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Botryosphaeriaceae from *Eucalyptus* plantations and adjacent plants in China

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Key words

Botryosphaeria
Cophinforma
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plant pathogen

Abstract The *Botryosphaeriaceae* is a species-rich family that includes pathogens of a wide variety of plants, including species of *Eucalyptus*. Recently, during disease surveys in China, diseased samples associated with species of *Botryosphaeriaceae* were collected from plantation *Eucalyptus* and other plants, including *Cunninghamina lanceolata*, *Dimocarpus longan*, *Melastoma sanguineum* and *Phoenix hanceana*, which were growing adjacent to *Eucalyptus*. In addition, few samples from *Araucaria cunninghamii* and *Cedrus deodara* in two gardens were also included in this study. Disease symptoms observed mainly included stem canker, shoot and twig blight. In this study, 105 isolates of *Botryosphaeriaceae* were collected from six provinces, of which 81 isolates were from *Eucalyptus* trees. These isolates were identified based on comparisons of the DNA sequences of the internal transcribed spacer regions and intervening 5.8S nrRNA gene (ITS), and partial translation elongation factor 1-alpha (*tef1*), β-tubulin (*tub*), DNA-directed RNA polymerase II subunit (*rpb2*) and calmodulin (*cmdA*) genes, the nuclear ribosomal large subunit (LSU) and the nuclear ribosomal small subunit (SSU), and combined with their morphological characteristics. Results showed that these isolates represent 12 species of *Botryosphaeriaceae*, including *Botryosphaeria fusispora*, *Cophinforma atrovirens*, *Lasiodiplodia brasiliense*, *L. pseudotheobromae*, *L. theobromae* and *Neofusicoccum parvum*, and six previously undescribed species of *Botryosphaeria* and *Neofusicoccum*, namely *B. pseudoramosa* sp. nov., *B. qingyuanensis* sp. nov., *B. wangensis* sp. nov., *N. hongkongense* sp. nov., *N. microconidium* sp. nov. and *N. sinoeucalypti* sp. nov. Aside from *B. wangensis*, *C. atrovirens* and *N. hongkongense*, the other nine *Botryosphaeriaceae* species were isolated from *Eucalyptus* trees in South China. *Botryosphaeria fusispora* (26 % of the isolates from *Eucalyptus*) is the dominant species, followed by *L. pseudotheobromae* (23 % of the isolates from *Eucalyptus*). In addition to species found on *Eucalyptus* trees, we also found *B. pseudoramosa* on *M. sanguineum*; *B. wangensis* on *C. deodara*; *C. atrovirens* on *D. longan*; *L. theobromae* on *C. lanceolata*, *D. longan* and *P. hanceana*; and *N. hongkongense* on *A. cunninghamii*. Pathogenicity tests showed that the 12 species of *Botryosphaeriaceae* are pathogenic to three *Eucalyptus* clones and that *Lasiodiplodia* species are the most aggressive. The results of our study suggest that many more species of the *Botryosphaeriaceae* remain to be discovered in China. This study also provides confirmation for the wide host range of *Botryosphaeriaceae* species on different plants.

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INTRODUCTION

The *Botryosphaeriaceae* includes a range of phylogenetically and morphologically diverse fungi with a broad host range and geographic distribution globally (Punithalingam 1980, Slippers & Wingfield 2007, Liu et al. 2012, Phillips et al. 2013). These fungi occur primarily on woody plants including both economically important crops and native trees (Slippers & Wingfield 2007). Many species of *Botryosphaeriaceae* are well-known pathogens that can cause stem canker, shoot blight and dieback on woody plants; however, some species of *Botryosphaeriaceae* have been described as latent pathogens or endophytes that cause disease when the plant is under stress conditions (Slippers & Wingfield 2007).

Species of *Eucalyptus* are widely planted in more than 100 countries, and because of the rapid growth of some *Eucalyptus* trees, they represent one of the most widely planted genera for commercial forestry worldwide, with approximately 20 million hectares (Mha) established in plantations (Iglesias-Trabad et al. 2009). In China, *Eucalyptus* plantations have expanded substantially during the past 30 years, with more than 4.5 Mha of *Eucalyptus* established in South China by the end of 2013 (Chen & Chen 2013). Industrial *Eucalyptus* plantations in China are typically single species or hybrid plantings, often from a few clones that share a common parentage (Wei 2005, Turnbull 2007, Zhou & Wingfield 2011). The model of large-scale plantations with few clones greatly increases the threat from pests and diseases (Wingfield 2003, Wingfield et al. 2008). In recent years, the sustainable development of *Eucalyptus* plantations in China has been increasingly threatened by pathogens and pests (Zhou & Wingfield 2011). The important diseases in Chinese *Eucalyptus* plantations include stem canker/wilt caused by species of *Botryosphaeriaceae* (Chen et al. 2011c), *Ceratocystis* (Chen et al. 2013, Liu et al. 2015), *Chrysoporthe* (Chen et al. 2010) and *Teratosphaeria* (Chen et al. 2011a); leaf blight/spot caused by species of *Teratosphaeriaceae* (Burgess et al. 2006), *Mycosphaerellaceae* (Burgess et al. 2007), *Calonectria* (Lombard et al. 2010, Chen et al. 2011b) and *Quambalaria* (Zhou et al. 2007); and bacterial wilt associated with *Ralstonia solanacearum* (Cao 1982, Old et al. 2003).

Relatively little research has been conducted on diseases caused by *Botryosphaeriaceae* on *Eucalyptus* trees in China (Chen et al. 2011c, Li et al. 2015a). Based on DNA sequence comparisons and morphological features, five species of *Botryosphaeriaceae* have been identified from *Eucalyptus* in China to date, including *Botryosphaeria fabicerciana* from FuJian,

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Fig. 1 Disease symptoms on *Eucalyptus* trees caused by *Botryosphaeriaceae*. a. Typical dieback of a *Eucalyptus grandis* clone in FunJian Province; b. dieback of *Eucalyptus globulus*; c–e. stem cankers and lesions on main stems of different *Eucalyptus* clones/genotypes; f. branch and twig blight of a *Eucalyptus grandis* clone; g. fruiting structures with abundant mature dark conidia on a *Eucalyptus* branch; h. new branches germinated after main stem infection.

GuangXi and HaiNan Provinces, *Lasiodiplodia pseudotheobromae* from GuangXi Province, *L. theobromae* from GuangDong and GuangXi Provinces, *Neofusicoccum parvum* from FuJian and GuangXi Provinces and *N. ribis* s.lat. from FuJian Province (Chen et al. 2011c, Li et al. 2015a). These species were collected from cankered stems and blighted branches or twigs, and pathogenicity tests showed that all five species could produce lesions on *Eucalyptus* seedlings or trees (Chen et al. 2011c, Li et al. 2015a).

In China, species of *Botryosphaeriaceae* also have been isolated from a number of other woody and horticultural plants, including *Acacia confusa* (Zhao et al. 2010), *Actinidia chinensis* (Zhou et al. 2015), *Bougainvillea spectabilis*, *Polyscias balfouriana* (Li et al. 2015a), *Juglans regia* (Li et al. 2015b, Yu et al. 2015), *Malus domestica* (Tang et al. 2012, Xu et al. 2015a), *Rosa rugosa* (Chen et al. 2016), *Vitis vinifera* (Yan et al. 2012, 2013) and *Vaccinium corymbosum* (Xu et al. 2015b). *Botryosphaeriaceae* species identified from these plants resided in *Botryosphaeria*, *Lasiodiplodia* and *Neofusicoccum*. These *Botryosphaeriaceae* were all isolated from diseased tissue of the respective plant hosts.

From 2013–2014, surveys were conducted on *Eucalyptus* in plantations and some plants adjacent to *Eucalyptus*, and diseases with symptoms typical of those caused by *Botryosphaeriaceae* were observed. Diseased samples were collected and the putative *Botryosphaeriaceae* fungi (based on microscopic morphology) were isolated. In addition, few samples previously collected from *Araucaria cunninghamii* and *Cedrus deodara* were also included in this study. The aims of this study are to:

- identify these species of *Botryosphaeriaceae* based on phylogenetic analyses and morphological characteristics;
- clarify the geographic distribution of these *Botryosphaeriaceae* species; and
- evaluate pathogenicity of the identified *Botryosphaeriaceae* species on different *Eucalyptus* clones.

MATERIALS AND METHODS

Disease symptoms, sample collection and fungal isolation

Disease surveys were mainly conducted on species of *Eucalyptus* in plantations distributed in FuJian, GuangDong, GuangXi and HaiNan Provinces. Disease symptoms typically caused by *Botryosphaeriaceae* include tree dieback, stem canker, branch canker and twig blight (Fig. 1). Other plants, including *Cunninghamina lanceolata*, *Dimocarpus longan*, *Melastoma sanguineum* and *Phoenix hanceana*, which were growing in close proximity to *Eucalyptus* trees, were also randomly surveyed in this study. These surveys were conducted during 2013–2014. Samples of diseased materials, including stems, branches and twigs that showed typical symptoms of *Botryosphaeriaceae* infection, were collected and taken to the laboratory for fungal isolation. Diseased branches of *C. deodara* in HeNan Province and *A. cunninghamii* in Hong Kong Region with similar symptoms typical of *Botryosphaeriaceae* collected previously, were also added in this study (Fig. 1).

Fungi were isolated from diseased stems, branches and twigs, as well as from pycnidia produced on diseased tissues of *Eucalyptus* and other plants. When pycnidia formed on the surface of diseased tissue, the pycnidia were scratched lightly with a sterile scalpel and transferred with a sterile steel needle to 2 % malt extract agar (MEA) media containing 20 g of malt extract powder (Beijing Shuangxuan Microbial Culture Medium Products Factory, Beijing, China) and 20 g of agar per litre of water (Beijing Solarbio Science & Technology Co., Ltd., Beijing, China) under a stereomicroscope (Carl Zeiss Ltd., Munchen, Germany). For diseased tissues that did not produce pycnidia, small tissue pieces (approximately 0.25 cm^2) were cut from inner wood and transferred to 2 % MEA. Pieces of pycnidia and wood were incubated at room temperature for 2–5 d until colonies formed. Colonies with morphological characteristics typical of *Botryosphaeriaceae* were transferred to fresh 2 % MEA plates. Pure cultures were obtained by transferring single hyphal tips from colonies to 2 % MEA. Cultures were deposited in the culture collection of the China Eucalypt Research Centre (CERC), Chinese Academy of Forestry (CAF), ZhanJiang, GuangDong Province, China. Isolates linked to type specimens of the fungal species were deposited in the China General Microbiological Culture Collection Center (CGMCC), Beijing, China. The specimens were deposited in the Collection of Central South Forestry Fungi of China (CSFF), GuangDong Province, China.

DNA extraction, PCR amplification and sequencing

DNA extractions and sequence comparisons were conducted on selected isolates collected from different trees and different regions (Table 1). For the selected isolates, mycelia were scraped from 7-d-old cultures using sterile scalpels and transferred to 2 mL Eppendorf tubes. A CTAB-based protocol, 'Method 5' described by Van Burik et al. (1998), was used to extract the DNA samples. The resulting DNA was checked for purity and concentration using a NanoDrop 2000 Spectrometer (Thermo Fisher Scientific Inc. Waltham, MA, USA). Prior to PCR amplification, each DNA sample was diluted to approximately 100 ng/μL with DNase/RNase-free ddH_2O (Sangon Biotech Co., Ltd., Shanghai, China). The internal transcribed spacer (ITS) region was amplified using the primers ITS1/ITS4 (White et al. 1990), a part of the translation elongation factor 1-alpha (*tef1*) gene was amplified using the primers EF1-728F/EF1-986R (Carbone & Kohn 1999) or EF1F/EF2R (Jacobs et al. 2004), a part of the β-tubulin (*tub*) gene was amplified using the primers BT-2a/BT-2b (Glass & Donaldson 1995), a part of DNA-directed RNA polymerase II subunit (*rpb2*) gene was amplified using the primers fRPB2-5F/fRPB2-7cR for *Botryosphaeria* and *Cophinforma* (Liu et al. 1999), rpb2-LasF/rpb2-LasR for *Lasiodiplodia* (Cruywagen et al. 2017) and RPB2bot6F/RPB-2bot7R for *Neofusicoccum* (Pavlic et al. 2009a, Sakalidis et al. 2011), the nuclear ribosomal large subunit (LSU) region was amplified using the primers LR0R/LR5 (Vilgalys & Hester 1990, Cubeta et al. 1991), the nuclear ribosomal small subunit (SSU) region was amplified using the primers NS1/NS4 (White et al. 1990). For the isolates of *Lasiodiplodia*, a portion of the calmodulin (*cmdA*) gene was amplified using the primers CAL-228F/CAL-737R (Carbone & Kohn 1999). All primers were synthesised by Life Technologies (Thermo Fisher Scientific Inc., Shanghai, China). The PCR mixtures to amplify the ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU, SSU regions used the TopTaq™ Master Mix Kit (Qiagen Inc., Hilden, Germany). All amplification reactions consisted of 25 μL TopTaq™ Master Mix (contain 1.25 U TopTaq™ DNA Polymerase, 200 μM of each dNTP and 1.5 mM $MgCl_2$), 0.2 mM of each primer and 50 ng template DNA (made up to a total volume of 50 μL with RNase-free water). The amplification conditions consisted of an initial denaturation step at 94 °C for 3 min, 35 cycles of 94 °C for 1 min, 55 °C (except 45 °C for SSU) for 1 min, and 72 °C for 1 min, followed by a final elongation step at 72 °C for 10 min.

PCR amplifications were carried out in a thermocycler (Bio-Rad Laboratories, Inc., Berkeley, California, USA). The PCR products were separated by electrophoresis in 1.5 % agarose gels with SYBR Safe DNA Gel Stain (Thermo Fisher Scientific Inc., USA) in 1× Tris-acetate-EDTA (TAE) buffer at a constant voltage (80 V) for 30 min. All PCR products were sequenced in both directions using the primers specified above by Beijing Genomics Institution, Guangzhou, GuangDong Province, China. The

Table 1 Isolates sequenced and used for phylogenetic analyses, morphological studies and pathogenicity tests in this study.

Species[1]	Isolate No.[2,3]	Genotype[4]	Host	Location	GPS information	Collector	GenBank accession No.[5]						
							ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU
Botryosphaeria fusispora	CERC1997	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277967	KX278072	KX278177	MF410116	N/A	MF410007	MF410205
	CERC2273	AAAA-AA	*Eucalyptus* hybrid	FuZhou Region, FuJian Province, China	N26°13'39" E119°10'51"	S.F. Chen & G.Q. Li	KX277968	KX278073	KX278178	MF410117	N/A	MF410008	MF410206
	CERC2274[6,7]	AAAA-AA	*Eucalyptus* hybrid	FuZhou Region, FuJian Province, China	N26°13'39" E119°10'51"	S.F. Chen & G.Q. Li	KX277969	KX278074	KX278179	MF410118	N/A	MF410009	MF410207
	CERC2910	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	Unknown	S.F. Chen & G.Q. Li	KX277970	KX278075	KX278180	MF410119	N/A	MF410010	MF410208
	CERC2912	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	Unknown	S.F. Chen & G.Q. Li	KX277971	KX278076	KX278181	MF410120	N/A	MF410011	MF410209
	CERC2913	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	Unknown	S.F. Chen & G.Q. Li	KX277972	KX278077	KX278182	MF410121	N/A	MF410012	MF410210
	CERC3441[6]	AAAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277974	KX278079	KX278184	MF410123	N/A	MF410014	MF410212
	CERC3469	AAAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277975	KX278080	KX278185	MF410124	N/A	MF410015	MF410213
	CERC3474	AAAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277976	KX278081	KX278186	MF410125	N/A	MF410016	MF410214
	CERC3426	AAAA-AB	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX277973	KX278078	KX278183	MF410122	N/A	MF410013	MF410211
	CERC1998[7]	ABAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277977	KX278082	KX278187	MF410126	N/A	MF410017	MF410215
	CERC2006	ABAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N21°15'26" E110°07'00"	S.F. Chen & G.Q. Li	KX277978	KX278083	KX278188	MF410127	N/A	MF410018	MF410216
	CERC2911[6]	ABAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	Unknown	S.F. Chen & G.Q. Li	KX277979	KX278084	KX278189	MF410128	N/A	MF410019	MF410217
	CERC2918[6]	ABAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277980	KX278085	KX278190	MF410129	N/A	MF410020	MF410218
	CERC2921	ABAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277981	KX278086	KX278191	MF410130	N/A	MF410021	MF410219
	CERC2925	ABAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277982	KX278087	KX278192	MF410131	N/A	MF410022	MF410220
	CERC2948	ABAA-AA	*Eucalyptus* hybrid	QingYuan Region, GuangDong Province, China	N23°51'44" E113°10'58"	S.F. Chen & G.Q. Li	KX277983	KX278088	KX278193	MF410132	N/A	MF410023	MF410221
	CERC2949	ABAA-AA	*Eucalyptus* hybrid	QingYuan Region, GuangDong Province, China	N23°51'44" E113°10'58"	S.F. Chen & G.Q. Li	KX277984	KX278089	KX278194	MF410133	N/A	MF410024	MF410222
	CERC2954	ABAA-AA	*Eucalyptus* hybrid	QingYuan Region, GuangDong Province, China	N23°51'44" E113°10'58"	S.F. Chen & G.Q. Li	KX277985	KX278090	KX278195	MF410134	N/A	MF410025	MF410223
	CERC3446[7]	ABAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277986	KX278091	MF409964	MF410135	N/A	MF410026	MF410224
	CERC2930[7]	ACAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277987	KX278092	KX278196	MF410136	N/A	MF410027	MF410225
B. pseudoramosa	CERC1999[6]	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277988	KX278093	KX278197	MF410139	N/A	MF410030	MF410228
	CERC2001 = CGMCC3.18739[6,7,8,9]	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277989	KX278094	KX278198	MF410140	N/A	MF410031	MF410229
	CERC2004[9]	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'41" E109°43'01"	S.F. Chen & G.Q. Li	KX277990	KX278095	KX278199	MF410141	N/A	MF410032	MF410230
	CERC2019	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	Unknown	S.F. Chen & G.Q. Li	KX277991	KX278096	KX278200	MF410142	N/A	MF410033	MF410231
	CERC2983 = CGMCC3.18740[6]	AAAA-AA	*Melastoma sanguineum*	ZhanJiang Region, GuangDong Province, China	N21°13'24" E110°24'04"	S.F. Chen	KX277992	KX278097	KX278201	MF410143	N/A	MF410034	MF410232
	CERC2985	AAAA-AA	*M. sanguineum*	ZhanJiang Region, GuangDong Province, China	N21°13'24" E110°24'04"	S.F. Chen	KX277993	KX278098	KX278202	MF410144	N/A	MF410035	MF410233
	CERC2987[6,9]	AAAA-AA	*M. sanguineum*	ZhanJiang Region, GuangDong Province, China	N21°13'24" E110°24'04"	S.F. Chen	KX277994	KX278099	KX278203	MF410145	N/A	MF410036	MF410234
	CERC2988[6]	AAAA-AA	*M. sanguineum*	ZhanJiang Region, GuangDong Province, China	N21°13'24" E110°24'04"	S.F. Chen	KX277995	KX278100	KX278204	MF410146	N/A	MF410037	MF410235
	CERC3452[7]	AAAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277996	KX278101	KX278205	MF410147	N/A	MF410038	MF410236
	CERC3455 = CGMCC3.18741[6]	AAAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277997	KX278102	KX278206	MF410148	N/A	MF410039	MF410237
	CERC3462	AAAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277998	KX278103	KX278207	MF410149	N/A	MF410040	MF410238
	CERC3472	AAAA-AA	*Eucalyptus* hybrid	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX277999	KX278104	KX278208	MF410150	N/A	MF410041	MF410239
B. qingyuanensis	**CERC2946 = CGMCC3.18742**[6,7,8,9]	AAAA-AA	*Eucalyptus* hybrid	QingYuan Region, GuangDong Province, China	N23°44'30" E112°48'49"	S.F. Chen & G.Q. Li	KX278000	KX278105	KX278209	MF410151	N/A	MF410042	MF410240
	CERC2947 = CGMCC3.18743[7,9]	AAAA-AA	*Eucalyptus* hybrid	QingYuan Region, GuangDong Province, China	N23°44'30" E112°48'49"	S.F. Chen & G.Q. Li	KX278001	KX278106	KX278210	MF410152	N/A	MF410043	MF410241
B. wangensis	**CERC2298 = CGMCC3.18744**[6,7,8,9]	AAAA-AA	*C. deodara*	XinZhuang, MangChuan, RuZhou Region, HeNan Province, China	N34°04'09.8" E112°49'00.7"	S.F. Chen	KX278002	KX278107	KX278211	MF410153	N/A	MF410044	MF410242
	CERC2299 = CGMCC3.18745[6,7]	AAAA-AA	*C. deodara*	XinZhuang, MangChuan, RuZhou Region, HeNan Province, China	N34°04'09.8" E112°49'00.7"	S.F. Chen	KX278003	KX278108	KX278212	MF410154	N/A	MF410045	MF410243
	CERC2300 = CGMCC3.18746[6,9]	AAAA-AA	*C. deodara*	XinZhuang, MangChuan, RuZhou Region, HeNan Province, China	N34°04'09.8" E112°49'00.7"	S.F. Chen	KX278004	KX278109	KX278213	MF410155	N/A	MF410046	MF410244
Cophinforma atrovirens	CERC3481	AAAA-AA	*Dimocarpus longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278005	KX278110	KX278214	MF410156	N/A	MF410047	MF410245
	CERC3482	AAAA-AA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278006	KX278111	KX278215	MF410157	N/A	MF410048	MF410246
	CERC3484[7]	AAAA-AA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278007	KX278112	KX278216	MF410158	N/A	MF410049	MF410247
	CERC3489[7]	BAAA-AA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278008	KX278113	KX278217	MF410159	N/A	MF410050	MF410248
	CERC3490	BAAA-AA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278009	KX278114	KX278218	MF410160	N/A	MF410051	MF410249
Lasiodiplodia brasiliense	**CERC2284**[6,7]	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278010	KX278115	KX278219	MF410163	MF409967	MF410054	MF410252
L. pseudotheobromae	CERC2262	AAAAAAA	*Eucalyptus* hybrid	YuLin Region, GuangXi Province, China	N22°09'12" E110°12'08"	S.F. Chen & G.Q. Li	KX278011	KX278116	KX278220	MF410164	MF409968	MF410055	MF410253
	CERC2280	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278012	KX278117	KX278221	MF410165	MF409969	MF410056	MF410254

Table 1 (cont.)

