



***Diaporthe*: formalizing the species-group concept**

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Abstract

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

Keywords – Diaporthaceae – Morphology – Phylogeny – Plant disease – Species complexes

Introduction

Fuckel (1867) established *Diaporthe* as the type of Diaporthaceae to accommodate *Diaporthe alnea* Fuckel, the type species (Index Fungorum 2022). *Phomopsis* (Sacc.) Bubák (1905) was introduced as the asexual morph. It has been a common practice to use two names for the fungal species with pleomorphic life cycles until the implementation of one fungus: one name (Taylor 2011). The name *Diaporthe* (1867) takes precedence over *Phomopsis* (1905) based on the

International Code for Nomenclature of Algae, Fungi and Plants (<http://www.iapptaxon.org/nomen/main.php?page=title>) (Rossman 2014). More than 1000 species have been named under *Diaporthe* in Index Fungorum (<http://www.indexfungorum.org/names/Names.asp>, November 2021). Dissanayake et al. (2017) provided a backbone phylogenetic tree for 171 species introduced from culture or directly sequenced specimens. The authors used molecular data to link species with their type.

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

Diaporthe species have been previously identified based on morphology and host specificity (Uecker 1988, Ferreira et al. 2015). However, overlapping morphological traits and association of several *Diaporthe* species with the same host make it difficult to identify characters that are taxonomically relevant at the species level (Rehner & Uecker 1994, Mostert et al. 2001, Gomes et al. 2013, Guarnaccia et al. 2016, Santos et al. 2010, Udayanga et al. 2011, 2014a, b, Dissanayake et al. 2017a, b). Thus, a molecular approach is essential to identify and comprehensively characterize *Diaporthe* (Santos & Phillips 2009, Diogo et al. 2010, Luongo et al. 2011, Udayanga et al. 2012a, b, Thomidis et al. 2013, Gao et al. 2017). However, sequence data from type material is unavailable for many *Diaporthe* species, while the phylogenetic relationships of genera in Diaporthaceae remain unclear (Delsuc et al. 2005, Manawasinghe et al. 2019). Hence, additional studies are needed focusing on neo- or epi- typification to clarify the taxonomic placement of these taxa. Using all the sequences classified under *Diaporthe*, Bhunjun et al. (2022) demonstrated that several species have been wrongly identified. Therefore, using larger dataset analyses in terms of taxa and loci is necessary to improve the taxonomic and phylogenetic resolution within *Diaporthe*. These approaches have been used successfully for other fungal taxa (Rokas & Carroll 2005, Norphanphoun et al. 2020, Bhunjun et al. 2020, 2021).

Herein, we have analysed a comprehensive dataset of five loci (nuclear ribosomal internal transcribed spacer (ITS), translation elongation factor 1- α (*efl1 α*), beta-tubulin (β -tubulin), calmodulin (*cal*), and histone (*his3*)), containing all species denoted as *Diaporthe* (559 strains) and all the genera in Diaporthaceae. Based on the resulting phylogenetic tree, we introduce 13 workable Species complexes of *Diaporthe*. Several genera and species are synonymised in Hongsanan et al. (in prep.) based on phylogenetic analyses and morphological characteristics. A list of *Diaporthe* species excluded from the genus is also provided, following Species Fungorum (2022), recent publications (Dissanayake et al. 2017c, Manawasinghe et al. 2019), and database in GenBank.

Materials & Methods

Phylogenetic analysis

Raw DNA sequence reads were edited and assembled into contigs using Geneious® version 11.1.5 (<http://www.geneious.com>). The new sequences were used as queries to perform BLASTn against the nr database in GenBank to check for contamination and retrieve Diaporthaceae sequences. The GenBank taxonomy browser was also used to check all sequences assigned as *Diaporthe* in the database (last accessed in April 2021). The BLASTn against nr and type sequences was used to identify sequences incorrectly assigned to *Diaporthe*. The ITSx 1.1, a Perl

based software tool, was used to extract ITS1, 5.8S and ITS2 regions (Bengtsson-Palme et al. 2013). Five genetic markers were used for phylogenetic analyses: *β-tubulin*, *cal*, *eflα*, *his3* and ITS. Open reading frames of protein-coding genes were determined using reference sequences in BioEdit version 7.2.3 (Hall 1999). For each genetic marker, two datasets were assembled; one containing *Diaporthe corylina* strains CBS 121124 and CBS 140348 as the outgroup, and the other containing *Cytospora disciformis* strain CBS 116827 and *C. leucostoma* strain SXYLt as the outgroup. For the latter two, genome data were used to extract the sequences needed for the analysis. *Cytospora* taxa were selected as the outgroup as they are closer to Diaporthaceae. The ITS dataset contained 534 taxa, *eflα* 510, *β-tubulin* 479, *cal* 383, and *his3* 343 taxa. The combined datasets consisted of 535 taxa. Taxa for which a single sequence (ITS) was available were excluded from the combined matrix. When included, most were not stable and impacted the robustness of the tree. Individual datasets for each genetic marker were also assembled. For ITS, an additional dataset was prepared, even including the 50 strains excluded from the initially combined dataset. All taxa used for these analyses are given in Table 1.

Datasets for each genetic marker were aligned separately using the MAFFT v.7.110 online tool (<http://mafft.cbrc.jp/alignment/server/>; Katoh & Standley 2013). BioEdit v. 7.0.5.3 was used for performing further manual adjustments where necessary (Hall 1999). TrimAl (available on Phylemon 2.0 platform, Sánchez et al. 2011) was used to trim ambiguously aligned positions or regions. A partition homogeneity test (PHT) was performed with PAUP* 4.0b10 to determine the congruency of genes and whether they could be combined (Swofford 2002). The combined sequence alignments were obtained from MEGA v. 7.0.14 and v. 10.1.0 (Kumar et al. 2018).

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

Results

Phylogenetic analysis

The results from the partition homogeneity tests (PHT) were not significant (level $\leq 95\%$), indicating that the individual datasets were congruent and could be combined. Phylogenetic trees from single loci were generated (Figs 2–7) to examine the overall topology and clade support. In this study, we introduce 13 species complexes containing extant species of *Diaporthe*. Nine singleton species were not assigned to any complex, and their phylogenetic placement was not robust. Almost all Diaporthaceae genera, except for *Paradiaporthe*, grouped and nested within *Diaporthe*. *Hyaliappendispora* and *Phaeodiaporthe* consistently formed a basal clade with strong support.

Phylogenetic analysis of the ITS region (609 bp) consisted of 534 strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the outgroup. Eight species complexes (*D. arecae*, *D. biconispora*, *D. decedens*, *D. alnea*, *D. oncostoma*, *D. rudis*, *D. toxica*, and *D. vawdreyi* species complexes) were recovered as in the combined gene tree (Fig. 1). The *Diaporthe alnea* species complex formed a well-resolved clade except for species *D. nomorae* and *D. citri*. As same as *Diaporthe pustulata* species complex that formed a well-resolved clade except for *D. obtusifoliae*. Most species in the *D. sojae* species complex clustered, except for some, which dispersed throughout the tree. Species in the *D. varians*, *D. carpini*, and *D. scobina* species complexes were dispersed throughout the tree and clustered with species from other clades (Fig. 2).

Table 1 GenBank accession numbers of the sequences used for phylogenetic analysis in this study.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	β -tubulin	<i>cal</i>	<i>his3</i>
<i>Cytospora disciformis</i>	CBS 116827 ^T	<i>Eucalyptus grandis</i>	Uruguay	KY051801	KX965072	KX964907	N/A	N/A
<i>C. leucostoma</i>	SXYLt*	<i>Prunus</i> sp.	China	LKEB00000000				
<i>Diaporthe absenteum</i>	LC3429 ^T	<i>Camellia sinensis</i>	China	KP267897	KP267971	KP293477	N/A	KP293547
<i>D. absenteum</i>	LC3564	<i>Camellia sinensis</i>	China	KP267912	KP267986	KP293492	N/A	KP293559
<i>D. acaciarum</i>	CBS 138862 ^T	<i>Acacia tortilis</i>	Tanzania	KP004460	N/A	KP004509	N/A	KP004504
<i>D. acaciigena</i>	CBS 129521 ^T	<i>Acacia retinodes</i>	Australia	KC343005	KC343731	KC343973	KC343247	KC343489
<i>D. acericola</i>	MFLUCC 17-0956 ^T	<i>Acer negundo</i>	Italy	KY964224	KY964180	KY964074	KY964137	N/A
<i>D. acerigena</i>	CFCC 52554 ^T	<i>Acer tataricum</i>	China	MH121489	MH121531	N/A	MH121413	MH121449
<i>D. acerigena</i>	CFCC 52555	<i>Acer tataricum</i>	China	MH121490	MH121532	N/A	MH121414	MH121450
<i>D. acerina</i>	CBS 137.27	<i>Acer saccharum</i>	Not stated	KC343006	KC343732	KC343974	KC343248	KC343490
<i>D. actinidiae</i>	ICMP 13683 ^T	<i>Actinidia deliciosa</i>	New Zealand	KC145886	KC145941	N/A	N/A	N/A
<i>D. actinidiae</i>	KFRD-7	<i>Actinidia deliciosa</i> var. <i>Miliang</i>	China	KX346886	KY404088	N/A	N/A	N/A
<i>D. actinidiae</i>	KFRD-8	<i>Actinidia chinensis</i> var. <i>Jinyan</i>	China	KX346887	KY404089	N/A	N/A	N/A
<i>D. actinidiae</i>	LP-2	<i>Actinidia</i> sp.	China	KX457968	KX457965	N/A	N/A	N/A
<i>D. acuta</i>	PSCG045	<i>Pyrus pyrifolia</i>	China	MK626956	MK654809	MK691223	MK691123	MK726160
<i>D. acuta</i>	CGMCC 3.19600 ^T	<i>Pyrus pyrifolia</i>	China	MK626957	MK654802	MK691225	MK691124	MK726161
<i>D. acutispora</i>	CGMCC 3.18285 ^T	<i>Coffea</i> sp.	China	KX986764	KX999155	KX999195	KX999274	N/A
<i>D. alangii</i>	CFCC 52556 ^T	<i>Alangium kurzii</i>	China	MH121491	MH121533	MH121573	MH121415	MH121451
<i>D. alleghaniensis</i>	CBS 495.72 ^T	<i>Betula</i> <i>alleghaniensis</i>	Canada	KC343007	KC343733	KC343975	KC343249	KC343491
<i>D. alnea</i>	CBS 146.46 ^T	<i>Alnus</i> sp.	Netherlands	KC343008	KC343734	KC343976	KC343250	KC343492
<i>D. amaranthophila</i>	MAFF 246900	<i>Amaranthus tricolor</i>	Japan	LC459575	LC459577	LC459579	LC459583	LC459581
<i>D. amaranthophila</i>	MAFF 246901	<i>Amaranthus tricolor</i>	Japan	LC459576	LC459578	LC459580	LC459584	LC459582
<i>D. ambigua</i>	CBS 114015 ^T	<i>Pyrus communis</i>	South Africa	KC343010	KC343736	KC343978	KC343252	KC343494
<i>D. ampelina</i>	CBS 114016 ^T	<i>Vitis vinifera</i>	France	AF230751	AY745056	JX275452	AY745026	N/A
<i>D. ampelina</i>	CBS 267.8	<i>Vitis vinifera</i>	Italy	KC343018	KC343744	KC343986	KC343260	KC343502
<i>D. amygdali</i>	CBS 115620	<i>Prunus persica</i> .	USA	KC343020	KC343746	KC343988	KC343262	KC343504
<i>D. amygdali</i>	CBS 111811	<i>Vitis vinifera</i>	South Africa	KC343019	KC343745	KC343987	KC343261	KC343503
<i>D. amygdali</i>	CBS 120840	<i>Prunus salicina</i>	South Africa	KC343021	KC343747	KC343989	KC343263	KC343505
<i>D. amygdali</i>	CBS 126679 ^T	<i>Prunus dulcis</i>	Portugal	KC343022	KC343748	KC343990	KC343264	KC343506

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. anacardii</i>	CBS 720.97 ^T	<i>Anacardium occidentale</i>	East Africa	KC343024	KC343750	KC343992	KC343266	KC343508
<i>D. angelicae</i>	CBS 111592 ^T	<i>Heracleum sphondylium</i>	Austria	KC343027	KC343753	KC343995	KC343269	KC343511
<i>D. anhuiensis</i>	CNUCC 201901 ^T	<i>Cunninghamia lanceolata</i>	China	MN219718	MN224668	MN227008	MN224549	MN224556
<i>D. anhuiensis</i>	CNUCC 201902	<i>Cunninghamia lanceolata</i>	China	MN219727	MN224669	MN227009	MN224550	MN224557
<i>D. apiculatum</i>	LC3418 ^T	<i>Camellia sinensis</i>	China	KP267896	KP267970	KP293476	N/A	N/A
<i>D. apiculatum</i>	CFCC 53069	<i>Rhus chinensis</i>	China	MK432652	MK578128	MK578055	MK442974	MK442999
<i>D. aquatica</i>	IFRDCC 3051 ^T	<i>Aquatic habitat</i>	China	JQ797437	N/A	N/A	N/A	N/A
<i>D. aquatica</i>	IFRDCC 3015	<i>Aquatic habitat</i>	China	JQ797438	N/A	N/A	N/A	N/A
<i>D. araucanorum</i>	CBS 145285 ^T	<i>Araucaria araucana</i>	Chile	NR_169994	MN509733	MN509722	MN974277	N/A
<i>D. araucanorum</i>	CBS 145286	<i>Araucaria araucana</i>	Chile	MN509712	MN509734	MN509723	N/A	N/A
<i>D. arctii</i>	CBS 139280 ^T	<i>Arctium lappa</i>	Austria	KJ590736	KJ590776	KJ610891	KJ612133	KJ659218
<i>D. arecae</i>	CBS 161.64 ^T	<i>Areca catechu</i>	India	KC343032	KC343758	KC344000	KC343274	KC343516
<i>D. arecae</i>	CBS 535.75	<i>Citrus</i> sp.	India	KC343033	KC343759	KC344001	KC343275	KC343517
<i>D. arengae</i>	CBS 114979 ^T	<i>Arenga engleri</i>	Hong Kong	KC343034	KC343760	KC344002	KC343276	KC343518
<i>D. aseana</i>	MFLUCC 12-0299a ^T	Unidentified dead leaf	Thailand	KT459414	KT459448	KT459432	KT459464	N/A
<i>D. asheicola</i>	CBS 136967 ^T	<i>Vaccinium ashei</i>	Chile	KJ160562	KJ160594	KJ160518	KJ160542	N/A
<i>D. asheicola</i>	CBS 136968	<i>Vaccinium ashei</i>	Chile	KJ160563	KJ160595	KJ160519	KJ160543	N/A
<i>D. aspalathi</i>	CBS 117169 ^T	<i>Aspalathus linearis</i>	South Africa	KC343036	KC343762	KC344004	KC343278	KC343520
<i>D. aspalathi</i>	CBS 117168	<i>Aspalathus linearis</i>	South Africa	KC343035	KC343761	KC344003	KC343277	KC343519
<i>D. australafricana</i>	CBS 111886 ^T	<i>Vitis vinifera</i>	Australia	KC343038	KC343764	KC344006	KC343280	KC343522
<i>D. australafricana</i>	CBS 113487	<i>Vitis vinifera</i>	Australia	KC343039	KC343765	KC344007	KC343281	KC343523
<i>D. avertroae</i>	SCHM 3605 ^T	<i>Averrhoa carambola</i>	China	AY618930	N/A	N/A	N/A	N/A
<i>D. azadirachtae</i>	TN 01	<i>Azadirachta indica</i>	India	KC631323	N/A	N/A	N/A	N/A

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. baccae</i>	CBS 136972 ^T	<i>Vaccinium</i> sp.	Italy	KJ160565	KJ160597	N/A	N/A	MF418264
<i>D. baccae</i>	CPC 20585	<i>Vaccinium</i> sp.	Italy	KJ160564	KJ160596	N/A	N/A	N/A
<i>D. batatas</i>	CBS 122.21 ^T	<i>Ipomoea batatas</i>	USA	KC343040	KC343766	KC344008	KC343282	KC343524
<i>D. bauhiniae</i>	CFCC 53071 ^T	<i>Bauhinia purpurea</i>	China	MK432648	MK578124	MK578051	MK442970	MK442995
<i>D. bauhiniae</i>	CFCC 53072	<i>Bauhinia purpurea</i>	China	MK432649	MK578125	MK578052	MK442971	MK442996
<i>D. beckhausii</i>	CBS 138.27	<i>Viburnum</i> sp.	Not stated	KC343041	KC343767	KC344009	KC343283	KC343525
<i>D. beilharziae</i>	BRIP 54792 ^T	<i>Indigofera australis</i>	Australia	JX862529	JX862535	KF170921	N/A	N/A
<i>D. benedicti</i>	SBen914 ^T	<i>Salix</i> sp.	USA	KM669929	KM669785	N/A	KM669862	N/A
<i>D. betulae</i>	CFCC 50469 ^T	<i>Betula platyphylla</i>	China	KT732950	KT733016	KT733020	KT732997	KT732999
<i>D. betulae</i>	CFCC 50470	<i>Betula platyphylla</i>	China	KT732951	KT733017	KT733021	KT732998	KT733000
<i>D. betulicola</i>	CFCC 51128 ^T	<i>Betula albosinensis</i>	China	KX024653	KX024655	KX024657	KX024659	KX024661
<i>D. betulicola</i>	CFCC 51129	<i>Betula albosinensis</i>	China	KX024654	KX024656	KX024658	KX024660	KX024662
<i>D. betulina</i>	CFCC 52560	<i>Betula albo-sinensis</i>	China	MH121495	MH121537	MH121577	MH121419	MH121455
<i>D. betulina</i>	CFCC 52561	<i>Betula costata</i>	China	MH121496	MH121538	MH121578	MH121420	MH121456
<i>D. bicincta</i>	CBS 121004 ^T	<i>Juglans</i> sp.	USA	KC343134	KC343860	KC344102	KC343376	KC343618
<i>D. biconispora</i>	CGMCC 3.17252 ^T	<i>Citrus grandis</i>	China	KJ490597	KJ490476	KJ490418	MT227578	KJ490539
<i>D. biconispora</i>	CGMCC 3.17251	<i>Fortunella margarita</i>	China	KJ490596	KJ490475	KJ490417	N/A	KJ490538
<i>D. biguttulata</i>	CFCC 52584	<i>Juglans regia</i>	China	MH121519	MH121561	MH121598	MH121437	MH121477
<i>D. biguttulata</i>	ZJUD47 ^T	<i>Citrus limon</i>	China	KJ490582	KJ490461	KJ490403	N/A	KJ490524
<i>D. bohemiae</i>	CBS 143347 ^T	<i>Vitis vinifera</i>	Czech Republic	MG281015	MG281536	MG281188	MG281710	MG281361
<i>D. bohemiae</i>	CBS 143348	<i>Vitis vinifera</i>	Czech Republic	MG281016	MG281537	MG281189	MG281711	MG281362
<i>D. brasiliensis</i>	CBS 133183 ^T	<i>Aspidosperma</i> sp.	Brazil	KC343042	KC343768	KC344010	KC343284	KC343526
<i>D. brasiliensis</i>	LGMF926	<i>Aspidosperma tomentosum</i>	Brazil	KC343043	KC343769	KC344011	KC343285	KC343527
<i>D. caatingaensis</i>	CBS 141542 ^T	<i>Tacinga inamoena</i>	Brazil	KY085927	KY115603	KY115600	N/A	KY115605
<i>D. caatingaensis</i>	URM7484	<i>Pilosocereus gounellei</i> sub sp.	Brazil	KY085928	N/A	KY115602	KY115599	KY115606
<i>D. camelliae-oleiferae</i>	HNZZ027 ^T	<i>Gounellei Camellia oleifera</i>	China	MZ509555	MZ504707	MZ504718	MZ504685	MZ504696

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. camelliae-oleiferae</i>	HNZZ030	<i>Camellia oleifera</i>	China	MZ509556	MZ504708	MZ504719	MZ504686	MZ504697
<i>D. camelliae-sinensis</i>	SAUCC194.92 ^T	<i>Camellia sinensis</i>	China	MT822620	MT855932	MT855817	MT855699	MT855588
<i>D. camelliae-sinensis</i>	SAUCC194.103	<i>Castanea mollissima</i>	China	MT822631	MT855943	MT855828	MT855710	MT855599
<i>D. camptothecae</i>	SCHM 3611 ^T	<i>Camptotheca acuminata</i>	China	AY622996	N/A	N/A	N/A	N/A
<i>D. canthii</i>	CBS 132533 ^T	<i>Canthium inerme</i>	South Africa	JX069864	KC843120	KC843230	KC843174	N/A
<i>D. caricae-papayae</i>	NIBM-ABIJP	<i>Carica papaya</i>	Malaysia	MN335224	N/A	N/A	N/A	N/A
<i>D. carpini</i>	CBS 114437	<i>Carpinus betulus</i>	Sweden	KC343044	KC343770	KC344012	KC343286	KC343528
<i>D. carpini</i>	CSB F191	<i>Brachiaria</i>	Kenya	KU680350	N/A	N/A	N/A	N/A
<i>D. caryae</i>	CFCC 52563 ^T	<i>Carya illinoensis</i>	China	MH121498	MH121540	MH121580	MH121422	MH121458
<i>D. caryae</i>	CFCC 52564	<i>Carya illinoensis</i>	China	MH121499	MH121541	MH121581	MH121423	MH121459
<i>D. cassines</i>	CPC 21916	<i>Cassine peragua</i>	South Africa	KF777155	KF777244	N/A	N/A	N/A
<i>D. caulivora</i>	CBS 127268 ^T	<i>Glycine max</i>	Croatia	KC343045	KC343771	KC344013	KC343287	KC343529
<i>D. celastrina</i>	CBS 139.27 ^T	<i>Celastrus</i> sp.	USA	KC343047	KC343773	KC344015	KC343289	KC343531
<i>D. celeris</i>	CBS 143349 ^T	<i>Vitis vinifera</i>	Czech Republic	MG281017	MG281538	MG281190	MG281712	MG281363
<i>D. celeris</i>	CBS 143350	<i>Vitis vinifera</i>	Czech Republic	MG281018	MG281539	MG281191	MG281713	MG281364
<i>D. ceratozamia</i>	CBS 131306 ^T	<i>Ceratozamia robusta</i>	Australia	JQ044420	N/A	N/A	N/A	N/A
<i>D. ceratozamia</i>	HCH260	<i>Artemisia lavandulifolia</i>	China	KU360597	N/A	N/A	N/A	N/A
<i>D. cercidis</i>	CFCC 52565 ^T	<i>Cercis chinensis</i>	China	MH121500	MH121542	MH121582	MH121424	MH121460
<i>D. chamaeropsis</i>	CBS 454.81 ^T	<i>Chamaerops humilis</i>	Greece	KC343048	KC343774	KC344016	KC343290	KC343532
<i>D. chamaeropsis</i>	CBS 753.70	<i>Spartium junceum</i>	Croatia	KC343049	KC343775	KC344017	KC343291	KC343533
<i>D. charlesworthii</i>	BRIP 54884m ^T	<i>Rapistrum rugostrum</i>	Australia	KJ197288	KJ197250	KJ197268	N/A	N/A
<i>D. chensiensis</i>	CFCC 52567 ^T	<i>Abies chensiensis</i>	China	MH121502	MH121544	MH121584	MH121426	MH121462
<i>D. chensiensis</i>	CFCC 52568	<i>Abies chensiensis</i>	China	MH121503	MH121545	MH121585	MH121427	MH121463
<i>D. chiangraiensis</i> (= <i>Chiangraiomyces bauhiniae</i>)	MFLUCC 17-1669 ^T	<i>Bauhinia</i> sp.	Thailand	MF190119	MF377598	N/A	N/A	N/A

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. chiangraiensis</i> (= <i>Ch. bauhiniæ</i>)	MFLUCC 17-1670	<i>Bauhinia</i> sp.	Thailand	MF190118	MF377599	N/A	N/A	N/A
<i>D. chimonanthe</i>	SCHM 3614 ^T	<i>Chimonanthus</i> <i>praecox</i>	China	AY622993	N/A	N/A	N/A	N/A
<i>D. chimonanthe</i>	G18 A2-24	<i>Luehea divaricata</i>	Brazil	EU878426	N/A	N/A	N/A	N/A
<i>D. chongqingensis</i>	CGMCC 3.19603 ^T	<i>Pyrus pyrifolia</i>	China	MK626916	MK654866	MK691321	MK691209	MK726257
<i>D. chongqingensis</i>	PSCG 436	<i>Pyrus pyrifolia</i>	China	MK626917	MK654867	MK691322	MK691208	MK726256
<i>D. cichorii</i>	MFLUCC 17-1023 ^T	<i>Cichorium intybus</i>	Italy	KY964220	KY964176	KY964104	KY964133	N/A
<i>D. cinerascens</i>	CBS 719.96	<i>Ficus carica</i>	Bulgaria	KC343050	KC343776	KC344018	KC343292	KC343534
<i>D. cinnamomic</i>	CFCC 52569 ^T	<i>Cinnamomum</i> sp.	China	MH121504	MH121546	MH121586	N/A	MH121464
<i>D. cinnamomic</i>	CFCC 52570	<i>Cinnamomum</i> sp.	China	MH121505	MH121547	MH121587	N/A	MH121465
<i>D. cissampeli</i>	CBS 141331 ^T	<i>Cissampelos</i> <i>capensis</i>	South Africa	KX228273	N/A	KX228384	N/A	KX228366
<i>D. citri</i>	CBS 135422 ^T	<i>Citrus</i> sp.	USA	KC843311	KC843071	KC843187	KC843157	N/A
<i>D. citri</i>	AR4469	<i>Citrus</i> sp.	USA	KC843321	KC843081	KC843197	KC843167	N/A
<i>D. citriasiana</i>	CGMCC 3.15224	<i>Citrus unshiu</i>	China	JQ954645	JQ954663	KC357459	KC357491	KJ490515
<i>D. citrichinensis</i>	ZJUD34 ^T	<i>Citrus</i> sp.	China	JQ954648	JQ954666	KJ490396	KC357494	KJ490516
<i>D. citrichinensis</i>	ZJUD38	<i>Citrus</i> sp.	China	KC357558	KC357527	KC357463	KC357495	KJ490517
<i>D. collariana</i>	MFLUCC 17-2636 ^T	<i>Magnolia</i> <i>champaca</i>	Thailand	MG806115	MG783040	MG783041	MG783042	N/A
<i>D. columnaris</i>	ICMP 16836	<i>Vaccinium vitis-</i> <i>idaea</i>	USA	KC145883	KC145999	N/A	N/A	N/A
<i>D. columnaris</i>	AR3612 ^T	<i>Vaccinium vitis-</i> <i>idaea</i>	USA	AF439625	N/A	N/A	N/A	N/A
<i>D. compacta</i>	CGMCC 3.17536 ^T	<i>Camellia sinensis</i>	China	KP267854	KP267928	KP293434	N/A	KP293508
<i>D. conica</i>	CFCC 52571 ^T	<i>Alangium chinense</i>	China	MH121506	MH121548	MH121588	MH121428	MH121466
<i>D. conica</i>	CFCC 52574	<i>Alangium chinense</i>	China	MH121509	MH121551	MH121591	MH121431	MH121469
<i>D. conorum</i>	MAFF 410330	<i>Abies firma</i>	Japan	AB201443	N/A	N/A	N/A	N/A
<i>D. conorum</i>	UAS002 ^T	<i>Nothapodytes</i> <i>nimmoniana</i>	India	FJ158120	N/A	N/A	N/A	N/A
<i>D. convolvuli</i>	CBS 124654 ^T	<i>Convolvulus</i> <i>arvensis</i>	Turkey	KC343054	KC343780	KC344022	KC343296	KC343538

