



Diversity of Fungal Communities Associated with Grapevine Trunk Diseases in China

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Abstract

Grapevine trunk diseases (GTDs) are one kind of the most common and destructive diseases worldwide which challenge the sustainable development of the grape industry and cause serious economic loss. From 2020 to 2022, grapevine trunk disease samples were collected from eight provinces in China and associated fungi were identified based on phylogenetic analyses and morphological observations. A total of 199 isolates were obtained, representing 40 species belonging to 21 genera in 10 families. Twenty-one species are reported as the first records in China and 13 as the first records on grapevine worldwide. *Diaporthe*, Botryosphaeriaceae, *Cylindrocarpon*-like and *Fusarium*-like genera were the most frequently isolated taxa. *Bartalinia*, *Botryosphaeria* and *Dactylonectria* species were widely distributed in China. The study provides an insight into the diversity of fungal species on the diseased grapevine, among which some may play the role of common or potential pathogens, endophytes, and saprobes. Relevant results provide the basis for further research on the interactions among fungal communities and strategies for managing grapevine trunk diseases.

Keywords – diversity – grapevine trunk diseases – morphology – new records – phylogenetic analyses

Introduction

Grapevine (*Vitis* spp.) is one of the most widely planted and economically important fruit crops in the world since historic times and served as table fruits or processed into wine and raisin (Gramaje et al. 2018). China ranks third among grape-cultivation countries, with a cultivation area of 783 Kha in 2021 (OIV 2022) with 15 million metric tons of annual production. However, *Vitis* species are susceptible to many fungal diseases. Among these, the grapevine trunk diseases (GTDs) are one of the most destructive diseases in the world, which have drawn considerable attention in the last decades (Reis et al. 2019). They reduce vineyard longevity, productivity and quality, and the loss caused is estimated to be \$1.5 billion per year (Hofstetter et al. 2012, Dissanayake et al. 2015a). The grapevine trunk diseases include a group of diseases associated with diverse vascular

and wood decay pathogens, mainly Esca complex, *Eutypa dieback*, *Botryosphaeria dieback*, black foot and *Phomopsis (Diaporthe) dieback* (Mondello et al. 2018, Ye et al. 2021a). Up to 2018, 133 fungal species belonging to 34 genera have been reported to be associated with grapevine trunk diseases (Gramaje et al. 2018). These fungi mainly act as latent pathogens, which can develop symptoms several years later after the infection (Hrycan et al. 2020).

Esca disease complex is one of the oldest and most severe trunk diseases caused by *Phaeomoniella chlamydospora*, *Phaeoacremonium minimum* and few other *Phaeoacremonium* spp. in all grapevine-growing areas worldwide (Gramaje et al. 2018). Furthermore, some basidiomycete fungi like *Fomitiporia* species were also reported to cause Esca diseases (Cloete et al. 2015). In 2021, Ye and colleagues provided the first detailed report on the Esca complex in China, confirming that both *F. punicata* and *P. minimum* are the causal agents of the Esca complex on Chinese grapevines (Ye et al. 2021b). This study also provided the first host record for *F. punicata* on the grapevine worldwide.

Botryosphaeria dieback is another important grapevine trunk disease which has been reported in most grape-growing countries (Yan et al. 2013). The causal organisms include *Botryosphaeriaceae* species, including *Botryosphaeria* spp., *Diplodia* spp., *Dothiorella* spp., *Lasiodiplodia* spp., *Neofusicoccum* spp., *Neoscytalidium* spp., *Phaeobotryosphaeria* spp. and *Spencermartinsia* spp. (Gramaje et al. 2018). In China, Yan et al. (2013) first reported *Botryosphaeria dieback* in detail with its causative agents, *Botryosphaeria dothidea*, *Diplodia seriata*, *Lasiodiplodia theobromae* and *Neofusicoccum parvum*. In addition to that, *Neofusicoccum mangiferae* and *Lasiodiplodia citricola* were also reported as pathogens of grapevine dieback in subsequent studies (Dissanayake et al. 2015b, Wu et al. 2021).

The black foot disease mainly occurs in grapevine nurseries and young plantations and is commonly associated with species belonging to *Campylocarpon*, *Cylindrocladiella*, *Dactylonectria*, *Ilyonectria*, *Neonectria*, *Pleiocarpon* and *Thelonectria* (Gramaje et al. 2018). Ye et al. (2021a) first reported the black foot disease in China caused by five pathogens, *Cylindrocladiella lageniformis*, *Dactylonectria alcacerensis*, *D. macrodidyma*, *D. torresensis* and *Neonectria* species. Recent studies have identified other fungi, such as *Campylocarpon fasciculare*, as causative agents of black foot disease on young grapevines in China (Abeywickrama et al. 2021).

Furthermore, *Diaporthe dieback* is another disease categorised in the grapevine trunk disease complex worldwide. Currently, around 30 *Diaporthe* species have been identified as causal organisms of *Diaporthe dieback* in grape-producing countries, among them ten were reported in China (Dissanayake et al. 2015a, Guarnaccia et al. 2018, Manawasinghe et al. 2019).

Eutypa dieback has been one of the most damaging diseases in Australia, France and California since the 1970s. To date, no effective measures are available to control this disease (Mondello et al. 2018). Among the 24 *Diatrypaceae* species that cause this disease, *Eutypa lata* is the most virulent and common (Gramaje et al. 2018). *Eutypa dieback* was first reported in China in 2007 with *Eutypella vitis* as the pathogen, but this has not been proved by Koch's postulates (Ye et al. 2021c).

There are more than 900 fungal species recorded on *Vitis* spp. in the world (Jayawardena et al. 2018). In addition to pathogenic fungi, diverse endophytes and saprobes also exist on healthy and/or diseased grapevines. Endophytes may have advantageous or neutral effects without causing disease symptoms, and saprobes can be the primary sources of inoculants (Dissanayake et al. 2018, Jayawardena et al. 2018). Several studies identified fungal endophytic and saprotrophic communities of grapevine using both traditional and culture-independent techniques. These studies revealed the development of fungal communities in grapevine in the early stage, the composition of primary organisms present in grapevine in its natural environment, as well as the emergence of fungi associated with grapevine trunk disease in perennial wood (Dissanayake et al. 2018, Jayawardena et al. 2018, Kraus et al. 2019). Moreover, antagonistic fungi have been isolated and identified from grapevine wood. *Fusarium lateritium* and *Cladosporium herbarum* have shown consistent efficiency in reducing infection by *Eutypa lata* (Munkvold 1993). *Trichoderma* species,

such as *T. aureoviride* and *T. harzianum* isolated from the grapevine can be applied to the control of grapevine trunk disease due to their antagonistic activities (González & Tello 2011, Bruez et al. 2016). These studies demonstrate that pathogenic and antagonistic fungi co-exist in grapevine woods (Kraus et al. 2019).

Numerous fungal species associated with grapevine trunk diseases have been identified. However, controlling the disease is still challenging because of the complex nature of mixed infections caused by several pathogens and the influence of the environment and climate. Since grapevine trunk diseases are caused by a number of different fungal groups, it is necessary to identify species accurately to control the grapevine trunk diseases. Therefore, the objectives of this study were to investigate the occurrence of grapevine trunk diseases in main cultivation regions in China, and isolate and identify the fungi associated with grapevine trunk diseases based on morphology and phylogenetic analyses. This study would update the grapevine trunk disease pathogens in China and strengthen the basis for further studies on the occurrence regularity and effective control strategies for the diseases.

Materials & Methods

Field sampling and fungal isolation

In 2021, grapevine trunk diseases were investigated in 14 grapevine orchards in Beijing, Fujian, Hebei, Hubei, Ningxia, Shaanxi, Shanxi and Yunnan Provinces, China (Fig. 1). Samples of the diseased trunk and root tissues were collected in zip-lock bags and taken to the laboratory. Some samples were posted by collaborators in different provinces.



Figure 1 – Sample collection sites of grapevine trunk diseases in eight provinces in China. BJ: Beijing. FJ: Fujian. HB: Hubei. HE: Hebei. NX: Ningxia. SN: Shaanxi. SX: Shanxi. YN: Yunnan.

Diseased samples were observed using the Nikon SMZ1500 stereomicroscope (Nikon, Japan). Fungal spore masses or fruiting bodies were scraped using sterile needles to make slides or spore suspensions. Slides were observed using the Nikon E200 compound microscope (Nikon, Japan) to speculate the groups according to the morphology and photographed. Measurements of morphological characters were recorded. Diseased samples without any fruiting bodies were cut

into small pieces, surface sterilized in 75% alcohol for 30 s and rinsed in sterile water three times. After drying on the sterilized filter paper, diseased tissues were transferred to potato dextrose agar (PDA) plates and incubated for 3–5 days at 25 °C. Hyphal tips of colonies were transferred onto fresh PDA plates, and single spore isolation was performed if sporulated (Senanayake et al. 2020). Purified isolates were preserved in PDA tubes at 4 °C. All isolates obtained in this study are deposited in the culture collection of the Institute of Plant Protection, Beijing Academy of Agriculture and Forestry Sciences (JZB), China.

DNA extraction, PCR amplification and sequencing

Purified isolates were cultured on PDA plates for seven days at 25 °C. Fresh mycelia grown on PDA plates were collected in 1.5 mL centrifuge tubes, and genomic DNA was extracted using CTAB (cetyltrimethylammonium bromide) method (Udayanga et al. 2012). Polymerase chain reactions (PCR) were performed to amplify the internal transcribed spacer region (ITS), partial translation elongation factor 1- α (*tef1*), β -tubulin (*tub2*), RNA polymerase II second largest subunit (*rpb2*), 28S large subunit of nuclear ribosomal RNA (LSU), histone H3 (*his3*), actin (*act*), calmodulin (*cal*), glyceraldehyde 3-phosphate dehydrogenase (*gapdh*) and chitin synthase (*chs*) with the primers shown in Tables 1, 2. After confirming the quality of the sequences, ITS sequences were searched against the GenBank database using the BLASTn tool (<https://blast.ncbi.nlm.nih.gov>) to identify their closest relatives. The 50 μ L volume of the PCR mixture includes 44 μ L of 1 \times Taq PCR Mix (TransGen Biotech, Beijing, China), 2 μ L of each forward and reverse primer (Sangon Biotech, Shanghai, China), and 2 μ L of DNA template. The PCR conditions were as follows: initial denaturation for 3 min at 95 °C, followed by 34 cycles of denaturation for 30 s at 95 °C, annealing for 30 s, 1 min elongation at 72 °C, and final extension for 10 min at 72 °C. The annealing temperatures for different primers were noted in Table 1. The PCR products were examined using agarose gel electrophoresis after staining with ethyl bromide and sequenced at SinoGenoMax Co., Ltd. (Beijing, China).

Morphological characterization

Purified isolates were cultured on PDA plates at 25 °C and 12/12 h light/dark cycle. The morphological characteristics of each species were examined. Colony colors were recorded following Rayner (1970), and colony diameters were measured. Micromorphology was photographed using Axio Imager Z2 photographic microscope (Carl Zeiss Microscopy, Oberkochen, Germany), and measurements were taken using ZEN PRO 2012. Pictures were processed and combined into photo plates using Adobe Photoshop CS6 Extended (V13.1.2). Dry cultures of new geographic records or new host records are deposited in the herbarium of the Institute of Plant Protection, Beijing Academy of Agriculture and Forestry Sciences (JZBH), China. Description and photo plates were provided for the new recorded species.

Phylogenetic analysis

Chromatograms of newly produced sequences were checked with BioEdit 7.0.9.0 to confirm sequence quality. Reference sequences for phylogenetic analyses were downloaded from NCBI (National Center for Biotechnology Information), following the relevant literature (Supplementary Table 1). Each dataset was aligned with MAFFT v. 7 (<https://mafft.cbrc.jp/alignment/server/>) (Kato et al. 2019) and manually adjusted in BioEdit, where necessary.

Phylogenetic analyses were conducted by using maximum likelihood (ML) and Bayesian posterior probability analysis (BYPP). The ML analysis was implemented through the tool RAxML-HPC2 on XSEDE (v.8.2.12) (Stamatakis et al. 2008; Stamatakis 2014) in the online platform CIPRES Science Gateway (<https://www.phylo.org/portal2>) (Miller et al. 2010). The model of evolution GTR + I + G with 1000 non-parametric bootstrapping iterations was applied. In Bayesian Inference (BI) analysis, posterior probabilities (PPs) were determined by Markov Chain Monte Carlo sampling (BMCMC), and different evolutionary models were used in response to the gene regions. For the combined dataset, six simultaneous Markov chains were run for 8,000,000

generations and trees were sampled at every 1000th generation. The first 25% of the generated trees were discarded and the remaining 75% of trees were used to calculate posterior probabilities (PP) of the majority rule consensus tree (Ronquist & Huelsenbeck 2003).

Phylogenetic trees were visualized using FigTree v. 1.4.0 (Rambaut 2012) and edited in Microsoft Office PowerPoint 2016. Phylogenetic results and notes for these identified taxa were presented under the relevant family and genus.

Table 1 Primers and their annealing temperatures, with sequences and sources.

Locus	Primer	Sequence (5'–3')	Annealing temperature (°C)	References
ITS	ITS1	TCCGTAGGTGAACCTGCGG	52	White et al. (1990)
	ITS4	TCCTCCGCTTATTGATATGC		
<i>tefl</i>	EF1-728F	CATCGAGAAGTTCGAGAAGG	54	Carbone & Kohn (1999)
	EF1-986R	TACTTGAAGGAACCCCTTACC		
	EF1-688F	CGGTCACCTTGATCTACAAGTGC	54	Alves et al. (2008)
	EF1-1251R	CCTCGAACTCACCAGTACCG	54	O'Donnell et al. (1998)
	EF1	ATGGGTAAAGGARGACAAGAC		
	EF2	GGARGTACCAGTSATCATG		
		EF1LLErev	AACTTGCAGGCAATGTGG	55
<i>tub2</i>	Bt2a	GGTAACCAAATCGGTGCTGCTTTC	58	Glass & Donaldson (1995)
	Bt2b	ACCCTCAGTGTAGTGACCCTTGCC		
	T1	AACATGCGTGAGATTGTAAGT	58	O'Donnell & Cigelnik (1997)
<i>rpb2</i>	RPB2-5f	GAYGAYMGWGATCAYTTYGG	56	Reeb et al. (2004)
	RPB2-7cR	CCCATRGCTTGYYTRCCCAT		Liu et al. (1999)
LSU	LR5	TCCTGAGGGAAACTTCG	52	Vilgalys & Hester (1990)
	LROR	ACCCGCTGAACTTAAGC		Rehner & Samuels (1994)
	LR7	TACTACCACCAAGATCT	50	Vilgalys & Hester (1990)
<i>his</i>	CYLH3F	AGGTCCACTGGTGCCAAG	58	Crous et al. (2004)
	CYLH3R	AGCTGGATGTCCTTGGACTG		
	H3-1a	ACTAAGCAGACCGCCCGCAGG	58	Glass & Donaldson (1995)
	H3-1b	GCGGGCGAGCTGGATGTCCTT		
<i>act</i>	ACT-512F	ATGTGCAAGGCCGTTTCGC	56	Carbone & Kohn (1999)
	ACT-783R	TACGAGTCCTTCTGGCCCAT		
<i>cal</i>	CAL-228F	GAGTTCAAGGAGGCCTTCTCCC	55	Carbone & Kohn (1999)
	CAL-737R	CATCTTTCTGGCCATCATGG	58	Weir et al. (2012)
	CL1C	GAATTCAAGGAGGCCTTCTC		
<i>gapdh</i>	CL2C	CTTCTGCATCATGAGCTGGAC		
	GDF	GCCGTCAACGACCCCTTCATTGA	54	Templeton et al. (1992)
	GDR	GGGTGGAGTCGTAAGTGGAGCATGT		
<i>gpd1</i>	gpd1	CAACGGCTTCGGTCGCATTG	58	Berbee et al. (1999)
	gpd2	GCCAAGCAGTTGGTTGTGC		
<i>chs-1</i>	CHS-79F	TGGGGCAAGGATGCTTGGGAAGAAG	58	Carbone & Kohn (1999)
	CHS-345R	TGGAAGAACCATCTGTGAGAGTTG		

The annealing temperature of EF1-728F/EF 2 is 56 °C.

Results

Disease symptoms of grapevine trunk diseases

Diseased grapevines exhibited several symptoms;

1) Weak tree vigor: low growth, stunted sprout, small leaves and short internodes. Leaves discolored or appear tiger-striped symptoms. Berries poorly developed or uneven ripening (Fig. 2).

2) Dieback: usually evident in early spring, the tree cannot sprout normally, and branches are dried-up, even the whole plant wilting or dead. The trunk shows discolored vascular tissues in a cross-section, sometimes appears canker lesions or black fruit bodies, and/or roots poorly developed (Fig. 2).

3) Fruits shrivelled or dry rotted, stem brown and wilting, sometimes appears black fruit bodies on the surface (Fig. 2).

The investigation results showed that plant decline, dieback, fruit shirking and fall-off are the major symptoms of grapevine trunk diseases in China, which lead to the reduction of productivity and life span of grapes. Grapevine trunk diseases were observed in nearly 20% of orchards, and the proportion of diseased plants was about 10% in the investigated fields, up to 100% in severe cases. Main grapevine trunk diseases including black foot, *Botryosphaeria* dieback and *Diaporthe* dieback were observed in this investigation.



Figure 2 – Symptoms of grapevine trunk diseases. a Stunted growth of plants. b Dried-up and discolored leaves. c Dead grapevine. d Tiger striped leaves. e Shriveled berries. f Uneven ripening of berries. g Withered shoot with fruiting bodies. h Necrotic root. i–j Internal symptoms of the diseased trunk. k Rotted berry with fruiting bodies. l Conidiomata on the necrotic trunk.

Isolation results of grapevine trunk disease samples

A total of 199 purified fungal isolates were obtained from 68 samples collected from eight provinces. Further, these isolates were identified into 40 species across 21 genera and ten families. Among them, 21 species were reported as new geographical records in China, and 13 were new host records (Table 3). *Diaporthe* was the most dominant (19.6%), followed by *Dactylonectria* (14.1%), *Fusarium* (10.6%), and *Botryosphaeria* (8.5%). Most *Botryosphaeriaceae*, *Pestalotiopsis*-like and *Colletotrichum* species were isolated from the trunk, while most *Dactylonectria* species were isolated from the root. *Diaporthe* and *Fusarium* were isolated from both trunk and root. *Dactylonectria*, *Botryosphaeria* and *Bartalinia* were widely distributed in China. Sequences generated in this study were deposited in the GenBank (Supplementary Table 2).

Table 2 Selected genes and primers for PCR amplification of each genus.

Genera	ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>Botryosphaeria</i> (Yan et al. 2013, Zhang et al. 2021)	ITS1/ ITS4	EF1-728F/ EF1-986R	Bt2a/ Bt2b							
<i>Lasiodiplodia</i> (Yan et al. 2013, Zhang et al. 2021)	ITS1/ ITS4	EF1-728F/ EF1-986R	Bt2a/ Bt2b							
<i>Neofusicoccum</i> (Yan et al. 2013, Zhang et al. 2021)	ITS1/ ITS4	EF1-728F/ EF1-986R	Bt2a/ Bt2b							
<i>Diplodia</i> (Yan et al. 2013, Zhang et al. 2021)	ITS1/ ITS4	EF1-728F/ EF1-986R	Bt2a/ Bt2b							
<i>Phaeobotryon</i> (Pan et al. 2019)	ITS1/ ITS4	EF1-688F/ EF1-1251R	Bt2a/ Bt2b		LR7/ LROR					
<i>Dactylonectria</i> (Ye et al. 2021a)	ITS1/ ITS4	EF1-688F/ EF1-1251R	T1/ Bt2b			CYLH3F/ CYLH3R				
<i>Ilyonectria</i> (Lu et al. 2020)	ITS1/ ITS4	EF1-688F/ EF1-1251R	T1/ Bt2b			CYLH3F/ CYLH3R				
<i>Cylindrocladiella</i> (Ye et al. 2021a)	ITS1/ ITS4	EF1-688F/ EF1-1251R	T1/ Bt2b							
<i>Fusarium</i> (Sandoval-Denis et al. 2018, Crous et al. 2021)	ITS1/ ITS4	EF1/ EF2		rpb2-5F2/ rpb2-7CR						
<i>Neocosmospora</i> (Sandoval-Denis et al. 2018, Crous et al. 2021)	ITS1/ ITS4	EF1/ EF2		rpb2-5F2/ rpb2-7CR						
<i>Bisifusarium</i> (Schroers et al. 2009, Crous et al. 2021)	ITS1/ ITS4	EF1/ EF2		rpb2-5F2/ rpb2-7CR						
<i>Diaporthe</i> (Manawasinghe et al. 2019, Norphanphoun et al. 2022)	ITS1/ ITS4	EF1-728F/ EF1-986R	Bt2a/ Bt2b					CAL-228F/ CAL-737R		
<i>Phaeoacremonium</i> (Ye et al. 2021b)			T1/ Bt2b				ACT-512F/ ACT-783R			
<i>Coniella</i> (Chethana et al. 2017)	ITS1/ ITS4	EF1-728F/ EF1-986R			LR5/ LROR	H3-1a/ H3-1b				
<i>Pestalotiopsis</i> (Li et al. 2021)	ITS1/ ITS4	EF1-728F/ EF1-986R	Bt2a/ Bt2b							
<i>Neopestalotiopsis</i> (Li et al. 2021)	ITS1/ ITS4	EF1-728F/ EF1-986R	Bt2a/ Bt2b							
<i>Bartalinia</i> (Tibpromma et al. 2020)	ITS1/ ITS4				LR5/ LROR					

Table 2 Continued.

Genera	ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>Colletotrichum</i> (Jayawardena et al. 2021)	ITS1/ ITS4		T1/ Bt2b				ACT-512F/ ACT-783R	CL1C/ CL2C	GDF/ GDR	CHS-79F/ CHS-345R
<i>Alternaria</i> (Woudenberg et al. 2013)	ITS1/ ITS4	EF1-728F/ EF1-986R		rpb2-5F2/ rpb2-7CR					gpd1/ gpd2	
<i>Trichoderma</i> (Zheng et al. 2021, Cai et al. 2022)	ITS1/ ITS4	EF1-728F/ EF1LLErev		rpb2-5F2/ rpb2-7CR						
<i>Cladosporium</i> (Bensch et al. 2012)	ITS1/ ITS4	EF1-728F/ EF1-986R					ACT-512F/ ACT-783R			

Table 3 Details of fungal taxa and sources.

No.	Family (count)	Genus (count)	Species	Count	Isolation source	Records on grapevine in China	Records on grapevine in other countries around the world
1	Botryosphaeriaceae (37)	<i>Botryosphaeria</i> (17)	<i>B. dothidea</i>	17	HB (T), YN (T, R), BJ (T), HE (T, TB)	Yan et al. (2012)	More than 20 countries
2		<i>Lasiodiplodia</i> (9)	<i>L. citricola</i>	4	HE (TB)	Wu et al. (2021)	Italy (Carlucci et al. 2015), Australia (Burgess et al. 2019)
3			<i>L. pseudotheobromae</i>	3	YN (T, R)	Dissanayake et al. (2015c)	Brazil (Correia et al. 2016), Tunisia (Rezgui et al. 2018), Australia (Burgess et al. 2019)
4			<i>L. theobromae</i>	2	HB (T)	Yan et al. (2013)	More than 15 countries (Farr & Rossman 2023)
5		<i>Diplodia</i> (3)	<i>D. seriata</i>	3	HE (T)	Yan et al. (2013)	More than 10 countries (Farr & Rossman 2023)
6		<i>Neofusicoccum</i> (2)	<i>N. parvum</i>	2	YN (T, R)	Yan et al. (2013)	More than 15 countries (Farr & Rossman 2023)
7		<i>Phaeobotryon</i> (6)	<i>P. rhois</i>	6	NX (T, R)	First report	First report
8	Nectriaceae (72)	<i>Dactylonectria</i> (28)	<i>D. novozelandica</i>	12	YN (R), HE (TB, R), BJ (R)	Tan et al. (2022)	USA (Lawrence et al. 2019), New Zealand (Lawrence et al. 2019), South Africa (Lombard et al. 2014), Spain (Berlanas et al. 2020)
9			<i>D. alcacerensis</i>	10	SX (R), BJ (TB, R), HE (R)	Ye et al. (2021a)	USA (Lawrence et al. 2019), Portugal (Carlucci et al. 2017),

Table 3 Continued.

No.	Family (count)	Genus (count)	Species	Count	Isolation source	Records on grapevine in China	Records on grapevine in other countries around the world	
							South Africa (Langenhoven et al. 2018), Spain (Berlanas et al. 2020), Turkey (Güngör-Savaş et al. 2020)	
10	Diaporthaceae (39)		<i>D. torresensis</i>	3	HE (R), NX (R)	Ye et al. (2021a)	More than 5 countries (Farr & Rossman 2023)	
11			<i>D. macrodidyma</i>	3	BJ (TB), YN (R)	Ye et al. (2021a)	USA (Lawrence et al. 2019), France (Pintos et al. 2018), Portugal (Carlucci et al. 2017), South Africa (Lombard et al. 2014), Spain (Berlanas et al. 2020)	
12		<i>Ilyonectria</i> (7)	<i>I. liriiodendri</i>	7	SX (R), NX (T), BJ (TB)	First report	More than 10 countries (Farr & Rossman 2023)	
13		<i>Cylindrocladiella</i> (3)	<i>C. viticola</i>	3	YN (R)	First report	South Africa (van Coller et al. 2005)	
14		<i>Fusarium</i> (21)	<i>F. oxysporum</i>	9	HE (R, T), YN (R), FJ (R)	Jayawardena et al. (2018)	Australia, Brazil, South Africa, Spain (Jayawardena et al. 2018), Italy (Lorenzini & Zapparoli, 2015), Egypt (Ziedan et al. 2011)	
15				<i>F. brachygibbosum</i>	4	BJ (R)	First report	First report
16				<i>F. acuminatum</i>	4	NX (T); SX (T)	First report	Spain (Jayawardena et al. 2018)
17				<i>F. hainanense</i>	2	YN (T)	First report	First report
18				<i>F. lacertarum</i>	1	SN (R)	First report	First report
19				<i>F. compactum</i>	1	YN (T)	First report	First report
20				<i>Neocosmospora</i> (11)	<i>N. falciformis</i>	7	SN (R); NX (T); BJ (R)	First report
21		<i>N. solani</i>	4			HE (R), FJ (R)	First report	Brazil, India (Jayawardena et al. 2018)
22		<i>Bisifusarium</i> (2)	<i>B. delphinoides</i>	2	HE (R)	First report	India (on <i>Plasmopara viticola</i>) (Ghule et al. 2018)	
23			<i>Diaporthe</i> (39)	<i>D. eres</i>	37	BJ (T, R), HE (T, TB, R)	Manawasinghe et al. (2019)	More than 10 countries (Farr & Rossman 2023)
24				<i>D. unshiuensis</i>	2	FJ (T)	Manawasinghe et al. (2019)	

Table 3 Continued.

No.	Family (count)	Genus (count)	Species	Count	Isolation source	Records on grapevine in China	Records on grapevine in other countries around the world
25	Togniniaceae (2)	<i>Phaeoacremonium</i> (2)	<i>P. iranianum</i>	2	HE (T)	First report	More than 5 countries (Farr & Rossman 2023)
26	Schizoparmaceae (7)	<i>Coniella</i> (7)	<i>C. vitis</i>	7	BJ (T), HE (T, R)	Chethana et al. (2017)	
27	Sporocadaceae (16)	<i>Pestalotiopsis</i> (6)	<i>P. kenyana</i>	3	FJ (T)	First report	First report
28			<i>P. rhodomyrtus</i>	2	FJ (T)	First report	First report
29			<i>P. adusta</i>	1	FJ (R)	First report	First report
30		<i>Neopestalotiopsis</i> (2)	<i>N. rosae</i>	2	YN (T, R)	First report	USA (Cosseboom & Hu 2021)
31		<i>Bartalinia</i> (8)	<i>B. kevinhydei</i>	8	YN (T), NX (T), HE (T), BJ (T)	First report	First report
32	Glomerellaceae (10)	<i>Colletotrichum</i> (10)	<i>C. viniferum</i>	6	FJ (S), BJ (T)	Yan et al. (2015)	Brazil (Echeverrigaray et al. 2020), Japan (Yokosawa et al. 2020), Korea (Oo & Oh 2017)
33			<i>C. nymphaeae</i>	3	FJ (S, T)	Liu et al. (2016)	Brazil (Echeverrigaray et al. 2020)
34			<i>C. kahawae</i>	1	YN (T)	First report	Brazil (Echeverrigaray et al. 2020)
35	Pleosporaceae (8)	<i>Alternaria</i> (8)	<i>A. alternata</i>	6	SX (T), HE (T, TB)	Jayawardena et al. (2018)	More than 10 countries (Farr & Rossman 2023)
36			<i>A. longipes</i>	2	FJ (T)	First report	First report
37	Hypocreaceae (6)	<i>Trichoderma</i> (6)	<i>T. asperellum</i>	3	YN (T, R)	First report	Italy (Lorenzini et al. 2016)
38			<i>T. guizhouense</i>	2	BJ (R)	First report	First report
39			<i>T. virens</i>	1	HE (R)	Bruetz et al. (2016)	First report
40	Cladosporiaceae (2)	<i>Cladosporium</i> (2)	<i>C. tenuissimum</i>	2	FJ (T)	Jayawardena et al. (2018)	
Total	10	21	40	199		21 first records	13 first records

T-trunk; R-root; TB-trunk base.

Phylogenetic analysis and morphological characterization

Botryosphaeriaceae Theiss. & Syd [as ‘Botryosphaeriaceae’], Anns mycol. 16(1/2): 16 (1918)

The Botryosphaeriaceae comprises a wide range of species as pathogens, endophytes or saprobes mainly on woody hosts. They are also known as opportunistic pathogens with changing environmental conditions and weak tree vigour (Phillips et al. 2013, Chethana et al. 2016).

Botryosphaeriaceae comprises 22 genera based on morphology and multi-gene phylogeny (Wijayawardene et al. 2021, Zhang et al. 2021), and eight genera have been reported to associate with grapevine trunk diseases (Gramaje et al. 2018).

In this study, thirty-seven isolates of Botryosphaeriaceae were obtained, belonging to *Botryosphaeria*, *Diplodia*, *Lasiodiplodia*, *Neofusicoccum* and *Phaeobotryon*, representing seven species. For taxonomic treatments of Botryosphaeriaceae, we follow Zhang et al. (2021).

Botryosphaeria Ces. & De Not., Comm. Soc. crittog. Ital. 1 (fasc. 4): 211 (1863)

Botryosphaeria dothidea (Moug.: Fr.) Ces. & De Not., Comm. Soc. crittog. Ital. 1 (fasc. 4): 212 (1863)

Index Fungorum number: IF183247; Facesoffungi number: FoF 03512

Description – see Phillips et al. (2013)

Material examined – China, Hubei Province, Wuhan City, on the trunk of *Vitis vinifera*, 28 April 2021, Linna Wu and Xinghong Li, living cultures JZB310204, JZB310205; *ibid.*, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB310206, JZB310211–JZB310214; *ibid.*, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB310207; *ibid.*, Beijing city, on the trunk of *Vitis vinifera*, 25 August 2021, Linna Wu and Xinghong Li, living cultures JZB310208–JZB310210; *ibid.*, 11 September 2021, Linna Wu and Xinghong Li, living cultures JZB310215, JZB310216; *ibid.*, Hebei Province, Qinhuangdao City, Changli County, on the trunk of *Vitis vinifera*, 18 October 2021, Linna Wu and Xinghong Li, living cultures JZB310217, JZB310218; *ibid.*, on the trunk-base of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB310219, JZB310220.

Notes – In the multi-locus phylogenetic analyses, 17 isolates clustered with *B. dothidea* with 69% ML bootstrap value and 0.95 BYPP (Fig. 3). *Botryosphaeria dothidea* is an opportunistic pathogen with a wide host range (Marsberg et al. 2017). Yan et al. (2013) have mentioned that *B. dothidea* was distributed in 18 provinces from north to south throughout China and took up 65% of all isolates among *Botryosphaeria* dieback pathogens in China (Yan et al. 2013).

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

Diplodia seriata De Not., Mém. R. Accad. Sci. Torino, Ser. 2 7: 26 (1845)

Index Fungorum number: IF180468; Facesoffungi number: FoF 03596

Description – see Phillips et al. (2013)

Material examined – China, Hebei Province, Zhangjiakou City, Huailai County, on the trunk of *Vitis vinifera*, 22 August 2020, Linna Wu and Xinghong Li, living cultures JZB3140015–JZB3140017.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *D. seriata* with 100% bootstrap value and 1.0 BYPP (Fig. 3). The species were shown to be weakly pathogenic to grapevines in California (Úrbez-Torres & Gubler 2009). In China, *D. seriata* was first reported by Yan et al. (2011b) and its pathogenicity was also shown moderate virulence on most grapevine cultivars in China (Yan et al. 2013).

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

Lasiodiplodia citricola Abdollahz., Javadi & A.J.L. Phillips, Persoonia 25: 4 (2010)

Index Fungorum number: IF516777; Facesoffungi number: FoF 09503

Description – see Phillips et al. (2013)

Material examined – China, Hebei Province, Qinhuangdao City, Changli County, on the trunk base of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB3130023–JZB3130026.

Notes – In the multi-locus phylogenetic analysis, four isolates clustered with *L. citricola* with 95% ML bootstrap value and 1.0 BYPP (Fig. 3). *Lasiodiplodia citricola* was first reported on the grapevine in Italy in 2015 and showed aggressive pathogenicity (Carlucci et al. 2015). In 2020, it was first reported in China (Wu et al. 2021), causing severe symptoms or death of grapevine.

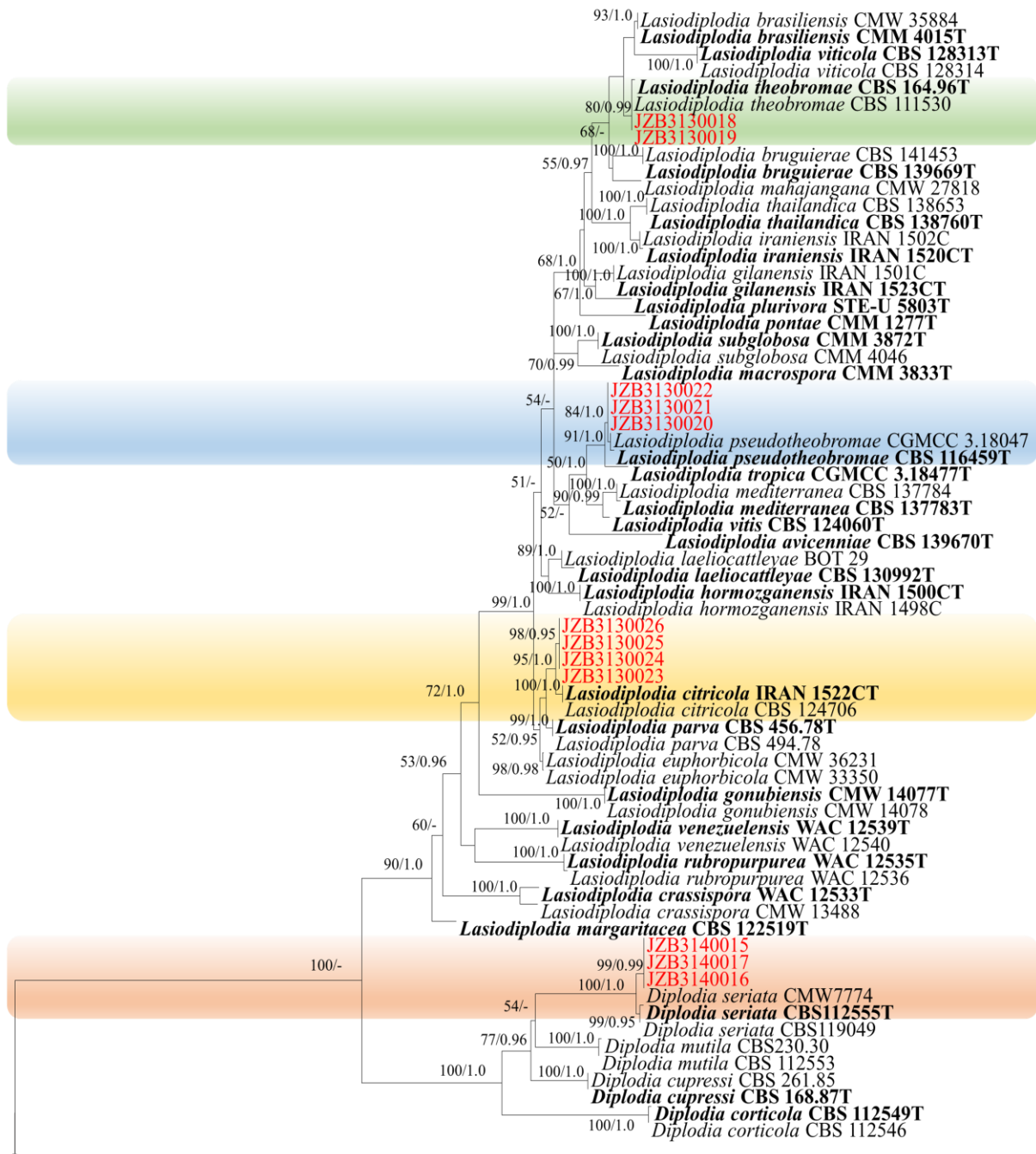


Figure 3 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tef1* and *tub2* sequence data of *Botryosphaeria*, *Lasiodiplodia*, *Neofusicoccum* and *Diplodia* species. *Phyllosticta citricarpa* (CBS 127454) was used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of -8506.960370 was presented. The matrix had 695 distinct alignment patterns, with 19.31% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.209952, C = 0.307342, G = 0.257379, T = 0.225327; substitution rates AC = 0.761022, AG = 2.876149, AT = 1.271062, CG = 1.067796, CT = 4.612694, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.659641$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (PP) are shown near the nodes. The scale bar indicates 0.08

changes per site. Isolates from the current study are in red and type specimens are in bold.

