Anacardiaceae | KC343191 KC343917 KC344159 KC343675 KC343433 | Tan et al. (2013) |
| **D. sclerotioides** | CBS 133181 (ex-type) | *Schinus terebinthifolius*, endophytic in leaf | Anacardiaceae | KC343192 KC343918 KC344160 KC343676 KC343434 | Thompson et al. (2015) |
| **D. sojae** | CBS 116017 | *Euphorbia nutans* | Euphorbiaceae | KC343195 KC343921 KC344163 KC343679 KC343437 | Gomes et al. (2013) |
| **D. sojae** | CBS 116017 | *Glycine max* | Fabaceae | KJ590719 KJ590762 KJ610875 KJ659208 - | - | Gomes et al. (2013) |
| **D. sterilis** | CBS 193.36 | - | - | FJ889448 GQ250324 - - | - | Lombard et al. (2014) |
| **D. stictica** | CBS 370.54 | *Buxus sampvirens, dead twig* | Buxaceae | KC343321 KC343938 KC344180 KC343696 KC343454 | Lombard et al. (2014) |
| **D. subclavata** | ZJUD 83, CGMCC 3.17253 | *Citrus grandis cv. Shatianyou* | 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 |
|----------------|------------------------|------------------|-------------|---------------------------|------------|
| † ZJUD 95, CGMCC 3.17257 | Citrus unshiu | Rosaceae | KJ490630 KJ490509 KJ490451 KJ490572 | - | Gomes et al. (2013) |
| † D. subordinaria | CBS 101711 | Plantago lanceolata | Plantaginaceae | KC343213 KC343939 KC344181 KC343697 KC343455 | Huang et al. (2015) |
| † D. tecoma | CBS 464.90 | Plantago lanceolata | Plantaginaceae | Kc343214 KC343940 KC344182 KC343698 KC343456 | Huang et al. (2015) |
| † D. tectonia | MFLUCC 12-0777 | Tabelua sp. | Bignoniacae | KU712430 KU743935 KU743977 - KU749345 | Gomes et al. (2013) |
| † D. tectonopsis | MFLUCC 14-1138 | Tabelua grandis | Verbenaceae | KU712439 KU743976 - KU743954 | Doilom et al. (2017) |
| † D. tectonigena | MFLUCC 12-0767 | Tabelua grandis | Verbenaceae | KU712432 | Doilom et al. (2017) |
| † D. terebinthifolii | CBS 534.93 (ex-type) | Schinus terebinthifolius | Anacardiaceae | KC343216 KC343942 KC344184 KC343700 KC343458 | Doilom et al. (2017) |
| † D. toxica | CBS 133.180 | Schinus terebinthifolius | Anacardiaceae | KC343220 KC343946 KC344188 KC343704 KC343462 | Udayanga et al. (2012) |
| † D. tulliensis | BRIP 62248a | Theobroma cacao | Sterculiaceae | KR936130 KR936133 KR936132 - - | Gomes et al. (2013) |
| † D. velutina | CGMCC 3.18286 = LC 6624 | Neolitsea sp., pathogen | Lauraceae | KX986789 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 KY491566 - | - | This study |
| † D. unshiensis | ZJUD 51, CGMCC 3.17568 | Fortunella margarita | Rutaceae | KJ490586 KJ400465 KJ490407 KJ490528 - | This study |
| † ZJUD 52, CGMCC 3.17569 | Citrus unshiu | Rosaceae | KJ490587 KJ400466 KJ490408 KJ490529 - | - | This study |
| † D. vaccinii | CBS 160.32 (ex-type) | Oxycoccus macrocarpos | Ericaceae | KC343228 KC343954 KC344196 KC343712 KC343470 | Huang et al. (2015) |
| † CBS 118571 | Vaccinium corymbosum | Ericaceae | KC343223 KC343949 KC344191 KC343701 KC343459 | Huang et al. (2015) |
| † D. vawdreyi | BRIP 57887a | Psidium guajava | Sterculiaceae | KR936126 KR936129 KR936128 - | - | Gomes et al. (2013) |
| † D. velutina | CGMCC 3.18286 = LC 4421 | Neolitsea s.p., pathogen | Lauraceae | KX986790 KX999182 KX999223 KX999261 | Crous et al. (2015) |
| † LC 4419 | Neolitsea s.p., 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 KX999296 KX999285 | - | This study |
| † LC 6708 | Camellia sinensis, pathogen | Theaceae | KX986787 KX999179 KX999220 KX999258 | - | This study |
| † D. virgilia | CMW 40755 (ex-type) | Solanum melongena | Solanaceae | KC343229 KC343955 KC344197 KC343713 KC343471 | - | This study |
| † LC 5519 | Virginia oroboides | Unknown | - | KP247573 - | - | This study |
Diaporthe is paraphyletic

