



Pathogenic *Diaporthe* from Italy and the first report of *D. foeniculina* associated with *Chenopodium* sp.

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Abstract

Diaporthe is an important genus composed of pathogenic, saprobic and endophytic species. A *Diaporthe* species was collected from a dead aerial branch of *Chenopodium* sp. from Italy. Multi-locus phylogeny of ITS, CAL, HIS, TEF1- α and TUB2 sequence data showed that our strain clusters with *Diaporthe foeniculina* with good statistical support. A comprehensive description, photographs of micromorphological characteristics and phylogenetic trees to show the placement of the taxon are provided. This is the first report of *D. foeniculina* on *Chenopodium* sp. from Italy. Previously, *Diaporthe foeniculina* has been recorded from Italy as a pathogen on different plant species. Based on the previous findings, a list of known pathogenic *Diaporthe* species reported from Italy is provided.

Keywords – Coelomycetes – Diaportheaceae – New record – Sordariomycetes – Taxonomy

Introduction

Chenopodium species are morphologically variable and comprise herbaceous and bushy annual or perennial plants growing in worldwide arid and semiarid zones (Bonifacio 2003). Most of the species of this genus are able to survive in adverse climatic and edaphic conditions (Bonifacio 2003, Fuentes-Bazan et al. 2012). This genus has important cultivable species which play diverse roles like crops for food (*C. album*, *C. giganteum*, *C. murale*, *C. quinoa*), animal feed production (*C. album*, *C. murale*, *C. opulifolium*) and medicinal uses (*C. album*, *C. amaranticolor*, *C. botrys*) (Bonifacio 2003, Fuentes-Bazan et al. 2012). *Chenopodium* sp. also constitutes major classes of phyto-constituents such as phenolics, ecdysteroids, flavonoids, triterpenoids and saponins (Bonifacio 2003, Kokanova-Nedialkova et al. 2009, de la Cruz Torres et al. 2013).

Several fungi associated with *Chenopodium* species have been recorded from various countries, including Australia (Cook & Dubé 1989), Brazil (Mendes et al. 1998), Canada (Conners 1967), China (Zhang et al. 1999), Germany (Van Der & Van Kesteren 1979), India (Sarbhoy 1971) and Italy (Choi et al. 2008). Earlier studies have reported *Oidium* sp. (Amano 1986) and *Peronospora* sp. (Greuter et al. 1991, Choi et al. 2008) as pathogens on different *Chenopodium* species from Italy.

Diaporthe was introduced with the type species *D. eres*, originally recorded on *Ulmus* sp. from Germany (Nitschke 1870). Species of *Diaporthe* have been reported as pathogens, endophytes and saprobes on a wide range of hosts in both temperate and tropical regions worldwide (Gomes et al. 2013, Udayanga et al. 2014a). In the early taxonomy, *Diaporthe* species were mainly defined on the basis of their micromorphology and host association (Santos & Phillips 2009). Later, it was understood that the host association of species has lesser taxonomic importance and the morphology alone is not sufficient to define a species (Santos & Phillips 2009). With the advances of molecular techniques, much progress has been made to define species using both morphological characteristics and DNA sequence data (Udayanga et al. 2012, Gao et al. 2017). The most commonly used sequence data for molecular characterization of *Diaporthe* species are the internal transcribed spacer region (ITS), beta-tubulin (TUB2), translation elongation factor-1alpha (TEF-1 α), partial histone H3 (HIS) and calmodulin (CAL) (Udayanga et al. 2012, Guarnaccia et al. 2018, Yang et al. 2018).

In the present study, a diaporthe-like strain was collected from a dead aerial branch of *Chenopodium* sp. from Italy. Combined ITS, CAL, HIS, TEF1- α and TUB2 phylogenetic analyses revealed that this fungus is *Diaporthe foeniculina*. This study, therefore, provides a new host record for *D. foeniculina* on *Chenopodium* sp. from Italy.

The accurate identification of a species in a genus, with a well resolved phylogeny, has much importance in plant pathology. It enables scientists to acquire knowledge on the host range and biogeography (Dugan et al. 2009, Udayanga et al. 2011), which will in turn help to expand their studies on coevolution, evolutionary adaptations and metabolite production. It has been discovered that the species of *Diaporthe* also have the ability to produce various secondary metabolites with antibiotic, cytotoxic and herbicidal activities (Gomes et al. 2013, Chepkirui & Stadler 2017). Furthermore, accurate species identification becomes particularly essential in cases where fungal diseases have to be controlled through the implementation of quarantine regulations (Rossman & Palm-Hernández 2008, Cai et al. 2011). Based on the previous findings, we provide a list of known pathogenic *Diaporthe* species reported from Italy.

Materials & Methods

Fungal isolation and morphological characterization

The dead aerial stem of *Chenopodium* sp. was collected from province of Forlì-Cesena in, Italy in February 2018. Specimen was brought to the laboratory in plastic bags. The sample was examined with a Motic SMZ 168 Series microscope. The hand cut sections of conidiomata were mounted in water for microscopic studies and photomicrography. The sections were examined using a Nikon ECLIPSE 80i compound microscope and photographed with a Canon 750D digital camera fitted to the microscope. Measurements were made with the Tarosoft (R) Image Frame Work program and images used for figures were processed with Adobe Photoshop CS6 Extended version 10.0 software (Adobe Systems, USA).

Single spore isolation was carried out following the method described in Senanayake et al. (2020). Germinated spores were individually transferred to potato dextrose agar (PDA) plates and incubated at 25 °C in daylight. Colony characteristics were observed and measured after 3 weeks. Herbarium specimens were deposited in the Mae Fah Luang University (MFLU) Herbarium, Chiang Rai, Thailand. Living cultures were deposited in the Culture Collection of Mae Fah Luang University (MFLUCC). Faces of Fungi number (FOF) was acquired, according to Jayasiri et al. (2015).

DNA extraction and PCR amplification and sequencing

Fungal isolates grown on PDA for 2 weeks at 25 °C were used to extract total genomic DNA. DNA was extracted from 50 to 100 mg of axenic mycelium of the growing cultures. The mycelium was ground to a fine powder with liquid nitrogen and fungal DNA was extracted using the OMEGA E.Z.N.A.® Forensic DNA Kit following the manufacturer's instructions. ITS, TUB2 and H3 genes were amplified as described in Manawasinghe et al. (2019). The attempts to obtain TEF1 α and CAL sequence data were unsuccessful. The PCR products were obtained according to optimized PCR protocols as described in Manawasinghe et al. (2019) and they were verified on 1% agarose electrophoresis gels stained with ethidium bromide. Thereafter, the amplified PCR fragments were purified and sequenced by Biomed Co. LTD, Beijing, China. Amplified nucleotide sequences were deposited in GenBank (Supplementary Table 1).

Phylogenetic analysis

Acquired sequences were verified and then subjected to a BLAST search in GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Related sequences were downloaded from GenBank following recent publications (Marin-Felix et al. 2019, Caio et al. 2020, Wrona et al. 2020). Single gene alignments were automatically done by MAFFT v. 7.036 (<http://mafft.cbrc.jp/alignment/server/large.html>, Katoh et al. 2019) using the default settings and later manually adjusted using BioEdit v. 7.0.5.2 where necessary, (Hall 1999).

Maximum likelihood trees were generated using RAxML-HPC2 on XSEDE (8.2.8) (Stamatakis et al. 2008, Stamatakis 2014) in the CIPRES Science Gateway platform (Miller et al. 2010). GTRGAMMA was used as the model of evolution and bootstrap support values were obtained by running 1000 pseudo replicates. Bayesian Inference (BI) analysis was conducted using MrBayes v. 3.1.2 (Ronquist & Huelsenbeck 2003). Six simultaneous Markov chains were run for 2,000,000 generations and trees were sampled every 1000th generation. The first 25% of generated trees representing the burn-in phase of the analyses were discarded and the remaining 75% of trees were used to calculate posterior probabilities (BYPP) in the majority rule consensus tree. Phylograms were visualized with FigTree v1.4.0 program (Rambaut 2011) and reorganized in Microsoft power point (2010). The reference strains used for the phylogenetic analyses in this study are listed in Supplementary Table 1.

Results

The strain observed and sequenced in this study was identified as *Diaporthe foeniculina* using morphology and molecular data.

Phylogenetic analyses

The initial phylogenetic tree was constructed using a combined ITS, CAL, HIS, TEF1- α and TUB2 data set which consisted of 249 taxa, including our strain (*Diaporthe foeniculina* MFLUCC 20-0151). Phylogenetic trees were rooted with *Diaporthella corylina* (CBS 121124) and *Diaporthella cryptica* (CBS 140348). The complete RAxML tree with 249 *Diaporthe* taxa with a final optimization likelihood value of -58281.827211 is shown in Supplementary Fig. 1. Placement of our strain, *Diaporthe foeniculina* (MFLUCC 20-0151) in the present study was identified from that tree and thereafter a final tree was constructed with 51 taxa. Maximum likelihood and Bayesian posterior probability analyses resulted in trees with similar topologies that did not differ significantly from one another (data not shown). The final RAxML tree with a final optimization likelihood value of -14994.433954 is shown in Fig. 1. The matrix had 1022 distinct alignment patterns, with 29.63% of undetermined characters or gaps.

Parameters for the GTRGAMMA model of the combined data set (ITS, CAL, HIS, TEF1- α and TUB2) were as follows: Estimated base frequencies; A = 0.220271, C = 0.318493, G = 0.237619, T = 0.223618; substitution rates AC = 1.306630, AG = 2.963307, AT = 0.997137, CG = 0.757166, CT = 4.658218, GT = 1.000000; proportion of invariable sites I = 0.319463; gamma distribution shape parameter α = 0.687349. Our strain of *Diaporthe foeniculina* (MFLUCC 20-

0151) clustered with the type strain of *Diaporthe foeniculina*, (CBS 111553) and other *Diaporthe foeniculina* strains (AR5145, CBS 111553, CBS 123208, MFLUCC 17-1068, MFLUCC 17-1020 and DP0454) in a well-supported clade (71% ML, 0.99 BYPP, Fig. 1).