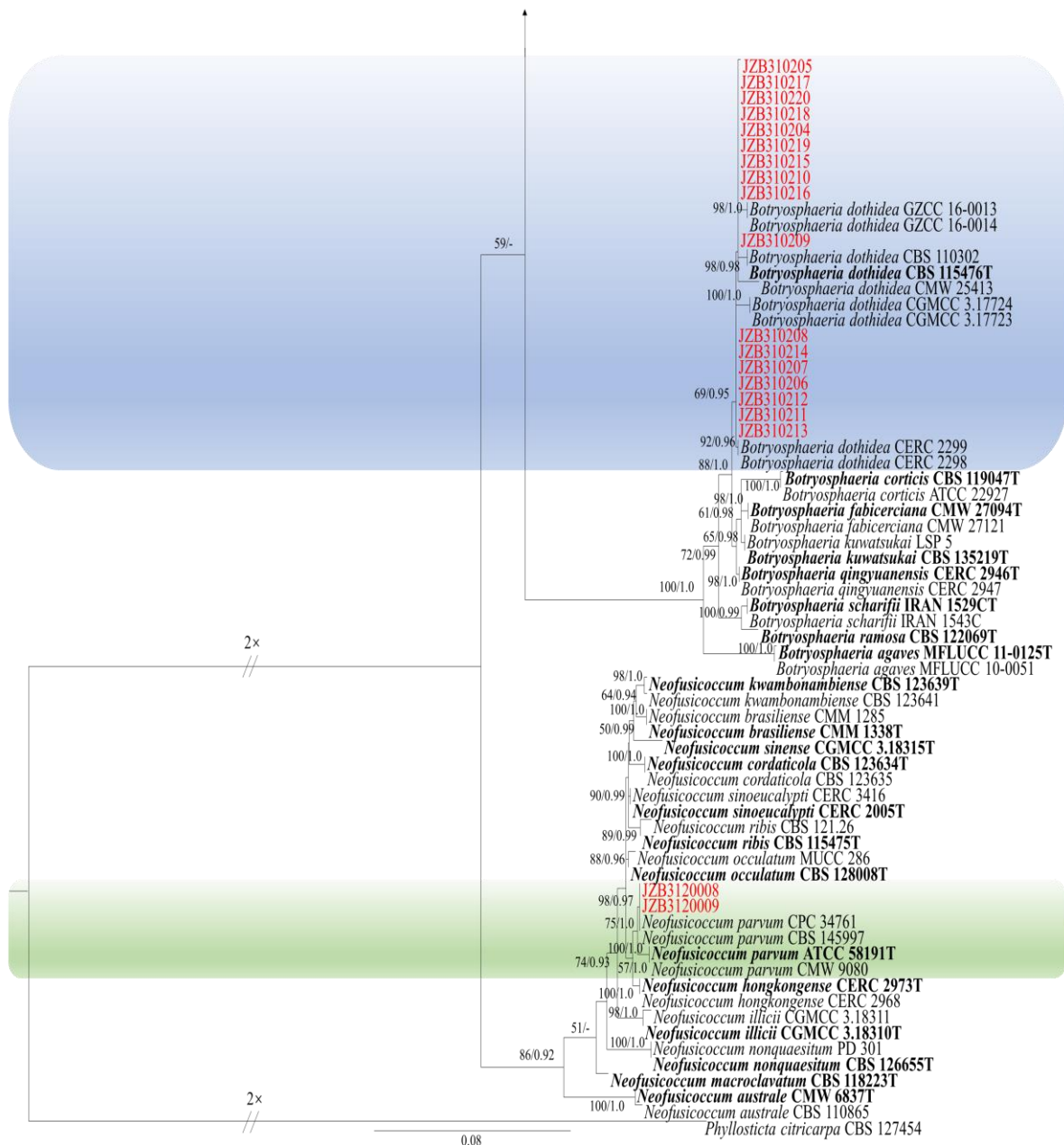


Figure 3 – Continued.

Lasiodiplodia pseudotheobromae A.J.L. Phillips, A. Alves & Crous, Fungal Diversity 28: 8 (2008)

Index Fungorum number: IF510941; Facesoffungi number: FoF 00166

Description – see Phillips et al. (2013)

Material examined – China, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB3130020; *ibid.*, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB3130021, JZB3130022.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *L. pseudotheobromae* with 84% ML bootstrap value and 1.0 BYPP (Fig. 3). *Lasiodiplodia pseudotheobromae* was first reported to cause the grapevine decline in Brazil (Correia et al. 2013) and was reported to cause pedicel and peduncle discolouration of grapes in China (Dissanayake et al. 2015c).

Lasiodiplodia theobromae (Pat.) Griffon & Maubl., Bull. Soc. mycol. Fr. 25: 57 (1909)

Index Fungorum number: IF188476; Facesoffungi number: FoF 00167

Description – see Phillips et al. (2013)

Material examined – China, Hubei Province, Wuhan City, on the trunk of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB3130018, JZB3130019.

Notes – In the multi-locus phylogenetic analyses, two isolates clustered with *L. theobromae* with 80% ML bootstrap value and 0.99 BYPP (Fig. 3). *Lasiodiplodia theobromae* is one of the most aggressive causal agents of Botryosphaeria dieback, especially in regions with hot climates (Úrbez-Torres & Gubler 2009, Paolinelli-Alfonso et al. 2016). In 2011, this species was first reported to cause severe grapevine decline in China and was shown to be the most virulent among Botryosphaeriaceae species on grapevines (Yan et al. 2011a, 2013).

Neofusicoccum Crous, Slippers & A.J.L. Phillips, Stud. Mycol. 55: 247 (2006)

Neofusicoccum parvum (Pennycook & Samuels) Crous, Slippers & A.J.L. Phillips, in Crous, Slippers, Wingfield, Rheeder, Marasas, Phillips, Alves, Burgess, Barber & Groenewald, Stud. Mycol. 55: 248 (2006)

Index Fungorum number: IF500879; Facesoffungi number: FoF 02411

Description – see Phillips et al. (2013)

Material examined – China, Yunnan Province, Binchuan County, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB3120008; *ibid.*, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB3120009.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *N. parvum* with 75% bootstrap value and 1.0 BYPP (Fig. 3). *Neofusicoccum parvum* is one of the most aggressive Botryosphaeria dieback pathogens worldwide. This species can cause internal cankers in the permanent woody structure of the vine (Úrbez-Torres & Gubler 2009, Massonnet et al. 2017). In China, *N. parvum* was first reported as a grapevine Botryosphaeria dieback pathogen in 2013 while it showed weak pathogenicity on grapevines (Yan et al. 2013).

Phaeobotryon Theiss. & Syd., Annls mycol. 13(5/6): 664 (1915)

Phaeobotryon rhois C.M. Tian, X.L. Fan & K.D. Hyde, in Fan, Hyde, Liu, Liang & Tian, Phytotaxa 205(2): 95 (2015)

Index Fungorum number: IF 811599; Facesoffungi number: FoF 00596

Asexual morph: *Conidiomata* stromatic, globose. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, formed from the cells lining the inner walls of the locules. *Conidia* 19–28 × 11–15 µm, ($\bar{x} \pm SD = 23.5 \pm 1.8 \times 12.5 \pm 1.0$ µm, n = 50), ellipsoid or ovoid, verruculose, initially hyaline, aseptate, and become brown with the time, 1-septate when mature (Fig. 4). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were initially white with fluffy aerial mycelium, and later produced dark green to black pigments (Fig. 4). Colonies reached 8.0 cm in diameter after 2 days at 25 °C.

Material examined – China, Ningxia Province, Yinchuan City, on the trunk of *Vitis vinifera*, 15 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3600001–JZBH3600003), living cultures JZB3600001–JZB3600003; *ibid.*, on the root of *Vitis vinifera*, 15 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3600004–JZBH3600006), living cultures JZB3600004–JZB3600006.

Notes – In the multi-locus phylogenetic analysis, six isolates clustered with *P. rhois* with 99% bootstrap value and 1.0 BYPP (Fig. 5). This species was reported to cause dieback and canker disease on *Rhus typhina* in China (Fan et al. 2015), as well as *Dioscorea nipponica*, *Platycladus orientalis* and *Rhamnus dahuricus* in China (Pan et al. 2019). This is the first report of *P. rhois* associated with grapevine trunk diseases in China.

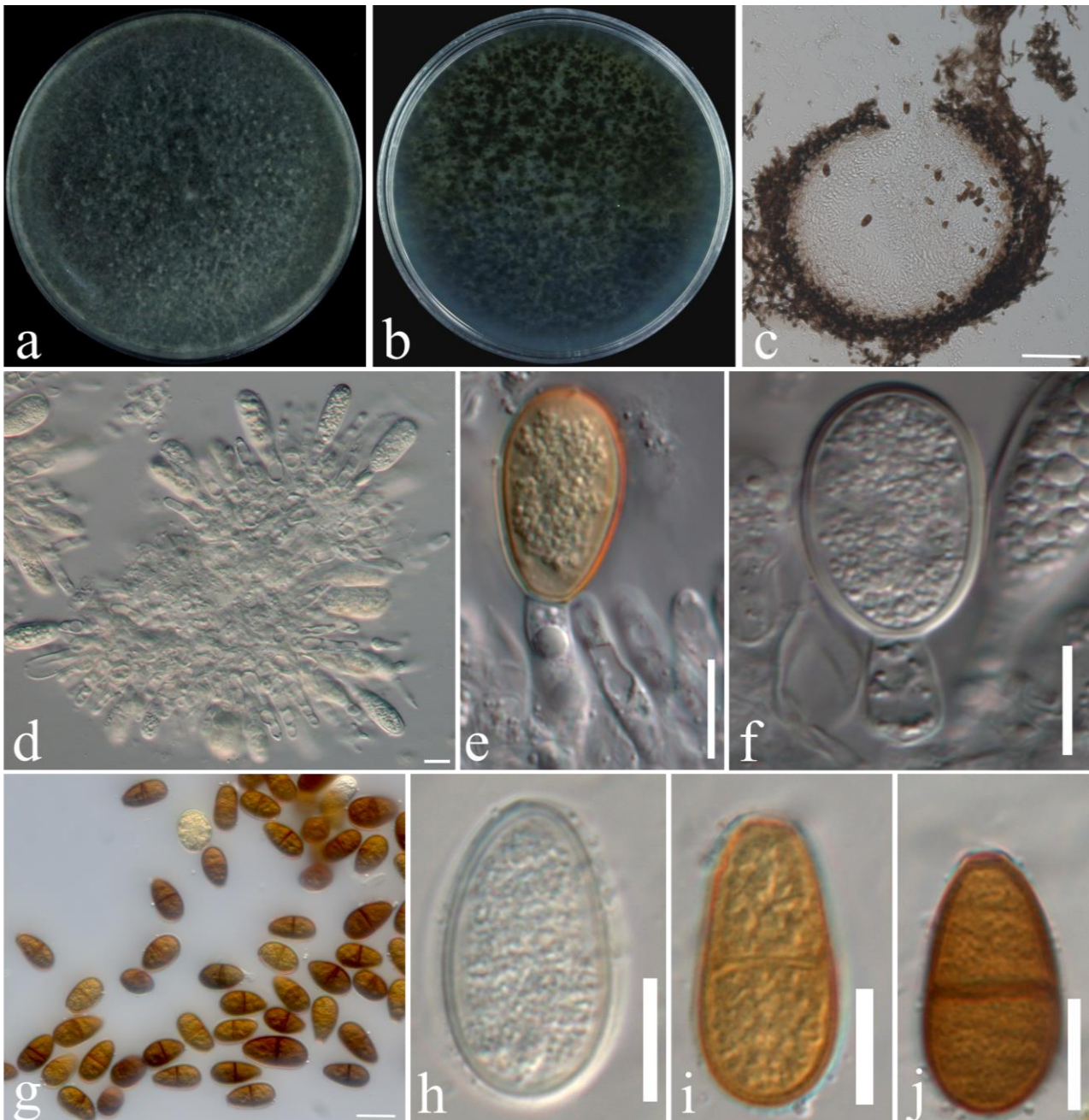


Figure 4 – Morphological characterization of *Phaeobotryon rhois* (JZB3600005). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c A cross section of a conidioma. d–f Conidiophores and conidiogenous cells. g–j Mature and immature conidia. Scale bars: c = 100 μ m, d–f, h–j = 10 μ m, g = 20 μ m.

Nectriaceae Tul. & C. Tul. [as ‘Nectrii’], Select. fung. carpol. (Paris) 3: 3 (1865)

***Cylindrocarpon*-like fungi**

Cylindrocarpon-like species are widely distributed, soil-borne fungi around the world, including *Campylocarpon*, *Cylindrocladiella*, *Cylindrodendrum*, *Dactylonectria*, *Ilyonectria*, *Neonectria*, *Pleioacarpon* and *Thelonectria* (Capote et al. 2022). This group is considered as saprophytic or pathogenic causing cankers, root rot and decay of grapevines and many other plants (Jankowiak et al. 2016, Capote et al. 2022). Among them, all genera except *Cylindrodendrum* have been reported on the grapevines (Ye et al. 2021a). In this study, thirty-nine isolates representing six species belonging to *Dactylonectria*, *Ilyonectria* and *Cylindrocladiella* were identified. For taxonomic treatments, we follow Lu et al. (2020) and Ye et al. (2021a).

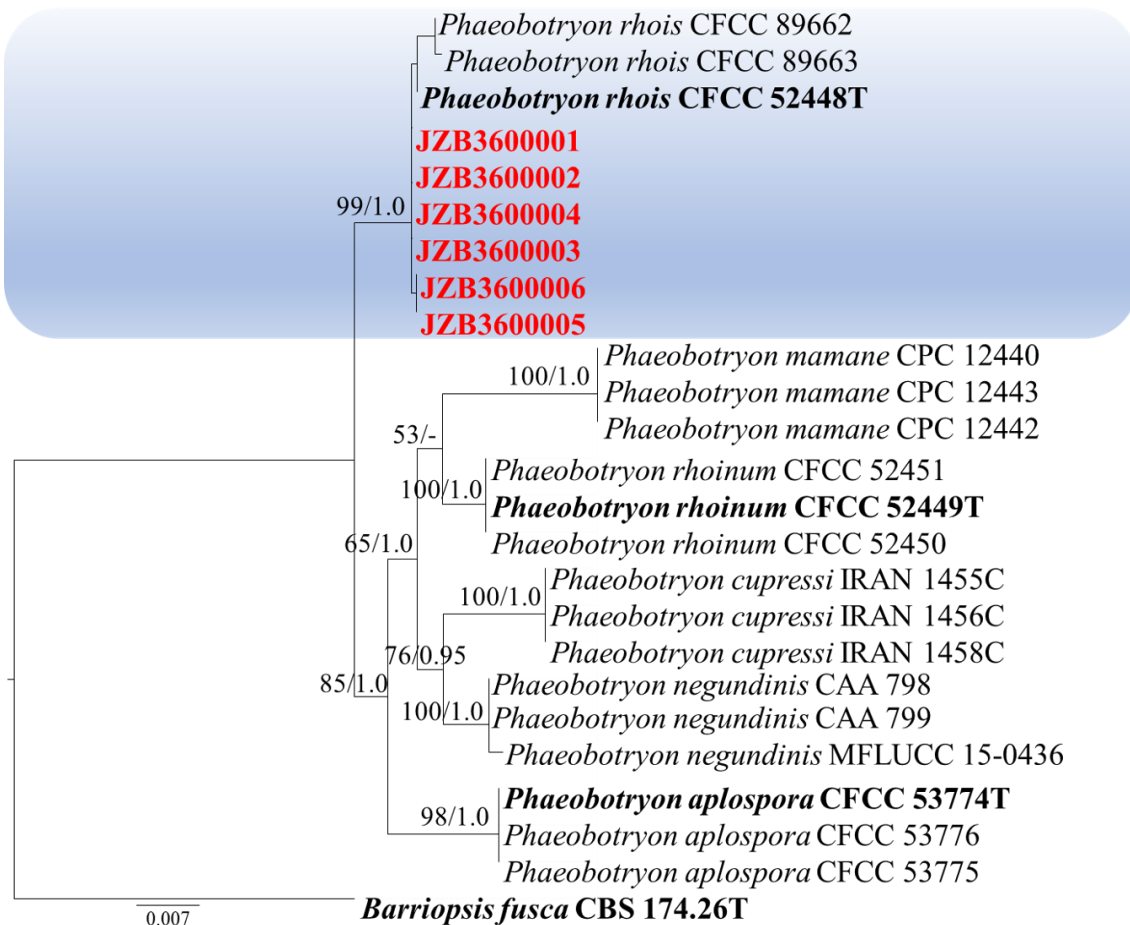


Figure 5 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tef1* and LSU sequence data of *Phaeobotryon* species. *Barriopsis fusca* (CBS 174.26) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -3653.517425 was presented. The matrix had 185 distinct alignment patterns, with 23.97% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.230084, C = 0.261877, G = 0.279321, T = 0.228718; substitution rates AC = 1.390053, AG = 2.937002, AT = 0.769951, CG = 0.806736, CT = 7.065592, GT = 1.000000; gamma distribution shape parameter α = 0.839033. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.007 changes per site. Isolates from the current study are in red and type specimens are in bold.

Dactylonectria novozelandica L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, *Phytopath. Mediterr.* 53(3): 523 (2014)

Index Fungorum number: IF810150; Facesoffungi number: FoF 14330

Description – see Lombard et al. (2014)

Material Examined – China, Yunnan Province, Binchuan County, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB3310031–JZB3310034; China, Hebei Province, Qinhuangdao City, Changli County, on the trunk-base of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB3310035, JZB3310036; *ibid.*, on the root of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB3310037, JZB3310038; China, Beijing City, on the root of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li, living cultures JZB3310039–JZB3310042.

Notes – In the multi-locus phylogenetic analysis, twelve isolates clustered with *D. novozelandica* with 96% bootstrap value and 0.95 BYPP (Fig. 6). *Dactylonectria novozelandica* has been reported to cause black foot disease from grapevines in China (Tan et al. 2022).

Dactylonectria alcacerensis (A. Cabral, H. Oliveira & Crous) L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, *Phytopath. Mediterr.* 53(3): 525 (2014)

Index Fungorum number: IF810143; Facesoffungi number: FoF 14331

Description – see Cabral et al. (2012)

Material Examined – China, Shanxi Province, Linfen City, on the root of *Vitis vinifera*, 23 June 2021, Linna Wu and Xinghong Li, living cultures JZB3310021–JZB3310024; China, Beijing City, on the root of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li, living cultures JZB3310025, JZB3310026; *ibid.*, 27 April 2021, Haiyun Hai and Xinghong Li, living cultures JZB3310029, JZB3310030; China, Hebei Province, Qinhuangdao City, Changli County, on the root of *Vitis vinifera*, 18 October 2021, Linna Wu and Xinghong Li, living cultures JZB3310027, JZB3310028.

Notes – In the multi-locus phylogenetic analysis, ten isolates clustered with *D. alcacerensis* with 99% bootstrap value and 1.0 BYPP (Fig. 6). *Dactylonectria alcacerensis* has been reported as a pathogen causing the black foot disease of grapevines in China (Ye et al. 2021a).

Dactylonectria torresensis (A. Cabral, Rego & Crous) L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, *Phytopath. Mediterr.* 53(3): 528 (2014)

Index Fungorum number: IF810153; Facesoffungi number: FoF 14332

Description – see Lombard et al. (2014)

Material Examined – China, Hebei Province, Huailai County, on the root of *Vitis vinifera*, 9 July 2021, Linna Wu and Xinghong Li, living cultures JZB3310046, JZB3310047; China, Ningxia Province, Yinchuan City, on the root of *Vitis vinifera*, 15 September 2021, Linna Wu and Xinghong Li, living cultures JZB3310048.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *D. torresensis* with 99% bootstrap value and 1.0 BYPP (Fig. 6). *Dactylonectria torresensis* has been reported to cause the black foot disease of grapevines in China (Ye et al. 2021a).

Dactylonectria macrodidyma (Halleen, Schroers & Crous) L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, *Phytopath. Mediterr.* 53(3): 527 (2014)

Index Fungorum number: IF810147; Facesoffungi number: FoF 14333

Description – see Halleen et al. (2004)

Material Examined – China, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB3310043, JZB3310044; China, Beijing City, on the transition region between trunk and root of *Vitis vinifera*, 27 April 2021, Haiyun Tan and Xinghong Li, living cultures JZB3310045.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *D. macrodidyma* with 100% bootstrap value and 1.0 BYPP (Fig. 6). *Dactylonectria macrodidyma* is one of the causal agents of the black foot disease of grapevine in China and was verified to be the most aggressive on detached green shoots among five species associated with black foot disease of grapevine (*C. lageniformis*, *D. alcacerensis*, *D. macrodidyma*, *D. torresensis* and *Neonectria* sp. 1) (Ye et al. 2021a).

Ilyonectria P. Chaverri & Salgado, in Chaverri, Salgado, Hirooka, Rossman & Samuels, *Stud. Mycol.* 68: 69 (2011)

Ilyonectria liriodendri (Halleen, Rego & Crous) P. Chaverri & Salgado, in Chaverri, Salgado, Hirooka, Rossman & Samuels, *Stud. Mycol.* 68: 71 (2011)

Index Fungorum number: IF518561; Facesoffungi number: FoF 14355

Asexual morph: *Macroconidia* predominating, 1–3-septate, straight to slightly curved, cylindrical, 3-septate macroconidia 24–40 × 4–7 µm ($\bar{x} \pm SD = 29.0 \pm 3.7 \times 5.1 \pm 0.5$ µm, n = 50). *Microconidia* ellipsoidal, subcylindrical to ovoid, 0–1-septate, 6–14 × 3–4 µm, ($\bar{x} \pm SD = 9.2 \pm 1.7 \times 3.5 \pm 0.4$ µm, n = 50) (Fig. 7). Sexual morph: Not observed.

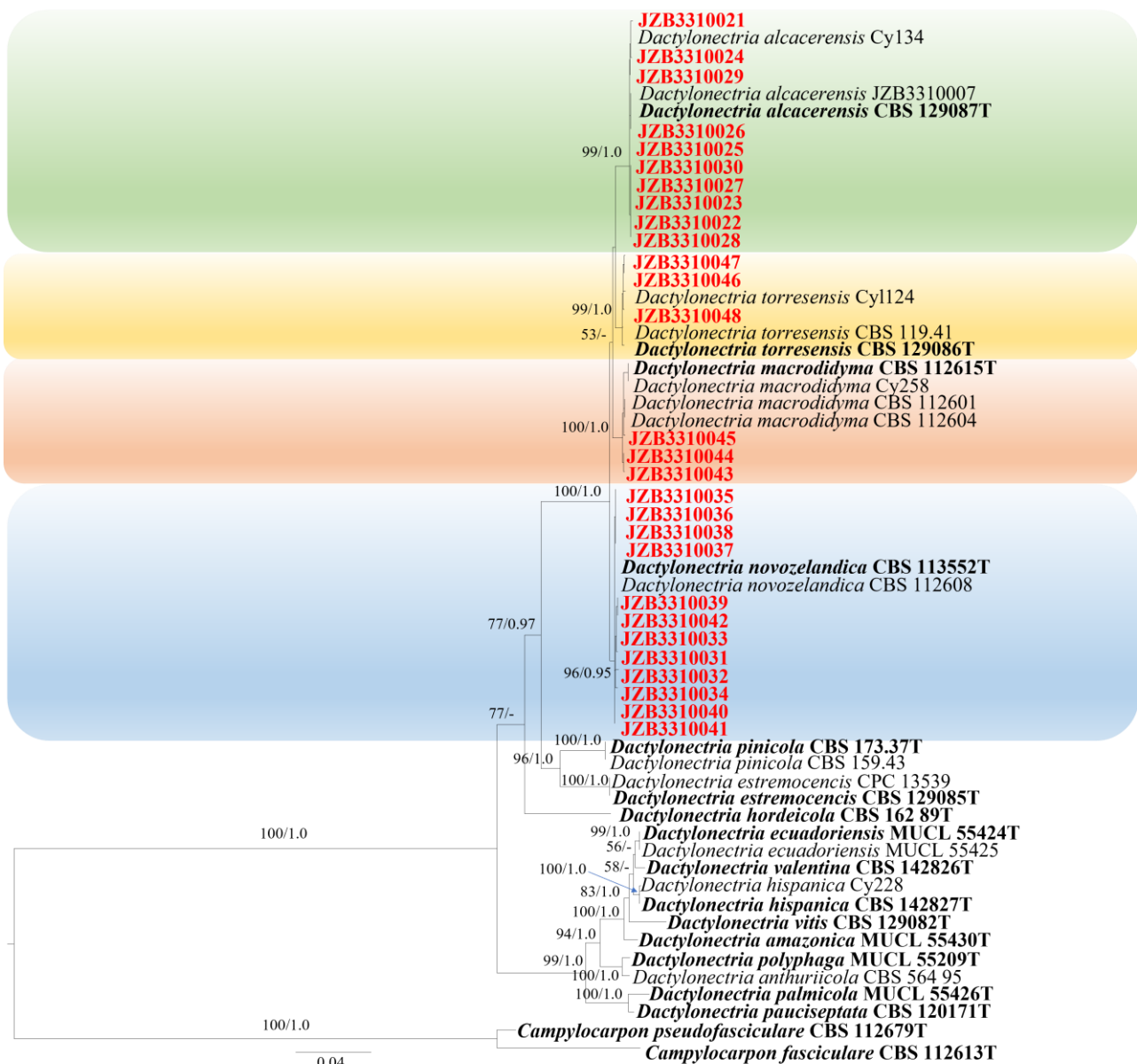


Figure 6 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tef1*, *tub2* and *his* sequence data of *Dactylonectria* species. *Campylocarpon pseudofasciculare* (CBS 112679) and *C. fasciculare* (CBS 112613) were used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -7792.518531 was presented. The matrix had 599 distinct alignment patterns with 14.58% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.221125, C = 0.327854, G = 0.223902, T = 0.227119; substitution rates AC = 1.748995, AG = 3.677564, AT = 1.718751, CG = 0.886389, CT = 6.913553, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.715661$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.04 changes per site. Isolates from the current study are in red and type specimens are in bold.

Culture characteristics – Colonies on PDA white with sparse aerial mycelium, reverse pale orange (Fig. 7), colonies reached 4.5 cm diam after 6 d.

Material Examined – China, Shanxi Province, Linfen City, on the root of *Vitis vinifera*, 23 June 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3610001, JZBH3610002), living cultures JZB3610001, JZB3610002; China, Ningxia Province, Yinchuan City, on the trunk of *Vitis vinifera*, 15 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures

JZBH3610003–JZBH3610006), living cultures JZB3610003–JZB3610006; China, Beijing City, on the transition region between trunk and root of *Vitis vinifera*, 27 April 2021, Haiyun Tan and Xinghong Li (Inactive dry cultures JZBH3610007), living cultures JZB3610007.

Notes – In the multi-locus phylogenetic analysis, seven isolates clustered with *I. liriiodendri* with 98% ML bootstrap value and 1.0 BYPP (Fig. 8). *Ilyonectria liriiodendri* (former *Neonectria liriiodendri*) has been reported as the pathogen of black foot of grapevines in many countries (Jayawardena et al. 2018). This is the first report of *I. liriiodendri* on grapevines in China.

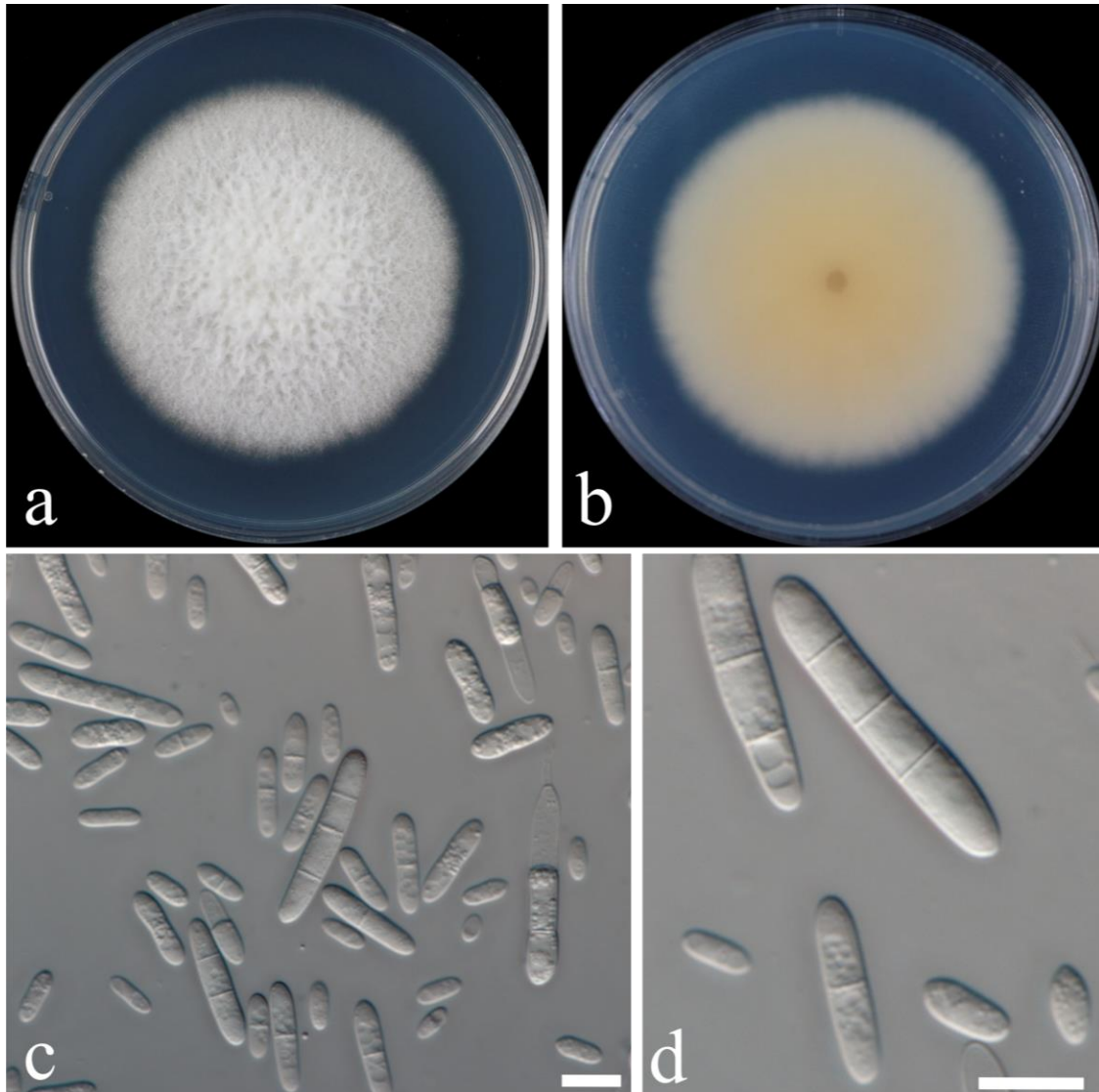


Figure 7 – *Ilyonectria liriiodendri* (JZB3610001). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c, d Macroconidia and microconidia. Scale bars: c, d = 10 µm.

Cylindrocladiella Boesew., Can. J. Bot. 60 (11): 2289 (1982)

Cylindrocladiella viticola Crous & Van Coller, in van Coller, Denman, Groenewald, Lamprecht & Crous, Australas. Pl. Path. 34(4): 493 (2005)

Index Fungorum: IF500187; Facesoffungi number: FoF 14356

Asexual morph: *Conidiophores* penicillate and subverticillate, hyaline. *Conidia* cylindrical, straight, rounded at both ends, straight, 1-septate, $8\text{--}16 \times 2\text{--}3 \mu\text{m}$ ($\bar{x} \pm \text{SD} = 12.1 \pm 1.4 \times 2.7 \pm 0.3 \mu\text{m}$, $n = 50$). *Chlamydospores* arranged in chains (Fig. 9). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA raised, cottony, yellow to umber, colonies reached 6.4 cm diam after 6 d (Fig. 9).



Figure 8 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tef1*, *tub2* and *his* sequence data of *Ilyonectria* species. *Campylocarpon pseudofasciculare* (CBS 112679) and *C. fasciculare* (CBS 112613) were used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of -8714.157328 was presented. The matrix had 555 distinct alignment patterns, with 9.38% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.218130, C = 0.328229, G = 0.229365, T = 0.224276; substitution rates AC = 1.504760, AG = 3.527434, AT = 1.562501, CG = 0.619652, CT = 6.790122, GT = 1.000000; gamma distribution shape parameter α = 0.587098. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.05 changes per site. Isolates from the current study are in red and type specimens are in bold.

Material Examined – China, Yunnan Province, Binchuan County, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3320005, JZBH3320006, JZBH3320007), living cultures JZB3320005, JZB3320006, JZB3320007.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *C. viticola* with 100% ML bootstrap value and 0.97 BYPP (Fig. 10). *Cylindrocladiella viticola* was reported to cause cutting rot on grapevine in South Africa (van Coller et al. 2005). This is the first report of *C. viticola* associated with grapevine trunk diseases in China.

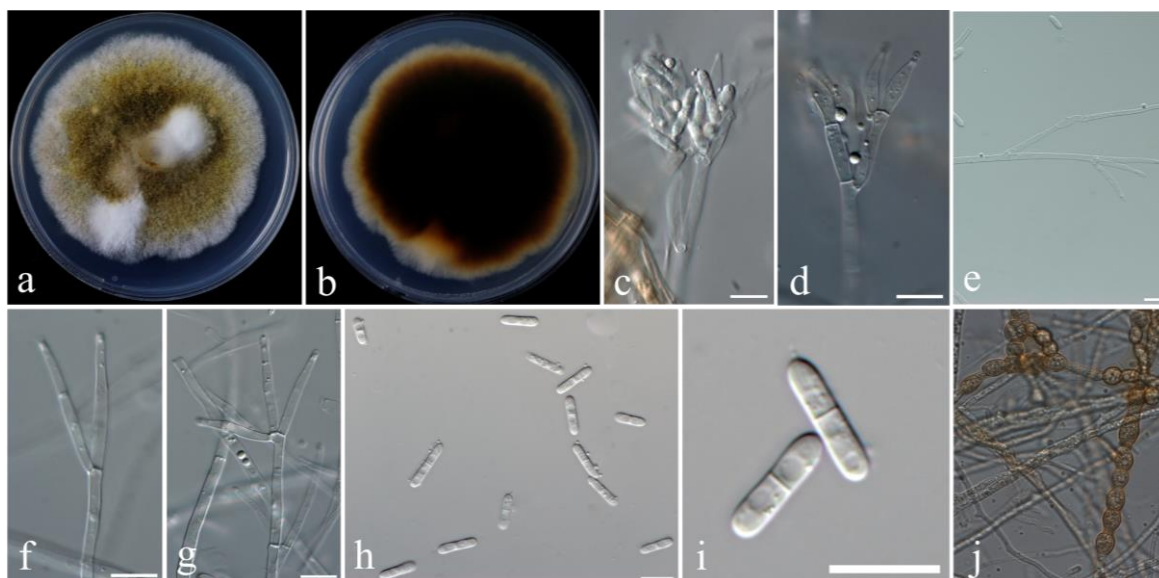


Figure 9 – Morphological characterization of *Cyindrocladiella viticola* (JZB3320006). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c, d Penicillate conidiophore. e-g Subverticillate conidiophore. h, i Conidia. j Chlamydospores. Scale bars: c–j =10 μm.

***Fusarium* and allied fusarioid genera**

Fusarium includes a large number of species as saprobes, endophytes or pathogens (Sandoval-Denis et al. 2018). Among them, *F. graminearum* and *F. oxysporum* are ranked as the top 10 fungal pathogens with scientific and economic importance (Dean et al. 2012). *Neocosmospora*, previously known as *F. solani* species complex (FFSC), includes the most important and ubiquitous groups of pathogens (Sandoval-Denis et al. 2019). *Bisifusarium* is a new genus proposed in recent years, encompasses species previously included in the *Fusarium dimerum* species complex (Sandoval-Denis et al. 2018).

In this study, thirty-four isolates from seven species belonging to *Fusarium*, *Neocosmospora* and *Bisifusarium* were identified (Fig. 11). For taxonomic treatments, we followed Crous et al. (2021).

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

Fusarium acuminatum Ellis & Everh., Proc. Acad. nat. Sci. Philad. 47: 441 (1895)

Index Fungorum: IF219366; Facesoffungi number: FoF 14334

Description – See Leslie & Summerell (2006)

Material Examined – China, Ningxia Province, Yinchuan City, on the trunk of *Vitis vinifera*, 15 September 2021, Wei Zhang and Xinghong Li, living cultures JZB3110195, JZB3110196; China, Shanxi Province, Linfen City, on the trunk of *Vitis vinifera*, 23 June 2021, Linna Wu and Xinghong Li, living cultures JZB3110197, JZB3110198.

Notes – In the multi-locus phylogenetic analysis, four isolates clustered with *F. acuminatum* with 98% bootstrap value and 1.0 BYPP (Fig. 11). *Fusarium acuminatum* has been reported as a pathogen of grapevine wilt in Spain (Jayawardena et al. 2018). This is the first report of *F. acuminatum* associated with grapevine trunk diseases in China.

Fusarium brachygibbosum Padwick, Mycol. Pap. 12: 11 (1945)

Index Fungorum: IF286508; Facesoffungi number: FoF 11683

Asexual morph: *Macroconidia* formed in orange sporodochia on the carnation leaf agar (CLA), slightly curved, with wide central cells, slightly sharp apical cell and distinct foot basal cells, usually have 5 septa, 23–59 × 5–6 μm ($\bar{x} \pm SD = 44.8 \pm 5.9 \times 5.7 \pm 0.4 \mu\text{m}$, n = 50). *Spherical chlamydospores* were produced from mycelium (Fig. 12). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were initially white with abundant aerial mycelium, turning light orange in the center, reverse orange (Fig. 12). Colonies reached 7.7 cm in diameter after 4 days at 25 °C.

Material Examined – China, Beijing City, on the root of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3110191–JZBH3110194), living cultures JZB3110191–JZB3110194.

Notes – In the multi-locus phylogenetic analysis, four isolates clustered with *F. brachygibbosum* with 100% bootstrap value and 1.0 BYPP (Fig. 11). *Fusarium brachygibbosum* was reported to cause root rot of soybean, tobacco and maize stalk rot in China (Shan et al. 2017, Wang et al. 2021, Qiu et al. 2021). This is the first report of *F. brachygibbosum* associated with grapevine trunk diseases in China.

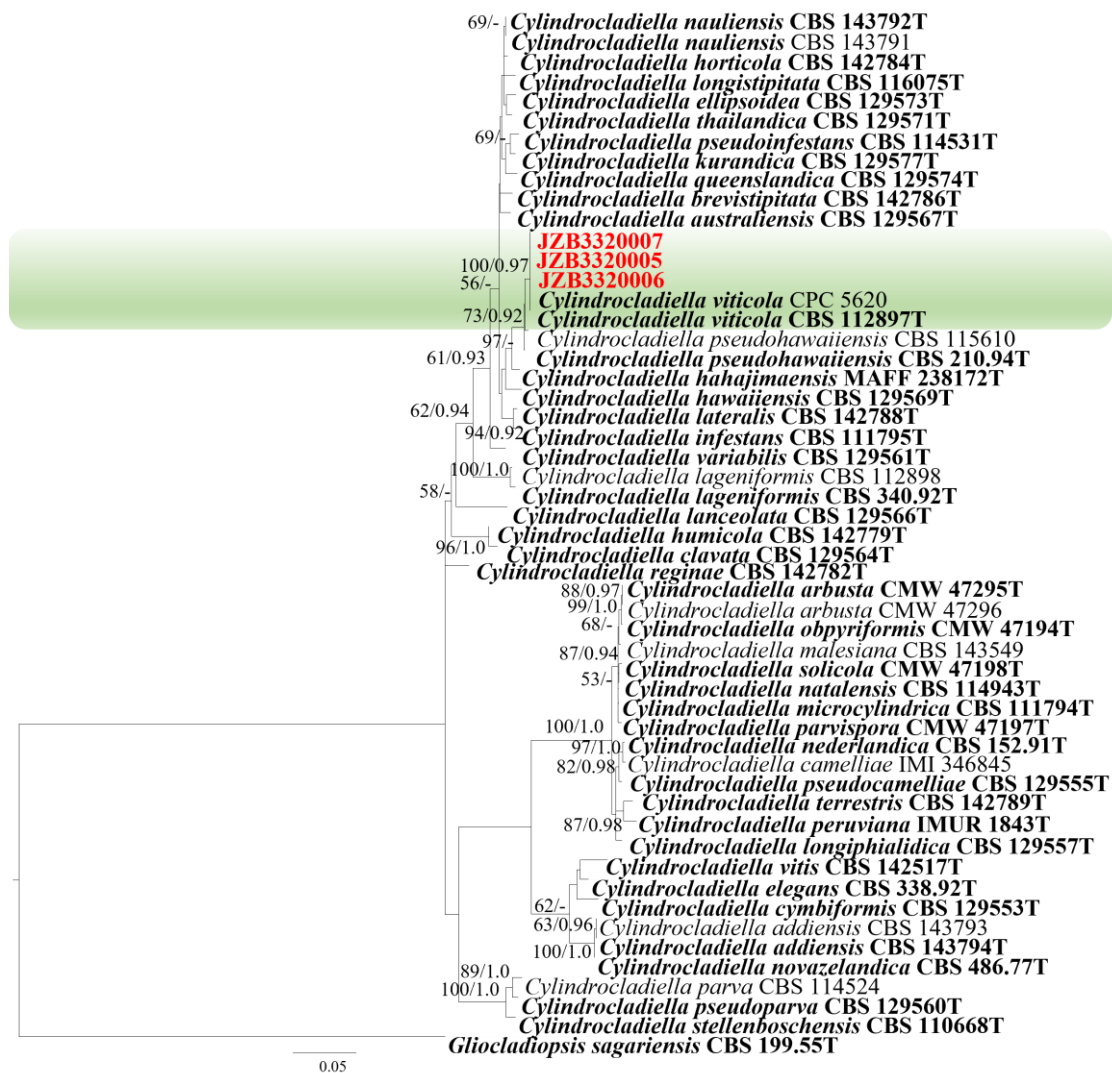


Figure 10 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tefl* and *tub2* sequence data of *Cyliandrocladiella* species. *Gliocladiopsis sagariensis* (CBS 199.55) was used as the outgroup taxon. The best scoring RAXML tree with a final likelihood value of -7461.214703 was presented. The matrix had 539 distinct alignment patterns, with 14.16% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.224070, C = 0.307547, G = 0.220194, T = 0.248188; substitution rates AC = 1.015860, AG = 3.279433, AT = 0.995371, CG = 0.438164, CT = 4.326124, GT = 1.000000; gamma distribution shape parameter α = 0.505492. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.05 changes per site. Isolates from the current study are in red and type specimens are in bold.