Table 2. (Continued).

| Species names | Culture collection no. | Isolation sources | Host family | GenBank Accession Numbers | References |
|---------------|------------------------|-------------------|-------------|---------------------------|------------|
|               |                        |                   |             | **ITS**                  | **TEF1**  | **TUB** | **HIS** | **CAL** |               |
|               |                        |                   |             |                           |           |         |         |         |               |
|               |                        |                   |             |                           |           |         |         |         |               |
| D. woodii     | CBS 558.93             | Lupinus sp.       | Fabaceae    | KC343244 - KC343970 - KC344212 - KC343728 - KC343486 | Gomes et al. (2013) |
| D. woolworthii| CBS 148.27             | Ulmus americana   | Ulmaceae    | KC343245 - KC343971 - KC344213 - KC343729 - KC343487 | Gomes et al. (2013) |
| D. xishuangbanica | CGMCC 3.18282= LC 6707 | *Camellia sinensis*, pathogen | Theaceae  | KX986783 - KX999175 - KX999216 - KX999255 | This study |
| D. xishuangbanica | LC 6744               | *Camellia sinensis*, pathogen | Theaceae  | KX986784 - KX999176 - KX999217 | - | This study |
| D. yunnanensis | CGMCC 3.18289 = LC6168 | Coffea sp., endophytes | Rubiaceae   | KX986796 - KX999188 - KX999228 - KX999267 - KX999290 | This study |
|                | LC 8106                | *Coffea* sp., endophytes | Rubiaceae   | KY491541 - KY491551 - KY491561 | - | KY491571 | This study |
|                | LC 8107                | *Coffea* sp., endophytes | Rubiaceae   | KY491542 - KY491552 - KY491562 | - | KY491572 | This study |
| Diaporthe sp. | LC 6496                | *Camellia sinensis*, endophytes | Theaceae  | KX986781 - KX999173 - KX999214 - KX999253 - KX999283 | Gomes et al. (2013) |
|                | LC 6512                | *Camellia sinensis*, endophyte | Theaceae  | KX986782 - KX999174 - KX999215 - KX999254 - KX999284 | This study |
|                | LC 6232                | *Theobroma cacao*, endophyte | Sterculiaceae | KX986797 - KX999189 - KX999229 - KX999268 - KX999291 | This study |
|                | LC 8108                | *Theobroma cacao*, endophyte | Sterculiaceae | KY491543 - KY491553 - KY491563 | - | KY491573 | This study |
|                | LC 8109                | *Theobroma cacao*, endophyte | Sterculiaceae | KY491544 - KY491554 - KY491564 | - | 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               | Glycine max, seed | Fabaceae   | KC343203 - KC343929 - KC344171 - KC343687 - KC343445 | Gomes et al. (2013) |
|                | CBS 119639             | Man, abscess      | - | KC343202 - KC343928 - KC344170 - KC343687 - KC343444 | Gomes et al. (2013) |
| Diaporthe sp. 1 | CGMCC 3.18292 = LC 0771 | *Alnus* sp., pathogen | Betulaceae | KX986799 - KX999191 - KX999231 - KX999270 - KX999282 | This study |
| Diaporthe sp. 2 | CGMCC 3.18291 = LC 6140 | *Acer* sp., endophyte | Aceraceae  | KX986799 - KX999191 - KX999231 - KX999270 - KX999282 | This study |
|                | LC8112                | *Acer* sp., endophyte | Aceraceae  | KX986799 - KX999191 - KX999231 - KX999270 - KX999282 | This study |
|                | LC8113                | *Acer* sp., endophyte | Aceraceae  | KX986799 - KX999191 - KX999231 - KX999270 - KX999282 | This study |
| Diaporthe collinea | CBS 121124           | Corylus sp., dying stems | Corylaceae | KC343004 - KC343730 - KC343972 - KC343488 - KC343246 | Gomes et al. (2013) |
| P. conorum    | CBS 587.79            | Pirus pentaphylla | Pinaceae   | KC343153 - KC343879 - KC344121 - KC343637 - KC343395 | Gomes et al. (2013) |
| P. emicis     | BRIP 45089a (ex-type) | Emex australis | Polygonaceae | JF957784 - JX275414 - JX275458 | - | JX197449 | Udayanga et al. (2012) |
| P. fukushii   | CBS 116863            | Pirus pyrifolia | Rosaceae   | KC343147 - KC343873 - KC344115 - KC343631 - KC343389 | Gomes et al. (2013) |
|                | BRIP 45089b           | Emex australis | Polygonaceae | JQ619898 - JX275415 - JX275459 | - | JX197450 | Udayanga et al. (2012) |