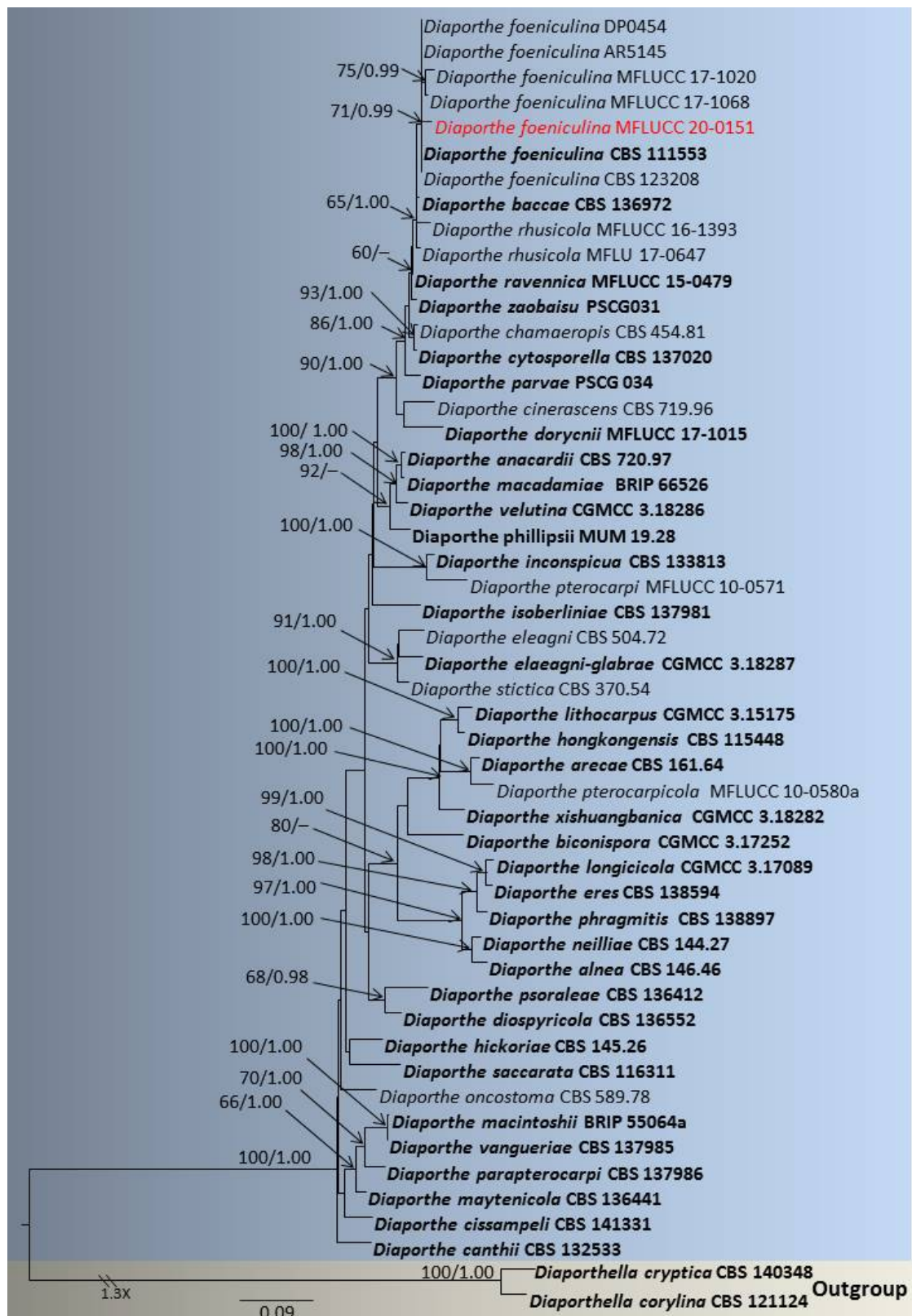


Fig. 1 – RAxML tree based on analysis of a combined dataset of ITS, CAL, HIS, TEF1- α and TUB2 sequences. Bootstrap support values for ML values equal to or >60% and BYPP values equal to or >0.95 are shown as ML/BYPP above the nodes. The isolate used for the present study is

shown in red and already known species are shown in black. Type strains are indicated in black bold. The tree is rooted using *Diaporthella corylina* and *Diaporthella cryptica*. The scale bar represents the expected number of nucleotide substitutions per site.

Taxonomy

Diaporthe foeniculina (Sacc.) Udayanga & Castl., *Persoonia* 32: 95 (2014)

Fig. 2

Facesoffungi number: FoF02183

Saprobic on dead aerial stem of *Chenopodium* sp. Asexual morph: Coelomycetous. *Conidiomata* 100–250 × 100–300 μm (\bar{x} = 175 × 200 μm, n = 5), pycnidial, scattered or gregarious, solitary, globose to subglobose, semi-immersed, unilocular, visible as small round to oval dark brown to black dots on the host surface. *Pycnidial wall* composed of 5–7 layers of cells of *textura angularis* almost similarly dense at the apex and base, outer 3–4 layers dark brown to black, inner 1–2 layers hyaline. *Paraphyses* lacking. *Conidiophores* 10–20 × 1–2 μm (\bar{x} = 15 × 1.5 μm, n = 20), hyaline, unbranched, cylindrical and straight to sinuous. *Conidiogenous cells* 0.5–1 μm diam, hyaline, cylindrical and terminal. *Conidia* 5–10 × 1–3 μm (\bar{x} = 7.5 × 2.5 μm, n = 40), aseptate, hyaline, ellipsoidal to cylindrical, rounded at both ends, thin and smooth-walled, with 2–3 guttules. Sexual morph: not observed (illustrated in Udayanga et al. (2014b)).

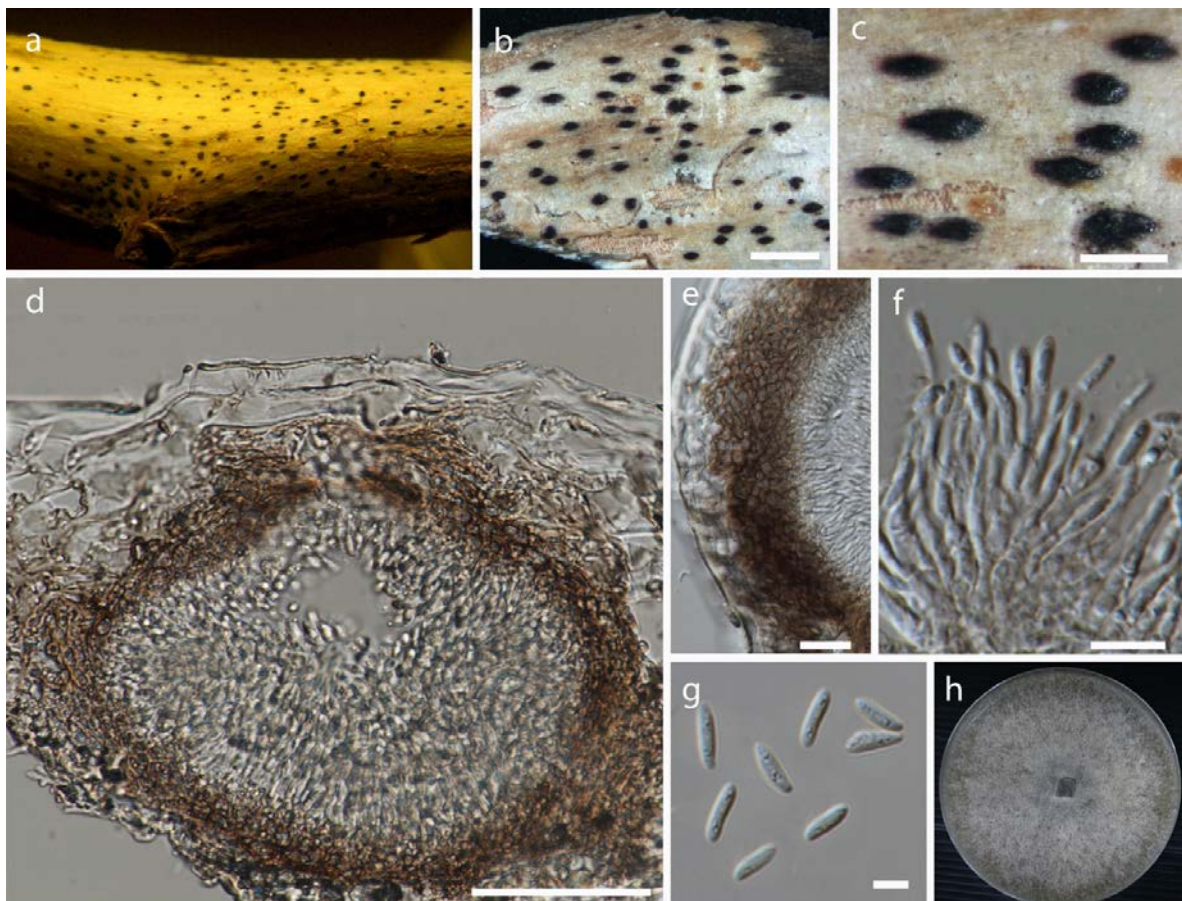


Fig. 2 – *Diaporthe foeniculina* (MFLU 18-0609). a *Chenopodium* sp. with conidiomata. b, c Close-up of conidiomata on the host. d Vertical section through conidioma. e Pycnidial wall in longitudinal section f Conidiogenous cells. g Conidia. h Colony on PDA. Scale bars: b = 500 μm, c = 200 μm, d = 100 μm, e = 20 μm, f = 10 μm, g = 5 μm.

Culture characteristics – Colonies on PDA reaching 90 mm diam. after 14 days at 25°C, colony circular, initially white, turning into brown with time (both front and reverse sides of the culture plate).

Material examined – ITALY, Province of Forlì–Cesena [FC], Forlì – Via Maria Ferrari, on dead aerial stem of *Chenopodium* sp., 06 February 2018, E. Camporesi, IT 3715 (MFLU 18-0609), living culture (MFLUCC 20-0151).

GenBank numbers – ITS = MW020272, HIS = MW057341, TUB2 = MW057340.

Notes – The strain of *Diaporthe foeniculina* (MFLUCC 20-0151) reported in the present study shares similar morphological features with the type strain of *D. foeniculina* (CBS 111553), with minor dimensional differences. The pycnidia of *Diaporthe foeniculina* (MFLUCC 20-0151) are comparatively smaller than those of *D. foeniculina* (CBS 111553) (100–300 µm diam. vs 400–700 µm diam.). *Diaporthe foeniculina* (MFLUCC 20-0151) comprises 5–7 cell layers in its pycnidial wall while *D. foeniculina* (CBS 111553) consists of only 2–3 layers (Udayanga et al. 2014b). The conidiophores are higher (12–20 × 1–2 µm vs 9–15 (–18) × 1–2 µm) and the conidia are smaller (7.5×2.5 µm vs 8.8 ± 0.3 × 2.4 ± 0.1 µm) (Udayanga et al. 2014b). These dimensional differences are probably due to environmental variation and host associations.