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>ef1a</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. corylicola</i>	CFCC 53986 ^T	stems of <i>Corylus heterophylla</i>	China	MW839880	MW815894	MW883977	MW836684	MW836717
<i>D. crataegi</i>	CBS 114435	<i>Crataegus rhipidophylla</i>	Sweden	KC343055	KC343781	KC344023	KC343297	KC343539
<i>D. crotalariae</i>	CBS 162.33 ^T	<i>Crotalaria spectabilis</i>	USA	KC343056	KC343782	KC344024	KC343298	KC343540
<i>D. crousii</i>	CAA819 ^T	<i>Vaccinium corymbosum</i>	China	MK792299	MK828071	MK837922	MK883827	MK871440
<i>D. crousii</i>	CAA820	<i>Vaccinium corymbosum</i>	China	MK792300	MK828072	MK837923	MK883828	MK871441
<i>D. cucurbitae</i>	CBS 136.25	<i>Arctium</i> sp.	Not stated	KC343031	KC343757	KC343999	KC343273	KC343515
<i>D. cucurbitae</i>	DAOM 42078 ^T	<i>Cucumis</i> sp.	Canada	KM453210	KM453211	KP118848	N/A	KM453212
<i>D. cuppatea</i>	CBS 117499 ^T	<i>Aspalathus linearis</i>	South Africa	KC343057	KC343783	KC344025	KC343299	KC343541
<i>D. cyatheae</i> (= <i>Ophiodiaporthe cyatheae</i>)	YMJ 1364 ^T	<i>Cyathea lepifera</i>	Taiwan	JX570889	KC465406	KC465403	KC465410	N/A
<i>D. cynaroidis</i>	CBS 122676 ^T	<i>Protea cynaroides</i>	South Africa	KC343058	KC343784	KC344026	KC343300	KC343542
<i>D. cytospora</i>	FAU461 ^T	<i>Citrus limon</i>	Italy	KC843307	KC843116	KC843221	KC843141	MF418283
<i>D. decedens</i>	CBS 109772	<i>Corylus avellana</i>	Austria	KC343059	KC343785	KC344027	KC343301	KC343543
<i>D. decedens</i>	CBS 114281	<i>Corylus avellana</i>	Austria	KC343060	KC343786	KC344028	KC343302	KC343544
<i>D. decorticans</i>	CBS 114649	<i>Alnus glutinosa</i>	Sweden	KC343170	KC343896	KC344138	KC343412	KC343654
<i>D. decorticans</i>	CBS 114200	<i>Prunus padus</i>	Sweden	KC343169	KC343895	KC344137	KC343411	KC343653
<i>D. detrusa</i>	CBS 109770	<i>Berberis vulgaris</i>	Austria	KC343061	KC343787	KC344029	KC343303	KC343545
<i>D. detrusa</i>	CBS 114652	<i>Berberis vulgaris</i>	Sweden	KC343062	KC343788	KC344030	KC343304	KC343546
<i>D. discoidispora</i>	ZJUD89 ^T	<i>Citrus unshiu</i>	China	KJ490624	KJ490503	KJ490445	N/A	KJ490566
<i>D. discoidispora</i>	ZJUD87	<i>Camellia sinensis</i>	China	KJ490622	KJ490501	KJ490443	N/A	KJ490564
<i>D. elaeagni-glabrae</i>	CGMCC 3.18287 ^T	<i>Elaeagnus glabra</i>	China	KX986779	KX999171	KX999212	KX999281	KX999251
<i>D. elaeagni-glabrae</i>	LC4806	<i>Elaeagnus glabra</i>	China	KX986780	KX999172	KX999213	KX999282	KX999252
<i>D. elonis</i>	6307	<i>Prunella vulgaris</i>	China	JN998101	N/A	N/A	N/A	N/A
<i>D. endocitricola</i>	ZHKUCC20-0012 ^T	<i>Citrus maxima</i>	China	MT355682	MT409336	MT409290	MT409312	N/A
<i>D. endocitricola</i>	ZHKUCC20-0013	<i>Citrus maxima</i>	China	MT355683	MT409337	MT409291	MT409313	N/A
<i>D. endophytica</i>	CBS 133811 ^T	<i>Schinus terebinthifolius</i>	Brazil	KC343065	KC343791	KC344033	KC343307	KC343549

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. endophytica</i>	LGMF911	<i>Schinus terebinthifolius</i>	Brazil	KC343066	KC343792	KC344034	KC343308	KC343550
<i>D. eres</i>	AR3519	<i>Corylus avellana</i>	Austria	KJ210523	KJ210547	KJ420789	KJ435008	KJ420839
<i>D. eres</i>	CBS 109767	<i>Acer</i> sp.	Austria	DQ491514	KC343801	KC344043	KC343317	KC343559
<i>D. eres</i>	AR3560	<i>Viburnum</i> sp.	Austria	JQ807425	JQ807351	KJ420795	KJ435011	KJ420846
<i>D. eres</i>	AR4346	<i>Prunus mume</i>	Korea	JQ807429	JQ807355	KJ420823	KJ435003	KJ420872
<i>D. eres</i>	AR4348	<i>Prunus persica</i>	Korea	JQ807431	JQ807357	KJ420811	KJ435004	KJ420862
<i>D. eres</i>	AR4363	<i>Malus</i> sp.	Korea	JQ807436	JQ807362	KJ420809	KJ435033	KJ420860
<i>D. eres</i>	AR4369	<i>Pyrus pyrifolia</i>	Korea	JQ807440	JQ807366	KJ420813	KJ435005	KJ420864
<i>D. eres</i>	AR4371	<i>Malus pumila</i>	Korea	JQ807441	JQ807367	KJ420796	KJ435034	KJ420847
<i>D. eres</i>	AR5197	<i>Rhododendron</i> sp.	Germany	KJ210531	KJ210552	KJ420812	KJ435014	KJ420863
<i>D. eres</i>	CBS 135428	<i>Juglans cinerea</i>	USA	KC843328	KC843121	KC843229	KC843155	KJ420840
<i>D. eres</i>	CBS 138594 ^T	<i>Ulmus laevis</i>	Germany	KJ210529	KJ210550	KJ420799	KJ434999	KJ420850
<i>D. eres</i>	CBS 138595	<i>Ulmus laevis</i>	Germany	KJ210533	KJ210554	KJ420817	KJ435006	KJ420866
<i>D. eres</i>	CBS 138597	<i>Vitis vinifera</i>	France	KJ210518	KJ210542	KJ420783	KJ434996	KJ420833
<i>D. eres</i>	CBS 138598	<i>Ulmus</i> sp.	USA	KJ210521	KJ210545	KJ420787	KJ435027	KJ420837
<i>D. eres</i>	CBS 138599	<i>Acer nugundo</i>	Germany	KJ210528	KJ210549	KJ420830	KJ435000	KJ420845
<i>D. eres</i>	DP0666	<i>Juglans cinerea</i>	USA	KJ210522	KJ210546	KJ420788	KJ435007	KJ420838
<i>D. eres</i>	DP0177	<i>Pyrus pyrifolia</i>	New Zealand	JQ807450	JQ807381	KJ420820	KJ435041	KJ420869
<i>D. eres</i>	DP0179	<i>Pyrus pyrifolia</i>	New Zealand	JQ807452	JQ807383	KJ420803	KJ435028	KJ420854
<i>D. eres</i>	DP0180	<i>Pyrus pyrifolia</i>	New Zealand	JQ807453	JQ807384	KJ420804	KJ435029	KJ420855
<i>D. eres</i>	DP0438	<i>Ulmus minor</i>	Austria	KJ210532	KJ210553	KJ420816	KJ435016	KJ420886
<i>D. eres</i>	FAU506	<i>Cornus florida</i>	USA	KJ210526	JQ807403	KJ420792	KJ435012	KJ420842
<i>D. eres</i>	DP0590	<i>Pyrus pyrifolia</i>	New Zealand	JQ807464	JQ807394	KJ420810	KJ435037	KJ420861
<i>D. eres</i>	DP0591	<i>Pyrus pyrifolia</i>	New Zealand	JQ807465	JQ807395	KJ420821	KJ435018	KJ420870
<i>D. eres</i>	FAU483	<i>Malus</i> sp.	Netherlands	KJ210537	KJ210556	KJ420827	KJ435022	KJ420874
<i>D. eres</i>	FAU522	<i>Sassafras albidum</i>	USA	KJ210525	JQ807406	KJ420791	KJ435010	KJ420841
<i>D. eres</i>	LCM11401b	<i>Ulmus</i> sp.	USA	KJ210520	KJ210544	KJ420786	KJ435026	KJ420836
<i>D. eres</i> (= <i>D. biguttusis</i>)	CGMCC 3.17081 ^T	<i>Lithocarpus glabra</i>	China	KF576282	KF576257	KF576306	N/A	N/A
<i>D. eres</i> (= <i>D. camptothecicola</i>)	CFCC 51632 ^T	<i>Camptotheca</i> sp.	China	KY203726	KY228887	KY228893	KY228877	KY228881

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. eres</i> (= <i>D. castaneae-mollissima</i>)	DNP128 ^T	<i>Castanea mollissima</i>	China	JF957786	KJ210561	KJ420801	JX197430	KJ420852
<i>D. eres</i> (= <i>D. cotoneastri</i>)	CBS 439.82 ^T	<i>Cotoneaster</i> sp.	UK	FJ889450	GQ250341	JX275437	JX197429	N/A
<i>D. eres</i> (= <i>D. fukushii</i>)	MAFF625033 ^T	<i>Pyrus pyrifolia</i>	Japan	JQ807468	JQ807417	KJ420814	KJ435017	KJ420865
<i>D. eres</i> (= <i>D. henanensis</i>)	HHAUP12290 ^T	<i>Ziziphus jujube</i>	China	KC898258	N/A	KF600608	N/A	KF600609
<i>D. eres</i> (= <i>D. longicicola</i>)	CGMCC 3.17089 ^T	<i>Lithocarpus glabra</i>	China	KF576267	KF576242	KF576291	N/A	N/A
<i>D. eres</i> (= <i>D. lonicerae</i>)	MFLUCC 17-0963 ^T	<i>Lonicera</i> sp.	Italy	KY964190	KY964146	KY964073	KY964116	N/A
<i>D. eres</i> (= <i>D. mahothocarpus</i>)	CGMCC 3.15181 ^T	<i>Lithocarpus glabra</i>	China	KC153096	KC153087	KF576312	N/A	N/A
<i>D. eres</i> (= <i>D. momicola</i>)	MFLUCC 16-0113 ^T	<i>Prunus persica</i>	China	KU557563	KU557631	KU557587	KU557611	N/A
<i>D. eres</i> (= <i>D. nobilis</i>)	CBS 113470	<i>Castanea sativa</i>	Korea	KC343146	KC343872	KC344114	KC343388	KC343630
<i>D. eres</i> (= <i>D. rosicola</i>)	MFLU 17-0646 ^T	<i>Rosa</i> sp.	UK	MG828895	MG829270	MG843877	MG829274	N/A
<i>D. eucalyptorum</i>	CBS 132525 ^T	<i>Eucalyptus</i> sp.	Australia	NR120157	N/A	N/A	N/A	N/A
<i>D. eucommiae</i>	SCHM 0020 ^T	<i>Eucommia ulmoides</i>	China	AY601921	N/A	N/A	N/A	N/A
<i>D. eucommiicola</i>	SCHM 3607 ^T	<i>Eucommia ulmoides</i> , <i>Styrax hypoglauca</i>	China	AY578071	N/A	N/A	N/A	N/A
<i>D. eugeniae</i>	DPFT23	<i>Mangifera indica</i>	Malaysia	MK110366	MK117267	MK122799	N/A	N/A
<i>D. eugeniae</i>	CBS 444.82 ^T	<i>Eugenia aromatica</i>	Indonesia	KC343098	KC343824	KC344066	KC343340	KC343582
<i>D. fibrosa</i>	CBS 109751	<i>Rhamnus cathartica</i>	Austria	KC343099	KC343825	KC344067	KC343341	KC343583
<i>D. fibrosa</i>	CBS 113830	<i>Rhamnus cathartica</i>	Sweden	KC343100	KC343826	KC344068	KC343342	KC343584
<i>D. foeniculina</i>	CBS 111553 ^T	<i>Foeniculum vulgare</i>	Portugal	KC843295	KC843104	KC843209	KC843129	N/A
<i>D. foeniculina</i> (= <i>D. foeniculacea</i>)	CBS 123208 ^T	<i>Foeniculum vulgare</i>	Portugal	KC343104	KC343830	KC344072	KC343346	KC343588

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. foeniculina</i> (= <i>D. rhoicola</i>)	CBS 129528 ^T	<i>Rhus pendulina</i>	South Africa	JF951146	KC843100	KC843205	KC843124	N/A
<i>D. foikelawen</i>	CBS 145289 ^T	<i>Drimys winteri</i>	Chile	NR_169995	MN509735	MN509724	MN974278	N/A
<i>D. foikelawen</i>	CBS 145288	<i>Drimys winteri</i>	Chile	MN509716	MN509738	MN509727	N/A	N/A
<i>D. forlicesenica</i>	MFLUCC 17-1015 ^T	<i>Dorycnium</i> <i>hirsutum</i>	Italy	KY964215	KY964171	KY964099	N/A	N/A
<i>D. fraxini-angustifoliae</i>	BRIP 54781 ^T	<i>Fraxinus</i> <i>angustifolia</i>	Australia	JX862528	JX862534	KF170920	N/A	N/A
<i>D. fraxini-angustifoliae</i>	MFLUCC 15-0748	<i>Vitis vinifera</i>	China	KT459428	KT459446	KT459430	KT459462	N/A
<i>D. fraxinicola</i>	CFCC 52582 ^T	<i>Fraxinus chinensis</i>	China	MH121517	MH121559	N/A	MH121435	N/A
<i>D. fructicola</i>	MAFF 246408 ^T	<i>Passiflora edulis</i> × <i>P. edulis</i> f. <i>flavicarpa</i>	Japan	LC342734	LC342735	LC342736	LC342738	LC342737
<i>D. fructicola</i>	MAFF 246409	<i>Passiflora edulis</i> × <i>P. edulis</i> f. <i>flavicarpa</i>	Japan	LC342739	LC342740	LC342741	LC342743	LC342742
<i>D. fulvicolor</i>	CGMCC 3.19601 ^T	<i>Pyrus pyrifolia</i>	China	MK626859	MK654806	MK691236	MK691132	MK726163
<i>D. fulvicolor</i>	PSCG 057	<i>Pyrus pyrifolia</i>	China	MK626858	MK654810	MK691233	MK691131	MK726164
<i>D. fusicola</i>	CGMCC 3.17087 ^T	<i>Lithocarpus glabra</i>	China	KF576281	KF576256	KF576305	KF576233	N/A
<i>D. fusicola</i>	GH3	Unidentified	China	MT499213	MT506473	MT506474	MT506476	MT506475
<i>D. ganjae</i>	CBS 180.91 ^T	<i>Cannabis sativa</i>	USA	KC343112	KC343838	KC344080	KC343354	N/A
<i>D. ganjae</i>	PSCG489	<i>Pyrus pyrifolia</i>	China	MK626955	MK654897	MK691287	MK691202	MK726204
<i>D. ganzhouensis</i>	CFCC 53087 ^T	Unidentified dead wood	China	MK432665	MK578139	MK578065	MK442985	MK443010
<i>D. ganzhouensis</i>	CFCC 53088	Unidentified dead wood	China	MK432666	MK578140	MK578066	MK442986	MK443011
<i>D. gardeniae</i>	CBS 288.56 ^T	<i>Gardenia</i> <i>jasminoides</i>	Italy	KC343113	KC343839	KC344081	KC343355	KC343597
<i>D. gardeniae</i>	step-1	<i>Gardenia</i> <i>jasminoides</i>	China	KY797655	MF158048	MF158050	N/A	MF158049
<i>D. garethjonesii</i>	MFLUCC 12-0542a ^T	Unidentified dead leaf	Thailand	KT459423	KT459457	KT459441	KT459470	N/A

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. glabrae</i>	SCHM 3622 ^T	<i>Bougainvillea glabra</i>	China	AY601918	N/A	N/A	N/A	N/A
<i>D. goulteri</i>	BRIP 55657a ^T	<i>Helianthus annuus</i>	Australia	KJ197290	KJ197252	KJ197270	N/A	N/A
<i>D. grandiflori</i>	SAUCC194.84 ^T	<i>Heterostemma grandiflorum</i>	China	MT822612	MT855924	MT855809	MT855691	MT855580
<i>D. guangdongensis</i>	ZHKUCC20-0014 ^T	<i>Citrus maxima</i>	China	MT355684	MT409338	MT409292	MT409314	N/A
<i>D. guangdongensis</i>	ZHKUCC20-0015	<i>Citrus maxima</i>	China	MT355685	MT409339	MT409293	MT409315	N/A
<i>D. guangxiensis</i>	JZB320094 ^T	<i>Vitis vinifera</i>	China	MK335772	MK523566	MK500168	MK736727	N/A
<i>D. guangxiensis</i>	JZB320091	<i>Vitis vinifera</i>	China	MK335769	MK523564	MK500165	MK736724	N/A
<i>D. gulyae</i>	BRIP 54025 ^T	<i>Helianthus annuus</i>	Australia	JF431299	JN645803	KJ197271	N/A	N/A
<i>D. gulyae</i>	MFLUCC 17-1026	<i>Heracleum sphondylium</i>	Italy	KY964223	KY964179	KY964107	KY964136	N/A
<i>D. helianthi</i>	CBS 592.81 ^T	<i>Helianthus annuus</i>	Serbia	KC343115	KC343841	KC344083	KC343357	KC343599
<i>D. heliconiae</i>	SAUCC194.77 ^T	<i>Heliconia metallica</i>	China	MT822605	MT855917	MT855802	MT855684	MT855573
<i>D. heterophyllae</i>	CBS 143769	<i>Acacia heterophylla</i>	France	MG600222	MG600224	MG600226	MG600218	MG600220
<i>D. heterostemmatis</i>	SAUCC194.85 ^T	<i>Heterostemma grandiflorum</i>	China	MT822613	MT855925	MT855810	MT855692	MT855581
<i>D. heterostemmatis</i>	SAUCC194.102	<i>Camellia sinensis</i>	China	MT822630	MT855942	MT855827	MT855709	MT855598
<i>D. heveae</i>	B23	<i>Atta cephalotes</i>	Brazil	KR812219	N/A	N/A	N/A	N/A
<i>D. hickoriae</i>	CBS 145.26 ^T	<i>Carya glabra</i>	USA	KC343118	KC343844	KC344086	KC343360	KC343602
<i>D. hispaniae</i>	CBS 143351 ^T	<i>Vitis vinifera</i>	Spain	MG281123	MG281644	MG281296	MG281820	MG281471
<i>D. hispaniae</i>	CBS 143352	<i>Vitis vinifera</i>	Spain	MG281124	MG281645	MG281297	MG281821	MG281472
<i>D. hongkongensis</i>	CBS 115448 ^T	<i>Dichroa febrifuga</i>	China	KC343119	KC343845	KC344087	KC343361	KC343603
<i>D. hongkongensis</i>	LC3079	<i>Camellia sinensis</i>	China	KP267851	KP267925	KP293431	N/A	KP293505
<i>D. hordei</i>	CBS 481.92 ^T	<i>Hordeum vulgare</i>	Norway	KC343120	KC343846	KC344088	KC343362	KC343604
<i>D. hordei</i>	HCH306	<i>Artemisia lavandulifolia</i>	China	KU360617	N/A	N/A	N/A	N/A
<i>D. huangshanensis</i>	CNUCC 201903 ^T	<i>Camellia oleifera</i>	China	MN219729	MN224670	MN227010	N/A	MN224558
<i>D. huangshanensis</i>	CNUCC 201904	<i>Camellia oleifera</i>	China	MN219730	MN224671	MN227011	N/A	MN224559
<i>D. hubeiensis</i>	JZB320123 ^T	<i>Vitis vinifera</i>	China	MK335809	MK523570	MK500147	MK500235	N/A
<i>D. hubeiensis</i>	JZB320128	<i>Vitis vinifera</i>	China	MK335814	MK523573	MK500152	MK500240	N/A
<i>D. hunanensis</i>	HNZZ023 ^T	<i>Camellia oleifera</i>	China	MZ509550	MZ504702	MZ504713	MZ504680	MZ504691

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. hunanensis</i>	HNZZ025	<i>Camellia oleifera</i>	China	MZ509551	MZ504703	MZ504714	MZ504681	MZ504692
<i>D. hungariae</i>	CBS 143353 ^T	<i>Vitis vinifera</i>	Hungary	MG281126	MG281647	MG281299	MG281823	MG281474
<i>D. hungariae</i>	CBS 143354	<i>Vitis vinifera</i>	Hungary	MG281127	MG281648	MG281300	MG281824	MG281475
<i>D. impuls</i>	CBS 114434	<i>Sorbus aucuparia</i>	Sweden	KC343121	KC343847	KC344089	KC343363	KC343605
<i>D. impuls</i>	CBS 141.27	<i>Sorbus americana</i>	Sweden	KC343122	KC343848	KC344090	KC343364	KC343606
<i>D. incompleta</i>	CGMCC 3.18288 ^T	<i>Camellia sinensis</i>	China	KX986794	KX999186	KX999226	KX999289	KX999265
<i>D. incompleta</i>	LC6706	<i>Camellia sinensis</i>	China	KX986793	KX999185	N/A	KX999288	KX999264
<i>D. inconspicua</i>	CBS 133813 ^T	<i>Maytenus ilicifolia</i>	Brazil	KC343123	KC343849	KC344091	KC343365	KC343607
<i>D. inconspicua</i>	URM7776	<i>Cenostigma pyramidale</i>	Brazil	MG696772	MG710414	MG710395	MG710391	MG710410
<i>D. infecunda</i>	CBS 133812 ^T	<i>Schinus</i> sp.	Brazil	KC343126	KC343852	KC344094	KC343368	KC343610
<i>D. infecunda</i>	CPC 20293	<i>Schinus terebinthifolius</i>	Brazil	KC343129	KC343855	KC344097	KC343371	KC343613
<i>D. infertilis</i>	CBS 230.52 ^T	<i>Citrus sinensis</i>	Suriname	KC343052	KC343778	KC344020	KC343294	KC343536
<i>D. infertilis</i>	CPC 20322	<i>Glycine max</i>	Brazil	KC343053	KC343779	KC344021	KC343295	KC343537
<i>D. isoberliniae</i>	CPC 22549 ^T	<i>Isoberlinia angolensis</i>	Zambia	KJ869133	N/A	KJ869245	N/A	N/A
<i>D. italiana</i>	MFLUCC 18-0091 ^T	<i>Morus alba</i>	Italy	NR_165892	MH853687	MH853689	MH853691	N/A
<i>D. italiana</i>	MFLUCC 18-0090	<i>Morus alba</i>	Italy	MH846237	MH853686	MH853688	MH853690	N/A
<i>D. juglandicola</i>	CFCC 51134 ^T	<i>Juglans mandshurica</i>	China	KU985101	KX024628	KX024634	KX024616	KX024622
<i>D. juglandicola</i>	CFCC 51135	<i>Juglans mandshurica</i>	China	KU985102	KX024629	KX024635	KX024617	KX024623
<i>D. kadsurae</i>	CFCC 52587	<i>Kadsura longipedunculata</i>	China	MH121522	MH121564	MH121601	MH121440	MH121480
<i>D. kadsurae</i>	CFCC 52586 ^T	<i>Kadsura longipedunculata</i>	China	MH121521	MH121563	MH121600	MH121439	MH121479
<i>D. kochmanii</i>	BRIP 54033 ^T	<i>Helianthus annuus</i>	Australia	JF431295	JN645809	N/A	N/A	N/A
<i>D. kochmanii</i>	BRIP 54034	<i>Helianthus annuus</i>	Australia	JF431296	JN645810	N/A	N/A	N/A
<i>D. kongii</i>	BRIP 54031 ^T	<i>Portulaca grandiflora</i>	Australia	JF431301	JN645797	N/A	N/A	N/A
<i>D. kongii</i>	BRIP 54032	<i>Portulaca grandiflora</i>	Australia	JF431300	JN645798	N/A	N/A	N/A
<i>D. krabiensis</i>	MFLUCC 17-2481 ^T	<i>marine based habitats</i>	Thailand	MN047101	MN433215	MN431495	N/A	N/A