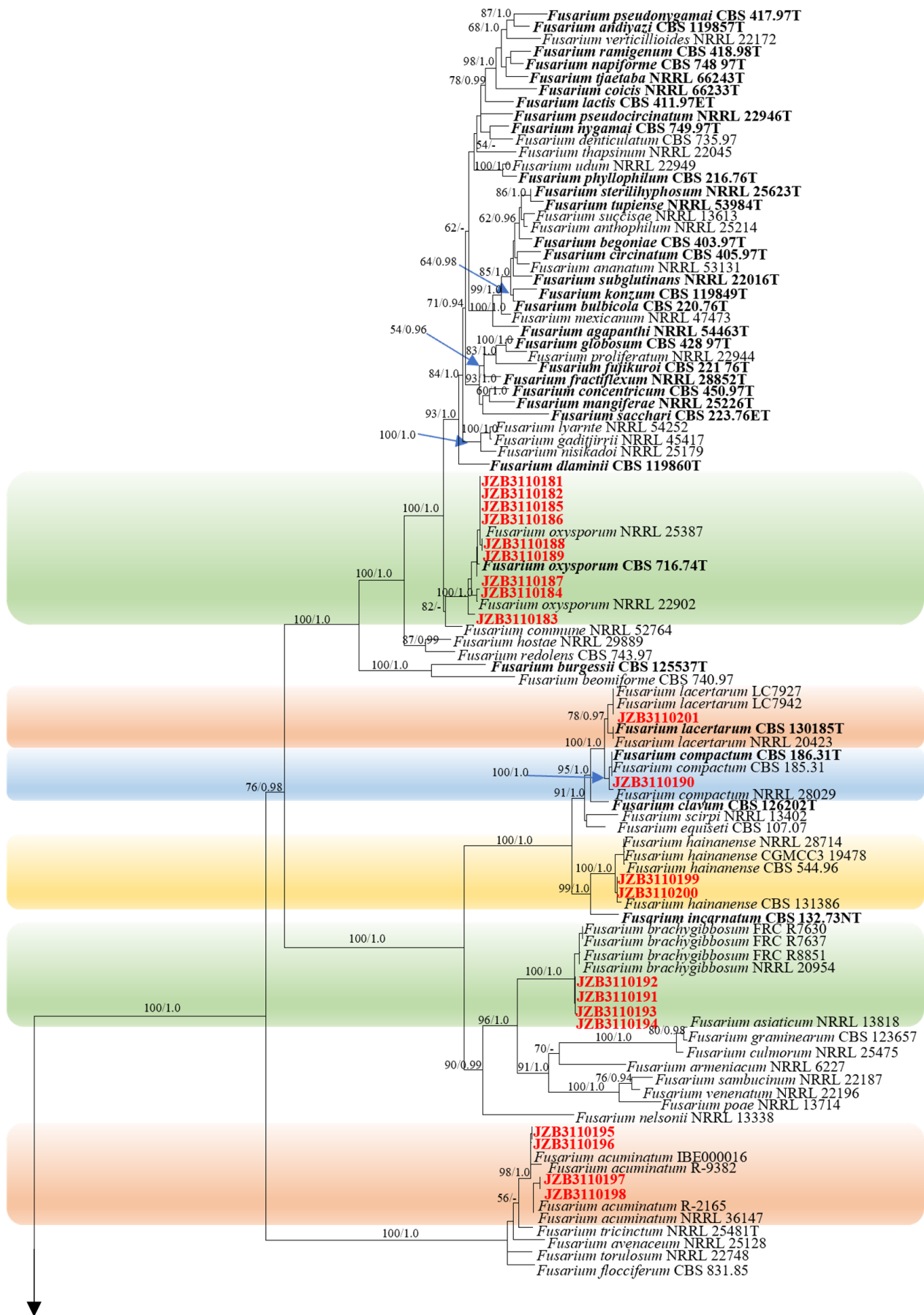


Figure 11 – Phylogenetic tree generated by maximum likelihood analysis of combined *tef1* and *rpb2* sequence data of *Fusarium*, *Neocosmospora* and *Bisifusarium* species. *Fusicolla*

aquaeductuum (CBS 734.79) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -18302.824510 was presented. The matrix had 945 distinct alignment patterns, with 15.67% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.251509, C = 0.269104, G = 0.244341, T = 0.235046; substitution rates AC = 1.483783, AG = 4.460272, AT = 1.757600, CG = 0.850730, CT = 9.879030, GT = 1.000000; gamma distribution shape parameter $\alpha = 1.224492$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.09 changes per site. Isolates from the current study are in red and type specimens are in bold.

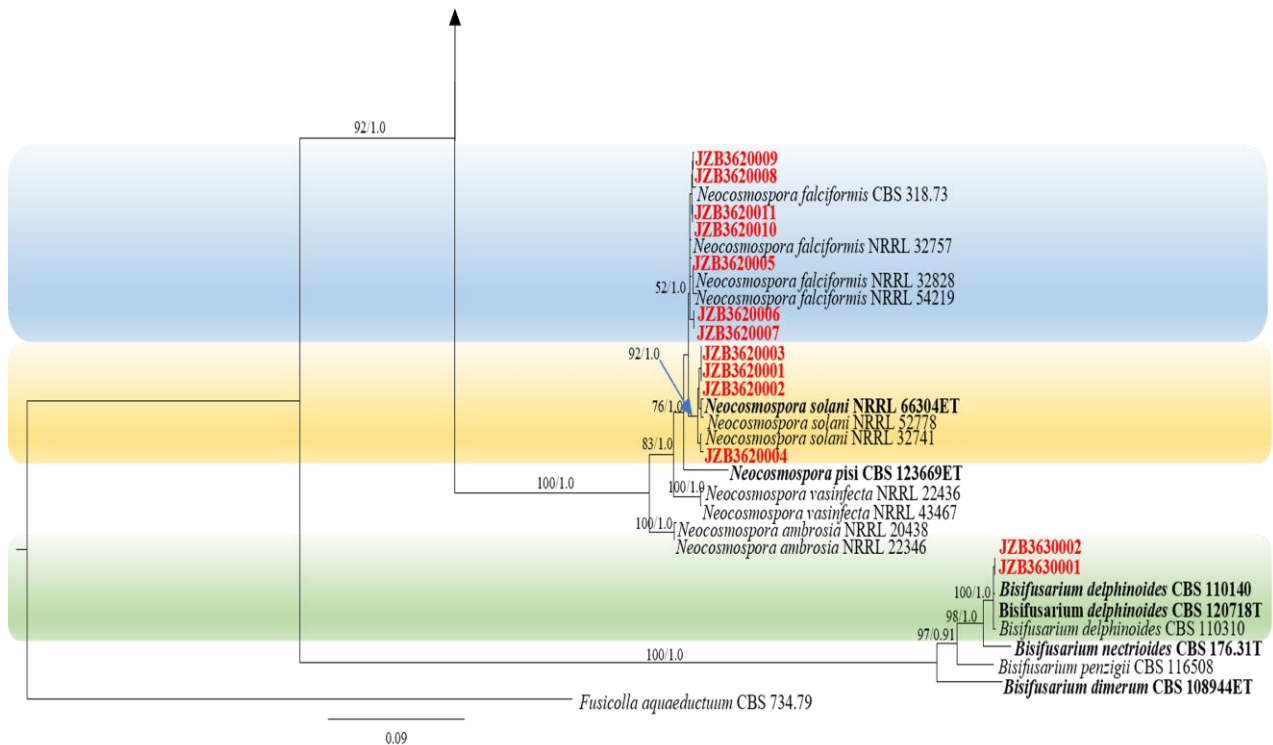


Figure 11– Continued.

Fusarium compactum (Wollenw.) Raillo, *Fungi of the Genus Fusarium*: 180 (1950)

Index Fungorum: IF297537; Facesoffungi number: FoF 14337

Asexual morph: Orange *sporodochia* formed on the CLA. *Macroconidia* produced from monophialides on branched conidiophores in sporodochia, have strong dorsi-ventral curvature with a pronounced foot cell and tapering elongate apical cell that is often needle like in appearance, usually 5-septate, $41\text{--}91 \times 3\text{--}7 \mu\text{m}$ ($\bar{x} \pm \text{SD} = 66.7 \pm 11.8 \times 5.0 \pm 0.6 \mu\text{m}$, $n = 50$) (Fig. 13). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were white with cottony, dense mycelium, and then turned light orange in center, reverse orange (Fig. 13). Colonies reached 6.9 cm in diameter after 4 days at 25 °C.

Material Examined – China, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3110190), living cultures JZB3110190.

Notes – In the multi-locus phylogenetic analysis, one isolate clustered with *F. compactum* with 100% bootstrap value and 1.0 BYPP (Fig. 11). *Fusarium compactum* was reported to cause wheat root and crown rot in Turkey (Tunali et al. 2008), or saprotroph on apples in Croatia (Sever et al. 2012). This is the first report of *F. compactum* associated with grapevine trunk diseases in the world.

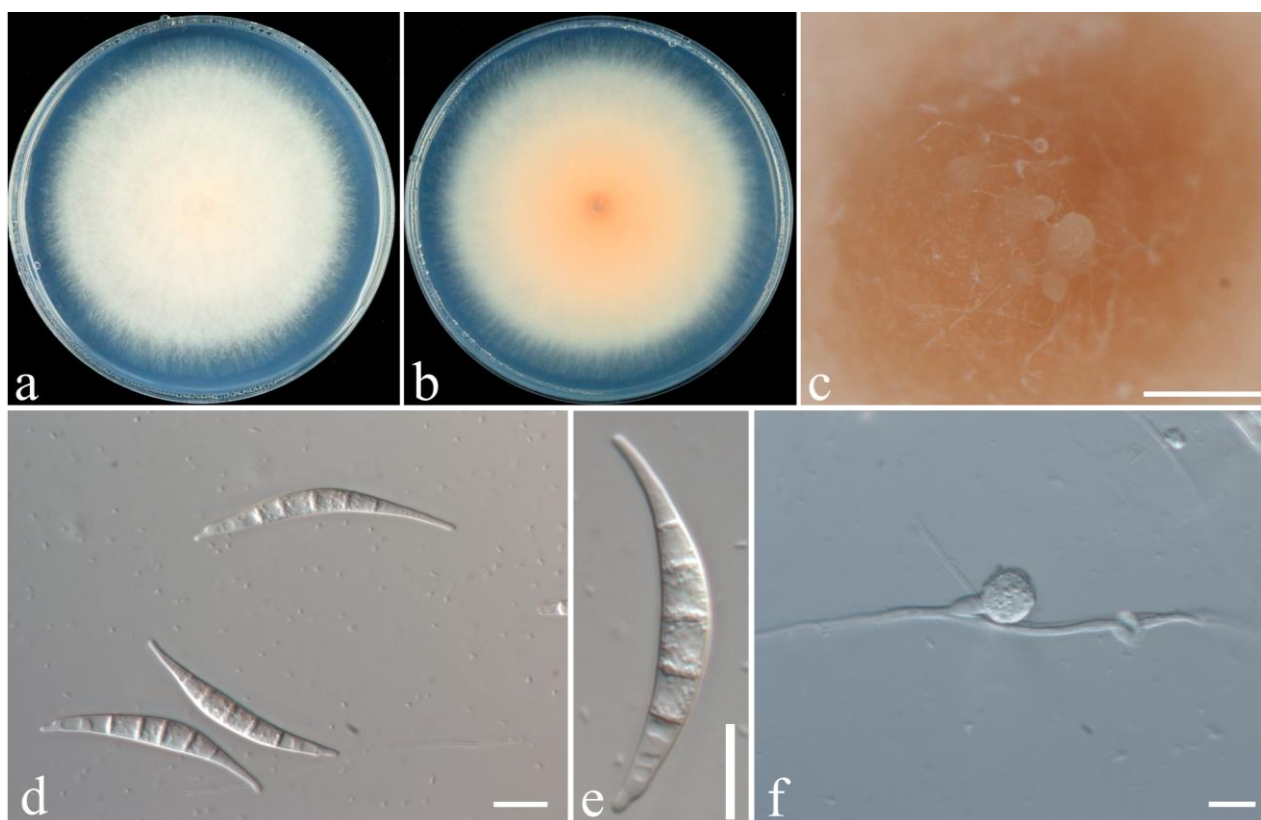


Figure 12 – Morphological characterization of *Fusarium brachygibbosum* (JZB3110191). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Sporodochia formed on the surface of carnation leaves. d, e Macroconidia. f Chlamydospore. Scale bars: c = 50 μm , d–f = 10 μm .

Fusarium hainanense M.M. Wang, Qian Chen & L. Cai, in Wang, Chen, Diao, Duan & Cai, *Persoonia* 43: 82 (2019)

Index Fungorum: IF829536; Facesoffungi number: FoF 14335

Asexual morph: *Sporodochia* light orange on CLA. *Conidiophores* unbranched. *Macroconidia* fusiform to falcate, straight to slightly curved, sometimes with constricted septa, have barely- to distinctly- notched basal cell and blunt to papillate apical cell, 1–5-septate, 17–39 \times 3–5 μm , ($\bar{x} \pm \text{SD} = 27.6 \pm 6.8 \times 4.1 \pm 0.5 \mu\text{m}$, n = 50) (Fig. 14). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were white with scant aerial mycelia, reverse pale orange in the center, white at the margin. Colonies reached 8.1 cm diam after 4 days at 25 $^{\circ}\text{C}$ (Fig. 14).

Material Examined – China, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3110199, JZBH3110200), living cultures JZB3110199, JZB3110200.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *F. hainanense* with 100% bootstrap value and 1.0 BYPP (Fig. 11). *Fusarium hainanense* was first isolated from rice as an endophyte in China (Wang et al. 2019). This is the first host report of *F. hainanense* associated with grapevine trunk diseases in China.

Fusarium lacertarum Subrahm. [as ‘laceratum’], *Mykosen* 26 (9): 478 (1983)

Index Fungorum: IF534970; Facesoffungi number: FoF 14336

Asexual morph: On CLA, *conidiophores* branched or unbranched. *Macroconidia* variable in size, fusiform to falcate, straight to slightly curved, with foot-shaped basal cells, tapering to hooked apical cells, 2–5-septate, 19–36 \times 3–5 μm ($\bar{x} \pm \text{SD} = 27.8 \pm 4.2 \times 4.2 \pm 0.5 \mu\text{m}$, n = 50) (Fig. 15). *Chlamydospores* were in abundance and present in chains. Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were white with floccose aerial mycelium, turning pale buff in the center. Colonies reached 7.4 cm diam after 4 days at 25 °C (Fig. 15).

Material Examined – China, Shannxi Province, Weinan City, on the root of *Vitis vinifera*, 29 June 2021, Wei Zhang (Inactive dry cultures JZBH3110201), living cultures JZB3110201.

Notes – In the multi-locus phylogenetic analysis, one isolate clustered with *F. lacertarum* with 78% bootstrap value and 0.97 BYPP (Fig. 11). *Fusarium lacertarum* was isolated from *Capsicum* in China (Wang et al. 2019) and reported to cause cladode rot in *Nopalea cochenillifera* in Brazil (Santiago et al. 2018) and the head blight on sorghum in North Carolina (Beacorn & Thiessen 2021). This is the first report of *F. lacertarum* associated with grapevine trunk diseases in the world.

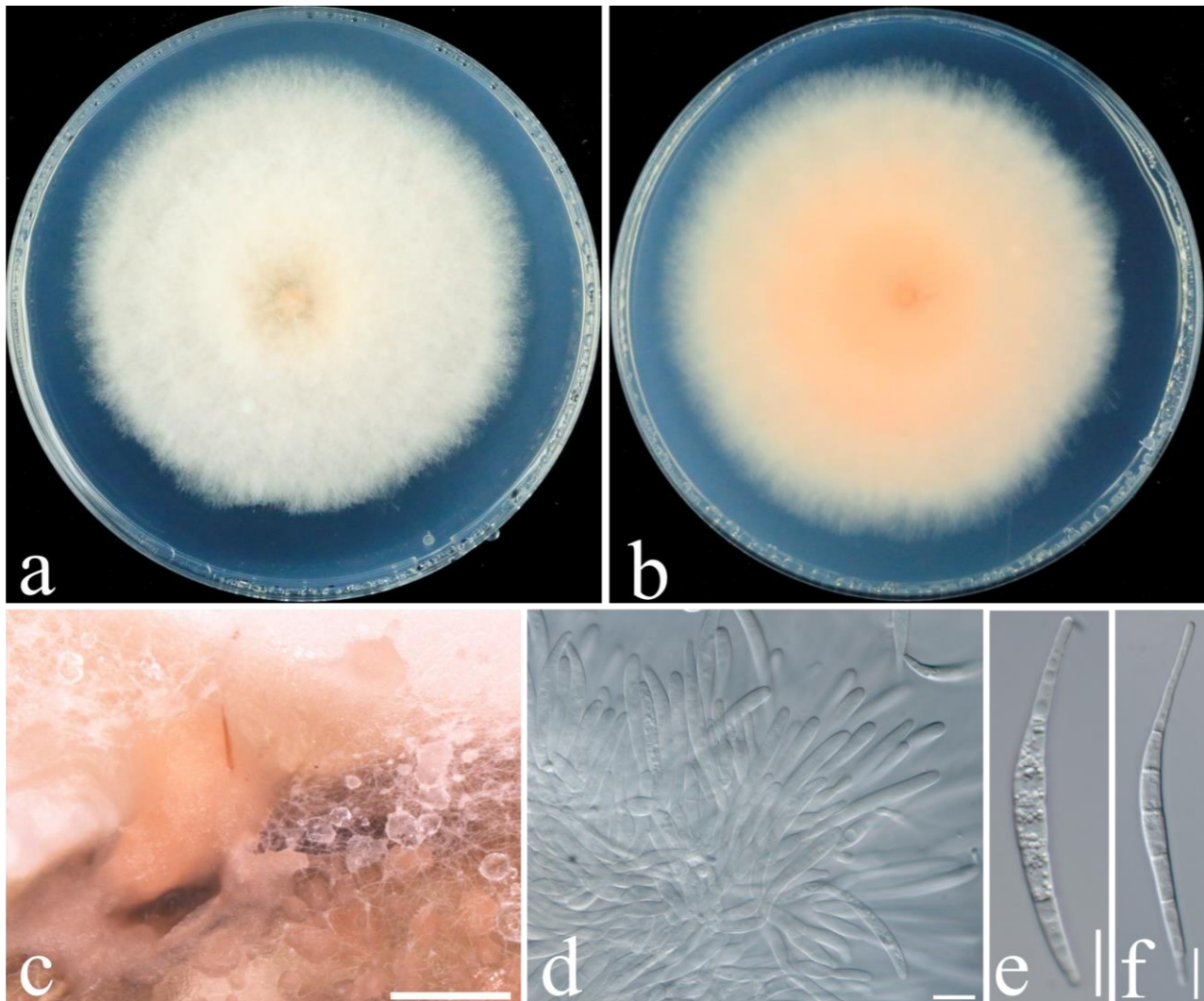


Figure 13 – Morphological characterization of *Fusarium compactum* (JZB3110190). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Sporodochia formed on the surface of carnation leaves. d Conidiophores. e, f Macroconidia. Scale bars: c = 50 µm, d–f = 10 µm.

Fusarium oxysporum Schldl., Fl. berol. (Berlin) 2: 139 (1824)

Index Fungorum: IF218372; Facesoffungi number: FoF 03824

Description – see Lombard et al. (2019)

Material Examined – China, Hebei Province, Qinhuangdao City, Changli County, on the root of *Vitis vinifera*, 18 October 2021, Linna Wu and Xinghong Li, living cultures JZB3110181, JZB3110184; *ibid.*, on the root of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB3110185, JZB3110186; *ibid.*, on the trunk of *Vitis vinifera*, 18 October 2021,

Linna Wu and Xinghong Li, living cultures JZB3110182, JZB3110183; China, Yunnan Province, Binchuan County, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living cultures JZB3110187; China, Fujian Province, Longyan City, Shanghang County, on the root of *Vitis vinifera*, 19 January 2022, Linna Wu and Xinghong Li, living cultures JZB3110188, JZB3110189.

Notes – In the multi-locus phylogenetic analysis, nine isolates clustered with *F. oxysporum* with 100% ML bootstrap value and 1.0 BYPP (Fig. 11). *Fusarium oxysporum* is reported to be associated with grapevine decline and dieback in Australia (Highet & Nair et al. 1995, Castillo-Pando et al. 2001), vascular wilt in Egypt (Ziedan et al. 2011) and withered rotten grapes in Italy (Lorenzini & Zapparoli 2015), or as an endophyte in Spain (González & Tello 2011), and saprotrophic fungi in China (Jayawardena et al. 2018).



Figure 14 – Morphological characterization of *Fusarium hainanense* (JZB3110199). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Sporodochia formed on the surface of carnation leaves. d Conidiophores. e–i Macroconidia. Scale bars: c = 50 μm , d–i = 10 μm .

Neocosmospora E.F. Sm., Bull. U.S. Department of Agriculture 17: 45 (1899)

Neocosmospora falciformis (Carrión) L. Lombard & Crous, Stud. Mycol. 80: 227 (2015)

Index Fungorum: IF810958; Facesoffungi number: FoF 14357

Asexual morph: *Sporodochia* formed abundantly on CLA. *Conidiophores* verticillately branched; phialides subcylindrical to doliiform, smooth- and thin-walled. *Macroconidia* slightly fusoid to falcate, with blunt apical cells and barely notched basal cell, 2–5-septate, 25–46 \times 5–8 μm , ($\bar{x} \pm \text{SD} = 39.4 \pm 4.7 \times 5.9 \pm 0.7 \mu\text{m}$, $n = 50$). *Microconidia* ellipsoidal to subcylindrical, straight or gently curved, 0–1-septate. *Chlamydospores* were globose to subglobose, single-celled, terminal and rough-walled (Fig. 16). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were white to pale-cream with sparse floccose aerial mycelium, growing in concentric rings, reverse beige. Colonies reached 4.9 cm diam after 4 days at 25 °C (Fig. 16).

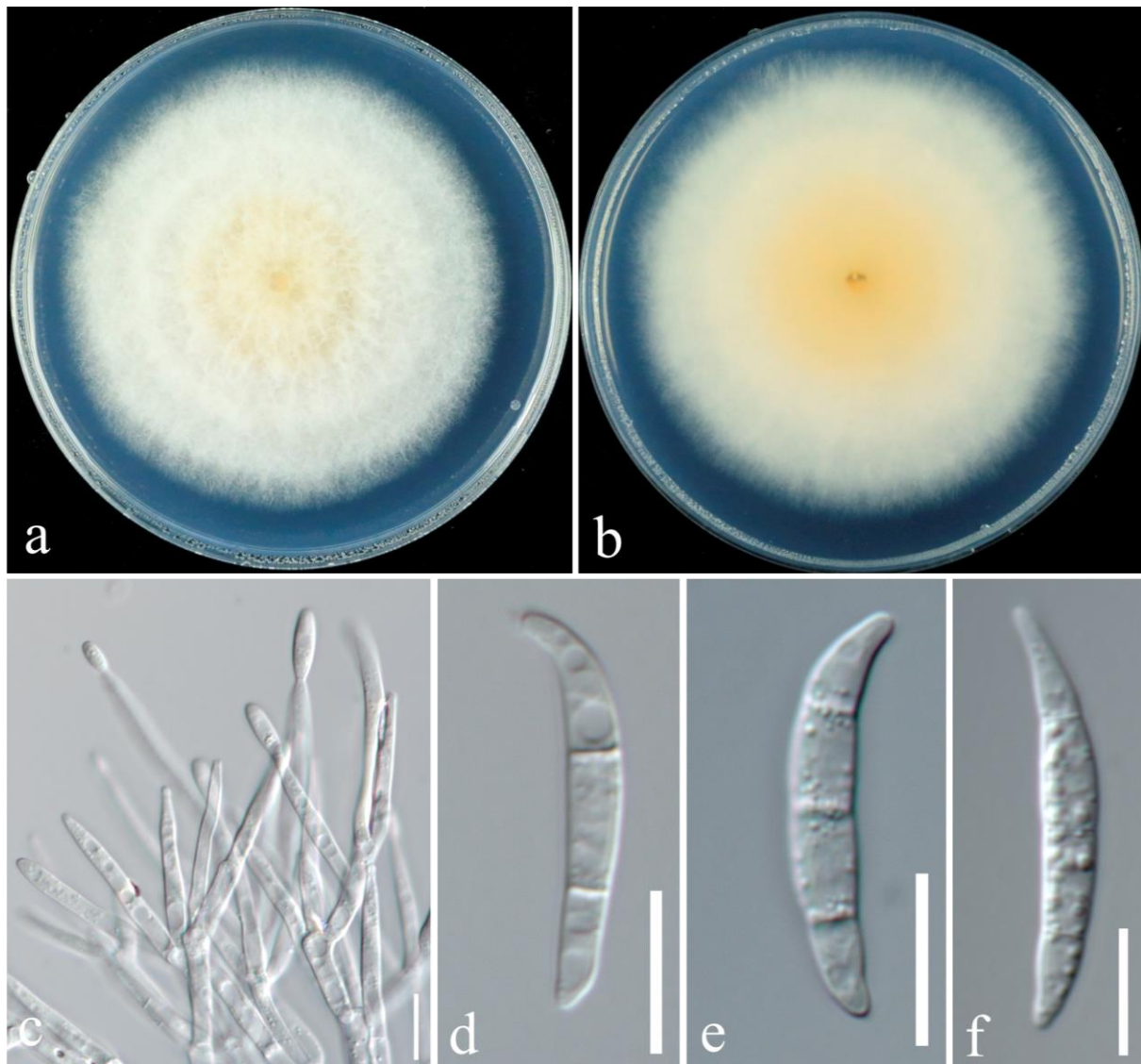


Figure 15 – Morphological characterization of *Fusarium lacertarum* (JZB3110201). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidiophores. d–f Macroconidia. Scale bars: c = 20 μ m, d–f = 10 μ m.

Material Examined – China, Shaanxi Province, Weinan City, on the root of *Vitis vinifera*, 29 June 2021, Wei Zhang (Inactive dry cultures JZBH3620005), living cultures JZB3620005; China, Ningxia Province, Yinchuan City, on the trunk of *Vitis vinifera*, 15 September 2021, Weizhang and Xinghong Li (Inactive dry cultures JZBH3620006, JZBH3620007), living cultures JZB3620006, JZB3620007; China, Beijing City, on the root of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3620008–JZBH3620011), living cultures JZB3620008–JZB3620011.

Notes – In the multi-locus phylogenetic analysis, seven isolates clustered with *N. falciformis* with 52% ML bootstrap value and 1.0 BYPP (Fig. 11). *Neocosmospora falciformis* (former *Fusarium falciforme*) was reported to cause root rot in *Weigela florida* and *Dioscorea polystachya* in China (Shen et al. 2020, Zhang et al. 2020), foot rot and wilt in tomatoes and maize stalk rot in Mexico (Vega-Gutiérrez et al. 2019, Douriet-Angulo et al. 2019). This is the first report of *N. falciformis* associated with grapevine trunk diseases in the world.

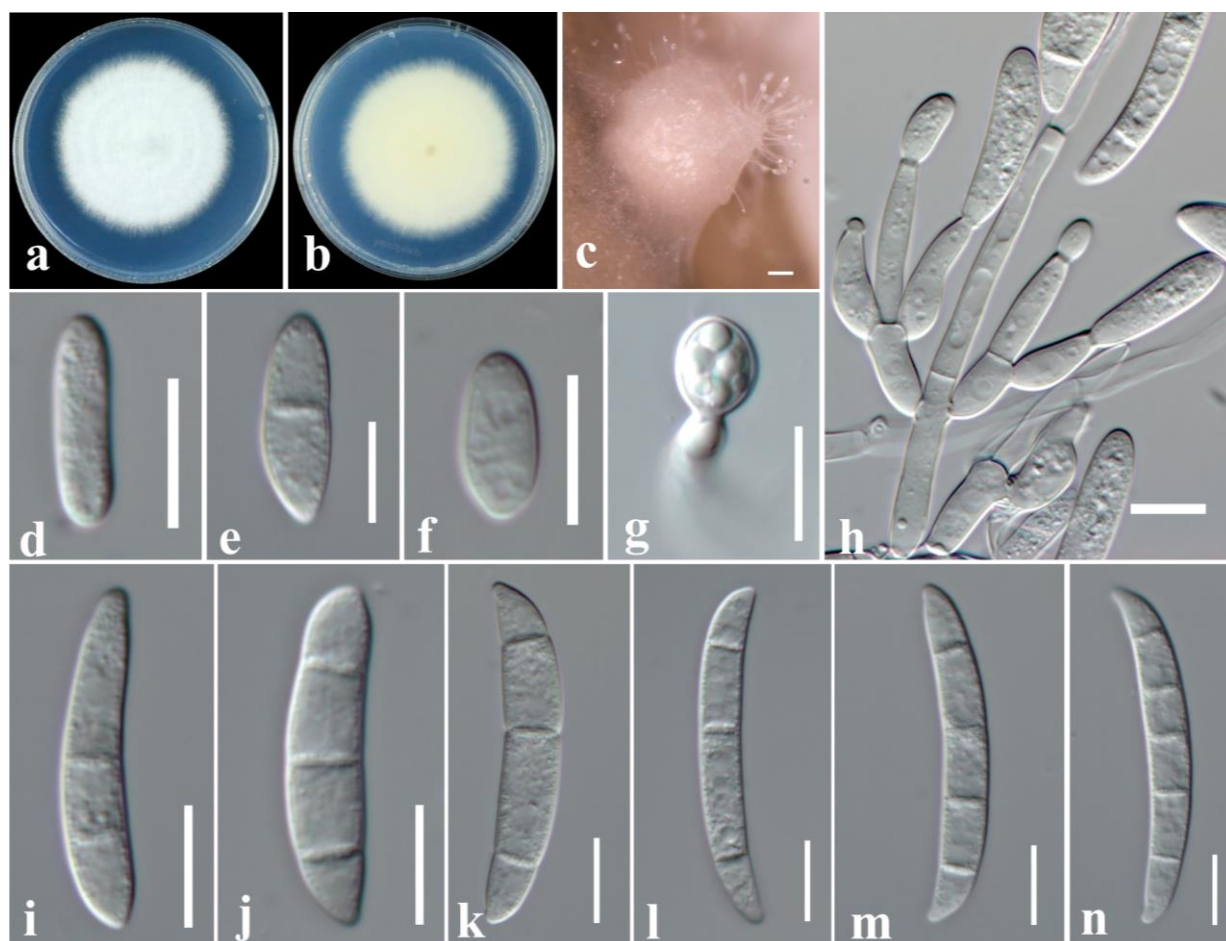


Figure 16 – Morphological characterization of *Neocosmospora falciformis* (JZB3620005). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Sporodochia formed on the surface of carnation leaves. d–f Microconidia. g Chlamydospore. h Conidiophores and phialides. i–n Macroconidia. Scale bars: c–n = 10 μ m.

Neocosmospora solani (Mart.) L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, Stud. Mycol. 80: 228 (2015)

Index Fungorum: IF810964; Facesoffungi number: FoF 14358

Asexual morph: Cream sporodochia formed abundantly on CLA. *Conidiophores* branched. *Macroconidia* are relatively wide falcate or fusoid, straight or slightly curved with blunt apical cells and notched or round basal cell, 3–5-septate, 25–58 \times 5–7 μ m ($\bar{x} \pm SD = 47.5 \pm 6.4 \times 6.1 \pm 0.5 \mu$ m, n = 50) (Fig. 17). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were white to cream with sparse aerial mycelium, growing in concentric rings. Colonies reached 4.5 cm diam after 4 days at 25 $^{\circ}$ C (Fig. 17).

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the root of *Vitis vinifera*, 19 January 2022, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3620001–JZBH3620003), living cultures JZB3620001–JZB3620003; China, Hebei Province, Qinhuangdao City, Changli County, on the root of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li (JZBH3620004), living cultures JZB3620004.

Notes – In the multi-locus phylogenetic analysis, four isolates clustered with *N. solani* with 92% ML bootstrap support values and 1.0 BYPP (Fig. 11). *Neocosmospora solani* (former *Fusarium solani*) is an important pathogen and the most common species with a wide host range (Sandoval-Denis et al. 2019). This species was isolated from grapevine in Brazil and India (Jayawardena et al. 2018). This is the first report of *N. solani* associated with grapevine trunk diseases in China.

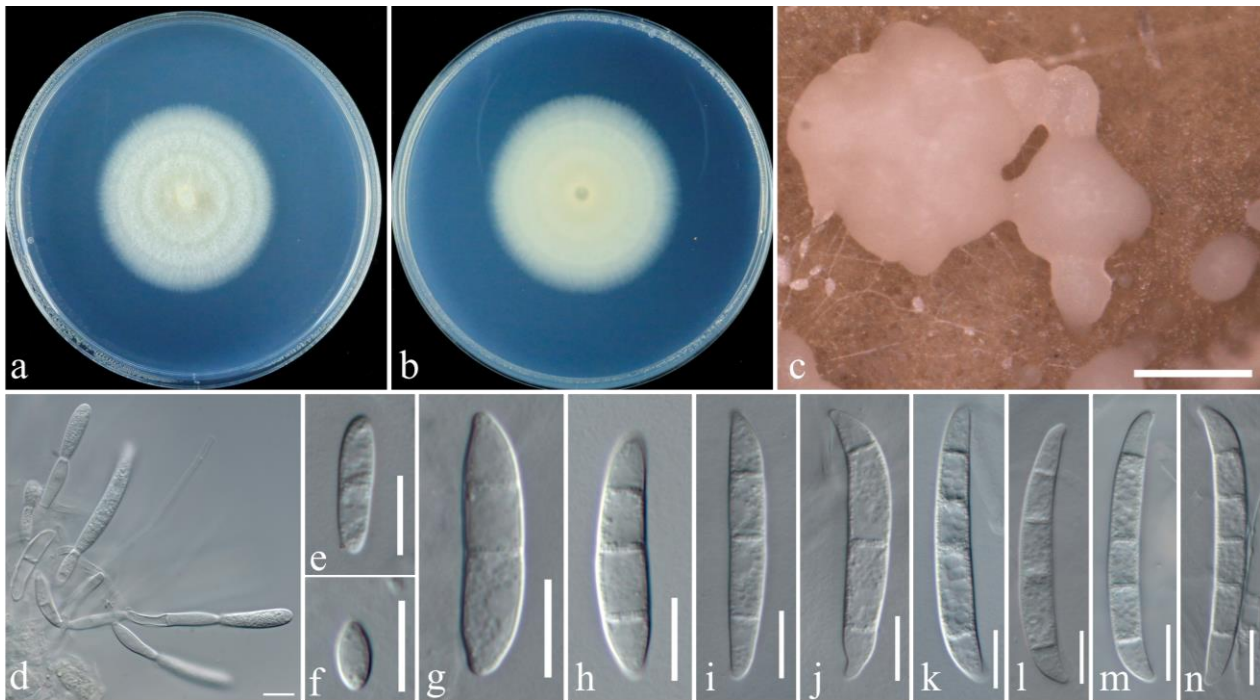


Figure 17 – Morphological characterization of *Neocosmospora solani* (JZB3620004). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Sporodochia formed on the surface of carnation leaves. d Conidiophores. e, f Microconidia. g–n Macroconidia. Scale bars: c = 100 μ m, d–n = 10 μ m.

Bisfusarium L. Lombard, Crous & W. Gams, in Lombard, van der Merwe, Groenewald & Crous, *Stud. Mycol.* 80: 223 (2015)

Bisfusarium delphinoides (Schroers, Summerb., O’Donnell & Lampr.) L. Lombard & Crous, in Lombard, van der Merwe, Groenewald & Crous, *Stud. Mycol.* 80: 224 (2015)

Index Fungorum: IF810228; Facesoffungi number: FoF 14364

Description – See Schroers (2009)

Material Examined – China, Hebei Province, Zhangjiakou City, Huailai County, on the root of *Vitis vinifera*, 9 July 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3630001, JZBH3630002), living cultures JZB3630001, JZB3630002.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *B. delphinoides* with 100% ML bootstrap value and 1.0 BYPP (Fig. 11). The species was isolated from *Citrus* in the USA (Schroers et al. 2009), oriental melon (nonpathogenic) in Korea (Seo & Kim 2017), and as putative mycoparasites of *Plasmopara viticola*, which cause downy mildew in grapevines (Ghule et al. 2018). This is the first report of *B. delphinoides* associated with grapevine trunk diseases in China.

Diaporthaceae Höhn. ex Wehm., *Am. J. Bot.* 13: 638 (1926)

Diaporthe Fuckel, *Fungi rhenani exsic.*, suppl., fasc. 5: no. 1988 (1867)

The genus *Diaporthe* comprises pathogenic, endophytic and saprobic species with wide host ranges and geographic distributions (Norphanphoun et al. 2022). The taxonomy of the species in this genus is complicated because of cryptic diversification and phenotypic plasticity within the genus (Udayanga et al. 2014). In this study, 39 isolates belonging to *Diaporthe* species were identified. For taxonomic treatments, we follow Norphanphoun et al. (2022).

Diaporthe eres Nitschke, *Pyrenomyc. Germ.* 2: 245 (1870)

Index Fungorum: IF172054; Facesoffungi number: FoF 02182

Description – See Udayanga et al. (2014)

Material Examined – China, Beijing City, on the trunk of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li, living cultures JZB320221–JZB320228, JZB320232–JZB320235; *ibid.*, on the root of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li, living cultures JZB320229–JZB320231, JZB320236; China, Hebei Province, Qinhuangdao City, Changli County, on the trunk of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB320237–JZB320239; *ibid.*, Changli County, on the trunk base of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB320240, JZB320241; *ibid.*, on the root of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB320242–JZB320244; *ibid.*, Zhangjiakou City, Huailai County, on the trunk of *Vitis vinifera*, 22 August 2021, Linna Wu and Xinghong Li, living cultures JZB320245–JZB320247; *ibid.*, on the trunk of *Vitis vinifera*, 24 October 2020, Linna Wu and Xinghong Li, living cultures JZB320248–JZB320251; *ibid.*, on the trunk of *Vitis vinifera*, 25 July 2020, Linna Wu and Xinghong Li, living cultures JZB320252; *ibid.*, on the root of *Vitis vinifera*, 9 July 2021, Linna Wu and Xinghong Li, living cultures JZB3202513–JZB3202567.

Notes – In the multi-locus phylogenetic analysis, forty-four isolates clustered with two clades of *D. eres* (Fig. 18). *Diaporthe eres* was regarded as the most prominent and widespread species associated with grapevine dieback in China (Manawasinghe et al. 2019).