Discussion

Several studies have confirmed that the species of *Diaporthe* have a wide host range, while some endophytic and plant pathogenic taxa have been found to be host-specific (Gomes et al. 2013). In this study, the focus has been on the particular species, *Diaporthe foeniculina*, identified for the first time from *Chenopodium* sp. in Italy. This newly acquired strain (MFLUCC 20-0151) clustered with the strains AR5145, CBS 111553, CBS 123208, MFLUCC 17-1068, MFLUCC 17-1020 and DP0454 with 71% ML, and 0.99 BYPP statistical supports in a monophyletic clade (Fig. 1). Furthermore, its asexual structures are similar to the asexual morph of the type strain of *D. foeniculina* (CBS 111553) (Udayanga et al. 2014b), which further confirms its identity. Epitypification of *Diaporthe foeniculina* was done by Udayanga et al. (2014b) and it has been recorded from different geographical locations, including Argentina, Australia, Europe (Greece, Portugal, Spain and Italy), New Zealand, South Africa and the USA (California) (Udayanga et al. 2014b, Farr & Rossman 2020). Still a few *Diaporthe* species has been recorded from *Chenopodium* species, namely, *D. arctii* from Georgia (Anonymous 1960, Hanlin 1963) *D. arctii* var. *achilleae* from New Jersey (Wehmeyer 1933) and *D. tulasnei* from Portugal (Unamuno 1941).

Previous studies have reported *Diaporthe foeniculina* as a pathogen or a saprobe on different host plant species from Italy (Table 1). *Diaporthe foeniculina* has been reported associated with blacktip and necrotic spots on hazelnut kernel in Chile (Guerrero et al. 2020), blueberry twig blight and dieback in Portugal (Hilário et al. 2020), post-harvest fruit rot in lemon in Turkey (Tekiner et al. 2020), twig blight, shoot blight and branch canker of citrus in Greece (Vakalounakis et al. 2019), reddish sunken cankers on apple trees in Uruguay (Sessa et al. 2017) and has caused disease on acacia (*Robinia pseudoacacia*) in Iran (Bavand et al. 2019).

This study presents the first report of *D. foeniculina* from a *Chenopodium* sp. from Italy. *Diaporthe foeniculina* has been reported as both opportunistic pathogen and endophyte on various host plants (Udayanga et al. 2014b, Guarnaccia et al. 2016). The stress factors for the plant due to changing environmental conditions can facilitate the fungi, to switch their life mode from endophytic or saprobic to the pathogenic mode being capable of colonizing new hosts (Manawasinghe et al. 2018). In this study, we found *D. foeniculina* as a saprobe on *Chenopodium* sp. This suggests that, the fungus may survive in the plant debris and have a possibility to be a pathogen on *Chenopodium* sp. when the environmental conditions are favourable. We were unable to conduct a pathogenicity test due to the practical difficulty faced as the fungus was reported on a host from Italy and the culture is located in Thailand. Therefore, we suggest a pathogenicity test for *Diaporthe foeniculina* on *Chenopodium* sp. in future studies to check whether it can be a pathogen on the particular host plant species.

Other than *D. foeniculina*, the species *Diaporthe baccae*, *D. caulivora*, *D. cytospora*, *D. eres*, *D. helianthi*, *D. novem*, *D. rudis*, *D. sclerotoides*, *D. sojiae*, *D. sterilis* and *D. torilicola* have been already reported as pathogens from Italy (Table 1). However, some species which are recorded as pathogenic have not been confirmed by pathogenicity tests. It will be useful if future

studies conduct pathogenicity tests to confirm whether those species are pathogenic on particular hosts.

The other *Diaporthe* species, which have been reported from Italy, do not have records as pathogens on the hosts from Italy, but most of them are known pathogens from other regions of the world. *Diaporthe ambigua* causes postharvest fruit rot on kiwifruit (*Actinidia deliciosa*) in Greece and Chile (Díaz et al. 2017, Thomidis et al. 2019). *Diaporthe ampelina* has been reported as a pathogen on grapevine wood in northern California, USA (Lawrence et al. 2015). *Diaporthe amygdali* has been reported as the causal agent of twig canker on walnut in China (Meng et al. 2018) and it has been reported as the main pathogen of almonds in Spain (León et al. 2020). *Diaporthe cynaroidis* has been found associated with walnut branch canker in Chile (Luna et al. 2020). *Diaporthe gardenia* has been reported from the cankers of gardenia in California, USA (Alfieri 1967). *Diaporthe gulyae* is associated with stem canker of sunflower (*Helianthus annuus*) in Australia, Argentina, Canada and China (Thompson et al. 2011, Mathew et al. 2015, Mancebo et al. 2019, Zhang et al. 2019). There are records that *Diaporthe gulyae* has caused stem disease on soybean and common buckwheat in North Dakota (Mathew et al. 2018, Duellman et al. 2019). *Diaporthe nobilis* has been reported causing post-harvest rot of blueberry, fruit decay of pepper, shoot dieback on apple and shoot canker on chestnut in China (Zhang et al. 2016, Yu et al. 2018, Zhang et al. 2018, Sun et al. 2020). *Diaporthe phaseolorum* has been found as a pathogen on sunflower in Russia (Gomzhina & Gannibal 2018).

In addition, *Diaporthe acericola*, *D. arctii*, *D. arezzoensis*, *D. camelliae*, *D. camporesii*, *D. cichorii*, *D. crataegi*, *D. dorycnii*, *D. euphorbiae*, *D. fasciculata*, *D. italiana*, *D. lonicerae*, *D. nigra*, *D. pardalota*, *D. podocarpi-macrophylli*, *D. pseudotsugae*, *D. pulla*, *D. ravennica*, *D. rumicicola*, *D. sarothamni*, *D. schoeni* and *D. stictica* have been reported from Italy. So far, those species do not have records as pathogens. However, as there is a possibility for *Diaporthe* species to become opportunistic pathogens, we would like to suggest pathogenicity tests for those species in future studies. It would be beneficial to prevent economic losses resulted by fungal diseases on commercial crop species, through implementation of quarantine regulations.

Table 1 *Diaporthe* species recorded from Italy, their mode of life and host range

Species	Host	Life mode	Disease/Disease symptoms	Original Reference
<i>Diaporthe acericola</i>	<i>Acer negundo</i>	Saprobic	–	Dissanayake et al. (2017)
<i>Diaporthe ambigua</i>	<i>Platanus acerifolia</i>	N/A	N/A	Gomes et al. (2013)
	<i>Helianthus annuus</i>	N/A	N/A	Gomes et al. (2013)
<i>Diaporthe ampelina</i>	<i>Vitis vinifera</i>	N/A	N/A	Gomes et al. (2013)
<i>Diaporthe amygdali</i>	<i>Prunus dulcis</i>	N/A	N/A	Santos et al. (2017)
<i>Diaporthe arctii</i>	<i>Cannabis sativa</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Eupatorium cannabinum</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Medicago sativa</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Melilotus officinalis</i>	N/A	N/A	Farr & Rossman (2020)
<i>Diaporthe arezzoensis</i>	<i>Cytisus</i> sp.	Saprobic	–	Li et al. (2020)
<i>Diaporthe baccae</i>	<i>Citrus limon</i>	Pathogenic	Twig dieback, Branch canker	Guarnaccia & Crous (2017)
	<i>Citrus paradisi</i>	Pathogenic	Branch canker	Guarnaccia & Crous (2017)
	<i>Citrus reticulata</i>	Pathogenic	Trunk canker	Guarnaccia & Crous (2017)
	<i>Citrus sinensis</i>	Pathogenic	Twig dieback, Trunk canker	Guarnaccia & Crous (2017)
	<i>Vaccinium corymbosum</i>	N/A	N/A	Lombard et al. (2014)
<i>Diaporthe camelliae</i>	<i>Camellia japonica</i>	N/A	N/A	Farr & Rossman (2020)
<i>Diaporthe camporesii</i>	<i>Urtica dioica</i>	Saprobic	–	Hyde et al. (2020)
<i>Diaporthe caulivora</i>	<i>Glycine max</i>	Pathogenic	Infection of seeds	Zhang et al. (1997)
<i>Diaporthe cichorii</i>	<i>Cichorium intybus</i>	Saprobic	–	Dissanayake et al. (2017)
<i>Diaporthe crataegi</i>	<i>Crataegus oxyacantha</i>	N/A	N/A	Farr & Rossman (2020)
<i>Diaporthe cynaroidis</i>	<i>Eupatorium cannabinum</i>	Saprobic	–	Hyde et al. (2020)
<i>Diaporthe cytospora</i>	<i>Citrus limonia</i>	Pathogenic	N/A	Udayanga et al. (2014b)

Table 1 Continued.

Species	Host	Life mode	Disease/Disease symptoms	Original Reference
<i>Diaporthe dorycnii</i> <i>Diaporthe eres</i>	<i>Citrus limon</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Dorycnium hirsutum</i>	Saprobic	–	Dissanayake et al. (2017)
	<i>Castanea vesca</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Ficus carica</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Galega officinalis</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Gleditsia triacanthos</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Juglans regia</i>	N/A	N/A	Gomes et al. (2013)
	<i>Lonicera</i> sp.	N/A	N/A	Dissanayake et al. (2017)
	<i>Ostrya carpinifolia</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Picea excelsa</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Pinus pinaster</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Populus nigra</i>	N/A	NA	Dissanayake et al. (2017)
	<i>Prunus persica</i>	Pathogenic	Stem canker	Prencipe et al. (2017)
	<i>Pyrus communis</i>	Pathogenic	Fruit rot	Bertetti et al. (2018)
	<i>Rhamnus alpina</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Salix caprea</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Sambucus nigra</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Sanguisorba minor</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Sonchus oleraceus</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Syringa vulgaris</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Vitis</i> sp.	Pathogenic	Canker	Jayawardena et al. (2018)
	<i>Vitis vinifera</i>	Pathogenic	Cane blight	Cinelli et al. (2016)
	<i>Diaporthe euphorbiae</i>	<i>Euphorbia amygdaloides</i>	N/A	N/A
<i>Diaporthe fasciculata</i>	<i>Robinia pseudoacacia</i>	N/A	N/A	Farr & Rossman (2020)
<i>Diaporthe foeniculina</i>	<i>Achillea millefolium</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Ailanthus altissima</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Arctium minus</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Asparagus</i> sp.	Saprobic	N/A	Hyde et al. (2020)
	<i>Camellia sinensis</i>	N/A	N/A	Gomes et al. (2013)
	<i>Castanea sativa</i>	Pathogenic	Stem and shoot cankers	Annesi et al. (2016)
	<i>Chenopodium</i> sp.	Saprobic	–	This study
	<i>Citrus limon</i>	Pathogenic	Twig dieback, Branch canker, Trunk canker	Guarnaccia & Crous (2017)
	<i>Citrus maxima</i>	Pathogenic	Branch canker	Guarnaccia & Crous (2017)
	<i>Citrus mitis</i>	Pathogenic	Twig dieback	Guarnaccia & Crous (2017)
	<i>Citrus paradisi</i>	Pathogenic	Branch canker	Guarnaccia & Crous (2017)
	<i>Citrus reticulata</i>	Pathogenic	Twig dieback	Guarnaccia & Crous (2017)
	<i>Citrus sinensis</i>	Pathogenic	Branch canker, Trunk canker	Guarnaccia & Crous (2017)
	<i>Cupressus sempervirens</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Diospyros kaki</i>	N/A	N/A	Gomes et al. (2013)
	<i>Eucalyptus camaldulensis</i>	Pathogenic	Cankers	Deidda et al. (2016)
	<i>Hemerocallis fulva</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Lunaria rediviva</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Melilotus officinalis</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Microcitrus australasica</i>	Pathogenic	Twig dieback	Guarnaccia & Crous (2017)
	<i>Persea americana</i>	Pathogenic	Branch cankers and stem-end rot	Guarnaccia et al. (2016)
	<i>Prunus amygdalus</i>	N/A	N/A	Gomes et al. (2013)
	<i>Prunus avium</i>	Saprobic or parasitic	–	Li et al. (2020)
<i>Rosa canina</i>	Pathogenic	N/A	Wanasinghe et al. (2018)	
<i>Vicia</i> sp.	N/A	N/A	Dissanayake et al. (2017)	
<i>Wisteria sinensis</i>	N/A	N/A	Dissanayake et al. (2017)	
<i>Amorpha fruticosa</i>	N/A	N/A	Dissanayake et al. (2017)	
<i>Angelica sylvestris</i>	N/A	N/A	Dissanayake et al. (2017)	