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. kyushuensis</i>	STE-U2675	grapevines	South Africa	AF230749	N/A	N/A	N/A	N/A
<i>D. kyushuensis</i>	ch-D-1 ^T	grapevine	Japan	AB302250	N/A	N/A	N/A	N/A
<i>D. lagerstroemiae</i>	SCHM 3608 ^T	<i>Lagerstroemia indica</i>	China	AY622994	N/A	N/A	N/A	N/A
<i>D. leucospermi</i>	CBS111980 ^T	<i>Leucospermum</i> sp.	Australia	JN712460	KY435632	KY435673	KY435663	KY435653
<i>D. limonicola</i>	CPC 27869	<i>Citrus limon</i>	Malta	MF418419	MF418498	MF418579	MF418253	MF418339
<i>D. limonicola</i>	CPC 28200 ^T	<i>Citrus limon</i>	Malta	NR_154980	MF418501	MF418582	MF418256	MF418342
<i>D. liquidambaris</i>	XSD-15	Unidentified	China	EU273505	N/A	N/A	N/A	N/A
<i>D. liquidambaris</i>	SCHM 3621 ^T	<i>Liquidambar formosana</i>	China	AY601919	N/A	N/A	N/A	N/A
<i>D. litchii</i>	SAUCC194.22 ^T	<i>Litchi chinensis</i>	China	MT822550	MT855863	MT855747	MT855635	MT855519
<i>D. litchii</i>	SAUCC194.12	<i>Elaeagnus conferta</i>	China	MT822540	MT855854	MT855737	MT855625	MT855509
<i>D. litchiicola</i>	BRIP 54900 ^T	<i>Litchi chinensis</i>	Australia	JX862533	JX862539	KF170925	N/A	N/A
<i>D. lithocarpus</i>	CGMCC 3.15175 ^T	<i>Lithocarpus glabra</i>	China	KC153104	KC153095	KF576311	KF576236	N/A
<i>D. lithocarpus</i>	CGMCC 3.17098	<i>Lithocarpus glaber</i>	China	KF576276	KF576251	KF576300	KF576228	N/A
<i>D. litoricola</i>	MFLUCC 16-1195	Unidentified	UK	MF190139	N/A	N/A	N/A	N/A
<i>D. litoricola</i>	MFLUCC 17-1657 ^T	Unidentified	UK	MF190140	N/A	N/A	N/A	N/A
<i>D. longispora</i>	CBS 194.36 ^T	<i>Ribes</i> sp.	Canada	KC343135	KC343861	KC344103	KC343377	KC343619
<i>D. loropetali</i>	SCHM 3615 ^T	<i>Loropetalum chinense</i>	China	AY601917	N/A	N/A	N/A	N/A
<i>D. lusitanicae</i>	CBS 123212	<i>Foeniculum vulgare</i>	Portugal	KC343136	KC343862	KC344104	KC343378	KC343620
<i>D. lusitanicae</i>	CBS 123213 ^T	<i>Foeniculum vulgare</i>	Portugal	MH863280	KC343863	KC344105	KC343379	KC343621
<i>D. lutescens</i>	SAUCC194.36 ^T	<i>Chrysalidocarpus lutescens</i>	China	MT822564	MT855877	MT855761	MT855647	MT855533
<i>D. macintoshii</i>	BRIP 55064a ^T	<i>Rapistrum rugostrum</i>	Australia	KJ197289	KJ197251	KJ197269	N/A	N/A
<i>D. macintoshii</i>	CAF013	Unidentified	China	KY420947	N/A	N/A	N/A	N/A
<i>D. macintoshii</i>	CAF027	Unidentified	China	KU821458	N/A	N/A	N/A	N/A
<i>D. magnoliicola</i>	SCHM 3001 ^T	<i>Magnolia coco</i>	China	AY622995	N/A	N/A	N/A	N/A
<i>D. malorum</i>	CAA734 ^T	<i>Malus domestica</i>	Portugal	KY435638	KY435627	KY435668	KY435658	KY435648
<i>D. malorum</i>	CAA953	<i>Eucalyptus globulus</i>	Portugal	MN190308	MT309430	MT309456	MT309447	MT309439

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. manihotia</i>	CBS 505.76	<i>Manihot utilissima</i>	Rwanda	KC343138	KC343864	KC344106	KC343380	KC343622
<i>D. manihotia</i>	MFLU 19-2826	<i>Camellia</i> sp.	China	MT012296	MW014359	MW018927	MW014358	N/A
<i>D. marina</i>	MFLU 17-2622 ^T	marine based habitats	Thailand	MN047102	N/A	N/A	N/A	N/A
<i>D. maritima</i>	NB464-3A	<i>Picea rubens</i>	Canada	KU552027	KU552022	KU574616	N/A	N/A
<i>D. maritima</i>	DAOM 695742 ^T	<i>Picea rubens</i>	Canada	KU552025	KU552023	KU574615	MN136126	MN136175
<i>D. masirevicii</i>	BRIP 57892a ^T	<i>Helianthus annuus</i>	Australia	KJ197276	KJ197239	KJ197257	N/A	N/A
<i>D. masirevicii</i>	LC6740	<i>Camellia sinensis</i>	China	KY011888	KY011899	N/A	N/A	N/A
<i>D. maytenicola</i>	CPC 21896 ^T	<i>Maytenus acuminata</i>	South Africa	KF777157	N/A	KF777250	N/A	N/A
<i>D. megalospora</i>	CBS 143.27 ^T	<i>Sambucus canadensis</i>	Not stated	KC343140	KC343866	KC344108	KC343382	KC343624
<i>D. melastomatis</i>	SAUCC194.55 ^T	<i>Melastoma malabathricum</i>	China	MT822583	MT855896	MT855780	MT855664	MT855551
<i>D. melastomatis</i>	SAUCC194.80	<i>Millettia reticulata</i>	China	MT822608	MT855920	MT855805	MT855687	MT855576
<i>D. melitensis</i>	CPC 27873 ^T	<i>Citrus limon</i>	Malta	MF418424	MF418503	MF418584	MF418258	MF418344
<i>D. melitensis</i>	CPC 27875	<i>Citrus limon</i>	Malta	MF418425	MF418504	MF418585	MF418259	MF418345
<i>D. melonis</i>	CBS 507.78 ^T	<i>Cucumis melo</i>	USA	KC343142	KC343868	KC344110	KC343384	KC343626
<i>D. melonis</i>	SoyYS1712	soybean	Myanmar	LC360101	LC377213	LC377206	N/A	N/A
<i>D. meridionalis</i>	stc-2	soybean	Not stated	AF001015	N/A	N/A	N/A	N/A
<i>D. meridionalis</i>	90-48	soybean	Not stated	AF000564	N/A	N/A	N/A	N/A
<i>D. michelina</i>	SCHM 3603 ^T	<i>Michelia alba</i>	China	AY620820	N/A	N/A	N/A	N/A
<i>D. middletonii</i>	BRIP 54884e ^T	<i>Rapistrum rugostrum</i>	Australia	KJ197286	KJ197248	KJ197266	N/A	N/A
<i>D. middletonii</i>	BRIP 57329	<i>Chrysanthemoides monilifera</i> subsp. <i>Rotundata</i>	Australia	KJ197285	KJ197247	KJ197265	N/A	N/A
<i>D. millettiae</i>	GUCC9167 ^T	<i>Millettia reticulata</i>	China	MK398674	MK480609	MK502089	MK502086	N/A
<i>D. minusculata</i>	CGMCC 3.20098 ^T	saprobic on decaying wood	China	MT385957	MT424692	MT424712	MW022475	MW022499

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. minusculata</i>	GZCC 19-0345	saprobic on decaying wood	China	MT797184	MT793027	MT793038	MW022476	MW022500
<i>D. miriciae</i>	BRIP 54736j ^T	<i>Helianthus annuus</i>	Australia	KJ197282	KJ197244	KJ197262	N/A	N/A
<i>D. miriciae</i>	CGMHD 1023	<i>Homo sapiens</i>	Taiwan	MH268404	MH368012	MH368009	MH368011	MH368010
<i>D. multiguttulata</i>	CGMCC 3.17258 ^T	<i>Citrus grandis</i>	China	KJ490633	KJ490512	KJ490454	N/A	KJ490575
<i>D. multiguttulata</i>	CFCC 53099	Unidentified	China	MK573958	MK574633	MK574653	MK574593	MK574613
<i>D. musigena</i>	CBS 129519 ^T	<i>Musa</i> sp.	Australia	KC343143	KC343869	KC344111	KC343385	KC343627
<i>D. musigena</i>	HKFZL006	<i>Khaya senegalensis</i>	China	MK050110	MK054238	MK079660	N/A	N/A
<i>D. myracrodruonis</i>	URM 7972 ^T	<i>Astronium urundeuva</i>	Brazil	MK205289	MK213408	MK205291	MK205290	N/A
<i>D. nebulae</i>	PMM1681 ^T	<i>Vitis vinifera</i>	South Africa	KY511337	MH708552	KY511369	N/A	N/A
<i>D. nebulae</i>	Phom240	<i>Vitis vinifera</i>	South Africa	KY511315	MH708543	KY511346	N/A	N/A
<i>D. neilliae</i>	CBS 144.27 ^T	<i>Spiraea</i> sp.	USA	KC343144	KC343870	KC344112	KC343386	KC343628
<i>D. nelumbonis</i>	A-SER3	<i>Persea americana</i>	Sri Lanka	MK907914	N/A	N/A	N/A	N/A
<i>D. nelumbonis</i>	R. Kirschner 4114 ^T	<i>Nelumbo nucifera</i>	Taiwan	KT821501	N/A	LC086652	N/A	N/A
<i>D. neoarctii</i>	CBS 109490 ^T	<i>Ambrosia trifida</i>	USA	KC343145	KC343871	KC344113	KC343387	KC343629
<i>D. neoraonikayaporum</i>	MFLUCC 14-1136 ^T	<i>Tectona grandis</i>	Thailand	KU712449	KU749369	KU743988	KU749356	N/A
<i>D. nigra</i>	JZB320170 ^T	<i>stem of Ballota nigra</i>	Italy	MN653009	MN892277	MN887113	N/A	N/A
<i>D. nitschkei</i>	AR5211 ^T	<i>Hedera helix</i>	France	KJ210538	KJ210559	KJ420828	KJ435043	KJ420875
<i>D. nomorae</i>	CBS 157.29	<i>Morus</i> sp.	Japan	KC343154	KC343880	KC344122	KC343396	KC343638
<i>D. nothofagi</i>	BRIP 54801 ^T	<i>Nothofagus cunninghamii</i>	Australia	JX862530	JX862536	KF170922	N/A	N/A
<i>D. obtusifoliae</i>	CPC 32336 ^T	<i>Acacia obtusifolia</i>	Australia	MG386072	N/A	N/A	N/A	MG386137
<i>D. ocoteae</i>	CBS 141330 ^T	<i>Ocotea obtusata</i>	France	KX228293	N/A	KX228388	N/A	N/A
<i>D. oculi</i>	HHUF 30565 ^T	<i>Homo sapiens</i>	Japan	LC373514	LC373516	LC373518	N/A	N/A
<i>D. oncostoma</i>	CBS 589.78	<i>Robinia pseudoacacia</i>	France	KC343162	KC343888	KC344130	KC343404	KC343646
<i>D. oncostoma</i>	CBS 100454	<i>Robinia pseudoacacia</i>	Germany	KC343160	KC343886	KC344128	KC343402	KC343644
<i>D. oraccinii</i>	CGMCC 3.17531 ^T	<i>Camellia sinensis</i>	China	KP267863	KP267937	KP293443	N/A	KP293517
<i>D. oraccinii</i>	LC3296	<i>Camellia sinensis</i>	China	KP267884	KP267958	KP293464	N/A	KP293536

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. osmanthi</i>	GUCC9165 ^T	<i>Osmanthus fragrans</i>	China	MK398675	MK480610	MK502091	MK502087	N/A
<i>D. ovalispora</i>	CGMCC 3.17256 ^T	<i>Citrus limon</i>	China	KJ490628	KJ490507	KJ490449	N/A	KJ490570
<i>D. ovoidea</i>	CGMCC 3.17092 ^T	<i>Lithocarpus glabra</i>	China	KF576264	KF576239	KF576288	KF576222	N/A
<i>D. ovoidea</i>	CGMCC 3.17093	<i>Lithocarpus glaber</i>	China	KF576265	KF576240	KF576289	KF576223	N/A
<i>D. oxe</i>	CBS 133186 ^T	<i>Maytenus ilicifolia</i>	Brazil	KC343164	KC343890	KC344132	KC343406	KC343648
<i>D. oxe</i>	CBS 133187	<i>Maytenus ilicifolia</i>	Brazil	KC343165	KC343891	KC344133	KC343407	KC343649
<i>D. padina</i>	CFCC 52590 ^T	<i>Padus racemosa</i>	China	MH121525	MH121567	MH121604	MH121443	MH121483
<i>D. padina</i>	CFCC 52591	<i>Padus racemosa</i>	China	MH121526	MH121568	MH121605	MH121444	MH121484
<i>D. pandanicola</i>	MFLUCC 17-0607 ^T	<i>Pandanus</i> sp.	Thailand	MG646974	N/A	MG646930	N/A	N/A
<i>D. paranensis</i>	CBS 133184 ^T	<i>Maytenus ilicifolia</i>	Brazil	KC343171	KC343897	KC344139	KC343413	KC343655
<i>D. paranensis</i>	LMICRO417	<i>Schinus terebinthifolia</i>	Brazil	KY461115	KY461116	N/A	N/A	N/A
<i>D. parapterocarpi</i>	CPC 22729 ^T	<i>Pterocarpus brenanii</i>	Zambia	KJ869138	N/A	KJ869248	N/A	N/A
<i>D. parva</i>	CGMCC 3.19599 ^T	<i>Pyrus × bretschneideri</i>	China	MK626919	MK654858	MK691248	N/A	MK726210
<i>D. parva</i>	PSCG035	<i>Pyrus × bretschneideri</i>	China	MK626920	MK654859	MK691249	MK691169	MK726211
<i>D. pascoei</i>	BRIP 54847 ^T	<i>Persea americana</i>	Australia	JX862532	JX862538	KF170924	N/A	N/A
<i>D. pascoei</i>	BPPCA147	<i>Mangifera indica</i>	Malaysia	MK111091	MK117255	MK122790	N/A	N/A
<i>D. passiflorae</i>	CBS 132527 ^T	<i>Passiflora edulis</i>	South America	JX069860	N/A	N/A	N/A	N/A
<i>D. passiflorae</i>	DJY16A1-5	<i>Actinidia</i> sp.	China	MH595929	MH621353	MH621349	N/A	N/A
<i>D. passifloricola</i>	CBS 141329 ^T	<i>Passiflora foetida</i>	Malaysia	KX228292	N/A	KX228387	N/A	KX228367
<i>D. passifloricola</i>	NFIF-3-11	<i>Citrus reticulata</i> cv. nanfengmiju	China	MG786598	MG925401	MG925398	MK238995	MK238998
<i>D. patagonica</i>	CBS 145291 ^T	<i>Aristotelia chilensis</i>	Chile	NR_169996	MN509739	MN509728	MN974279	N/A
<i>D. patagonica</i>	CBS 145755	<i>Aristotelia chilensis</i>	Chile	MN509718	MN509740	MN509729	N/A	N/A
<i>D. penetrитеum</i>	CGMCC 3.17532 ^T	<i>Camellia sinensis</i>	China	KP714505	KP714517	KP714529	N/A	KP714493
<i>D. penetrитеum</i>	LC3215	<i>Camellia sinensis</i>	China	KP267879	KP267953	KP293459	N/A	KP293532
<i>D. perijuncta</i>	CBS 109745 ^T	<i>Ulmus glabra</i>	Austria	KC343172	KC343898	KC344140	KC343414	KC343656
<i>D. pernicioosa</i>	ATCC 38578	Unidentified	Not stated	HQ908492	N/A	N/A	N/A	N/A

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. perseae</i>	CBS 151.73 ^T	<i>Persea gratissima</i>	Netherlands	KC343173	KC343899	KC344141	KC343415	KC343657
<i>D. perseae</i>	BPPCA257	<i>Mangifera indica</i>	Malaysia	MK111098	MK117256	MK122791	N/A	N/A
<i>D. pescicola</i>	MFLUCC 16-0105 ^T	<i>Prunus persica</i>	China	KU557555	KU557623	KU557579	KU557603	N/A
<i>D. pescicola</i>	PSCG036	<i>Pyrus x bretschneideri</i>	China	MK626855	MK654796	MK691226	MK691116	MK726159
<i>D. phaseolorum</i>	AR4203 ^T	<i>Phaseolus vulgaris</i>	USA	KJ590738	KJ590739	KJ610893	KJ612135	KJ659220
<i>D. phaseolorum</i>	CBS 116019	<i>Caperonia palustris</i>	USA	KC343175	KC343901	KC344143	KC343417	KC343659
<i>D. phillipsii</i>	CAA817 ^T	<i>Vaccinium corymbosum</i>	Portugal	MK792305	MK828076	MN000351	MK883831	MK871445
<i>D. phillipsii</i>	CAA818	<i>Vaccinium corymbosum</i>	Portugal	MK792307	MK828078	MN000352	MK883833	MK871447
<i>D. phoenicicola</i>	CBS 161.64 ^T	<i>Areca catechu</i>	India	MH858400	GQ250349	JX275440	JX197432	N/A
<i>D. phoenicicola</i>	PBMR345	<i>Mangifera indica</i>	Malaysia	MK111088	MK117275	MK122810	N/A	N/A
<i>D. phoenicicola</i>	PBMR340	<i>Mangifera indica</i>	Malaysia	MK111086	MK117271	MK122805	N/A	N/A
<i>D. phoenicicola</i>	KUC21243	<i>Sargassum</i> sp.	South Korea	KT207761	N/A	KT207659	N/A	N/A
<i>D. phoenicicola</i>	KUC21217	<i>Sargassum</i> sp.	South Korea	KT207733	N/A	KT207633	N/A	N/A
<i>D. phragmitis</i>	CBS 138897 ^T	<i>Phragmites australis</i>	China	KP004445	N/A	KP004507	N/A	KP004503
<i>D. phyllanthicola</i>	SCHM 3680 ^T	<i>Phyllanthus emblica</i>	China	AY620819	N/A	N/A	N/A	N/A
<i>D. phyllanthicola</i>	RS 129	<i>Medicinal plant</i>	India	MK398278	N/A	N/A	N/A	N/A
<i>D. podocarpi-macrophylli</i>	CGMCC 3.18281 ^T	<i>Podocarpus macrophyllus</i>	China	KX986774	KX999167	KX999207	KX999278	KX999246
<i>D. podocarpi-macrophylli</i>	LC6229	<i>Olea europaea</i>	Italy	KX986771	KX999164	KX999204	KX999277	KX999243
<i>D. poincianellae</i>	URM 7932 ^T	<i>Cenostigma pyramidale</i>	Brazil	MH989509	MH989538	MH989537	MH989540	MH989539
<i>D. portugallica</i>	CPC 34247 ^T	<i>Camellia sinensis</i>	Portugal	MH063905	MH063911	MH063917	MH063893	MH063899
<i>D. portugallica</i>	CPC 34248	<i>Camellia sinensis</i>	Portugal	MH063906	MH063912	MH063918	MH063894	MH063900
<i>D. pseudoalnea</i>	CFCC 54190 ^T	<i>Alnus glutinosa</i>	Netherlands	MZ727037	MZ816343	MZ753487	MZ753468	MZ781302
<i>D. pseudoalnea</i>	M2A	<i>Alnus glutinosa</i>	Netherlands	MZ727038	MZ816344	MZ753488	MZ753469	MZ753478
<i>D. pseudoinconspicua</i>	URM 7873	<i>Cenostigma pyramidale</i>	Brazil	MH122535	MH122530	MH122521	MH122525	MH122518

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. pseudoinconspicua</i>	URM 7874 ^T	<i>Cenostigma pyramidale</i>	Brazil	MH122538	MH122533	MH122524	MH122528	MH122517
<i>D. pseudolongicolla</i> (= <i>D. novem</i>)	PL42 ^T	<i>Glycine max</i>	Serbia	JQ697843	JQ697856	N/A	N/A	N/A
<i>D. pseudolongicolla</i> (= <i>D. novem</i>)	CBS 127270	<i>Glycine max</i>	Croatia	KC343156	KC343882	KC344124	KC343398	KC343640
<i>D. pseudomangiferae</i>	CBS 101339 ^T	<i>Mangifera indica</i>	Dominican Republic	KC343181	KC343907	KC344149	KC343423	KC343665
<i>D. pseudomangiferae</i>	CBS 388.89	<i>Mangifera indica</i>	Mexico	KC343182	KC343908	KC344150	KC343424	KC343666
<i>D. pseudooculi</i>	HHUF 30617 ^T	<i>Homo sapiens</i>	Japan	NR_161019	LC373517	LC373519	N/A	N/A
<i>D. pseudooculi</i>	B3180	<i>tamarind</i>	Malaysia	MT043790	N/A	N/A	N/A	N/A
<i>D. pseudophoenicicola</i>	CBS 462.69 ^T	<i>Phoenix dactylifera</i>	Spain	KC343184	KC343910	KC344152	KC343426	KC343668
<i>D. pseudophoenicicola</i>	HNQZ01	<i>Areca catechu</i>	China	MN424520	MN424562	MN424534	MN424576	MN424548
<i>D. pseudotsugae</i>	MFLU 15-3228 ^T	<i>Pseudotsuga menziesii</i>	Italy	N/A	KY964181	KY964108	KY964138	N/A
<i>D. psoraleae</i>	CBS 136412 ^T	<i>Psoralea pinnata</i>	South Africa	KF777158	KF777245	KF777251	N/A	N/A
<i>D. psoraleae-pinnatae</i>	CBS 136413 ^T	<i>Psoralea pinnata</i>	South Africa	KF777159	N/A	KF777252	N/A	N/A
<i>D. pterocarpi</i>	MFLUCC 10-0571 ^T	<i>Pterocarpus indicus</i>	Thailand	JQ619899	JX275416	JX275460	JX197451	N/A
<i>D. pterocarpi</i>	MFLUCC 10-0588	<i>Pterocarpus indicus</i>	Thailand	JQ619900	JX275417	JX275461	JX197452	N/A
<i>D. pterocarpicola</i>	MFLUCC 10-0580 ^T	<i>Pterocarpus indicus</i>	Thailand	JQ619887	JX275403	JX275441	JX197433	N/A
<i>D. pulla</i>	CBS 338.89 ^T	<i>Hedera helix</i>	Yugoslavia	KC343152	KC343878	KC344120	KC343394	KC343636
<i>D. pungensis</i>	SAUCC194.112 ^T	<i>Elaeagnus pungens</i>	China	MT822640	MT855952	MT855837	MT855719	MT855607
<i>D. pungensis</i>	SAUCC194.89	<i>Camellia sinensis</i>	China	MT822617	MT855929	MT855814	MT855696	MT855585
<i>D. pustulata</i>	CBS 109742	<i>Acer pseudoplatanus</i>	Austria	KC343185	KC343911	KC344153	KC343427	KC343669
<i>D. pustulata</i>	CBS 109784	<i>Prunus padus</i>	Austria	KC343187	KC343913	KC344155	KC343429	KC343671
<i>D. pyracanthae</i>	CBS 142384 ^T	<i>Pyracantha coccinea</i>	Portugal	KY435635	KY435625	KY435666	KY435656	KY435646
<i>D. pyracanthae</i>	CAA487	<i>Pyracantha coccinea</i>	Portugal	KY435636	KY435626	KY435667	KY435657	KY435647

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. racemosae</i>	CPC 26646 ^T	<i>Euclea racemosa</i>	South Africa	MG600223	MG600225	MG600227	MG600219	MG600221
<i>D. raonikayaporum</i>	CBS 133182 ^T	<i>Spondias mombin</i>	Brazil	KC343188	KC343914	KC344156	KC343430	KC343672
<i>D. ravennica</i>	MFLUCC 15-0479 ^T	<i>Tamarix</i> sp.	Italy	KU900335	KX365197	KX432254	N/A	N/A
<i>D. ravennica</i>	MFLUCC 17-1029	<i>Salvia</i> sp.	Italy	KY964191	KY964147	KY964075	N/A	N/A
<i>D. rhoina</i>	CBS 146.27	<i>Rhus toxicodendron</i>	Not stated	MH854907	KC343915	KC344157	KC343431	KC343673
<i>D. rosae</i>	MFLUCC 17-2658 ^T	<i>Rosa</i> sp.	Thailand	MG828894	N/A	MG843878	MG829273	N/A
<i>D. rosae</i>	MFLUCC 17-2574	<i>Senna siamea</i>	Thailand	MG906793	MG968954	MG968952	N/A	N/A
<i>D. rosiphthora</i>	COAD 2913	<i>Rosa</i> sp.	Brazil	MT311196	MT313692	N/A	MT313690	N/A
<i>D. rosiphthora</i>	COAD 2914 ^T	<i>Rosa</i> sp.	Brazil	MT311197	MT313693	N/A	MT313691	N/A
<i>D. rossmaniae</i>	CAA762 ^T	<i>Vaccinium corymbosum</i>	Portugal	MK792290	MK828063	MK837914	MK883822	MK871432
<i>D. rossmaniae</i>	CAA763	<i>Vaccinium corymbosum</i>	Portugal	MK792291	MK828064	MK837915	MK883823	MK871433
<i>D. rostrata</i>	CFCC 50062 ^T	<i>Juglans mandshurica</i>	China	KP208847	KP208853	KP208855	KP208849	KP208851
<i>D. rostrata</i>	CFCC 50063	<i>Juglans mandshurica</i>	China	KP208848	KP208854	KP208856	KP208850	KP208852
<i>D. rudis</i>	AR3422 ^T	<i>Laburnum anagyroides</i>	Austria	KC843331	KC843090	KC843177	KC843146	
<i>D. rudis</i>	CBS 113201	<i>Vitis vinifera</i>	Portugal	MH862916	KC343960	KC344202	KC343476	KC343718
<i>D. rumicicola</i>	MFLUCC18-0739	<i>Rumex</i> sp.	Italy	MH846233	MK049554	MK049555	N/A	N/A
<i>D. rumicicola</i>	JZB320006 ^T	<i>Scrophularia canina</i>	Italy	MK066126	MK078545	MK078546	N/A	N/A
<i>D. saccharata</i>	CBS 116311 ^T	<i>Protea repens</i>	South Africa	KC343190	KC343916	KC344158	KC343432	KC343674
<i>D. sackstonii</i>	BRIP 54669b ^T	<i>Helianthus annuus</i>	Australia	KJ197287	KJ197249	KJ197267	N/A	N/A
<i>D. salicicola</i>	BRIP 54825 ^T	<i>Salix purpurea</i>	Australia	JX862531	JX862537	KF170923	N/A	N/A
<i>D. salinicola</i>	MFLU 17-2592	<i>Xylocarpus</i> sp.	Thailand	MN047099	MN077074	N/A	N/A	N/A
<i>D. salinicola</i>	MFLU 18-0553 ^T	<i>Xylocarpus</i> sp.	Thailand	MN047098	MN077073	N/A	N/A	N/A
<i>D. salsuginosa</i>	NFCCI-4385	<i>Avicennia marina</i>	India	MN061372	N/A	MN431500	N/A	N/A
<i>D. sambucusii</i>	CFCC 51986 ^T	<i>Sambucus williamsii</i>	China	KY852495	KY852507	KY852511	KY852499	KY852503
<i>D. sambucusii</i>	CFCC 51987	<i>Sambucus williamsii</i>	China	KY852496	KY852508	KY852512	KY852500	KY852504