Diaporthe unshiuensis F. Huang, K.D. Hyde & Hong Y. Li, in Huang, Udayanga, Mei, Fu, Hyde & Li, Fungal Biology 119(5): 344 (2015)

Index Fungorum: IF810845; Facesoffungi number: FoF 09422

Description – See Huang et al. (2015)

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the trunk of *Vitis vinifera*, 19 January 2022, Linna Wu and Xinghong Li, living cultures JZB320258, JZB320259.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *D. unshiuensis* with 100% ML bootstrap value and 1.0 BYPP (Fig. 18). *Diaporthe unshiuensis* has been recorded to be associated with Diaporthe dieback in China (Manawasinghe et al. 2019).

Togniniaceae Réblová, L. Mostert, W. Gams & Crous, Stud. Mycol. 50(2): 540 (2004)

Phaeoacremonium W. Gams, Crous & M.J. Wingf., Mycologia 88 (5): 789 (1996)

Phaeoacremonium spp. are common pathogens on stems and branches on a wide range of woody hosts, especially on grapevine (Gramaje et al. 2015). In 2021, *Phaeoacremonium minimum* was first reported as a pathogen of Esca disease in China (Ye et al. 2020). In this study, we follow Ye et al. (2021b) for taxonomic treatments.

Phaeoacremonium iranianum L. Mostert, Gräfenhan, W. Gams & Crous, in Mostert, Groenewald, Summerbell, Gams & Crous, Stud. Mycol. 54: 83 (2006)

Index Fungorum: IF500227; Facesoffungi number: FoF 14338

Asexual morph: *Conidiophores* unbranched, erect. *Phialides* mostly monophialidic, have three types: type I phialides the shortest, cylindrical; type II phialides medium sized, elongate-ampulliform to navicular; type III phialides were long, subcylindrical to navicular, some tapering towards the apex to form a thin neck. *Conidia* oblong-ellipsoidal, 4–9 × 2–3 μm ($\bar{x} \pm SD = 6.1 \pm 1.2 \times 2.3 \pm 0.3 \mu\text{m}$, n = 50) (Fig. 19). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA felty, olive-brown, in reverse dark brown. Colonies reached 7.7 cm diam after 28 days at 25 °C (Fig. 19).

Material Examined – China, Hebei Province, Changli County, on the trunk of *Vitis vinifera*, 18 October 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3190013, JZBH3190014), living cultures JZB3190013, JZB3190014.

support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.2 changes per site. Isolates from the current study are in red and type specimens are in bold.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *P. iranianum* with 100% ML bootstrap value and 1.0 BYPP (Fig. 20). *Phaeoacremonium iranianum* was initially isolated from kiwi fruit and grapevines in Iran and Italy (Mostert et al. 2006) and reported to cause Esca disease of grapevine in Canada, Italy, South Africa and Spain (Gramaje et al. 2015). This is the first report of *P. iranianum* associated with grapevine trunk diseases in China.

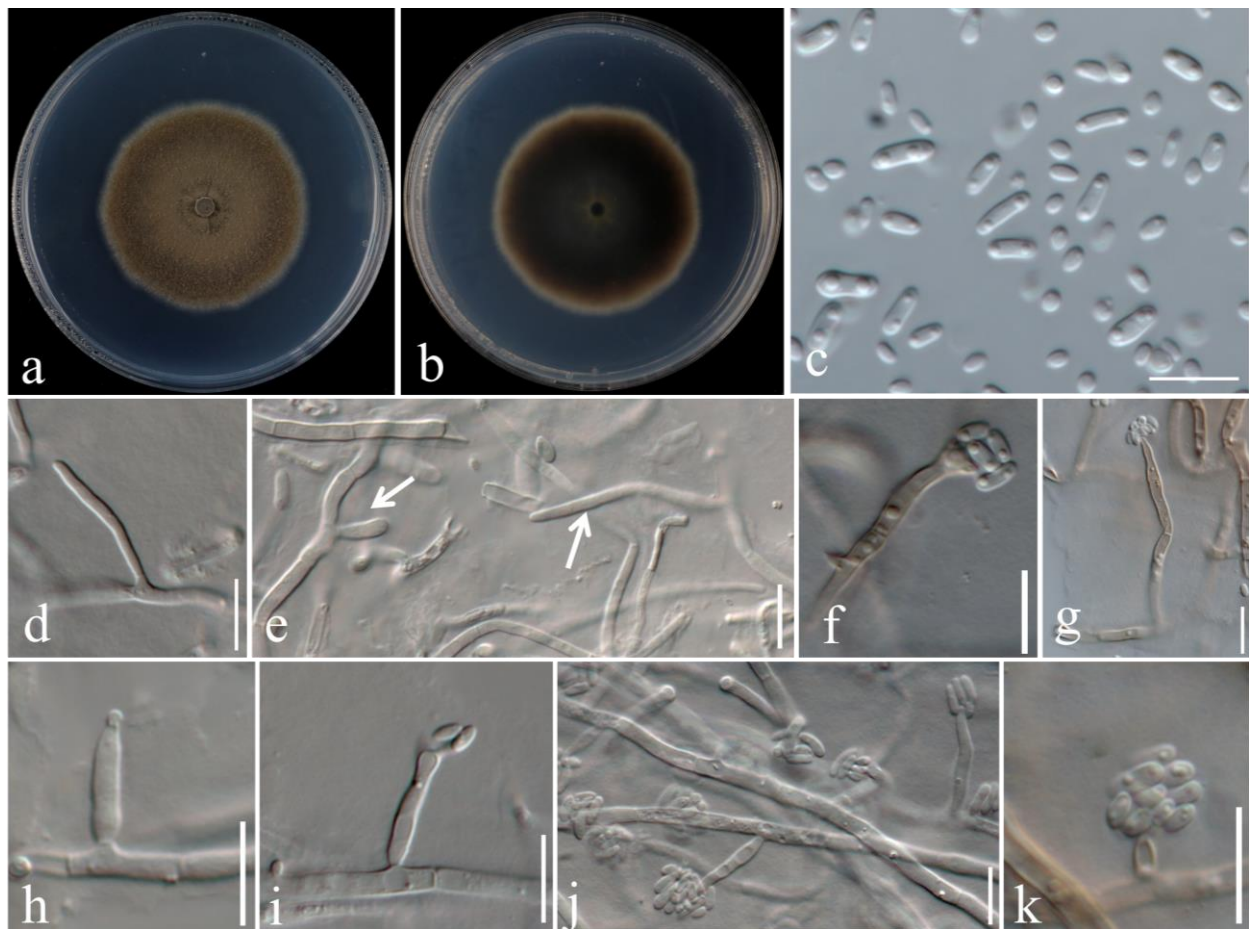


Figure 19 – Morphological characterization of *Phaeoacremonium iranianum* (JZB3190014). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidia. d, e Conidiophore. f, g Type III phialides. h, i Type II Phialides. j, k Type I phialides. Scale bars: c–k = 10 μm .

Schizoparmaceae Rossman, D.F. Farr & Castl. [as ‘Schizoparmeaceae’], Mycoscience 48 (3): 137 (2007)

Coniella Höhn., Ber. dt. bot. Ges. 36 (7): 316 (1918)

For taxonomic treatments, we follow Chethana et al. (2017).

Coniella vitis Chethana, J.Y. Yan, X.H. Li & K.D. Hyde, in Chethana, Zhou, Zhang, Liu, Xing, Hyde, Yan & Li, Pl. Dis. 101 (12): 2129 (2017)

Index Fungorum: IF819365; Facesoffungi number: FoF 02722

Description – See Chethana et al. (2017)

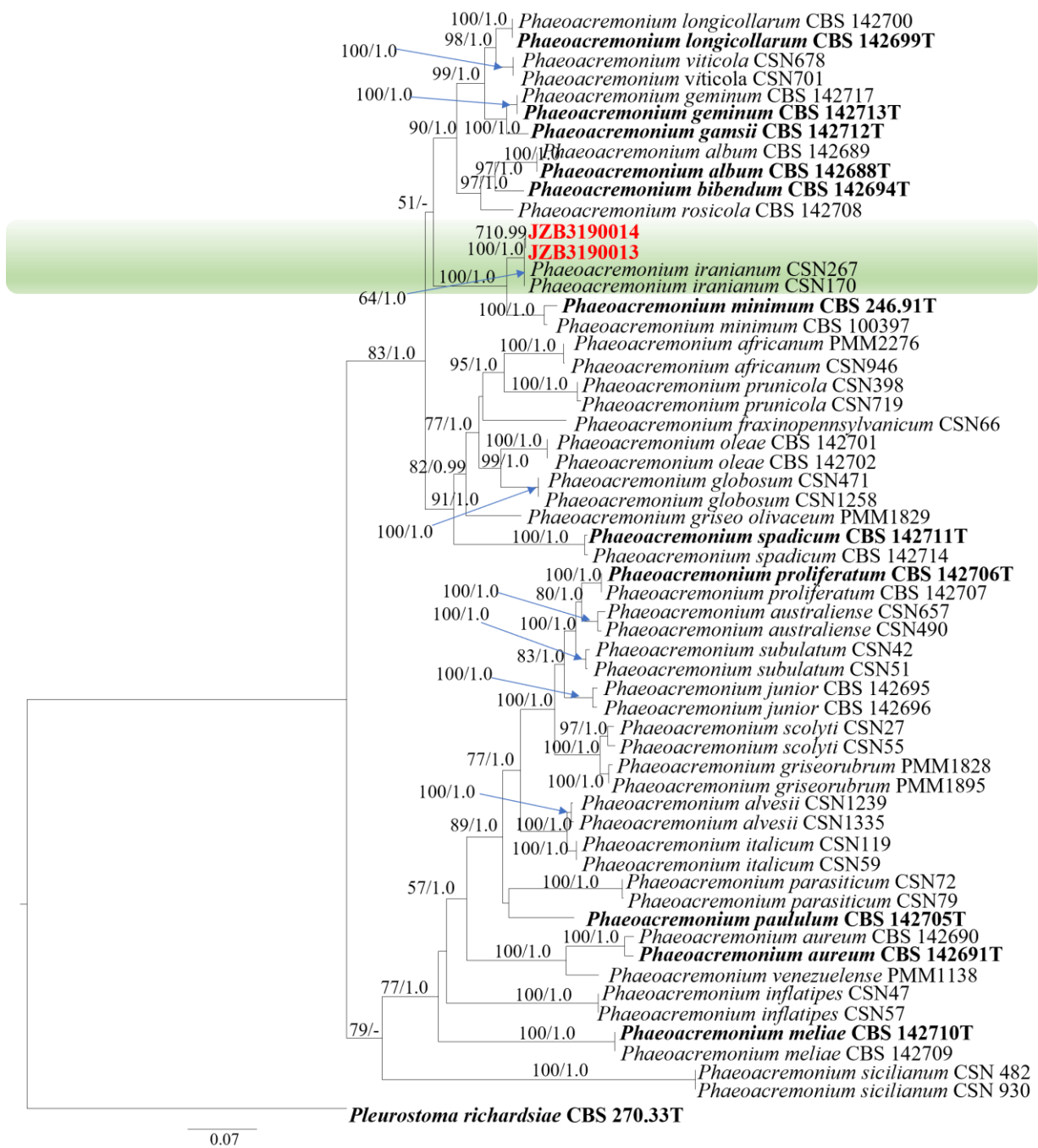


Figure 20 – Phylogenetic tree generated by maximum likelihood analysis of combined *act* and *tub2* sequence data of *Phaeoacremonium* species. *Pleurostoma richardsiae* (CBS 270.33) was used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of -10031.367491 was presented. The matrix had 622 distinct alignment patterns, with 12.24% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.216115, C = 0.316660, G = 0.225016, T = 0.242209; substitution rates AC = 1.424857, AG = 5.577572, AT = 1.486155, CG = 1.182568, CT = 5.200674, GT = 1.000000; gamma distribution shape parameter α = 2.279586. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.07 changes per site. Isolates from the current study are in red and type specimens are in bold.

Material Examined – China, Beijing City, on the trunk of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li, living cultures JZB3700081, JZB3700082; China, Hebei Province, Changli County, on the trunk of *Vitis vinifera*, 18 October 2021, Linna Wu and Xinghong Li, living

cultures JZB3700083, JZB3700084; *ibid.*, on the root of *Vitis vinifera*, 18 October 2021, Linna Wu and Xinghong Li, living cultures JZB3700085–JZB3700087.

Notes – In the multi-locus phylogenetic analysis, seven isolates clustered with *C. vitis* with 85% ML bootstrap values and 0.97 BYPP (Fig. 21). *Coniella vitis* was described as a novel species causing white rot in grapevine berries in China (Chethana et al. 2017).

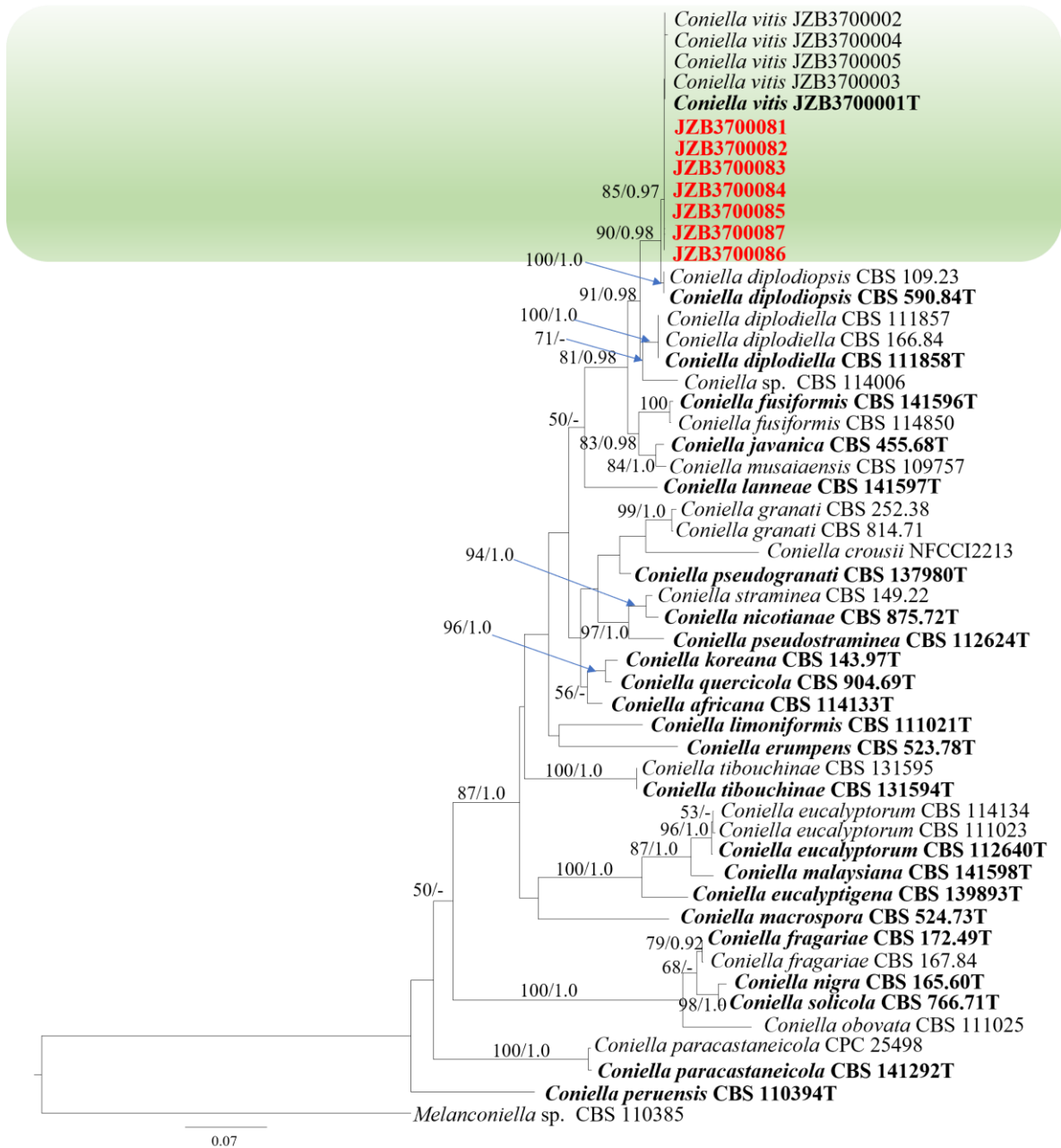


Figure 21 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *his*, LSU and *tef1* sequence data of *Coniella* species. *Melanconiella* sp. (CBS 110385) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -12111.406531 was presented. The matrix had 688 distinct alignment patterns, with 21.86% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.245494, C = 0.247696, G = 0.255443, T = 0.251367; substitution rates AC = 1.306162, AG = 2.579472, AT = 1.571029, CG = 0.884497, CT = 5.752512, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.397636$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.07 changes per site. Isolates from the current study are in red and type specimens are in bold.

Sporocadaceae Corda [as ‘Sporocadeae’], *Icon. fung.* (Prague) 5: 34 (1842)

Species of Sporocadaceae are endophytes, phytopathogens or saprobes with a wide host range, which are characterized by producing appendaged conidia (Liu et al. 2019). *Neopestalotiopsis* and *Pestalotiopsis*, generally known as Pestalotioid fungi, are important pathogens causing postharvest fruit rot and trunk diseases on grapevines in many countries (Jayawardena et al. 2015, Maharachchikumbura et al. 2016). In this study, sixteen isolates were obtained from Sporocadaceae belonging to *Pestalotiopsis*, *Neopestalotiopsis* and *Bartalinia*, representing five species. For taxonomic treatments of Sporocadaceae, we follow Tibpromma et al. (2020) and Li et al. (2021).

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

Pestalotiopsis kenyana Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, *Stud. Mycol.* 79: 166 (2014)

Index Fungorum: IF809741; Facesoffungi number: FoF 06981

Asexual morph: *Conidiogenous* cells discrete, lageniform to subcylindrical, hyaline. *Conidia* fusoid to subcylindrical, straight to slightly curved, 4-septate, $23\text{--}29 \times 7\text{--}9 \mu\text{m}$ ($\bar{x} \pm \text{SD} = 25.2 \pm 1.7 \times 7.7 \pm 0.5 \mu\text{m}$, $n = 50$); basal cell conic to obconic, hyaline; three median cells doliiform, wall verruculose concolourous, brown, septa darker than the rest of the cell; apical cell subcylindrical, hyaline, with two to three tubular appendages arising from the apex of the apical cell, one filiform, basal appendage (Fig. 22). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA white with wavy edge. Colonies reached 6.7 cm diam after 5 days at 25 °C (Fig. 22).

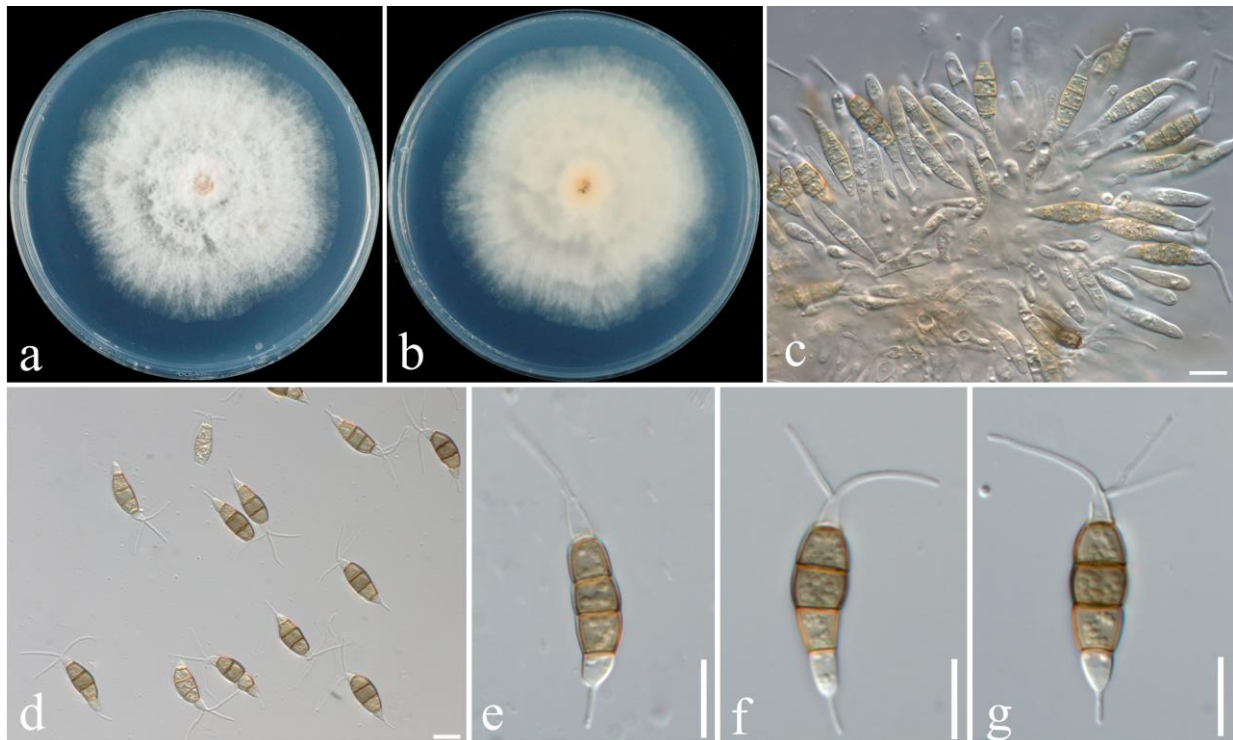


Figure 22 – Morphological characterization of *Pestalotiopsis kenyana* (JZB340076). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidiogenous cells and conidia. d–g Conidia. Scale bars: c–g =10 μm .

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the trunk of *Vitis vinifera*, 4 January 2022, Linna Wu and Xinghong Li (Inactive dry cultures JZBH340076–JZBH340078), living cultures JZB340076–JZB340078.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *P. kenya* with 94% ML bootstrap value and 1.0 BYPP (Fig. 23). *Pestalotiopsis kenya* was reported on *Camellia sinensis* in China (Liu et al. 2017). This is the first report of this species associated with grapevine trunk diseases in the world.

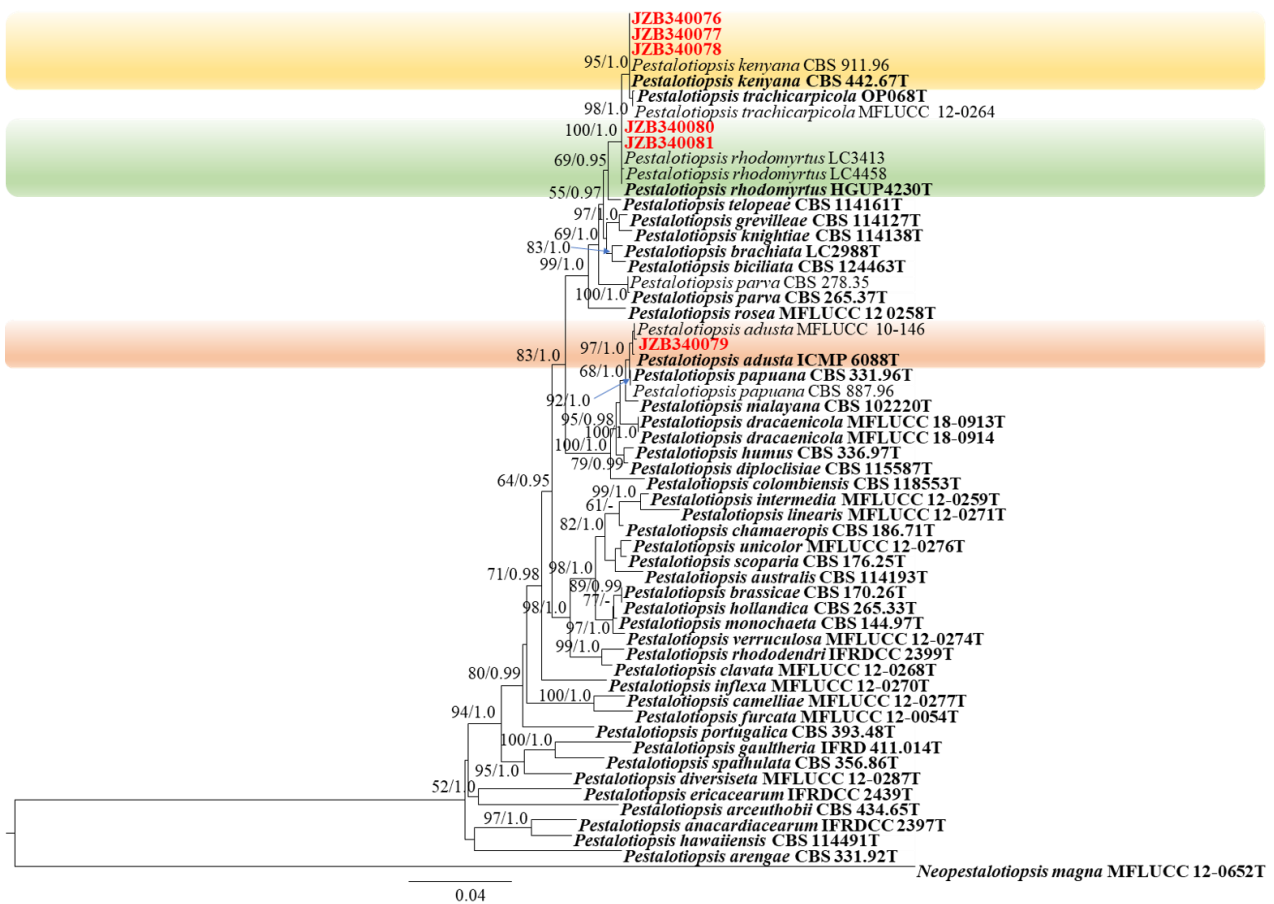


Figure 23 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tub2* and *tefl* sequence data of *Pestalotiopsis* species. *Neopestalotiopsis magna* (MFLUCC 12-0652) was used as the outgroup taxon. The best-scoring RAXML tree with a final likelihood value of -9698.046952 was presented. The matrix had 733 distinct alignment patterns, with 15.42% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.239513, C = 0.293756, G = 0.215210, T = 0.251521; substitution rates AC = 1.226778, AG = 3.764525, AT = 1.325866, CG = 1.211293, CT = 5.305853, GT = 1.000000; gamma distribution shape parameter α = 0.597712. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.04 changes per site. Isolates from the current study are in red and type specimens are in bold.

Pestalotiopsis rhodomyrtus Y. Song, K. Geng, K.D. Hyde & Yong Wang, Phytotaxa 126: 27. 2013.

Index Fungorum: IF846110; Facesoffungi number: FoF 09398

Asexual morph: *Conidiomata* scattered, black. *Conidiogenous cells* discrete, filiform, hyaline. *Conidia* fusoid, straight or slightly curved, 4-septate, $25\text{--}32 \times 5\text{--}7 \mu\text{m}$ ($\bar{x} \pm \text{SD} = 28.6 \pm 1.9 \times 6.0 \pm 0.5 \mu\text{m}$, $n = 50$); basal cell conic to obconic, hyaline; three median cells doliiform, concolorous, brown, septate and periclinal walls darker than the rest of the cell, verruculose; apical cell subcylindrical to obconic, hyaline, with 2–3 tubular appendages arising from the apex of the apical cell, with one filiform, basal appendage (Fig. 24). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were white with crenate edge, reverse light orange with white margin (Fig. 24). Colonies reached 6.9 cm diam after 5 days at 25 °C.

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the trunk of *Vitis vinifera*, 19 January 2022, Linna Wu and Xinghong Li (Inactive dry cultures JZBH340080–JZBH340081), living cultures JZB340080–JZB340081.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *P. rhodomyrtus* with 100% ML bootstrap value and 1.0 BYPP (Fig. 23). *Pestalotiopsis rhodomyrtus* was reported on *Rhodomyrtus tomentosa* and *Camellia sinensis* in China (Liu et al. 2017, Song et al. 2013). This is the first report of this species associated with grapevine trunk diseases in the world.

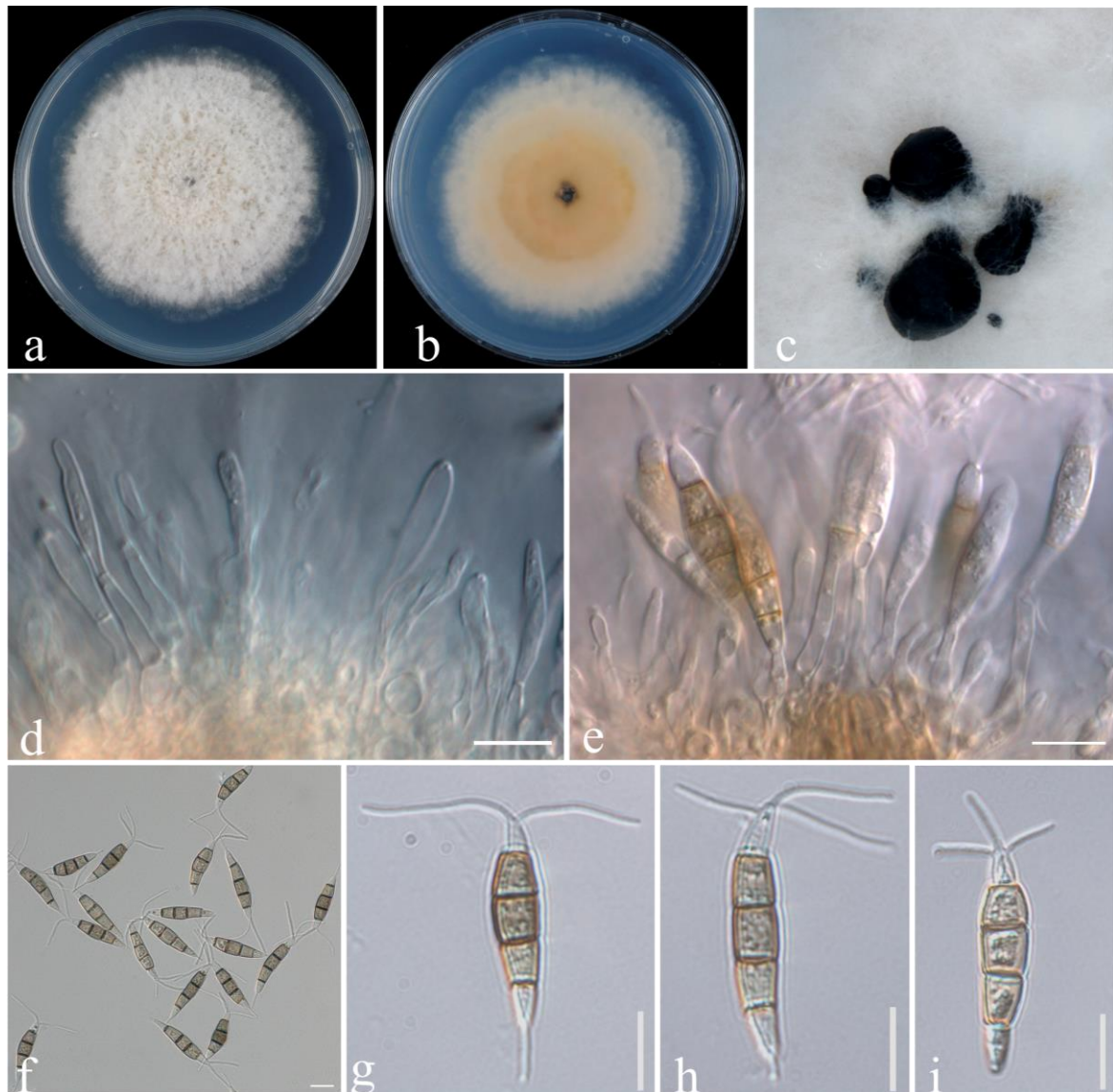


Figure 24 – Morphological characterization of *Pestalotiopsis rhodomyrtus* (JZB340080). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidiomata sporulating on PDA. d, e Conidiogenous cells and conidia. f–i Conidia. Scale bars: c = 100 μ m, d–i = 10 μ m.

Pestalotiopsis adusta (Ellis & Everh.) Steyaert, Trans. Br. mycol. Soc. 36(2): 82 (1953)

Index Fungorum: IF302600; Facesoffungi number: FoF 14323

Asexual morph: *Conidiomata* globose, black. *Conidiogenous cells* discrete, filiform, hyaline. *Conidia* fusiform to ellipsoid, straight or slightly curved, 4-septate, 17–27 \times 5–7 μ m ($\bar{x} \pm SD = 21.7 \pm 2.0 \times 5.8 \pm 0.6 \mu$ m, n = 50); basal cell obtuse, hyaline; three median cells doliiform, concolorous, olivaceous, septate and periclinal walls darker than the rest of the cell, verruculose; apical cell obconic, hyaline, with 2–3 tubular appendages arising from the apex of the apical cell, with one filiform, basal appendage (Fig. 25). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA white with undulate edge, reverse orange (Fig. 25). Colonies reached 8.0 cm diam. after 5 days at 25 °C.

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the root of *Vitis vinifera*, 4 January 2022, Linna Wu and Xinghong Li (Inactive dry cultures JZBH340079), living cultures JZB340079.

Notes – In the multi-locus phylogenetic analysis, one isolate clustered with *P. adusta* with 99% ML bootstrap value and 1.0 BYPP (Fig. 23). *Pestalotiopsis adusta* was reported to cause leaf spot on raspberry and mongo in China (Yan et al. 2019, Shu et al. 2020). This is the first report of the species associated with grapevine trunk diseases in the world.

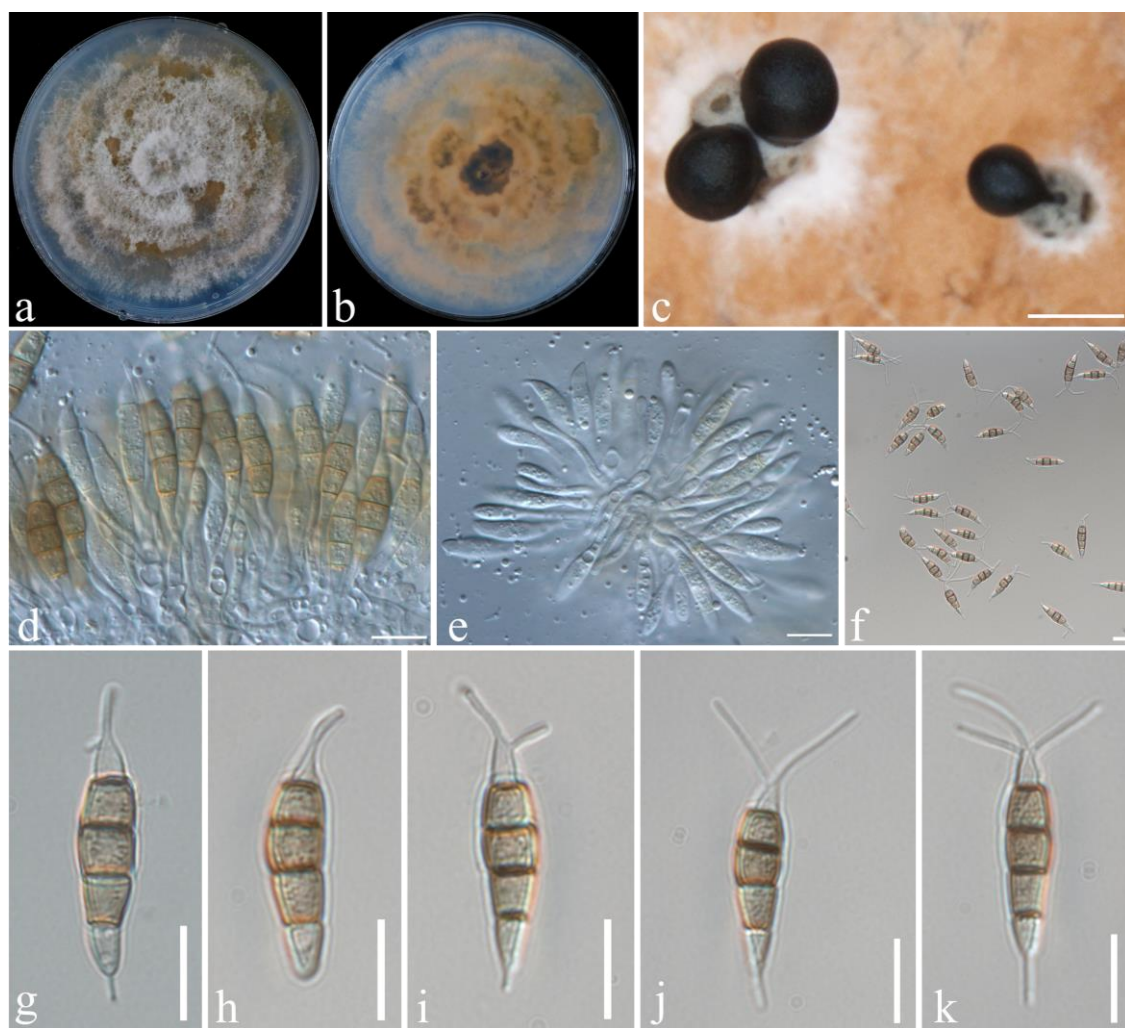


Figure 25 – Morphological characterization of *Pestalotiopsis adusta* (JZB340079). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidiomata sporulating on PDA. d, e Conidiogenous cells and conidia. f–k Conidia. Scale bars: c = 100 μ m, d–k = 10 μ m.

Neopestalotiopsis Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 135 (2014)

Neopestalotiopsis rosae Maharachch., K.D. Hyde & Crous, in Maharachchikumbura, Hyde, Groenewald, Xu & Crous, Stud. Mycol. 79: 147 (2014)

Index Fungorum: IF809777; Facesoffungi number: FoF 03890

Description – See Maharachchikumbura et al. (2014)

Material Examined – China, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living culture JZB340082; *ibid.*, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li, living culture JZB340083.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *N. rosae* with 70% ML bootstrap value and 1.0 BYPP (Fig. 26). The morphological characteristics of these isolates were similar to the type of *N. rosae* (CBS 101057) (Maharachchikumbura et al. 2014). *Neopestalotiopsis rosae* was reported to cause grape rot in the USA (Cosseboom & Hu 2021). This is the first report of *N. rosae* associated with grapevine trunk diseases in China.

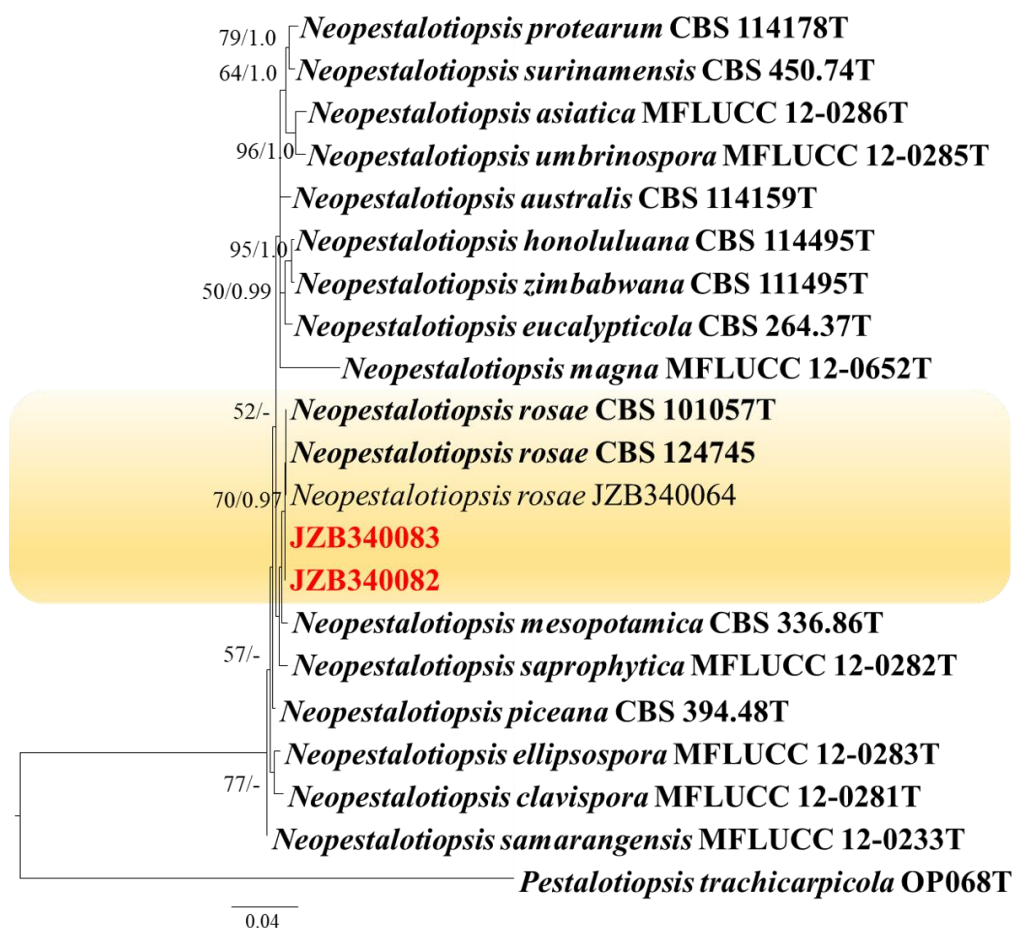


Figure 26 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tub2* and *tef1* sequence data of *Neopestalotiopsis* species. *Pestalotiopsis trachicarpicola* (OP068T) was used as the outgroup taxon. The best-scoring RAxML tree with a final likelihood value of -4690.057697 was presented. The matrix had 220 distinct alignment patterns, with 9.61% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.237087, C = 0.273572, G = 0.213431, T = 0.275910; substitution rates AC = 0.728700, AG = 4.270377, AT = 1.372478, CG = 0.528762, CT = 5.131524, GT = 1.000000; gamma distribution shape parameter α = 0.791052. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.90 (BYPP) are shown near the nodes. The scale bar indicates 0.04 changes per site. Isolates from the current study are in red and type specimens are in bold.