Species[1]	Isolate No.[2,3]	Genotype[4]	Host	Location	GPS information	Collector	GenBank accession No.[5]						
							ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU
L. pseudotheobromae (cont.)	CERC2281	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278013	KX278118	KX278222	MF410166	MF409970	MF410057	MF410255
	CERC2282	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278014	KX278119	KX278223	MF410167	MF409971	MF410058	MF410256
	CERC2283	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278015	KX278120	KX278224	MF410168	MF409972	MF410059	MF410257
	CERC2286[6,7]	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278016	KX278121	KX278225	MF410169	MF409973	MF410060	MF410258
	CERC2287[6]	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278017	KX278122	KX278226	MF410170	MF409974	MF410061	MF410259
	CERC2288	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278018	KX278123	KX278227	MF410171	MF409975	MF410062	MF410260
	CERC2289	AAAAAAA	*Eucalyptus* hybrid	ZhangZhou Region, FuJian Province, China	N24°46'06" E117°51'02"	S.F. Chen & G.Q. Li	KX278019	KX278124	KX278228	MF410172	MF409976	MF410063	MF410261
	CERC2960	AAAAAAA	*Eucalyptus* hybrid	YunFu Region, GuangDong Province, China	N23°15'12" E111°41'51"	S.F. Chen & G.Q. Li	KX278020	KX278125	KX278229	MF410173	MF409977	MF410064	MF410262
	CERC2961	AAAAAAA	*Eucalyptus* hybrid	YunFu Region, GuangDong Province, China	N23°15'12" E111°41'51"	S.F. Chen & G.Q. Li	KX278021	KX278126	KX278230	MF410174	MF409978	MF410065	MF410263
	CERC3417[7]	AAAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278023	KX278128	KX278232	MF410176	MF409980	MF410067	MF410265
	CERC3432[6]	AAAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278024	KX278129	KX278233	MF410177	MF409981	MF410068	MF410266
	CERC3434	AAAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278025	KX278130	KX278234	MF410178	MF409982	MF410069	MF410267
	CERC3438	AAAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278026	KX278131	KX278235	MF410179	MF409983	MF410070	MF410268
	CERC3475	AAAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278027	KX278132	KX278236	MF410180	MF409984	MF410071	MF410269
	CERC3495[7]	AAAAAAA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278028	KX278133	KX278237	MF410181	MF409985	MF410072	MF410270
	CERC3496	AAAAAAA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278029	KX278134	KX278238	MF410182	MF409986	MF410073	MF410271
	CERC2962	AAAAABA	*Eucalyptus* hybrid	YunFu Region, GuangDong Province, China	N23°15'12" E111°41'51"	S.F. Chen & G.Q. Li	KX278022	KX278127	KX278231	MF410175	MF409979	MF410066	MF410264
L. theobromae	**CERC2024**[6]	AAAAAAA	*Phoenix hanceana*	ZhanJiang Region, GuangDong Province, China	N21°15'26" E110°07'01"	S.F. Chen & G.Q. Li	KX278030	KX278135	KX278239	MF410183	MF409987	MF410074	MF410272
	CERC3420[6,7]	AAAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278031	KX278136	KX278240	MF410184	MF409988	MF410075	MF410273
	CERC3424[6]	AAAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278032	KX278137	KX278241	MF410185	MF409989	MF410076	MF410274
	CERC2025	ABAAAAA	*P. hanceana*	ZhanJiang Region, GuangDong Province, China	N21°15'26" E110°07'01"	S.F. Chen & G.Q. Li	KX278033	KX278138	KX278242	MF410186	MF409990	MF410077	MF410275
	CERC2264	ABAAAAA	*E. urophylla* × *E. grandis*	YuLin Region, GuangXi Province, China	N22°09'12" E110°12'08"	S.F. Chen & G.Q. Li	KX278034	KX278139	KX278243	MF410187	MF409991	MF410078	MF410276
	CERC2275	ABAAAAA	*E. urophylla* × *E. grandis*	YongAn Region, FuJian Province, China	N26°01'40" E117°27'11"	S.F. Chen & G.Q. Li	KX278035	KX278140	KX278244	MF410188	MF409992	MF410079	MF410277
	CERC2934	ABAAAAA	*Eucalyptus* hybrid	DingAn County, HaiNan Province, China	N19°36'41" E110°17'16"	S.F. Chen & G.Q. Li	KX278036	KX278141	KX278245	MF410189	MF409993	MF410080	MF410278
	CERC2957	ABAAAAA	*Cunninghamina lanceolata*	ShaoGuan Region, GuangDong Province, China	N24°31'32" E113°37'40"	S.F. Chen & G.Q. Li	KX278037	KX278142	KX278246	MF410190	MF409994	MF410081	MF410279
	CERC2958	ABAAAAA	*C. lanceolata*	ShaoGuan Region, GuangDong Province, China	N24°31'32" E113°37'40"	S.F. Chen & G.Q. Li	KX278038	KX278143	KX278247	MF410191	MF409995	MF410082	MF410280
	CERC2963	ABAAAAA	*Eucalyptus* hybrid	YunFu Region, GuangDong Province, China	N23°15'12" E111°41'51"	S.F. Chen & G.Q. Li	KX278039	KX278144	KX278248	MF410192	MF409996	MF410083	MF410281
	CERC3418	ABAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278040	KX278145	KX278249	MF410193	MF409997	MF410084	MF410282
	CERC3422	ABAAAAA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278041	KX278146	KX278250	MF410194	MF409998	MF410085	MF410283
	CERC3485	ABAAAAA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278042	KX278147	KX278251	MF410195	MF409999	MF410086	MF410284
	CERC3486	ABAAAAA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278043	KX278148	KX278252	MF410196	MF410000	MF410087	MF410285
	CERC3487	ABAAAAA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278044	KX278149	KX278253	MF410197	MF410001	MF410088	MF410286
	CERC3491	ABAAAAA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278045	KX278150	KX278254	MF410198	MF410002	MF410089	MF410287
	CERC3493	ABAAAAA	*D. longan*	ZhanJiang Region, GuangDong Province, China	Unknown	S.F. Chen	KX278046	KX278151	KX278255	MF410199	MF410003	MF410090	MF410288
	CERC3513[6,7]	ABAAAAA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278047	KX278152	KX278256	MF410200	MF410004	MF410091	MF410289
	CERC3514	ABAAAAA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278048	KX278153	KX278257	MF410201	MF410005	MF410092	MF410290
	CERC3516[7]	ABAAAAA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278049	KX278154	KX278258	MF410202	MF410006	MF410093	MF410291
Neofusicoccum hongkongense	**CERC2967 = CGMCC3.18747**	AAAA-AA	*Araucaria cunninghamii*	Hong Kong, China	Unknown	S.F. Chen	KX278050	KX278155	KX278259	KX278281	N/A	MF410094	MF410292
	CERC2968 = CGMCC3.18748[6,7,9]	AABA-AA	*A. cunninghamii*	Hong Kong, China	Unknown	S.F. Chen	KX278051	KX278156	KX278260	KX278282	N/A	MF410095	MF410293
	CERC2973 = CGMCC3.18749[6,7,8,9]	AABA-AA	*A. cunninghamii*	Hong Kong, China	Unknown	S.F. Chen	KX278052	KX278157	KX278261	KX278283	N/A	MF410096	MF410294
N. microconidium	**CERC3497 = CGMCC3.18750**[6,7,8,9]	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278053	KX278158	KX278262	MF410203	N/A	MF410097	MF410295
	CERC3498 = CGMCC3.18751 [6,7,9]	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278054	KX278159	KX278263	MF410204	N/A	MF410098	MF410296
N. parvum	**CERC2951**[7]	AAAA-AA	*E. urophylla* × *E. grandis*	QingYuan Region, GuangDong Province, China	N23°51'44" E113°10'58"	S.F. Chen & G.Q. Li	KX278055	KX278160	KX278264	KX278284	N/A	MF410099	MF410297
	CERC3508	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278056	KX278161	KX278265	KX278285	N/A	MF410100	MF410298
	CERC3509[7]	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278057	KX278162	KX278266	KX278286	N/A	MF410101	MF410299
	CERC3502	ABAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278058	KX278163	KX278267	KX278287	N/A	MF410102	MF410300
	CERC3503[6]	ABAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278059	KX278164	KX278268	KX278288	N/A	MF410103	MF410301
	CERC3504[6,7]	ABAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278060	KX278165	KX278269	KX278289	N/A	MF410104	MF410302

Table 1 (cont.)

Species[1]	Isolate No.[2,3]	Genotype[4]	Host	Location	GPS information	Collector	GenBank accession No.[5]					
							ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU
N. sinoeucalypti	**CERC2005 = CGMCC3.18752**[6,7,8,9]	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N21°15'26" E110°07'00"	S.F. Chen & G.Q. Li	KX278061	KX278166	KX278270	KX278290	N/A	MF410105	MF410303
	CERC3415[6]	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278063	KX278168	KX278272	KX278292	N/A	MF410107	MF410305
	CERC3416 = CGMCC3.18754[6]	AAAA-AA	*Eucalyptus* hybrid	BeiHai Region, GuangXi Province, China	N21°35'49" E109°43'49"	S.F. Chen & G.Q. Li	KX278064	KX278169	KX278273	KX278293	N/A	MF410108	MF410306
	CERC3457	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX278066	KX278171	KX278275	KX278295	N/A	MF410110	MF410308
	CERC3458	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX278067	KX278172	KX278276	KX278296	N/A	MF410111	MF410309
	CERC3463[7]	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX278068	KX278173	KX278277	KX278297	N/A	MF410112	MF410310
	CERC3464	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX278069	KX278174	KX278278	KX278298	N/A	MF410113	MF410311
	CERC3467	AAAA-AA	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX278070	KX278175	KX278279	KX278299	N/A	MF410114	MF410312
	CERC3517	AAAA-AB	*E. urophylla* × *E. grandis*	YuLin Region, GuangXi Province, China	N21°13'31" E110°23'47"	S.F. Chen & G.Q. Li	KX278071	KX278176	KX278280	KX278300	N/A	MF410115	MF410313
	CERC2265 = CGMCC3.18753[8,9]	AAAA-AB	*E. urophylla* × *E. grandis*		N22°08'55" E110°12'00"	S.F. Chen & G.Q. Li	KX278062	KX278167	KX278271	KX278291	N/A	MF410106	MF410304
	CERC3451	AAAA-AB	*E. urophylla* × *E. grandis*	ZhanJiang Region, GuangDong Province, China	N20°41'20" E110°01'17"	S.F. Chen & G.Q. Li	KX278065	KX278170	KX278274	KX278294	N/A	MF410109	MF410307

[1] Species names in **bold** are novel species described in this study.
[2] Isolates in **bold** are in the phylogenetic trees.
[3] CERC: Culture Collection of China Eucalypt Research Centre, Chinese Academy of Forestry, ZhanJiang, GuangDong Province, China; CGMCC: China General Microbiological Culture Collection Center, Beijing, China.
[4] Genotype within each identified species, determined by ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU and SSU regions; '–' means not available.
[5] ITS, internal transcribed spacer region and intervening 5.8S nrRNA gene; *tef1*, translation elongation factor 1-alpha; *tub*, β-tubulin; *rpb2*, DNA-directed RNA polymerase II subunit; *cmdA*, calmodulin; LSU, nuclear ribosomal large subunit; SSU, nuclear ribosomal small subunit; N/A = not available.
[6] Isolates used for morphological studies.
[7] Isolates used for pathogenicity tests on three *Eucalyptus* clones.
[8] Isolates represent ex-type.
[9] Isolates used for culture growth studies.

nucleotide sequences were edited with MEGA v. 6.0.5 software (Tamura et al. 2013). Sequences obtained in this study were all deposited in GenBank (http://www.ncbi.nlm.nih.gov) (Table 1).

Phylogenetic analyses

The preliminary identities of the isolates sequenced in this study were obtained by conducting a standard nucleotide BLAST search using the ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU, SSU sequences. The sequences of the ex-type strains that were closely related to the *Botryosphaeriaceae* isolates sequenced in this study were downloaded from NCBI (http://www.ncbi.nlm.nih.gov/) and used for polygenetic analyses (Table 2). Sequences were aligned using MAFFT online v. 7 (http://mafft.cbrc.jp/alignment/server/) (Katoh & Standley 2013), with the iterative refinement method (FFT-NS-i setting). The alignments were further edited manually with MEGA v. 6.0.5 software (Tamura et al. 2013). Resulting alignments and phylogenetic trees for all the datasets were deposited in TreeBASE (http://treebase.org).

The BLAST results showed that the isolates collected in this study were grouped in the genera *Botryosphaeria*, *Cophinforma*, *Lasiodiplodia* and *Neofusicoccum*. Phylogenetic analyses were conducted for each of the ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU and SSU datasets for genera *Botryosphaeria*/*Cophinforma*, *Lasiodiplodia* and *Neofusicoccum*, respectively. As the *cmdA* sequences are only available for *Lasiodiplodia*, and not for *Botryosphaeria*, *Cophinforma* and *Neofusicoccum*, the analyses for *cmdA* sequences were only conducted for the genus *Lasiodiplodia*.

Phylogenetic analyses were also conducted for combined datasets, as the LSU and SSU sequences are not available for some of the previously described species of *Botryosphaeria*, *Cophinforma*, *Lasiodiplodia* and *Neofusicoccum*, and the *rpb2* sequences are not available for some species of *Botryosphaeria*. The ITS, *tef1* and *tub* sequences were combined for phylogenetic analyses of *Botryosphaeria*/*Cophinforma* isolates, the ITS, *tef1*, *tub*, *rpb2* and *cmdA* sequences were combined for *Lasiodiplodia* isolates, and ITS, *tef1*, *tub* and *rpb2* sequences were combined for *Neofusicoccum* isolates.

Two phylogenetic analysis methods were used: PAUP v. 4.0b10 (Swofford 2003) for the maximum parsimony (MP) analyses and PhyML v. 3.0 (Guindon et al. 2010) for maximum likelihood (ML) tests. For MP analyses, gaps are treated as a fifth character and the characters are unordered and of equal weight with 1 000 random addition replicates. The equally most parsimonious trees were obtained using the heuristic search function and tree bisection and reconstruction (TBR) as the branch swapping algorithms. MAXTREES were limited to 5 000, and branch lengths of zero were collapsed. A bootstrap analysis (50 % majority rule, 1 000 replicates) was performed to determine the confidence levels of the tree-branching points (Felsenstein 1985). Tree length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC) and homoplasy index (HI) were used to evaluate the trees (Hillis & Huelsenbeck 1992).

For ML analyses of each dataset, the best models of nucleotide substitution were determined using jModelTest v. 2.1.5 (Darriba et al. 2012). Additional ML parameters in PhyML include the retention of the maximum number of 1 000 trees and the determination of nodal support by non-parametric bootstrapping with 1 000 replicates. All phylogenetic trees were viewed using MEGA v. 6.0.5 (Tamura et al. 2013). *Neofusicoccum parvum* (ATCC 58191) was used as the outgroup taxon for analyses of *Botryosphaeria* and *Cophinforma*; *Botryosphaeria dothidea* (CBS 115476) was used as the outgroup taxon for analyses of *Lasiodiplodia* and *Neofusicoccum* (Table 2).

Table 2 Isolates from other studies used in the phylogenetic analyses for this study.