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. schimae</i>	CFCC 53103 ^T	<i>Schima superba</i>	China	MK432640	MK578116	MK578043	MK442962	MK442987
<i>D. schimae</i>	CFCC 53104	<i>Schima superba</i>	China	MK432641	MK578117	MK578044	MK442963	MK442988
<i>D. schini</i>	CBS 133181 ^T	<i>Schinus</i>	Brazil	KC343191	KC343917	KC344159	KC343433	KC343675
		<i>terebinthifolius</i>						
<i>D. schini</i>	CPC 20286	<i>Schinus</i>	Brazil	KC343192	KC343918	KC344160	KC343434	KC343676
		<i>terebinthifolius</i>						
<i>D. schisandrae</i>	CFCC 51988 ^T	<i>Schisandra</i>	China	KY852497	KY852509	KY852513	KY852501	KY852505
		<i>chinensis</i>						
<i>D. schisandrae</i>	CFCC 51989	<i>Schisandra</i>	China	KY852498	KY852510	KY852514	KY852502	KY852506
		<i>chinensis</i>						
<i>D. schoeni</i>	MFLU 15-1279 ^T	<i>Schoenus nigricans</i>	Italy	KY964226	KY964182	KY964109	KY964139	N/A
<i>D. schoeni</i>	MFLU 15-2609	<i>Plantago</i> sp.	Italy	KY964229	KY964185	KY964112	KY964141	N/A
<i>D. sclerotioides</i>	CBS 296.67 ^T	<i>Cucumis sativus</i>	Netherlands	KC343193	KC343919	KC344161	KC343435	KC343677
<i>D. sclerotioides</i>	CBS 710.76	<i>Cucumis sativus</i>	Netherlands	KC343194	KC343920	KC344162	KC343436	KC343678
<i>D. scobina</i>	CBS 251.38	<i>Fraxinus excelsior</i>	UK	KC343195	KC343921	KC344163	KC343437	KC343679
<i>D. searlei</i>	CBS 146456 ^T	<i>Macadamia</i>	Australia	MN708231	N/A	MN696540	N/A	N/A
<i>D. sennae</i>	CFCC 51636 ^T	<i>Senna bicapsularis</i>	China	KY203724	KY228885	KY228891	KY228875	N/A
<i>D. sennae</i>	CFCC 51637	<i>Senna bicapsularis</i>	China	KY203725	KY228886	KY228892	KY228876	N/A
<i>D. sennicola</i>	CFCC 51634 ^T	<i>Senna bicapsularis</i>	China	KY203722	KY228883	KY228889	KY228873	KY228879
<i>D. sennicola</i>	CFCC 51635	<i>Senna bicapsularis</i>	China	KY203723	KY228884	KY228890	KY228874	KY228880
<i>D. serafiniae</i>	BRIP 55665a ^T	<i>Helianthus annuus</i>	Australia	KJ197274	KJ197236	KJ197254	N/A	N/A
<i>D. serafiniae</i>	BRIP 54136	<i>Lupinus albus</i>	Australia	KJ197273	KJ197235	KJ197253	N/A	N/A
<i>D. shaanxiensis</i>	CFCC 53106 ^T	on branches of	China	MK432654	MK578130	N/A	MK442976	MK443001
		liana						
<i>D. shaanxiensis</i>	CFCC 53107	on branches of	China	MK432655	MK578131	N/A	MK442977	MK443002
		liana						
<i>D. shennongjiaensis</i>	CNUCC 201906	<i>Juglans regia</i>	China	MN216228	MN224673	MN227013	MN224552	MN224561
<i>D. shennongjiaensis</i>	CNUCC 201905 ^T	<i>Juglans regia</i>	China	MN216229	MN224672	MN227012	MN224551	MN224560
<i>D. siamensis</i>	MFLUCC 10-573a ^T	<i>Dasymaschalon</i> sp.	Thailand	JQ619879	JX275393	JX275429	JX197422	N/A
<i>D. siamensis</i>	MFLUCC 12-0300	dead leaf	Thailand	KT459417	KT459451	KT459435	KT459467	N/A
<i>D. silvicola</i>	CFCC 54191 ^T	<i>Fraxinus excelsior</i>	Netherlands	MZ727041	MZ816347	MZ753491	MZ753472	MZ753481
<i>D. silvicola</i>	M79	<i>Fraxinus excelsior</i>	Netherlands	MZ727042	MZ816348	MZ753492	MZ753473	MZ753482
<i>D. sinensis</i>	ZJUP0033-4 ^T	<i>Amaranthus</i> sp.	China	MK637451	MK660449	MK660447	N/A	MK660451

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. sinensis</i>	ZJUP0038-3	<i>Amaranthus</i> sp.	China	MN442428	MN448493	MN448494	N/A	MN448492
<i>D. sojae</i>	DP0605	<i>Glycine max</i>	USA	KJ590707	KJ590750	KJ610863	KJ612104	KJ659196
<i>D. sojae</i>	FAU459	<i>Stokesia laevis</i>	USA	KJ590709	KJ590752	KJ610865	KJ612106	KJ659198
<i>D. sojae</i>	FAU499	<i>Asparagus officinalis</i>	USA	KJ590717	KJ590760	KJ610873	KJ612114	KJ659206
<i>D. sojae</i>	FAU604	<i>Glycine max</i>	USA	KJ590716	KJ590759	KJ610872	KJ612113	KJ659205
<i>D. sojae</i>	FAU635 ^T	<i>Glycine max</i>	USA	KJ590719	KJ590762	KJ610875	KJ612116	KJ659208
<i>D. sojae</i>	FAU636	<i>Glycine max</i>	USA	KJ590718	KJ590761	KJ610874	KJ612115	KJ659207
<i>D. sophorae</i>	JAC12639	<i>Sophora microphylla</i>	New Zealand	MK432728	N/A	N/A	N/A	N/A
<i>D. sophorae</i>	PDD95984	Unidentified	New Zealand	JQ694115	N/A	N/A	N/A	N/A
<i>D. spartinicola</i>	CBS 140003 ^T	<i>Spartium junceum</i>	Spain	KR611879	N/A	N/A	N/A	KR857696
<i>D. spinosa</i>	CGMCC 3.19602 ^T	<i>Pyrus pyrifolia</i>	China	MK626849	MK654811	MK691234	MK691129	MK726156
<i>D. spinosa</i>	PSCG388	<i>Pyrus pyrifolia</i>	China	MK626860	MK654798	MK691229	MK691128	MK726171
<i>D. sterilis</i>	CBS 136969 ^T	<i>Vaccinium corymbosum</i>	Italy	KJ160579	KJ160611	KJ160528	KJ160548	MF418350
<i>D. sterilis</i>	MFLUCC 17-1011	<i>Cytisus</i> sp.	Italy	KY964211	KY964167	KY964095	KY964126	N/A
<i>D. stewartii</i>	CBS 193.36 ^T	<i>Cosmos bipinnatus</i>	Not stated	MH867279	GQ250324	JX275421	JX197415	N/A
<i>D. stewartii</i>	MN1	<i>Helianthus annuus</i>	US	KX668416	KX852355	N/A	N/A	N/A
<i>D. stictica</i>	CBS 370.54 ^T	<i>Buxus sempervirens</i>	Italy	KC343212	KC343938	KC344180	KC343454	KC343696
<i>D. subclavata</i>	ZJUD83	<i>Citrus maxima</i> cv. Shatianyou	China	KJ490618	KJ490497	KJ490439	N/A	KJ490560
<i>D. subclavata</i>	CGMCC 3.17257 ^T	<i>Citrus unshiu</i>	China	KJ490630	KJ490509	KJ490451	N/A	KJ490572
<i>D. subcylindrospora</i>	KUMCC 17-0151 ^T	<i>Salix</i> sp.	China	MG746629	MG746630	MG746631	N/A	N/A
<i>D. subellipicola</i>	KUMCC 17-0153 ^T	on dead wood	China	MG746632	MG746633	MG746634	N/A	N/A
<i>D. subordinaria</i>	CBS 464.90 ^T	<i>Plantago lanceolata</i>	New Zealand	KC343214	KC343940	KC344182	KC343456	KC343698
<i>D. subordinaria</i>	CBS 101711	<i>Plantago lanceolata</i>	New Zealand	KC343213	KC343939	KC344181	KC343455	KC343697
<i>D. taiwanensis</i>	NTUCC 18-105-1 ^T	<i>Ixora chinensis</i>	Taiwan	MT241257	MT251199	MT251202	MT251196	N/A
<i>D. taiwanensis</i>	NTUCC 18-105-2	<i>Ixora chinensis</i>	Taiwan	MT241258	MT251200	MT251203	MT251197	N/A

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. tanakae</i>	MAFF 410600	<i>Malus pumila</i> var. <i>domestica</i>	Japan	AB245077	N/A	N/A	N/A	N/A
<i>D. tanakae</i>	MAFF 410127	<i>Malus pumila</i> var. <i>domestica</i>	Japan	AB245075	N/A	N/A	N/A	N/A
<i>D. taoicola</i>	MFLUCC 16-0117 ^T	<i>Prunus persica</i>	China	KU557567	KU557635	KU557591	N/A	N/A
<i>D. taoicola</i>	PSCG485	<i>Pyrus pyrifolia</i>	China	MK626869	MK654812	MK691227	MK691120	MK726173
<i>D. tarchonanathi</i>	CBS 146073 ^T	<i>Tarchonanthus littoralis</i>	South Africa	MT223794	N/A	MT223733	N/A	MT223759
<i>D. tecomae</i>	CBS 100547 ^T	<i>Tabebuia</i> sp.	Brazil	KC343215	KC343941	KC344183	KC343457	KC343699
<i>D. tectonae</i>	MFLUCC 12-0777 ^T	<i>Tectona grandis</i>	Thailand	NR147590	KU749359	KU743977	KU749345	N/A
<i>D. tectonae</i>	MFLUCC 14-1139	<i>Tectona grandis</i>	Thailand	KU712438	KU749366	KU743985	KU749353	N/A
<i>D. tectonendophytica</i>	MFLUCC 13-0471 ^T	<i>Tectona grandis</i>	Thailand	NR_147591	KU749367	KU743986	KU749354	N/A
<i>D. tectonendophytica</i>	LC8115	Unidentified	China	KY491550	KY491560	KY491570	N/A	N/A
<i>D. tectonigena</i>	MFLUCC 12-0767 ^T	<i>Tectona grandis</i>	China	KU712429	KU749371	KU743976	KU749358	N/A
<i>D. tectonigena</i>	LC6512	<i>Camellia sinensis</i>	China	KX986782	KX999174	KX999215	KX999284	KX999254
<i>D. terebinthifolii</i>	CBS 133180 ^T	<i>Schinus terebinthifolius</i>	Brazil	KC343216	KC343942	KC344184	KC343458	KC343700
<i>D. terebinthifolii</i>	CPC 20285	<i>Schinus terebinthifolius</i>	Brazil	KC343218	KC343944	KC344186	KC343460	KC343702
<i>D. ternstroemia</i>	CGMCC 3.15183 ^T	<i>Ternstroemia gymnanthera</i>	China	NR_147523	KC153089	N/A	N/A	N/A
<i>D. ternstroemia</i>	CGMCC 3.15184	<i>Ternstroemia gymnanthera</i>	China	KC153099	KC153090	N/A	N/A	N/A
<i>D. tersa</i>	FS441	deep-sea sediments of the Indian Ocean	China	MK592793	N/A	N/A	N/A	N/A
<i>D. tersa</i>	BCKSKMP-8	<i>Butea monosperma</i>	India	MG049670	N/A	N/A	N/A	N/A
<i>D. thunbergiae</i>	MFLUCC 10-0576a ^T	<i>Thunbergia laurifolia</i>	Thailand	JQ619893	JX275409	JX275449	JX197440	N/A
<i>D. thunbergiae</i>	MFLUCC 10-0576b	Unidentified	Not stated	JQ619894	JX275410	JX275450	JX197441	N/A
<i>D. thunbergiicola</i>	MFLUCC 12-0033 ^T	<i>Thunbergia laurifolia</i>	Thailand	KP715097	KP715098	N/A	N/A	N/A
<i>D. tibetensis</i>	CFCC 51999 ^T	<i>Juglans regia</i>	China	MF279843	MF279858	MF279873	MF279888	MF279828
<i>D. tibetensis</i>	CFCC 52000	<i>Juglans regia</i>	China	MF279844	MF279859	MF279874	MF279889	MF279829

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. torilicola</i>	MFLUCC 17-1051 ^T	<i>Torilis arvensis</i>	Italy	KY964212	KY964168	KY964096	KY964127	N/A
<i>D. toxica</i>	CBS 534.93 ^T	<i>Lupinus angustifolius</i>	Australia	KC343220	KC343946	KC344188	KC343462	KC343704
<i>D. toxica</i>	CBS 546.93	<i>Lupinus</i> sp.	Australia	KC343222	KC343948	KC344190	KC343464	KC343706
<i>D. toxicodendri</i>	TFM FP-10740 ^T	<i>Toxicodendron vernicifluum</i>	Japan	NR_158416	N/A	N/A	N/A	N/A
<i>D. toxicodendri</i>	FFPRI420990	<i>Toxicodendron vernicifluum</i>	Japan	LC275193	LC275217	LC275225	LC275201	LC275209
<i>D. tulliensis</i>	BRIP 62248a ^T	<i>Theobroma cacao</i>	Australia	KR936130	KR936133	KR936132	N/A	N/A
<i>D. tulliensis</i>	RST-1	<i>Ricinus communis</i>	China	MN911382	MT121969	N/A	N/A	N/A
<i>D. ueckeri</i>	FAU656 ^T	<i>Cucumis melo</i>	USA	KJ590726	KJ590747	KJ610881	KJ612122	KJ659215
<i>D. ueckeri</i>	HNWN01	<i>Areca catechu</i>	China	MN424522	MN424564	MN424536	MN424578	MN424550
<i>D. ukurunduensis</i>	CFCC 52592 ^T	<i>Acer ukurunduense</i>	China	MH121527	MH121569	N/A	MH121445	MH121485
<i>D. ukurunduensis</i>	CFCC 52593	<i>Acer ukurunduense</i>	China	MH121528	MH121570	N/A	MH121446	MH121486
<i>D. undulata</i>	CGMCC 3.18293 ^T	Unidentified leaf	China-Laos border	KX986798	KX999190	KX999230	N/A	KX999269
<i>D. undulata</i>	LC8111	Unidentified	China	KY491546	KY491556	KY491566	N/A	N/A
<i>D. unshiuensis</i>	CGMCC 3.17566 ^T	<i>Fortunella margarita</i>	China	KJ490584	KJ490463	KJ490405	N/A	KJ490526
<i>D. unshiuensis</i>	PSCG339	<i>Pyrus pyrifolia</i>	China	MK626928	MK654879	MK691300	MK691181	MK726188
<i>D. vaccinii</i>	CBS 160.32 ^T	<i>Oxycoccus macrocarpos</i>	USA	KC343228	KC343954	KC344196	KC343470	KC343712
<i>D. vaccinii</i>	CBS 122116	<i>Vaccinium corymbosum</i>	USA	KC343227	KC343953	KC344195	KC343469	KC343711
<i>D. vacuae</i>	CAA829 ^T	<i>Vaccinium corymbosum</i>	Portugal	MK792306	MK828077	MK837928	MK883832	MK871446
<i>D. vacuae</i>	CAA830	<i>Vaccinium corymbosum</i>	Portugal	MK792309	MK828080	MK837931	MK883834	MK871449
<i>D. vangeriae</i>	CPC 22703 ^T	<i>Vangeria infausta</i>	Zambia	KJ869137	N/A	KJ869247	N/A	N/A
<i>D. varians</i>	LC8112	<i>Acer</i> sp.	Japan	KY491547	KY491557	KY491567	KY491575	N/A
<i>D. varians</i>	LC8113	<i>Acer</i> sp.	Japan	KY491548	KY491558	KY491568	KY491576	N/A
<i>D. vawdreyi</i>	BRIP 57887a ^T	<i>Psidium guajava</i>	Australia	KR936126	KR936129	KR936128	N/A	N/A
<i>D. velutina</i>	CGMCC 3.18286 ^T	<i>Neolitsea</i> sp.	China	KX986790	KX999182	KX999223	N/A	KX999261

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>efla</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>D. velutina</i>	LC4419	<i>Neolitsea</i> sp.	China	KX986789	KX999181	KX999222	KX999286	KX999260
<i>D. verniciicola</i>	CFCC 53109 ^T	<i>Vernicia montana</i>	China	MK573944	MK574619	MK574639	MK574583	MK574599
<i>D. verniciicola</i>	CFCC 53110	<i>Vernicia montana</i>	China	MK573945	MK574620	MK574640	MK574584	MK574600
<i>D. vexans</i>	CBS 127.14	<i>Solanum</i>	USA	KC343229	KC343955	KC344197	KC343471	KC343713
		<i>melongena</i>						
<i>D. vexans</i>	FAU597	<i>Solanum</i> sp.	Dominican Republic	KJ590734	KJ590774	KJ610889	KJ612131	KJ659216
<i>D. viburni</i>	CBS 158.29 ^T	Unidentified	Not stated	MH855030	N/A	N/A	N/A	N/A
<i>D. viniferae</i>	JZB320071 ^T	<i>Vitis vinifera</i>	China	MK341550	MK500107	MK500112	MK500119	N/A
<i>D. viniferae</i>	JZB320072	<i>Vitis vinifera</i>	China	MK341551	MK500108	MK500113	MK500120	N/A
<i>D. virgiliae</i>	CMW40748 ^T	<i>Virgilia oroboides</i>	South Africa	KP247566	N/A	KP247575	N/A	N/A
<i>D. virgiliae</i>	CMW40749	Unidentified	Not stated	KP247567	N/A	KP247576	N/A	N/A
<i>D. vochysiae</i>	LGMF1583 ^T	<i>Vochysia divergens</i>	Brazil	MG976391	MK007526	MK007527	MK007528	MK033323
<i>D. woodii</i>	CBS 558.93	<i>Lupinus</i> sp.	Australia	KC343244	KC343970	KC344212	KC343486	KC343728
<i>D. woolworthii</i>	CBS 148.27	<i>Ulmus americana</i>	Not stated	KC343245	KC343971	KC344213	KC343487	KC343729
<i>D. xishuangbanica</i>	CGMCC 3.18283 ^T	<i>Camellia sinensis</i>	China	KX986784	KX999176	KX999217	N/A	N/A
<i>D. xishuangbanica</i>	CGMCC 3.18282	<i>Camellia sinensis</i>	China	KX986783	KX999175	KX999216	N/A	KX999255
<i>D. xunwuensis</i>	CFCC 53085 ^T	Unidentified dead wood	China	MK432663	MK578137	MK578063	MK442983	MK443008
<i>D. xunwuensis</i>	CFCC 53086	Unidentified dead wood	China	MK432664	MK578138	MK578064	MK442984	MK443009
<i>D. yunnanensis</i>	CGMCC 3.18289 ^T	<i>Coffea</i> sp.	China	KX986796	KX999188	KX999228	KX999290	N/A
<i>D. yunnanensis</i>	LC8107	<i>Coffea</i> sp.	China	KY491542	KY491552	KY491562	KY491572	N/A
<i>D. zaobaisu</i>	CGMCC 3.19598 ^T	<i>Pyrus</i> × <i>bretschneideri</i>	China	MK626922	MK654855	MK691245	N/A	MK726207
<i>D. zaobaisu</i>	PSCG032	<i>Pyrus</i> × <i>bretschneideri</i>	China	MK626923	MK654856	MK691246	N/A	MK726208
<i>Hyaliappendispora galii</i>	MFLUCC 16-1208 ^T	<i>Galium</i> sp.	Italy	NR_154107	MF377587	N/A	N/A	N/A
<i>H. galii</i>	MFLU 15-2269	<i>Galium</i> sp.	Italy	MF190150	MF377588	N/A	N/A	N/A
<i>Massariothea</i> sp.	MFLUCC 15-0452	<i>Thysanolaena</i> sp.	Thailand	MG967672	MH137275	N/A	N/A	N/A
<i>Massariothea</i> sp.	MFLUCC 14-0585	Poaceae sp.	Thailand	MG967671	MH104871	N/A	N/A	N/A
<i>Massariothea</i> sp.	MFLUCC 15-0458	Poaceae sp.	Thailand	MG967674	MH171171	N/A	N/A	N/A

Table 1 Continued.

Species	Isolate	Host	Location	GenBank accession numbers				
				ITS	<i>ef1a</i>	<i>β-tubulin</i>	<i>cal</i>	<i>his3</i>
<i>Paradiaporthes artemisiae</i>	MFLUCC 14-0850 ^T	<i>Artemisia</i>	Italy	MF190155	MF377583	N/A	N/A	N/A
<i>P. artemisiae</i>	MFLUCC 17-1663	<i>Artemisia</i>	Italy	MF190156	MF377584	N/A	N/A	N/A
<i>Phaeocystostroma ambiguum</i>	CFMS 1295	<i>Zea mays</i>	Brazil	KU323508	KU351848	N/A	N/A	N/A
<i>Ph. ambiguum</i>	CPC 17079	<i>Zea mays</i>	South Africa	FR748043	FR748075	N/A	N/A	N/A
<i>Ph. megalosporum</i>	CBS 284.65	<i>Rice-field soil</i>	India	FR748045	FR748077	N/A	N/A	N/A
<i>Ph. plurivorum</i>	CBS 113835	Unidentified	Portugal	MH862945	FR748078	N/A	N/A	N/A
<i>Ph. sacchari</i>	CBS 275.34	Unidentified	Japan	MH855512	FR748079	N/A	N/A	N/A
<i>Phaeodiaporthes appendiculata</i>	CBS 123821 ^T	<i>Acer campestre</i>	Austria	NR_154299	N/A	N/A	N/A	N/A
<i>Stenocarpella macrospora</i>	CBS 117560 ^T	<i>Zea mays</i>	South Africa	NR_157418	MG934504	N/A	N/A	N/A
<i>S. macrospora</i>	YZ-1	<i>Zea mays</i>	China	KY012337	MF076787	N/A	N/A	N/A
<i>S. maydis</i>	CPC 16789	<i>Zea mays</i>	South Africa	FR748064	FR748093	N/A	N/A	N/A
<i>S. maydis</i>	CBS 117559	<i>Zea mays</i>	South Africa	FR748052	FR748081	N/A	N/A	N/A
<i>S. maydis</i>	A1-1*	<i>Zea mays</i>	USA	NQMI00000000				

* Whole genomic DNA strain; ^T Type; (-) synonymized taxa in previous research and this study.

Another phylogenetic analysis was performed using the ITS dataset (609 bp), which included the 50 strains that only have ITS sequence and excluded from the combined dataset (Fig. 1). This dataset consisted of 784 Diaporthaceae strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the outgroup taxa. The tree topology was similar to the previously obtained ITS tree (Fig. 2). Those 50 strains dispersed throughout the tree, but placements and memberships in different sections were not impacted (Fig. 3).

Phylogenetic analysis of the *ef1a* gene (381 bp) consisted of 510 strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the outgroup taxa. The *D. arecae*, *D. biconispora*, *D. carpini*, *D. decedens*, *D. oncostoma*, *D. pustulata*, *D. rudis*, *D. sojae*, *D. varians*, and *D. vawdreyi* species complexes were recovered as in the combined gene tree. The *Diaporthes alnea* species complex formed a well-resolved clade except for *D. shennongjiaensis*. *Diaporthes scobina* and *D. toxica* species complexes were dispersed throughout the tree and clustered with species from other clades (Fig. 4).

Phylogenetic analysis using the *β-tubulin* gene (763 bp) consisted of 479 strains. *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt) were used as the outgroup taxa. The *D. alnea*, *D. arecae*, *D. biconispora*, *D. carpini*, *D. decedens*, *D. oncostoma*, *D. pustulata*, *D. rudis*, *D. toxica*, *D. varians*, and *D. vawdreyi* species complexes were recovered as in the combined gene tree (Fig. 1). *Diaporthes scobina*, *D. sojae* and *D. varians* species complexes formed a well-resolved species complex except for some species (Fig. 5).