*: not provided in literatures.
**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 µm diam, often with a yellowish conidial cirrus exuding from the ostioles. Conidiophores 10–34.5 × 2–3 µm, cylindrical, hyaline, septate, branched, straight or slightly curved, tapering towards the apex. *Alpha conidia* abundant in culture, 7–10.5 × 2–3 µm (\(\bar{X} = 8.4 \pm 0.7 \times 2.6 \pm 0.2, n = 30\)), aseptate, hyaline, elliptoidal to fusoid, multi-guttulate. *Beta conidia* not observed.

*Culture characters:* Cultures incubated on PDA at 25 °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 |
|-------------|---------|------------------|--------------------|-------------------|------------------|------------|
| Coffea      | *P. coffeae* | 200–250          | 12–16 × 2          | 8–9 × 2.5         | -                | Uecker (1988) |
| Camellia    | *D. acutispora* | 99–473            | 10–34.5 × 2–3      | 6.9–10.4 × 2.1–3.1 | -                | This study  |
|             | *D. amygdali* | 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) |
|             | *D. apiculata* | 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) |
|             | *D. compacta* | 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) |
|             | *D. discoidispora* | 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) |
|             | *D. eres* | 200–250           | 10–15 × 2–3        | (6–8.5(–9) × 3–4 | (18–22–28(29) × 1–1.5 | Udayanga et al. (2014b) |
|             | *D. foeniculacea* | 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) |
|             | *D. foeniculina* | 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) |
|             | *D. hongkongensis* | to 200           | 5–12 × 2–4         | (5–)6–7(–8) × (2–)2.5(–3) | 18–22 × 1.5–2 | Gomes et al. (2013) |
|             | *D. oraccinii* | 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) |
|             | *D. penetriteum* | 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) |
|             | *D. uckerae* | 150–200           | (9–)12–28(–30) × 1.5–2.5 | (6–)4–8(–8.6) × (2–)2.3–3 | - | Udayanga et al. (2014a) |
|             | *D. xishuangbanica* | 180–310         | 13–34.5 × 1.5–3    | 7–9.5 × 2.5–3.5   | -                | This study  |
|             | *D. yunnanensis* | 195–880          | -                  | 3–6.5 × 1–2.5     | 13.5–33.5 × 1–1.5 | This study  |
|             | *P. acaciicola* | -                 | -                  | 7–9 × 3–3.5       | -                | Diedicke (1911) |
|             | *P. theae* | 40 × 25           | -                  | 6–8 × 1.5–2       | 18–24 × 0.75     | Petch (1925) |
| Elaeagnus   | *P. amoldae* | 900 × 500         | 6–12 × 1–2         | 5.5–11 × 1.5–2    | 15–20           | Uecker (1988) |
|             | *P. elaeagni* | 500–750           | 20–25 × 1–1.5      | 6–10 × 2–3        | -                | Uecker (1988) |
|             | *P. elaeagnicola* | 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) |
|             | *P. elaeagni-glabrae* | 330–1170       | 16–28 × 1.5–2.5    | 6–13 × 1.5–3    | 7.5–22.5 × 1–2  | This study  |
|             | *D. incompleta* | 207–650          | 8–22 × 1–2.5       | -                | 19–44 × 0.5–1.5 | This study  |
| Neolitsea   | *D. valutina* | 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 Paraña, 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.
Description: On PDA: Conidiomata globose, to 330–1170 µm, erumpent, with slightly elongated black necks, yellowish or dirty white, spiral conidial cirri extruding from ostioles. Conidiophores 16–28 × 1.5–2.5 µm, cylindrical, phialidic, septate, branched, sometimes inflated. Alpha conidia 6–13 × 1.5–3 µm (X = 8.3 ± 1.4 × 2.2 ± 0.3, n = 30), hyaline, fusiform or oval, usually biguttulate. Beta conidia 7.5–22.5 × 1–2 µm (X = 15.1 ± 3.5 × 1.2 ± 0.2, n = 40), hyaline, filiform, smooth, curved, base truncate.