Bartalinia Tassi, Bulletin Labor. Orto Bot. de R. Univ. Siena 3: 4 (1900)

Bartalinia kevinhydei Doilom, Tibpromma & D.J. Bhat, in Tibpromma, Karunarathna, Mortimer, Xu, Doilom & Lumyong, Phytotaxa 474(1): 32 (2020)

Index Fungorum: IF557718; Facesoffungi number: FoF 08146

Asexual morph: *Conidiomata* subglobose. *Conidiogenous cells* ampulliform to subcylindrical, hyaline. *Conidia* subcylindrical, straight or slightly curved, 4-septate, $19\text{--}26 \times 3\text{--}6 \mu\text{m}$ ($\bar{x} \pm \text{SD} = 21.4 \pm 1.7 \times 4.7 \pm 0.6 \mu\text{m}$, $n = 50$); basal cell conic, hyaline, sometimes pale brown, paler than

second to fourth cells; three median cells doliiform, concolorous, pale brown, septate with periclinal walls darker than the rest of the cell; apical cell conical, hyaline, with 3 tubular appendages arising from the apex of the apical cell with one filiform, basal appendage (Fig. 27). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA were yellow-brown in the center and cream color at edge (Fig. 27). Colonies reached 6.2 cm diam after 5 days at 25 °C.

Material Examined – China, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3640001, JZBH3640002), living cultures JZB3640001, JZB3640002; *ibid.*, Ningxia Province, Yinchuan City, on the trunk of *Vitis vinifera*, 15 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3640003, JZBH3640004), living cultures JZB3640003, JZB3640004; *ibid.*, Hebei Province, Changli County, on the trunk of *Vitis vinifera*, 18 October 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3640005, JZB3640006), living cultures JZB3640005, JZB3640006; *ibid.*, Beijing City, Fangshan District, on the trunk of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3640007, JZBH3640008), living cultures JZB3640007, JZB3640008.

Notes – In the multi-locus phylogenetic analysis, eight isolates clustered with *B. kevinhydei* with 67% ML bootstrap value and 1.0 BYPP (Fig. 28). *Bartalinia kevinhydei* is a new leaf-spot causing fungus on teak from Northern Thailand (Tibpromma et al. 2020). This is the first report of *B. kevinhydei* associated with grapevine trunk diseases in the world.

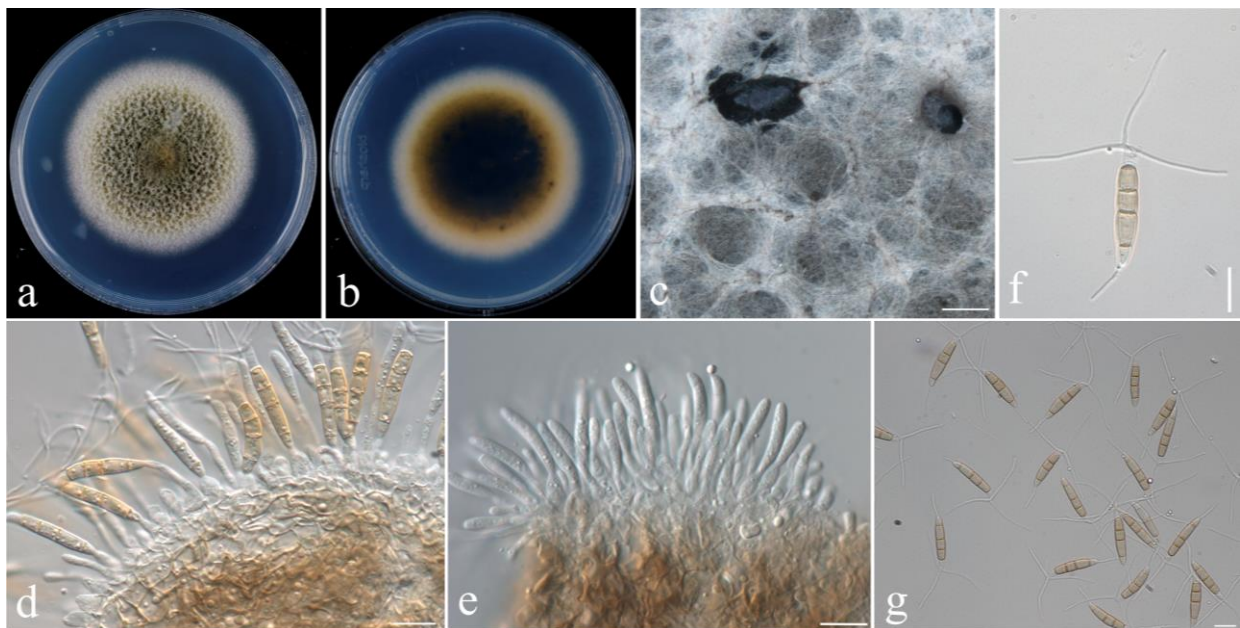


Figure 27 – Morphological characterization of *Bartalinia kevinhydei* (JZB3640003). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidiomata sporulating on PDA. d, e Conidiogenous cells and conidia. f, g Conidia. Scale bars: c = 100 µm, d–g = 10 µm.

Glomerellaceae Locq. ex Seifert & W. Gams, in Zhang, Castlebury, Miller, Huhndorf, Schoch, Seifert, Rossman, Rogers, Kohlmeyer, Volkmann-Kohlmeyer & Sung, *Mycologia* 98(6): 1083 (2007) [2006]

Colletotrichum Corda, in Sturm, *Deutschl. Fl.*, 3 Abt. (Pilze Deutschl.) 3(12): 41 (1831)

Colletotrichum is the only genus in Glomerellaceae and is regarded as one of the top 10 phytopathogenic fungal genera in the world, causing anthracnose on leaves, fruits, stems and other more organs (Dean et al. 2012, Liu et al. 2022). In this study, we follow Liu et al. (2022) for taxonomic treatments.

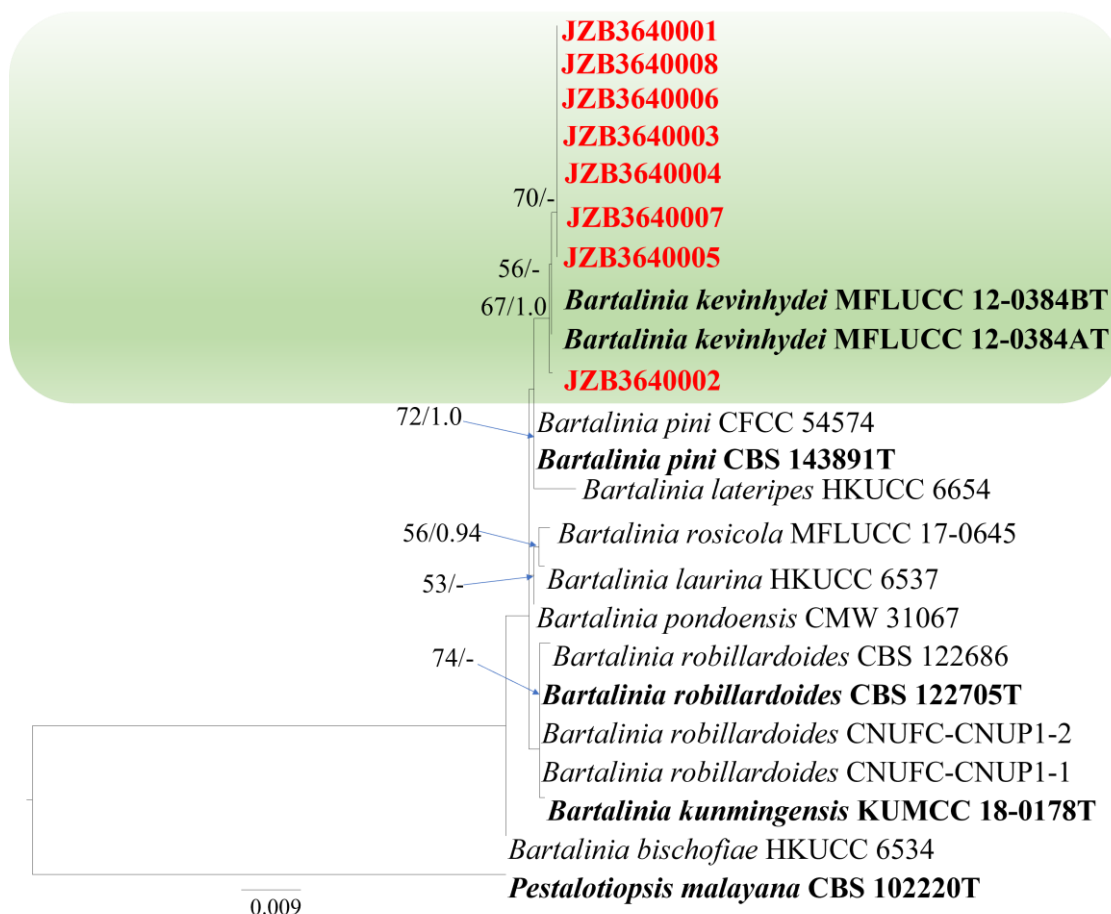


Figure 28 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS and LSU sequence data of *Bartalinia* species. *Pestalotiopsis malayana* (CBS 102220) was used as outgroup taxon. The best scoring RAxML tree with a final likelihood value of -2455.231222 was presented. The matrix had 64 distinct alignment patterns, with 9.62% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.259785, C = 0.205067, G = 0.256605, T = 0.278543; substitution rates AC = 0.000100, AG = 6.135642, AT = 5.163560, CG = 7.199006, CT = 22.594137, GT = 1.000000; gamma distribution shape parameter $\alpha = 1000.000000$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.009 changes per site. Isolates from the current study are in red and type specimens are in bold.

Colletotrichum viniferum Li J. Peng, L. Cai, K.D. Hyde & Zi Y. Ying, Mycoscience 54(1): 36 (2013)

Index Fungorum: IF563086; Facesoffungi number: FoF 03600

Description – See Peng et al. (2013)

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the shoot of *Vitis vinifera*, 20 May 2021, Linna Wu and Xinghong Li, living cultures JZB330319–JZB330322; *ibid.*, Beijing City, on the trunk of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li, living cultures JZB330323, JZB330324.

Notes – In the multi-locus phylogenetic analysis, six isolates clustered with *C. viniferum* with 100% ML bootstrap value and 1.0 BYPP (Fig. 29). *Colletotrichum viniferum* was reported to cause fruit anthracnose and leaf lesions of grapevines in China (Peng et al. 2013, Yan et al. 2015).

Colletotrichum nymphaeae (Pass.) Aa, Netherlands Journal of Plant Pathology, Supplement 1 84(3): 110 (1978)

Index Fungorum: IF311502; Facesoffungi number: FoF 14339

Description – See Damm et al. (2012)

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the shoot of *Vitis vinifera*, 20 May 2021, Linna Wu and Xinghong Li, living cultures JZB330325; *ibid.*, on the trunk of *Vitis vinifera*, 4 January 2022, Linna Wu and Xinghong Li, living cultures JZB330326, JZB330327.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *C. nymphaeae* with 96% ML bootstrap value and 1.0 BYPP (Fig. 29). *Colletotrichum nymphaeae* was reported to cause twig anthracnose on grapevines in China (Liu et al. 2016).

Colletotrichum kahawae J.M. Waller & Bridge, Mycol. Res. 97(8): 993 (1993)

Index Fungorum: IF360355; Facesoffungi number: FoF 14359

Asexual morph: *Conidiophores* hyaline, one-celled, not branching. *Conidia* cylindrical, 10–15 × 5–8 μm ($\bar{x} \pm SD = 12.8 \pm 1.1 \times 6.5 \pm 0.6$ μm, n = 50). *Appressoria* spherical, ovoid or slightly irregular (Figure 30). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA white to pale grey, reverse dark gray with white margin. Colonies reached 6.5 mm diam. after 5 days at 25 °C (Fig. 30).

Material Examined – China, Yunnan Province, Mile City, on the trunk of *Vitis vinifera*, 9 September 2020, Linna Wu and Xinghong Li (Inactive dry cultures JZBH330328), living cultures JZB330328.

Notes – In the multi-locus phylogenetic analysis, one isolate clustered with *C. kahawae* with 89% ML bootstrap value and 1.0 BYPP (Fig. 29). *Colletotrichum kahawae* was reported to cause grape ripe rot disease in Brazil (Echeverrigaray et al. 2020). This is the first report of *C. kahawae* associated with grapevine trunk disease in China.

Pleosporaceae Nitschke, Verh. naturh. Ver. preuss. Rheinl. 26: 74 (1869)

Alternaria Nees, Syst. Pilze (Würzburg): 72 (1816) [1816-17]

Alternaria widely distributed in various substrates as saprobes, endophytes and pathogens, and has numerous hosts including grapevine (Woudenberg et al. 2013, Tao et al. 2014). In this study, eight isolates belonging to two *Alternaria* species were identified. For taxonomic treatments, we follow Woudenberg et al. (2013).

Alternaria alternata (Fr.) Keissl., Beih. bot. Zbl., Abt. 2 29: 434 (1912)

Index Fungorum: IF119834; Facesoffungi number: FoF 03825

Description – See Woudenberg et al. (2013)

Asexual morph: China, Shanxi Province, Linfen City, on the trunk of *Vitis vinifera*, 23 June 2021, Linna Wu and Xinghong Li, living cultures JZB3180127, JZB3180128; *ibid.*, Hebei Province, Zhangjiakou City, Huailai County, on the trunk of *Vitis vinifera*, 9 July 2021, Linna Wu and Xinghong Li, living cultures JZB3180129, JZB3180130; *ibid.*, Qinhuangdao City, Changli County, on the trunk of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li, living cultures JZB3180131; *ibid.*, Fujian Province, Longyan City, Shanghang County, on the trunk of *Vitis vinifera*, 4 January 2022, Linna Wu and Xinghong Li, living culture JZB3180132.

Notes – In the multi-locus phylogenetic analysis, six isolates clustered in two clades of *A. alternata* with 97% ML bootstrap value and 1.0 BYPP (Fig. 31). *Alternaria* is a widespread fungus, which includes saprobic, endophytic and pathogenic species. *Alternaria alternata* is a well-known plant pathogen around the world, and is reported to cause grapevine fruit rot and also act as endophytes and saprotrophs on grapevine (Jayawardena et al. 2018).

Alternaria longipes (Ellis & Everh.) E.W. Mason, Annot. Acct Fungi rec'd Bur. Mycol. 2(1): 19 (1928)

Index Fungorum: IF269712; Facesoffungi number: FoF 14360

Asexual morph: *Conidiophores* light to dark brown with one or a few regular septa, mostly unbranched. *Conidia* obclavate, brown, with three to eight transverse and zero to two longitudinal or oblique septa, 10–32 × 6–14 μm ($\bar{x} \pm SD = 20.0 \pm 5.3 \times 10.7 \pm 2.0 \mu\text{m}$, n = 50), and concatenated in long, sometimes branched chains (Fig. 32). Sexual morph: Not observed.



Figure 29 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *gapdh*, *act*, *chs* and *tub2* sequence data of *Colletotrichum* species. *Monilochaetes infuscans* (CBS 869.96)

was used as the outgroup taxon. The best scoring RAxML tree with a final likelihood value of -11791.239474 was presented. The matrix had 941 distinct alignment patterns, with 13.45% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.232433, C = 0.302405, G = 0.240309, T = 0.224853; substitution rates AC = 1.238239, AG = 3.563826, AT = 1.094851, CG = 0.802739, CT = 5.163031, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.983971$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.07 changes per site. Isolates from the current study are in red and type specimens are in bold.

Culture characteristics – Colonies on PDA were initially white and became grayish brown over time, reverse dark brown with white margin (Fig. 32). Colonies reached 6.5 mm diam. after 6 days at 25 °C.

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the trunk of *Vitis vinifera*, 4 January 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3180133, JZBH3180134), living cultures JZB3180133, JZB3180134.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *A. longipes* with 100% ML bootstrap value and 1.0 BYPP (Fig. 31). *Alternaria longipes* has been reported to cause leaf spot disease in tea and some medicinal plants in China (Tan et al. 2012, Yin et al. 2021). This is the first report of *A. longipes* associated with grapevine trunk disease in the world.

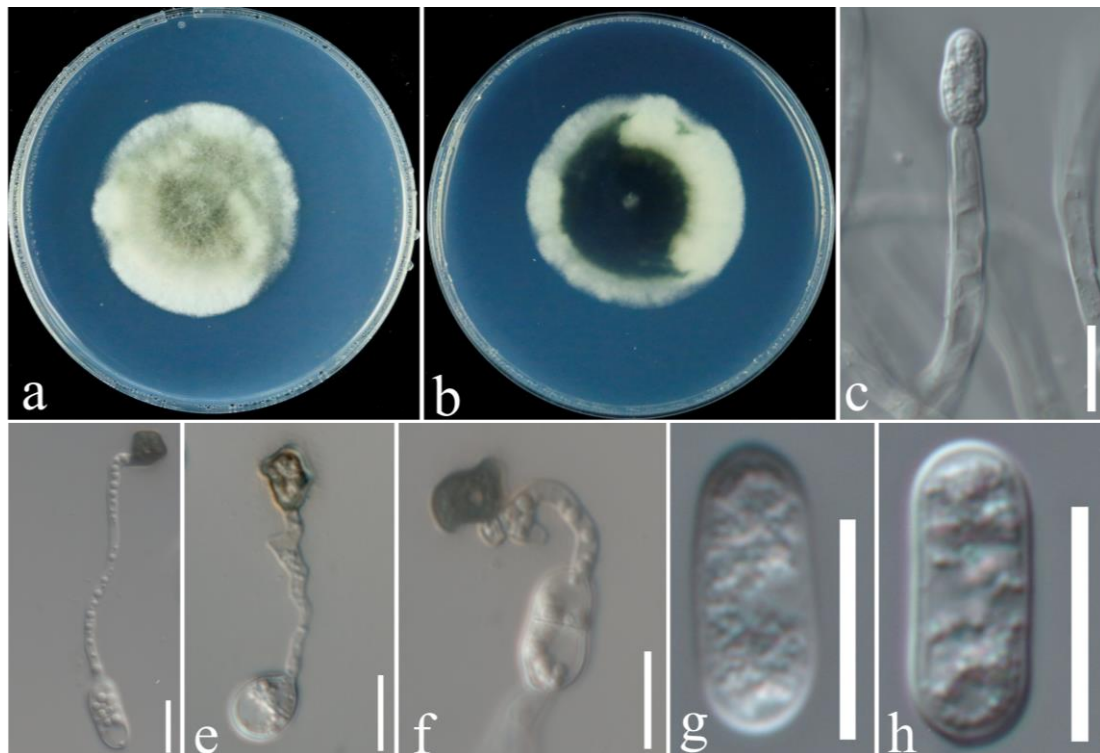


Figure 30 – Morphological characterization of *Colletotrichum kahawae* (JZB330328). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidiophores. d–f Appressoria. g, h Conidia. Scale bars: c–h = 10 μ m.

Hypocreaceae De Not. [as ‘Hypocreacei’], G. bot. ital. 2(1): 48 (1844)

Trichoderma Pers., Neues Mag. Bot. 1: 92 (1794)

Trichoderma is a widespread genus with abilities or potentials to be developed as biocontrol agents, for their potent degradative machinery for decomposition of heterogeneous substrates (Schuster & Schmoll 2010). In this study, six isolates belonging to three *Trichoderma* species were identified. For taxonomic treatments, we follow Cai et al. (2022).

Trichoderma asperellum Samuels, Lieckf. & Nirenberg, Sydowia 51(1): 81 (1999)

Index Fungorum: IF461012; Facesoffungi number: FoF 14361

Asexual morph: *Conidiophores* tree-like, with repeated, paired branching with a main central branch. Phialides flask-shaped, enlarged in the middle. *Conidia* globose to oval, green, smooth, 3–4 × 2–3 μm ($\bar{x} \pm SD = 3.2 \pm 0.2 \times 2.8 \pm 0.2 \mu\text{m}$, n = 50). *Chlamydospores* elliptic or round (Fig. 33). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA initially whitish, downy, gradually green sporulation spread throughout the whole plate, reverse grayish with the formation of concentric rings (Fig. 33). Colonies reached 6.0 mm diam. after 2 days at 25 °C.

Material Examined – China, Yunnan Province, Binchuan County, on the trunk of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3360013), living culture JZB3360013; *ibid.*, on the root of *Vitis vinifera*, 23 July 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3360014, JZBH3360015), living cultures JZB3360014, JZB3360015.

Notes – In the multi-locus phylogenetic analysis, three isolates clustered with *T. asperellum* with 98% ML bootstrap value and 1.0 BYPP (Fig. 34). *Trichoderma asperellum* was reported to isolate from withered grape in Italy (Lorenzini et al. 2016). This is the first report of *T. asperellum* associated with grapevine trunk disease in China.

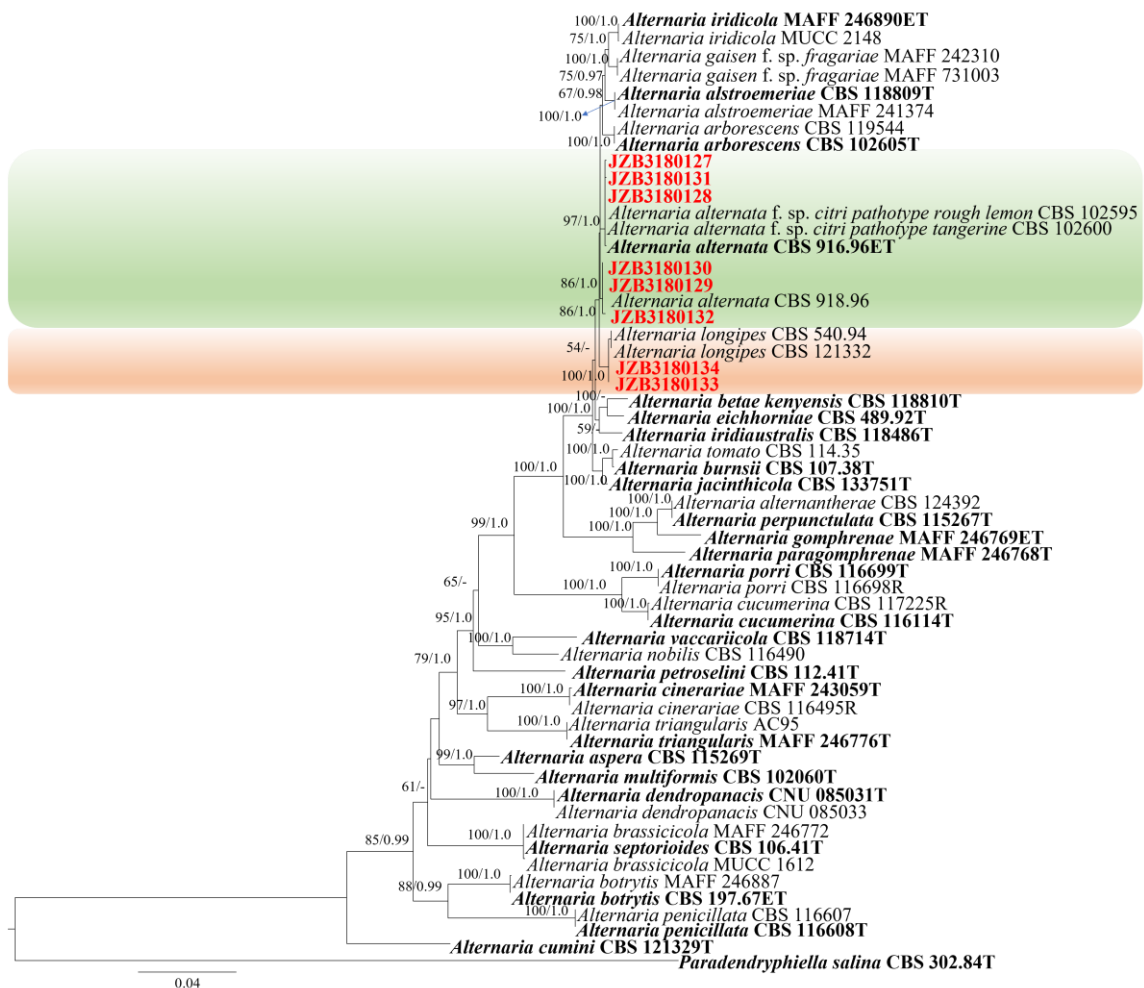


Figure 31 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tef1*, *rpb2* and *gapdh* sequence data of *Alternaria* species. *Paradendryphiella salina* (CBS 302.84) was used as the outgroup taxon. The best scoring RAXML tree with a final likelihood value of -11419.172816 was presented. The matrix had 820 distinct alignment patterns, with 11.89% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.241820, C = 0.277132, G = 0.247459, T = 0.233589; substitution rates AC = 1.364113, AG = 4.480928, AT =

1.081367, CG = 0.860134, CT = 10.450729, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.900455$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.04 changes per site. Isolates from the current study are in red and type specimens are in bold.

Trichoderma guizhouense Q.R. Li, McKenzie & Yong Wang bis, in Li, Tan, Jiang, Hyde, McKenzie, Bahkali, Kang & Wang, Mycol. Progr. 12(2): 170 (2012) [2013]

Index Fungorum: IF563664; Facesoffungi number: FoF 07838

Asexual morph: *Conidiophores* verticillate. *Phialides* ampulliform to lageniform, mostly in whorls of 2–3. *Conidia* oval to globose, yellow-green, smooth, $3\text{--}4 \times 2\text{--}3 \mu\text{m}$ ($\bar{x} \pm \text{SD} = 3.2 \pm 0.2 \times 2.8 \pm 0.2 \mu\text{m}$, $n = 50$). *Chlamydospores* elliptic or round, terminal (Fig. 35). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA cottony, dark green, forming concentric rings. Colonies reached 6.8 mm diam. after 2 days at 25 °C (Fig. 35).

Material Examined – China, Beijing City, on the root of *Vitis vinifera*, 11 September 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3360016, JZBH3360017), living cultures JZB3360016, JZB3360017.

Notes – In the multi-locus phylogenetic analysis, two isolates clustered with *T. guizhouense* with 90% ML bootstrap value and 1.0 BYPP (Fig. 34). *Tritroderma guizhouense* was initially isolated from soil in Guizhou Province, China (Li et al. 2013). This is the first report of *T. guizhouense* associated with grapevine trunk diseases.

Trichoderma virens (J.H. Mill., Giddens & A.A. Foster) Arx, Beih. Nova Hedwigia 87: 288 (1987)

Index Fungorum: IF128198; Facesoffungi number: FoF 14362

Asexual morph: *Conidiophores* erect, asymmetrical branched. *Phialides* flask-shaped to ampulliform. *Conidia* sub-globose to elliptical, green, smooth, $4\text{--}6 \times 3\text{--}5 \mu\text{m}$ ($\bar{x} \pm \text{SD} = 4.5 \pm 0.4 \times 3.8 \pm 0.3 \mu\text{m}$, $n = 50$). *Chlamydospores* elliptic or round (Fig. 36). Sexual morph: Not observed.

Culture characteristics – Colonies on PDA initially whitish, gradually became deep green, reverse grayish. Colonies reached 5.9 mm diam. after 2 days at 25 °C (Fig. 36).

Material Examined – China, Hebei Province, Qinhuangdao City, Changli County, on the root of *Vitis vinifera*, 13 November 2021, Linna Wu and Xinghong Li (Inactive dry cultures JZBH3360018), living cultures JZB3360018.

Notes – In the multi-locus phylogenetic analysis, one isolate clustered with *T. virens* with 100% ML bootstrap value and 1.0 BYPP (Fig. 34). *Trichoderma virens* was commonly isolated from the soil, and also reported as an endophyte of sugarcane and coffee (Romão-Dumaresq et al. 2016, Rodríguez et al. 2021). *Trichoderma virens* was isolated from a 42-year-old grapevine free of grapevine trunk disease symptoms in France (Bruez et al. 2016). This is the first report of *T. virens* associated with grapevine trunk disease in China.

Cladosporiaceae Chalm. & R.G. Archibald, Yearbook of Tropical Medicine and Hygiene: 25 (1915)

Cladosporium Link, Mag. Gesell. naturf. Freunde, Berlin 7: 37 (1816) [1815]

Cladosporium is a ubiquitous genus with small conidia in large numbers, spread easily over long distances. *Cladosporium* species are common endophytes, and also could be secondary invaders after other plant pathogens, causing leaf spots (Bensch et al. 2012). In this study, we follow Bensch et al. (2012) for taxonomic treatments.

Cladosporium tenuissimum Cooke, Grevillea 6(no. 40): 140 (1878)

Index Fungorum: IF145672; Facesoffungi number: FoF 09313

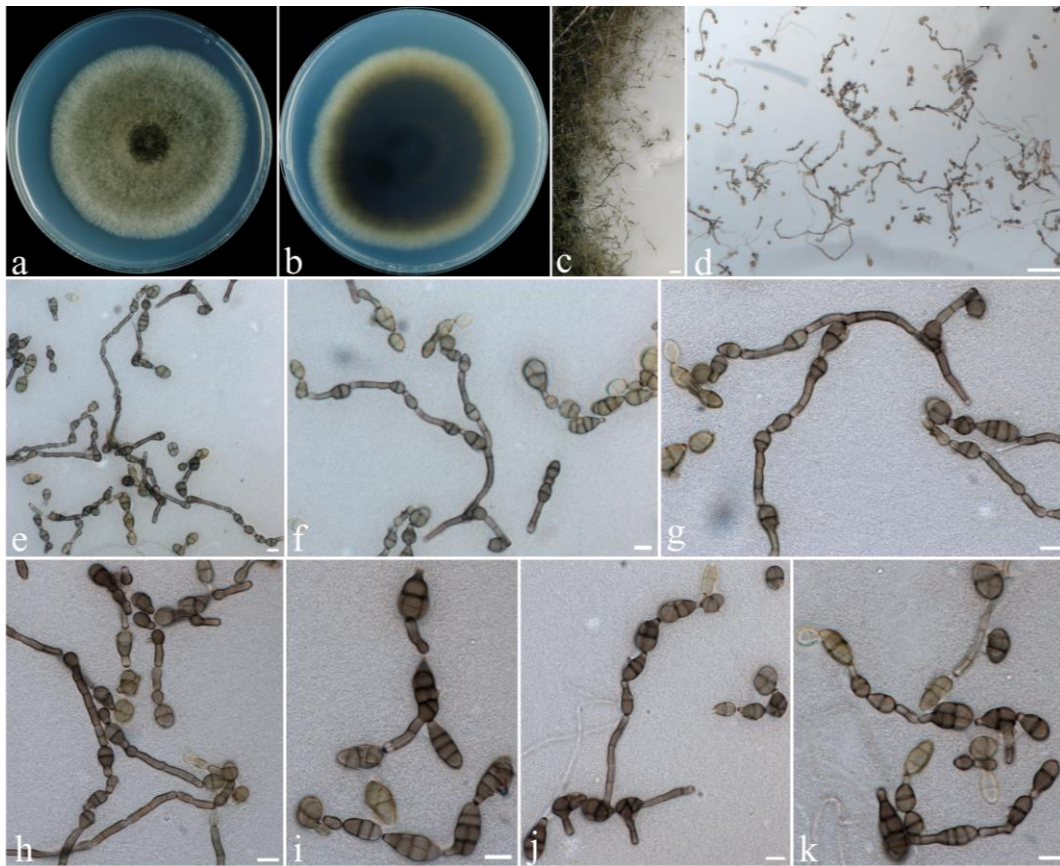


Figure 32 – Morphological characterization of *Alternaria longipes* (JZB3180133). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c–k Conidia and conidiophores. Scale bars: c = 500 μ m, d = 100 μ m, e–k = 10 μ m.

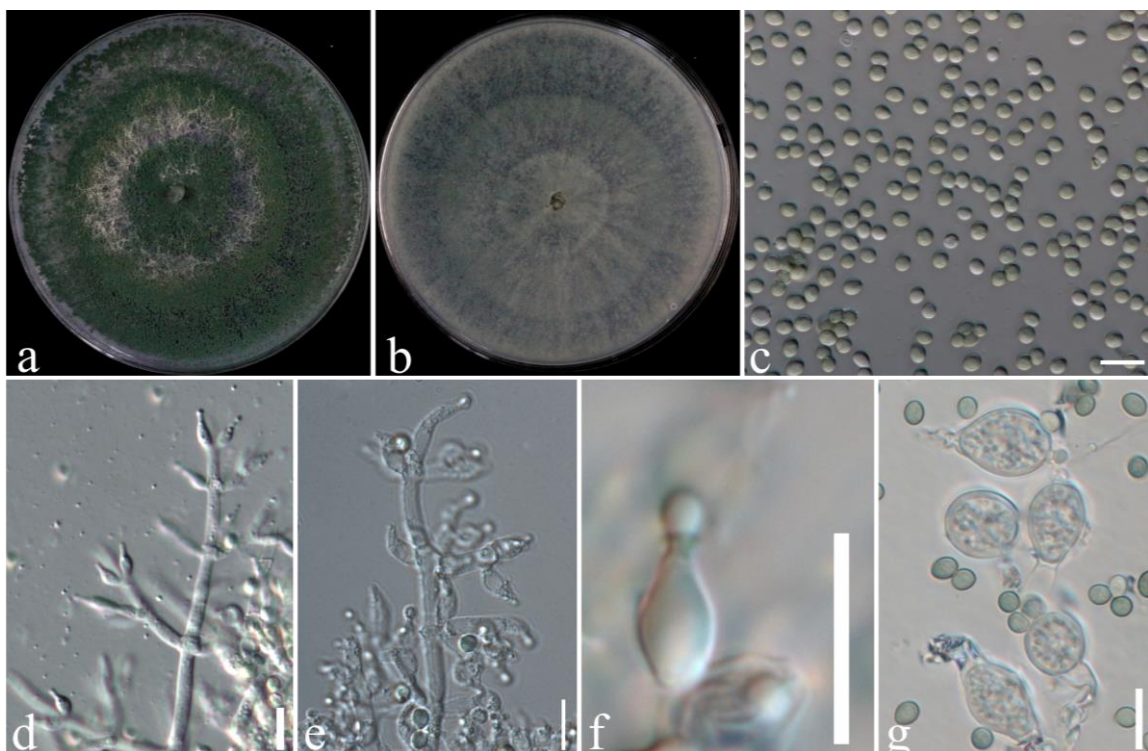


Figure 33 – Morphological characterization of *Trichoderma asperellum* (JZB3360013). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidia. d, e Conidiophores. f phialide. g Chlamydospores. Scale bars: c–g = 10 μ m.

Description – See Bensch et al. 2012

Material Examined – China, Fujian Province, Longyan City, Shanghang County, on the trunk of *Vitis vinifera*, 4 January 2021, Linna Wu and Xinghong Li, living cultures JZB390038, JZB390039.

Notes – In the multi-locus phylogenetic analysis, eight isolates clustered with *C. tenuissimum* with 99% ML bootstrap value and 1.0 BYPP (Fig. 37). *Cladosporium tenuissimum* was reported as a pathogen causing grapevine fruit rot and/or as an endophytic fungus on grapevines in China (Dissanayake et al. 2018, Jayawardena et al. 2018).

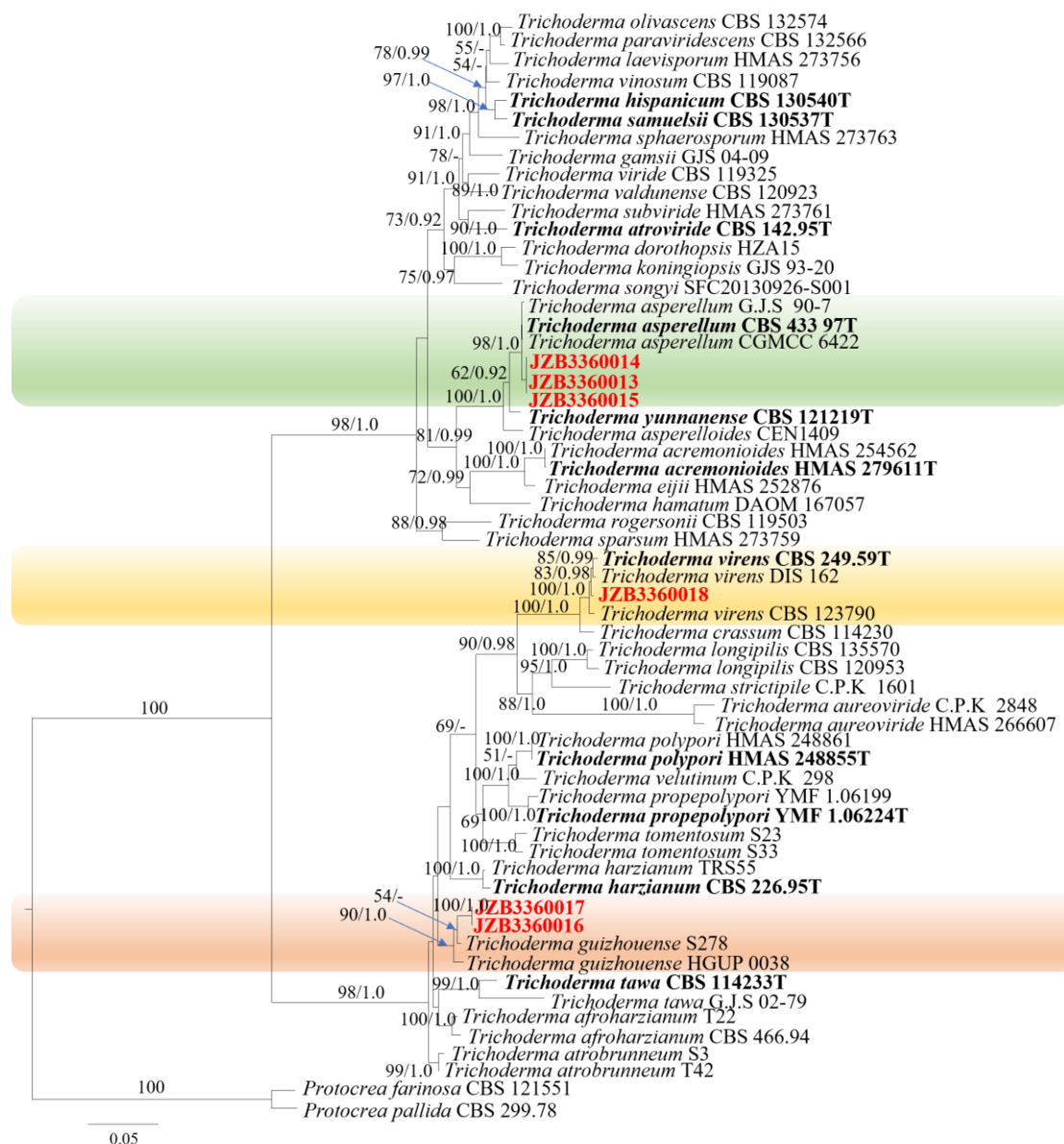


Figure 34 – Phylogenetic tree generated by maximum likelihood analysis of combined *tef1* and *rpb2* sequence data of *Trichoderma* species. *Protocrea farinosa* (CBS 121551) and *Protocrea pallida* (CBS 299.78) were used as the outgroup taxa. The best-scoring RAxML tree with a final likelihood value of -16356.159894 was presented. The matrix had 916 distinct alignment patterns, with 17.53% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.235351, C = 0.280622, G = 0.241553, T = 0.242473; substitution rates AC = 0.812912, AG = 3.702497, AT = 1.233164, CG = 0.719097, CT = 5.223883, GT = 1.000000; gamma distribution shape parameter $\alpha = 1.063259$. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.05 changes per site. Isolates from the current study are in red and type specimens are in bold.