Species	Isolate numbers[1]	Host	Location	Collector	GenBank accession numbers[2]							Reference
					ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU	
Botryosphaeria agaves	MFLUCC 11-0125 = CBS 133992[3]	*Agave* sp.	Thailand	R. Phookamsak	JX646791	JX646856	JX646841	N/A	N/A	JX646808	JX646825	Liu et al. (2012)
	MFLUCC 10-0051	*Agave* sp.	Thailand	P. Chomnunti	JX646790	JX646855	JX646840	N/A	N/A	JX646807	JX646824	Liu et al. (2012)
B. auasmontanum	CMW 25413 = CBS 121769[3]	*Acacia mellifera*	Namibia	F.J.J. van der Walt & J. Roux	EU101303	EU101348	N/A	N/A	N/A	KF766332	KF766252	Slippers et al. (2013, 2014)
B. corticis	CBS 119047[3]	*Vaccinium corymbosum*	USA	P.V. Oudemans	DQ299245	EU017539	EU673107	N/A	N/A	EU673244	EU673175	Phillips et al. (2006, 2008), Lazzizera et al. (2008)
	ATCC 22927	*Vaccinium* sp.	USA	R.D. Millholland	DQ299247	EU673291	EU673108	N/A	N/A	EU673245	EU673176	Phillips et al. (2006, 2008)
B. dothidea	CBS 115476 = CMW 8000[3]	*Prunus* sp.	Switzerland	B. Slippers	AY236949	AY236898	AY236927	EU339577	N/A	AY928047	EU673173	Slippers et al. (2004a), Phillips et al. (2008)
	CBS 110302	*Vitis vinifera*	Portugal	A.J.L. Phillips	AY259092	AY573218	EU673106	N/A	N/A	EU673243	EU673174	Alves et al. (2004), Phillips et al. (2008)
B. fabicerciana	CMW 27094 = CBS 127193[3]	*Eucalyptus* sp.	China	M.J. Wingfield	HQ332197	HQ332213	KF779068	MF410137	N/A	MF410028	MF410226	Chen et al. (2011c), This study
	CMW 27121 = CBS 127194	*Eucalyptus* sp.	China	M.J. Wingfield	HQ332198	HQ332214	KF779069	MF410138	N/A	MF410029	MF410227	Chen et al. (2011c), This study
B. fusispora	MFLUCC 10-0098[3]	*Entada* sp.	Thailand	S. Boonmee	JX646789	JX646854	JX646839	N/A	N/A	JX646806	JX646823	Liu et al. (2012)
	MFLUCC 11-0507	*Entada* sp.	Thailand	R. Cheewangkoon	JX646788	JX646853	JX646838	N/A	N/A	JX646805	JX646822	Liu et al. (2012)
B. kuwatsukai	CBS 135219 = PG 2[3]	*Malus domestica*	China	C.S. Wang	KJ433388	KJ433410	N/A	N/A	N/A	N/A	N/A	Xu et al. (2015a)
	LSP 5	*Pyrus* sp.	China	C.S. Wang	KJ433395	KJ433417	N/A	N/A	N/A	N/A	N/A	Xu et al. (2015a)
B. minutispermatia	GZCC 16-0013[3]	Dead wood	Guizhou, China	H.A. Ariyawansa	KX447675	KX447678	N/A	N/A	N/A	N/A	N/A	Ariyawansa et al. (2016)
	GZCC 16-0014	Dead wood	Guizhou, China	H.A. Ariyawansa	KX447676	KX447679	N/A	N/A	N/A	N/A	N/A	Ariyawansa et al. (2016)
B. ramosa	CBS 122069 = CMW 26167[3]	*Eucalyptus camaldulensis*	Australia	T.I. Burgess	EU144055	EU144070	KF766132	N/A	N/A	KF766333	KF766253	Pavlic et al. (2008), Slippers et al. (2013)
B. rosaceae	CGMCC3.18007[3]	*Malus* sp.	Shandong, China	Y. Zhang & J.Q. Zhang	KX197074	KX197094	KX197101	N/A	N/A	KX197083	N/A	Zhou et al. (2017)
	CGMCC3.18008	*Amygdalus* sp.	Shandong, China	Y. Zhang, J.Q. Zhang & Z.P. Dou	KX197075	KX197095	KX197102	N/A	N/A	KX197084	N/A	Zhou et al. (2017)
B. scharifii	IRAN 1529C = CBS 124703[3]	*Mangifera indica*	Iran	J. Abdollahzadeh	JQ772020	JQ772057	N/A	N/A	N/A	N/A	N/A	Abdollahzadeh et al. (2013)
	IRAN 1543C = CBS 124702	*Mangifera indica*	Iran	J. Abdollahzadeh & A. Javadi	JQ772019	JQ772056	N/A	N/A	N/A	N/A	N/A	Abdollahzadeh et al. (2013)
B. sinensia	CGMCC3.17723	*Morus* sp.	Henan, China	Z.P. Dou	KT343254	KU221233	KX197107	N/A	N/A	KX197090	N/A	Zhou et al. (2016, 2017)
	CGMCC3.17724	*Juglans regia*	Henan, China	Z.P. Dou	KT343256	KU221234	KX197108	N/A	N/A	N/A	N/A	Zhou et al. (2016, 2017)
Cophinforma atrovirens	CBS 124934 = CMW 22674[3]	*Pterocarpus angolensis*	South Africa	J. Mehl & J. Roux	FJ888473	FJ888456	N/A	N/A	N/A	N/A	N/A	Mehl et al. (2011)
	CBS 124935 = CMW 22682	*Pterocarpus angolensis*	South Africa	J. Mehl & J. Roux	FJ888476	FJ888457	N/A	N/A	N/A	N/A	N/A	Mehl et al. (2011)
	CBS 117445 = CMW 13425	*Acacia mangium*	Venezuela	S. Mohali	EF118046	GU134939	N/A	N/A	N/A	N/A	N/A	Mohali et al. (2007)
	CBS 117446 = CMW 13429	*Eucalyptus hybrid*	Venezuela	S. Mohali	EF118048	GU134940	N/A	N/A	N/A	N/A	N/A	Mohali et al. (2007)
Lasiodiplodia avicenniae	CMW 41467[3]	*Avicennia marina*	South Africa	J.A. Osorio & J. Roux	KP860835	KP860680	KP860758	KU587878	N/A	N/A	N/A	Osorio et al. (2017)
	LAS 199 (DNA)	*Avicennia marina*	South Africa	J.A. Osorio & J. Roux	KU587957	KU587947	KU587868	KU587880	N/A	N/A	N/A	Osorio et al. (2017)
L. americana	CERC1961 = CFCC50065[3]	*Pistachia vera*	Arizona, USA	T.J. Michailides	KP217059	KP217067	KP217075	MF410161	MF409965	MF410052	MF410250	Chen et al. (2015), This study
	CERC1960 = CFCC50064	*Pistachia vera*	Arizona, USA	T.J. Michailides	KP217058	KP217066	KP217074	MF410162	MF409966	MF410053	MF410251	Chen et al. (2015), This study
L. brasiliense	CMM 4015[3]	*Mangifera indica*	Brazil	M.W. Marques	JX464063	JX464049	N/A	N/A	N/A	N/A	N/A	Netto et al. (2014)
	CMW 35884	*Adansonia madagascariensis*	Madagascar		KU887094	KU886972	KU887466	KU696345	KU886755	N/A	N/A	Cruywagen et al. (2017)
L. bruguierae	CMW 41470[3]	*Bruguiera gymnorrhiza*	South Africa	J.A. Osorio & J. Roux	KP860833	KP860678	KP860756	KU587875	N/A	N/A	N/A	Osorio et al. (2017)
	CMW 41614	*Bruguiera gymnorrhiza*	South Africa	J.A. Osorio & J. Roux	KP860834	KP860679	KP860757	KU587877	N/A	N/A	N/A	Osorio et al. (2017)
L. caatinguensis	CMM 1325[3]	*Citrus sinensis*	Itarema, Ceará, Brazil	I.B.L. Coutinho & J.S. Lima	KT154760	KT008006	KT154767	N/A	N/A	N/A	N/A	Coutinho et al. (2017)

Table 2 (cont.)

Species	Isolate numbers[1]	Host	Location	Collector	GenBank accession numbers[2]							Reference
					ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU	
L. caatinguensis (cont.)	IBL 40	*Spondias mombin*	Itarema, Ceará, Brazil	J.S. Lima & J.E. Cardoso	KT154762	KT154755	KT154769	N/A	N/A	N/A	N/A	Coutinho et al. (2017)
L. chinensis	CGMCC3.18061[3]	Unknown	China	W. He & Z.P. Dou	KX499889	KX499927	KX500002	KX499965	N/A	N/A	N/A	Dou et al. (2017a)
	CGMCC3.18066	*Hevea brasiliensis*	China	Y. Zhang & Y.P. Zhou	KX499899	KX499937	KX500012	KX499974	N/A	N/A	N/A	Dou et al. (2017a)
L. citricola	CBS 124707 = IRAN 1522C[3]	*Citrus* sp.	Iran	J. Abdollahzadeh & A. Javadi	GU945354	GU945340	KU887505	KU696351	KU886760	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
	CBS 124706 = IRAN 1521C	*Citrus* sp.	Iran	A. Shekari	GU945353	GU945339	KU887504	KU696350	KU886759	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
L. crassispora	CBS 118741 = WAC12533[3]	*Santalum album*	Kununurra, Australia	T.I. Burgess & B. Dell	DQ103550	EU673303	KU887506	KU696353	KU886761	DQ377901	N/A	Burgess et al. (2006), Phillips et al. (2008), Cruywagen et al. (2017)
	CBS 110492	Unknown	Unknown	Unknown	EF622086	EF622066	EU673134	N/A	N/A	EU673251	N/A	Alves et al. (2008), Phillips et al. (2008)
L. euphorbicola	CMM 3609[3]	*Jatropha curcas*	Brazil	A.R. Machado & O.L. Pereira	KF234543	KF226689	KF254926	N/A	N/A	N/A	N/A	Machado et al. (2014)
	CMW 33350	*Adansonia digitata*	Botswana		KU887149	KU887026	KU887455	KU696346	KU886754	N/A	N/A	Cruywagen et al. (2017)
L. exigua	CBS 137785[3]	*Retama raetam*	Tunisia	B.T. Linaldeddu	KJ638317	KJ638336	KU887509	KU696355	KU886764	N/A	N/A	Linaldeddu et al. (2015), Cruywagen et al. (2017)
	BL 184	*Retama raetam*	Tunisia	B.T. Linaldeddu	KJ638318	KJ638337	N/A	N/A	N/A	N/A	N/A	Linaldeddu et al. (2015)
L. gilanensis	CBS 124704 = IRAN 1523C[3]	Unknown	Iran	J. Abdollahzadeh & A. Javadi	GU945351	GU945342	KU887511	KU696357	KU886765	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
	CBS 124705 = IRAN 1501C	Unknown	Iran	J. Abdollahzadeh & A. Javadi	GU945352	GU945341	KU887510	KU696356	KU886766	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
L. gonubiensis	CBS 115812 = CMW 14077[3]	*Syzygium cordatum*	South Africa	D. Pavlic	AY639595	DQ103566	DQ458860	KU696359	KU886768	DQ377902	EU673193	Pavlic et al. (2004), Burgess et al. (2006), Phillips et al. (2008), Cruywagen et al. (2017)
	CBS 116355 = CMW 14078	*Syzygium cordatum*	South Africa	D. Pavlic	AY639594	DQ103567	EU673126	KU696358	KU886767	EU673252	EU673194	Pavlic et al. (2004), Burgess et al. (2006), Phillips et al. (2008), Cruywagen et al. (2017)
L. gravistriata	CMM 4564[3]	*Anacardium humile*	Brazil	M.S.B. Netto	KT250949	KT250950	N/A	N/A	N/A	N/A	N/A	Netto et al. (2017)
	CMM 4565	*Anacardium humile*	Brazil	M.S.B. Netto	KT250947	KT266812	N/A	N/A	N/A	N/A	N/A	Netto et al. (2017)
L. hormozganensis	CBS 124709 = IRAN 1500C[3]	*Olea* sp.	Iran	J. Abdollahzadeh & A. Javadi	GU945355	GU945343	KU887515	KU696361	KU886770	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
	CBS 124708 = IRAN 1498C	*Mangifera indica*	Iran	J. Abdollahzadeh & A. Javadi	GU945356	GU945344	KU887514	KU696360	KU886769	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
L. hyalina	CGMCC3.17975[3]	*Acacia confusa*	China	Y. Zhang & Y.P. Zhou	KX499879	KX499917	KX499992	KX499955	N/A	N/A	N/A	Dou et al. (2017b)
	CGMCC3.18383 = B 6180	Unknown tree	China	Z.P. Dou & Z.C. Liu	KY767661	KY751302	KY751299	KY751296	N/A	N/A	N/A	Dou et al. (2017b)
L. indica	IBP 01[3]	*Angiospermous* tree	India	I.B. Prasher & G. Singh	KM376151	N/A	N/A	N/A	N/A	N/A	N/A	Prasher & Singh (2014)
L. iraniensis	IRAN 1520C[3]	*Salvadora persica*	Iran	J. Abdollahzadeh & A. Javadi	GU945348	GU945336	KU887516	KU696363	KU886771	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
	IRAN 1502C	*Juglans* sp.	Iran	A. Javadi	GU945347	GU945335	KU887517	KU696362	KU886772	N/A	N/A	Abdollahzadeh et al. (2010), Cruywagen et al. (2017)
L. laeliocattleyae	CBS 167.28[3]	*Laeliocattleya*	Italy	C. Sibilia	KU507487	KU507454	N/A	N/A	N/A	DQ377892	N/A	Crous et al. (2006), Rodríguez-Gálvez et al. (2017)
	LAREP1	*Mangifera indica*	Repartidor, Peru	P. Guerrero	KU507484	KU507451	N/A	N/A	N/A	N/A	N/A	Rodríguez-Gálvez et al. (2017)
L. lignicola	MFLUCC 11-0435 = CBS134112[3]	Unknown	Thailand	A.D. Ariyawansa	JX646797	KU887003	JX646845	KU696364	N/A	JX646814	JX646830	Liu et al. (2012), Cruywagen et al. (2017)
L. macrospora	CMM 3833[3]	*Jatropha curcas*	Brazil	A.R. Machado & O.L. Pereira	KF234557	KF226718	KF254941	N/A	N/A	N/A	N/A	Machado et al. (2014)
L. mahajangana	CBS 124925 = CMW 27801[3]	*Terminalia catappa*	Madagascar	J. Roux	FJ900595	FJ900641	FJ900630	KU696365	KU886773	N/A	N/A	Begoude et al. (2010), Cruywagen et al. (2017)
	CBS 124926 = CMW 27820	*Terminalia catappa*	Madagascar	J. Roux	FJ900596	FJ900642	KU887519	KU696366	KU886774	N/A	N/A	Begoude et al. (2010), Cruywagen et al. (2017)
L. margaritacea	CBS 122519 = CMW 26162[3]	*Adansonia gibbosa*	WA, Tunnel Creek Gorge	T.I. Burgess	EU144050	EU144065	KU887520	KU696367	KU886775	KX464354	N/A	Pavlic et al. (2008), Cruywagen et al. (2017)
L. mediterranea	CBS 137783[3]	*Quercus ilex*	Italy	B.T. Linaldeddu	KJ638312	KJ638331	KU887521	KU696368	KU886776	N/A	N/A	Linaldeddu et al. (2015)
	CBS 137784	*Vitis vinifera*	Italy	S. Serra	KJ638311	KJ638330	KU887522	KU696369	KU886777	N/A	N/A	Linaldeddu et al. (2015)
L. missouriana	CBS 128311 = UCD2193MO[3]	*Vitis* sp. × *Vitis labruscana*	Missouri, USA	K. Striegler & G.M. Leavitt	HQ288225	HQ288267	HQ288304	KU696370	KU886778	N/A	N/A	Úrbez-Torres et al. (2012), Cruywagen et al. (2017)
	CBS 128312 = UCD2199MO	*Vitis* sp. × *Vitis labruscana*	Missouri, USA	K. Striegler & G.M. Leavitt	HQ288226	HQ288268	HQ288305	KU696371	KU886779	N/A	N/A	Úrbez-Torres et al. (2012), Cruywagen et al. (2017)
L. parva	CBS 456.78[3]	Cassava-field soil	Colombia	O. Rangel	EF622083	EF622063	KU887523	KU696372	KU886780	KF766362	N/A	Alves et al. (2008), Cruywagen et al. (2017)

Table 2 (cont.)

Species	Isolate numbers[1]	Host	Location	Collector	GenBank accession numbers[2]							Reference
					ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU	
L. parva (cont.)	CBS 494.78	Cassava-field soil	Colombia	O. Rangel	EF622084	EF622064	EU673114	KU696373	KU886781	EU673258	EU673201	Alves et al. (2008), Phillips et al. (2008), Cruywagen et al. (2017)
L. plurivora	CBS 120832[3]	*Prunus salicina*	Stellenbosch, Western Cape, South Africa	U. Damm	EF445362	EF445395	KU887524	KU696374	KU886782	KX464356	N/A	Damm et al. (2007), Cruywagen et al. (2017)
	CBS 121103	*Vitis vinifera*	South Africa	F. Halleen	AY343482	EF445396	KU887525	KU696375	KU886783	KX464357	N/A	Damm et al. (2007), Cruywagen et al. (2017)
L. pontae	CMM 1277[3]	*Spondias purpurea*	Pio-IX/Piauí/Brazil	J.S. Lima & F.C.O. Freire	KT151794	KT151791	KT151797	N/A	N/A	N/A	N/A	Coutinho et al. (2017)
L. pseudotheobromae	CBS 116459[3]	*Gmelina arborea*	Costa Rica	J. Carranza & Velásquez	EF622077	EF622057	EU673111	KU696376	KU886784	EU673256	EU673199	Alves et al. (2008), Phillips et al. (2008), Cruywagen et al. (2017)
	CMM 3887	*Jatropha curcas*	Brazil	A. R. Machado	KF234559	KF226722	KF254943	N/A	N/A	N/A	N/A	Machado et al. (2014)
L. pyriformis	CBS 121770 = CMW 25414[3]	*Acacia mellifera*	Dordabis, Namibia	F.J.J. van der Walt & J. Roux	EU101307	EU101352	KU887527	KU696378	KU886786	N/A	N/A	Slippers et al. (2014), Cruywagen et al. (2017)
	CBS 121771 = CMW 25415	*Acacia mellifera*	Dordabis, Namibia	F.J.J. van der Walt & J. Roux	EU101308	EU101353	KU887528	KU696379	KU886787	N/A	N/A	Slippers et al. (2014), Cruywagen et al. (2017)
L. rubropurpurea	CBS 118740 = CMW 14700 = WAC 12535[3]	*Eucalyptus grandis*	Tully, Queensland	T.I. Burgess & G. Pegg	DQ103553	DQ103571	EU673136	KU696380	KU886788	DQ377903	EU673191	Burgess et al. (2006), Phillips et al. (2008), Cruywagen et al. (2017)
	WAC 12536 = CMW 15207	*Eucalyptus grandis*	Tully, Queensland	T.I. Burgess & G. Pegg	DQ103554	DQ103572	KU887530	KU696381	N/A	N/A	N/A	Burgess et al. (2006), Cruywagen et al. (2017)
L. sterculiae	CBS 342.78[3]	*Sterculia oblonga*	Germany	S. Bruhn	KX464140	KX464634	KX464908	KX463989	N/A	JX681073	N/A	Yang et al. (2017)
L. subglobosa	CMM 3872[3]	*Jatropha curcas*	Brazil	A.R. Machado & O.L. Pereira	KF234558	KF226721	KF254942	N/A	N/A	N/A	N/A	Machado et al. (2014)
	CMM 4046	*Jatropha curcas*	Brazil	A.R. Machado & O.L. Pereira	KF234560	KF226723	KF254944	N/A	N/A	N/A	N/A	Machado et al. (2014)
L. thailandica	CPC 22795[3]	*Mangifera indica*	Thailand	T. Trakunyingcharoen	KJ193637	KJ193681	N/A	N/A	N/A	N/A	N/A	Trakunyingcharoen et al. (2015)
	CPC 22755	*Phyllanthus acidus*	Thailand	T. Trakunyingcharoen	KM006433	KM006464	N/A	N/A	N/A	N/A	N/A	Trakunyingcharoen et al. (2015)
L. theobromae	CBS 164.96[3]	Fruit along coral reef coast	New Guinea	A. Aptroot	AY640255	AY640258	KU887532	KU696383	KU886789	EU673253	EU673196	Alves et al. (2008), Phillips et al. (2008), Cruywagen et al. (2017)
	CBS 111530	Unknown	Unknown	Unknown	EF622074	EF622054	KU887531	KU696382	KU886790	N/A	N/A	Alves et al. (2008), Cruywagen et al. (2017)
L. venezuelensis	CBS 118739 = CMW 13511 = WAC 12539[3]	*Acacia mangium*	Acarigua, Venezuela	S. Mohali	DQ103547	DQ103568	KU887533	KU696384	KU886791	DQ377904	EU673192	Burgess et al. (2006), Phillips et al. (2008), Cruywagen et al. (2017)
	CMW 13512 = WAC 12540	*Acacia mangium*	Acarigua, Venezuela	S. Mohali	DQ103548	DQ103569	KU887534	N/A	KU886792	N/A	N/A	Burgess et al. (2006), Cruywagen et al. (2017)
L. viticola	CBS 128313 = UCD 2553AR[3]	*Vitis vinifera*	USA	K. Striegler & G.M. Leavitt	HQ288227	HQ288269	HQ288306	KU696385	KU886793	N/A	N/A	Úrbez-Torres et al. (2012), Cruywagen et al. (2017)
	CBS 128315 = UCD 2604MO	*Vitis vinifera*	USA	K. Striegler & G.M. Leavitt	HQ288228	HQ288270	HQ288307	KU696386	KU886794	N/A	N/A	Úrbez-Torres et al. (2012), Cruywagen et al. (2017)
L. vitis	CBS 124060[3]	*Vitis vinifera*	Italy	S. Burruano	KX464148	KX464642	KX464917	KX463994	N/A	KX464367	N/A	Yang et al. (2017)
Neofusicoccum algeriense	CBS 137504 = ALG 1[3]	*Vitis vinifera*	Algeria	A. Berraf-Tebbal	KJ657702	KJ657715	KX505915	N/A	N/A	N/A	N/A	Berraf-Tebbal et al. (2014), Lopes et al. (2017)
	CAA 322	*Malus domestica*	Portugal		KX505906	KX505894	KX505916	N/A	N/A	N/A	N/A	Lopes et al. (2017)
N. andinum	CBS 117453 = CMW 13455[3]	*Eucalyptus* sp.	Me' rida state, Venezuela	S. Mohali	AY693976	AY693977	KX464923	KX464002	N/A	KX464373	N/A	Mohali et al. (2006), Yang et al. (2017)
	CBS 117452 = CMW 13446	*Eucalyptus* sp.	Me' rida state, Venezuela	S. Mohali	DQ306263	DQ306264	KX464922	KX464001	N/A	DQ377914	N/A	Mohali et al. (2006), Yang et al. (2017)
N. arbuti	CBS 116131[3]	*Arbutus menziesii*	Washington, USA	M. Elliott	AY819720	KF531792	KF531793	KX464003	N/A	DQ377915	KF531814	Farr et al. (2005), Crous et al. (2006), Phillips et al. (2013), Yang et al. (2017)
	CBS 117090	*Arbutus menziesii*	California, USA	M. Elliott	AY819724	KF531791	KF531794	N/A	N/A	DQ377919	KF531813	Farr et al. (2005), Crous et al. (2006), Phillips et al. (2013)
N. australe	CMW 6837[3]	*Acacia* sp.	Batemans Bay, Australia	M.J. Wingfield	AY339262	AY339270	AY339254	EU339573	N/A	KF766367	N/A	Slippers et al. (2004b, 2013), Burgess et al. (2007)
	CBS 110865 = CPC 4599	*Vitis vinifera*	South Africa	F. Halleen	AY343408	KX464661	KX464937	KX464005	N/A	KX464385	N/A	Van Niekerk et al. (2004), Yang et al. (2017)
N. batangarum	CBS 124924 = CMW 28363[3]	*Terminalia catappa*	Cameroon	D. Begoude & J. Roux	FJ900607	FJ900653	FJ900634	FJ900615	N/A	KX464401	N/A	Begoude et al. (2010), Yang et al. (2017)

Table 2 (cont.)