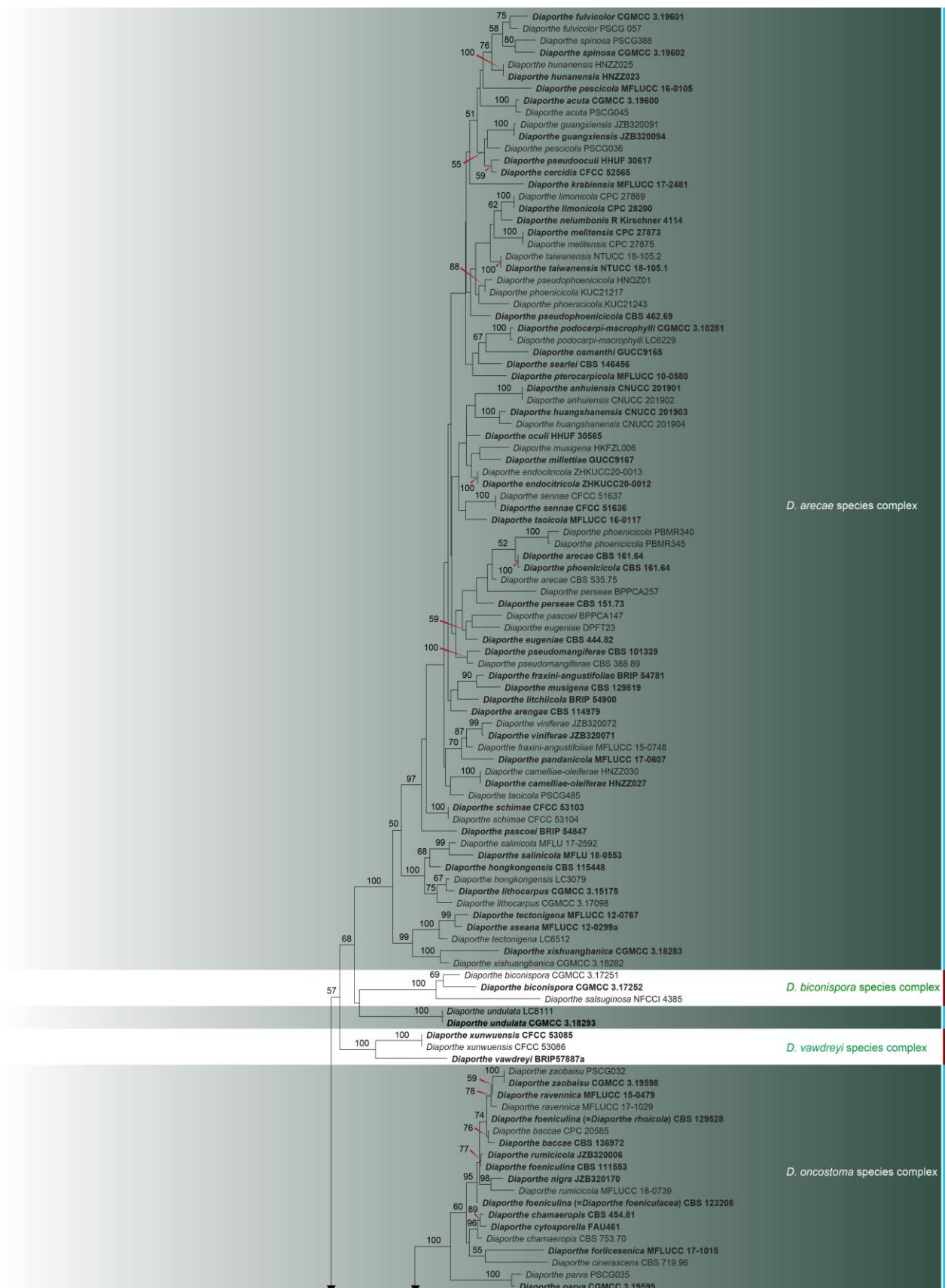


Figure 1 – Maximum likelihood phylogenetic tree inferred from combined ITS1+ITS2, 5.8S, *efl* α , β -tubulin, *cal*, and *his3* sequence data of 535 strains of Diaporthaceae. The tree is artificially rooted with *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values $\leq 50\%$ are given at the nodes. The species synonymized are in blue and the ex-type taxa are in bold.

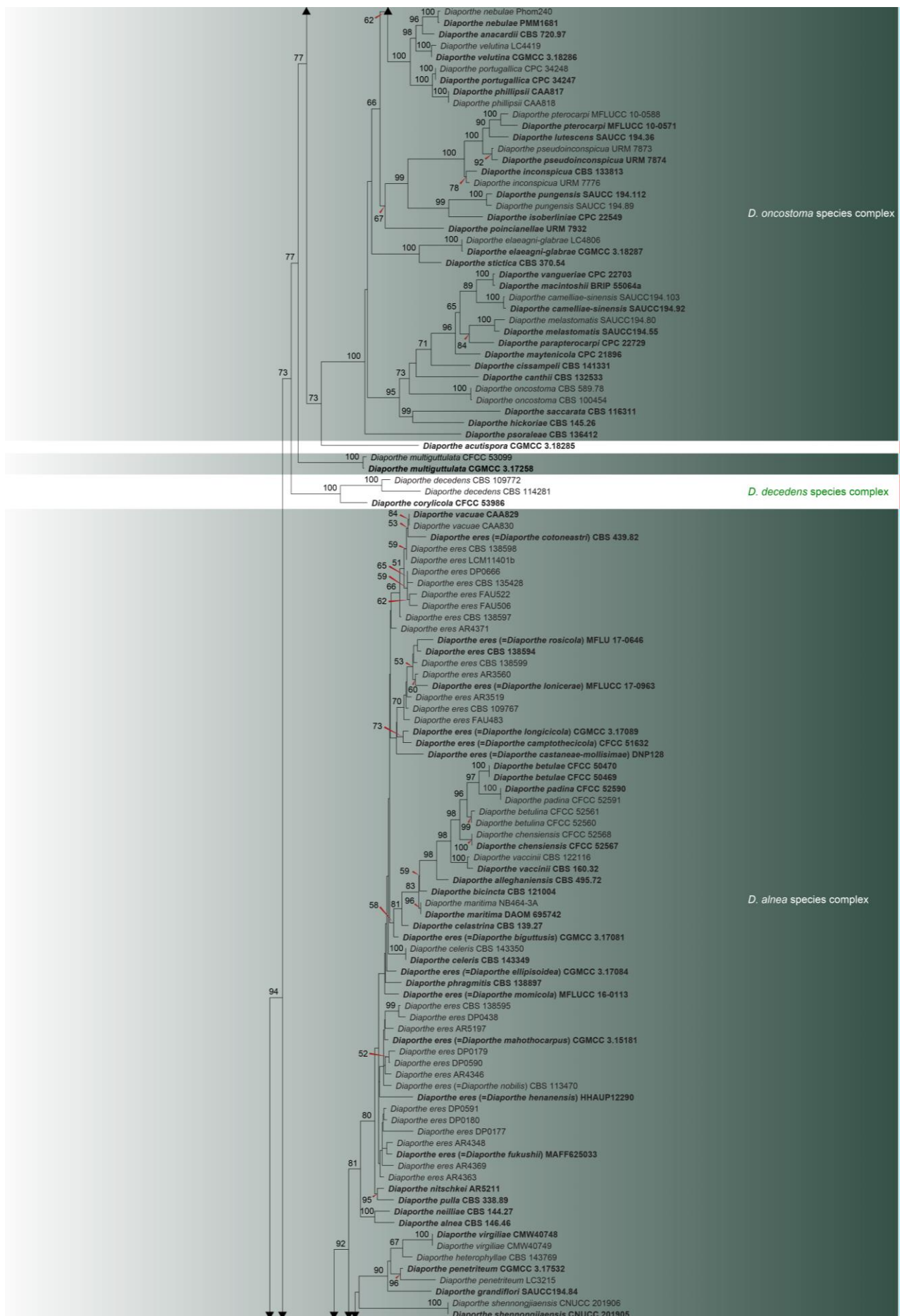


Figure 1 – Continued.

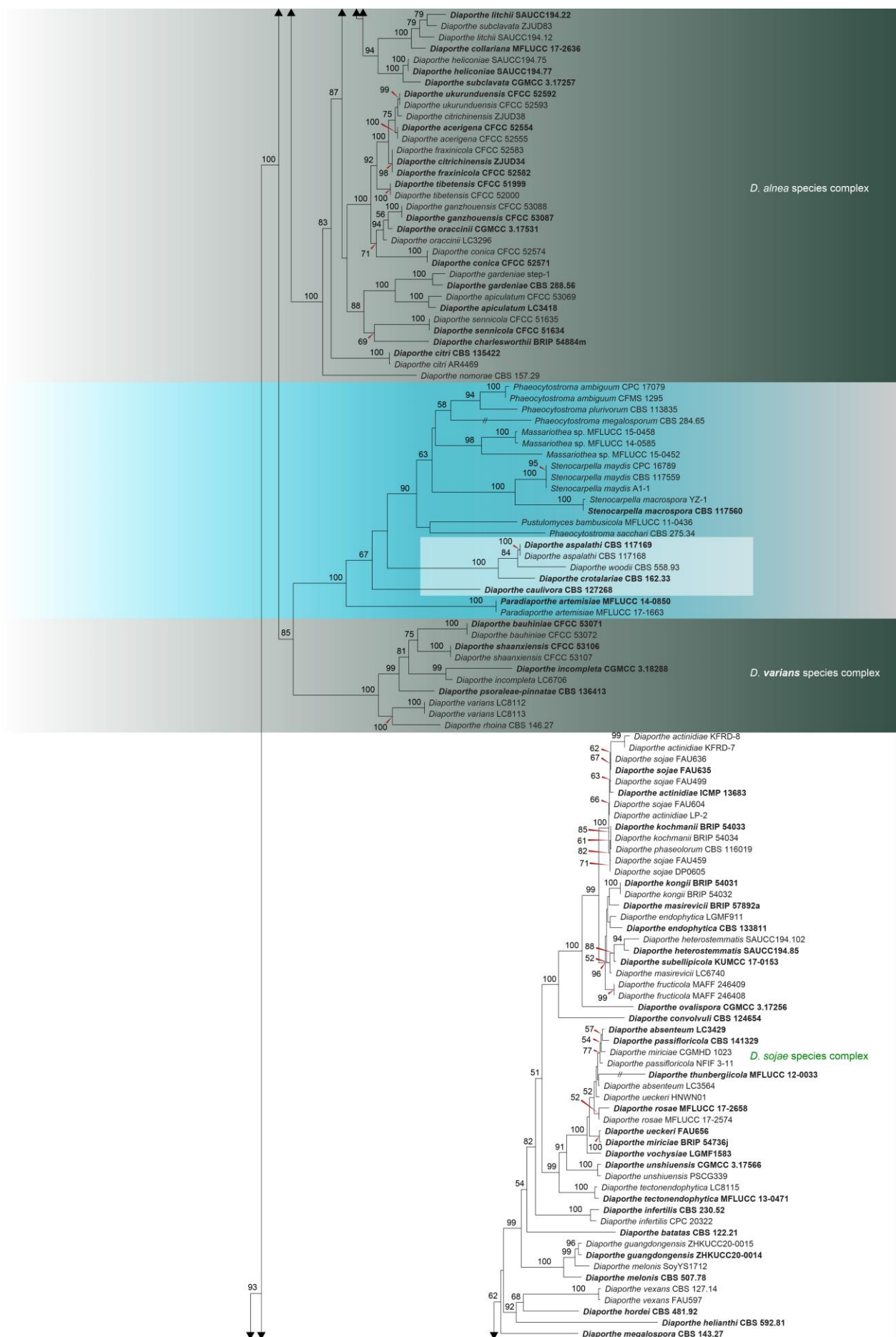


Figure 1 – Continued.



Figure 1 – Continued.

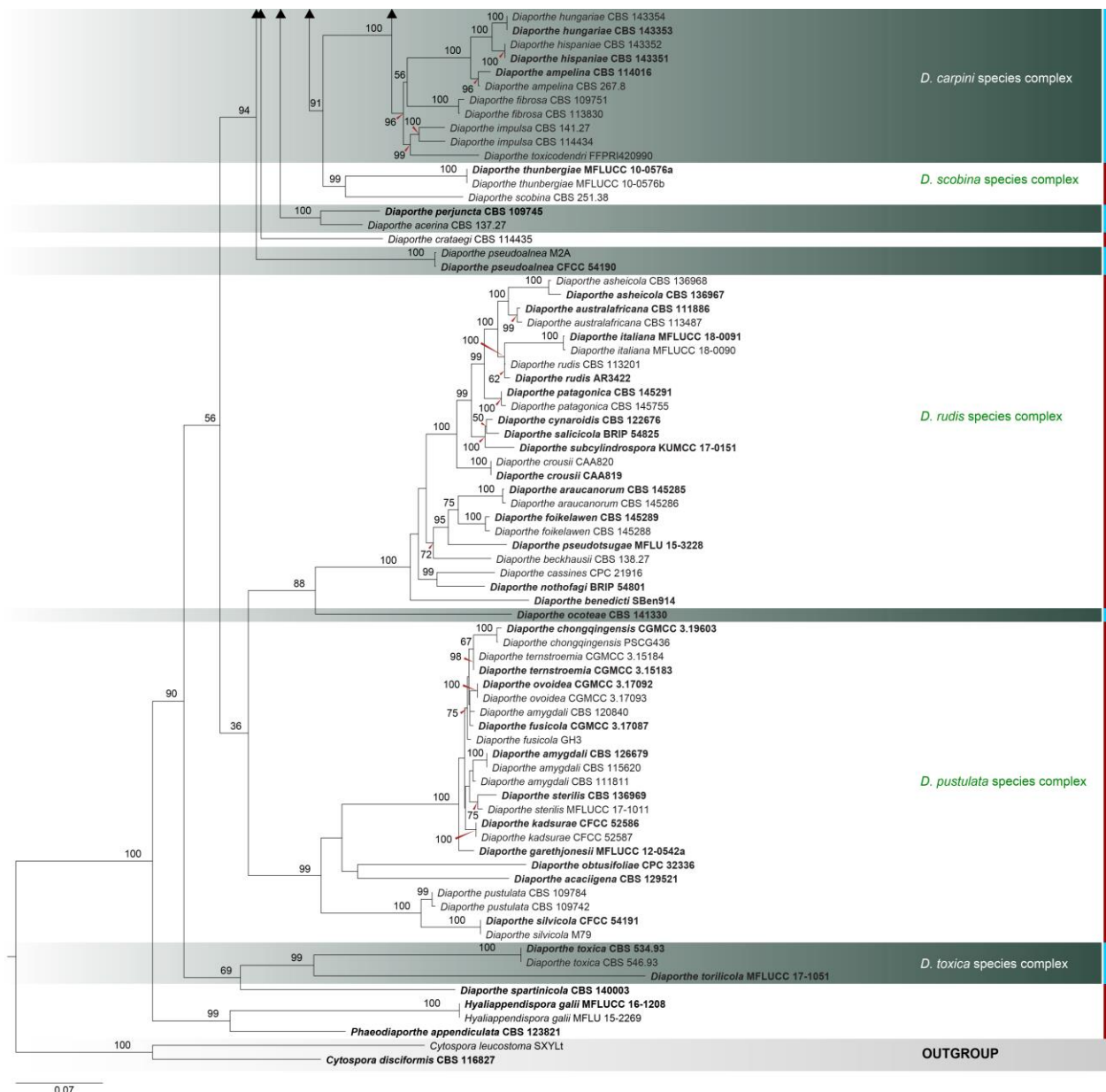


Figure 1 – Continued.

Phylogenetic analysis using the *cal* gene (694 bp) consisted of 383 strains. *Cytospora leucostoma* (SXYLt) was used as the outgroup taxon. The *D. alnea*, *D. carpini*, *D. decedens*, *D. oncostoma*, *D. rudis*, *D. scobina*, *D. toxica*, *D. varians*, and *D. vawdreyi* species complexes were recovered as in the combined gene tree (Fig. 1). *Diaporthe arecae*, *D. biconispora*, *D. pustulata*, and *D. sojae* species complexes were well-resolved, except for some species (Fig. 6).

Phylogenetic analysis using the *his3* gene (474 bp) consisted of 343 strains. *Cytospora leucostoma* (SXYLt) was used as the outgroup taxa. The *D. arecae*, *D. oncostoma*, *D. vawdreyi*, *D. carpini*, *D. pustulata*, *D. rudis*, and *D. toxica* species complexes were recovered as in the combined gene tree. *Diaporthe alnea* species complex was recovered as in the combined gene tree except for *D. penetratum*. Similarly, the *D. sojae* species complex was recovered except for *D. tarchonantheri*, which did not cluster within the clade. *Diaporthe varians* species complex formed a well-resolved clade except for *D. incomplete* strain CGMCC 3.18288. This species complex formed a sister clade to *D. sojae* species complex and some genera in Diaporthaceae. One species of the *D. scobina* species complex clustered within the *D. carpini* species complex, and that was the only species with *his3* sequence in the clade (Fig. 7). Species of the *D. biconispora* species complex clustered within *D. arecae* species complex.

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

Species complexes

There are 13 species complexes:

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

Diaporthe alnea species complex

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

Notes – Forty species are included in the *D. alnea* species complex based on the maximum likelihood analysis of the combined gene tree (100%, Fig. 1). This is the second largest species complex in *Diaporthe* genus, while included the generic type, *D. alnea*. Its members are mostly pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). The species complex was named as *Diaporthe eres* (Udayanga et al. 2014), based on *Diaporthe* introduced by Nitschke (1870). According to nomenclatural articles, it conserves the oldest name. Therefore, *Diaporthe alnea*, the type species of *Diaporthe* introduced by Fuckel in 1867, is used to describe this species complex. The clade was not well-resolved in ITS, *efl**a*, *cal*, and *his3* single-locus trees, but β -*tubulin* topology provided a better resolution for this species complex similar to the combined gene tree (Figs 1–7). *Diaporthe eres* strains collected from different hosts were dispersed in the clade.

Diaporthe arecae species complex

Species included in the *D. arecae* species complex – *Diaporthe acuta*, *D. anhuiensis*, *D. arecae*, *D. arengae*, *D. aseana*, *D. camelliae-oleiferae*, *D. cercidis*, *D. endocitricola*, *D. eugeniae*, *D. fraxini-angustifoliae*, *D. fulvicolor*, *D. guangxiensis*, *D. hongkongensis*, *D. huangshanensis*, *D. hunanensis*, *D. krabiensis*, *D. limonicola*, *D. litchiicola*, *D. lithocarpus*,

D. melitensis, *D. millettiae*, *D. musigena*, *D. nelumbonis*, *D. oculi*, *D. osmanthi*, *D. pandanicola*, *D. pascoei*, *D. perseae*, *D. pescicola*, *D. phoenicicola*, *D. podocarpi-macrophylli*, *D. pseudomangiferae*, *D. pseudooculi*, *D. pseudophoenicicola*, *D. pterocarpicola*, *D. salinicola*, *D. schimae*, *D. searlei*, *D. sennae*, *D. spinosa*, *D. taiwanensis*, *D. taoicola*, *D. tectonigena*, *D. viniferae*, *D. xishuangbanica*

Notes – Forty-five species are included in the *Diaporthe arecae* species complex based on maximum likelihood analysis (100%, Fig. 1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of host plants (Table 1), while some species were described as human pathogens (Arciuolo et al. 2020). The name *Diaporthe arecae* species complex is used for this species complex as mentioned in Huang et al. (2015) and Ozawa et al. (2019). This species complex was recovered in all single gene trees (Figs 2–7) and combined analysis gene tree (Fig. 1).

***Diaporthe biconispora* species complex**

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

Notes – Two species are included in the *D. biconispora* species complex based on maximum likelihood analysis (91%, Fig. 1). Members of this section include a pathogen associated with an unidentified host and an endophyte from *Citrus grandis* and *Fortunella margarita* (Table 1). *Diaporthe biconispora* is used to describe this species complex based on the publication year (2015). Huang et al. (2015) introduced *Diaporthe biconispora*, as an endophytic on *Citrus grandis* in China. This clade was not well-resolved based on single-locus *his3* trees, while ITS, *efl* α , β -*tubulin*, and *cal* topologies provided better resolution for this species complex, similar to the combined gene tree (Figs 1–7).

***Diaporthe carpini* species complex**

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

Notes – Sixteen species are included in the *D. carpini* species complex based on maximum likelihood analysis of combined gene tree (100%, Fig. 1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe carpini* is used to describe this species complex. This clade was not well-resolved based on single-locus ITS and β -*tubulin* trees but *efl* α , *cal*, and *his3* topologies provided a better resolution for this species complex, similar to the combined gene tree (Figs 1–7).

***Diaporthe decedens* species complex**

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

Notes – Two species are included in the *D. decedens* species complex based on maximum likelihood analysis (100%, Fig. 1). The clade for this species complex is robust and recovered in all analyses (Figs 1–7), except for the *cal* tree, in which *D. decedens* strain CBS 114281 grouped with the *D. sojae* species complex.

***Diaporthe oncostoma* species complex**

Species included in the *D. oncostoma* species complex – *Diaporthe anacardii*, *D. baccae*, *D. camelliae-sinensis*, *D. canthii*, *D. chamaeropsis*, *D. cinerascens*, *D. cissampeli*, *D. cytospora*, *D. elaeagni-glabrae*, *D. foeniculina*, *D. forlicesenica*, *D. hickoriae*, *D. inconspicua*, *D. isoberliniae*, *D. lutescens*, *D. macintoshii*, *D. maytenicola*, *D. melastomatis*, *D. nebulae*, *D. nigra*, *D. oncostoma*, *D. parapterocarpi*, *D. parva*, *D. phillipsii*, *D. poincianellae*, *D. portugallica*, *D. pseudoinconspicua*, *D. psoraleae*, *D. pterocarpi*, *D. pungensis*, *D. ravennica*, *D. rumicicola*, *D. saccharata*, *D. stictica*, *D. vangeriae*, *D. velutina*, *D. zaobaisu*

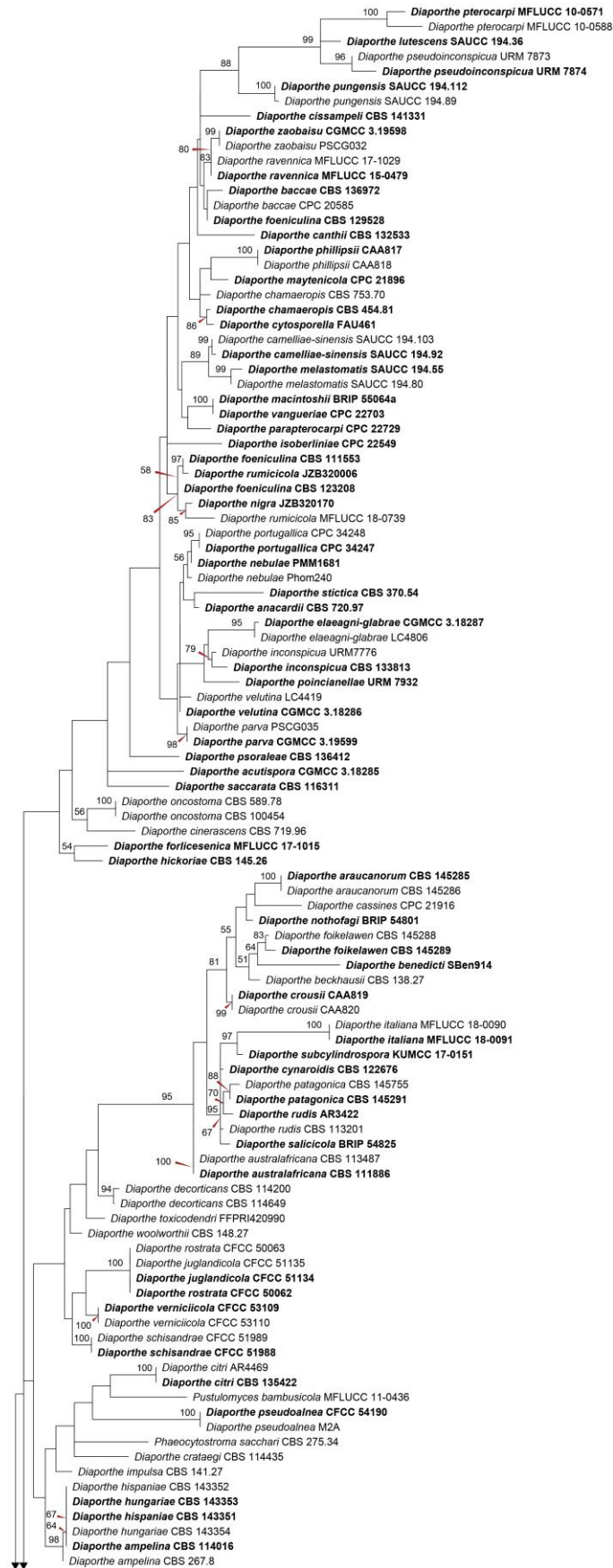


Figure 2 – Phylogram generated using maximum likelihood analysis based on ITS sequence data from 534 strains. The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values $\leq 50\%$ are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