Culture characters: Cultures incubated on PDA at 25 °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 µm diam. Conidiophores cylindrical, straight or sinuous, apical or base sometimes swelling, 11.5–23.5 × 1.8–3.5 µm (X = 16 ± 3 × 2.5 ± 0.5, n = 30). Beta conidia filiform, hamate or slightly curved, base truncate, tapering towards one apex, 11.5–32 × 0.5–2 µm (X = 20 ± 7.5 × 1 ± 0.4, n = 20). Alpha conidia not observed.

Culture characters: Cultures on PDA at 25 °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) (Mutanola-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.
Diaporthe is paraphyletic

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 µm diam, cream to pale luteous conidial droplets exuding from the central ostioles. *Conidiophores* 8–22 × 1–2.5 µm, cylindrical, hyaline, septate, unbranched, smooth, slightly curved, tapering towards apex. *Alpha conidia* not observed. *Beta conidia* 19–44 × 0.5–1.5 µm (X = 30.5 ± 8.7 × 1.1 ± 0.4, n = 30), smooth, hyaline, filiform, base subtruncate, straight or curved.

*Culture characters:* Cultures incubated on PDA at 25 °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 lobe, 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.
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 µm; E–G = 10 µm.

**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-
Diaporthe is paraphyletic

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 × 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 × 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 × 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 × 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 °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. 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.*
**Diaporthe undulata** Y.H. Gao & L. Cai, **sp. nov.**
MycoBank MB820683

*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 µm; **E–G =** 10 µm.

**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

**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 µm long, coated with short hyphae, one to several necks forming from a single pycnidium. Conidiophores obpyriform, hyaline, phialidic, septate, branched, 5–17.5 × 2–3 µm (\(T = 9.7 \pm 4.0 \times 2.4 \pm 0.5, n = 20\)). Alpha conidia ellipsoid, hyaline, biguttulate, rounded at both ends, 5–6.5 × 2–3 (\(T = 5.8 \pm 0.4 \times 2.3 \pm 0.3, n = 50\)). Beta conidia not observed.

**Culture characters:** Cultures incubated on PDA at 25 °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
Diaporthe is paraphyletic

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 µm diam, cream translucent drop of conidia exuded from the central ostioles. Conidiophores 10–23 × 1–2.5 µm, cylindrical, hyaline, branched, densely aggregated, slightly tapering towards the apex, sometimes slightly curved. Alpha conidia 5.5–10 × 2–2.5 µm (X = 6.9 ± 0.9 × 2.2 ± 0.2, n = 50), unicellular, aseptate, hyaline, fusoid to ellipsoid or clavate, bi-guttulate or multi-guttulate. Beta conidia 11–27.5 × 0.5–1.5 µm (X = 16.1 ± 5.0 × 0.8 ± 0.4, n = 30), smooth, hyaline, apex acutely rounded, curved.