Species	Isolate numbers[1]	Host	Location	Collector	GenBank accession numbers[2]							Reference
					ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU	
N. batangarum (cont.)	CBS 124923 = CMW 28320	*Terminalia catappa*	Cameroon	D. Begoude & J. Roux	FJ900608	FJ900654	FJ900635	FJ900616	N/A	KX464400	N/A	Begoude et al. (2010), Yang et al. (2017)
N. brasiliense	CMM 1338[3]	*Mangifera indica*	Brazil	M.W. Marques	JX513630	JX513610	KC794031	N/A	N/A	N/A	N/A	Marques et al. (2013)
	CMM 1285	*Mangifera indica*	Brazil	M.W. Marques	JX513628	JX513608	KC794030	N/A	N/A	N/A	N/A	Marques et al. (2013)
N. buxi	CBS 116.75[3]	*Buxus sempervirens*	France	H.A. van der Aa	KX464165	KX464678	N/A	KX464010	N/A	KX464406	N/A	Yang et al. (2017)
	CBS 113714	*Buxus sempervirens*	Sweden	O. Constantinescu	KX464164	KX464677	KX464954	KX464009	N/A	KX464405	N/A	Yang et al. (2017)
N. cordaticola	CBS 123634 = CMW 13992[3]	*Syzigium cordatum*	South Africa	D. Pavlic	EU821898	EU821868	EU821838	EU821928	N/A	KX464409	N/A	Pavlic et al. (2009b), Yang et al. (2017)
	CBS 123635 = CMW 14056	*Syzigium cordatum*	South Africa	D. Pavlic	EU821903	EU821873	EU821843	EU821933	N/A	KX464410	N/A	Pavlic et al. (2009b), Yang et al. (2017)
N. cryptoaustrale	CMW 23785 = CBS 122813[3]	*Eucalyptus* trees	South Africa	H.M. Maleme	FJ752742	FJ752713	FJ752756	KX464014	N/A	KX464416	N/A	Crous et al. (2013), Yang et al. (2017)
N. eucalypticola	CBS 115679 = CMW 6539[3]	*Eucalyptus grandis*	Orbost, Victoria, Australia	M.J. Wingfield	AY615141	AY615133	AY615125	N/A	N/A	KF766368	KF766288	Slippers et al. (2004c, 2013)
	CBS 115766 = CMW 6217	*Eucalyptus rossii*	Tidbinbilla, NSW, Australia	M.J. Wingfield	AY615143	AY615135	AY615127	N/A	N/A	N/A	N/A	Slippers et al. (2004c, 2013)
N. eucalyptorum	CBS 115791 = CMW 10125[3]	*Eucalyptus grandis*	South Africa	H. Smith	AF283686	AY236891	AY236920	N/A	N/A	N/A	N/A	Smith et al. (2001), Slippers et al. (2004b)
	CMW 10126	*Eucalyptus grandis*	South Africa	H. Smith	AF283687	AY236892	AY236921	N/A	N/A	N/A	N/A	Smith et al. (2001), Slippers et al. (2004b)
N. grevilleae	CBS 129518 = CPC 16999[3]	*Grevillea aurea*	Australia	P.W. Crous & R.G. Shivas	JF951137	N/A	N/A	N/A	N/A	JF951157	N/A	Crous et al. (2011)
N. hellenicum	CERC1947 = CFCC50067[3]	*Pistachia vera*	Thessaloniki, Greece	T.J. Michailides	KP217053	KP217061	KP217069	N/A	N/A	N/A	N/A	Chen et al. (2015)
	CERC1948 = CFCC50068	*Pistachia vera*	Aghios Mamas, Chalkidiki, Greece	T.J. Michailides	KP217054	KP217062	KP217070	N/A	N/A	N/A	N/A	Chen et al. (2015)
N. illicii	CGMCC3.18310[3]	*Illicium verum*	Guangxi, China	L. Wang	KY350149	N/A	KY350155	N/A	N/A	N/A	N/A	Zhang et al. (2017)
	CGMCC3.18311	*Illicium verum*	Guangxi, China	L. Wang	KY350150	KY817756	KY350156	N/A	N/A	N/A	N/A	Zhang et al. (2017)
N. kwambonambiense	CBS 123639 = CMW 14023[3]	*Syzigium cordatum*	South Africa	D. Pavlic	EU821900	EU821870	EU821840	EU821930	N/A	KX464422	N/A	Pavlic et al. (2009b), Yang et al. (2017)
	CBS 123641 = CMW 14140	*Syzigium cordatum*	South Africa	D. Pavlic	EU821919	EU821889	EU821859	EU821949	N/A	KX464424	N/A	Pavlic et al. (2009b), Yang et al. (2017)
N. lumnitzerae	CMW 41469[3]	*Lumnitzera racemosa*	South Africa	J.A. Osorio & J. Roux	KP860881	KP860724	KP860801	KU587925	N/A	N/A	N/A	Osorio et al. (2017)
	CMW 41228	*Lumnitzera racemosa*	South Africa	J.A. Osorio & J. Roux	KP860882	KP860725	KP860803	KU587926	N/A	N/A	N/A	Osorio et al. (2017)
N. luteum	CBS 562.92 = ATCC 58193[3]	*Actinidia deliciosa*, lesion on ripe fruit	New Zealand	S.R. Pennycook	KX464170	KX464690	KX464968	KX464020	N/A	KX464430	N/A	Yang et al. (2017)
N. macroclavatum	CBS 118223 = WAC 12444[3]	*Eucalyptus globulus*	Western Australia	T. Burgess	DQ093196	DQ093217	DQ093206	KX464022	N/A	KX464436	N/A	Burgess et al. (2005), Yang et al. (2017)
N. mangiferae	CBS 118531 = CMW 7024[3]	*Mangifera indica*	Australia	G.I. Johnson	AY615185	DQ093221	AY615172	N/A	N/A	DQ377920	EU673153	Slippers et al. (2005), Phillips et al. (2008)
	CBS 118532 = CMW 7797	*Mangifera indica*	Australia	G.I. Johnson	AY615186	DQ093220	AY615173	KX464023	N/A	DQ377921	EU673154	Slippers et al. (2005), Phillips et al. (2008), Yang et al. (2017)
N. mangroviorum	CMW 41365[3]	*Avicennia marina*	South Africa	J.A. Osorio & J. Roux	KP860859	KP860702	KP860779	KU587905	N/A	N/A	N/A	Osorio et al. (2017)
	CMW 42481	*Bruguiera gymnorrhiza*	South Africa	J.A. Osorio & J. Roux	KP860848	KP860692	KP860770	KU587895	N/A	N/A	N/A	Osorio et al. (2017)
N. mediterraneum	CBS 121718 = CPC 13137[3]	*Eucalyptus* sp.	Greece	P.W. Crous, M.J. Wingfield & A.J.L. Phillips	GU251176	GU251308	GU251836	KX464024	N/A	N/A	N/A	Crous et al. (2007), Yang et al. (2017)
N. nonquaesitum	CBS 126655 = PD 484[3]	*Umbellularia californica*	USA	F.P. Trouillas	GU251163	GU251295	GU251823	KX464025	N/A	KX464437	N/A	Inderbitzin et al. (2010), Yang et al. (2017)
	PD 301	*Vaccinum corymbosum* cv. Elliot	Chile	E.X. Bricenõ, J.G. Espinoza, B.A. Latorre & J.G. Espinoza	GU251164	GU251296	GU251824	N/A	N/A	N/A	N/A	Inderbitzin et al. (2010)
N. occulatum	CBS 128008 = MUCC 227[3]	*Eucalyptus grandis* hybrid	Australia	T.I. Burgess	EU301030	EU339509	EU339472	EU339558	N/A	KX464438	N/A	Sakalidis et al. (2011), Yang et al. (2017)

Table 2 (cont.)

Species	Isolate numbers[1]	Host	Location	Collector	GenBank accession numbers[2]							Reference
					ITS	*tef1*	*tub*	*rpb2*	*cmdA*	LSU	SSU	
N. occulatum (cont.)	MUCC 286 = WAC 12395	*Eucalyptus pellita*	Australia	T.I. Burgess	EU736947	EU339511	EU339474	EU339560	N/A	N/A	N/A	Sakalidis et al. (2011)
N. parvum	ATCC 58191 = CMW 9081[3]	*Populus nigra*	New Zealand	G.J. Samuels	AY236943	AY236888	AY236917	EU821963	N/A	AY928045	EU673151	Slippers et al. (2004a), Alves et al. (2005), Phillips et al. (2008), Pavlic et al. (2009b)
	CMW 9080 = ICMP 8002	*Populus nigra*	New Zealand	G.J. Samuels	AY236942	AY236887	AY236916	EU821962	N/A	N/A	N/A	Slippers et al. (2004a), Pavlic et al. (2009b)
N. pennatisporum	WAC 13153 = MUCC 510[3]	*Allocasuarina fraseriana*	Western Australia	K.M. Taylor	EF591925	EF591976	EF591959	N/A	N/A	EF591942	N/A	Taylor et al. (2009)
N. pistaciae	CBS 595.76[3]	*Pistacia vera*	Greece	D.G. Zachos	KX464163	KX464676	KX464953	KX464008	N/A	KX464404	N/A	Yang et al. (2017)
N. pistaciarum	CBS 113083 = CPC 5263[3]	*Pistacia vera*	USA	T.J. Michailides	KX464186	KX464712	KX464998	KX464027	N/A	KX464465	N/A	Yang et al. (2017)
	CBS 113084 = CPC 5284	Redwood	USA	T.J. Michailides	KX464187	KX464713	KX464999	KX464028	N/A	KX464466	N/A	Yang et al. (2017)
N. protearum	CBS 114176 = STE-U 1775[3]	*Leucadendron salignum*	South Africa	S. Denman	AF452539	KX464720	KX465006	KX464029	N/A	JX556245	N/A	Denman et al. (2003), Yang et al. (2017)
	CBS 111200 = CPC 1357	*Leucadendron* sp.	South Africa	P.W. Crous	KX464193	KX464719	KX465005	N/A	N/A	KX464472	N/A	Yang et al. (2017)
N. ribis	CBS 115475 = CMW 7772[3]	*Ribes* sp.	USA	B. Slippers & G. Hudler	AY236935	AY236877	AY236906	EU821958	N/A	AY928044	KF766292	Slippers et al. (2004a, 2013), Alves et al. (2005), Pavlic et al. (2009b)
	CBS 121.26 = CMW 7054	*Ribes rubrum*	USA	N.E. Stevens	AF241177	AY236879	AY236908	EU821960	N/A	KX464473	N/A	Slippers et al. (2004a), Pavlic et al. (2009b), Yang et al. (2017)
N. sinense	CGMCC3.18315[3]	Unknown woody plant	Guizhou, China	J.J. Gan	KY350148	KY817755	KY350154	N/A	N/A	N/A	N/A	Zhang et al. (2017)
N. stellenboschiana	CBS 110864 = CPC 4598[3]	*Vitis vinifera*	South Africa	F. Halleen	AY343407	AY343348	KX465047	KX464042	N/A	KX464513	N/A	Van Niekerk et al. (2004), Yang et al. (2017)
N. terminaliae	CBS 125263 = CMW 26679[3]	*Terminalia sericea*	South Africa	D. Begoude & J. Roux	GQ471802	GQ471780	KX465052	KX464045	N/A	KX464518	N/A	Begoude (2010), Yang et al. (2017)
	CBS 125264 = CMW 26683	*Terminalia sericea*	South Africa	D. Begoude & J. Roux	GQ471804	GQ471782	KX465053	KX464046	N/A	KX464519	N/A	Begoude (2010), Yang et al. (2017)
N. umdonicola	CBS 123645 = CMW 14058[3]	*Syzigium cordatum*	South Africa	D. Pavlic	EU821904	EU821874	EU821844	EU821934	N/A	KX464522	N/A	Pavlic et al. (2009b), Yang et al. (2017)
	CBS 123646 = CMW 14060	*Syzigium cordatum*	South Africa	D. Pavlic	EU821905	EU821875	EU821845	EU821935	N/A	KX464523	N/A	Pavlic et al. (2009b), Yang et al. (2017)
N. ursorum	CMW 24480 = CBS 122811[3]	*Eucalyptus* trees	South Africa	H.M. Maleme	FJ752746	FJ752709	KX465056	KX464047	N/A	N/A	N/A	Crous et al. (2013), Yang et al. (2017)
	CMW 23790	*Eucalyptus* trees	South Africa	H.M. Maleme	FJ752745	FJ752708	KX465057	N/A	N/A	N/A	N/A	Crous et al. (2013), Yang et al. (2017)
N. viticlavatum	CBS 112878 = STE-U 5044[3]	*Vitis vinifera*	South Africa	F. Halleen	AY343381	AY343342	KX465058	KX464048	N/A	KX464527	N/A	Phillips et al. (2013), Yang et al. (2017)
	CBS 112977 = STE-U 5041	*Vitis vinifera*	South Africa	F. Halleen	AY343380	AY343341	KX465059	N/A	N/A	KX464528	N/A	Phillips et al. (2013), Yang et al. (2017)
N. vitifusiforme	CBS 110887 = STE-U 5252[3]	*Vitis vinifera*	South Africa	J.M. van Niekerk	AY343383	AY343343	KX465061	KX464049	N/A	KX464530	N/A	Van Niekerk et al. (2004), Yang et al. (2017)
	CBS 110880 = STE-U 5050	*Vitis vinifera*	South Africa	J.M. van Niekerk	AY343382	AY343344	KX465008	N/A	N/A	KX464475	N/A	Van Niekerk et al. (2004), Yang et al. (2017)

[1] ALG: Personal culture collection A. Berraf-Tebbal; ATCC: American Type Culture Collection, Virginia, USA; BL: Personal number of B.T. Linaldeddu; CAA: Personal culture collection Artur Alves, Universidade de Aveiro, Portugal; CBS: CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands; CERC: Culture collection of China Eucalypt Research Centre, Chinese Academy of Forestry, ZhanJiang, GuangDong, China; CFCC: China Forestry Culture Collection Center, Beijing, China; CGMCC: China General Microbiological Culture Collection Center, Beijing, China; CMM: Culture Collection of Phytopathogenic Fungi 'Prof. Maria Menezes', Universidade Federal Rural de Pernambuco, Recife, Brazil; CMW: Tree Pathology Co-operative Program, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa; CPC: Working collection of P.W. Crous, housed at CBS; GZCC: Guizhou Academy of Agricultural Sciences Culture Collection, GuiZhou, China; IBL: Personal culture collection, I.B.L. Coutinho; IBP: Personal culture collection, I.B. Prasher; ICMP: International Collection of Microorganisms from Plants, Auckland, New Zealand; IRAN: Iranian Fungal Culture Collection, Iranian Research Institute of Plant Protection, Iran; MFLUCC: Mae Fah Luang University Culture Collection, Chiang Rai, Thailand; MUCC: Culture collection of Murdoch University, Perth, Australia; STE-U: Culture collection of the Department of Plant Pathology, University of Stellenbosch, South Africa; UCD: University of California, Davis, Plant Pathology Department Culture Collection; WAC: Department of Agriculture, Western Australia Plant Pathogen Collection, South Perth, Western Australia.

[2] ITS, internal transcribed spacer region and intervening 5.8S nrRNA gene; *tef1*, translation elongation factor 1-alpha; *tub*, β-tubulin; *rpb2*, DNA-directed RNA polymerase II subunit; *cmdA*, calmodulin; LSU, nuclear ribosomal large subunit; SSU, nuclear ribosomal small subunit; N/A = not available.

[3] Isolates represent ex-type or are from samples that have been linked morphologically to type materials of the species.

Morphology

Representative isolates for each genotype of *Botryosphaeriaceae* species identified by DNA sequence comparisons were selected for morphological study. To induce sporulation, selected isolates were transferred to 2 % water agar (WA) media (20 g of agar per litre of water) with double-sterilised pine needles placed on the surface of the media (Smith et al. 1996). These cultures were incubated at 25 °C under near-ultraviolet light for 4–6 wk. Conidia in the pycnidia were mounted in one drop of 80 % lactic acid on glass slides and examined under a stereomicroscope (Carl Zeiss Ltd., Munchen, Germany). Conidia and other structures were examined and recorded using a Zeiss Axio Imager A1 microscope and a Zeiss AxioCam MRc digital camera with Zeiss Axio Vision v. 4.8 software (Carl Zeiss Ltd.). Measurements of conidiomata, conidiophores and conidiogenous cells were made to determine the smallest and the largest values. For the isolates selected as a holotype, the lengths and widths of 100 conidia per isolate were measured, as well as 25 measurements of the remaining isolates of each taxon. Average (mean), standard deviation (SD), minimum (min) and maximum (max) measurements are presented as (min–)(mean–SD)–(mean+SD)(–max). The average length/average width ratio (L/W) of the conidial measurements was calculated.

Colony morphology was characterised by cultures grown on 2 % MEA for 7 d and colony colour was determined using the colour charts of Rayner (1970). For growth studies, a 5-mm-diam plug from the growing margin of 7-d-old colonies of each representative isolate was placed in the centre of 90-mm-diam Petri plates containing 2 % MEA. These cultures were incubated in the dark at 5 °C intervals from 5–40 °C. Five replicate plates of each isolate at each temperature were conducted. Two diameter measurements, orthogonally, were recorded daily until the fastest growing culture reached the edge of the Petri plate. The experiment was repeated once and the average for each of the eight temperatures was calculated.

Pathogenicity tests

To determine the pathogenicity of the identified species on *Eucalyptus* seedlings, representative isolates of all *Botryosphaeriaceae* species identified in this study were selected to inoculate on *Eucalyptus* seedlings. Three *Eucalyptus* clones, CEPT-11 (*Eucalyptus urophylla* × *E. grandis*), CEPT-12 (*E. urophylla*) and CEPT-13 (*E. urophylla* × *E. tereticornis*), were used for inoculations. The *Eucalyptus* seedlings were 1-yr-old, approximately 1.7 m in height, and had a 2.0 cm diam at the root collar. For each clone, 10 seedlings were inoculated with each isolate. On each inoculated seedling, a 5-mm-diam wound was made on the tree stem using a cork borer to remove the bark and expose the xylem. The wounds are located approximately 30 cm above the root collar. For inoculation, 5-mm-diam plugs of mycelia from the margins of colonies grown on 2 % MEA for 7 d in the dark were taken and placed into the wounds with the mycelia facing the cambium. Inoculated wounds were encased with masking tape to prevent contamination and desiccation. Ten seedlings of each *Eucalyptus* clone were inoculated with sterile MEA plugs to serve as negative controls. One month after inoculation, the bark of inoculated seedlings was removed and the internal lesion/wound length on the cambium was measured. The inoculated fungi were re-isolated by cutting small pieces of wood from the edges of the lesions and cultivating them in 2 % MEA at 25 °C. Re-isolations were made from the seedlings inoculated by mycelium plugs and MEA plugs. The data were analysed by one-way analyses of variance (ANOVA) using SAS v. 9.3 (SAS Institute Inc. 2011).

RESULTS

Fungal isolation

In this study, 105 isolates from *Eucalyptus* and other plants that show typical morphology of *Botryosphaeriaceae* were isolated. Eighty-one isolates were collected from *Eucalyptus* trees: 12 from FuJian Province, 39 from GuangDong Province, 29 from GuangXi Province and one from HaiNan Province. Eighteen isolates with typical characteristics of *Botryosphaeriaceae* were collected from other plants which were growing in close proximity to *Eucalyptus*: two from *C. lanceolata*, 10 from *D. longan*, four from *M. sanguineum*, and two from *P. hanceana*. In addition, three isolates were collected from *A. cunninghamii* and *C. deodara*, respectively (Table 1).