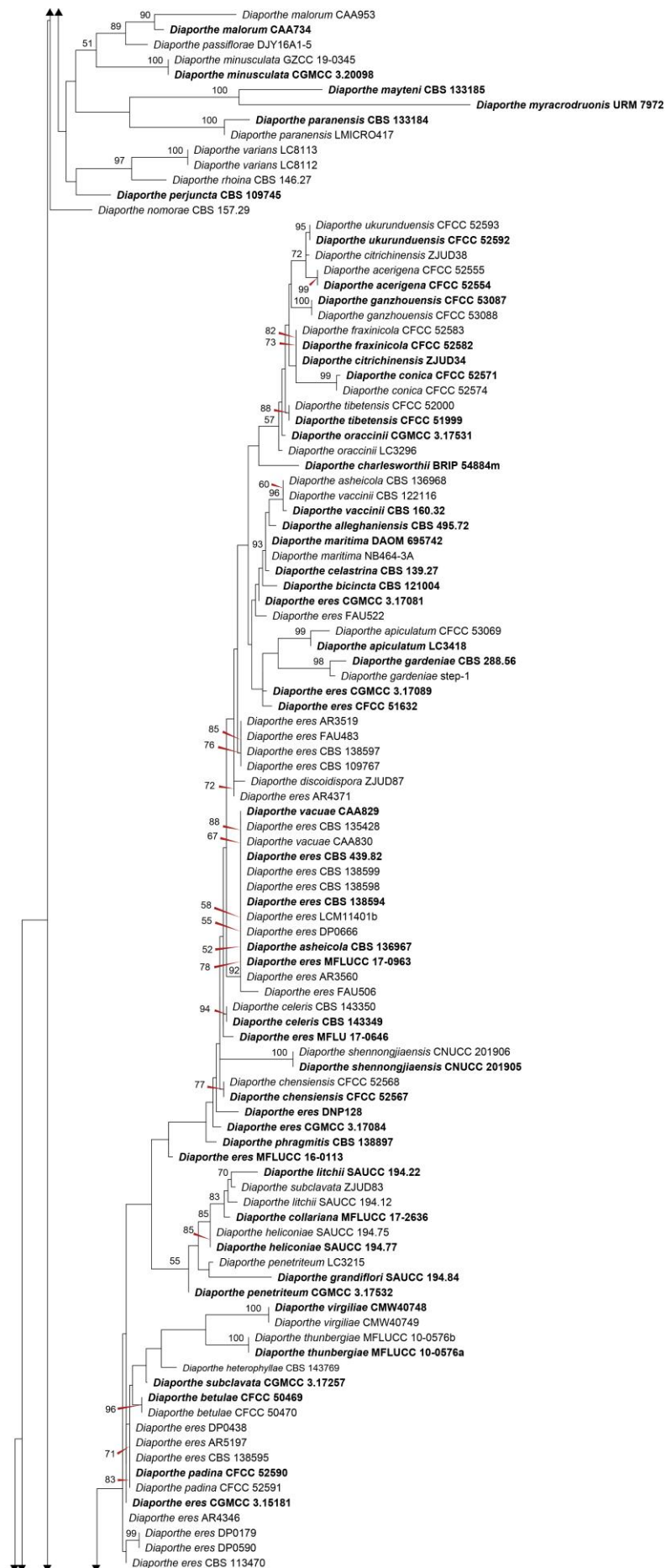


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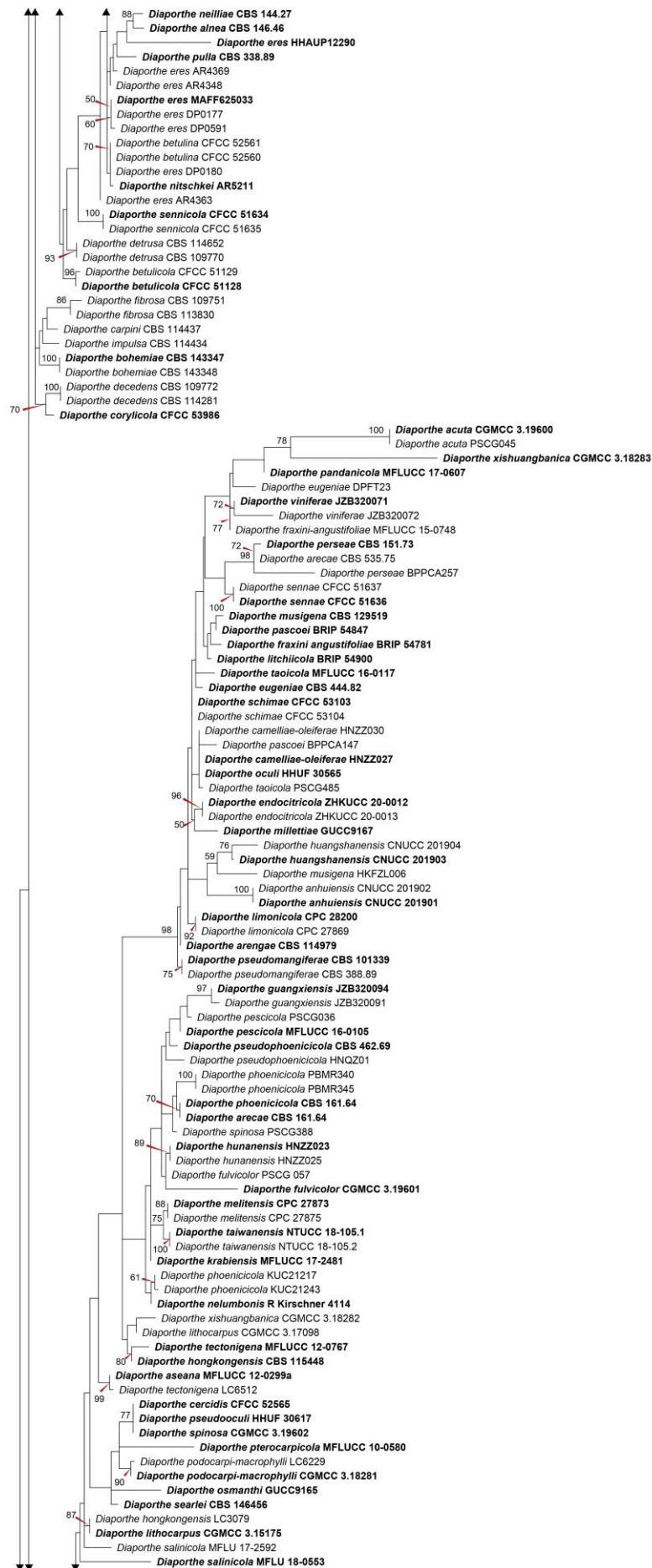


Figure 2 – Continued.



Figure 2 – Continued.

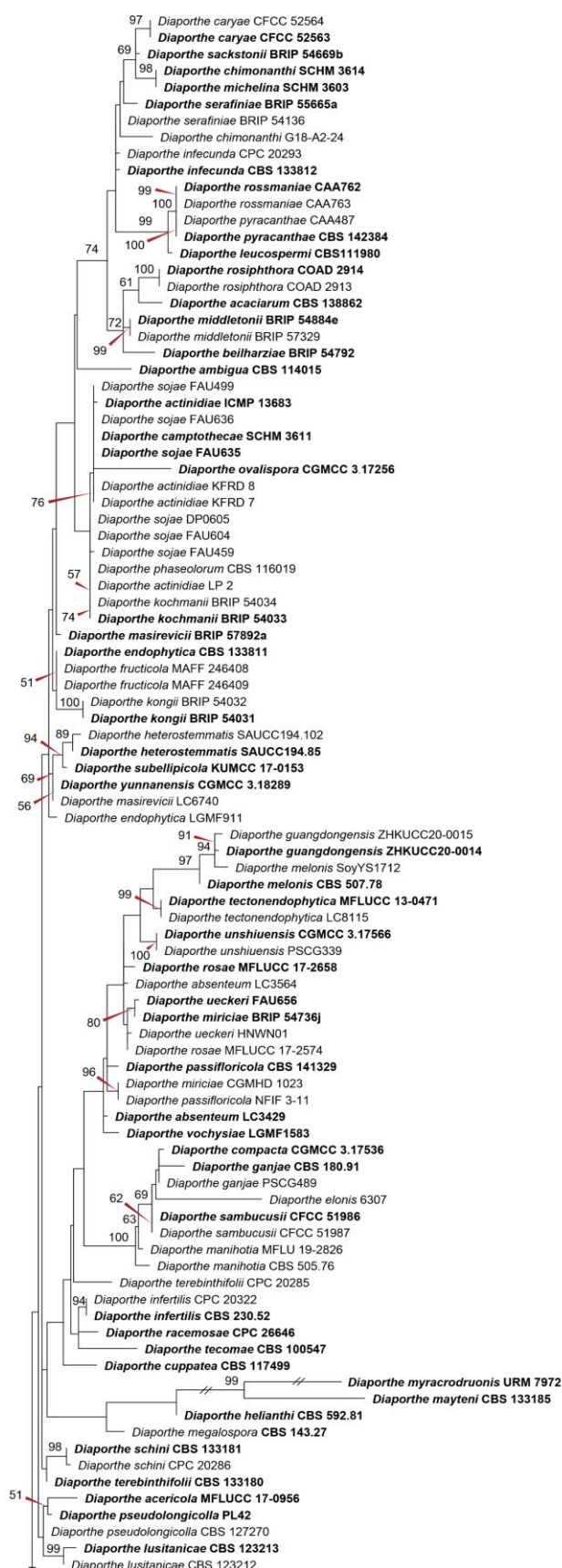


Figure 3 – Phylogram generated using maximum likelihood analysis based on ITS sequence data from 584 strains (included 50 strains that only have the ITS region). The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values $\leq 50\%$ are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

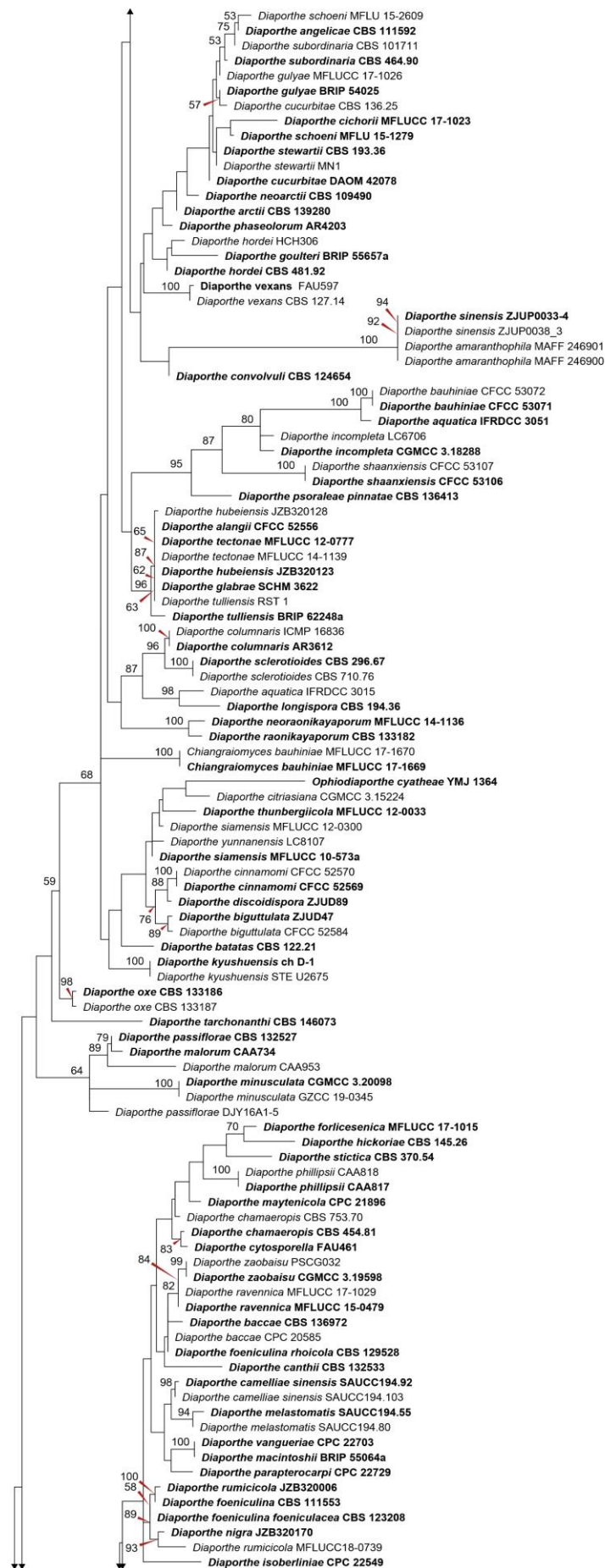


Figure 3 – Continued.

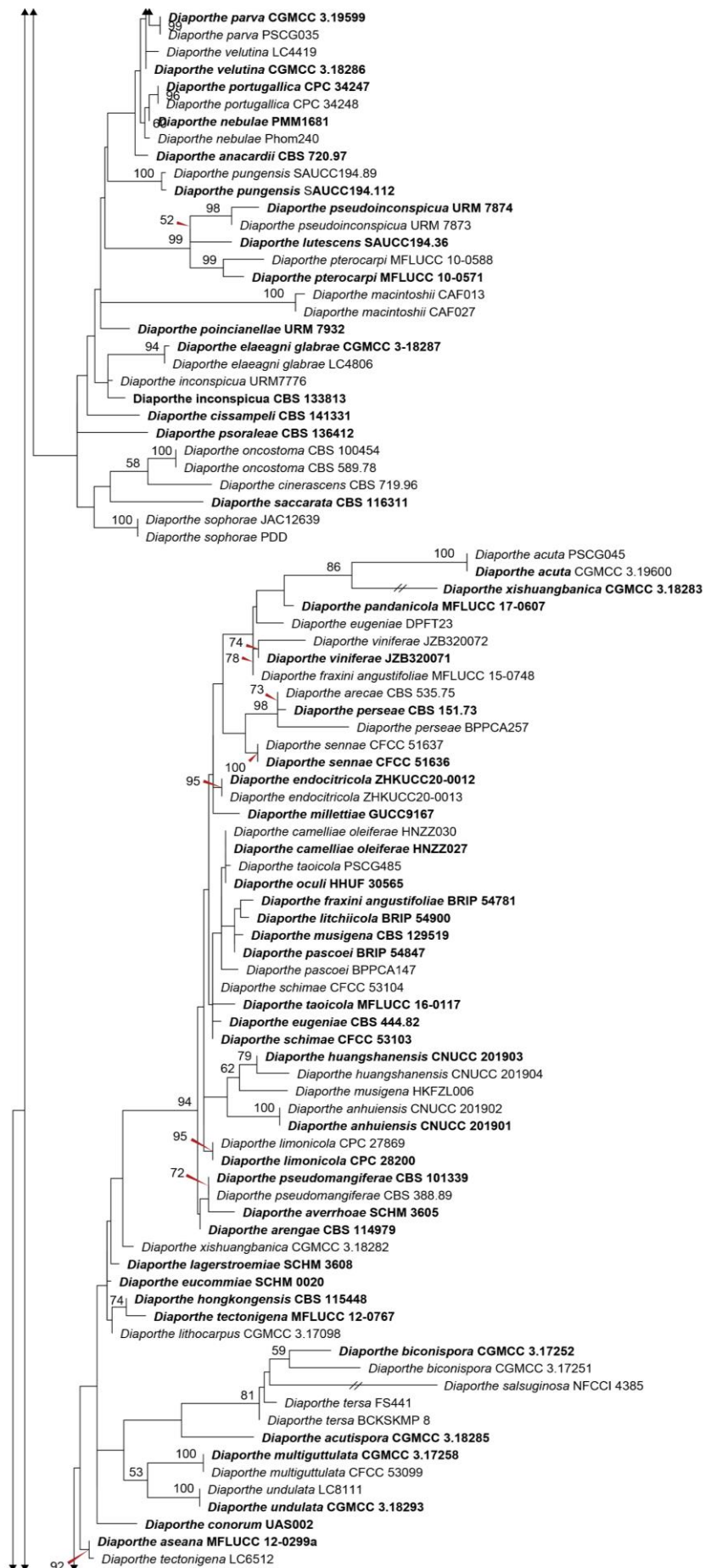


Figure 3 – Continued.

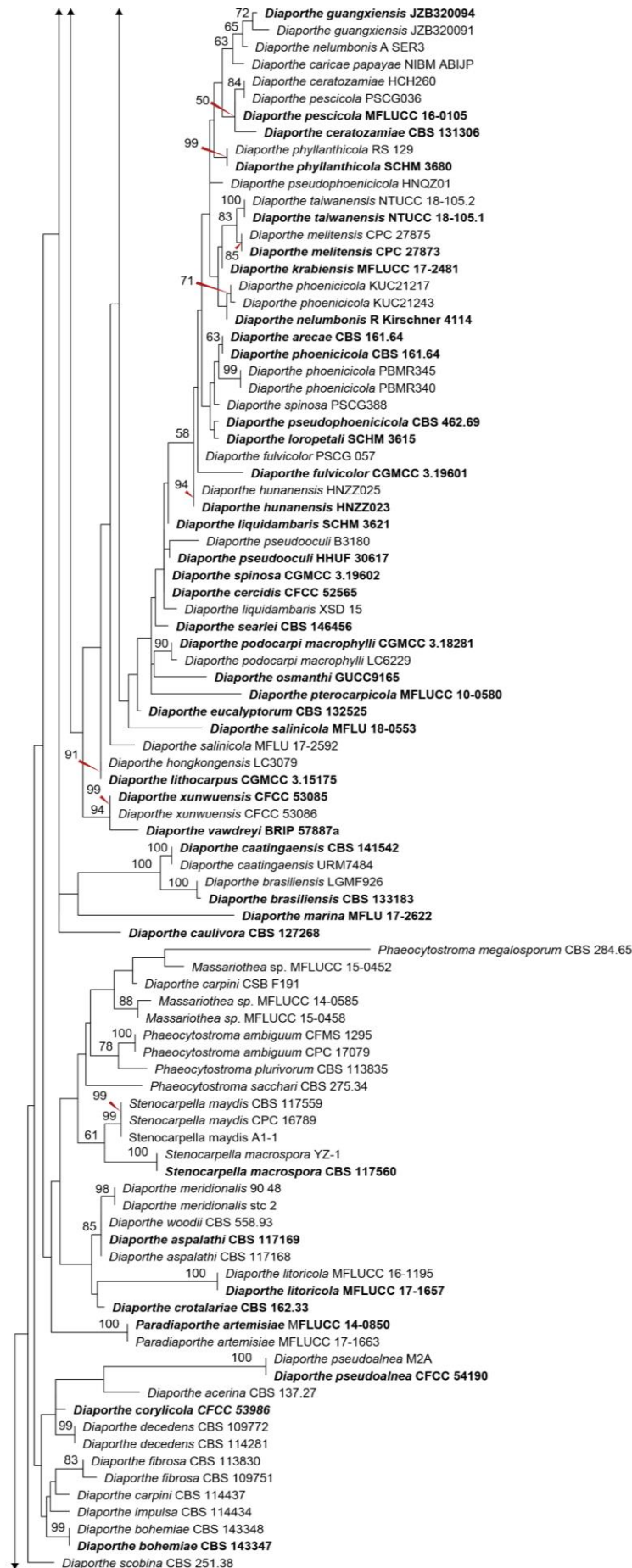


Figure 3 – Continued.

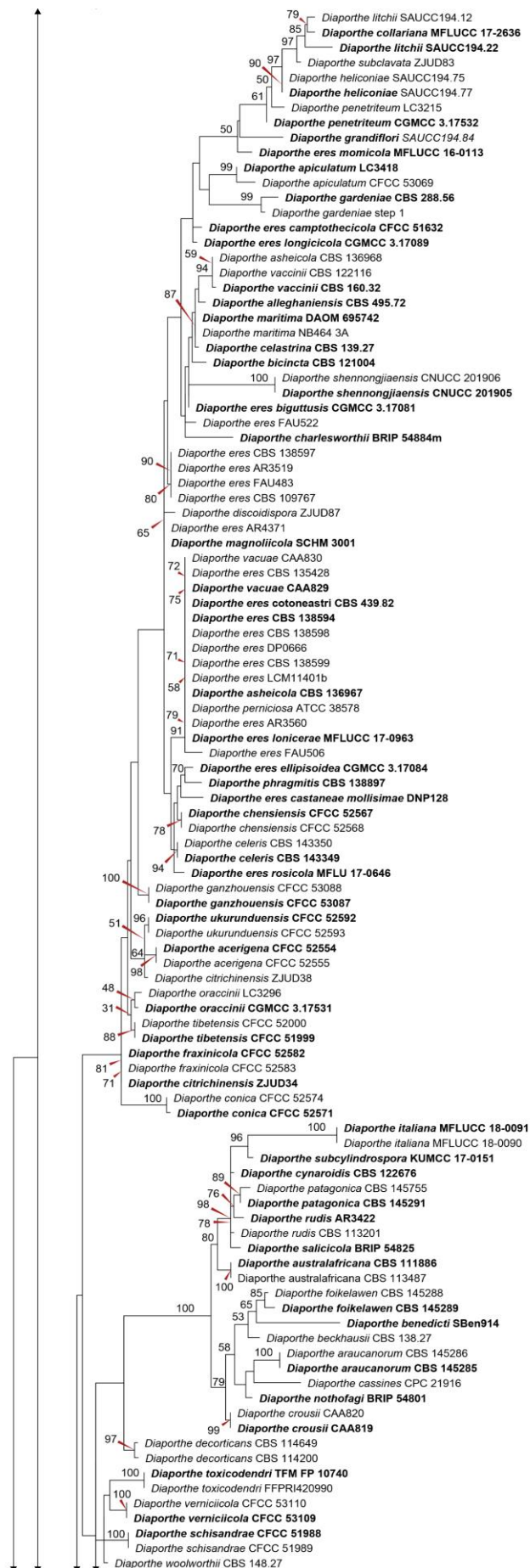


Figure 3 – Continued.



Figure 3 – Continued.

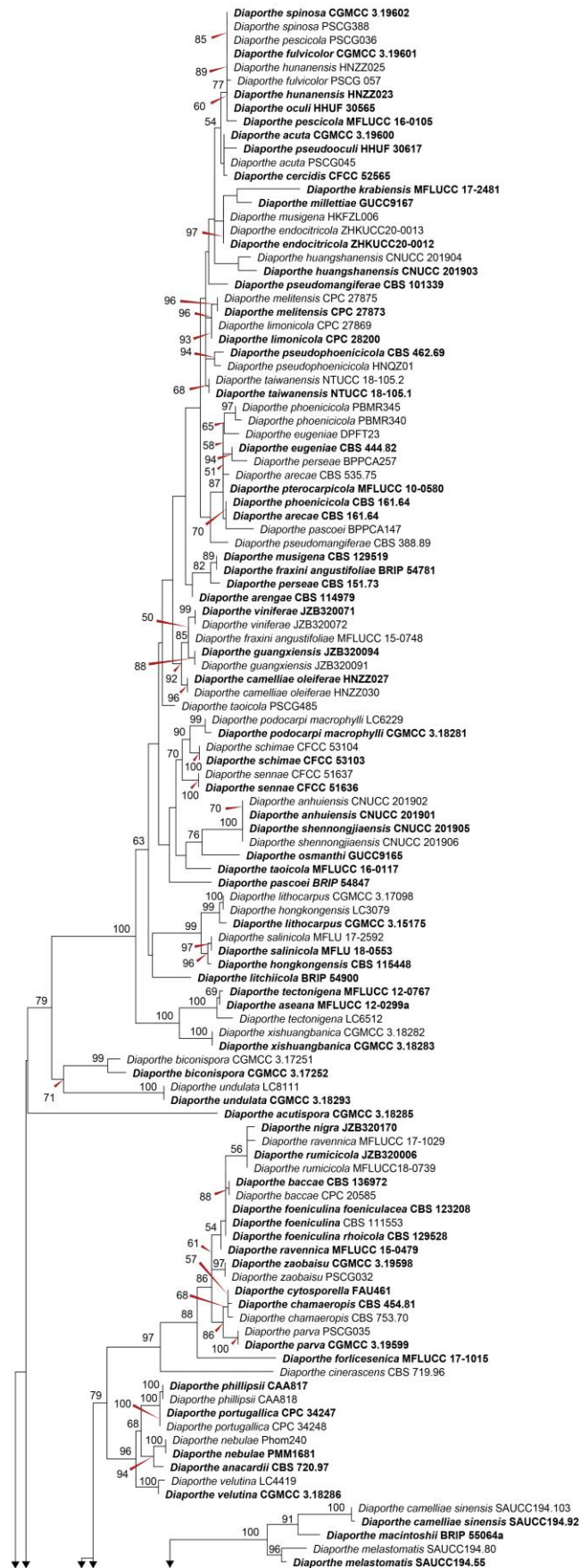


Figure 4 – Phylogram generated using maximum likelihood analysis based on *efl* α sequence data from 510 strains. The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values $\leq 50\%$ are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

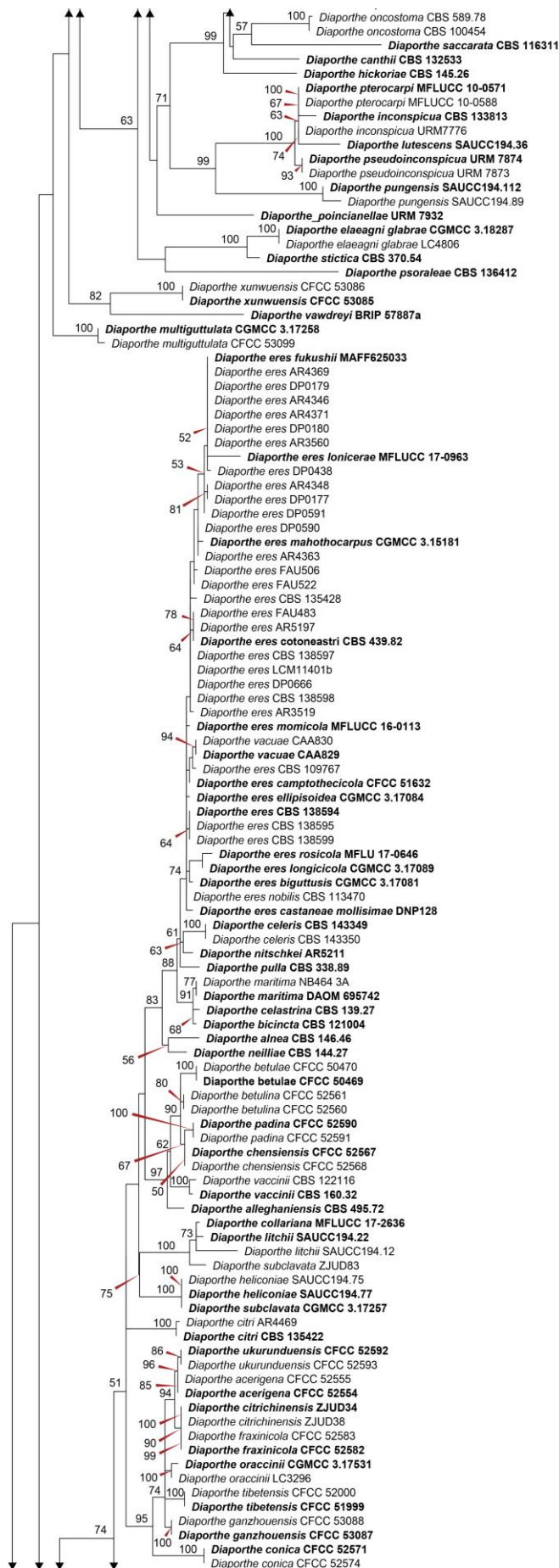


Figure 4 – Continued.