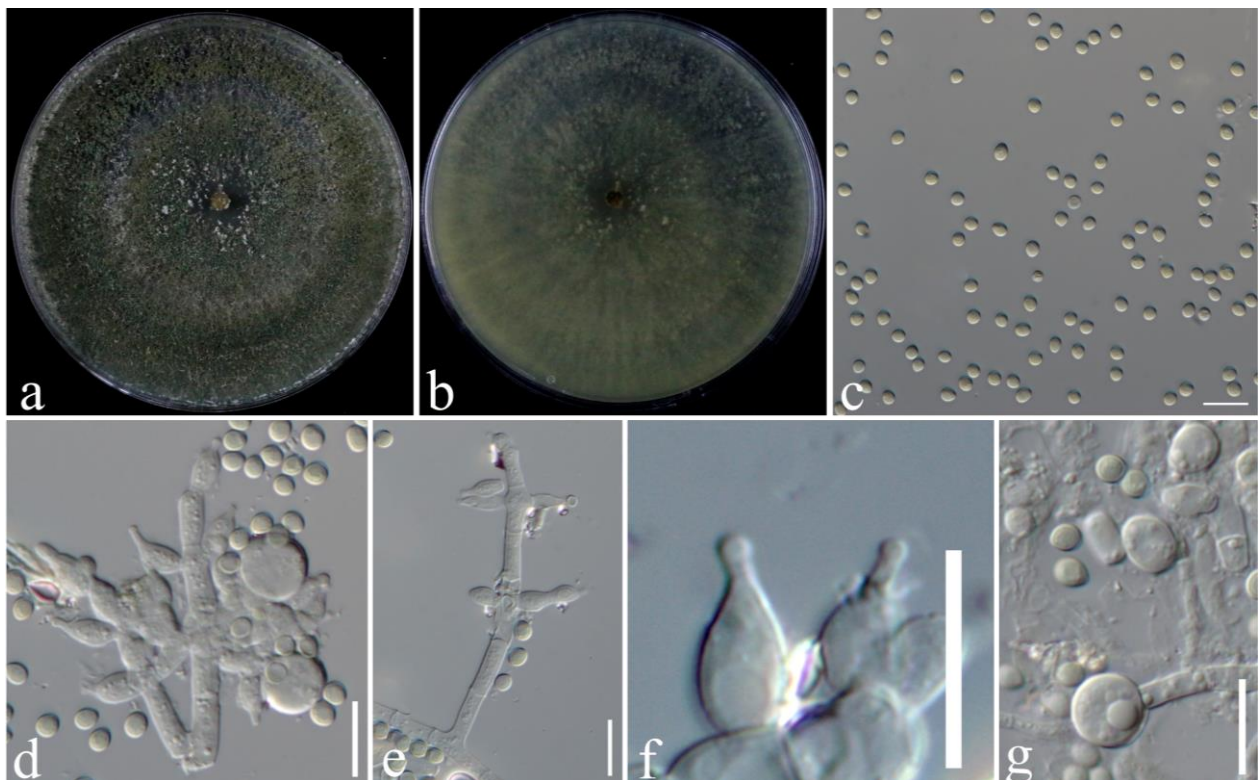


Figure 35 – Morphological characterization of *Trichoderma guizhouense* (JZB3360016). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidia. d, e Conidiophores. f phialide. g Chlamydospores. Scale bars: c–g = 10 μ m.

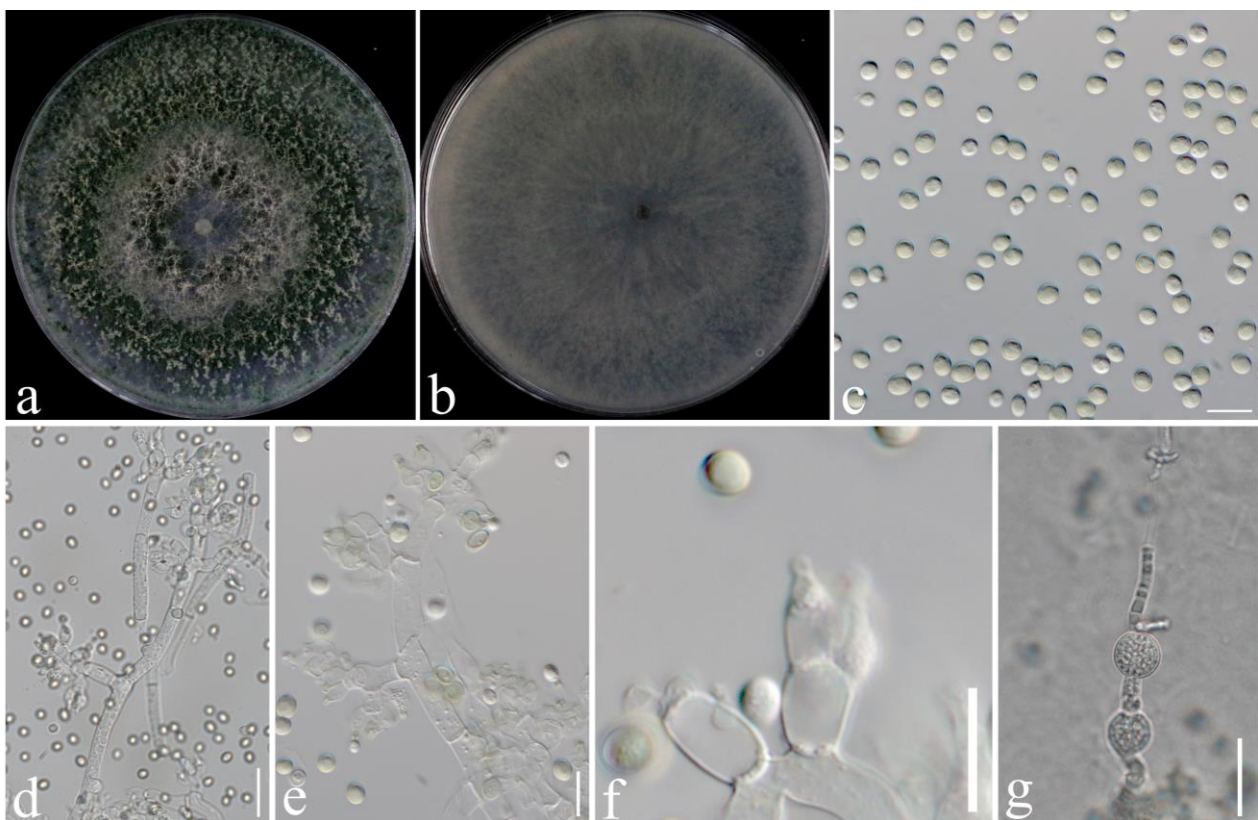


Figure 36 – Morphological characterization of *Trichoderma virens* (JZB3360018). a Upper view of the colony on PDA. b Reverse view of the colony on PDA. c Conidia. d, e Conidiophores. f phialide. g Chlamydospores. Scale bars: c–g = 10 μ m.

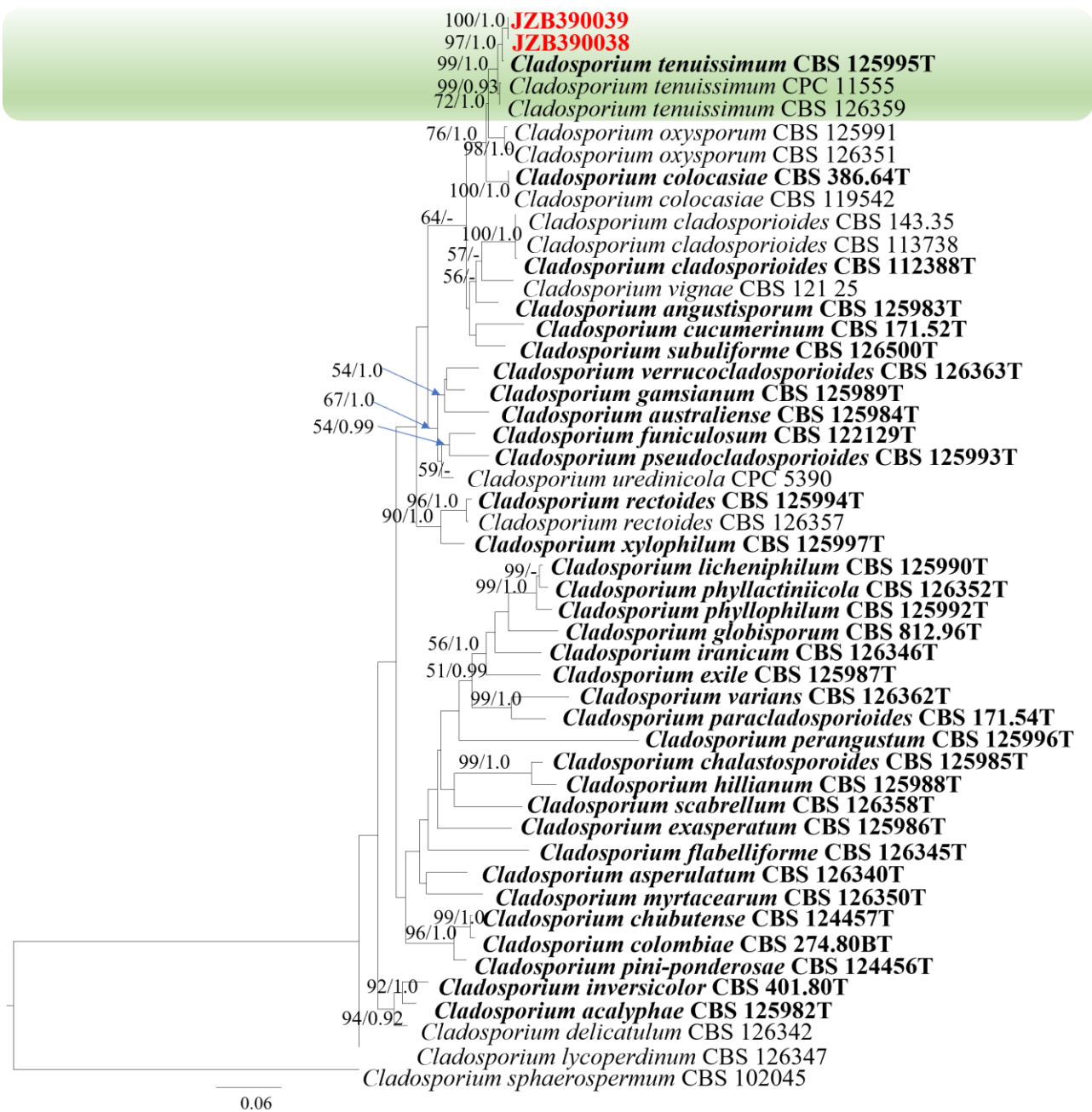


Figure 37 – Phylogenetic tree generated by maximum likelihood analysis of combined ITS, *tef1* and LSU sequence data of *Cladosporium* species. *Cladosporium sphaerospermum* (CBS 102045) was used as the outgroup taxon. The best scoring RAXML tree with a final likelihood value of -6579.450688 was presented. The matrix had 293 distinct alignment patterns, with 4.16% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.224955, C = 0.297835, G = 0.240548, T = 0.236662; substitution rates AC = 2.713837, AG = 5.914225, AT = 2.658810, CG = 1.741064, CT = 8.493258, GT = 1.000000; gamma distribution shape parameter α = 0.651559. ML bootstrap support values $\geq 50\%$ (BT) and Bayesian posterior probabilities ≥ 0.95 (BYPP) are shown near the nodes. The scale bar indicates 0.06 changes per site. Isolates from the current study are in red and type specimens are in bold.

Discussion

Grapevine trunk diseases are a huge threat to the sustainable development of the viticulture and viniculture industries, resulting in reduced yields and limited vineyard lifespans (Úrbez-Torres et al. 2020). At the same time, multiple fungal taxa have been recognized to be associated with a

specific disease, and field symptoms are complex due to the mixed infection of different pathogens (Patanita et al. 2022). Roles of potential pathogens, effects of endophyte and saprobes, and their interactions among the fungal communities remain unclear. In this study, a total of 40 species belonging to 21 genera in 10 families were identified based on multi-locus phylogenetic analyses and morphological observations. Among them, 22 were first reports on grapevine in China and 13 species were first recorded on grapevine in the world. The top three taxa, *Diaporthe* (19.6%), *Cylindrocarpon*-like fungi (19.1%) and Botryosphaeriaceae (18.6%) accounted for more than half of the total isolates, which are well-established as pathogens causing grapevine trunk disease.

Diaporthe is an important fungal pathogen of grapevine trunk disease around the world, and extensive research has been done on the disease; *Diaporthe dieback*. In China, *Diaporthe eres* was proved to be the most commonly isolated species in both studies in 2015 and 2019 (Dissanayake et al. 2015a, Manawasinghe et al. 2019). Thus, the result from the present study also accepts this conclusion. Black foot disease is a devastating grapevine trunk disease caused by *Cylindrocarpon*-like fungi, which are common in nurseries and young plantations worldwide (Lawrence et al. 2019). In this study, six *Cylindrocarpon*-like fungal species, belonging to *Dactylonectria*, *Ilyonectria* and *Cylindrocladiella* were identified. Ye et al. (2021a) reported *D. alcacerensis*, *D. torresensis*, *D. macrodidyma* for the first time in China, and *D. novozelandica* has been recently proven to be grapevine pathogens (Tan et al. 2022). *Ilyonectria liriodendri* and *Cylindrocladiella viticola* are common pathogens in many countries, however they have never been reported in China from grapevine previously.

Botryosphaeriaceae encompasses diverse members of pathogens and are regarded as plant opportunistic fungal pathogens (Phillips et al. 2013, Chethana et al. 2016). These species are important pathogens on grapevine and are associated with a series of diseases including leaf spots, shoot dieback, perennial cankers, vascular discoloration and fruit rots (Úrbez-Torres 2011). More than 20 species from Botryosphaeriaceae have been reported to cause Botryosphaeria dieback (Gramaje et al. 2018). Most Botryosphaeriaceae species isolated and identified in this study have been proven to cause Botryosphaeria dieback in China (Yan et al. 2013, Jayawardena et al. 2018, Wu et al. 2021). *Phaeobotryon rhois* which belongs to Botryosphaeriaceae, has not reported for causing diseases on grapevine. However, this species has been reported to cause branch wilt of *Ulmus pumila* L. and *Rubus crataegifolius* Bge in China (Liu et al. 2020, Zhu et al. 2020).

In addition, two *Phaeoacremonium iranianum* isolates were identified in this study. *Phaeoacremonium* has been reported worldwide for its association with Esca disease, which has become a major concern in all grape-growing countries during the past decades (Hofstetter et al. 2012). However, *Phaeoacremonium iranianum* has not been reported from grapevine in China before. Therefore, based on our collection, this species might be also Esca pathogen which required further confirmation with pathogenicity tests. Pestalotiopsis-like fungi can also cause grapevine trunk disease showing wedge-shaped cankers and bleached canes with slitting (Jayawardena et al. 2015), while species in the current study (*P. kenyana*, *P. rhodomyrtus* and *P. adusta*) have not been reported from grapevine in the world yet.

In addition to the grapevine trunk diseases, several species isolated from this study are associated with grapevines causing different diseases. *Coniella* and *Colletotrichum* are commonly known as grape-fruit pathogens. *Coniella vitis* first reported in 2017 as a novel species causing white rot in China (Chethana et al. 2017). *Colletotrichum* species, including *C. nymphaeae* and *C. viniferum* reported in this study, were reported to cause anthracnose with symptoms of fruit ripe rot and twig dieback (Yan et al. 2015, Liu et al. 2016). *Pestalotiopsis*-like species were also reported to cause fruit rot (Jayawardena et al. 2015). This may prove that the grapevine pathogens not only exist in the main tissues, but also infect other tissues. The roles of these pathogenic taxa on the trunk and root need to be further explored.

Fusarium-like genera comprise many taxa with economic importance, acting as pathogens, saprophytes or endophytes, as well as secondary pathogens (Leslie & Summerell 2006, Crous et al. 2021). In 1995, *Fusarium oxysporum* was isolated from the roots of declining grapevine in Australia (Highet & Nair 1995). Recent studies have also identified *Fusarium* species in grapevine

nurseries and vineyards. Several *Fusarium* species have been reported as pathogens on grapevines, indicating that *Fusarium* can transfer to being weak or latent pathogens in grapevines from endophytic phases under favourable conditions (Úrbez-Torres et al. 2020). In this study, nine *Fusarium*-like species were identified, belonging to *Fusarium*, *Neocosmospora* and *Bisifusarium*. Except for *F. oxysporum*, other species have not been reported on grapevines in China (Jayawardena et al. 2018). However, the exact life mode and pathogenicity mechanisms of these isolates need to be further explored.

According to the above results, these isolated fungal taxa may have different effects on the grapevine. Grapevine wood is a highly competitive habitat, with the simultaneous presence of plant pathogens and beneficial, potentially protective fungi (Kraus et al. 2019). Pathogenic fungi can change the biotrophic mode from pathogenic to saprotrophic, and become active again once the conditions become favourable, being the primary source of inoculant in a vineyard (Jayawardena et al. 2018). On the other hand, the effect of endophytes on plant disease can be antagonistic, and fungal endophytes diversity can influence the severity of plant diseases (Busby et al. 2016). Thus, the roles of saprotroph, endophyte, and pathogen need to be clarified by pathogenicity tests, and interactions between different communities need to be explored.

Rather than focus on one of the grapevine trunk diseases, our study conducted an extensive survey on the diverse fungi that covered the main grapevine trunk disease symptoms in China in recent years. This results not only reported new records on the grapevine but also expanded the isolation source of some species compared to previous studies in China (Yan et al. 2013, Ye et al. 2021a, b). For example, *Botryosphaeria dothidea*, *Dactylonectria novozelandica*, *D. macrodidyma*, *Lasiodiplodia pseudotheobromae* and *Neofusicoccum parvum* were first recorded in Yunnan Province; *Alternaria alternata*, *Cladosporium tenuissimum*, *Colletotrichum nymphaeae*, *C. viniferum* and *Diaporthe unshiuensis* were first reported in Fujian Province; *Dactylonectria alcacerensis* and *D. macrodidyma* were first recorded in Beijing; *Dactylonectria alcacerensis* and *L. pseudotheobromae* were first recorded in Hebei Province; and *D. torresensis* was first recorded in Ningxia Province. This may be because of the increase of investigated regions, the transfer of fungi between hosts, as well as the transportation of seedlings carrying pathogens (Manawasinghe et al. 2018).

In addition to the parts of sampling and collection site, their distribution, diversity and proportion of fungal taxa may be influenced by climate, environment, and management practices (Mondello et al. 2018). The previous research on the geographical distribution of Botryosphaeriaceae species causing grapevine dieback in China showed that *L. theobromae* was isolated primarily from subtropical monsoon climate regions of China, *Diplodia seriata* isolated primarily from temperate monsoon climate regions, *Neofusicoccum parvum* primarily isolated from central and south China, and *Botryosphaeria dothidea* was isolated from north to south throughout China (Yan et al. 2013). Our results also support these conclusions. Furthermore, these infections may occur through the wounds made during the grapevine planting, or the propagation process, including pruning, retraining, trimming, and de-suckering (Gramaje et al. 2018, Berlanas et al. 2020). To determine the occurrence dynamics of the fungi associated with grapevine trunk disease throughout China, the field of investigation should further enlarge, and more samples should be collected.

The grapevine trunk diseases in fields are usually a mix of different disease types caused by various pathogens rather than a single one. Due to the complexity of the disease and the lack of the most effective chemical products, the management of grapevine trunk diseases is difficult (Gramaje et al. 2018). For pathogens inhabiting vascular tissues, chemical sprays and dips used for controlling surface pathogens could hardly penetrate dormant grapevine cuttings sufficiently (Waite & May 2005). It is well-accepted that grapevine trunk diseases should be managed by an integrated disease management strategy, including biological control (Gramaje et al. 2018). *Trichoderma* species are capable of efficient utilization of neighbouring substrates, as well as competitive aggression by secreting antibiotic metabolites and enzymes. With their antagonistic ability, some species have successfully been used in the commercial biological control of fungal pathogens

(Schuster & Schmoll 2010, Lopes et al. 2012). The control efficiency of *Trichoderma* on fungi associated with grapevine trunk disease was demonstrated in the field and nurseries (Kraus et al. 2019). For example, *T. atroviride* and *T. harzianum* applied to the control of Esca caused by *Phaeoconiella chlamydospora* and *Phaeoacremonium* species in nurseries (Pertot et al. 2016, Marco & Osti 2007), and *T. harzianum* was applied to prevent infection of *Eutypa lata* on grapevine pruning wounds (John et al. 2005). In the current study, three *Trichoderma* species were identified. *Trichoderma virens* is one of the most common biological control agents (BCAs). It has excellent control compared to other fungicides against *Pythium ultimum* infecting cotton and *Rhizoctonia solani* infecting tobacco (Benítez et al. 2004) and was observed to have mediate resistance in tomatoes against Fusarium wilt (Jogaiah et al. 2018). *Trichoderma asperellum* also showed inhibitory activities against *R. solani* on maize and rice, *Sclerotium oryzae* on rice, *A. alternata* on apple, as well as *C. musae* and *F. oxysporum* causing banana fruit rot (Adebesin et al. 2009, Hariharan et al. 2022). Galarza et al. (2015) have assessed the antagonistic activities of *Trichoderma* species against the phytopathogenic fungi from Ecuador and Japan. They have found *T. virens* and *T. asperellum* showing strong inhibitory activities against some *Fusarium*, *Moniliophthora* and *Rosellinia* species (Galarza et al. 2015). *Trichoderma guizhouense* showed a significant effect on root rot of *Vigna unguiculata* caused by *R. solani* (Wang & Zhuang 2019). *Trichoderma guizhouense* isolates from Italy were evaluated for their potential activity as BCAs in vitro against the canker-causing fungi *Diplodia seriata*, *Eutypa lata* and *Neofusicoccum parvum* (Úrbez-Torres et al. 2020). Interestingly, the isolation results showed that *Cylindrocarpon*-like fungi were sometimes isolated simultaneously with *Trichoderma* isolates. The three *Trichoderma* species in this study, namely *Trichoderma guizhouense*, *T. virens* and *T. asperellum*, may also have the promising ability to become as biocontrol agents for grapevine trunk diseases. According to the former study by Munkvold & Marois (1993), *Fusarium* and *Cladosporium* showing the antagonistic effect on grapevine trunk disease pathogens. However, antagonistic activities and biocontrol potential of *Alternaria*, *Cladosporium* and *Fusarium* species reported in this study need to be further studied.

In conclusion, this study provides new insights into the diversity of fungi on symptomatic grapevine trunks and roots, including typical grapevine trunk disease agents, a pathogen associated with other diseases, endophytes with biocontrol potential and others. The relevant results reveal common fungal species associated with grapevine trunk diseases in China and establish the basis for research on the occurrence and management strategies of the grapevine trunk diseases worldwide.

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Supplementary Table 1 Strains used in phylogenetic analyses and their GenBank accession numbers.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>Botryosphaeria agaves</i>	MFLUCC 11-0125T	JX646791	JX646856	JX646841						
<i>B. agaves</i>	MFLUCC 10-0051	JX646790	JX646855	JX646840						
<i>B. corticis</i>	CBS 119047T	DQ299245	EU017539	EU673107						
<i>B. corticis</i>	ATCC 22927	DQ299247	EU673291	EU673108						
<i>B. dothidea</i>	CMW 25413	EU101303	EU101348	N/A						
(<i>B. auasmontanum</i>)										
<i>B. dothidea</i>	CBS 115476T	AY236949	AY236898	AY236927						
<i>B. dothidea</i>	CBS 110302	AY259092	AY573218	EU673106						
<i>B. dothidea</i>	GZCC 16-0013	KX447675	KX447678	N/A						
(<i>B. minutispermata</i>)										
<i>B. dothidea</i>	GZCC 16-0014	KX447676	KX447679	N/A						
(<i>B. minutispermata</i>)										
<i>B. dothidea</i>	CGMCC 3.17723	KT343254	KU221233	KX197107						
(<i>B. sinensia</i>)										
<i>B. dothidea</i>	CGMCC 3.17724	KT343256	KU221234	KX197108						
(<i>B. sinensia</i>)										
<i>B. dothidea</i>	CERC2298	KX278002	KX278107	KX278211						
(<i>B. wangensis</i>)										
<i>B. dothidea</i>	CERC2299	KX278003	KX278108	KX278212						
(<i>B. wangensis</i>)										
<i>B. fabicerciana</i>	CMW 27094T	HQ332197	HQ332213	KF779068						
<i>B. fabicerciana</i>	CMW 27121	HQ332198	HQ332214	KF779069						
<i>B. kuwatsukai</i>	CBS 135219T	KJ433388	KJ433410	N/A						
<i>B. kuwatsukai</i>	LSP 5	KJ433395	KJ433417	N/A						
<i>B. qingyuanensis</i>	CERC2946T	KX278000	KX278105	KX278209						
<i>B. qingyuanensis</i>	CERC2947	KX278001	KX278106	KX278210						
<i>B. ramosa</i>	CBS 122069T	EU144055	EU144070	KF766132						
<i>B. scharifii</i>	IRAN 1529CT	JQ772020	JQ772057	N/A						
<i>B. scharifii</i>	IRAN 1543C	JQ772019	JQ772056	N/A						
<i>Lasiodiplodia avicenniae</i>	CBS 139670T	KP860835	KP860680	KP860758						
<i>L. brasiliensis</i>	CMM 4015T	JX464063	JX464049	N/A						
<i>L. brasiliensis</i>	CMW 35884	KU887094	KU886972	KU887466						
<i>L. bruguierae</i>	CBS 139669T	KP860833	KP860678	KP860756						
<i>L. bruguierae</i>	CBS 141453	KP860832	KP860677	KP860755						
<i>L. citricola</i>	IRAN 1522CT	GU945354	GU945340	KU887505						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>L. citricola</i>	CBS 124706	GU945353	GU945339	KU887504						
<i>L. crassispora</i>	WAC 12533T	DQ103550	DQ103557	KU887506						
<i>L. crassispora</i>	CMW 13488	DQ103552	DQ103559	KU887507						
<i>L. euphorbicola</i>	CMW 33350	KU887149	KU887026	KU887455						
<i>L. euphorbicola</i>	CMW 36231	KU887187	KU887063	KU887494						
<i>L. gilanensis</i>	IRAN 1523CT	GU945351	GU945342	KU887511						
<i>L. gilanensis</i>	IRAN 1501C	GU945352	GU945341	KU887510						
<i>L. gonubiensis</i>	CMW 14077T	AY639595	DQ103566	DQ458860						
<i>L. gonubiensis</i>	CMW 14078	AY639594	DQ103567	EU673126						
<i>L. hormozganensis</i>	IRAN 1500CT	GU945355	GU945343	KU887515						
<i>L. hormozganensis</i>	IRAN 1498C	GU945356	GU945344	KU887514						
<i>L. iraniensis</i>	IRAN 1520CT	GU945348	GU945336	KU887516						
<i>L. iraniensis</i>	IRAN 1502C	GU945347	GU945335	KU887517						
<i>L. laeliocattleyae</i>	CBS 130992T	JN814397	JN814424	KU887508						
<i>L. laeliocattleyae</i>	BOT 29	JN814401	JN814428	N/A						
<i>L. macrospora</i>	CMM 3833T	KF234557	KF226718	KF254941						
<i>L. mahajangana</i>	CMW 27818	FJ900596	FJ900642	FJ900631						
<i>L. margaritacea</i>	CBS 122519T	EU144050	EU144065	KU887520						
<i>L. mediterranea</i>	CBS 137783T	KJ638312	KJ638331	KU887521						
<i>L. mediterranea</i>	CBS 137784	KJ638311	KJ638330	KU887522						
<i>L. parva</i>	CBS 456.78T	EF622083	EF622063	KU887523						
<i>L. parva</i>	CBS 494.78	EF622084	EF622064	EU673114						
<i>L. plurivora</i>	STE-U 5803T	EF445362	EF445395	KP872421						
<i>L. pontae</i>	CMM 1277T	KT151794	KT151791	KT151797						
<i>L. pseudotheobromae</i>	CBS 116459T	EF622077	EF622057	EU673111						
<i>L. pseudotheobromae</i>	CGMCC 3.18047	KX499876	KX499914	KX499989						
<i>L. rubropurpurea</i>	WAC 12535T	DQ103553	DQ103571	EU673136						
<i>L. rubropurpurea</i>	WAC 12536	DQ103554	DQ103572	KU887530						
<i>L. subglobosa</i>	CMM 4046	KF234560	KF226723	KF254944						
<i>L. subglobosa</i>	CMM 3872T	KF234558	KF226721	KF254942						
<i>L. thailandica</i>	CBS 138760T	KJ193637	KJ193681	N/A						
<i>L. thailandica</i>	CBS 138653	KM00643	KM00646	N/A						
		3	4							
<i>L. theobromae</i>	CBS 111530	EF622074	EF622054	KU887531						
<i>L. theobromae</i>	CBS 164.96T	AY640255	AY640258	KU887532						
<i>L. tropica</i>	CGMCC 3.18477T	KY783454	KY848616	KY848540						
<i>L. venezuelensis</i>	WAC 12539T	DQ103547	DQ103568	KU887533						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>L. venezuelensis</i>	WAC 12540	DQ103548	DQ103569	KU887534						
<i>L. viticola</i>	CBS 128313T	HQ288227	HQ288269	HQ288306						
<i>L. viticola</i>	CBS 128314	HQ288228	HQ288270	HQ288307						
<i>L. vitis</i>	CBS 124060T	KX464148	KX464642	KX464917						
<i>Diplodia corticola</i>	CBS 112546	AY259090	EU673310	EU673117						
<i>D. corticola</i>	CBS 112549T	AY259100	AY573227	DQ458853						
<i>D. cupressi</i>	CBS 168.87T	DQ458893	DQ458878	DQ458861						
<i>D. cupressi</i>	CBS 261.85	DQ458894	DQ458879	DQ458862						
<i>D. mutila</i>	CBS 112553	AY259093	AY573219	DQ458850						
<i>D. mutila</i>	CBS 230.30	DQ458886	DQ458869	DQ458849						
<i>D. seriata</i>	CBS 119049	DQ458889	DQ458874	DQ458857						
<i>D. seriata</i>	CBS 112555T	AY259094	AY573220	DQ458856						
<i>D. seriata</i>	CMW 7774	AY236953	AY236902	AY236931						
<i>Neofusicoccum australe</i>	CMW 6837T	AY339262	AY339270	AY339254						
<i>N. australe</i>	CBS 110865	AY343408	KX464661	KX464937						
<i>N. brasiliense</i>	CMM 1338T	JX513630	JX513610	KC794031						
<i>N. brasiliense</i>	CMM 1285	JX513628	JX513608	KC794030						
<i>N. cordaticola</i>	CBS 123634T	EU821898	EU821868	EU821838						
<i>N. cordaticola</i>	CBS 123635	EU821903	EU821873	EU821843						
<i>N. hongkongense</i>	CERC 2968	KX278051	KX278156	KX278260						
<i>N. hongkongense</i>	CERC 2973T	KX278052	KX278157	KX278261						
<i>N. illicii</i>	CGMCC 3.18310T	KY350149	N/A	KY350155						
<i>N. illicii</i>	CGMCC 3.18311	KY350150	KY817756	KY350156						
<i>N. kwambonambiense</i>	CBS 123639T	EU821900	EU821870	EU821840						
<i>N. kwambonambiense</i>	CBS 123641	EU821919	EU821889	EU821859						
<i>N. macroclavatum</i>	CBS 118223T	DQ093196	DQ093217	DQ093206						
<i>N. nonquaesitum</i>	CBS 126655T	GU251163	GU251295	GU251823						
<i>N. nonquaesitum</i>	PD 301	GU251164	GU251296	GU251824						
<i>N. occulatum</i>	CBS 128008T	EU301030	EU339509	EU339472						
<i>N. occulatum</i>	MUCC 286	EU736947	EU339511	EU339474						
<i>N. parvum</i>	ATCC 58191T	AY236943	AY236888	AY236917						
<i>N. parvum</i>	CMW 9080	AY236942	AY236887	AY236916						
<i>N. parvum</i>	CBS 145997	MT587449	MT592159	MT592649						
<i>N. parvum</i>	CPC 34761	MT587452	MT592161	MT592652						
<i>N. ribis</i>	CBS 115475T	AY236935	AY236877	AY236906						
<i>N. ribis</i>	CBS 121.26	AF241177	AY236879	AY236908						
<i>N. sinense</i>	CGMCC 3.18315T	KY350148	KY817755	KY350154						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>N. sinoeucalypti</i>	CERC 2005T	KX278061	KX278166	KX278270							
<i>N. sinoeucalypti</i>	CERC 3416	KX278064	KX278169	KX278273							
<i>Guignardia citricarpa</i>	CBS 127454	JF343583	JF343604	N/A							
<i>Phaeobotryon aplospora</i>	CFCC 53774T	MN21583	MN20599			MN21587					
		6	6			1					
<i>P. aplospora</i>	CFCC 53775	MN21583	N/A			MN21587					
		7				2					
<i>P. aplospora</i>	CFCC 53776	MN21583	MN20599			MN21587					
		8	7			3					
<i>P. cupressi</i>	IRAN 1456C	FJ919670	FJ919659			N/A					
<i>P. cupressi</i>	IRAN 1458C	FJ919671	FJ919660			N/A					
<i>P. cupressi</i>	IRAN 1455C	FJ919672	FJ919661			N/A					
<i>P. mamane</i>	CPC 12442	EU673333	EU673299			DQ377899					
<i>P. mamane</i>	CPC 12440	KF766209	EU673298			EU673248					
<i>P. mamane</i>	CPC 12443	EU673334	EU673300			EU673249					
<i>P. negundinis</i>	CAA798	KX061514	KX061508			N/A					
<i>P. negundinis</i>	CAA799	KX061515	KX061509			N/A					
<i>P. negundinis</i>	MFLUCC 15-0436	KU820970	KU853997			KU820971					
<i>P. rhoinum</i>	CFCC 52449T	MH13392	MH13395			MH13394					
		3	7			0					
<i>P. rhoinum</i>	CFCC 52450	MH13392	MH13395			MH13394					
		4	8			1					
<i>P. rhoinum</i>	CFCC 52451	MH13392	MH13395			MH13394					
		5	9			2					
<i>P. rhois</i>	CFCC 89662	KM03058	KM03059			KM03059					
		4	8			1					
<i>P. rhois</i>	CFCC 89663	KM03058	KM03059			KM03059					
		5	9			2					
<i>P. rhois</i>	CFCC 52448T	MH13392	MH13395			MH13393					
		2	6			9					
<i>Barriopsis fusca</i>	CBS 174.26T	EU673330	EU673296			DQ377857					
<i>Dactylonectria alcacerensis</i>	CBS 129087T	JF735333	JF735819	N/A			JF735630				
<i>D. alcacerensis</i>	Cy134	JF735332	JF735818	N/A			JF735629				
<i>D. alcacerensis</i>	JZB3310007	MN98871	MN95638	MN95852			MN95853				
		6	1	8			9				
<i>D. amazonica</i>	MUCL 55430T	MF683706	MF683664	MF683643			MF683686				

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>D. anthuriicola</i>	CBS 564.95	JF735302	JF735768	JF735430			JF735579				
<i>D. ecuadoriensis</i>	MUCL 55424T	MF683704	MF683662	MF683641			MF683684				
<i>D. ecuadoriensis</i>	MUCL 55425	MF683705	MF683663	MF683642			MF683684				
<i>D. estremocencis</i>	CPC 13539	JF735330	JF735816	JF735458			JF735627				
<i>D. estremocencis</i>	CBS 129085T	JF735320	JF735806	JF735448			JF735617				
<i>D. hispanica</i>	CBS 142827T	KY676882	KY676870	KY676876			KY676864				
<i>D. hispanica</i>	Cy228	JF735301	JF735767	JF735429			JF735578				
<i>D. hordeicola</i>	CBS 162.89T	AM41906	JF735799	AM41908			JF735610				
		0		4							
<i>D. macrodidyma</i>	CBS 112601	MH86289	JF735833	AY677229			JF735644				
		8									
<i>D. macrodidyma</i>	CBS 112615T	AY677290	JF268750	AY677233			JF735647				
<i>D. macrodidyma</i>	Cy258	JF735348	JF735845	JF735477			JF735656				
<i>D. macrodidyma</i>	CBS 112604	AY677284	JF735833	AY677229			JF735644				
<i>D. novozelandica</i>	CBS 112608	AY677288	JF735821	AY677235			JF735632				
<i>D. novozelandica</i>	CBS 113552T	JF735334	JF735822	AY677237			JF735633				
<i>D. palmicola</i>	MUCL 55426T	MF683708	MF683666	MF683645			MF683687				
<i>D. pauciseptata</i>	CBS 120171T	EF607089	JF735776	EF607066			JF735587				
<i>D. pinicola</i>	CBS 159.43	JF735318	JF735802	JF735446			JF735613				
<i>D. pinicola</i>	CBS 173.37T	JF735319	JF735803	JF735447			JF735614				
<i>D. polyphaga</i>	MUCL 55209T	MF683689	MF683647	MF683626			MF683668				
<i>D. torresensis</i>	CBS 119.41	JF735349	JF735846	JF735478			JF735657				
<i>D. torresensis</i>	Cyl124	KP823912	KP823881	KP823891			KP823900				
<i>D. torresensis</i>	CBS 129086T	JF735362	JF735870.	JF735492			JF735681				
			1								
<i>D. valentina</i>	CBS 142826T	KY676881	KY676869	KY676875			KY676863				
<i>D. vitis</i>	CBS 129082T	JF735303	JF735769.	JF735431			JF735580				
			1								
<i>Ilyonectria capensis</i>	CBS 132815T	JX231151	JX231119	JX231103			JX231135				
<i>I. capensis</i>	CBS 132816	JX231160	JX231128	JX231112			JX231144				
<i>I. changbaiensis</i>	CGMCC 3.18789T	MF350464	MF350491	MF350410			MF350437				
<i>I. changbaiensis</i>	72R2	MF350465	MF350492	MF350411			MF350438				
<i>I. communis</i>	CGMCC 3.18788T	MF350456	MF350483	MF350402			MF350429				
<i>I. communis</i>	J410	MF350457	MF350484	MF350403			MF350430				
<i>I. coprosmae</i>	CBS 119606T	JF735260	JF735694	JF735373			JF735505				
<i>I. crassa</i>	CBS 139.30T	JF735275	JF735723	JF735393			JF735534				
<i>I. crassa</i>	CBS 158.31	JF735276	JF735724	JF735394			JF735535				