Phylogenetic analyses

For all the 105 isolates in this study, ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU and SSU sequence data were generated and deposited in GenBank (Table 1). The PCR fragments are approximately 520 bps for the ITS region, 280 bps for the *tef1* region, 430 bps for the *tub* region, 610 bps for the *rpb2* region, 850 bps for the LSU region and 1040 bps for the SSU region. The genotype for each isolate was determined by the ITS, *tef1*, *tub*, *rpb2*, LSU, SSU sequences for isolates in the genera *Botryosphaeria*, *Cophinforma* and *Neofusicoccum*, and by ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU, SSU sequences for isolates in the genus *Lasiodiplodia* (Table 1). The preliminary identities of the isolates were determined from conducting a standard nucleotide BLAST with the sequences of ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU and SSU, the results consistently showed that the isolates sequenced in this study resided in *Botryosphaeria*, *Cophinforma*, *Lasiodiplodia* or *Neofusicoccum*. One to two isolates of each genotype were selected and used for phylogenetic analyses, depending on the number of isolates of each genotype (Table 1). Based on the comparisons for six to seven region sequences generated in this study and published sequences from ex-type strains of *Botryosphaeriaceae* downloaded from NCBI, sequences of *Botryosphaeria*, *Cophinforma*, *Lasiodiplodia* or *Neofusicoccum* related to species emerging from this study were used for analyses (Table 2). The aligned sequences of each region of ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU, SSU, as well as the combined sequences of three to five (*Botryosphaeria*/*Cophinforma*: three; *Lasiodiplodia*: five; *Neofusicoccum*: four) regions were deposited in TreeBASE (No. 21430). These datasets for genera *Botryosphaeria*/*Cophinforma*, *Lasiodiplodia* and *Neofusicoccum*, as well as statistical values for the trees for the MP analyses and parameters for the best-fit substitution models of ML analyses, are provided in Table 3.

Species residing in Botryosphaeria

For the isolates grouping in the genus *Botryosphaeria*, isolates clustered into four phylogenetic groups (Groups A–D) for each of the ITS, *tef1*, *tub*, *rpb2* and ITS/*tef1*/*tub* datasets (Fig. 2a–d, g). For each of the LSU and SSU datasets, Groups A, C and D clustered together (Fig. 2e–f). The ITS sequences of *Botryosphaeria fabicerciana*, *B. fusispora*, *B. kuwatsukai*, *B. rosaceae* and the six Chinese isolates (CERC2274, CERC2911, CERC2918, CERC2930, CERC3426 and CERC3441) in Group A are consistent, and all of them grouped into one phylogenetic clade (Fig. 2a). For the *tef1* sequence analyses, the isolates in Group A clustered closely to *B. fabicerciana* and *B. fusispora* (Fig. 2b). For the *tub* sequences, the isolates in Group A resided in the same phylogenetic clade with *B. fusispora* (Fig. 2c). For the *rpb2*, LSU and SSU sequences, the isolates in Group A clustered to the same clade with *B. fabicerciana* and *B. fusispora* (*rpb2* is not available to *B. fusispora*) (Fig. 2d–f). The phylogenetic analyses for ITS, *tef1*, *tub*, *rpb2*, LSU and SSU sequences

Table 3 Datasets used and statistics resulting from phylogenetic analyses.

Genus	Dataset	No. of taxa	No. of bp[1]	Maximum parsimony						
				PIC[2]	No. of trees	Tree length	CI[3]	RI[4]	RC[5]	HI[6]
Botryosphaeria/*Cophinforma*	ITS	45	543	42	18	67	0.8209	0.9506	0.7804	0.1791
	tef1	45	356	147	875	206	0.8932	0.9677	0.8643	0.1068
	tub	34	415	43	8	58	0.9138	0.9688	0.8852	0.0862
	rpb2	22	718	92	2	116	0.9397	0.9809	0.9217	0.0603
	LSU	34	847	21	3	24	0.9583	0.9865	0.9454	0.0417
	SSU	31	1024	9	342	9	1.0000	1.0000	1.0000	1.0000
	ITS/*tef1*/*tub*	45	1314	232	5000	337	0.8665	0.9585	0.8305	0.1335
Lasiodiplodia	ITS	76	526	48	5000	87	0.6897	0.8945	0.6169	0.3103
	tef1	75	332	142	852	402	0.6219	0.9067	0.5639	0.3781
	tub	67	409	41	5000	60	0.7667	0.9352	0.7170	0.2333
	rpb2	57	532	104	861	190	0.6421	0.8761	0.5626	0.3579
	cmdA	45	521	74	496	91	0.9121	0.9776	0.8916	0.0879
	LSU	28	835	20	3	27	0.7407	0.9247	0.6850	0.2593
	SSU	19	1020	17	2	23	0.8261	0.9048	0.7474	0.1739
	ITS/*tef1*/*tub*/*rpb2*/*cmdA*	76	2320	409	5000	948	0.5918	0.8713	0.5156	0.4082
Neofusicoccum	ITS	77	532	81	1404	187	0.5615	0.8707	0.4889	0.4385
	tef1	75	307	147	5000	303	0.7426	0.9321	0.6922	0.2574
	tub	75	424	71	1430	141	0.6170	0.8784	0.5420	0.3830
	rpb2	55	607	114	652	191	0.7173	0.9069	0.6505	0.2827
	LSU	55	841	33	3260	70	0.5714	0.8324	0.4757	0.4286
	SSU	21	1027	3	1	3	1.0000	1.0000	1.0000	1.0000
	ITS/*tef1*/*tub*/*rpb2*	77	1870	413	336	884	0.6267	0.8824	0.5530	0.3733

Genus	Dataset	Maximum likelihood									
		Subst. model[7]	NST[8]	Rate matrix					Ti/Tv ratio[9]	p-inv	Gamma	Rates
Botryosphaeria/*Cophinforma*	ITS	TrN+I	6	1.0000	1.4207	1.0000	1.0000	8.3891	–	0.8010	–	Equal
	tef1	TPM2uf+G	6	1.7386	4.6965	1.7386	1.0000	4.6965	–	–	0.4470	Gamma
	tub	HKY+G	2	–	–	–	–	–	4.1414	–	0.0220	Gamma
	rpb2	TrN+G	6	1.0000	3.1864	1.0000	1.0000	10.4238	–	–	0.2610	Gamma
	LSU	TrN+I	6	1.0000	5.1213	1.0000	1.0000	14.2608	–	0.8440	–	Equal
	SSU	TIM2	6	0.2353	0.4397	0.2353	1.0000	3.3084	–	–	–	Equal
	ITS/*tef1*/*tub*	TrN+G	6	1.0000	3.2977	1.0000	1.0000	5.9498	–	–	0.0970	Gamma
Lasiodiplodia	ITS	TPM1uf+I+G	6	1.0000	8.3075	3.1185	3.1185	8.3075	–	0.6760	0.7400	Gamma
	tef1	TrN+G	6	1.0000	3.6014	1.0000	1.0000	5.5149	–	–	0.3870	Gamma
	tub	TIM3+G	6	2.6761	3.8909	1.0000	2.6761	10.7362	–	–	0.4190	Gamma
	rpb2	TrN+G	6	1.0000	4.8566	1.0000	1.0000	13.8753	–	–	0.3530	Gamma
	cmdA	HKY+I	2	–	–	–	–	–	2.7918	0.5470	–	Equal
	LSU	TrN+I	6	1.0000	7.7385	1.0000	1.0000	16.1138	–	0.7970	–	Equal
	SSU	TIM2+I	6	3.1234	3.8646	3.1234	1.0000	15.5731	–	0.9220	–	Equal
	ITS/*tef1*/*tub*/*rpb2*/*cmdA*	TIM3+I+G	6	0.6986	3.2898	1.0000	0.6986	5.4586	–	0.5380	0.6730	Gamma
Neofusicoccum	ITS	TIM1+I+G	6	1.0000	11.6895	3.1944	3.1944	22.131	–	0.5510	0.6030	Gamma
	tef1	HKY+G	2	–	–	–	–	–	2.8135	0.0740	0.6810	Gamma
	tub	TrN+G	6	1.0000	4.0352	1.0000	1.0000	7.8348	–	–	0.1980	Gamma
	rpb2	TIM3+G	6	1.9463	7.0524	1.0000	1.9463	19.4804	–	–	0.2840	Gamma
	LSU	TrN+I	6	1.0000	6.0800	1.0000	1.0000	25.6908	–	0.9010	–	Equal
	SSU	TrN	6	1.0000	0.9096	1.0000	1.0000	7.9272	–	–	–	Equal
	ITS/*tef1*/*tub*/*rpb2*	TrN+I+G	6	1.0000	4.8874	1.0000	1.0000	9.1711	–	0.4320	0.7150	Gamma

[1] bp = base pairs.
[2] PIC = number of parsimony informative characters.
[3] CI = consistency index.
[4] RI = retention index.
[5] RC = rescaled consistency index.
[6] HI = homoplasy index.
[7] Subst. model = best fit substitution model.
[8] NST = number of substitution rate categories.
[9] Ti/Tv ratio = transition/transversion ratio.

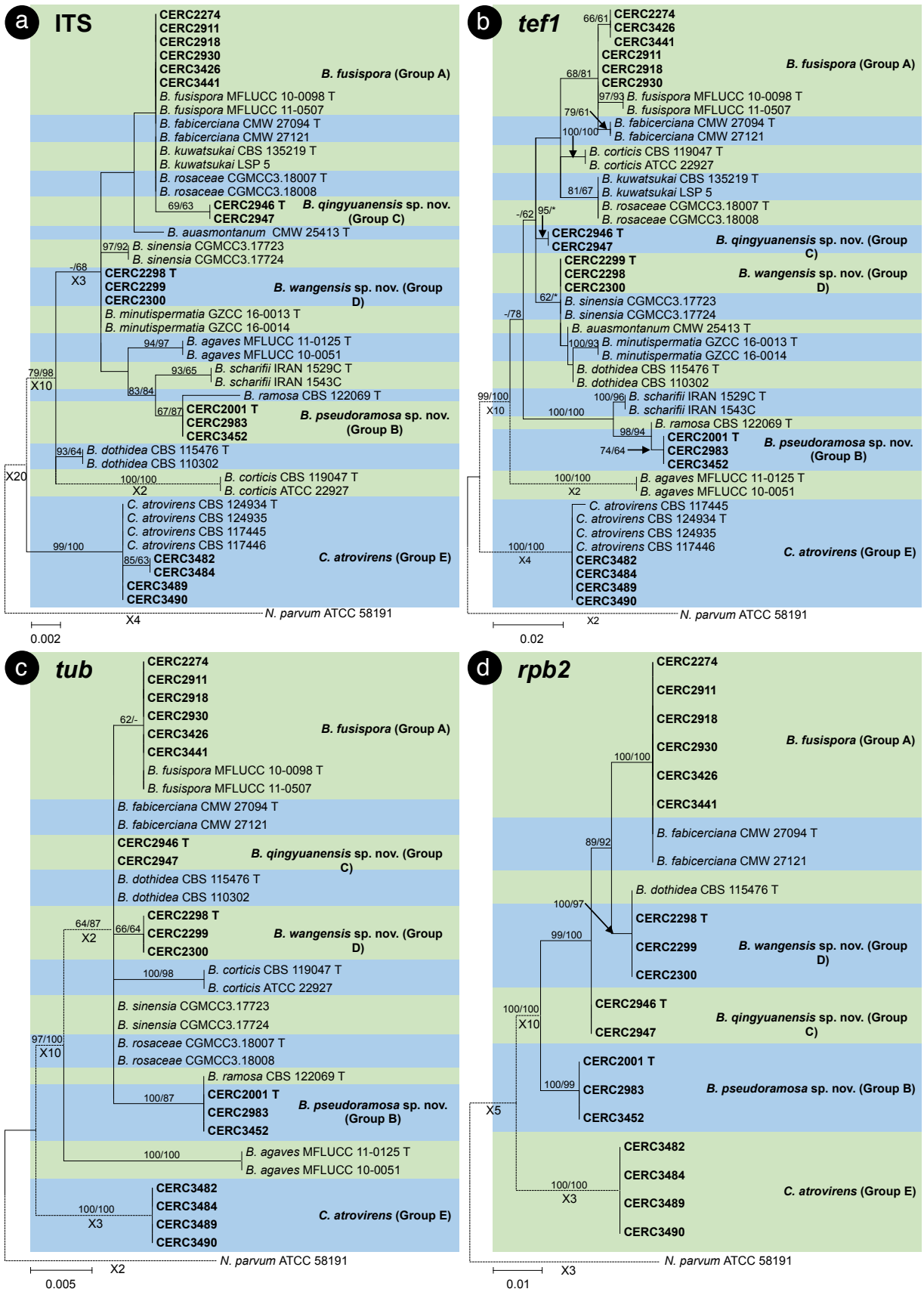
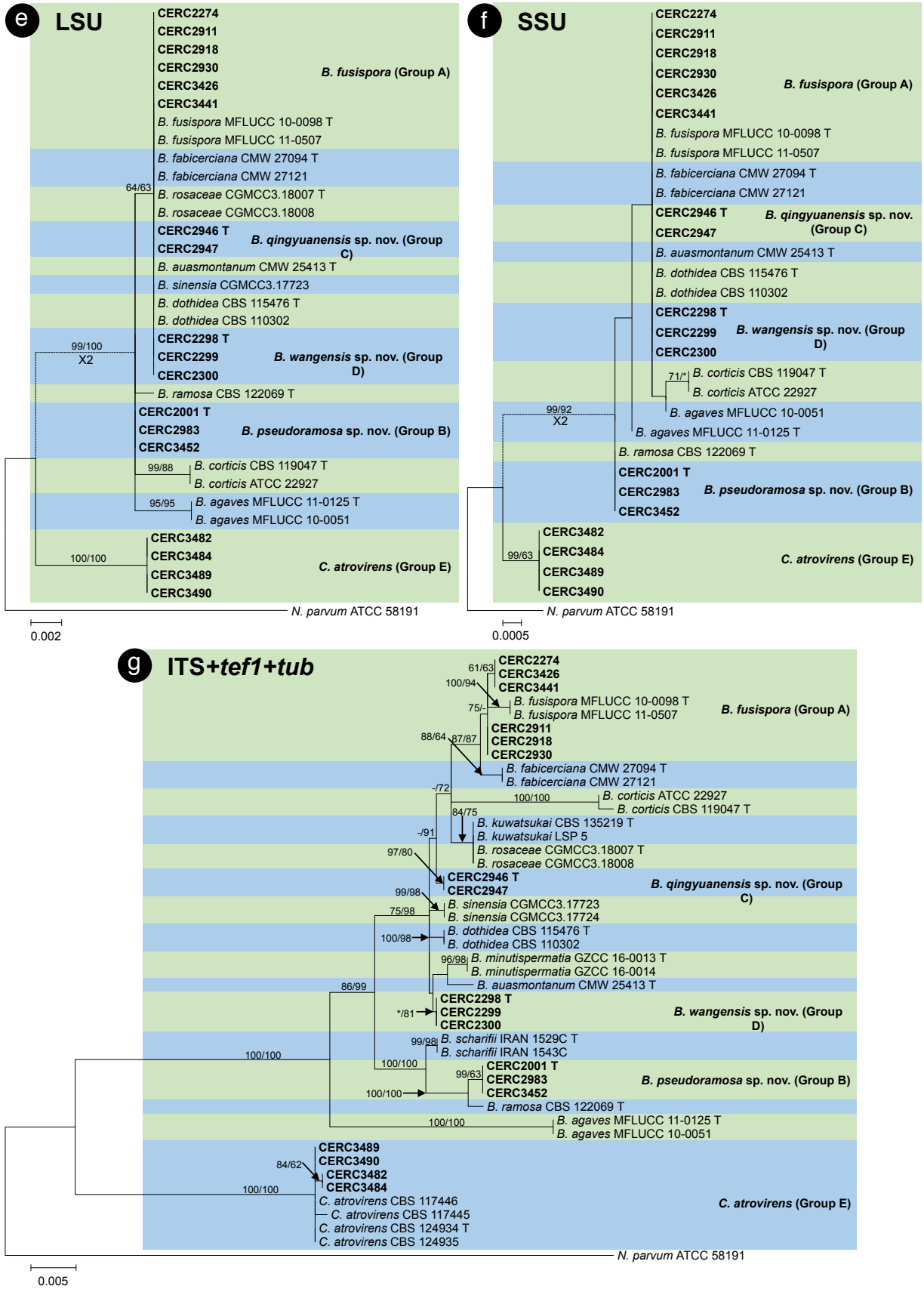


Fig. 2 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Botryosphaeria* and *Cophinforma*. a. ITS region; b. *tef1* gene region; c. *tub* gene region; d. *rpb2* gene region; e. LSU region; f. SSU region; g. combination of ITS, *tef1* and *tub* regions. Isolates sequenced in this study are in **bold**. Bootstrap support values ≥ 60 % for ML and MP are presented above branches as follows: ML/MP, bootstrap support values < 60 % are marked with '–', and absent (< 50 %) are marked with '*'. Isolates representing ex-type sequences are marked with 'T'. *Neofusicoccum parvum* (ATCC 58191) was used as the outgroup taxon.

Fig. 2 (cont.)


e LSU
CERC2274
CERC2911
CERC2918
CERC2930
CERC3426
CERC3441
B. fusispora (Group A)
B. fusispora MFLUCC 10-0098 T
B. fusispora MFLUCC 11-0507
B. fabicerciana CMW 27094 T
B. fabicerciana CMW 27121
64/63
B. rosaceae CGMCC3.18007 T
B. rosaceae CGMCC3.18008
CERC2946 T
CERC2947
B. qingyuanensis sp. nov. (Group C)
B. auasmontanum CMW 25413 T
B. sinensia CGMCC3.17723
B. dothidea CBS 115476 T
B. dothidea CBS 110302
99/100
X2
CERC2298 T
CERC2299
CERC2300
B. wangensis sp. nov. (Group D)
B. ramosa CBS 122069 T
CERC2001 T
CERC2983
CERC3452
B. pseudoramosa sp. nov. (Group B)
99/88
B. corticis CBS 119047 T
B. corticis ATCC 22927
95/95
B. agaves MFLUCC 11-0125 T
B. agaves MFLUCC 10-0051
CERC3482
100/100
CERC3484
CERC3489
CERC3490
C. atrovirens (Group E)
N. parvum ATCC 58191
0.002
f SSU
CERC2274
CERC2911
CERC2918
CERC2930
CERC3426
CERC3441
B. fusispora (Group A)
B. fusispora MFLUCC 10-0098 T
B. fusispora MFLUCC 11-0507
B. fabicerciana CMW 27094 T
B. fabicerciana CMW 27121
CERC2946 T
CERC2947
B. qingyuanensis sp. nov. (Group C)
B. auasmontanum CMW 25413 T
B. dothidea CBS 115476 T
B. dothidea CBS 110302
CERC2298 T
CERC2299
CERC2300
B. wangensis sp. nov. (Group D)
71/*
B. corticis CBS 119047 T
B. corticis ATCC 22927
99/92
X2
B. agaves MFLUCC 10-0051
B. agaves MFLUCC 11-0125 T
B. ramosa CBS 122069 T
CERC2001 T
CERC2983
CERC3452
B. pseudoramosa sp. nov. (Group B)
CERC3482
99/63
CERC3484
CERC3489
CERC3490
C. atrovirens (Group E)
N. parvum ATCC 58191
0.0005
g ITS+tef1+tub
61/63
CERC2274
CERC3426
100/94
CERC3441
B. fusispora MFLUCC 10-0098 T
75/-
B. fusispora MFLUCC 11-0507
B. fusispora (Group A)
88/64
87/87
CERC2911
CERC2918
CERC2930
B. fabicerciana CMW 27094 T
B. fabicerciana CMW 27121
-/72
100/100
B. corticis ATCC 22927
B. corticis CBS 119047 T
84/75
B. kuwatsukai CBS 135219 T
-/91
B. kuwatsukai LSP 5
97/80
B. rosaceae CGMCC3.18007 T
B. rosaceae CGMCC3.18008
CERC2946 T
CERC2947
B. qingyuanensis sp. nov. (Group C)
99/98
B. sinensia CGMCC3.17723
75/98
B. sinensia CGMCC3.17724
B. dothidea CBS 115476 T
100/98
B. dothidea CBS 110302
96/98
B. minutispermatia GZCC 16-0013 T
B. minutispermatia GZCC 16-0014
86/99
B. auasmontanum CMW 25413 T
CERC2298 T
*/81
CERC2299
CERC2300
B. wangensis sp. nov. (Group D)
99/98
B. scharifii IRAN 1529C T
100/100
B. scharifii IRAN 1543C
100/100
CERC2001 T
99/63
CERC2983
CERC3452
B. pseudoramosa sp. nov. (Group B)
100/100
B. ramosa CBS 122069 T
100/100
B. agaves MFLUCC 11-0125 T
B. agaves MFLUCC 10-0051
CERC3489
84/62
CERC3490
CERC3482
100/100
CERC3484
C. atrovirens CBS 117446
C. atrovirens CBS 117445
C. atrovirens CBS 124934 T
C. atrovirens CBS 124935
C. atrovirens (Group E)
N. parvum ATCC 58191
0.005