**Culture characters:** Cultures incubated on PDA at 25 °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 cinea, 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. tectonigena* in several loci (98 % in ITS, 90 % in TEF1, and 96 % in TUB)
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 µm 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 × 1–2.5 µm (\(\bar{x} = 5.5 \pm 1 \times 2 \pm 0.5, n = 30\)), fusiform, hyaline, biguttulate, with one end obtuse and the other acute. Beta conidia 13.5–33.5 × 1–1.5 µm (\(\bar{x} = 27.5 \pm 5.5 \times 1.5 \pm 0.3, n = 30\)), hyaline,

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 is paraphyletic

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 µm, yellowish drop of conidia diffusing from the central ostioles. Conidiophores 6.5–19.5 × 1–3 µm, cylindrical, hyaline, septate, branched, straight to sinuous, base inflated, slightly tapering towards the apex. Alpha conidia 7.5–13.5 × 2–3.5 µm (\( \bar{X} = 9.9 \pm 1.4 \times 2.8 \pm 0.4, n = 30 \)), unicellular, hyaline, fusoid to ellipsoid or clavate, two or several large guttulae observed, base subtruncate. Beta conidia 15–40.5 × 1–2.5 µm (\( \bar{X} = 26.0 \pm 5.8 \times 1.8 \pm 0.5, n = 30 \)), 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 118°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. celastrina, D. eres, D. helicis, D. neilliae, D. pulla, and D. vaccinia. Gao et al. (2016) examined 17 isolates belonging to the D. eres 7-d-old culture on PDA; C. Conidiomata; D. Conidiophores; E. Alpha and beta conidia; F. Beta conidia. Bars: C = 100 µm; D–F = 10 µm.

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 µm; D–F = 10 µm.
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 is paraphyletic

**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 8112; *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. inconspicuca, D. infecunda, D. asheiica, and D. steriliis* (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., *Mycosistema* 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., *Mycosistema* 24: 145 (2005).

*Type* **China:** Hunan Province: on living branches of Campotheca acuminate, 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., *Mycosistema* 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 ‘eucommi’.

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

*MycoBank MB821441*

*Basionym:* Phomopsis eucommiiicola C.Q. Chang et al., *Mycosistema* 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 glabae** (C.Q. Chang et al.) Y.H. Gao & L. Cai, **comb. nov.**

*MycoBank MB821443*

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

*Type* **China:** Hunan Province: on living branches of Loropetaleum 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., *Mycosistema* 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., Mycosistema 24: 9 (2005); as ‘micheliana’.

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., Mycosistema 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 diaporthalean sexual morph (Gomes et al. 2013), a paraphyletic nature is revealed in the present study (Fig. 1). Several genera, notably *Ophidiaparthe* (Fu et al. 2013), *Pustulomyces* (Dai et al. 2014), *Phaeocytostroma*, 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, *Ophidiaparthe* produces only one type of globose or subglobose conidia that differs from the dimorphic (fusiform and filiform) conidia of *Diaporthe* (Fu et al. 2013); *Phaeocytostroma* 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). *Phaeocytostroma* and *Stenocarpella* were originally suspected to be members of *Botryosphaeriaceae* (*Botryosphaeriales*) because of their pigmented alpha conidia and diploidea-like morphology (Crous et al. 2006). However, they were subsequently allocated to *Diaporthales* based on phylogenetic analysis (Lamprecht et al. 2011), which is confirmed in this study.

The large “*Diaporthe*” clade embedded with the heterogeneous genera *Ophidiaparthe*, *Pustulomyces*, *Phaeocytostroma*, 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 *Ophidiaparthe* is associated with *Cytisus lepidula* (a fern), while *Pustulomyces* is bambusicolous (Dai et al. 2014). On the contrary, none of the previously named over 1900 *Diaporthe / Phomopsis* species was recorded from a fern or *Bambusaceae* (https://nt.ars-grin.gov/fungaldatabases/). It is therefore reasonable to speculate that the speciation of *Ophidiaparthe* and *Pustulomyces*, as well as the distinctly different morphologies from their close *Diaporthe* allies, are the consequences of evolutionary adaption to new hosts. Similarly, *Phaeocytostroma* 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 can be distributed as endophytes or latent pathogens with global trade.

ACKNOWLEDGEMENTS

We thank all the members in LC’s lab for help and assistance. This work was supported by grants from the National Natural Science Foundation of China (NSFC 31110103906), and the Ministry of Science and Technology, China (MOST 2014FY120100).

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