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>I. cyclaminicola</i>	CBS 302.93T	JF735304	JF735770	JF735432			JF735581			
<i>I. destructans</i>	CBS 264.65T	AY677273	JF735695	AY677256			JF735506			
<i>I. europaea</i>	CBS 129078T	JF735294	JF735756	JF735421			JF735567			
<i>I. europaea</i>	CBS 537.92	EF607079	JF735757	EF607064			JF735568			
<i>I. gamsii</i>	CBS 940.97T	AM41906	JF735766	AM41908			JF735577			
		5		9						
<i>I. leucospermi</i>	CBS 132809T	JX231161	JX231129	JX231113			JX231145			
<i>I. leucospermi</i>	CBS 132810	JX231162	JX231130	JX231114			JX231146			
<i>I. liliigena</i>	CBS 189.49T	JF735297	JF735762	JF735425			JF735573			
<i>I. liliigena</i>	CBS 732.74	JF735298	JF735763	JF735426			JF735574			
<i>I. liriiodendri</i>	CBS 110.81T	DQ178163	JF735696	DQ178170			JF735507			
<i>I. liriiodendri</i>	CBS 117526	DQ178164	JF735697	DQ178171			JF735508			
<i>I. lusitanica</i>	CBS 129080T	JF735296	JF735759	JF735423			JF735570			
<i>I. mors-panacis</i>	CBS 306.35T	JF735288	JF735746	JF735414			JF735557			
<i>I. mors-panacis</i>	CBS 124662	JF735290	JF735748	JF735416			JF735559			
<i>I. palmarum</i>	CBS 135754T	HF937431	HF922614	HF922608			HF922620			
<i>I. palmarum</i>	CBS 135753	HF937432	HF922615	HF922609			HF922621			
<i>I. panacis</i>	CBS 129079T	AY295316	JF735761	JF735424			JF735572			
<i>I. protearum</i>	CBS 132811T	JX231157	JX231125	JX231109			JX231141			
<i>I. protearum</i>	CBS 132812	JX231165	JX231133	JX231117			JX231149			
<i>I. pseudodestructans</i>	CBS 129081T	AJ875330	JF735752	AM41909			JF735563			
				1						
<i>I. pseudodestructans</i>	CBS 117824	JF735292	JF735751	JF735419			JF735562			
<i>I. qitaiheensis</i>	CGMCC 3.18787T	MF350472	MF350499	MF350418			MF350445			
<i>I. qitaiheensis</i>	J919	MF350473	MF350500	MF350419			MF350446			
<i>I. robusta</i>	CBS 308.35T	JF735264	JF735707	JF735377			JF735518			
<i>I. robusta</i>	CBS 129084	JF735273	JF735721	JF735391			JF735532			
<i>I. rufa</i>	CBS 153.37T	AY677271	JF735729	AY677251			JF735540			
<i>I. rufa</i>	CBS 640.77	JF735277	JF735731	JF735399			JF735542			
<i>I. strelitziae</i>	CBS 142253T	KY304649	KY304727	KY304755			KY304621			
<i>I. strelitziae</i>	CBS 142254	KY304651	KY304729	KY304757			KY304623			
<i>I. venezuelensis</i>	CBS 102032T	AM41905	JF735760	AY677255			JF735571			
		9								
<i>I. vredenhoekensis</i>	CBS 132807T	JX231155	JX231123	JX231107			JX231139			
<i>I. vredenhoekensis</i>	CBS 132808	JX231159	JX231127	JX231111			JX231143			
<i>Campylocarpon fasciculare</i>	CBS 112613T	AY677301	JF735691	AY677221			JF735502			

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>C. pseudofasciculare</i>	CBS 112679T	AY677306	JF735692	KJ022328			JF735503			
<i>Cylindrocladiella addiensis</i>	CBS 143794T	MH11138		MH11138			N/A			
<i>C. addiensis</i>	CBS 143793	MH11138		MH11139			N/A			
<i>C. arbusta</i>	CMW 47295T	MH01701		MH01695			MH01699			
<i>C. arbusta</i>	CMW 47296	MH01701		MH01695			MH01699			
<i>C. australiensis</i>	CBS 129567T	JN100624		JN098747			JN098932			
<i>C. brevistipitata</i>	CBS 142786T	N/A		MF444926			N/A			
<i>C. camelliae</i>	IMI 346845	AF220952		AY793471			AY793509			
<i>C. clavata</i>	CBS 129564T	JN099095		JN098752			JN098858			
<i>C. cymbiformis</i>	CBS 129553T	JN099103		JN098753			JN098866			
<i>C. elegans</i>	CBS 338.92T	AY793444		AY793474			AY793512			
<i>C. ellipsoidea</i>	CBS 129573T	JN099094		JN098757			JN098857			
<i>C. hahajimaensis</i>	MAFF 238172T	JN687561		N/A			N/A			
<i>C. hawaiiensis</i>	CBS 129569T	JN100621		JN098761			JN098929			
<i>C. horticola</i>	CBS 142784T	MF444911		MF444924			N/A			
<i>C. humicola</i>	CBS 142779T	MF444906		MF444919			N/A			
<i>C. infestans</i>	CBS 111795T	AF220955		AF320190			AY793513			
<i>C. kurandica</i>	CBS 129577T	JN100646		JN098765			JN098953			
<i>C. lageniformis</i>	CBS 112898	AY793445		AY725652			AY725699			
<i>C. lageniformis</i>	CBS 340.92T	MH86236		AY793481			AY793520			
<i>C. lanceolata</i>	CBS 129566T	JN099099		JN098789			JN098862			
<i>C. lateralis</i>	CBS 142788T	MF444914		MF444928			N/A			
<i>C. longiphialidica</i>	CBS 129557T	JN100585		JN098790			JN098851			
<i>C. longistipitata</i>	CBS 116075T	AF220958		AY793506			AY793546			
<i>C. malesiana</i>	CBS 143549	MH01701		MH01696			MH01699			
<i>C. microcylindrica</i>	CBS 111794T	AY793452		AY793483			AY793523			
<i>C. natalensis</i>	CBS 114943T	JN100588		JN098794			JN098895			
<i>C. nauliensis</i>	CBS 143792T	MH11138		MH11139			N/A			
<i>C. nauliensis</i>	CBS 143791	MH11138		MH11139			N/A			

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>C. nederlandica</i>	CBS 152.91T	JN100603		JN098800			JN098910				
<i>C. novazelandica</i>	CBS 486.77T	AF220963		AY793485			AY793525				
<i>C. obpyriformis</i>	CMW 47194T	MH01702		MH01696			MH01700				
		2		5			3				
<i>C. parva</i>	CBS 114524	AF220964		AY793486			AY793526				
<i>C. parvispora</i>	CMW 47197T	MH01702		MH01696			MH01700				
		5		8			6				
<i>C. peruviana</i>	IMUR 1843T	AF220966		AY793500			AY793540				
<i>C. pseudocamelliae</i>	CBS 129555T	JN100577		JN098814			JN098843				
<i>C. pseudohawaiiensis</i>	CBS 210.94T	JN099128		JN098819			JN098890				
<i>C. pseudohawaiiensis</i>	CBS 115610	JN100594		JN098820			JN098901				
<i>C. pseudoinfestans</i>	CBS 114531T	AF220957		AY793508			AY793548				
<i>C. pseudoparva</i>	CBS 129560T	JN100620		JN098824			JN098927				
<i>C. queenslandica</i>	CBS 129574T	JN099098		JN098826			JN098861				
<i>C. reginae</i>	CBS 142782T	MF444909		MF444922			N/A				
<i>C. solicola</i>	CMW 47198T	MH01702		MH01696			MH01700				
		1		4			2				
<i>C. stellenboschensis</i>	CBS 110668T	JN100615		JN098829			JN098922				
<i>C. terrestris</i>	CBS 142789T	MF444915		MF444929			N/A				
<i>C. thailandica</i>	CBS 129571T	JN100582		JN098834			JN098848				
<i>C. variabilis</i>	CBS 129561T	JN100643		JN098719			JN098950				
<i>C. viticola</i>	CBS 112897T	AY793468		AY793504			AY793544				
<i>C. viticola</i>	CPC 5620	AY793469		AY793505			AY793545				
<i>C. vitis</i>	CBS 142517T	KY979751		KY979918			N/A				
<i>Gliocladiopsis sagariensis</i>	CBS 199.55T	NR147628		JQ666141			JQ666031				
<i>Fusarium acuminatum</i>	NRRL 36147		GQ505420		GQ505484						
<i>F. acuminatum</i>	IBE000016		EF531240		N/A						
<i>F. acuminatum</i>	R-9382		FJ154733		N/A						
<i>F. acuminatum</i>	R-2165		FJ154735		N/A						
<i>F. agapanthi</i>	NRRL 54463T		KU900630		KU900625						
<i>F. ananatum</i>	NRRL 53131		HM34712		HM34721						
			8		3						
<i>F. andiyazi</i>	CBS 119857T		LT996092		LT996138						
<i>F. anthophilum</i>	NRRL 25214		KF466414		KU171696						
<i>F. armeniacum</i>	NRRL 6227		N/A		JX171560						
<i>F. asiaticum</i>	NRRL 13818		N/A		JX171573						
<i>F. avenaceum</i>	NRRL 25128		JF740751		JF741079						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>F. begoniae</i>	CBS 403.97T		AF160293		LT996140						
<i>F. beomiforme</i>	CBS 740.97		N/A		JX171619						
<i>F. brachygibbosum</i>	FRC R7630		MW23317		MW23351						
			3		7						
<i>F. brachygibbosum</i>	FRC R7637		MW23317		MW23351						
			4		8						
<i>F. brachygibbosum</i>	FRC R8851		MW23319		MW23354						
			8		2						
<i>F. brachygibbosum</i>	NRRL 20954		MW23307		MW23341						
			5		8						
<i>F. bulbicola</i>	CBS 220.76T		KF466415		KF466404						
<i>F. burgessii</i>	CBS 125537T		N/A		HQ646393						
<i>F. circinatum</i>	CBS 405.97T		KM23194		HM06835						
			3		4						
<i>F. clavum</i>	CBS 126202T		MN17045		MN17038						
			6		9						
<i>F. coicis</i>	NRRL 66233T		KP083251		KP083274						
<i>F. commune</i>	NRRL 52764		JF740838		JF741002						
<i>F. compactum</i>	CBS 185.31		GQ505646		GQ505824						
<i>F. compactum</i>	CBS 186.31T		GQ505648		GQ505826						
<i>F. compactum</i>	NRRL 28029		GQ505602		GQ505780						
<i>F. concentricum</i>	CBS 450.97T		AF160282		JF741086						
<i>F. culmorum</i>	NRRL 25475		N/A		JX171628						
<i>F. denticulatum</i>	CBS 735.97		AF160269		LT996143						
<i>F. dlaminii</i>	CBS 119860T		AF160277		KU171701						
<i>F. equiseti</i>	CBS 107.07		GQ505644		GQ505822						
<i>F. flocciferum</i>	CBS 831.85		N/A		JX171627						
<i>F. fractiflexum</i>	NRRL 28852T		AF160288		LT575064						
<i>F. fujikuroi</i>	CBS 221.76T		AF160279		MW83400						
					5						
<i>F. gaditjirrii</i>	NRRL 45417		N/A		KU171704						
<i>F. globosum</i>	CBS 428.97T		KF466417		KF466406						
<i>F. graminearum</i>	CBS 123657		AY452957		JX171644						
<i>F. hainanense</i>	CBS 131386		MN17051		MN17044						
			0		3						
<i>F. hainanense</i>	CBS 544.96		GQ505598		GQ505776						
<i>F. hainanense</i>	NRRL 28714		GQ505604		GQ505782						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>F. hainanense</i>	CGMCC3.19478		MK28958		MK28973						
			1		5						
<i>F. hostae</i>	NRRL 29889		N/A		JX171640						
<i>F. incarnatum</i>	CBS 132.73NT		MN17047		MN17040						
			6		9						
<i>F. konzum</i>	CBS 119849T		LT996098		LT996148						
<i>F. lacertarum</i>	NRRL 20423		GQ505593		JX171581						
<i>F. lacertarum</i>	CBS 130185T		GQ505593		GQ505771						
<i>F. lacertarum</i>	LC7927		MK28963		MK28979						
			7		1						
<i>F. lacertarum</i>	LC7942		MK28964		MK28979						
			3		7						
<i>F. lactis</i>	CBS 411.97ET		AF160272		LT996149						
<i>F. lyarnte</i>	NRRL 54252		N/A		JX171661						
<i>F. mangiferae</i>	NRRL 25226T		AF160281		JX171622						
<i>F. mexicanum</i>	NRRL 47473		GU737416		LR792615						
<i>F. napiforme</i>	CBS 748.97T		AF160266		EF470117						
<i>F. nelsonii</i>	NRRL 13338		GQ505402		JX171561						
<i>F. nisikadoi</i>	NRRL 25179		N/A		JX171620						
<i>F. nygamai</i>	CBS 749.97T		AF160273		EF470114						
<i>F. oxysporum</i>	CBS 716.74T		AF008479		JX171583						
<i>F. oxysporum</i>	NRRL 25387		HM34711		HM34720						
			7		9						
<i>F. oxysporum</i>	NRRL 22902		AF160312		LT575065						
<i>F. phyllophilum</i>	CBS 216.76T		KF466421		KF466410						
<i>F. poae</i>	NRRL 13714		N/A		JX171572						
<i>F. proliferatum</i>	NRRL 22944		AF160280		HM06835						
					2						
<i>F. pseudocircinatum</i>	NRRL 22946T		AF160271		N/A						
<i>F. pseudonygamai</i>	CBS 417.97T		AF160263		LT996152						
<i>F. ramigenum</i>	CBS 418.98T		KF466423		KF466412						
<i>F. redolens</i>	CBS 743.97		MT409452		JX171616						
<i>F. sacchari</i>	CBS 223.76ET		AF160278		JX171580						
<i>F. sambucinum</i>	NRRL 22187		MW83427		JX171606						
			7								
<i>F. scirpi</i>	NRRL 13402		GQ505592		JX171566						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>F. sterilihyphosum</i>	NRRL 25623T		AF160300		MN19389 7						
<i>F. subglutinans</i>	NRRL 22016T		AF160289		JX171599						
<i>F. succisae</i>	NRRL 13613		AF160291		LT996154						
<i>F. thapsinum</i>	NRRL 22045		AF160270		JX171600						
<i>F. tjaetaba</i>	NRRL 66243T		KP083263		KP083275						
<i>F. torulosum</i>	NRRL 22748		N/A		JX171615						
<i>F. tricinctum</i>	NRRL 25481T		HM06830 7		HM06832 7						
<i>F. tuiense</i>	NRRL 53984T		GU737404		LR792619						
<i>F. udum</i>	NRRL 22949		AF160275		LT996172						
<i>F. venenatum</i>	NRRL 22196		N/A		JX171607						
<i>F. verticillioides</i>	NRRL 22172		AF160262		EF470122						
<i>Neocosmospora ambrosia</i>	NRRL 20438		AF178332		JX171584						
<i>N. ambrosia</i>	NRRL 22346		FJ240350		EU329503						
<i>N. falciformis</i>	NRRL 32757		DQ247075		EU329614						
<i>N. falciformis</i>	NRRL 32828		DQ247135		EU329626						
<i>N. falciformis</i>	CBS 318.73		JX435158		JX435258						
<i>N. falciformis</i>	NRRL 54219		HQ401721		HQ401723						
<i>N. pisi</i>	CBS 123669ET		LR583636		LR583862						
<i>N. solani</i>	NRRL 52778		JF740846		JF741172						
<i>N. solani</i>	NRRL 66304ET		KT313611		KT313623						
<i>N. solani</i>	NRRL 32741		DQ247061		EU329608						
<i>N. vasinfecta</i>	NRRL 22436		AF178348		JX171610						
<i>N. vasinfecta</i>	NRRL 43467		EF452940		EF469979						
<i>Bisifusarium delphinoides</i>	CBS 110140		EU926302		HM34721 9						
<i>B. delphinoides</i>	CBS 120718T		EU926296		N/A						
<i>B. delphinoides</i>	CBS 110310		EU926307		N/A						
<i>B. dimerum</i>	CBS 108944ET		KR673912		HM34721 8						
<i>B. nectrioides</i>	CBS 176.31T		EU926312		JX171591						
<i>B. penzigii</i>	CBS 116508		EU926323		HM34721 7						
<i>Fusicolla aquaeductuum</i>	CBS 734.79		HQ897742		MW84790 5						
<i>Diaporthe acaciaram</i>	CBS 138862T	KP004460	N/A	KP004509					N/A		

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>D.acerigena</i>	CFCC 52554T	MH12148 9	MH12153 1	N/A					MH12141 3		
<i>D.alleghaniensis</i>	CBS 495.72T	KC343007	KC343733	KC343975					KC343249		
<i>D.alnea</i>	CBS 146.46T	KC343008	KC343734	KC343976					KC343250		
<i>D.batatas</i>	CBS 122.21T	KC343040	KC343766	KC344008					KC343282		
<i>D.betulae</i>	CFCC 50469T	KT732950	KT733016	KT733020					KT732997		
<i>D.betulina</i>	CFCC 52560	MH12149 5	MH12153 7	MH12157 7					MH12141 9		
<i>D.bicincta</i>	CBS 121004T	KC343134	KC343860	KC344102					KC343376		
<i>D.caryae</i>	CFCC 52563T	MH12149 8	MH12154 0	MH12158 0					MH12142 2		
<i>D.celastrina</i>	CBS 139.27T	KC343047	KC343773	KC344015					KC343289		
<i>D.celeris</i>	CBS 143349T	MG28101 7	MG28153 8	MG28119 0					MG28171 2		
<i>D.celeris</i>	CBS 143350	MG28101 8	MG28153 9	MG28119 1					MG28171 3		
<i>D.charlesworthii</i>	BRIP 54884mT	KJ197288	KJ197250	KJ197268					N/A		
<i>D.chensiensis</i>	CFCC 52567T	MH12150 2	MH12154 4	MH12158 4					MH12142 6		
<i>D.citri</i>	CBS 135422T	KC843311	KC843071	KC843187					KC843157		
<i>D.citrichinensis</i>	ZJUD34T	JQ954648	JQ954666	KJ490396					KC357494		
<i>D.collariana</i>	MFLUCC 17- 2636T	MG80611 5	MG78304 0	MG78304 1					MG78304 2		
<i>D.conica</i>	CFCC 52571T	MH12150 6	MH12154 8	MH12158 8					MH12142 8		
<i>D.convolvuli</i>	CBS 124654T	KC343054	KC343780	KC344022					KC343296		
<i>D.endophytica</i>	CBS 133811T	KC343065	KC343791	KC344033					KC343307		
<i>D.eres</i>	AR4369	JQ807440	JQ807366	KJ420813					KJ435005		
<i>D.eres</i>	CBS 138594T	KJ210529	KJ210550	KJ420799					KJ434999		
<i>D.eres</i>	CBS 138595	KJ210533	KJ210554	KJ420817					KJ435006		
<i>D.eres</i>	DP0180	JQ807453	JQ807384	KJ420804					KJ435029		
<i>D.eres</i>	DP0438	KJ210532	KJ210553	KJ420816					KJ435016		
<i>D.eres</i>	JZB320029	MK33571 7	MK52362 0	MK50017 7					MK50006 9		
<i>D.eres</i>	JZB320030	MK33571 8	MK52362 1	MK50017 8					MK50007 0		

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>D.eres</i>	JZB320065	MK33574 9	MK52361 5	MK50020 8					MK50010 1		
<i>D.eres</i> (= <i>D. biguttusis</i>)	CGMCC 3.17081T	KF576282	KF576257	KF576306					N/A		
<i>D.eres</i> (= <i>D. camptothecicola</i>)	CFCC 51632T	KY203726	KY228887	KY228893					KY228877		
<i>D.eres</i> (= <i>D. fukushii</i>)	MAFF625033T	JQ807468	JQ807417	KJ420814					KJ435017		
<i>D.eres</i> (= <i>D. longicicola</i>)	CGMCC 3.17089T	KF576267	KF576242	KF576291					N/A		
<i>D.eres</i> (= <i>D. lonicerae</i>)	MFLUCC 17-0963T	KY964190	KY964146	KY964073					KY964116		
<i>D.eres</i> (= <i>D. mahothocarpus</i>)	CGMCC 3.15181T	KC153096	KC153087	KF576312					N/A		
<i>D.eres</i> (= <i>D. momicola</i>)	MFLUCC 16-0113T	KU557563	KU557631	KU557587					KU557611		
<i>D.eres</i> (= <i>D. nobilis</i>)	CBS 113470	KC343146	KC343872	KC344114					KC343388		
<i>D.eres</i> (= <i>D. rosicola</i>)	MFLU 17-0646T	MG82889 5	MG82927 0	MG84387 7					MG82927 4		
<i>D.fraxinicola</i>	CFCC 52582T	MH12151 7	MH12155 9	N/A					MH12143 5		
<i>D.helianthi</i>	CBS 592.81T	KC343115	KC343841	KC344083					KC343357		
<i>D.heterophyllae</i>	CBS 143769	MG60022 2	MG60022 4	MG60022 6					MG60021 8		
<i>D.kongii</i>	BRIP 54031T	JF431301	JN645797	N/A					N/A		
<i>D.maritima</i>	DAOM 695742T	KU552025	KU552023	KU574615					MN13612 6		
<i>D.masirevicii</i>	BRIP 57892aT	KJ197276	KJ197239	KJ197257					N/A		
<i>D.melonis</i>	CBS 507.78T	KC343142	KC343868	KC344110					KC343384		
<i>D.middletonii</i>	BRIP 54884eT	KJ197286	KJ197248	KJ197266					N/A		
<i>D.miriciae</i>	BRIP 54736jT	KJ197282	KJ197244	KJ197262					N/A		
<i>D.neilliae</i>	CBS 144.27T	KC343144	KC343870	KC344112					KC343386		
<i>D.oraccinii</i>	CGMCC 3.17531T	KP267863	KP267937	KP293443					N/A		
<i>D.padina</i>	CFCC 52590T	MH12152 5	MH12156 7	MH12160 4					MH12144 3		
<i>D.penitriteum</i>	CGMCC 3.17532T	KP714505	KP714517	KP714529					N/A		
<i>D.phragmitis</i>	CBS 138897T	KP004445	N/A	KP004507					N/A		
<i>D.pulla</i>	CBS 338.89T	KC343152	KC343878	KC344120					KC343394		
<i>D.sackstonii</i>	BRIP 54669bT	KJ197287	KJ197249	KJ197267					N/A		
<i>D.schini</i>	CBS 133181T	KC343191	KC343917	KC344159					KC343433		

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>D.sennicola</i>	CFCC 51634T	KY203722	KY228883	KY228889					KY228873		
<i>D.sojae</i>	DP0605	KJ590707	KJ590750	KJ610863					KJ612104		
<i>D.sojae</i>	FAU635T	KJ590719	KJ590762	KJ610875					KJ612116		
<i>D.subclavata</i>	CGMCC 3.17257T	KJ490630	KJ490509	KJ490451					N/A		
<i>D.terebinthifolii</i>	CBS 133180T	KC343216	KC343942	KC344184					KC343458		
<i>D.thunbergiicola</i>	MFLUCC 12- 0033T	KP715097	KP715098	N/A					N/A		
<i>D.tibetensis</i>	CFCC 51999T	MF279843	MF279858	MF279873					MF279888		
<i>D.ukurunduensis</i>	CFCC 52592T	MH12152 7	MH12156 9	N/A					MH12144 5		
<i>D.unshiuensis</i>	CGMCC 3.17566T	KJ490584	KJ490463	KJ490405					N/A		
<i>D.unshiuensis</i>	PSCG339	MK62692 8	MK65487 9	MK69130 0					MK69118 1		
<i>D.unshiuensis</i>	ZJUD52	KJ490587	KJ490466	KJ490408					N/A		
<i>D.unshiuensis</i>	CFCC 52595	MH12153 0	MH12157 2	MH12160 7					N/A		
<i>D.vaccinii</i>	CBS 160.32T	KC343228	KC343954	KC344196					KC343470		
<i>D.virgiliae</i>	CMW40748T	KP247566	N/A	KP247575					N/A		
<i>Diaporthella corylina</i>	CBS 121124T	KC343004	KC343730	KC343972					KC343246		
<i>Phaeoacremonium africanum</i>	CSN946			KY906773				KY906772			
<i>P. africanum</i>	PMM2276			KY906927				KY906926			
<i>P. album</i>	CBS 142688T			KY906885				KY906884			
<i>P. album</i>	CBS 142689			KY906925				KY906924			
<i>P. alvesii</i>	CSN1239			KY906785				KY906784			
<i>P. alvesii</i>	CSN1335			KY906801				KY906800			
<i>P. aureum</i>	CBS 142690			KY906799				KY906798			
<i>P. aureum</i>	CBS 142691T			KY906657				KY906656			
<i>P. australiense</i>	CSN490			KY906729				KY906728			
<i>P. australiense</i>	CSN657			KY906735				KY906734			
<i>P. bibendum</i>	CBS 142694T			KY906759				KY906758			
<i>P. fraxinopennsylvanicum</i>	CSN66			KY906681				KY906680			
<i>P. gamsii</i>	CBS 142712T			KY906741				KY906740			
<i>P. geminum</i>	CBS 142713T			KY906649				KY906648			
<i>P. geminum</i>	CBS 142717			KY906647				KY906646			

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tefl</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>P. globosum</i>	CSN471			KY906725				KY906724		
<i>P. globosum</i>	CSN1258			KY906797				KY906796		
<i>P. griseo-olivaceum</i>	PMM1829			KY906853				KY906852		
<i>P. griseorubrum</i>	PMM1828			KY906851				KY906850		
<i>P. griseorubrum</i>	PMM1895			KY906875				KY906874		
<i>P. inflatipes</i>	CSN47			KY906665				KY906664		
<i>P. inflatipes</i>	CSN57			KY906675				KY906674		
<i>P. iranianum</i>	CSN170			KY906695				KY906694		
<i>P. iranianum</i>	CSN267			KY906707				KY906706		
<i>P. italicum</i>	CSN59			KY906677				KY906676		
<i>P. italicum</i>	CSN119			KY906691				KY906690		
<i>P. junior</i>	CBS 142695			KY906651				KY906650		
<i>P. junior</i>	CBS 142696			KY906653				KY906652		
<i>P. longicollarum</i>	CBS 142699T			KY906689				KY906688		
<i>P. longicollarum</i>	CBS 142700			KY906879				KY906878		
<i>P. meliae</i>	CBS 142709			KY906705				KY906704		
<i>P. meliae</i>	CBS 142710T			KY906825				KY906824		
<i>P. minimum</i>	CBS 246.91T			AF246811				AY735497		
<i>P. minimum</i>	CBS 100397			AF246806				AY735498		
<i>P. oleae</i>	CBS 142701			KY906719				KY906718		
<i>P. oleae</i>	CBS 142702			KY906771				KY906770		
<i>P. parasiticum</i>	CSN72			KY906683				KY906682		
<i>P. parasiticum</i>	CSN79			KY906687				KY906686		
<i>P. paululum</i>	CBS 142705T			KY906881				KY906880		
<i>P. proliferatum</i>	CBS 142706T			KY906903				KY906902		
<i>P. proliferatum</i>	CBS 142707			KY906827				KY906826		
<i>P. prunicola</i>	CSN398			KY906717				KY906716		
<i>P. prunicola</i>	CSN719			KY906753				KY906752		
<i>P. rosicola</i>	CBS 142708			KY906831				KY906830		
<i>P. scolyti</i>	CSN27			KY906661				KY906660		
<i>P. scolyti</i>	CSN55			KY906671				KY906670		
<i>P. sicilianum</i>	CSN 482			KY906727				KY906726		
<i>P. sicilianum</i>	CSN 930			KY906769				KY906768		
<i>P. spadicum</i>	CBS 142711T			KY906839				KY906838		
<i>P. spadicum</i>	CBS 142714			KY906667				KY906666		
<i>P. subulatum</i>	CSN42			KY906663				KY906662		
<i>P. subulatum</i>	CSN51			KY906669				KY906668		

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>P. venezuelense</i>	PMM1138			KY906835				KY906834			
<i>P. viticola</i>	CSN678			KY906745				KY906744			
<i>P. viticola</i>	CSN701			KY906749				KY906748			
<i>Pleurostoma richardsiae</i>	CBS 270.33T			AY579334				AY579271			
<i>Coniella africana</i>	CBS 114133T	AY339344	AY339364			AY339293	AY339309				
<i>C. crousii</i>	NFCCI2213	HQ264189	N/A			N/A	N/A				
<i>C. diplodiella</i>	CBS 111858T	AY339323	AY339355			AY339284	AY339297				
<i>C. diplodiella</i>	CBS 166.84	AY339325	AY339356			AY339285	AY339299				
<i>C. diplodiella</i>	CBS 111857	AY339331	AY339357			AY339286	AY339305				
<i>C. diplodiopsis</i>	CBS 590.84T	AY339334	AY339359			AY339288	AY339308				
<i>C. diplodiopsis</i>	CBS 109.23	AY339332	AY339358			AY339287	AY339306				
<i>C. erumpens</i>	CBS 523.78T	KX833533	KX833630			KX833361	N/A				
<i>C. eucalyptigena</i>	CBS 139893T	KR476725	N/A			KR476760	N/A				
<i>C. eucalyptorum</i>	CBS 112640T	AY339338	KX833637			AY339290	N/A				
<i>C. eucalyptorum</i>	CBS 114134	AY339339	AY339361			AY339289	N/A				
<i>C. eucalyptorum</i>	CBS 111023	AY339337	AY339360			KX833363	N/A				
<i>C. fragariae</i>	CBS 172.49T	AY339317	AY339352			AY339282	N/A				
<i>C. fragariae</i>	CBS 167.84	AY339318	KX833662			EU754149	N/A				
<i>C. fusiformis</i>	CBS 141596T	KX833576	KX833674			KX833397	N/A				
<i>C. fusiformis</i>	CBS 114850	KX833574	KX833672			KX833395	N/A				
<i>C. granati</i>	CBS 252.38	AY339342	AY339362			AY339291	N/A				
<i>C. granati</i>	CBS 814.71	KX833582	KX833682			AY408380	N/A				
<i>C. javanica</i>	CBS 455.68T	KX833583	KX833683			KX833403	N/A				
<i>C. koreana</i>	CBS 143.97T	KX833584	KX833684			AF408378	N/A				
<i>C. lanneae</i>	CBS 141597T	KX833585	KX833685			KX833404	N/A				
<i>C. limoniformis</i>	CBS 111021T	AY339346	KX833686			KX833405	AY339310				
<i>C. macrospora</i>	CBS 524.73T	AY339343	AY339363			AY339292	N/A				
<i>C. malaysiana</i>	CBS 141598T	KX833588	KX833688			KX833406	N/A				
<i>C. musaiaensis</i>	CBS 109757	KX833589	KX833689			AF408337	N/A				
<i>C. nicotianae</i>	CBS 875.72T	KX833590	KX833690			KX833407	N/A				
<i>C. nigra</i>	CBS 165.60T	AY339319	KX833691			KX833408	N/A				
<i>C. obovata</i>	CBS 111025	AY339313	KX833692			KX833409	N/A				
<i>C. paracastaneicola</i>	CBS 141292T	KX833591	KX833693			KX833410	N/A				
<i>C. paracastaneicola</i>	CPC 25498	KX833592	KX833694			KX833411	N/A				
<i>C. peruensis</i>	CBS 110394T	KJ710463	KX833695			KJ710441	N/A				
<i>C. pseudogranati</i>	CBS 137980T	KJ869132	N/A			KJ869189	N/A				
<i>C. pseudostraminea</i>	CBS 112624T	KX833593	KX833696			KX833412	N/A				

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>C. quercicola</i>	CBS 904.69T	KX833595	KX833698			KX833414	N/A				
<i>C. solicola</i>	CBS 766.71T	KX833597	KX833701			KX833416	N/A				
<i>C. sp.</i>	CBS 114006	AY339347	KX833703			AY339295	AY339311				
<i>C. straminea</i>	CBS 149.22	AY339348	AY339366			AY339296	AY339312				
<i>C. tibouchinae</i>	CBS 131594T	JQ281774	JQ281778			JQ281776	N/A				
<i>C. tibouchinae</i>	CBS 131595	JQ281775	JQ281779			JQ281777	N/A				
<i>C. vitis</i>	JZB3700001T	KX890008	KX890058			KX890083	KX890033				
<i>C. vitis</i>	JZB3700002	KX889992	KX890042			KX890067	KX890017				
<i>C. vitis</i>	JZB3700003	KX889993	KX890043			KX890068	KX890018				
<i>C. vitis</i>	JZB3700004	KX889994	KX890044			KX890069	KX890019				
<i>C. vitis</i>	JZB3700005	KX889995	KX890045			KX890070	KX890020				
<i>Melanconiella sp.</i>	CBS 110385	KX833599	KX833707			KX833420	N/A				
<i>Pestalotiopsis adusta</i>	ICMP 6088T	JX399006	JX399070	JX399037							
<i>P. adusta</i>	MFLUCC 10-146	JX399007	JX399071	JX399038							
<i>P. anacardiacearum</i>	IFRDCC 2397T	KC247154	KC247156	KC247155							
<i>P. arceuthobii</i>	CBS 434.65T	KM19934	KM19951	KM19942							
		1	6	7							
<i>P. arengae</i>	CBS 331.92T	KM19934	KM19951	KM19942							
		0	5	6							
<i>P. australis</i>	CBS 114193T	KM19933	KM19947	KM19938							
		2	5	3							
<i>P. biciliata</i>	CBS 124463T	KM19930	KM19950	KM19939							
		8	5	9							
<i>P. brachiata</i>	LC2988T	KX894933	KX895150	KX895265							
<i>P. brassicae</i>	CBS 170.26T	KM19937	KM19955	N/A							
		9	8								
<i>P. camelliae</i>	MFLUCC 12-0277T	JX399010	JX399074	JX399041							
<i>P. chamaeropsis</i>	CBS 186.71T	KM19932	KM19947	KM19939							
		6	3	1							
<i>P. clavata</i>	MFLUCC 12-0268T	JX398990	JX399056	JX399025							
<i>P. colombiensis</i>	CBS 118553T	KM19930	KM19948	KM19942							
		7	8	1							
<i>P. diploclisiae</i>	CBS 115587T	KM19932	KM19948	KM19941							
		0	6	9							

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>P. diversiseta</i>	MFLUCC 12-0287T	NR120187	JX399073	JX399040						
<i>P. dracaenicola</i>	MFLUCC 18-0913T	MN96273 1	MN96273 2	MN96273 3						
<i>P. dracaenicola</i>	MFLUCC 18-0914	MN96273 4	MN96273 5	MN96273 6						
<i>P. ericacearum</i>	IFRDCC 2439T	KC537807	KC537814	KC537821						
<i>P. furcata</i>	MFLUCC 12-0054T	JQ683724	JQ683740	JQ683708						
<i>P. gaultheria</i>	IFRD 411-014T	KC537805	KC537812	KC537819						
<i>P. grevilleae</i>	CBS 114127T	KM19930 0	KM19950 4	KM19940 7						
<i>P. hawaiiensis</i>	CBS 114491T	KM19933 9	KM19951 4	KM19942 8						
<i>P. hollandica</i>	CBS 265.33T	KM19932 8	KM19948 1	KM19938 8						
<i>P. humus</i>	CBS 336.97T	KM19931 7	KM19948 4	KM19942 0						
<i>P. inflexa</i>	MFLUCC 12-0270T	JX399008	JX399072	JX399039						
<i>P. intermedia</i>	MFLUCC 12-0259T	JX398993	JX399059	JX399028						
<i>P. kenya</i>	CBS 442.67T	KM19930 2	KM19950 2	KM19939 5						
<i>P. kenya</i>	CBS 911.96	KM19930 3	KM19950 3	KM19939 6						
<i>P. knightiae</i>	CBS 114138T	KM19931 0	KM19949 7	KM19940 8						
<i>P. linearis</i>	MFLUCC 12-0271T	JX398992	JX399058	JX399027						
<i>P. malayana</i>	CBS 102220T	KM19930 6	KM19948 2	KM19941 1						
<i>P. monochaeta</i>	CBS 144.97T	KM19932 7	KM19947 9	KM19938 6						
<i>P. papuana</i>	CBS 331.96T	KM19932 1	KM19949 1	KM19941 3						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>P. papuana</i>	CBS 887.96	KM19931	KM19949	KM19941						
		8	2	5						
<i>P. parva</i>	CBS 265.37T	KM19931	KM19950	KM19940						
		2	8	4						
<i>P. parva</i>	CBS 278.35	KM19931	KM19950	KM19940						
		3	9	5						
<i>P. portugalica</i>	CBS 393.48T	KM19933	KM19951	KM19942						
		5	0	2						
<i>P. rhododendri</i>	IFRDCC 2399T	KC537804	KC537811	KC537818						
<i>P. rhodomyrtus</i>	HGUP4230T	KF412648	KF412645	KF412642						
<i>P. rhodomyrtus</i>	LC4458	KX895010	KX895228	KX895342						
<i>P. rhodomyrtus</i>	LC3413	KX894981	KX895198	KX895313						
<i>P. rosea</i>	MFLUCC 12-0258T	JX399005	JX399069	JX399036						
<i>P. scoparia</i>	CBS 176.25T	KM19933	KM19947	KM19939						
		0	8	3						
<i>P. spathulata</i>	CBS 356.86T	KM19933	KM19951	KM19942						
		8	3	3						
<i>P. telopeae</i>	CBS 114161T	KM19929	KM19950	KM19940						
		6	0	3						
<i>P. trachicarpicola</i>	MFLUCC 12-0264	JX399004	JX399068	JX399035						
<i>P. trachicarpicola</i>	OP068T	JQ845947	JQ845946	JQ845945						
<i>P. unicolor</i>	MFLUCC 12-0276T	JX398999	N/A	JX399030						
<i>P. verruculosa</i>	MFLUCC 12-0274T	JX398996	JX399061	N/A						
<i>Neopetalotiopsis asiatica</i>	MFLUCC 12-0286T	JX398983	JX399049	JX399018						
<i>N. australis</i>	CBS 114159T	KM19934	KM19953	KM19943						
		8	7	2						
<i>N. clavispora</i>	MFLUCC 12-0281T	JX398979	JX399045	JX399014						
<i>N. ellipsospora</i>	MFLUCC 12-0283T	JX398980	JX399047	JX399016						
<i>N. eucalypticola</i>	CBS 264.37T	KM19937	KM19955	KM19943						
		6	1	1						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers								
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>
<i>N. honoluluana</i>	CBS 114495T	KM19936 4	KM19954 8	KM19945 7						
<i>N. magna</i>	MFLUCC 12-0652T	KF582795	KF582791	KF582793						
<i>N. mesopotamica</i>	CBS 336.86T	KM19936 2	KM19955 5	KM19944 1						
<i>N. piceana</i>	CBS 394.48T	KM19936 8	KM19952 7	KM19945 3						
<i>N. protearum</i>	CBS 114178T	JN712498	KM19954 2	KM19946 3						
<i>N. rosae</i>	CBS 101057T	KM19935 9	KM19952 3	KM19942 9						
<i>N. rosae</i>	CBS 124745	KM19936 0	KM19952 4	KM19943 0						
<i>N. rosae</i>	JZB340064	MN49597 2	MN96832 8	MN96833 6						
<i>N. samarangensis</i>	MFLUCC 12-0233T	JQ968609	JQ968611	JQ968610						
<i>N. saprophytica</i>	MFLUCC 12-0282T	KM19934 5	KM19953 8	KM19943 3						
<i>N. surinamensis</i>	CBS 450.74T	KM19935 1	KM19951 8	KM19946 5						
<i>N. umbrinospora</i>	MFLUCC 12-0285T	JX398984	JX399050	JX399019						
<i>N. zimbabwana</i>	CBS 111495T	JX556231	KM19954 5	KM19945 6						
<i>Pseudopezalotiopsis cocos</i>	CBS 272.29T	KM19937 8	KM19955 3	KM19946 7						
<i>Bartalinia bischoffiae</i>	HKUCC 6534	N/A				AF382367				
<i>B. kevinhydei</i>	MFLUCC 12-0384AT	MT477057				MT477059				
<i>B. kevinhydei</i>	MFLUCC 12-0384BT	MT477058				MT477060				
<i>B. kunmingensis</i>	KUMCC 18-0178T	MK35308 3				MK35308 5				
<i>B. lateripes</i>	HKUCC 6654	N/A				AF382368				
<i>B. laurina</i>	HKUCC 6537	AF405302				AF382369				