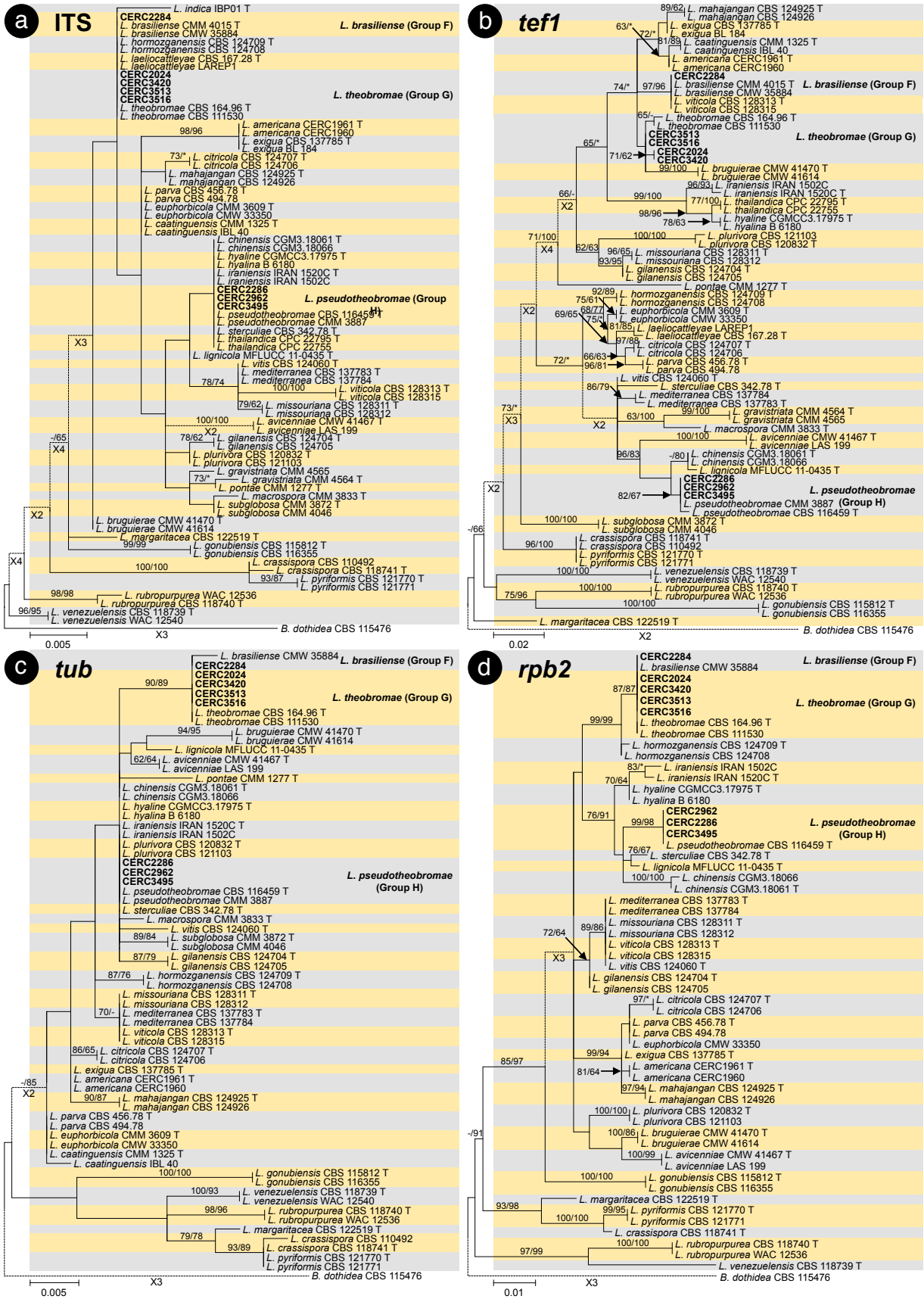
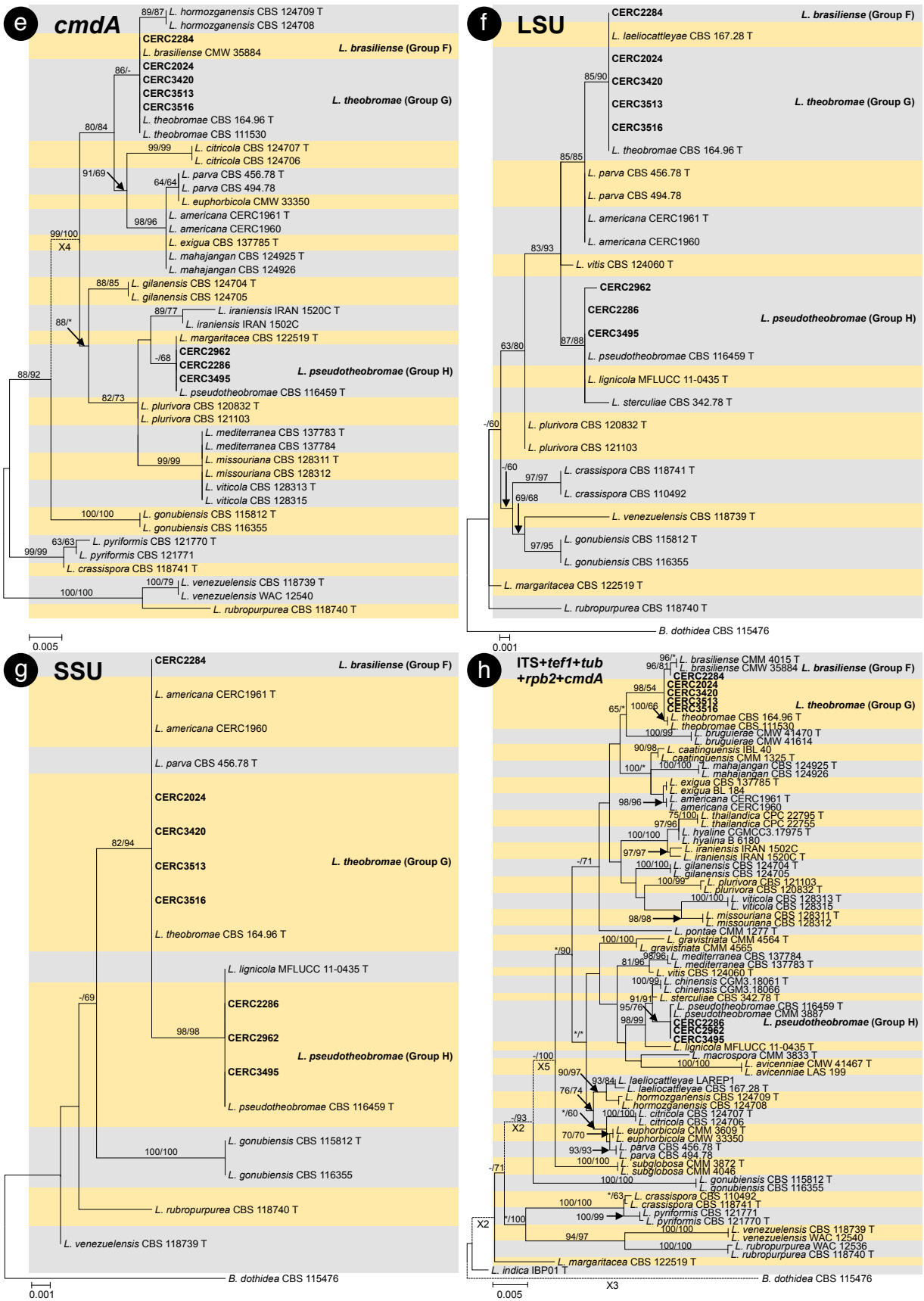


Fig. 3 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Lasiodiplodia*. a. ITS region; b. *tef1* gene region; c. *tub* gene region; d. *rpb2* gene region; e. *cmdA* gene region; f. LSU region; g. SSU region; h. combination of ITS, *tef1*, *tub*, *rpb2* and *cmdA* regions. Isolates sequenced in this study are in **bold**. Bootstrap support values ≥ 60 % for ML and MP are presented above branches as follows: ML/MP, bootstrap values < 60 % are marked with '–', and absent (< 50 %) are marked with '*'. Isolates representing ex-type sequences are marked with 'T'. *Botryosphaeria dothidea* (CBS 115476) was used as the outgroup taxon.

Fig. 3 (cont.)


e
cmdA
L. hormozganensis CBS 124709 T
L. hormozganensis CBS 124708
CERC2284
L. brasiliense CMW 35884
L. brasiliense (Group F)
CERC2024
CERC3420
CERC3513
CERC3516
L. theobromae (Group G)
L. theobromae CBS 164.96 T
L. theobromae CBS 111530
L. citricola CBS 124707 T
L. citricola CBS 124706
L. parva CBS 456.78 T
L. parva CBS 494.78
L. euphorbicola CMW 33350
L. americana CERC1961 T
L. americana CERC1960
L. exigua CBS 137785 T
L. mahajangan CBS 124925 T
L. mahajangan CBS 124926
L. gilanensis CBS 124704 T
L. gilanensis CBS 124705
L. iraniensis IRAN 1520C T
L. iraniensis IRAN 1502C
L. margaritacea CBS 122519 T
CERC2962
CERC2286
CERC3495
L. pseudotheobromae (Group H)
L. pseudotheobromae CBS 116459 T
L. plurivora CBS 120832 T
L. plurivora CBS 121103
L. mediterranea CBS 137783 T
L. mediterranea CBS 137784
L. missouriana CBS 128311 T
L. missouriana CBS 128312
L. viticola CBS 128313 T
L. viticola CBS 128315
L. gonubiensis CBS 115812 T
L. gonubiensis CBS 116355
L. pyriformis CBS 121770 T
L. pyriformis CBS 121771
L. crassispora CBS 118741 T
L. venezuelensis CBS 118739 T
L. venezuelensis WAC 12540
L. rubropurpurea CBS 118740 T
0.005
f
LSU
CERC2284
L. brasiliense (Group F)
L. laeliocattleyae CBS 167.28 T
CERC2024
CERC3420
CERC3513
CERC3516
L. theobromae (Group G)
L. theobromae CBS 164.96 T
L. parva CBS 456.78 T
L. parva CBS 494.78
L. americana CERC1961 T
L. americana CERC1960
L. vitis CBS 124060 T
CERC2962
CERC2286
CERC3495
L. pseudotheobromae (Group H)
L. pseudotheobromae CBS 116459 T
L. lignicola MFLUCC 11-0435 T
L. sterculiae CBS 342.78 T
L. plurivora CBS 120832 T
L. plurivora CBS 121103
L. crassispora CBS 118741 T
L. crassispora CBS 110492
L. venezuelensis CBS 118739 T
L. gonubiensis CBS 115812 T
L. gonubiensis CBS 116355
L. margaritacea CBS 122519 T
L. rubropurpurea CBS 118740 T
B. dothidea CBS 115476
0.001
g
SSU
CERC2284
L. brasiliense (Group F)
L. americana CERC1961 T
L. americana CERC1960
L. parva CBS 456.78 T
CERC2024
CERC3420
CERC3513
CERC3516
L. theobromae (Group G)
L. theobromae CBS 164.96 T
L. lignicola MFLUCC 11-0435 T
CERC2286
CERC2962
CERC3495
L. pseudotheobromae (Group H)
L. pseudotheobromae CBS 116459 T
L. gonubiensis CBS 115812 T
L. gonubiensis CBS 116355
L. rubropurpurea CBS 118740 T
L. venezuelensis CBS 118739 T
B. dothidea CBS 115476
0.001
h
ITS+tef1+tub +rpb2+cmdA
L. brasiliense CMM 4015 T
L. brasiliense CMW 35884
L. brasiliense (Group F)
CERC2284
CERC2024
CERC3420
CERC3513
CERC3516
L. theobromae (Group G)
L. theobromae CBS 164.96 T
L. theobromae CBS 111530
L. bruguierae CMW 41470 T
L. bruguierae CMW 41614
L. caatinguensis IBL 40
L. caatinguensis CMM 1325 T
L. mahajangan CBS 124925 T
L. mahajangan CBS 124926
L. exigua CBS 137785 T
L. exigua BL 184
L. americana CERC1961 T
L. americana CERC1960
L. thailandica CPC 22795 T
L. thailandica CPC 22755
L. hyaline CGMCC3.17975 T
L. hyalina B 6180
L. iraniensis IRAN 1502C
L. iraniensis IRAN 1520C T
L. gilanensis CBS 124704 T
L. gilanensis CBS 124705
L. plurivora CBS 121103
L. plurivora CBS 120832 T
L. viticola CBS 128313 T
L. viticola CBS 128315
L. missouriana CBS 128311 T
L. missouriana CBS 128312
L. pontae CMM 1277 T
L. gravistriata CMM 4564 T
L. gravistriata CMM 4565
L. mediterranea CBS 137784
L. mediterranea CBS 137783 T
L. vitis CBS 124060 T
L. chinensis CGM3.18061 T
L. chinensis CGM3.18066
L. sterculiae CBS 342.78 T
L. pseudotheobromae CBS 116459 T
L. pseudotheobromae CMM 3887
CERC2286
CERC2962
CERC3495
L. pseudotheobromae (Group H)
L. lignicola MFLUCC 11-0435 T
L. macrospora CMM 3833 T
L. avicenniae CMW 41467 T
L. avicenniae LAS 199
L. laeliocattleyae LAREP1
L. laeliocattleyae CBS 167.28 T
L. hormozganensis CBS 124709 T
L. hormozganensis CBS 124708
L. citricola CBS 124707 T
L. citricola CBS 124706
L. euphorbicola CMM 3609 T
L. euphorbicola CMW 33350
L. parva CBS 456.78 T
L. parva CBS 494.78
L. subglobosa CMM 3872 T
L. subglobosa CMM 4046
L. gonubiensis CBS 115812 T
L. gonubiensis CBS 116355
L. crassispora CBS 110492
L. crassispora CBS 118741 T
L. pyriformis CBS 121771
L. pyriformis CBS 121770 T
L. venezuelensis CBS 118739 T
L. venezuelensis WAC 12540
L. rubropurpurea WAC 12536
L. rubropurpurea CBS 118740 T
L. margaritacea CBS 122519 T
L. indica IBP01 T
B. dothidea CBS 115476
X2
X3
X4
X5
0.005

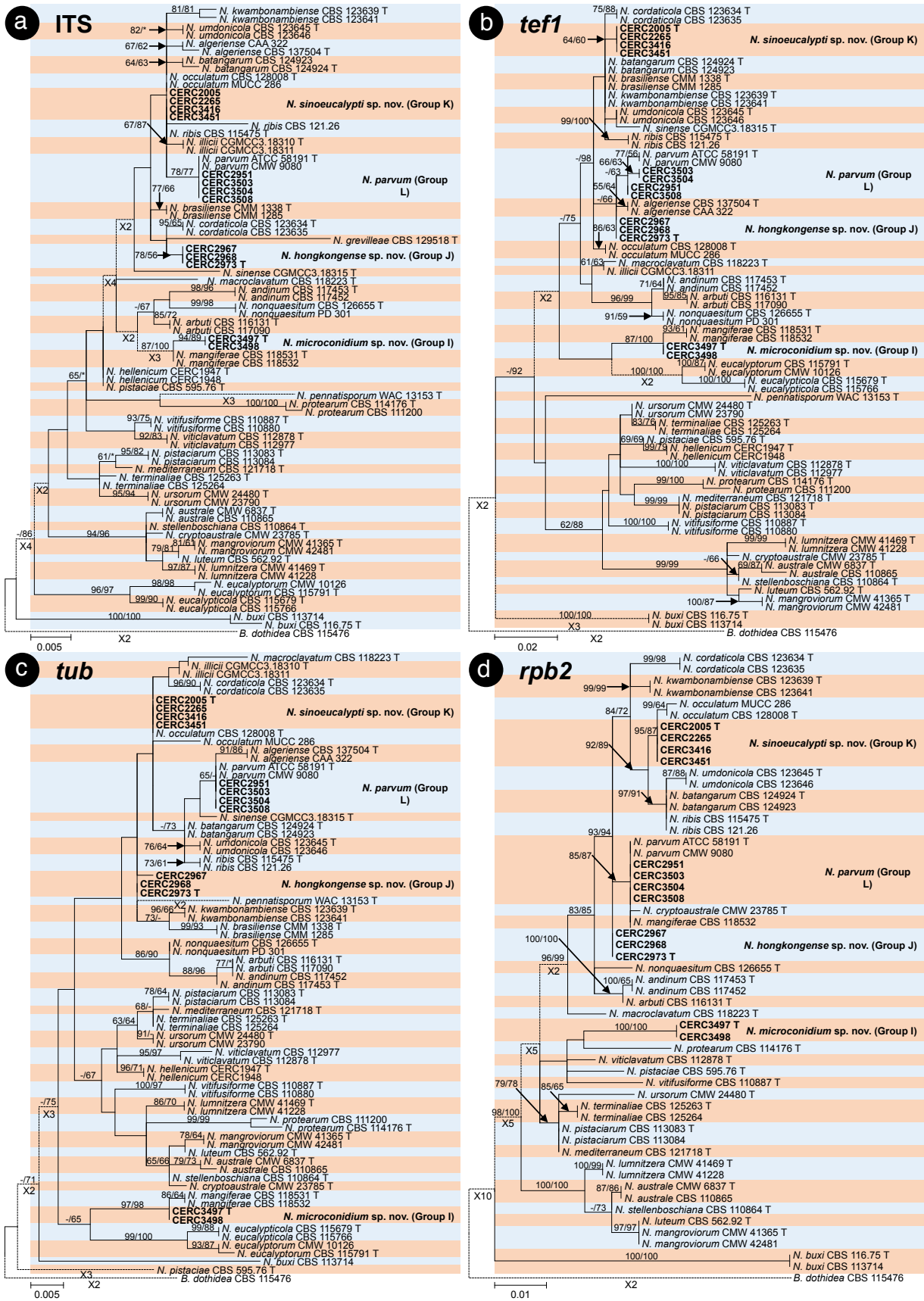
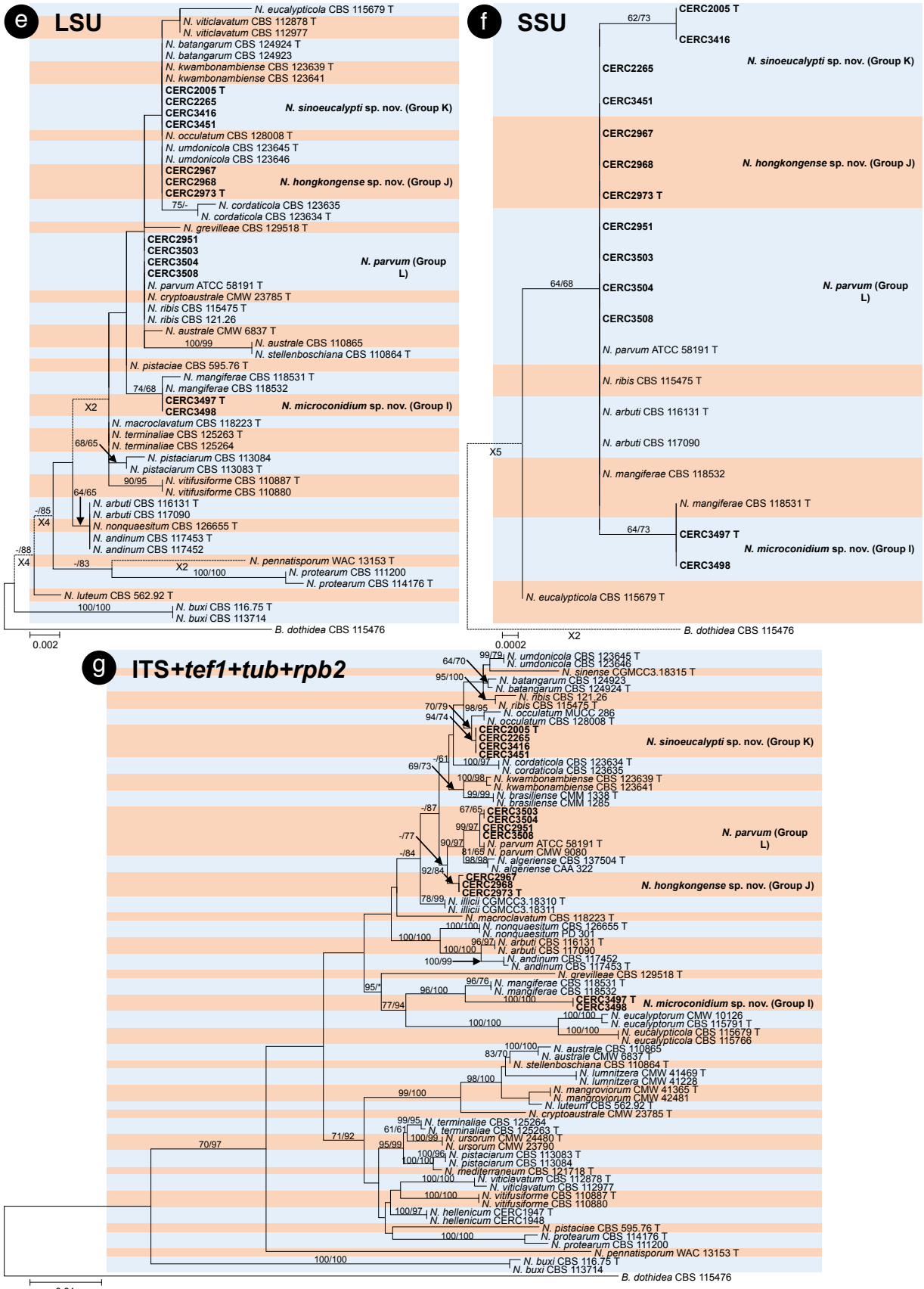


Fig. 4 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Neofusicoccum*. a. ITS region; b. *tef1* gene region; c. *tub* gene region; d. *rpb2* gene region; e. LSU region; f. SSU region; g. combination of ITS, *tef1*, *tub* and *rpb2* regions. Isolates sequenced in this study are in **bold**. Bootstrap support values ≥ 60 % for ML and MP are presented above branches as follows: ML/MP, bootstrap support values < 60 % are marked with '–', and absent (< 50 %) are marked with '*'. Isolates representing ex-type sequences are marked with 'T'. *Botryosphaeria dothidea* (CBS 115476) was used as the outgroup taxon.