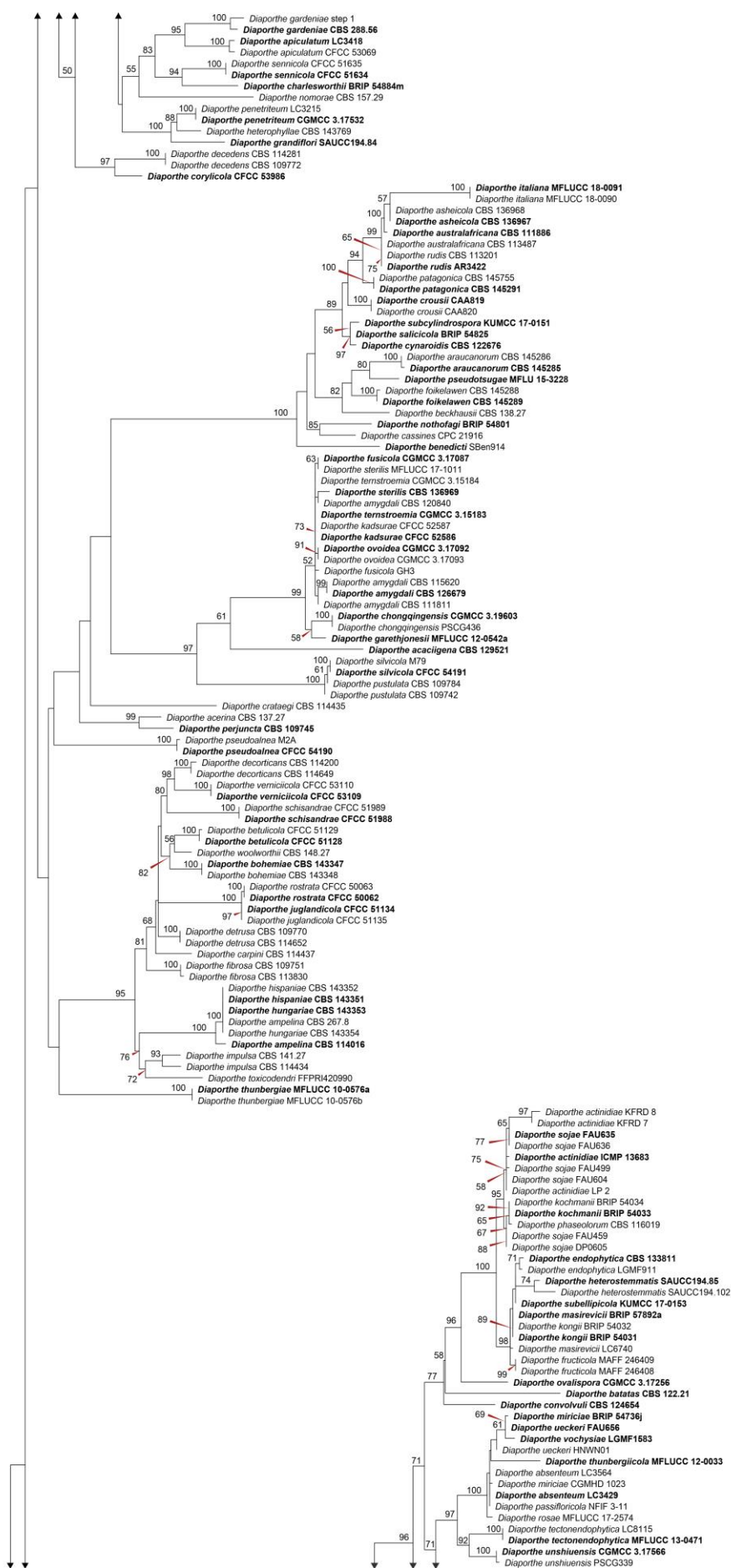


Figure 4 – Continued.

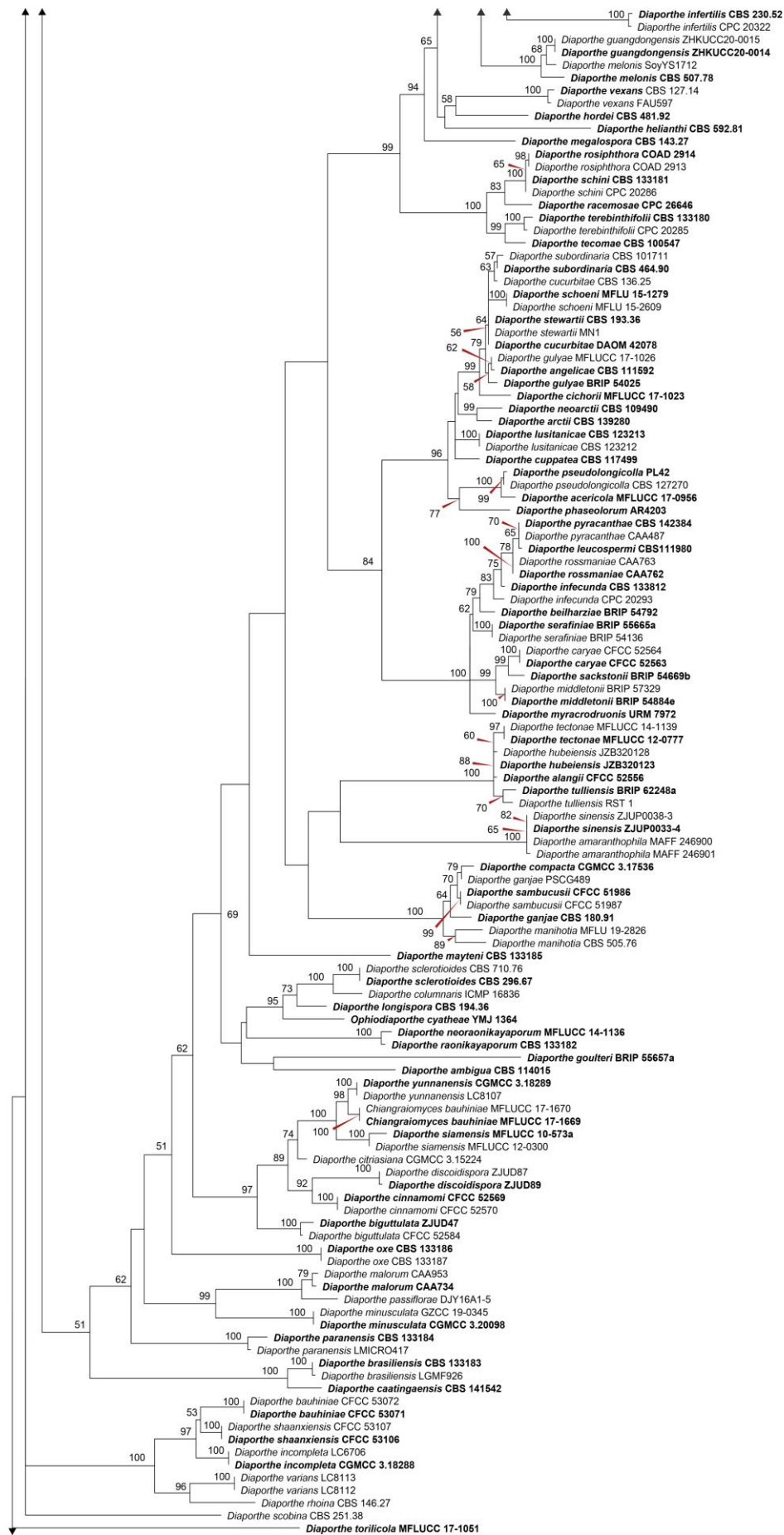


Figure 4 – Continued.

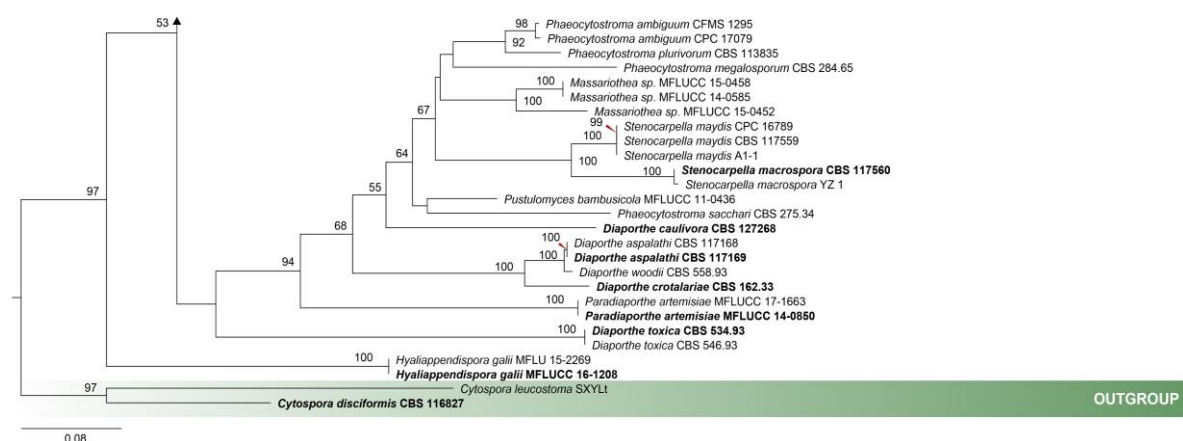


Figure 4 – Continued.

Notes – Thirty-seven species are included in the *D. oncostoma* species complex based on the maximum likelihood analysis (100%, Fig. 1). Members of this section are mostly pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe oncostoma* is used to describe this species complex based on the publication year (1870). The clade for this species complex is robust and recovered in the multi- and single-locus trees (except for the *cal* tree, in which *D. parvae* grouped to *D. alnea* species complex) (Figs 1–7).

***Diaporthe pustulata* species complex**

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

Notes – Twelve species are included in the *D. pustulata* species complex, which is strongly supported in the combined gene tree (94%, Fig. 1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe pustulata* is used to describe this species complex based on the publication year. This species complex clade was robust and recovered in all single-locus tree analyses and in the combined gene tree (Figs 1–7).

***Diaporthe rudis* species complex**

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

Notes – Sixteen species are included in the *D. rudis* species complex, which has the maximum statistical support (100%, Fig. 1). Members of this section are pathogenic, endophytic, and saprobic on a broad range of hosts (Table 1). *Diaporthe rudis*, the oldest species found within the clade, used to describe this species complex based on the publication year. This species complex clade was robust and recovered in most single-locus trees and in the combined gene tree, except for the ITS single-locus tree topology that was not well-resolved (Figs 1–7).

***Diaporthe scobina* species complex**

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

Notes – Two species are included in the *D. scobina* species complex based on the maximum likelihood analysis of the combined gene tree (97%, Fig. 1). Members of this section are associated with *Fraxinus excelsior* and *Thunbergia laurifolia* (Table 1, Mulyenko et al. 2008, Udayanga et al. 2012a, b). *Diaporthe scobina* is used to describe this species complex based on the publication year. This clade was not well-resolved based on ITS, *efl* α , and *his3* single-locus trees, but β -*tubulin* and *cal* topologies provided a better resolution for this species complex similar to the combined gene tree (Figs 1–7).

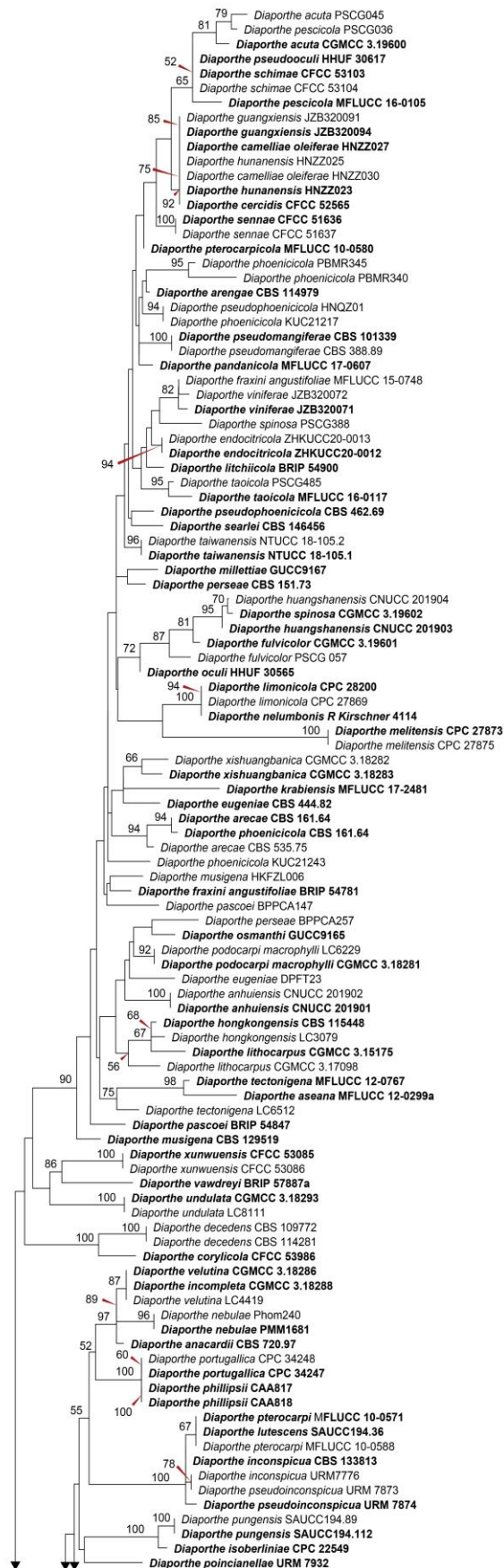


Figure 5 – Phylogram generated using maximum likelihood analysis based on β -tubulin sequence data from 479 strains. The tree is artificially rooted to *Cytospora disciformis* (CBS 116827) and *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values $\leq 50\%$ are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

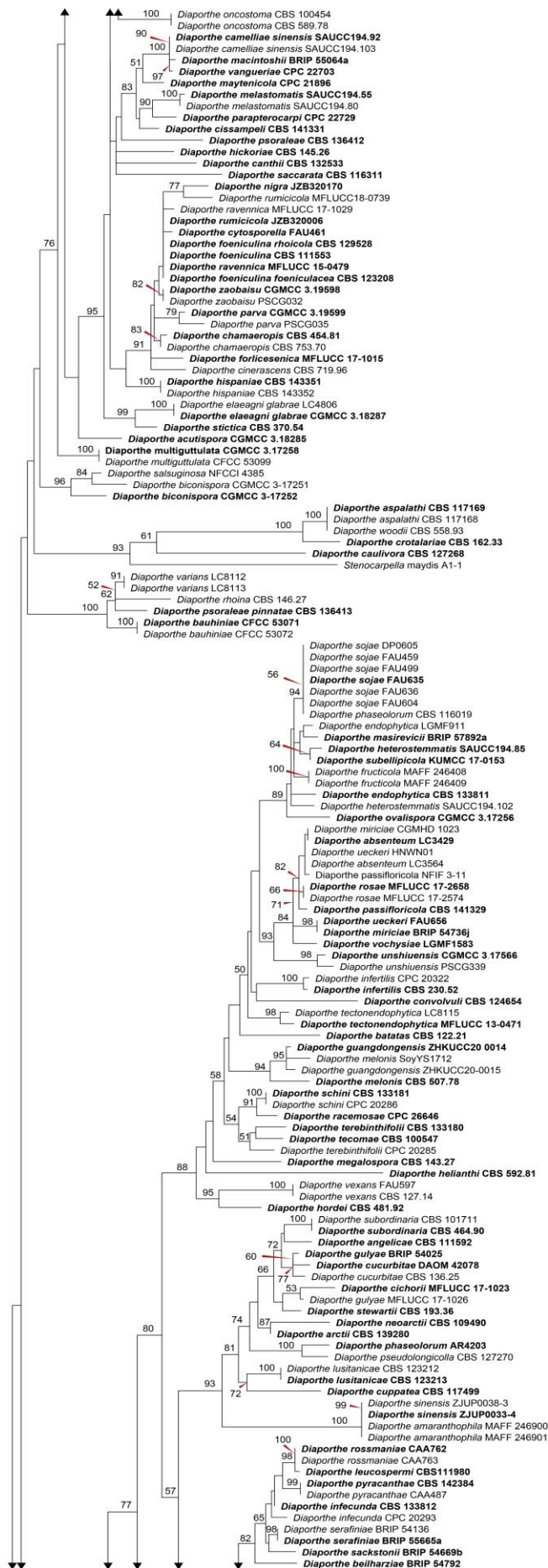


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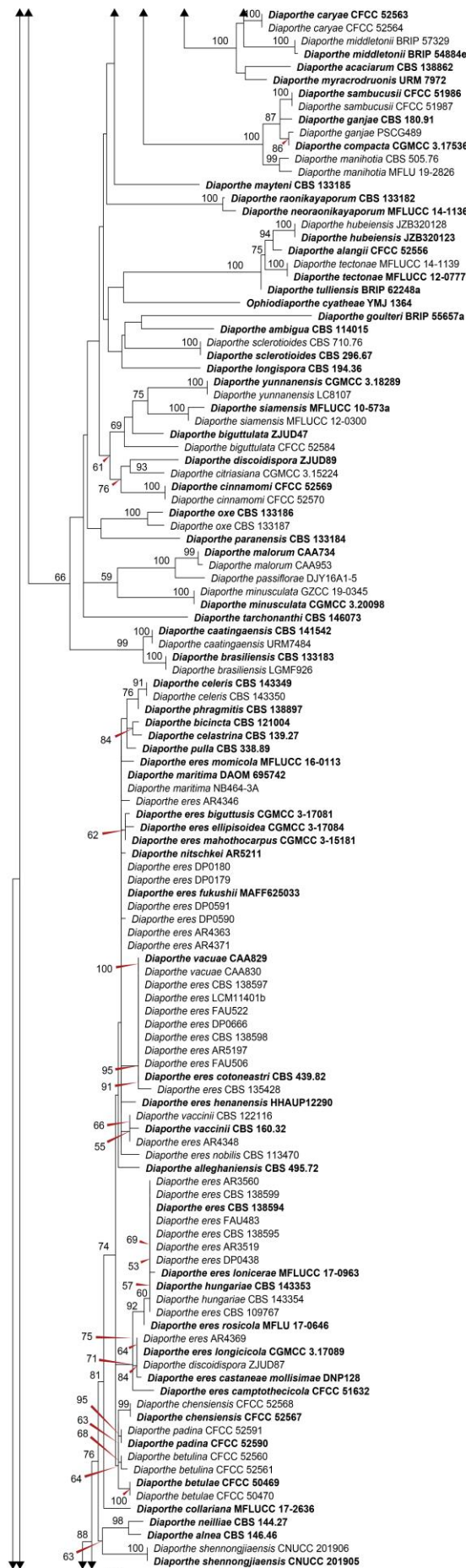


Figure 5 – Continued.



Figure 5 – Continued.

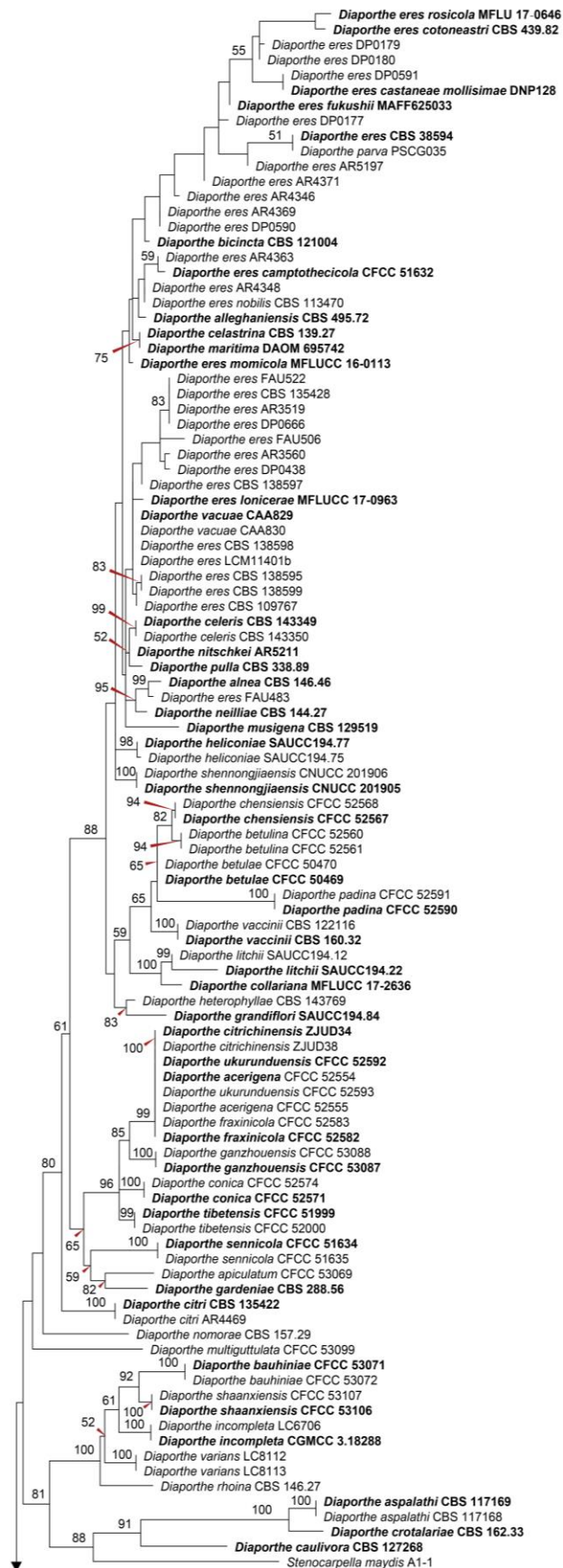


Figure 6 – Phylogram generated using maximum likelihood analysis based on *cal* sequence data from 383 strains. The tree is artificially rooted to *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values $\leq 50\%$ are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

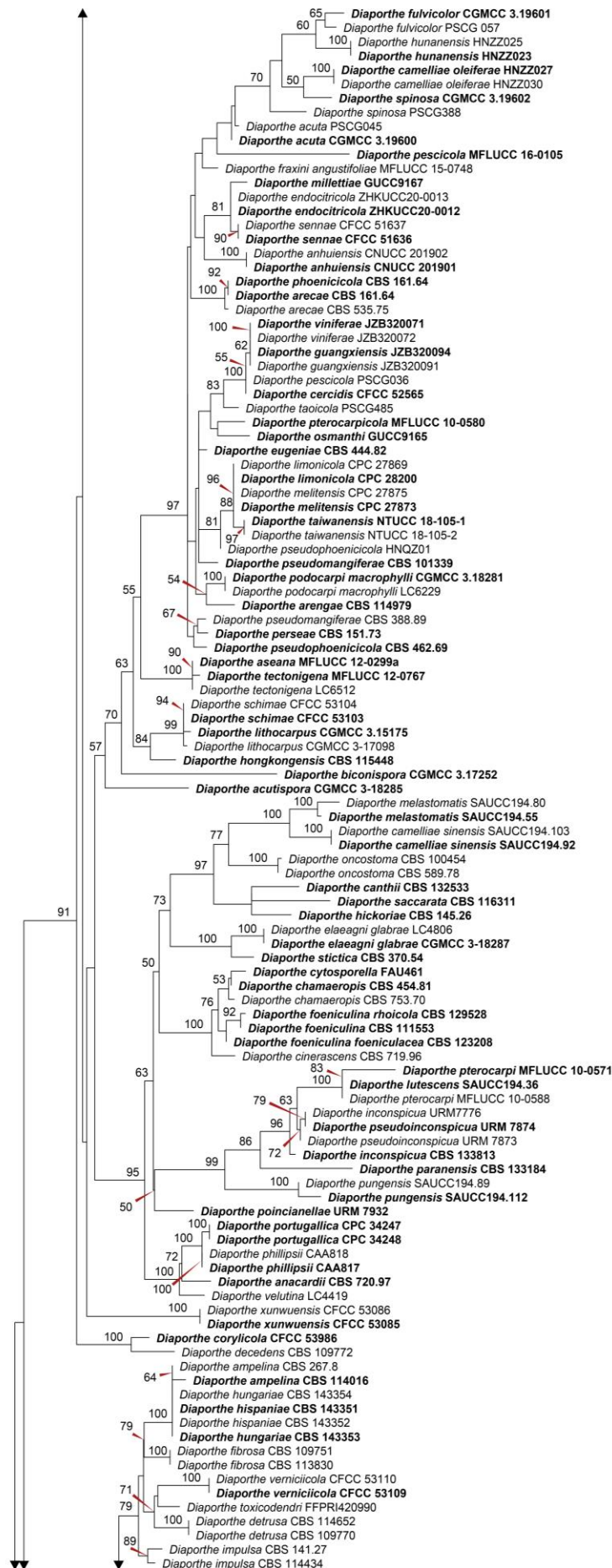


Figure 6 – Continued.