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>B. pini</i>	CBS 143891T	MH55412				MH55433					
		5				0					
<i>B. pini</i>	CFCC 54574	MW36428				MW36427					
		5				6					
<i>B. pondoensis</i>	CMW 31067	NR153599				N/A					
<i>B. robillardoides</i>	CBS 122686	EU552102				N/A					
<i>B. robillardoides</i>	CBS 122705T	LT853104				N/A					
<i>B. robillardoides</i>	CNUFC-CNUP1-1	MH48284				MH48285					
		7				3					
<i>B. robillardoides</i>	CNUFC-CNUP1-2	MH48284				MH48285					
		8				4					
<i>B. rosicola</i>	MFLUCC 17-0645	MG82887				MG82898					
		2				8					
<i>Colletotrichum abscissum</i>	COAD 1877T	KP843126		KP843135				KP843141		KP843129	KP843132
<i>C. acerbum</i>	CBS 128530T	JQ948459		JQ950110				JQ949780		JQ948790	JQ949120
<i>C. acutatum</i>	CBS 112996T	JQ005776		JQ005860				JQ005839		JQ948677	JQ005797
<i>C. aenigma</i>	ICMP 18608T	JX010244		JX010389				JX009443		JX010044	JX009774
<i>C. aenigma</i>	ICMP 18686	JX010243		JX010390				JX009519		JX009913	JX009789
<i>C. aeschynomenes</i>	ICMP 17673T	JX010176		JX010392				JX009483		JX009930	JX009799
<i>C. alatae</i>	CBS 304.67T	JX010190		JX010383				JX009471		JX009990	JX009837
<i>C. alienum</i>	ICMP 12071T	JX010251		JX010411				JX009572		JX010028	JX009882
<i>C. aotearoa</i>	ICMP 18537T	JX010205		JX010420				JX009564		JX010005	JX009853
<i>C. asianum</i>	ICMP 18580T	FJ972612		JX010406				JX009584		JX010053	JX009867
<i>C. australe</i>	CBS 116478T	JQ948455		JQ950106				JQ949776		JQ948786	JQ949116
<i>C. brisbanense</i>	CBS 292.67T	JQ948291		JQ949942				JQ949612		JQ948621	JQ948952
<i>C. cairnsense</i>	BRIP 63642T	KU923672		KU923688				KU923716		KU923704	KU923710
<i>C. carthami</i>	SAPA100011T	AB696998		AB696992				N/A		N/A	N/A
<i>C. chrysanthemi</i>	IMI 364540	JQ948273		JQ949924				JQ949594		JQ948603	JQ948934
<i>C. clidemiae</i>	ICMP 18658T	JX010265		JX010438				JX009537		JX009989	JX009877
<i>C. cordylinicola</i>	ICMP 18579T	JX010226		JX010440				HM470235		JX009975	JX009864
<i>C. cosmi</i>	CBS 853.73T	JQ948274		JQ949925				JQ949595		JQ948604	JQ948935
<i>C. costaricense</i>	CBS 330.75T	JQ948180		JQ949831				JQ949501		JQ948510	JQ948841
<i>C. cuscutae</i>	IMI 304802T	JQ948195		JQ949846				JQ949516		JQ948525	JQ948856
<i>C. fioriniae</i>	CBS 125396	JQ948299		JQ949950				JQ949620		JQ948629	JQ948960
<i>C. fioriniae</i>	IMI 324996	JQ948301		JQ949952				JQ949622		JQ948631	JQ948962
<i>C. fioriniae</i>	CBS 126526	JQ948323		JQ949974				JQ949644		JQ948653	JQ948984

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tefl</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>C. fruticicola</i>	ICMP 18581T	JX010165		JX010405				FJ907426		JX010033	JX009866
<i>C. fruticicola</i>	ICMP 18613	JX010167		JX010388				JX009491		JX009998	JX009772
<i>C. fruticicola</i>	ICMP 18727	JX010179		JX010394				JX009565		JX010035	JX009812
<i>C. gloeosporioides</i>	IMI 356878T	JX010152		JX010445				JX009531		JX010056	JX009818
<i>C. gloeosporioides</i>	ICMP 12939	JX010149		N/A				JX009462		JX009931	JX009747
<i>C. gloeosporioides</i>	ICMP 18695	JX010153		N/A				JX009494		JX009979	JX009779
<i>C. godetiae</i>	CBS 133.44T	JQ948402		JQ950053				JQ949723		JQ948733	JQ949063
<i>C. hebeiense</i>	CGMCC 3.17464T	KF156863		KF288975				KF377532		KF377495	KF289008
<i>C. horii</i>	ICMP 10492T	GQ329690		JX010450				JX009438		GQ329681	JX009752
<i>C. johnstonii</i>	CBS 128532T	JQ948444		JQ950095				JQ949765		JQ948775	JQ949105
<i>C. kahawae</i> subsp. <i>ciggaro</i>	ICMP 18539T	JX010230		JX010434				JX009523		JX009966	JX009800
<i>C. kahawae</i> subsp. <i>ciggaro</i>	ICMP 18534	JX010227		JX010427				JX009473		JX009904	JX009765
<i>C. kahawae</i> subsp. <i>ciggaro</i>	ICMP 12952	JX010214		JX010426				JX009431		JX009971	JX009757
<i>C. kahawae</i> subsp. <i>kahawae</i>	IMI 319418T	JX010231		JX010444				JX009452		JX010012	JX009813
<i>C. kinghornii</i>	CBS 198.35T	JQ948454		JQ950105				JQ949775		JQ948785	JQ949115
<i>C. laticiphilum</i>	CBS 112989T	JQ948289		JQ949940				JQ949610		JQ948619	JQ948950
<i>C. lupini</i>	CBS 109225T	JQ948155		JQ949806				JQ949476		JQ948485	JQ948816
<i>C. musae</i>	CBS 116870T	JX010146		HQ596280				JX009433		JX010050	JX009896
<i>C. nupharicola</i>	CBS 470.96T	JX010187		JX010398				JX009437		JX009972	JX009835
<i>C. nymphaeae</i>	CBS 515.78T	JQ948197		JQ949848				JQ949518		JQ948527	JQ948858
<i>C. nymphaeae</i>	CBS 134234	KC293582		KC293662				KY855974		KC293742	KY856139
<i>C. nymphaeae</i>	CBS 516.78	JQ948198		JQ949849				JQ949519		JQ948528	JQ948859
<i>C. paranaense</i>	CBS 134729T	KC204992		KC205060				KC205077		KC205026	KC205043
<i>C. paxtonii</i>	IMI 165753T	JQ948285		JQ949936				JQ949606		JQ948615	JQ948946
<i>C. phormii</i>	CBS 118194T	JQ948446		JQ950097				JQ949767		JQ948777	JQ949107
<i>C. psidii</i>	CBS 145.29T	JX010219		JX010443				JX009515		JX009967	JX009901
<i>C. pyricola</i>	CBS 128531T	JQ948445		JQ950096				JQ949766		JQ948776	JQ949106
<i>C. queenslandicum</i>	ICMP 1778T	JX010276		JX010414				JX009447		JX009934	JX009899
<i>C. rhombiforme</i>	CBS 129953T	JQ948457		JQ950108				JQ949778		JQ948788	JQ949118
<i>C. salicis</i>	CBS 607.94T	JQ948460		JQ950111				JQ949781		JQ948791	JQ949121
<i>C. salsolae</i>	ICMP 19051T	JX010242		JX010403				JX009562		JX009916	JX009863
<i>C. siamense</i>	ICMP 18578T	JX010171		JX010404				FJ907423		JX009924	JX009865
<i>C. siamense</i>	ICMP 17795	JX010162		JX010393				JX009506		JX010051	JX009805

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tefl</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>C. simmondsii</i>	CBS 122122T	JQ948276		JQ949927				JQ949597		JQ948606	JQ948937
<i>C. sloanei</i>	IMI 364297T	JQ948287		JQ949938				JQ949608		JQ948617	JQ948948
<i>C. tamarilloi</i>	CBS 129814T	JQ948184		JQ949835				JQ949505		JQ948514	JQ948845
<i>C. temperatum</i>	CBS 133122T	JX145159		JX145211				N/A		N/A	N/A
<i>C. temperatum</i>	CBS 133120	JX145135		JX145186				N/A		N/A	N/A
<i>C. theobromicola</i>	CBS 124945T	JX010294		JX010447				JX009444		JX010006	JX009869
<i>C. ti</i>	ICMP 4832T	JX010269		JX010442				JX009520		JX009952	JX009898
<i>C. tropicale</i>	CBS 124949T	JX010264		JX010407				JX009489		JX010007	JX009870
<i>C. viniferum</i>	GZAAS 5.08601T	JN412804		JN412813				JN412795		JN412798	N/A
<i>C. viniferum</i>	GZAAS5.08608	JN412802		JN412811				JN412793		JN412800	N/A
<i>C. viniferum</i>	GZAAS5.08616	JN412807		JN412809				JN412790		JN412799	N/A
<i>C. viniferum</i>	GZAAS5.08622	JN412806		JN412812				JN412791		JN412796	N/A
<i>C. walleri</i>	CBS 125472T	JQ948275		JQ949926				JQ949596		JQ948605	JQ948936
<i>C. wuxiense</i>	CGMCC 3.17894T	KU251591		KU252200				KU251672		KU252045	KU251939
<i>C. wuxiense</i>	JS1A44	KU251592		KU252201				KU251673		KU252046	KU251940
<i>C. xanthorrhoeae</i>	ICMP 17903T	JX010261		JX010448				JX009478		JX009927	JX009823
<i>Monilochaefes infuscans</i>	CBS 869.96T	JQ005780		JQ005864				JQ005843		JX546612	JQ005801
<i>Alternaria alstroemeriae</i>	MAFF 241374	AB678214	LC275050		LC275231					AB744034	
<i>A. alstroemeriae</i>	CBS 118809T	KP124297	KP125072		KP124765					KP124154	
<i>A. alternantherae</i>	CBS 124392	KC584179	KC584633		KC584374					KC584096	
<i>A. alternata</i>	CBS 916.96ET	AF347031	KC584634		KC584375					AY278808	
<i>A. alternata</i>	CBS 918.96	AF347032	KC584693		KC584435					AY278809	
<i>A. alternata</i> f. sp. citri pathotype rough lemon	CBS 102595	FJ266476	KC584666		KC584408					AY562411	
<i>A. alternata</i> f. sp. citri pathotype tangerine	CBS 102600	KP124331	KP125107		KP124799					KP124186	
<i>A. arborescens</i> species complex	CBS 102605T	AF347033	KC584636		KC584377					AY278810	
<i>A. arborescens</i> species complex	CBS 119544	KP124408	KP125186		KP124878					JQ646321	
<i>A. aspera</i>	CBS 115269T	KC584242	KC584734		KC584474					KC584166	
<i>A. betae-kenyensis</i>	CBS 118810T	KP124419	KP125197		KP124888					KP124270	
<i>A. botrytis</i>	MAFF 246887	LC440625	LC480252		LC476834					LC482047	
<i>A. botrytis</i>	CBS 197.67ET	KC584243	KC584736		KC584476					KC584168	
<i>A. brassicicola</i>	MAFF 246772	LC440585	LC480212		LC476792					LC482007	
<i>A. brassicicola</i>	MUCC 1612	LC440586	AB862981		AB862975					AB862969	
<i>A. burnsii</i>	CBS 107.38T	KP124420	KP125198		KP124889					JQ646305	

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tefl</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>A. cinerariae</i>	MAFF 243059T	AB906673	LC480247		LC476828						AB906670
<i>A. cinerariae</i>	CBS 116495R	KC584190	KC584648		KC584389						KC584109
<i>A. cucumerina</i>	CBS 117225R	KJ718154	KJ718502		KJ718327						KJ718001
<i>A. cucumerina</i>	CBS 116114T	KJ718153	KJ718501		KJ718326						KJ718000
<i>A. cumini</i>	CBS 121329T	KC584191	KC584650		KC584391						KC584110
<i>A. dendropanacis</i>	CNU 085031T	HQ203210	KP877992		KP877985						KF516506
<i>A. dendropanacis</i>	CNU 085033	N/A	KP877993		KP877986						KF516507
<i>A. eichhorniae</i>	CBS 489.92T	KC146356	KP125204		KP124895						KP124276
<i>A. gaisen f. sp. fragariae</i>	MAFF 242310	LC269973	LC275059		LC275239						LC270141
<i>A. gaisen f. sp. fragariae</i>	MAFF 731003	LC164852	LC167150		LC169133						LC169127
<i>A. gomphrenae</i>	MAFF 246769ET	LC440579	LC480206		LC476782						LC481999
<i>A. iridialustralis</i>	CBS 118486T	KP124435	KP125214		KP124905						KP124284
<i>A. iridicola</i>	MUCC 2148	LC269974	LC275060		LC275240						LC270142
<i>A. iridicola</i>	MAFF 246890ET	LC269975	LC275061		LC275241						LC270143
<i>A. jacinthicola</i>	CBS 133751T	KP124438	KP125217		KP124908						KP124287
<i>A. longipes</i>	CBS 540.94R	AY278835	KC584667		KC584409						AY278811
<i>A. longipes</i>	CBS 121332R	KP124443	KP125222		KP124913						KP124292
<i>A. multiformis</i>	CBS 102060T	FJ266486	KC584744		KC584484						KC584174
<i>A. nobilis</i>	CBS 116490R	KC584208	KC584673		KC584415						KC584127
<i>A. paragonphrenae</i>	MAFF 246768T	N/A	LC480207		LC476783						LC482000
<i>A. penicillata</i>	CBS 116608T	FJ357311	KC584698		KC584440						FJ357299
<i>A. penicillata</i>	CBS 116607	KC584229	KC584706		KC584447						KC584153
<i>A. perpunctulata</i>	CBS 115267T	KC584210	KC584676		KC584418						KC584129
<i>A. petroselini</i>	CBS 112.41T	KC584211	KC584677		KC584419						KC584130
<i>A. porri</i>	CBS 116699T	KJ718218	KJ718564		KJ718391						KJ718053
<i>A. porri</i>	CBS 116698R	DQ323700	KC584679		KC584421						KC584132
<i>A. septorioides</i>	CBS 106.41T	KC584216	KC584685		KC584427						KC584136
<i>A. tomato</i>	CBS 114.35	KP124446	KP125225		KP124916						KP124295
<i>A. triangularis</i>	MAFF 246776T	LC440629	LC480255		LC476837						LC482050
<i>A. triangularis</i>	AC95	LC440630	LC480256		LC476838						LC482051
<i>A. vaccariicola</i>	CBS 118714T	KC584224	KC584697		KC584439						KC584147
<i>Paradendryphiella salina</i>	CBS 302.84T	JN383486	KC584709		KC584450						JN383467
<i>Trichoderma acremonioides</i>	HMAS 279611T		MH61237		MH61236						
			5		9						
<i>T. acremonioides</i>	HMAS 254562		MH61237		MH61236						
			4		8						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>T. afroharzianum</i>	CBS 466.94		KP008851		KP009150						
<i>T. afroharzianum</i>	T22		KP008850		KP009145						
<i>T. asperelloides</i>	CEN1409		MK69664		MK69680						
			7		8						
<i>T. asperellum</i>	CGMCC 6422		KF425756		KF425755						
<i>T. asperellum</i>	CBS 433.97T		AY376058		EU248617						
<i>T. asperellum</i>	G.J.S. 90-7		EU338333		EU338337						
<i>T. atrobrunneum</i>	T42		KX632629		KX632572						
<i>T. atrobrunneum</i>	S3		KJ665376		KJ665241						
<i>T. atroviride</i>	CBS 142.95T		AY376051		EU241500						
<i>T. aureoviride</i>	C.P.K. 2848		FJ860615		FJ860523						
<i>T. aureoviride</i>	HMAS 266607		KF923280		KF923306						
<i>T. crassum</i>	CBS 114230		JN133572		AY481587						
<i>T. dorotheopsis</i>	HZA15		MK85083		MH64780						
			7		5						
<i>T. eijii</i>	HMAS 252876		KJ634775		KJ634742						
<i>T. gamsii</i>	GJS 04-09		DQ307541		JN133561						
<i>T. guizhouense</i>	S278		KF134799		KF134791						
<i>T. guizhouense</i>	HGUP 0038		JN215484		JQ901400						
<i>T. hamatum</i>	DAOM 167057		EU279965		AF545548						
<i>T. harzianum</i>	CBS 226.95T		AF534621		AF545549						
<i>T. harzianum</i>	TRS55		KP008803		KP009121						
<i>T. hispanicum</i>	CBS 130540T		JN715659		JN715600						
<i>T. koningiopsis</i>	GJS 93-20		DQ284966		EU241506						
<i>T. laevisporum</i>	HMAS 273756		KU529128		KU529139						
<i>T. longipilis</i>	CBS 120953		FJ860643		FJ860542						
<i>T. longipilis</i>	CBS 135570		KJ665556		KJ665292						
<i>T. olivascens</i>	CBS 132574		KC285624		KC285752						
<i>T. paraviridescens</i>	CBS 132566		KC285671		KC285764						
<i>T. polypori</i>	HMAS 248855T		KY688058		KY687994						
<i>T. polypori</i>	HMAS 248861		KY688059		KY688000						
<i>T. propepolypori</i>	YMF 1.06224T		MT070158		MT052181						
<i>T. propepolypori</i>	YMF 1.06199		MT070157		MT052182						
<i>T. rogersonii</i>	CBS 119503		FJ860690		FJ860583						
<i>T. samuelsii</i>	CBS 130537T		JN715651		JN715599						
<i>T. songyi</i>	SFC20130926-S001		KJ636525		KJ636518						

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>T. sparsum</i>	HMAS 273759		KU529136		KU529147						
<i>T. sphaerosporum</i>	HMAS 273763		KU529134		KU529145						
<i>T. strictipile</i>	C.P.K. 1601		FJ860704		FJ860594						
<i>T. subviride</i>	HMAS 273761		KU529131		KU529142						
<i>T. tawa</i>	G.J.S 02-79		AY392003		AY391955						
<i>T. tawa</i>	CBS 114233T		AY392004		AY391956						
<i>T. tomentosum</i>	S23		KJ665759		KJ665351						
<i>T. tomentosum</i>	S33		KF134801		KF134793						
<i>T. valdunense</i>	CBS 120923		FJ860717		FJ860605						
<i>T. velutinum</i>	C.P.K. 298		KJ665769		KF134794						
<i>T. vinosum</i>	CBS 119087		N/A		KC285779						
<i>T. virens</i>	CBS 249.59T		AF534631		AF545558						
<i>T. virens</i>	DIS 162		FJ463367		FJ442696						
<i>T. virens</i>	CBS 123790		AY750894		EU341804						
<i>T. viride</i>	CBS 119325		DQ672615		EU711362						
<i>T. yunnanense</i>	CBS 121219T		GU198243		GU198274						
<i>Protocrea farinosa</i>	CBS 121551		EU703889		EU703935						
<i>Protocrea pallida</i>	CBS 299.78		EU703900		EU703948						
<i>Cladosporium acalyphae</i>	CBS 125982T	HM14799	HM14823							HM148481	
		4	5								
<i>C. angustisporum</i>	CBS 125983T	HM14799	HM14823							HM148482	
		5	6								
<i>C. asperulatum</i>	CBS 126340T	HM14799	HM14823							HM148485	
		8	9								
<i>C. australiense</i>	CBS 125984T	HM14799	HM14824							HM148486	
		9	0								
<i>C. chalastosporoides</i>	CBS 125985T	HM14800	HM14824							HM148488	
		1	2								
<i>C. chubutense</i>	CBS 124457T	FJ936158	FJ936161							FJ936165	
<i>C. cladosporioides</i>	CBS 112388T	HM14800	HM14824							HM148490	
		3	4								
<i>C. cladosporioides</i>	CBS 113738	HM14800	HM14824							HM148491	
		4	5								
<i>C. cladosporioides</i>	CBS 143.35	HM14801	HM14825							HM148498	
		1	2								
<i>C. colocasiae</i>	CBS 386.64T	HM14806	HM14831							HM148555	
		7	0								

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>C. colocasiae</i>	CBS 119542	HM14806 6	HM14830 9					HM148554			
<i>C. colombiae</i>	CBS 274.80BT	FJ936159	FJ936163					FJ936166			
<i>C. cucumerinum</i>	CBS 171.52T	HM14807 2	HM14831 6					HM148561			
<i>C. delicatulum</i>	CBS 126342	HM14807 9	HM14832 3					HM148568			
<i>C. exasperatum</i>	CBS 125986T	HM14809 0	HM14833 4					HM148579			
<i>C. exile</i>	CBS 125987T	HM14809 1	HM14833 5					HM148580			
<i>C. flabelliforme</i>	CBS 126345T	HM14809 2	HM14833 6					HM148581			
<i>C. funiculosum</i>	CBS 122129T	HM14809 4	HM14833 8					HM148583			
<i>C. gamsianum</i>	CBS 125989T	HM14809 5	HM14833 9					HM148584			
<i>C. globisporum</i>	CBS 812.96T	HM14809 6	HM14834 0					HM148585			
<i>C. hillianum</i>	CBS 125988T	HM14809 7	HM14834 1					HM148586			
<i>C. inversicolor</i>	CBS 401.80T	HM14810 1	HM14834 5					HM148590			
<i>C. iranicum</i>	CBS 126346T	HM14811 0	HM14835 4					HM148599			
<i>C. licheniphilum</i>	CBS 125990T	HM14811 1	HM14835 5					HM148600			
<i>C. lycoperdinum</i>	CBS 126347	HM14811 2	HM14835 6					HM148601			
<i>C. myrtacearum</i>	CBS 126350T	HM14811 7	HM14836 1					HM148606			
<i>C. oxysporum</i>	CBS 125991	HM14811 8	HM14836 2					HM148607			
<i>C. oxysporum</i>	CBS 126351	HM14811 9	HM14836 3					HM148608			

Supplementary Table 1 Continued.

Species	Isolate	GenBank accession numbers									
		ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
<i>C. paracladosporioides</i>	CBS 171.54T	HM14812 0	HM14836 4					HM148609			
<i>C. perangustum</i>	CBS 125996T	HM14812 1	HM14836 5					HM148610			
<i>C. phyllactiniicola</i>	CBS 126352T	HM14815 0	HM14839 4					HM148639			
<i>C. phyllophilum</i>	CBS 125992T	HM14815 4	HM14839 8					HM148643			
<i>C. pini-ponderosae</i>	CBS 124456T	FJ936160	FJ936164					FJ936167			
<i>C. pseudocladosporioides</i>	CBS 125993T	HM14815 8	HM14840 2					HM148647			
<i>C. rectoides</i>	CBS 125994T	HM14819 3	HM14843 8					HM148683			
<i>C. rectoides</i>	CBS 126357	HM14819 4	HM14843 9					HM148684			
<i>C. scabrellum</i>	CBS 126358T	HM14819 5	HM14844 0					HM148685			
<i>C. subuliforme</i>	CBS 126500T	HM14819 6	HM14844 1					HM148686			
<i>C. tenuissimum</i>	CBS 125995T	HM14819 7	HM14844 2					HM148687			
<i>C. tenuissimum</i>	CBS 126359	HM14819 8	HM14844 3					HM148688			
<i>C. tenuissimum</i>	CPC 11555	HM14820 5	HM14845 0					HM148695			
<i>C. uredinicola</i>	CPC 5390	AY251071 7	HM14846 7					HM148712			
<i>C. varians</i>	CBS 126362T	HM14822 4	HM14847 0					HM148715			
<i>C. verrucocladosporioides</i>	CBS 126363T	HM14822 6	HM14847 2					HM148717			
<i>C. vignae</i>	CBS 121.25	HM14822 7	HM14847 3					HM148718			
<i>C. xylophilum</i>	CBS 125997T	HM14823 0	HM14847 6					HM148721			
<i>C. sphaerospermum</i>	CBS 102045	DQ780351	EU570262					EF101378			

Supplementary Table 2 Details of fungal taxa and source.

No.	Species	ID	GenBank accession numbers									
			ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
1	<i>B. dothidea</i>	JZB310204	ON891635	ON890442	ON911723							
		JZB310205	ON891636	ON890443	ON911724							
		JZB310206	ON891637	ON890444	ON911725							
		JZB310207	ON891638	ON890445	ON911726							
		JZB310208	ON891639	ON890446	ON911727							
		JZB310209	ON891640	ON890447	N/A							
		JZB310210	ON891641	ON890448	ON911728							
		JZB310211	ON891642	ON890449	ON911729							
		JZB310212	ON891643	ON890450	ON911730							
		JZB310213	ON891644	ON890451	ON911731							
		JZB310214	ON891645	ON890452	ON911732							
		JZB310215	ON891646	ON890453	ON911733							
		JZB310216	ON891647	ON890454	ON911734							
		JZB310217	ON891648	ON890455	ON911735							
		JZB310218	ON891649	ON890456	ON911736							
		JZB310219	ON891650	ON890457	ON911737							
		JZB310220	ON891651	ON890458	ON911738							
2	<i>L. citricola</i>	JZB3130023	OP223326	OP225411	OP225418							
		JZB3130024	OP223327	OP225412	OP225419							
		JZB3130025	OP223328	OP225413	OP225420							
		JZB3130026	OP223329	OP225414	OP225421							
3	<i>L. pseudotheobromae</i>	JZB3130020	OP223323	OP225408	OP225415							
		JZB3130021	OP223324	OP225409	OP225416							
		JZB3130022	OP223325	OP225410	OP225417							
4	<i>L. theobromae</i>	JZB3130018	OP216759	OP225403	OP225405							
		JZB3130019	OP216760	OP225404	N/A							
5	<i>D. seriata</i>	JZB3140015	OP223425	OP225437	OP225442							
		JZB3140016	OP223426	OP225438	OP225443							
		JZB3140017	OP223427	OP225439	OP225444							
6	<i>N. parvum</i>	JZB3120008	OP223418	OP225429	OP225440							
		JZB3120009	OP223419	OP225430	OP225441							
7	<i>P. rhois</i>	JZB3600001	OP223420	OP225431		N/A						
		JZB3600002	OP223421	OP225432		OP225930						
		JZB3600003	OP223422	OP225433		OP225931						
		JZB3600004	OP223423	OP225434		OP225932						
		JZB3600005	N/A	OP225435		OP225933						

Supplementary Table 2 Continued.

No.	Species	ID	GenBank accession numbers									
			ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
		JZB3600006	OP223424	OP225436				OP225934				
8	<i>D. novozelandica</i>	JZB3310031	OQ119068	OQ122032	OQ129652				OQ123934			
		JZB3310032	OQ119069	OQ122033	OQ129653				OQ123935			
		JZB3310033	OQ119070	OQ122034	OQ129654				OQ123936			
		JZB3310034	OQ119071	OQ122035	OQ129655				OQ123937			
		JZB3310035	OQ119072	OQ122036	N/A				OQ123938			
		JZB3310036	OQ119073	OQ122037	N/A				OQ123939			
		JZB3310037	OQ119074	OQ122038	OQ129656				OQ123940			
		JZB3310038	OQ119075	OQ122039	OQ129657				OQ123941			
		JZB3310039	OQ119076	OQ122040	OQ129658				OQ123942			
		JZB3310040	OQ119077	OQ122041	N/A				OQ123943			
		JZB3310041	OQ119078	OQ122042	N/A				OQ123944			
		JZB3310042	OQ119079	OQ122043	OQ129659				OQ123945			
9	<i>D. alcacerensis</i>	JZB3310021	OQ119058	OQ122023	OQ129643				OQ123926			
		JZB3310022	OQ119059	OQ122024	OQ129644				OQ123927			
		JZB3310023	OQ119060	OQ122025	OQ129645				OQ123928			
		JZB3310024	OQ119061	OQ122026	OQ129646				OQ123929			
		JZB3310025	OQ119062	OQ122027	OQ129647				OQ123930			
		JZB3310026	OQ119063	OQ122028	OQ129648				N/A			
		JZB3310027	OQ119064	OQ122029	OQ129649				OQ123931			
		JZB3310028	OQ119065	N/A	N/A				OQ123932			
		JZB3310029	OQ119066	OQ122030	OQ129650				N/A			
		JZB3310030	OQ119067	OQ122031	OQ129651				OQ123933			
10	<i>D. torresensis</i>	JZB3310046	OQ119083	OQ122047	OQ129662				OQ123949			
		JZB3310047	OQ119084	OQ122048	OQ129663				OQ123950			
		JZB3310048	OQ119085	OQ122049	OQ129664				OQ123951			
11	<i>D. macrodidyma</i>	JZB3310043	OQ119080	OQ122044	OQ129660				OQ123946			
		JZB3310044	OQ119081	OQ122045	OQ129661				OQ123947			
		JZB3310045	OQ119082	OQ122046	N/A				OQ123948			
12	<i>I. liriodendri</i>	JZB3610001	OQ119086	OQ129739	OQ122016				OQ123952			
		JZB3610002	OQ119087	OQ129740	OQ122017				OQ123953			
		JZB3610003	OQ119088	OQ129741	OQ122018				OQ123954			
		JZB3610004	OQ119089	OQ129742	OQ122019				OQ123955			
		JZB3610005	OQ119090	OQ129743	OQ122020				OQ123956			
		JZB3610006	OQ119091	OQ129744	OQ122021				OQ123957			
		JZB3610007	OQ119092	OQ129745	OQ122022				OQ123958			

Supplementary Table 2 Continued.

No.	Species	ID	GenBank accession numbers									
			ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
13	<i>C. viticola</i>	JZB3320005	OQ119040	OQ122013	OQ129640							
		JZB3320006	OQ119041	OQ122014	OQ129641							
		JZB3320007	OQ119042	OQ122015	OQ129642							
14	<i>F. oxysporum</i>	JZB3110181		OQ122050		OQ124015						
		JZB3110182		OQ122051		OQ124016						
		JZB3110183		OQ122052		OQ124017						
		JZB3110184		OQ122053		OQ124018						
		JZB3110185		OQ122054		OQ124019						
		JZB3110186		OQ122055		OQ124020						
		JZB3110187		OQ122056		OQ124021						
		JZB3110188		OQ122057		OQ124022						
		JZB3110189		OQ122058		OQ124023						
15	<i>F. brachygibbosum</i>	JZB3110191		OQ122060		OQ124025						
		JZB3110192		OQ122061		OQ124026						
		JZB3110193		OQ122062		OQ124027						
		JZB3110194		N/A		OQ124028						
16	<i>F. acuminatum</i>	JZB3110195		OQ122063		OQ124029						
		JZB3110196		OQ122064		OQ124030						
		JZB3110197		OQ122065		OQ124031						
		JZB3110198		OQ122066		OQ124032						
17	<i>F. hainanense</i>	JZB3110199		OQ122067		OQ124033						
		JZB3110200		OQ122068		OQ124034						
18	<i>F. lacertarum</i>	JZB3110201		OQ122069		OQ124035						
19	<i>F. compactum</i>	JZB3110190		OQ122059		OQ124024						
20	<i>N. falciformis</i>	JZB3620005		OQ122074		OQ124040						
		JZB3620006		OQ122075		N/A						
		JZB3620007		OQ122076		N/A						
		JZB3620008		OQ122077		N/A						
		JZB3620009		OQ122078		OQ124041						
		JZB3620010		OQ122079		N/A						
		JZB3620011		OQ122080		OQ124042						
21	<i>N. solani</i>	JZB3620001		OQ122070		OQ124036						
		JZB3620002		OQ122071		OQ124037						
		JZB3620003		OQ122072		OQ124038						
		JZB3620004		OQ122073		OQ124039						

Supplementary Table 2 Continued.

No.	Species	ID	GenBank accession numbers									
			ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
22	<i>B. delphinoides</i>	JZB3630001		OQ122081		OQ124043						
		JZB3630002		OQ122082		OQ124044						
23	<i>D. eres</i>	JZB320221	OQ119101	OQ123959	OQ129700					OQ129665		
		JZB320222	OQ119102	OQ123960	OQ129701					OQ129666		
		JZB320223	OQ119103	OQ123961	OQ129702					OQ129667		
		JZB320224	OQ119104	OQ123962	OQ129703					OQ129668		
		JZB320225	OQ119105	OQ123963	OQ129704					OQ129669		
		JZB320226	OQ119106	OQ123964	OQ129705					OQ129670		
		JZB320227	OQ119107	OQ123965	OQ129706					OQ129671		
		JZB320228	OQ119108	OQ123966	OQ129707					OQ129672		
		JZB320229	OQ119109	OQ123967	OQ129708					OQ129673		
		JZB320230	OQ119110	OQ123968	OQ129709					OQ129674		
		JZB320231	OQ119111	OQ123969	N/A					OQ129675		
		JZB320232	OQ119112	OQ123970	OQ129710					OQ129676		
		JZB320233	OQ119113	OQ123971	N/A					OQ129677		
		JZB320234	OQ119114	OQ123972	OQ129711					OQ129678		
		JZB320235	OQ119115	OQ123973	N/A					OQ129679		
		JZB320236	OQ119116	OQ123974	OQ129712					OQ129680		
		JZB320237	OQ119117	OQ123975	OQ129713					OQ129681		
		JZB320238	OQ119118	OQ123976	OQ129714					OQ129682		
		JZB320239	OQ119119	OQ123977	OQ129715					OQ129683		
		JZB320240	OQ119120	OQ123978	OQ129716					OQ129684		
		JZB320241	OQ119121	OQ123979	OQ129717					OQ129685		
		JZB320242	OQ119122	OQ123980	OQ129718					OQ129686		
		JZB320243	OQ119123	OQ123981	OQ129719					OQ129687		
		JZB320244	OQ119124	OQ123982	OQ129720					OQ129688		
		JZB320245	OQ119125	OQ123983	OQ129721					N/A		
		JZB320246	OQ119126	OQ123984	OQ129722					N/A		
		JZB320247	OQ119127	OQ123985	OQ129723					N/A		
		JZB320248	OQ119128	OQ123986	OQ129724					OQ129689		
		JZB320249	OQ119129	N/A	OQ129725					N/A		
		JZB320250	N/A	OQ123987	OQ129726					OQ129690		
		JZB320251	OQ119130	OQ123988	OQ129727					OQ129691		
JZB320252	OQ119131	OQ123989	OQ129728					OQ129692				
JZB320253	OQ119132	OQ123990	OQ129729					OQ129693				
JZB320254	OQ119133	OQ123991	OQ129730					OQ129694				
JZB320255	OQ119134	OQ123992	OQ129731					OQ129695				

Supplementary Table 2 Continued.

No.	Species	ID	GenBank accession numbers									
			ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>
		JZB320256	OQ119135	OQ123993	OQ129732						OQ129696	
		JZB320257	OQ119136	OQ123994	OQ129733						OQ129697	
24	<i>D. unshiuensis</i>	JZB320258	OQ119137	OQ123995	OQ129734						OQ129698	
		JZB320259	OQ119138	OQ123996	N/A						OQ129699	
25	<i>P. iranianum</i>	JZB3190013			OQ124013						OQ124011	
		JZB3190014			OQ124014						OQ124012	
26	<i>C. vitis</i>	JZB3700081	OQ123804	OQ122008		OQ119043	OQ129636					
		JZB3700082	OQ123805	OQ122009		OQ119044	OQ129637					
		JZB3700083	OQ123806	OQ122010		OQ119045	OQ129638					
		JZB3700084	OQ123807	OQ122011		OQ119046	OQ129639					
		JZB3700085	OQ123808	N/A		N/A	N/A					
		JZB3700086	OQ123809	N/A		OQ119047	N/A					
		JZB3700087	OQ123810	OQ122012		OQ119048	N/A					
27	<i>P. kenyaana</i>	JZB340076	OQ119093	OQ129746	OQ129754							
		JZB340077	OQ119094	OQ129747	OQ129755							
		JZB340078	OQ119095	OQ129748	OQ129756							
28	<i>P. rhodomyrtus</i>	JZB340080	OQ119097	OQ129750	OQ129758							
		JZB340081	OQ119098	OQ129751	OQ129759							
29	<i>P. adusta</i>	JZB340079	OQ119096	OQ129749	OQ129757							
30	<i>N. rosae</i>	JZB340082	OQ119099	OQ129752	OQ129760							
		JZB340083	OQ119100	OQ129753	OQ129761							
31	<i>B. kevinhydei</i>	JZB3640001	OQ119032			OQ119050						
		JZB3640002	OQ119033			OQ119051						
		JZB3640003	OQ119034			OQ119052						
		JZB3640004	OQ119035			OQ119053						
		JZB3640005	OQ119036			OQ119054						
		JZB3640006	OQ119037			OQ119055						
		JZB3640007	OQ119038			OQ119056						
		JZB3640008	OQ119039			OQ119057						
32	<i>C. viniferum</i>	JZB330319	OQ109024		OQ116727			OQ121999		OQ123916	OQ129626	
		JZB330320	OQ109025		OQ116728			OQ122000		OQ123917	OQ129627	
		JZB330321	OQ109026		OQ116729			N/A		OQ123918	OQ129628	
		JZB330322	OQ109027		OQ116730			OQ122001		OQ123919	OQ129629	
		JZB330323	OQ109028		OQ116731			OQ122002		OQ123920	OQ129630	
		JZB330324	OQ109029		OQ116732			OQ122003		OQ123921	OQ129631	

Supplementary Table 2 Continued.

No.	Species	ID	GenBank accession numbers										
			ITS	<i>tef1</i>	<i>tub2</i>	<i>rpb2</i>	LSU	<i>his</i>	<i>act</i>	<i>cal</i>	<i>gapdh</i>	<i>chs</i>	
33	<i>C. nymphaeae</i>	JZB330325	OQ109030		OQ116733					OQ122004		OQ123922	OQ129632
		JZB330326	OQ109031		OQ116734					OQ122005		OQ123923	OQ129633
		JZB330327	OQ109032		OQ116735					OQ122006		OQ123924	OQ129634
34	<i>C. kahawae</i>	JZB330328	OQ109033		OQ116736				OQ122007		OQ123925	OQ129635	
35	<i>A. alternata</i>	JZB3180127	OQ119022	OQ123902		OQ123908						OQ129619	
		JZB3180128	OQ119023	OQ123903		OQ123909						OQ129620	
		JZB3180129	OQ119024	OQ123904		OQ123910						OQ129621	
		JZB3180130	OQ119025	OQ123905		OQ123911						OQ129622	
		JZB3180131	OQ119026	OQ123906		OQ123912						OQ129623	
		JZB3180132	OQ119027	N/A		OQ123913						OQ129624	
36	<i>A. longipes</i>	JZB3180133	OQ119028	N/A		OQ123914						N/A	
		JZB3180134	OQ119029	OQ123906		OQ123915						OQ129625	
37	<i>T. asperellum</i>	JZB3360013		OQ123997		OQ124003							
		JZB3360014		OQ123998		N/A							
		JZB3360015		OQ123999		N/A							
38	<i>T. guizhouense</i>	JZB3360016		OQ124000		OQ124004							
		JZB3360017		OQ124001		OQ124005							
39	<i>T. virens</i>	JZB3360018		OQ124002		OQ124006							
40	<i>C. tenuissimum</i>	JZB390038	OQ119030	OQ129735						OQ129737			
		JZB390039	OQ119031	OQ129736						OQ129738			