Fig. 4 (cont.)


e LSU
N. eucalypticola CBS 115679 T
N. viticlavatum CBS 112878 T
N. viticlavatum CBS 112977
N. batangarum CBS 124924 T
N. batangarum CBS 124923
N. kwambonambiense CBS 123639 T
N. kwambonambiense CBS 123641
CERC2005 T
CERC2265
CERC3416
CERC3451
N. sinoeucalypti sp. nov. (Group K)
N. occultatum CBS 128008 T
N. umdonicola CBS 123645 T
N. umdonicola CBS 123646
CERC2967
CERC2968
CERC2973 T
N. hongkongense sp. nov. (Group J)
N. cordaticola CBS 123635
N. cordaticola CBS 123634 T
N. grevilleae CBS 129518 T
CERC2951
CERC3503
CERC3504
CERC3508
N. parvum (Group L)
N. parvum ATCC 58191 T
N. cryptoaustrale CMW 23785 T
N. ribis CBS 115475 T
N. ribis CBS 121.26
N. australe CMW 6837 T
N. australe CBS 110865
N. stellenboschiana CBS 110864 T
N. pistaciae CBS 595.76 T
N. mangiferae CBS 118531 T
N. mangiferae CBS 118532
CERC3497 T
CERC3498
N. microconidium sp. nov. (Group I)
N. macroclavatum CBS 118223 T
N. terminaliae CBS 125263 T
N. terminaliae CBS 125264
N. pistaciarum CBS 113084
N. pistaciarum CBS 113083 T
N. vitifusiforme CBS 110887 T
N. vitifusiforme CBS 110880
N. arbuti CBS 116131 T
N. arbuti CBS 117090
N. nonquaesitum CBS 126655 T
N. andinum CBS 117453 T
N. andinum CBS 117452
N. pennatisporum WAC 13153 T
N. protearum CBS 111200
N. protearum CBS 114176 T
N. luteum CBS 562.92 T
N. buxi CBS 116.75 T
N. buxi CBS 113714
B. dothidea CBS 115476
0.002
f SSU
CERC2005 T
CERC3416
N. sinoeucalypti sp. nov. (Group K)
CERC2265
CERC3451
CERC2967
CERC2968
N. hongkongense sp. nov. (Group J)
CERC2973 T
CERC2951
CERC3503
CERC3504
N. parvum (Group L)
CERC3508
N. parvum ATCC 58191 T
N. ribis CBS 115475 T
N. arbuti CBS 116131 T
N. arbuti CBS 117090
N. mangiferae CBS 118532
N. mangiferae CBS 118531 T
CERC3497 T
CERC3498
N. microconidium sp. nov. (Group I)
N. eucalypticola CBS 115679 T
B. dothidea CBS 115476
X2
0.0002
g ITS+tef1+tub+rpb2
N. umdonicola CBS 123645 T
N. umdonicola CBS 123646
N. sinense CGMCC3.18315 T
N. batangarum CBS 124923
N. batangarum CBS 124924 T
N. ribis CBS 121.26
N. ribis CBS 115475 T
N. occultatum MUCC 286
N. occultatum CBS 128008 T
CERC2005 T
CERC2265
CERC3416
CERC3451
N. sinoeucalypti sp. nov. (Group K)
N. cordaticola CBS 123634 T
N. cordaticola CBS 123635
N. kwambonambiense CBS 123639 T
N. kwambonambiense CBS 123641
N. brasiliense CMM 1338 T
N. brasiliense CMM 1285
CERC3503
CERC3504
CERC2951
CERC3508
N. parvum (Group L)
N. parvum ATCC 58191 T
N. parvum CMW 9080
N. algeriense CBS 137504 T
N. algeriense CAA 322
CERC2967
CERC2968
CERC2973 T
N. hongkongense sp. nov. (Group J)
N. illicii CGMCC3.18310 T
N. illicii CGMCC3.18311
N. macroclavatum CBS 118223 T
N. nonquaesitum CBS 126655 T
N. nonquaesitum PD 301
N. arbuti CBS 116131 T
N. arbuti CBS 117090
N. andinum CBS 117452
N. andinum CBS 117453 T
N. grevilleae CBS 129518 T
N. mangiferae CBS 118531 T
N. mangiferae CBS 118532
CERC3497 T
CERC3498
N. microconidium sp. nov. (Group I)
N. eucalyptorum CMW 10126
N. eucalyptorum CBS 115791 T
N. eucalypticola CBS 115679 T
N. eucalypticola CBS 115766
N. australe CBS 110865
N. australe CMW 6837 T
N. stellenboschiana CBS 110864 T
N. lumnitzera CMW 41469 T
N. lumnitzera CMW 41228
N. mangroviorum CMW 41365 T
N. mangroviorum CMW 42481
N. luteum CBS 562.92 T
N. cryptoaustrale CMW 23785 T
N. terminaliae CBS 125264
N. terminaliae CBS 125263 T
N. ursorum CMW 24480 T
N. ursorum CMW 23790
N. pistaciarum CBS 113083 T
N. pistaciarum CBS 113084
N. mediterraneum CBS 121718 T
N. viticlavatum CBS 112878 T
N. viticlavatum CBS 112977
N. vitifusiforme CBS 110887 T
N. vitifusiforme CBS 110880
N. hellenicum CERC1947 T
N. hellenicum CERC1948
N. pistaciae CBS 595.76 T
N. protearum CBS 114176 T
N. protearum CBS 111200
N. pennatisporum WAC 13153 T
N. buxi CBS 116.75 T
N. buxi CBS 113714
B. dothidea CBS 115476
0.01

showed that the six Chinese isolates in Group A are most closely related to *B. fabicerciana* and *B. fusispora* (Fig. 2a–f). The analyses of the combination of ITS, *tef1* and *tub* sequences indicated that the six isolates are not forming a well-resolved clade, but are phylogenetically more closely related to *B. fusispora* than to *B. fabicerciana* (Fig. 2g). Based on the phylogenetic analyses for ITS, *tef1*, *tub*, *rpb2*, LSU, SSU and the combination of the ITS, *tef1* and *tub* sequences, the six isolates were identified as *B. fusispora*.

Isolates in Group B (CERC2001, CERC2983 and CERC3452) and Group C (CERC2946 and CERC2947) were found to be consistently distinct from other known phylogenetically related species of *Botryosphaeria* by congruent distinction in the multiple datasets (Group B: ITS, *tef1*, *rpb2* and LSU datasets; Group C: ITS, *tef1* and *rpb2* datasets) (Fig. 2a–f). The analyses of the combination of ITS, *tef1* and *tub* sequences indicated that the isolates in Group B and Group C form two well-resolved clades supported by relatively high bootstrap values (Fig. 2g). Isolates in Groups B and C represent two previously undescribed species of *Botryosphaeria*.

The phylogenetic analyses based on ITS, *tef1*, *tub*, *rpb2*, LSU and SSU sequences consistently showed that three isolates (CERC2298, CERC2299 and CERC2300) in Group D were phylogenetically most closely related to *B. auasmontanum*, *B. dothidea*, *B. minutispermatia* and *B. sinensia* (Fig. 2a–f). The analyses of combined ITS, *tef1* and *tub* sequences showed that isolates in Group D form one well-resolved clade (Fig. 2g). Isolates in Group D were identified as a new species of *Botryosphaeria*.

Species residing in Cophinforma

The BLAST results for ITS sequences show that isolates CERC3482, CERC3484, CERC3489 and CERC3490 (Group E) are related to the genus *Cophinforma*. Only two species of *Cophinforma* have previously been described, *Cophinforma atrovirens* (Mehl et al. 2011, Phillips et al. 2013) and *C. mamane* (Gardner 1997, Phillips et al. 2013). The two species of *Cophinforma* are morphologically very similar, but can be distinguished based on ITS sequence data. BLAST results of the ITS sequences indicate that the four Chinese isolates are more closely related to *C. atrovirens* than to *C. mamane*. A BLAST search of the *tef1* sequences show that the Chinese isolates and the ex-type isolate of *C. atrovirens* (CBS 124934) are identical. *Cophinforma mamane* does not have a *tef1* sequence and cultures are not available (Phillips et al. 2013). Based on the sequence comparisons of the ITS and *tef1* regions (*tub* gene sequences are not available for species of *Cophinforma*), isolates in Group E were identified as *C. atrovirens* (Fig. 2a–b, g).

Species residing in Lasiodiplodia

The isolates in our study that clustered in the genus *Lasiodiplodia* grouped into three phylogenetic groups for the *tef1* dataset (Group F: CERC2284; Group G: CERC2024, CERC3420, CERC3513, CERC3516; Group H: CERC2286, CERC2962, CERC3495) (Fig. 3b), and two clades (Group F = Group G; Group H) for the ITS, *tub*, *rpb2*, *cmdA*, LSU and SSU datasets (Fig. 3a, c–g). For Group F, the sequence analyses of the ITS, *tef1*, *tub*, *rpb2*, *cmdA* datasets showed that the Chinese isolates clustered into the same (ITS, *tef1*, *rpb2* and *cmdA*) clade or close (*tub*) to *L. brasiliense* (LSU and SSU sequences are not available to *L. brasiliense*) (Fig. 3a–g). The analyses indicated that isolates in Group G and Group H clustered into the same (ITS, *tub*, *rpb2*, *cmdA*, LSU and SSU) clade or close (*tef1*) to *L. theobromae* and *L. pseudotheobromae*, respectively (Fig. 3a–g). The analyses of the combination of the ITS, *tef1*, *tub*, *rpb2* and *cmdA* sequences indicated that the isolates in Groups F, G and H are phylogenetically most closely related to *L. brasiliense*, *L. theobromae* and *L. pseudotheobromae*, respectively (Fig. 3h). Altogether, the results of these phylogenetic analyses identified isolates in Groups F, G and H as *L. brasiliense*, *L. theobromae* and *L. pseudotheobromae*, respectively.

Species residing in Neofusicoccum

For the Chinese isolates that grouped in the genus *Neofusicoccum*, the isolates in this study clustered into four phylogenetic groups for the ITS, *tef1*, *tub* and *rpb2* datasets (Group I: CERC3497, CERC3498; Group J: CERC2967, CERC2968, CERC2973; Group K: CERC2005, CERC2265, CERC3416, CERC3451; Group L: CERC2951, CERC3503, CERC3504, CERC3508) (Fig. 4a–d). The Chinese *Neofusicoccum* isolates clustered into three groups (Group I, Group J = Group K, Group L) for the LSU dataset, and two groups (Group I, Group J = Group K = Group L) for the SSU dataset (Fig. 4e–f).

Previous studies have shown that phylogenetic analyses of the ITS, *tef1*, *tub* and *rpb2* sequences, especially a combination of the four gene sequences, is an efficient method for species identification in *Neofusicoccum* (Pavlic et al. 2009a, Sakalidis et al. 2011, Osorio et al. 2017). The isolates in each of Group I and J were found to be consistently distinct from other known phylogenetically closely related species of *Neofusicoccum* by congruent distinction in all the ITS, *tef1*, *tub* and *rpb2* datasets (Fig. 4a–d). Isolates in Group K formed a single independent clade that was distinct from any known *Neofusicoccum* species in the *tef1* and *rpb2* datasets (Fig. 4b, d). The analyses of the combination of the ITS, *tef1*, *tub* and *rpb2* sequences indicated that isolates in each of Groups I, J and K formed a well-resolved clade that was distinct from any described *Neofusicoccum* species which are supported by high bootstrap values (Fig. 4g). Therefore, we considered isolates in Groups I, J and K to represent three undescribed species of *Neofusicoccum*.

The Chinese isolates in Group L grouped in the same clade as *N. parvum* based on the ITS, *tub*, *rpb2*, LSU and SSU sequence analyses (Fig. 4a, c–f), and close to *N. parvum* on the *tef1* sequence analysis (Fig. 4b). In the phylogenetic analyses combining four gene regions, isolates in Group L were identified as *N. parvum* (Fig. 4g).

Morphology and taxonomy

Representative isolates (Table 1, 4) selected for morphological studies produced asexual fruiting structures on pine needles on WA media within 4–6 wk. No sexual structures were observed during the same period of time. For the 12 phylogenetic groups of *Botryosphaeriaceae* which were distinguished by DNA sequences, morphological studies, including culture and conidia characteristics, show that isolates in each of Group A, E, F, G, H and L were morphologically similar to the type specimens linked to it via sequence data, especially in the morphological characterisation of conidia (Table 4), namely *B. fusispora*, *C. atrovirens*, *L. brasiliense*, *L. theobromae*, *L. pseudotheobromae* and *N. parvum*, respectively. For phylogenetic groups B, C, D, I, J and K, morphological differences were observed compared to the phylogenetically most closely related species based on sequence data, and consequently each of the six groups were considered as new species. Based on the phylogenetic analyses and the morphological characteristics, the fungi collected from *Eucalyptus* and other plants in this study represent 12 species of *Botryosphaeriaceae*, including six previously undescribed species. These new species are described as follows.

Table 4 Conidial measurements of *Botryosphaeriaceae* species examined in this study and comparison with measurements described in previous studies.

Species[1]	Conidial size (μm) (L × W)[2]	Mean (μm) (L × W)[3]	L/W[4]	Reference
Botryosphaeria auasmontanum	(8.1–)8.8–11.3(–13) × (2.5–)2.9–3.9(–5)	10.1 × 3.4	3.0	Slippers et al. (2014)
B. corticis	(20.5–)23.5–32.5(–34.5) × (5.0–)5.5–7(–7.5)	28.9 × 6.4	4.5	Phillips et al. (2006)
B. dothidea	(20–)23–27(–30) × 4–5(–6)	26.2 × 5.4	4.9	Slippers et al. (2004a)
B. fabicerciana	(16.5–)19.5–24.5(–26) × (4.5–)5–6.5(–7.5)	22.0 × 5.8	3.8	Chen et al. (2011c)
B. fusispora	**(16.5–)19–23.5(–28.5) × 5–6(–8)**	**21.2 × 5.6**	**3.8**	**This study**
B. fusispora	16–22 × 4–5.5	20.0 × 5.0	4.0	Liu et al. (2012)
B. kuwatsukai	(18.5–)20–24.5(–26) × 5–7(–8)	22.3 × 6.2	3.6	Xu et al. (2015a)
B. minutispermatia	8–14 × 3–4	13.0 × 3.5	3.7	Ariyawansa et al. (2016)
B. pseudoramosa[5]	**(8–)10–13(–16) × (4–)4.5–5(–6)**	**11.5 × 4.6**	**2.5**	**This study**
B. qingyuanensis[5]	**(15–)19.5–24.5(–28.5) × (5–)6–6.5(–7.5)**	**22.0 × 6.2**	**3.5**	**This study**
B. ramosa	(11–)12–15(–16) × (4.7–)5–6(–7)	13.5 × 5.5	2.3	Pavlic et al. (2008)
B. rosaceae	20–31 × 6–8	26.2 × 6.7	3.9	Zhou et al. (2017)
B. scharifii	(11.5–)13–17(–19) × 4–6.5	15.4 × 5.2	2.7	Abdollahzadeh et al. (2013)
B. sinensia	(15–)19–29 × 5–7	24.3 × 5.9	4.1	Zhou et al. (2016)
B. wangensis[5]	**(20.5–)22–26(–29) × (4.5–)5.5–6.5(–7.5)**	**23.8 × 6.0**	**3.9**	**This study**
Lasiodiplodia brasiliense	22.7–29.2 × 11.7–17	26.0 × 14.6	1.8	Netto et al. (2014)
L. brasiliense	**(22–)25–27(–28) × (12–)13.5–15(–15.5)**	**26.0 × 14.4**	**1.8**	**This study**
L. pseudotheobromae	(22.5–)23.5–32(–33) × (13.5–)14–18(–20)	28.0 × 16.0	1.7	Alves et al. (2008)
L. pseudotheobromae	**(22.5–)24.5–28.5(–31.5) × (12–)13–15(–16)**	**26.5 × 13.8**	**1.9**	**This study**
L. theobromae	(19–)21–31(–32.5) × (12–)13–15.5(–18.5)	26.2 × 14.2	1.9	Alves et al. (2008)
L. theobromae	**(21–)24–26.5(–29.5) × (11–)12.5–14(–16)**	**25.3 × 13.1**	**1.9**	**This study**
Neofusicoccum algeriense	(14.5–)17–18(–21) × (4.5–)5.5–5.7(–6.5)	17.6 × 5.6	3.1	Berraf-Tebbal et al. (2014)
N. batangarum	(12–)14–17.5(–20) × (4–)4.5–6(–6.5)	15.5 × 5.5	2.9	Begoude et al. (2010)
N. cordaticola	18–28 × 4.5–7	23.3 × 5.3	4.3	Pavlic et al. (2009b)
N. hongkongense[5]	**(11.5–)13–15.5(–17.5) × (4–)4.5–5(–5.5)**	**14.1 × 4.7**	**3.0**	**This study**
N. kwambonambiense	16–28 × 5–8	22.3 × 6.3	3.6	Pavlic et al. (2009b)
N. microconidium[5]	**(10–)11.5–13(–14.5) × (4–)4.5–5.5(–6)**	**12.3 × 5.0**	**2.5**	**This study**
N. mangiferae	(11–)12–15(–17.5) × 5–6.6	13.6 × 5.4	2.0–2.5	Slippers et al. (2005)
N. occulatum	14–22 × 3.5–7.5	18.3 × 5.2	3.5	Sakalidis et al. (2011)
N. parvum	(12–)13.5–21(–24) × 4–6(–10)	17.1 × 5.5	3.2	Phillips et al. (2013)
N. parvum	**(15.5–)16.5–19(–21) × (4.5–)5–6(–6.5)**	**17.9 × 5.5**	**3.3**	**This study**
N. ribis	(16–)19–23(–24) × 5–6(–7)	20.8 × 5.5	3.8	Slippers et al. (2004a)
N. sinense	(15.2–)17.6–20.4(–23) × (6.9–)7.4–8(–9)	18.7 × 7.7	2.4	Zhang et al. (2017)
N. sinoeucalypti[5]	**(13–)15–20.5(–25.5) × (4–)5–5.5(–6.5)**	**17.7 × 5.2**	**3.4**	**This study**
N. umdonicola	15–23.5 × 4.5–6.5	19.4 × 5.5	3.5	Pavlic et al. (2009b)

[1] Isolates and measurements in **bold** were examined in this study.
[2] Minimum–(average – standard deviation)–(average + standard deviation)–maximum or minimum–maximum, L × W = length × width.
[3] L × W = average length × average width.
[4] L/W = average length/average width.
[5] Novel species described in this study.

TAXONOMY

Botryosphaeria pseudoramosa G.Q. Li & S.F. Chen, *sp. nov.* — MycoBank MB822323; Fig. 5

Etymology. Named for its phylogenetic resemblance to *B. ramosa*.

Sexual morph unknown. *Conidiomata* pycnidial, produced on pine needles on WA within 2–4 wk, globose to ovoid, dark brown to black, up to 698 μm wide, sometimes with a neck up to 1 660 μm long, arising from the substrate, covered by hyphal hairs, embedded in needle tissue, semi-immersed to superficial, unilocular, with a central ostiole. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, discrete, hyaline, cylindrical to lageniform, phialidic with periclinal thickening, (10–)11–16(–22.5) × (1–)2–3.5(–4) μm. *Paraphyses* not seen. *Conidia* hyaline, thin-walled, smooth with granular contents, unicellular, aseptate ellipsoid to fusoid, base subtruncate to bluntly rounded, (8–)10–13(–16) × (4–)4.5–5(–6) μm (av. = 11.5 × 4.6 μm, n = 100; L/W = 2.5) (Table 4).