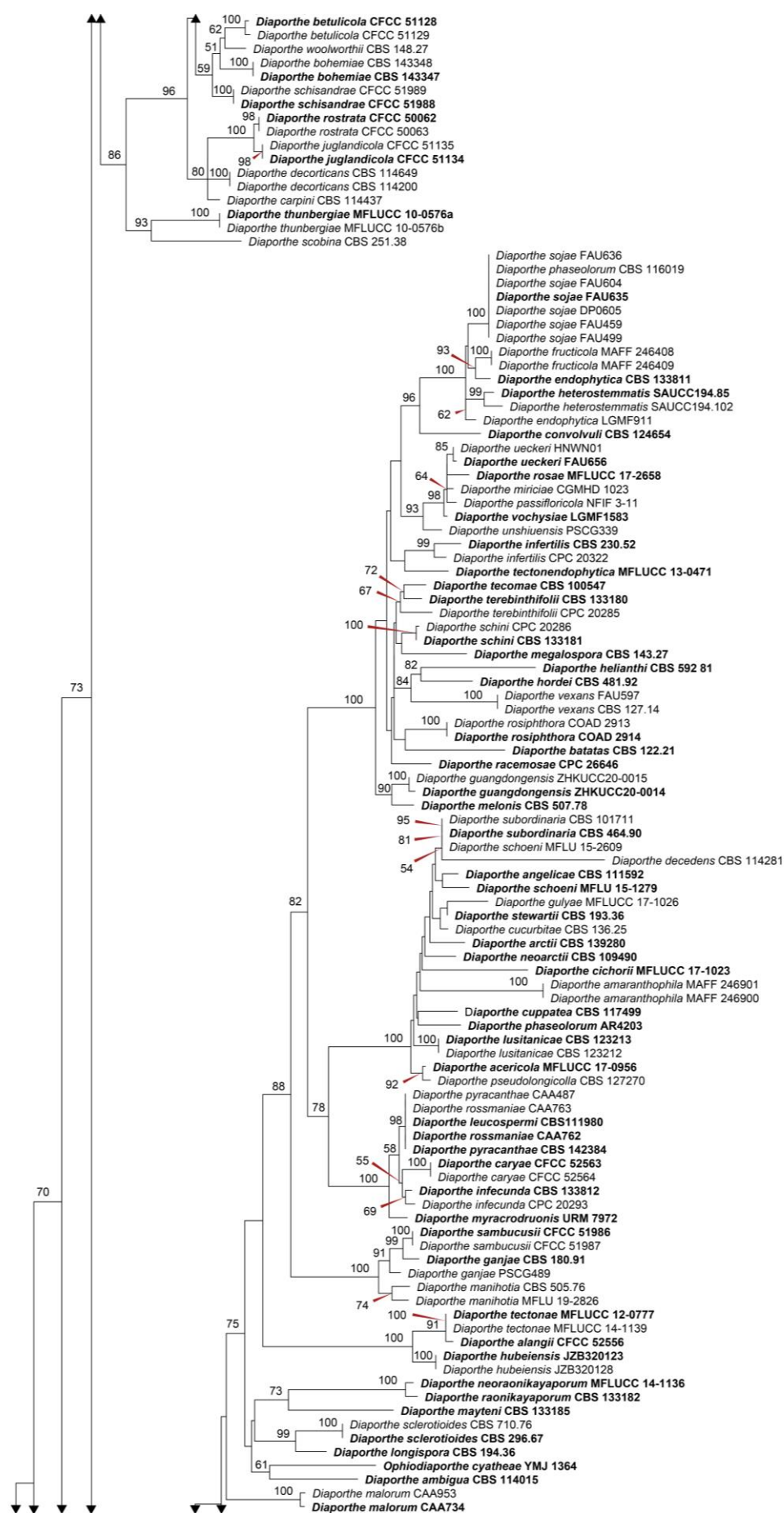


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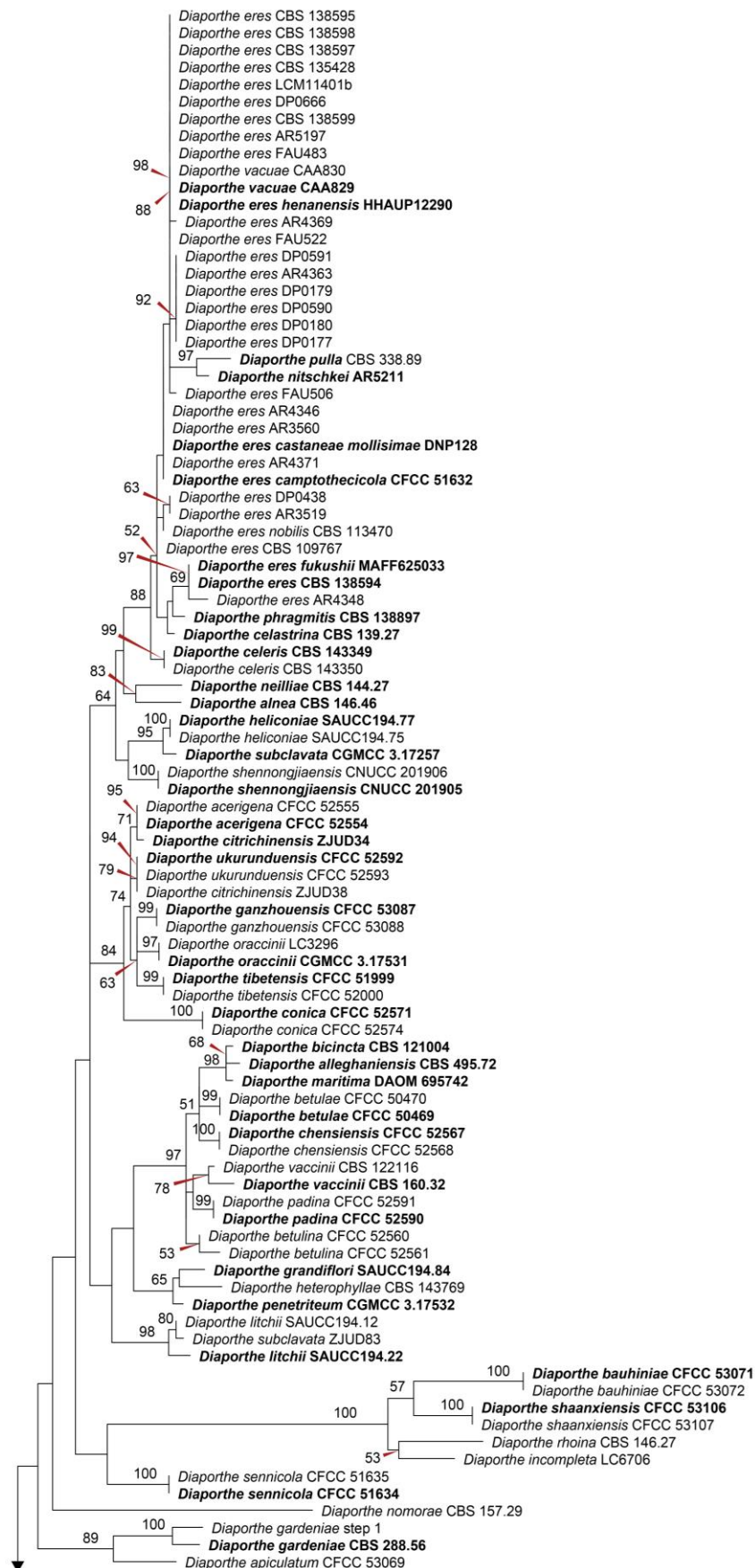


Figure 7 – Phylogram generated using maximum likelihood analysis based on *his3* sequence data from 343 strains. The tree is artificially rooted to *C. leucostoma* (SXYLt). Maximum likelihood bootstrap values $\leq 50\%$ are given at the nodes in this order. The species synonymized are in blue and ex-type taxa are in bold.

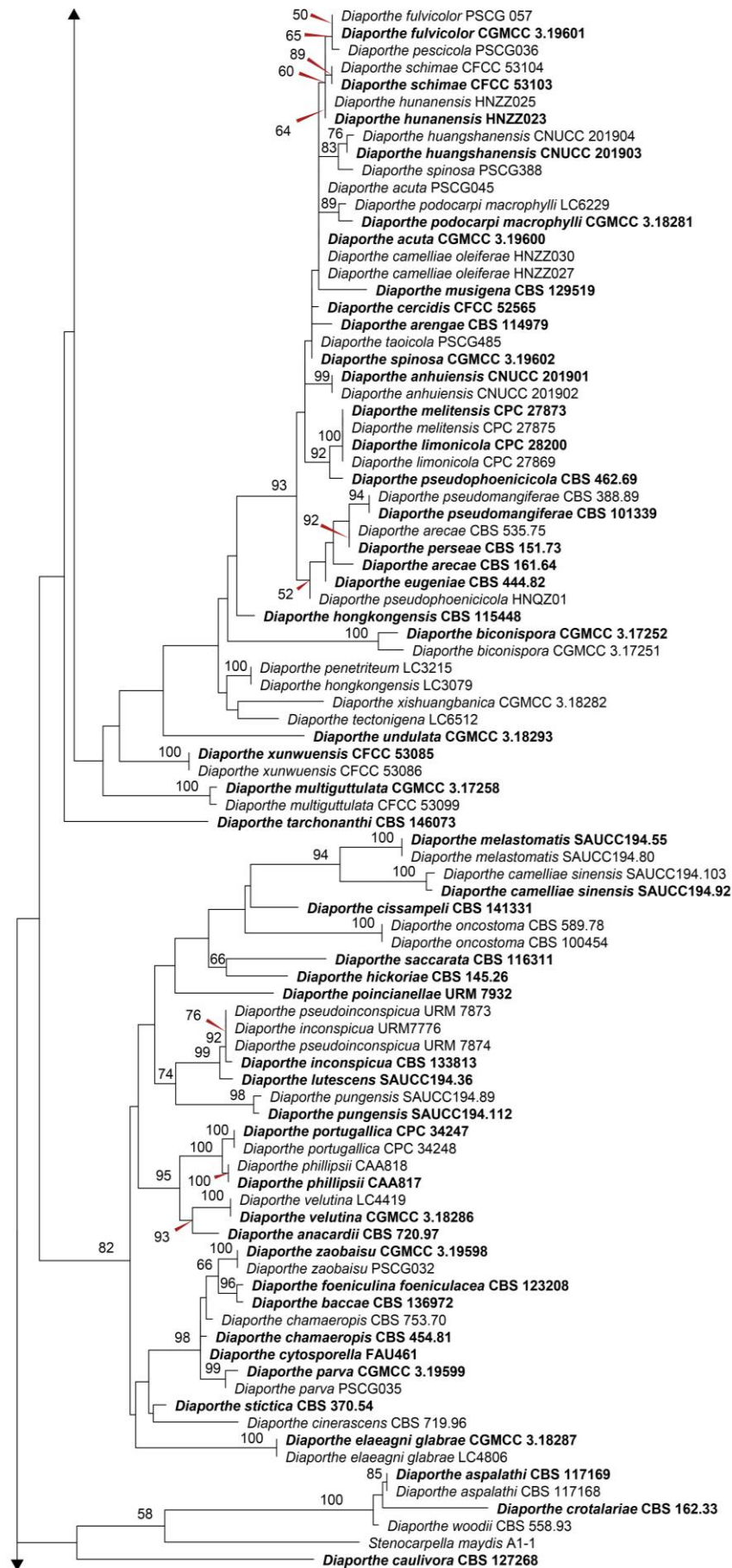


Figure 7 – Continued.

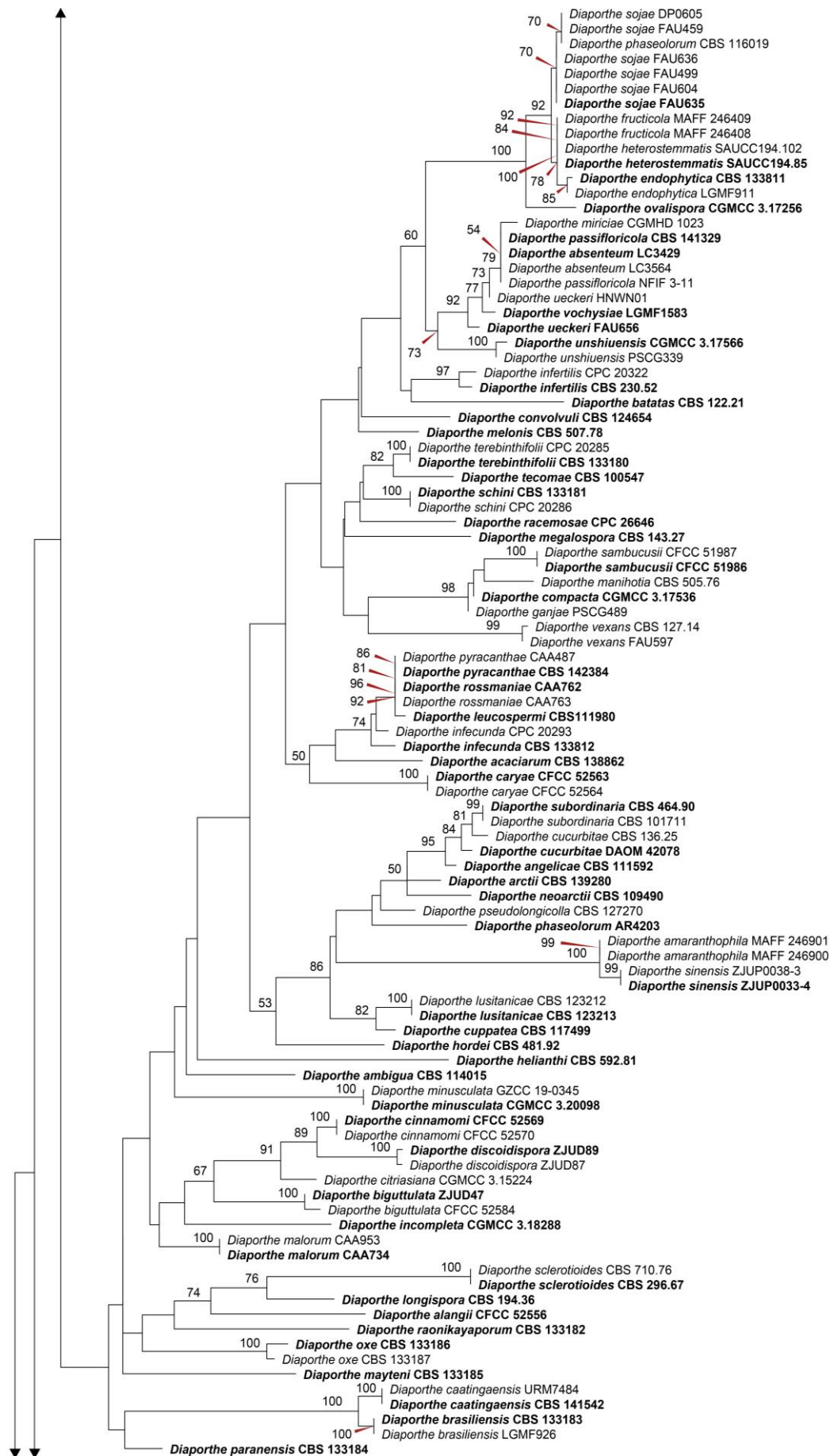


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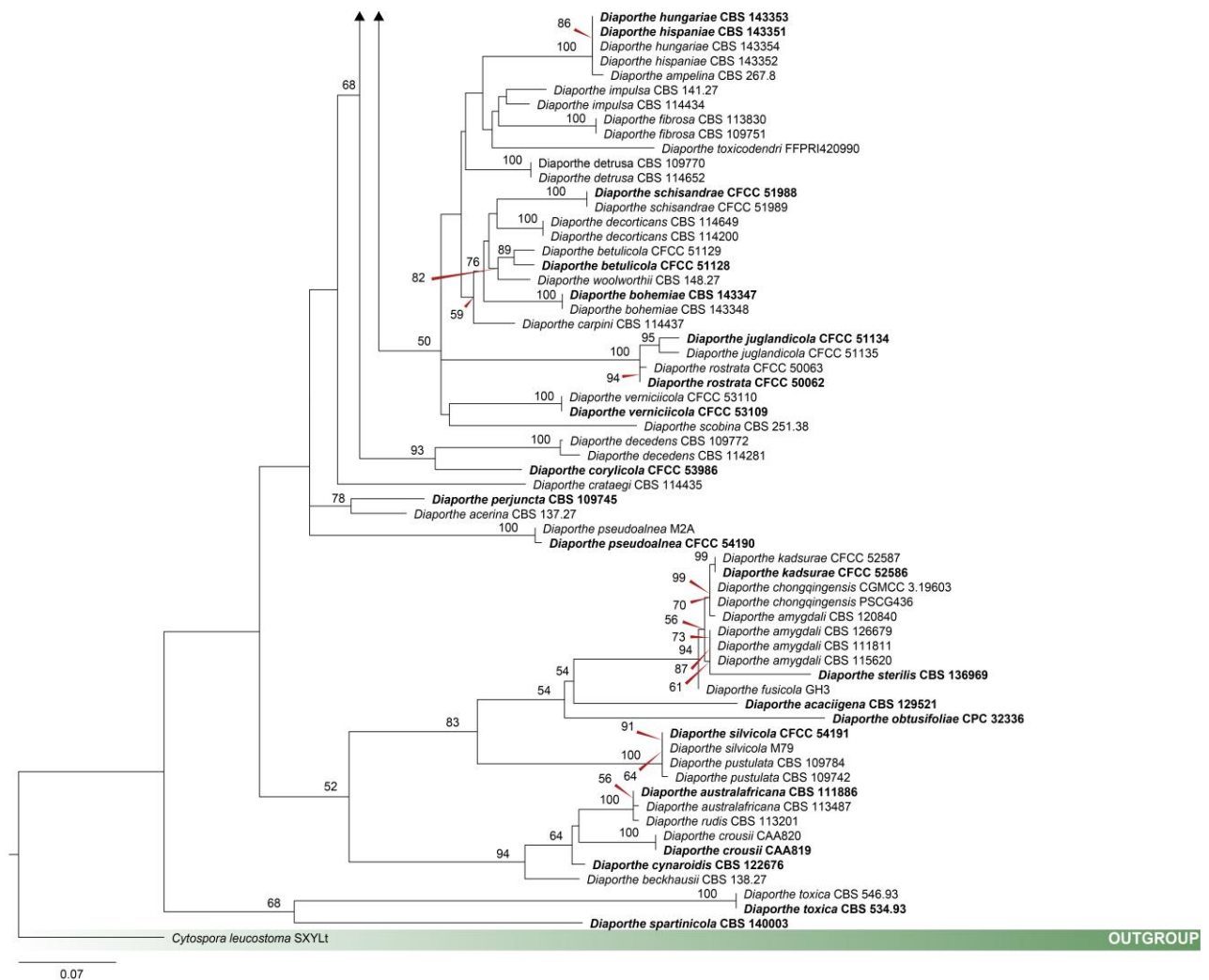


Figure 7 – Continued.

Notes – Ninety-two species are included in the *D. sojae* species complex, which is strongly supported in the combined gene tree (99%, Fig. 1). Members of this section are mostly pathogenic, endophytic, and saprobic on a broad range of host plants (Table 1), and some species are human pathogens (Garcia-Reyne et al. 2011, Iriart et al. 2011, Mattei et al. 2013). The clade was named as *Diaporthe sojae* species complex as defined in Udayanga et al. (2015), broadening the limits with more species in this study. Some species members in this species complex were not well-resolved based on ITS and β -tubulin and *his3* single-locus trees, but *efla* and *cal* topologies provided a better resolution for this species complex as did the combined gene tree (Figs 1–7). This is the largest species complex clade of *Diaporthe*. Most species that only have ITS sequence data and not included in the combined gene tree are grouped in this clade (Fig. 3).

Diaporthe toxica species complex

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

Notes – Two species are included in the *D. toxica* species complex based on the maximum likelihood analysis (94%, Fig. 1). The members are pathogens and endophytes on *Lupinus angustifolius* and *Torilis arvensis* (Dissanayake et al. 2017c, Gomes et al. 2013). *Diaporthe toxica* produces secondary metabolites that cause lupinosis in sheep (Williamson et al. 1994, Table 1). *Diaporthe toxica* is used to describe this species complex based on the publication year. This clade was not well-resolved based on the *efla* single-locus tree, while ITS, β -tubulin, *cal*, and *his3* topologies provided a better resolution for this species complex as did the combined gene tree (Figs 1–7).

***Diaporthe varians* species complex**

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

Notes – Six species are included in the *D. varians* species complex, which has maximum statistical support in the combined gene tree (100%, Fig. 1). Members of this section are reported as pathogenic and saprobic fungi on a broad range of hosts (*Acer* sp., *Bauhinia purpurea*, *Camellia sinensis*, *Psoralea pinnata*, *Rhus toxicodendron*) as mentioned in Table 1. *Diaporthe varians* is used to describe this species complex based on the publication year (1870). This clade was not resolved in the single-locus trees of ITS and *his3*, but β -tubulin, *efl* α , and *cal* topologies provided a better resolution for this species complex as in the combined gene tree (Figs 1–7).

***Diaporthe vawdreyi* species complex**

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

Notes – Two species are included in the *D. vawdreyi* species complex, which is strongly supported (100%, Fig. 1). Members of this section are pathogenic on *Psidium guajava* and saprobic fungi from unidentified dead wood (Table 1). *Diaporthe vawdreyi* is used to describe this species complex based on the publication year (2015), a pathogenic species that causes fruit rot disease of *Psidium guajava* in Australia (Crous et al. 2015). The clade for this species complex is robust and recovered in all analyses (Figs 1–7).

Discussion

Diaporthe species are associated with economically important hosts as pathogens, endophytes, and saprobes on a wide range of hosts and have a broad geographic distribution (Uecker 1988, Ferreira et al. 2015). *Diaporthe* taxonomy and species descriptions have previously been based on morphology and host-specificity. However, the overlap of morphological traits and association with the same host made the identification of taxonomically relevant characters at the species level difficult and species delimitation based on morphology was problematic (Rehner & Uecker 1994, Mostert et al. 2001, Gomes et al. 2013, Guarnaccia et al. 2016, Santos et al. 2010, Udayanga et al. 2011, 2014a, b, Dissanayake et al. 2017a, b). Hence, a molecular approach is essential to identify and comprehensively characterize members of *Diaporthe* (Santos & Phillips 2009, Diogo et al. 2010, Luongo et al. 2011, Udayanga et al. 2012a, b, Thomidis et al. 2013, Gao et al. 2017). However, sequence data from type material is not available for many *Diaporthe* species, and even some known species do not have enough molecular data to justify their introduction as novel taxa. More than 500 taxa have been recorded and named as species of *Diaporthe* (<http://www.indexfungorum.org>, accessed on May 5, 2022).

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

been introduced successfully for *Fusarium* (O'Donnell et al. 2013, 2015, Al-Hatmi et al. 2016), *Colletotrichum* (Cannon et al. 2012, Damm et al. 2019, Jayawardena et al. 2016, da Silva et al. 2020), and *Phyllosticta* (Norphanhoun et al. 2020).

Using broad sampling in terms of taxa and genes is necessary for improving the phylogenetic resolution at low and high taxonomic levels within Diaporthaceae. Single (Figs 2–7) and multiple gene phylogenies along with statistical support were considered to introduce the *Diaporthe* species complexes (Fig. 1). The placement of the proposed species complexes and the species they contain are mostly similar in the single gene trees and the combined gene tree (Fig. 1). The topology of *efla* most closely resembled that of the combined tree with only a handful of incongruences, followed by *β-tubulin*. Nonetheless, within the complexes, the placement of some species remains problematic, and additional loci are likely needed for taxonomic resolution. These include *D. actinidiae*, *D. eres*, *D. foeniculina*, *D. amygdali*, *D. phoenicicola*, and *D. sojae*. Delimiting species of *Diaporthe* will not only provide a better understanding of inter and intraspecific variation within the broader species complexes but also at the genus and family levels.

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

In our analysis, *Diaporthe* is not monophyletic similar to previous results (Gao et al. 2017, Huang et al. 2021). *Massariothea*, *Stenocarpella*, *Phaecystroma*, and *Pustulomyces* nested within *Diaporthe* in all the single gene trees and the combined gene tree. *Diaporthe caulivora*, *D. crotalariae*, *D. woodii*, and *D. aspalathi* formed a strongly supported clade with these genera in the combined gene tree and the *efla* tree. These four *Diaporthe* species were not introduced as members of any species complex as their placements are unstable in single gene trees. In contrast, *Hyaliappendispora* and *Phaeodiaporthe* were consistently placed separately from *Diaporthe* and the rest of the genera at the base of the Diaporthaceae tree with high statistical support. (Figs 2–7).

Demarcation of individual taxa within the genus is essential for a better understanding of the lifestyles, ecology, and overall biology of these individual taxa and their impact and control in various ecosystems. Hence, some strains were excluded from the Diaporthaceae tree, as they do not belong to *Diaporthe* based on BLAST search and phylogenetic analysis, viz. *D. scabra* strain CBS 127746, DCDSL 69/96, DCDSL 11/96, DCDSL 102/96, *D. columnaris* strain CBS 109873, *D. elonis* strain d91, *D. liquidambaris* strain SA1, *D. oncostoma* strain WU 32007, *D. phyllanthicola* strain TW23, msy54, *D. rhoina* strain IPBCC 15.1322, IPBCC 15.1323, and *D. apiculate* strain CGMCC 3.17533, LC3187. Two taxa, *Ophiodiaporthe cyatheae* and *Chiangraiomyces bauhiniae*, are synonymized under *Diaporthe*, *D. cyatheae* ($\equiv$ *O. cyatheae*) and *D. pseudobauhiniae* ($\equiv$ *C. bauhiniae*), respectively based on phylogenetic analysis (Figs 1–7) (Fu et al. 2013, Senanayake et al. 2017). *Apiosphaeria guaranitica* (UB23801, UB23795, UB23750, UB23561, UB23518, UB23484, UB23393, UB22757, CDUB247), *Chaetoconis polygoni* (CBS 405.95), *Mazzantia galii* (CBS 125529), *M. napelli* (AR 3498, AFTOL-ID 2126) were removed from the Diaporthaceae tree.

The paraphyletic nature of the genus *Diaporthe* based on single gene trees and the combined gene trees has been observed by various authors and in this study. Sequences split into several distinct and genetically divergent clades, which could represent separate genera however determining the extent of discordance between morphology and molecular data (dense and broad taxon sampling, careful examination of morphology) and the suitability of genetic markers used (phylogenomic analyses) will assist substantially towards resolving this question. Further studies are also needed to establish whether these species are host-specific, determine their habitats and lifestyles, the conditions under which they might switch lifestyle and their interactions with their plant hosts.

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