Table 1 Continued.

Species	Host	Life mode	Disease/Disease symptoms	Original Reference
	<i>Platanus hybrida</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Prunus</i> sp.	N/A	N/A	Hyde et al. (2017)
	<i>Rubus</i> sp.	N/A	N/A	Dissanayake et al. (2017)
<i>Diaporthe gardeniae</i>	<i>Gardenia florida</i>	N/A	N/A	Gomes et al. (2013)
	<i>Gardenia jasminoides</i>	N/A	N/A	Fan et al. (2018)
<i>Diaporthe gulyae</i>	<i>Heracleum sphondylium</i>	N/A	N/A	Dissanayake et al. (2017)
<i>Diaporthe helianthi</i>	<i>Helianthus annuus</i>	Pathogenic	Stem canker	Pecchia et al. (2004)
<i>Diaporthe italiana</i>	<i>Morus alba</i>	Saprobic	–	Hyde et al. (2019)
<i>Diaporthe lonicerae</i>	<i>Lonicera</i> sp.	Saprobic	–	Dissanayake et al. (2017)
	<i>Laurus nobilis</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Torilis arvensis</i>	N/A	N/A	Dissanayake et al. (2017)
<i>Diaporthe nigra</i>	<i>Ballota nigra</i>	Saprobic	–	Hyde et al. (2020)
<i>Diaporthe nobilis</i>	<i>Vitis vinifera</i>	N/A	N/A	Lorenzini et al. (2016)
<i>Diaporthe novem</i>	<i>Citrus aurantifolia</i>	Pathogenic	Twig dieback	Guarnaccia & Crous (2017)
	<i>Citrus japonica</i>	Pathogenic	Twig dieback	Guarnaccia & Crous (2017)
	<i>Galium</i> sp.	N/A	N/A	Dissanayake et al. (2017)
<i>Diaporthe pardalota</i>	<i>Euonymus japonicus</i>	N/A	N/A	Farr & Rossman (2020)
	<i>Yucca gloriosa</i>	N/A	N/A	Farr & Rossman (2020)
<i>Diaporthe phaseolorum</i>	<i>Glycine max</i>	N/A	N/A	Luongo et al. (2011)
<i>Diaporthe podocarpi-macrophylli</i>	<i>Olea europaea</i>	N/A	N/A	Gao et al. (2017)
<i>Diaporthe pseudotsugae</i>	<i>Pseudotsuga menziesii</i>	N/A	N/A	Dissanayake et al. (2017)
<i>Diaporthe pulla</i>	<i>Hedera helix</i>	N/A	N/A	Farr & Rossman (2020)
<i>Diaporthe ravennica</i>	<i>Salvia</i> sp.	N/A	N/A	Dissanayake et al. (2017)
	<i>Tamarix</i> sp.	Saprobic	–	Thambugala et al. (2017)
<i>Diaporthe rudis</i>	<i>Acer campestre</i>	N/A	N/A	Guterres et al. (2018)
	<i>Acer opalus</i>	N/A	N/A	Udayanga et al. (2014b)
	<i>Anthoxanthum odoratum</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Carlina vulgaris</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Cornus</i> sp.	N/A	N/A	Dissanayake et al. (2017)
	<i>Dioscorea communis</i>	N/A	N/A	Dissanayake et al. (2017)
	<i>Vaccinium corymbosum</i>	Pathogenic	Blight and dieback	Guarnaccia et al. (2020)
	<i>Vitis</i> sp.	Pathogenic	Canker	Jayawardena et al. (2018)
	<i>Vitis vinifera</i>	N/A	N/A	Udayanga et al. (2014b)
<i>Diaporthe rumicicola</i>	<i>Rumex</i> sp.	Saprobic	–	Hyde et al. (2019)
<i>Diaporthe sarothamni</i>	<i>Solanum dulcamara</i>	N/A	N/A	Farr & Rossman (2020)
<i>Diaporthe schoeni</i>	<i>Schoenus nigricans</i>	Saprobic	–	Dissanayake et al. (2017)
	<i>Carduus</i> sp.	N/A	N/A	Dissanayake et al. (2017)
	<i>Plantago</i> sp.	N/A	N/A	Dissanayake et al. (2017)
<i>Diaporthe sclerotioides</i>	<i>Cucumis sativus</i>	Pathogenic	Black root rot	Fukada et al. (2018)
<i>Diaporthe sojae</i>	<i>Glycine soja</i>	N/A	N/A	Gomes et al. (2013)
	<i>Glycine max</i>	Pathogenic	Seed death	Farr & Rossman (2020)
<i>Diaporthe sterilis</i>	<i>Cytisus</i> sp.	N/A	N/A	Dissanayake et al. (2017)
	<i>Persea americana</i>	Pathogenic	Branch and shoot cankers	Guarnaccia et al. (2016)
	<i>Vaccinium corymbosum</i>	N/A	N/A	Lombard et al. (2014)
<i>Diaporthe stictica</i>	<i>Buxus sempervirens</i>	N/A	N/A	Gomes et al. (2013)
<i>Diaporthe torilicola</i>	<i>Torilis arvensis</i>	Pathogenic	Dieback	Dissanayake et al. (2017)

N/A – Not Available, The known pathogenic *Diaporthe* sp. are in **bold**. The records are taken from the literature and some pathogenic species has not been confirmed by pathogenicity tests.

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Supplementary data

Supplementary Table 1 Selected taxa with their corresponding GenBank accession numbers of *Diaporthe* used in the phylogenetic analyses. Type species are marked with an asterisk and the newly generated sequences are in blue.

Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. acaciarum</i>	CBS 138862*	KP004460	KP004509	KP004504	–	–
<i>D. acaciigena</i>	CBS 129521*	KC343005	KC343973	KC343489	KC343731	KC343247
<i>D. acericola</i>	MFLUCC 17-0956*	KY964224	KY964074	–	KY964180	KY964137
<i>D. acerina</i>	CBS 137.27	KC343006	KC343974	KC343490	KC343732	KC343248
<i>D. acuta</i>	PSCG 047*	MK626957	MK691225	MK726161	MK654802	MK691124
<i>D. acutispora</i>	CGMCC 3.18285*	KX986764	KX999195	KX999235	KX999155	KX999274
<i>D. albosinensis</i>	CFCC 53066*	MK432659	MK578059	MK443004	MK578133	MK442979
<i>D. alleghaniensis</i>	CBS 495.72*	FJ889444	KC843228	KC343491	GQ250298	KC343249
<i>D. alnea</i>	CBS 146.46*	KC343008	KC343976	KC343492	KC343734	KC343250
<i>D. ambigua</i>	CBS 114015*	KC343010	KC343978	KC343494	KC343736	KC343252
<i>D. ampelina</i>	CBS 114016*	AF230751	JX275452	–	GQ250351	JX197443
<i>D. amygdali</i>	CBS 126679*	KC343022	KC343990	KC343506	KC343748	KC343264
<i>D. anacardii</i>	CBS 720.97*	KC343024	KC343992	KC343508	KC343750	KC343266
<i>D. angelicae</i>	CBS 111592*	KC343026	KC343994	KC343511	KC343752	KC343268
<i>D. anhuiensis</i>	CNUCC 201901	MN219718	MN227008	MN224556	MN224668	MN224549
<i>D. apiculatum</i>	LC 3418*	KP267896	KP293476	–	KP267970	–
<i>D. aquatica</i>	IFRDCC 3051*	JQ797437	–	–	–	–
<i>D. araucanorum</i>	RGM 2546	MN509711	MN509722	–	MN509733	MN974277
<i>D. arctii</i>	CBS 136.25	KC343031	KC343999	KC343515	KC343757	KC343273
<i>D. arecae</i>	CBS 161.64*	KC343032	KC344000	KC343516	KC343758	KC343274
<i>D. arengae</i>	CBS 114979*	KC343034	KC344002	KC343518	KC343760	KC343276
<i>D. arezzoensis</i>	MFLU 19-2880*	MT185503	MT454055	–	MT454019	–
<i>D. aseana</i>	MFLUCC 12-0299a*	KT459414	KT459432	–	KT459448	KT459464
<i>D. asheicola</i>	CBS 136967*	KJ160562	KJ160518	–	KJ160594	KJ160542
<i>D. aspalathi</i>	CBS 117169*	KC343036	KC344004	KC343520	KC343762	KC343278
<i>D. australafricana</i>	CBS 111886*	KC343038	KC344006	KC343522	KC343764	KC343280
<i>D. australiana</i>	BRIP 66145*	MN708222	MN696530	–	MN696522	–
<i>D. baccae</i>	CBS 136972*	KJ160565	MF418509	MF418264	KJ160597	–
<i>D. batatas</i>	CBS 122.21	KC343040	KC344008	KC343524	KC343766	KC343282
<i>D. beckhausii</i>	CBS 138.27	KC343041	KC344009	KC343525	KC343767	KC343283
<i>D. beilharziae</i>	BRIP 54792*	JX862529	KF170921	–	JX862535	–
<i>D. benedicti</i>	CFCC 50062*	KP208847	KP208855	KP208851	KP208853	KP208849
<i>D. betulae</i>	CFCC 50469*	KT732950	KT733020	KT732999	KT733016	KT732997

Supplementary Table 1 Continued.

Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. betulicola</i>	CFCC 51128*	KX024653	KX024657	KX024661	KX024655	KX024659
<i>D. bicincta</i>	CBS 121004*	KC343134	KC344102	KC343618	KC343860	KC343376
<i>D. biconispora</i>	CGMCC 3.17252*	KJ490597	KJ490418	KJ490539	KJ490476	–
<i>D. biguttulata</i>	ICMP20657*	KJ490582	KJ490403	KJ490524	KJ490461	–
<i>D. biguttusis</i>	CGMCC 3.17081*	KF576282	KF576306	–	KF576257	–
<i>D. bohemiae</i>	CBS 143347*	MG281015	MG281188	MG281361	MG281536	MG281710
<i>D. brasiliensis</i>	CBS 133183*	KC343042	KC344010	KC343526	KC343768	KC343284
<i>D. caatingaensis</i>	CBS 141542*	KY085927	KY115600	KY115605	KY115603	KY115597
<i>D. camptothecicola</i>	CFCC 51632*	KY203726	KY228893	KY228881	KY228887	KY228877
<i>D. canthii</i>	CBS 132533*	JX069864	KC843230	–	KC843120	KC843174
<i>D. carpini</i>	CBS 114437	KC343044	KC344012	KC343528	KC343770	KC343286
<i>D. cassines</i>	CBS 136440*	KF777155	–	–	KF777244	–
<i>D. caulivora</i>	CBS 127268*	KC343045	KC344013	KC343529	KC343771	KC343287
<i>D. celastrina</i>	CBS 139.27*	KC343047	KC344015	KC343531	KC343773	KC343289
<i>D. celeris</i>	CBS 143349*	MG281017	MG281190	MG281363	MG281538	MG281712
<i>D. ceratozamia</i>	CBS 131306*	JQ044420	–	–	–	–
<i>D. chamaeropsis</i>	CBS 454.81	KC343048	KC344016	KC343532	KC343774	KC343290
<i>D. charlesworthii</i>	BRIP 54884m*	KJ197288	KJ197268	–	KJ197250	–
<i>D. chongqingensis</i>	PSCG435*	MK626916	MK691321	MK726257	MK654866	MK691209
<i>D. cichorii</i>	MFLUCC 17-1023*	KY964220	KY964104	–	KY964176	KY964133
<i>D. cinerascens</i>	CBS 719.96	KC343050	KC344018	KC343534	KC343776	KC343292
<i>D. cissampeli</i>	CBS 141331*	KX228273	KX228384	KX228366	–	–
<i>D. citri</i>	CBS 135422*	KC843311	KC843187	MF418281	KC843071	KC843157
<i>D. citriasiana</i>	CBS 134240*	JQ954645	KC357459	MF418282	JQ954663	KC357491
<i>D. citrichinensis</i>	CBS 134242*	JQ954648	MF418524	KJ420880	JQ954666	KC357494
<i>D. compacta</i>	LC3083*	KP267854	KP293434	KP293508	KP267928	–
<i>D. convolvuli</i>	CBS 124654	KC343054	KC344022	KC343538	KC343780	KC343296
<i>D. coryli</i>	CFCC 53083*	MK432661	MK578061	MK443006	MK578135	MK442981
<i>D. crataegi</i>	CBS 114435	KC343055	KC344023	KC343539	KC343781	KC343297
<i>D. crotalariae</i>	CBS 162.33*	KC343056	KC344024	KC343540	KC343782	KC343298
<i>D. crousii</i>	CAA823*	MK792311	MK837932	MK871450	MK828081	MK883835
<i>D. cucurbitae</i>	DAOM 42078*	KM453210	KP118848	KM453212	KM453211	–
<i>D. cuppatea</i>	CBS 117499*	AY339322	JX275420	KC343541	AY339354	JX197414
<i>D. cynaroidis</i>	CBS 122676	KC343058	KC344026	KC343542	KC343784	KC343300
<i>D. cytosporella</i>	CBS 137020*	KC843307	KC843221	MF418283	KC843116	KC843141

Supplementary Table 1 Continued.

Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. decedens</i>	CBS 109772	KC343059	KC344027	KC343543	KC343785	KC343301
<i>D. decorticans</i>	CBS 114200	KC343169	KC344137	KC343653	KC343895	KC343411
<i>D. destruens</i>	SPL15025*	MH465671	–	–	MH560611	MH560612
<i>D. detrusa</i>	CBS 109770	KC343061	KC344029	KC343545	KC343787	KC343303
<i>D. diospyricola</i>	CBS 136552*	KF777156	–	–	–	–
<i>D. discoidispora</i>	ICMP20662*	KJ490624	KJ490445	KJ490566	KJ490503	–
<i>D. dorycnii</i>	MFLUCC 17-1015*	KY964215	KY964099	–	KY964171	–
<i>D. drenthii</i>	BRIP 66524*	MN708229	MN696537	–	MN696526	–
<i>D. durionigena</i>	KCSR1812.8*	MN453530	MT276159	–	MT276157	–
<i>D. elaeagni-glabrae</i>	CGMCC 3.18287*	KX986779	KX999212	KX999251	KX999171	KX999281
<i>D. eleagni</i>	CBS 504.72	KC343064	KC344032	KC343548	KC343790	KC343306
<i>D. ellipicola</i>	CGMCC 3.17084*	KF576270	KF576291	–	KF576245	–
<i>D. endophytica</i>	CBS 133811*	KC343065	KC344033	KC343549	KC343791	KC343307
<i>D. eres</i>	CBS 138594*	KJ210529	KJ420799	KJ420850	KJ210550	KJ434999
<i>D. eucalyptorum</i>	CBS 132525*	JX069862	–	–	–	–
<i>D. eugeniae</i>	CBS 444.82	KC343098	KC344066	KC343582	KC343824	KC343340
<i>D. fibrosa</i>	CBS 109751	KC343099	KC344067	KC343583	KC343825	KC343341
<i>D. foeniculina</i>	MFLUCC 17-1068	KY964188	KY964071	–	KY964144	–
<i>D. foeniculina</i>	MFLUCC 17-1020	KY964218	KY964102	–	KY964174	–
<i>D. foeniculina</i>	AR5145	KC843306	KC843220	–	KC843115	KC843140
<i>D. foeniculina</i>	DP0454	KC843297	KC843211	–	KC843106	KC843131
<i>D. foeniculacea</i>	CBS 123208	KC343104	KC344072	KC343588	KC343830	KC343346
<i>D. foeniculina</i>	CBS 111553*	KC343101	KC344069	KC343585	KC343827	KC343343
<i>D. foeniculina</i>	MFLUCC 20-0151	MW020272	MW057340	MW057341	–	–
<i>D. foikelawen</i>	RGM 2539*	MN509713	MN509724	–	MN509735	MN974278
<i>D. fraxini-angustifoliae</i>	BRIP 54781*	JX862528	KF170920	–	JX852534	–
<i>D. fructicola</i>	MAFF 246408*	LC342734	LC342736	LC342737	LC342735	LC342738
<i>D. fulvicolor</i>	PSCG 051*	MK626859	MK691236	MK726163	MK654806	MK691132
<i>D. fusicola</i>	CGMCC 3.17087*	KF576281	KF576305	–	KF576256	KF576233
<i>D. ganjae</i>	CBS 180.91*	KC343112	KC344080	KC343596	KC343838	KC343354
<i>D. gardeniae</i>	CBS 288.56	KC343113	KC344081	KC343597	KC343839	KC343355
<i>D. Garethjonesii</i>	MFLUCC 12-0542a*	KT459423	KT459441	–	KT459457	KT459470
<i>D. goulteri</i>	BRIP 55657a*	KJ197290	KJ197270	–	KJ197252	–
<i>D. Guangxiensis</i>	JZB320094*	MK335772	MK500168	–	MK523566	MK736727
<i>D. gulyae</i>	BRIP 54025*	JF431299	KJ197271	–	JN645803	–

Supplementary Table 1 Continued.

Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. helianthi</i>	CBS 592.81*	KC343115	KC344083	KC343599	KC343841	JX197454
<i>D. heterophyllae</i>	CBS 143769*	MG600222	MG600226	MG600220	MG600224	MG600218
<i>D. heveae</i>	CBS 852.97	KC343116	KC344084	KC343600	KC343842	KC343358
<i>D. heveae</i>	CBS 681.84	KC343117	KC344085	KC343601	KC343843	KC343359
<i>D. hickoriae</i>	CBS 145.26*	KC343118	KC344086	KC343602	KC343844	KC343360
<i>D. hispaniae</i>	CBS 143351*	MG281123	MG281296	MG281471	MG281644	MG281820
<i>D. hongkongensis</i>	CBS 115448*	KC343119	KC344087	KC343603	KC343845	KC343361
<i>D. hordei</i>	CBS 481.92	KC343120	KC344088	KC343604	KC343846	KC343362
<i>D. huangshanensis</i>	CNUCC 201903*	MN219729	MN227010	MN224558	MN224670	–
<i>D. hubeiensis</i>	JZB320123*	MK335809	MK500148	–	MK523570	MK500235
<i>D. hungariae</i>	CBS 143353*	MG281126	MG281299	MG281474	MG281647	MG281823
<i>D. impulsa</i>	CBS 114434	KC343121	KC344089	KC343605	KC343847	KC343363
<i>D. incompleta</i>	CGMCC 3.18288*	KX986794	KX999226	KX999265	KX999186	KX999289
<i>D. inconspicua</i>	CBS 133813*	KC343123	KC344091	KC343607	KC343849	KC343365
<i>D. infecunda</i>	CBS 133812*	KC343126	KC344094	KC343610	KC343852	KC343368
<i>D. isoberliniae</i>	CBS 137981*	KJ869133	KJ869245	–	–	–
<i>D. italiana</i>	MFLUCC:18-0091*	MH846238	MH853689	–	MH853687	MH853691
<i>D. juglandicola</i>	CFCC 51134*	KU985101	KX024634	–	KX024628	KX024616
<i>D. kochmanii</i>	BRIP 54033*	JF431295	–	–	JN645809	–
<i>D. kongii</i>	BRIP 54031*	JF431301	KJ197272	–	JN645797	–
<i>D. krabiensis</i>	MFLUCC 17-2481*	MN047100	MN431495	–	MN433215	–
<i>D. leucospermi</i>	CBS 111980*	JN712460	KY435673	KY435653	KY435632	KY435663
<i>D. limonicola</i>	CBS 142549*	MF418422	MF418582	MF418342	MF418501	MF418256
<i>D. litchicola</i>	BRIP 54900*	JX862533	KF170925	–	JX862539	–
<i>D. lithocarpus</i>	CGMCC 3.15175*	KC153104	KF576311	–	KC153095	–
<i>D. longicicola</i>	CGMCC 3.17089*	KF576267	KF576291	–	KF576242	–
<i>D. longicolla</i>	FAU 599*	KJ590728	KJ610883	KJ659188	KJ590767	KJ612124
<i>D. longispora</i>	CBS 194.36*	KC343135	KC344103	KC343619	KC343861	KC343377
<i>D. loniceriae</i>	MFLUCC 17-0963*	KY964190	KY964073	–	KY964146	KY964116
<i>D. lusitanicae</i>	CBS 123212*	KC343136	KC344104	KC343620	KC343862	KC343378
<i>D. macadamiae</i>	BRIP 66526*	MN708230	MN696539	–	MN696528	–
<i>D. macintoshii</i>	BRIP 55064a*	KJ197289	KJ197269	–	KJ197251	–
<i>D. mahothocarpus</i>	CGMCC 3.15181	KC153096	–	–	KC153087	–
<i>D. malorum</i>	CBS142383*	KY435638	KY435668	KY435648	KY435627	KY435658
<i>D. manihotia</i>	CBS 505.76	KC343138	KC344106	KC343622	KC343864	KC343380
<i>D. marina</i>	MFLU 17-2622*	MN047102	–	–	–	–

Supplementary Table 1 Continued.

Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. maritima</i>	DAOMC 250563*	KU552025	KU574615	–	KU552023	–
<i>D. masirevicii</i>	BRIP 57892a*	KJ197277	KJ197257	–	KJ197239	–
<i>D. mayteni</i>	CBS 133185*	KC343139	KC344107	KC343623	KC343865	KC343381
<i>D. maytenicola</i>	CBS 136441*	KF777157	KF777250	–	–	–
<i>D. megalospora</i>	CBS 143.27	KC343140	KC344108	KC343624	KC343866	KC343382
<i>D. melitensis</i>	CBS 142551*	MF418424	MF418584	MF418344	MF418503	MF418258
<i>D. melonis</i>	CBS 507.78*	KC343142	KC344110	KC343626	KC343868	KC343384
<i>D. middletonii</i>	BRIP 54884e*	KJ197286	KJ197266	–	KJ197248	–
<i>D. millettiae</i>	GUCC9167*	MK398674	MK460488	–	MK480609	MK502086
<i>D. miriciae</i>	BRIP 54736j*	KJ197283	KJ197263	–	KJ197245	–
<i>D. momicola</i>	MFLUCC 16-0113*	KU557563	KU557587	–	KU557631	KU557611
<i>D. multigutullata</i>	ICMP20656*	KJ490633	KJ490454	KJ490575	KJ490512	–
<i>D. musigena</i>	CBS 129519*	KC343143	KC344111	KC343627	KC343869	KC343385
<i>D. myracrodruonis</i>	URM 7972*	NR_163320	MK205291	–	MK213408	MK205290
<i>D. neilliae</i>	CBS 144.27*	KC343144	KC344112	KC343628	KC343870	KC343386
<i>D. neoarctii</i>	CBS 109490	KC343145	KC344113	KC343629	KC343871	KC343387
<i>D. nomurai</i>	CBS 157.29	KC343154	KC344122	KC343638	KC343880	KC343396
<i>D. nothofagi</i>	BRIP 54801*	JX862530	KF170922	–	JX862536	–
<i>D. novem</i>	CBS 127271*	KC343157	KC344125	KC343641	KC343883	KC343399
<i>D. obtusifoliae</i>	CBS 143449*	MG386072	–	MG386137	–	–
<i>D. ocoteae</i>	CBS 141330*	KX228293	KX228388	–	–	–
<i>D. oncostoma</i>	CBS 589.78	KC343162	KC344130	KC343646	KC343888	KC343404
<i>D. oraccinii</i>	LC 3166*	KP267863	KP293443	KP293517	KP267937	–
<i>D. osmanthi</i>	GUCC9165*	MK398675	MK502091	–	MK480610	MK502087
<i>D. ovalispora</i>	ICMP20659*	KJ490628	KJ490449	KJ490570	KJ490507	–
<i>D. ovoicicola</i>	CGMCC 3.17092*	KF576264	KF576288	–	KF576239	KF576222
<i>D. oxe</i>	CBS 133186*	KC343164	KC344132	KC343648	KC343890	KC343406
<i>D. paranensis</i>	CBS 133184	KC343171	KC344139	KC343655	KC343897	KC343413
<i>D. parapterocarpi</i>	CBS 137986*	KJ869138	KJ869248	–	–	–
<i>D. parvae</i>	PSCG 034*	MK626919	MK691248	MK726210	MK654858	–
<i>D. patagonica</i>	RGM 2473*	MN509717	MN509728	–	MN509739	MN974279
<i>D. pascoei</i>	BRIP 54847*	JX862532	KF170924	–	JX862538	–
<i>D. passiflorae</i>	CBS 132527*	JX069860	KY435674	KY435654	KY435633	KY435664
<i>D. passifloricola</i>	CBS 141329*	KX228292	KX228387	KX228367	–	–
<i>D. penetrитеum</i>	LC 3353	KP714505	KP714529	KP714493	KP714517	–
<i>D. perjuncta</i>	CBS 109745*	KC343172	KC344140	KC343656	KC343898	KC343414

Supplementary Table 1 Continued.

Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. pernicios</i>	CBS 124030	KC343149	KC344117	KC343633	KC343875	KC343391
<i>D. perseae</i>	CBS 151.73	KC343173	KC344141	KC343657	KC343899	KC343415
<i>D. pescicola</i>	MFLUCC 16-0105*	KU557555	KU557579	–	KU557623	KU557603
<i>D. phaseolorum</i>	CBS 113425	KC343174	KC344142	KC343658	KC343900	KC343416
<i>D. phillipsii</i>	MUM 19.28*	MK792305	MN000351	MK871445	MK828076	MK883831
<i>D. phragmitis</i>	CBS 138897*	KP004445	KP004507	KP004503	–	–
<i>D. podocarpimacrophylli</i>	CGMCC3.18281*	KX986774	KX999207	KX999246	KX999167	KX999278
<i>D. pseudomangiferae</i>	CBS 101339*	KC343181	KC344149	KC343665	KC343907	KC343423
<i>D.pseudophoenicicola</i>	CBS 462.69*	KC343184	KC344152	KC343668	KC343910	KC343426
<i>D. pseudotsugae</i>	MFLU 15-3228	KY964225	KY964108	–	KY964181	KY964138
<i>D. psoraleae</i>	CBS 136412*	KF777158	KF777251	–	KF777245	–
<i>D. psoraleae-pinnatae</i>	CBS 136413*	KF777159	KF777252	–	–	–
<i>D. pterocarp</i>	MFLUCC 10-0571	JQ619899	JX275460	–	JX275416	JX197451
<i>D. pterocarpicola</i>	MFLUCC 10-0580a	JQ619887	JX275441	–	JX275403	JX197433
<i>D. pustulata</i>	CBS 109742	KC343185	KC344153	KC343669	KC343911	KC343427
<i>D. pyracanthae</i>	CBS142384*	KY435635	KY435666	KY435645	KY435625	KY435656
<i>D. racemosae</i>	CBS 143770*	MG600223	MG600227	MG600221	MG600225	MG600219
<i>D. raonikayaporum</i>	CBS 133182*	KC343188	KC344156	KC343672	KC343914	KC343430
<i>D. ravennica</i>	MFLUCC 15-0479*	KU900335	KX432254	–	–	–
<i>D. rhoia</i>	CBS 146.27	KC343189	KC344157	KC343673	KC343915	KC343431
<i>D. rhusicola</i>	MFLU 17-0647	MG828893	MG922552	–	MG922551	–
<i>D. rhusicola</i>	MFLUCC 16-1393	KY684947	KY684945	–	KY684946	–
<i>D. rosiphthora</i>	COAD 2914*	MT311197	–	–	–	–
<i>D. rosmaniae</i>	MUM 19.30*	MK792290	MK837914	MK871432	MK828063	MK883822
<i>D. rostrata</i>	CFCC 50062*	KP208847	KP208855	KP208851	KP208853	KP208849
<i>D. rudis</i>	CBS 113201	KC343234	KC344202	KC343718	KC343960	KC343476
<i>D. saccarata</i>	CBS 116311*	KC343190	KC344158	KC343674	KC343916	KC343432
<i>D. sackstonii</i>	BRIP 54669b*	KJ197287	KJ197267	–	KJ197249	–
<i>D. salicicola</i>	BRIP 54825*	JX862531	KF170923	–	JX862537	–
<i>D. salinicola</i>	MFLUCC 18-0553 *	MN047098	–	–	MN077073	–
<i>D. sambucusii</i>	CFCC 51986*	KY852495	KY852511	KY852503	KY852507	KY852499
<i>D. schini</i>	CBS 133181*	KC343191	KC344159	KC343675	KC343917	KC343433
<i>D. schisandrae</i>	CFCC 51988*	KY852497	KY852513	KY852505	KY852509	KY852501
<i>D. schoeni</i>	MFLU 15-1279*	KY964226	KY964109	–	KY964182	KY964139

Supplementary Table 1 Continued.

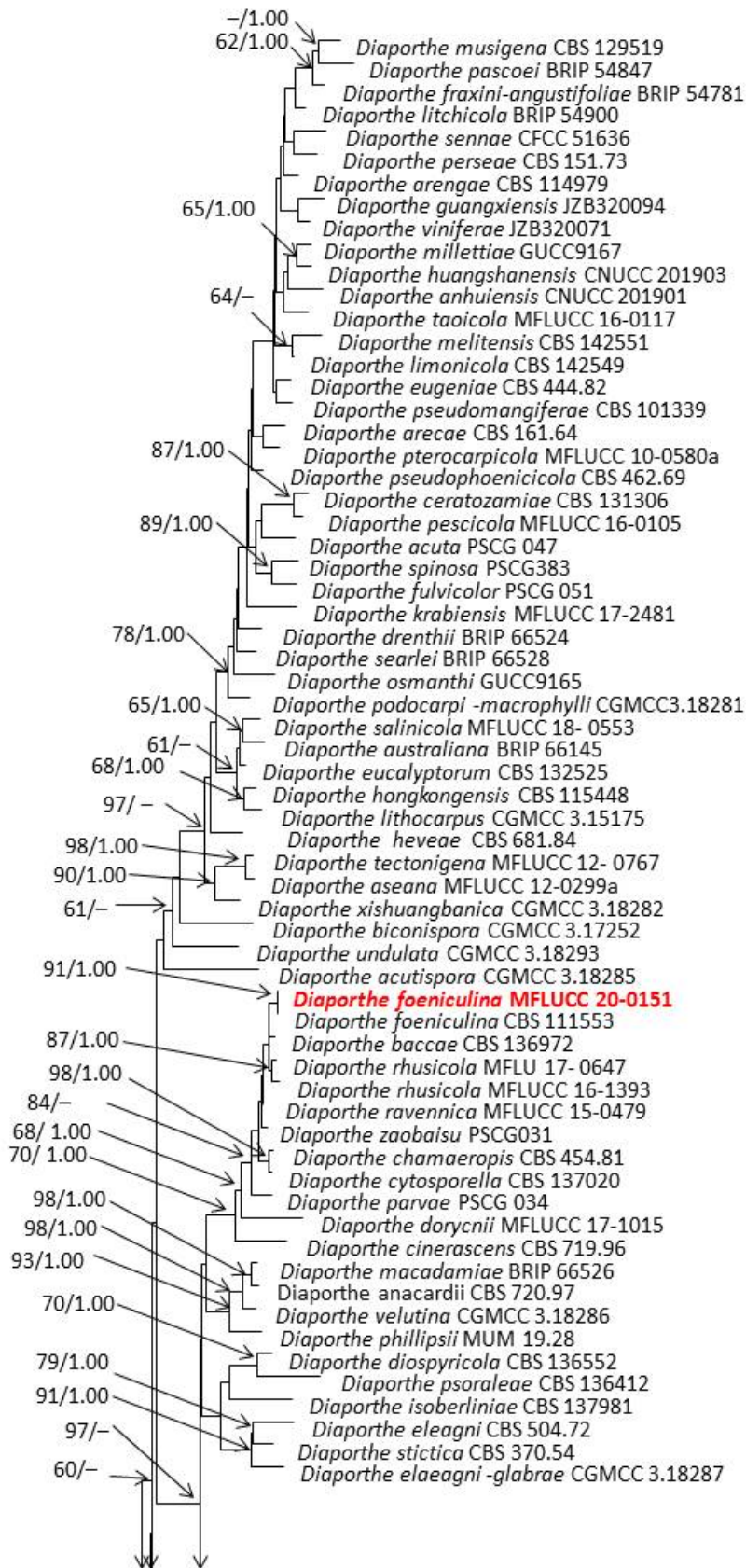
Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. sclerotioides</i>	CBS 296.67*	KC343193	KC344161	KC343677	KC343919	KC343435
<i>D. scobina</i>	CBS 251.38	KC343195	KC344163	KC343679	KC343921	KC343437
<i>D. searlei</i>	BRIP 66528*	MN708231	MN696540	–	–	–
<i>D. sennae</i>	CFCC 51636*	KY203724	KY228891	–	KY228885	KY228875
<i>D. sennicola</i>	CFCC 51634*	KY203722	KY228889	–	KY228883	KY228873
<i>D. serafiniae</i>	BRIP 55665a*	KJ197274	KJ197254	–	KJ197236	–
<i>D. shaanxiensis</i>	CFCC 53106*	MK432654	–	MK443001	MK578130	MK442976
<i>D. shennongjiaensis</i>	CNUCC 201905*	MN216229	MN227012	MN224560	MN224672	MN224551
<i>D. siamensis</i>	MFLUCC 10-0573a	JQ619879	JX275429	–	JX275393	–
<i>D. sojiae</i>	CBS 139282*	KJ590719	KJ610875	KJ659208	KJ590762	KJ612116
<i>D. spinosa</i>	PSCG383*	MK626849	MK691234	MK726156	MK654811	MK691129
<i>D. sterilis</i>	CBS 136969*	KJ160579	KJ160528	MF418350	KJ160611	KJ160548
<i>D. stewartii</i>	CBS 193.36	FJ889448	–	–	GQ250324	–
<i>D. stictica</i>	CBS 370.54	KC343212	KC344180	KC343696	KC343938	KC343454
<i>D. subclavata</i>	ICMP20663*	KJ490630	KJ490451	KJ490572	KJ490509	–
<i>D. subordinaria</i>	CBS 101711	KC343213	KC344181	KC343697	KC343939	KC343455
<i>D. taicola</i>	MFLUCC 16-0117*	KU557567	KU557591	–	KU557635	–
<i>D. tarchonantheri</i>	CPC 37479*	MT223794	MT223733	MT223759	–	–
<i>D. tecomae</i>	CBS 100547	KC343215	KC344183	KC343699	KC343941	KC343457
<i>D. tectonae</i>	MFLUCC 12-0777*	KU712430	KU743977	–	KU749359	KU749345
<i>D. tectonendophytica</i>	MFLUCC 13-0471*	KU712439	KU743986	–	KU749367	KU749354
<i>D. tectonigena</i>	MFLUCC 12-0767*	KU712429	KU743976	–	KU749371	KU749358
<i>D. terebinthifolii</i>	CBS 133180*	KC343216	KC344184	KC343700	KC343942	KC343458
<i>D. ternstroemia</i>	CGMCC 3.15183*	KC153098	–	–	KC153089	–
<i>D. thunbergii</i>	MFLUCC 10-0756a	JQ619893	JX275449	–	JX275409	JX197440
<i>D. toxicodendri</i>	FFPRI420987	LC275192	LC275224	LC275216	LC275216	LC275200
<i>D. tulliensis</i>	BRIP 62248a	KR936130	KR936132	–	KR936133	–
<i>D. ueckerae</i>	FAU 656	KJ590726	KJ610881	KJ659215	KJ590747	KJ612122
<i>D. undulata</i>	CGMCC 3.18293*	KX986798	KX999230	KX999269	KX999190	–
<i>D. unshiuensis</i>	CGMCC3.17569*	KJ490587	KJ490408	KJ490529	KJ490466	–
<i>D. vaccinii</i>	CBS 160.32*	AF317578	KC344196	KC343712	GQ250326	KC343470
<i>D. vacuae</i>	MUM 19.31*	MK792309	MK837931	MK871449	MK828080	MK883834
<i>D. vancouveriae</i>	CBS 137985*	KJ869137	KJ869247	–	–	–
<i>D. vawdreyi</i>	BRIP 57887a	KR936126	KR936128	–	KR936129	–
<i>D. velutina</i>	CGMCC 3.18286*	KX986790	KX999223	KX999261	KX999182	–
<i>D. vexans</i>	CBS 127.14	KC343229	KC344197	KC343713	KC343955	KC343471

Supplementary Table 1 Continued.

Species	Culture collection/ Herbarium number	GenBank accession numbers				
		ITS	TUB2	HIS	TEF1- α	CAL
<i>D. viniferae</i>	JZB320071*	MK341550	MK500112	–	MK500107	MK500119
<i>D. virgiliae</i>	CBS 138788*	KP247573	KP247582	–	–	–
<i>D. woodii</i>	CBS 558.93	KC343244	KC344212	KC343728	KC343970	KC343486
<i>D. woolworthii</i>	CBS 148.27	KC343245	KC344213	KC343729	KC343971	KC343487
<i>D. xishuangbanica</i>	CGMCC 3.18282*	KX986783	KX999216	KX999255	KX999175	–
<i>D. yunnanensis</i>	CGMCC 3.18289*	KX986796	KX999228	KX999267	KX999188	KX999290
<i>D. zaobaisu</i>	PSCG031*	MK626922	MK691245	MK726207	MK654855	–

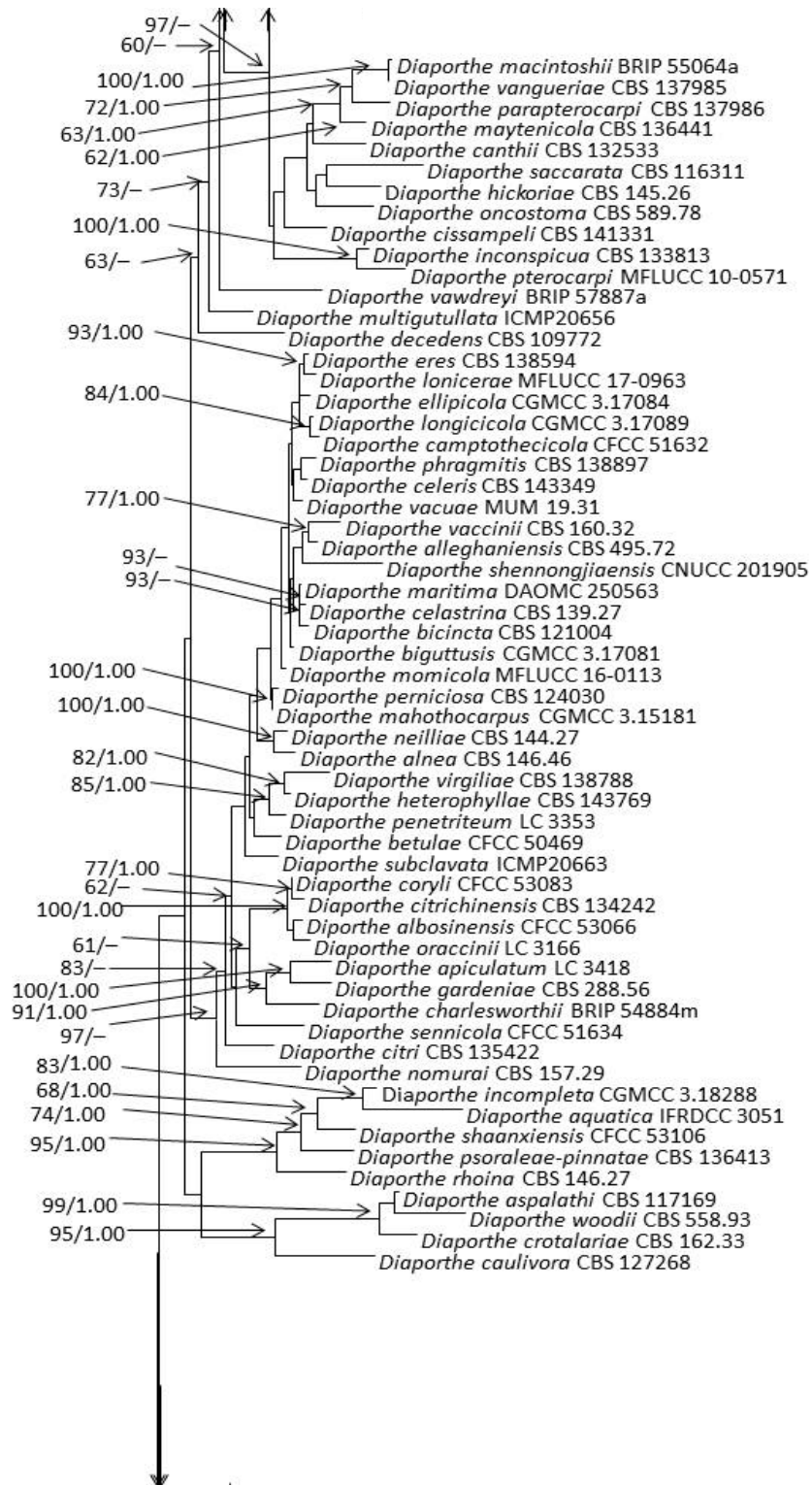
¹BRIP: Queensland Plant Pathology Herbarium, Brisbane, Australia; CBS: Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands; CFCC: China Forestry Culture Collection Center, Beijing, China; CGMCC: Chinese General Microbiological Culture Collection Center, Beijing, China; DAOM: Plant Research Institute, Department of Agriculture (Mycology), Ottawa, Canada; DAOMC: Canadian Collection of Fungal Cultures, Ottawa, Canada; FAU: Isolates in culture collection of Systematic Mycology and Microbiology Laboratory; FFPRI: Forestry and Forest Products Research Institute, Japan; ICMP: International Collection of Micro-organisms from Plants, Landcare Research, Private Bag 92170, Auckland, New Zealand; IFRDCC: International Fungal Research and Development Culture Collection; MFLU: Mae Fah Luang University herbarium, Thailand; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; LC: Working collection of Lei Cai, housed at Institute of Microbiology, Chinese Academy of Sciences, Beijing, China. Asterix (*) indicates ex-type strains.

²ITS: internal transcribed spacers and intervening 5.8S nrDNA; TUB2: partial β -tubulin gene; HIS: partial histone H3 gene; TEF1- α : partial elongation factor 1-alpha gene; CAL: partial calmodulin gene

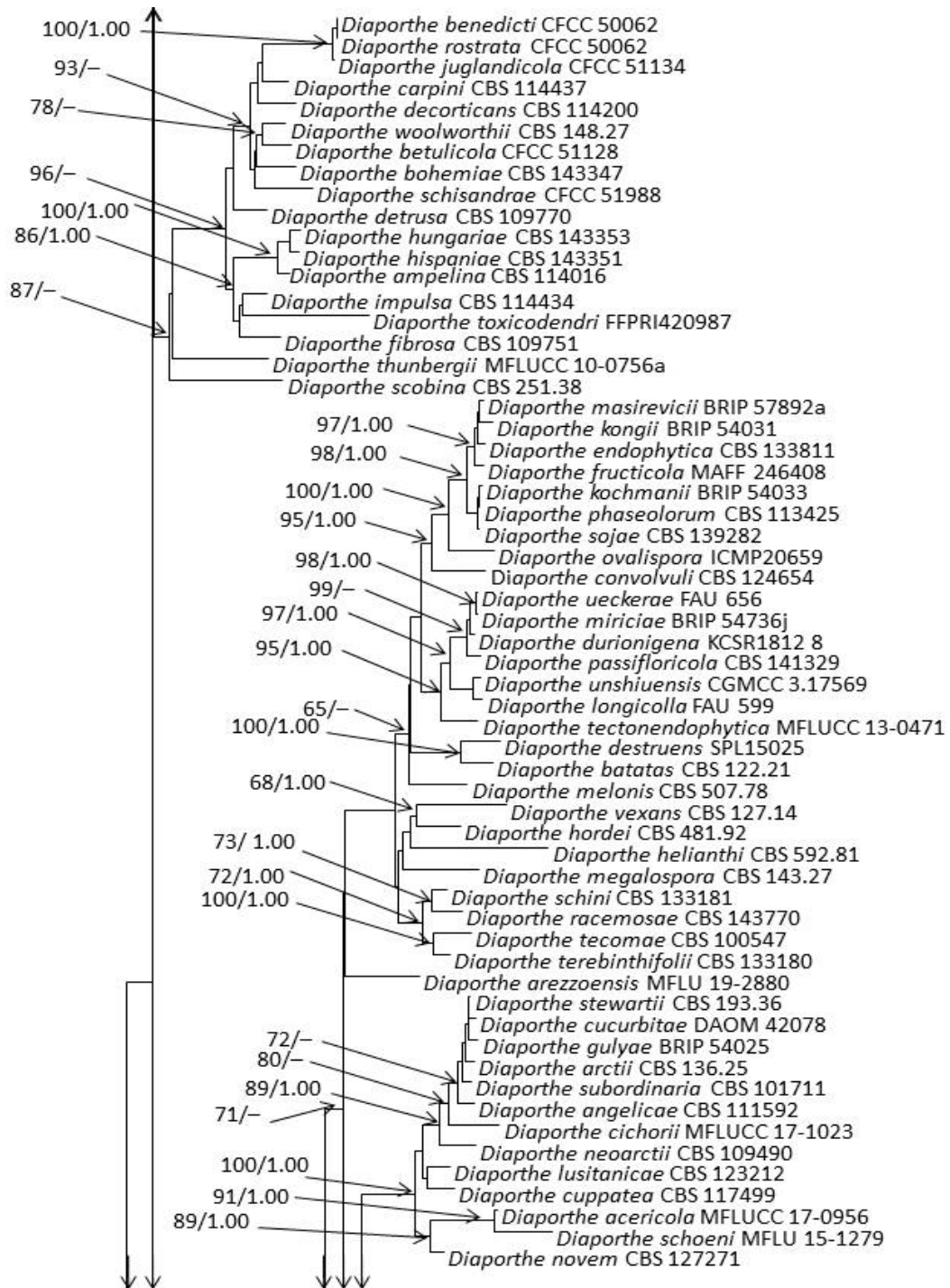


Supplementary Fig. 1 – Phylogram generated from the best scoring of the RAxML tree based on combined data set (ITS, CAL, HIS, TEF1- α and TUB2) of 249 taxa in *Diaporthe*. *Diaporthella corylina* (CBS 121124) and *Diaporthella cryptica* (CBS 140348) are selected as the outgroup taxon. The best RAxML tree with a final likelihood value of -58281.827211 is presented. RAxML analysis yielded 1390 distinct alignment patterns and 29.63% of undetermined characters or gaps.

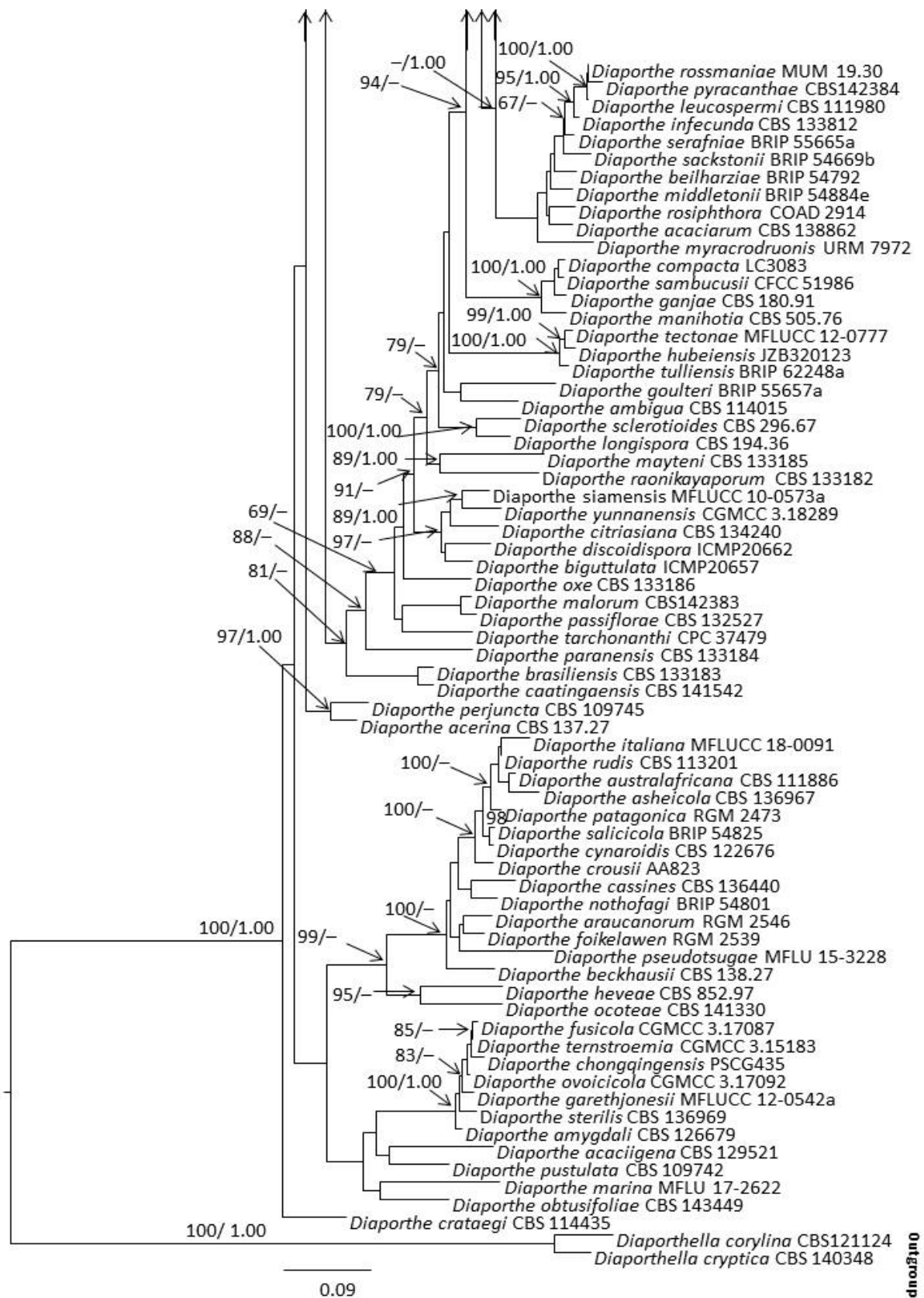
Estimated base frequencies were as follows: A = 0.217907, C = 0.312897, G = 0.242800, T = 0.226396, with substitution rates. The gamma distribution shape parameter $\alpha=0.165747$. Bayesian posterior probabilities (BYPP) from MCMC were evaluated with final average standard deviation of split frequencies AC = 1.148527, AG = 3.407871, AT = 1.179852, CG = 0.925771, CT = 4.859002, GT = 1.000000. Bootstrap support values for maximum likelihood (ML) equal to or greater than 60%; BYPP equal to or greater than 0.95 are given above or below the nodes as ML/BYPP. Type sequences are in black and newly generated sequences are indicated in red bold



Supplementary Fig. 1 – Continued.



Supplementary Fig. 1 – Continued.



Supplementary Fig. 1 – Continued.