Culture characteristics — Colonies on MEA have fluffy mycelia with an uneven margin and a few cottony aerial mycelia reaching to the lid of the Petri plate, with an appressed mycelial mat that is sparse to moderately dense. Colony mycelia initially white, becoming smoke grey (21'''f) to pale mouse grey (15'''d) at the surface and olivaceous (21''k) to iron grey (23'''k) at the reverse within 10–14 d. Optimal growth temperature is 30 °C, covering the 90 mm plates after 5 d. No growth at 5 °C. After 5 d, colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C, 35 °C and 40 °C reached 17 mm, 20 mm, 64 mm, 80 mm, 87 mm, 33 mm and 8 mm, respectively.

Specimens examined. China, GuangXi, from twigs of one *Eucalyptus* tree, fruiting structures induced on needles of *Pinus* sp. on water agar, 24 May 2014, *S.F. Chen & G.Q. Li* (holotype CSFF2025, culture ex-type CERC2001 = CGMCC3.18739); GuangDong, from twigs of one *Eucalyptus* tree, 24 May 2014, *S.F. Chen & G.Q. Li* (CSFF2026, culture CERC3455 = CGMCC3.18741); GuangDong, from twigs of one *Melastoma sanguineum* plant, 17 Mar. 2014, *S.F. Chen* (CSFF2027, culture CERC2983 = CGMCC3.18740).

Notes — *Botryosphaeria pseudoramosa* is phylogenetically closely related to *B. ramosa* and *B. scharifii*. *Botryosphaeria pseudoramosa* can be distinguished from *B. ramosa* and *B. scharifii* based on the morphology of their conidia. Conidia of *B. pseudoramosa* (av. 11.5 × 4.6; L/W = 2.5) are smaller than *B. ramosa* (av. 13.5 × 5.5; L/W = 2.3) (Pavlic et al. 2008) and *B. scharifii* (av. 15.4 × 5.2; L/W = 2.7) (Abdollahzadeh et al. 2013) (Table 4).

Botryosphaeria qingyuanensis G.Q. Li & S.F. Chen, *sp. nov.* — MycoBank MB822324; Fig. 6

Etymology. Named for the QingYuan Region where the fungus was isolated for the first time.

Sexual morph unknown. *Conidiomata* pycnidial, produced on pine needles on WA within 2–4 wk, solitary, globose to ovoid, dark brown to black, up to 317 μm wide, 229 μm high, embedded in needle tissue, semi-immersed to superficial, unilocular, with a central ostiole. *Conidiophores* absent. *Conidiogenous cells* holoblastic, discrete, hyaline, cylindrical to lageniform, phialidic with periclinal thickening, (7–)7.5–12(–14.5) × (2–)2.5–3.5 μm. *Paraphyses* not seen. *Conidia* hyaline, thin-walled, smooth with

granular contents, unicellular, aseptate narrowly fusiform, base subtruncate to bluntly rounded, (15–)19.5–24.5(–28.5) × (5–)6–6.5(–7.5) µm (av. = 22 × 6.2 µm, n = 100; L/W = 3.5) (Table 4).

Culture characteristics — Colonies on MEA have fluffy mycelia with an uneven margin and few cottony aerial mycelia reaching to the lid of the Petri plate, with an appressed mycelial mat that is sparse to moderately dense. Colony mycelia initially white, becoming smoke grey (21""f) to pale mouse grey (15""d) at the surface and smoke grey (21""f) to iron grey (23""k) at the reverse within 10–14 d. Optimal growth temperature is (25–)30 °C, reaching the edge of the 90 mm plates after 5 d. No growth is observed at 5 °C and 40 °C. After 5 d, colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C and 35 °C reach 14 mm, 22 mm, 52 mm, 73 mm, 74 mm and 12 mm, respectively.

Specimens examined. China, GuangDong, from twigs of one *Eucalyptus* tree, fruiting structures induced on needles of *Pinus* sp. on water agar, 4 Dec. 2013, *S.F. Chen & G.Q. Li* (holotype CSFF2028, culture ex-type CERC2946 = CGMCC3.18742); GuangDong, from twigs of one *Eucalyptus* hybrid tree, fruiting structures induced on needles of *Pinus* sp. on water agar, 4 Dec. 2013, *S.F. Chen & G.Q. Li* (CSFF2029, culture CERC2947 = CGMCC3.18743).

Notes — *Botryosphaeria qingyuanensis* is phylogenetically closely related to *B. corticis*, *B. fabicerciana*, *B. fusispora*, *B. kuwatsukai* and *B. rosaceae*, but can be distinguished from these species based on morphological or growth characteristics. Conidia of *B. qingyuanensis* (av. 22 × 6.2; L/W = 3.5) are wider than these of *B. fabicerciana* (av. 22 × 5.8; L/W = 3.8) and the optimal growth temperature of *B. qingyuanensis* ((25–)30 °C) is different from that of *B. fabicerciana* (25(–30) °C) (Chen et al. 2011c). Conidia of *B. qingyuanensis* are longer and wider than *B. fusispora* (av. 20 × 5; L/W = 4) (Liu et al. 2012). Conidia of *B. qingyuanensis* are smaller than *B. corticis* (av. 28.9 × 6.4; L/W = 4.5) (Phillips et al. 2006) and *B. rosaceae* (av. 26.2 × 6.7; L/W = 3.9) (Zhou et al. 2017). Conidia of *B. qingyuanensis* are slightly shorter than *B. kuwatsukai* (av. 22.3 × 6.2; L/W = 3.6) (Xu et al. 2015a) and no conidia or microconidia are observed for *B. qingyuanensis*, but conidia with 1–3 septa before germination and microconidia (3–8 × 1–2 µm) have been found for *B. kuwatsukai* (Xu et al. 2015a) (Table 4).

Botryosphaeria wangensis G.Q. Li & S.F. Chen, *sp. nov.* — MycoBank MB822325; Fig. 7

Etymology. Named after the Wang village where the fungus was isolated for the first time.

Sexual morph unknown. *Conidiomata* pycnidial, produced on pine needles on WA within 2–4 wk, solitary, globose to ovoid, dark brown to black, up to 698 µm wide, 484 µm high, embedded in needle tissue, semi-immersed to superficial, unilocular, with a central ostiole, exuding conidia in a yellow mucoid mass. *Conidiophores* absent. *Conidiogenous cells* holoblastic, discrete, hyaline, cylindrical to lageniform, phialidic with periclinal thickening, (6–)8.5–13.5(–15) × 2–3(–3.5) µm. *Paraphyses* not seen. *Conidia* hyaline, thin-walled, smooth with granular contents, unicellular, aseptate, becoming 1-septate before germination, narrowly fusiform, base subtruncate to bluntly rounded, (20.5–)22–26(–29) × (4.5–)5.5–6.5(–7.5) µm (av. = 23.8 × 6 µm, n = 100; L/W = 3.9) (Table 4). *Spermatophores* hyaline, smooth, branched, cylindrical to subcylindrical (Fig. 7f). *Spermatogenous cells* discrete or integrated, hyaline, smooth, cylindrical, producing spermatia on their tips, holoblastic or proliferating via phialides with periclinal thickenings, 6.5–16 × 1.5–2.5 µm. *Spermatia* unicellular, aseptate, hyaline, thin-walled, allantoid to rod-shaped, 3.5–4.5 × 1–1.5 µm, L/W = 2.9.

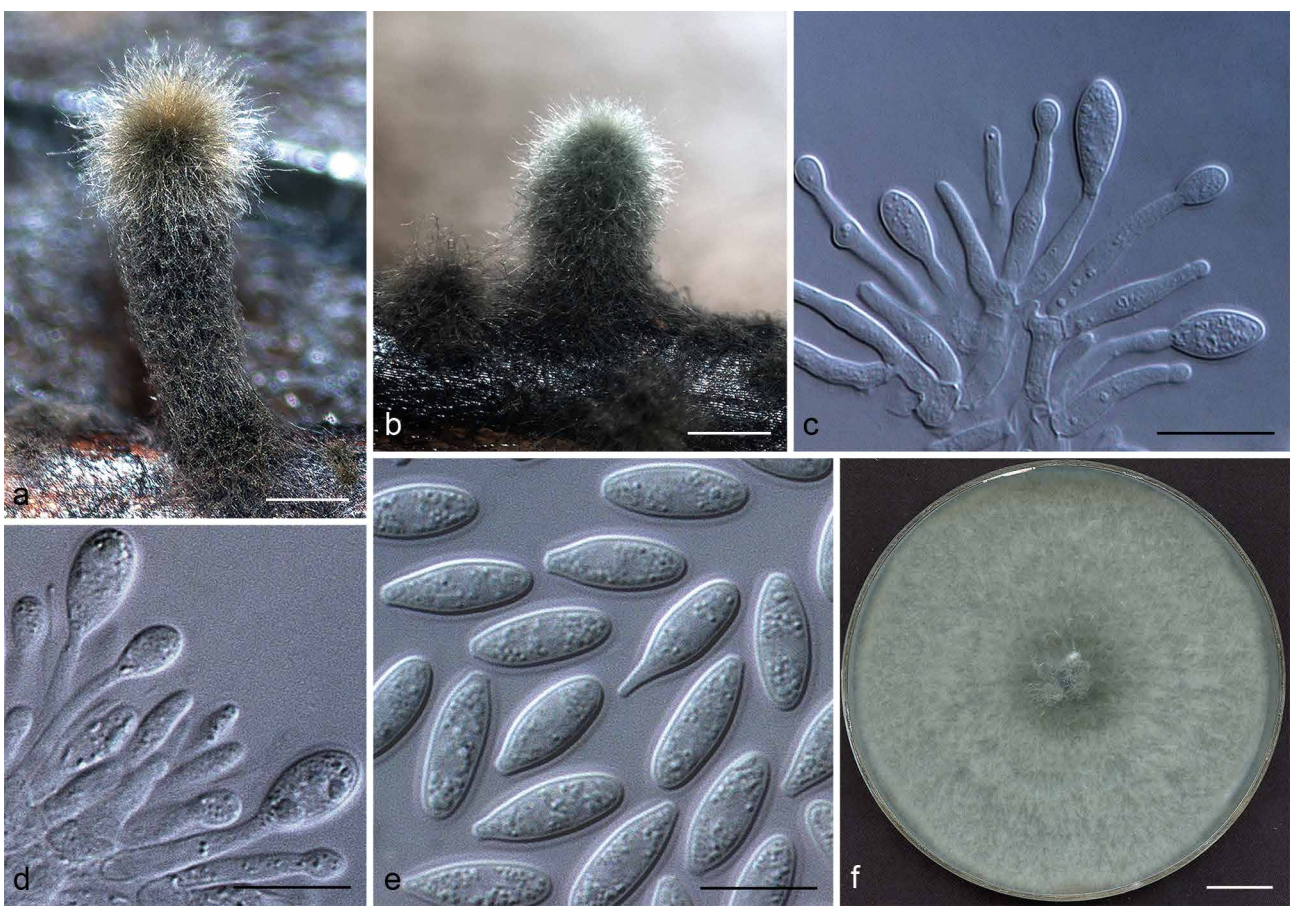


Fig. 5 *Botryosphaeria pseudoramosa*. a–b. Conidiomata formed on pine needle culture; c–d. conidiogenous cells and developing conidia; e. conidia; f. living culture after 10 d on 2 % MEA (front). — Scale bars: a–b = 500 µm; c–e = 10 µm; f = 1 cm.

Culture characteristics — Colonies on MEA have fluffy mycelia with an uneven margin and a few cottony aerial mycelia reaching to the lid of the Petri plate, with an appressed mycelial mat that is sparse to moderately dense. Colony mycelia initially white, becoming smoke grey (21’’’’f) to mouse grey (13’’’’i) at the surface and olivaceous grey (21’’’’i) to iron grey (23’’’’k) at the reverse within 10–14 d. Optimal growth temperature is 30 °C, covering the 90 mm plates after 5 d. No growth at 5 °C and 40 °C. After 5 d, colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C and 35 °C reach 15 mm, 21 mm, 50 mm, 69 mm, 89 mm and 24 mm, respectively.

Specimens examined. China, HeNan, from twigs of one *Cedrus deodara* tree, fruiting structures induced on needles of *Pinus* sp. on water agar, 26 Nov. 2013, *S.F. Chen* (holotype CSFF2030, culture ex-type CERC2298 = CGMCC3.18744); HeNan, from twigs of one *Cedrus deodara* tree, 26 Nov. 2013, *S.F. Chen* (CSFF2031, culture CERC2300 = CGMCC3.18746).

Notes — *Botryosphaeria wangensis* is phylogenetically closely related to *B. auasmontanum*, *B. dothidea*, *B. minutispermatia* and *B. sinensia*. *Botryosphaeria wangensis* can be distinguished from its phylogenetically closely related species by the size of their conidia. Conidia of *B. wangensis* (av. 23.8 × 6; L/W = 3.9) are longer and wider than those of *B. auasmontanum* (av. 10.1 × 3.4; L/W = 3) (Slippers et al. 2014) and *B. minutispermatia* (av. 13 × 3.5; L/W = 3.7) (Ariyawansa et al. 2016) and shorter and wider than those of *B. dothidea* (av. 26.2 × 5.4; L/W = 4.9) (Slippers et al. 2004a) and *B. sinensia* (av. 24.3 × 5.9; L/W = 4.1) (Zhou et al. 2016) (Table 4).

Fig. 6 *Botryosphaeria qingyuanensis*. a. Conidiomata formed on pine needle culture; b–c. conidiogenous cells and developing conidia; d. conidia; e. living culture after 10 d on 2 % MEA (front). — Scale bars: a = 500 µm; b–d = 10 µm; e = 1 cm.

Neofusicoccum hongkongense G.Q. Li & S.F. Chen, *sp. nov.* — MycoBank MB822328; Fig. 8

Etymology. Named after the Hong Kong Region where it was isolated for the first time.

Sexual morph unknown. *Conidiomata* pycnidial, produced on pine needles on WA within 2–4 wk, solitary, globose to ovoid, dark brown to black, up to 694 µm wide, up to 776 µm high, embedded in needle tissue, semi-immersed to superficial, unilocular, with a central ostiole. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* holoblastic, discrete, hyaline, cylindrical, phialidic with periclinal thickening, (9.5–)12–18.5(–22) × (1.5–)2–2.5(–3) µm. *Paraphyses* not seen. *Conidia* hyaline, thin-walled, smooth with granular contents, unicellular, aseptate narrowly fusiform, base subtruncate to bluntly rounded, (11.5–)13–15.5(–17.5) × (4–)4.5–5(–5.5) µm (av. = 14.1 × 4.7 µm, n = 100; L/W = 3) (Table 4).

Culture characteristics — Colonies on MEA have fluffy mycelia with an uneven margin and a few cottony aerial mycelia reaching to the lid of the Petri plate, with an appressed mycelial mat that is sparse to moderately dense. Colony mycelia initially white, becoming smoke grey (21''''f) to grey olivaceous (21''''b) at the surface and grey olivaceous (21''''b) to olivaceous grey (21''''i) at the reverse within 10–14 d. Optimal growth temperature is 25 °C, covering the 90 mm plates after 5 d. No growth at 5 °C or 40 °C. After 5 d, colonies grown at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C and 35 °C reach 25 mm, 41 mm, 66 mm, 90 mm, 84 mm and 9 mm, respectively.

Specimens examined. China, Hong Kong, from twigs of *Araucaria cunninghamii*, fruiting structures induced on needles of *Pinus* sp. on water agar, 11 Mar. 2014, *S.F. Chen* (holotype CSFF2034, culture ex-type CERC2973 = CGMCC3.18749); Hong Kong, from twigs of *Araucaria cunninghamii*, 11 Mar. 2014, *S.F. Chen* (CSFF2035, culture CERC2968 = CGMCC3.18748).

Notes — Based on phylogenetic analyses, *N. hongkongense* phylogenetically clustered in the *N. parvum*/*N. ribis* species complex. *Neofusicoccum hongkongense* can be distinguished from other species in the *N. parvum*/*N. ribis* complex by the size and shape of their conidia. The conidia of *N. hongkongense*

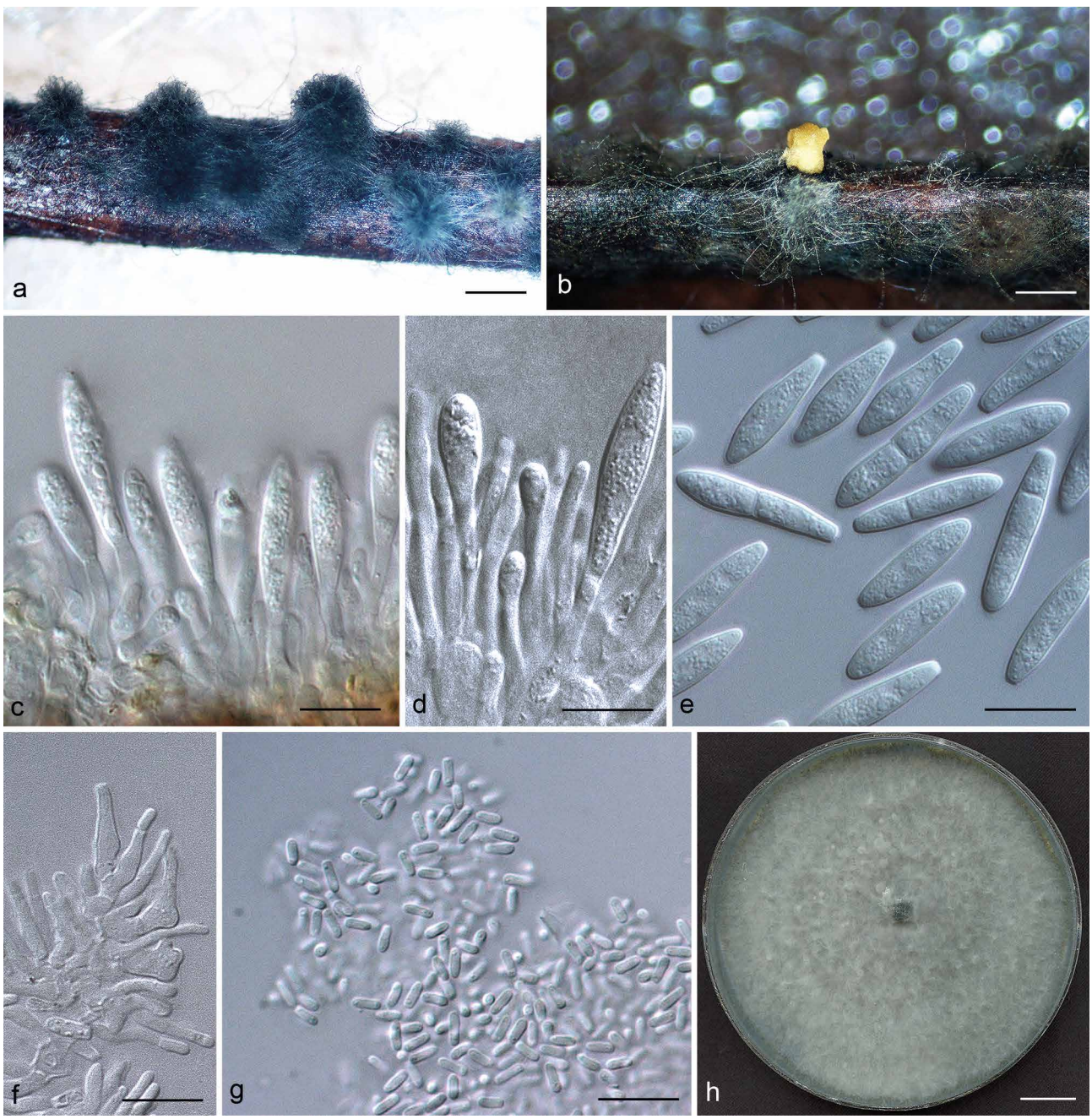


Fig. 7 *Botryosphaeria wangensis*. a–b. Conidiomata on pine needle culture; c–d. conidiogenous cells and developing conidia; e. conidia with 1 septum; f. spermatogenous cells; g. spermatia; h. living culture after 10 d on 2 % MEA (front). — Scale bars: a–b = 500 µm; c–g = 10 µm; h = 1 cm.

(av. 14.1 × 4.7; L/W = 3) are shorter and narrower than those of *N. algeriense* (av. 17.6 × 5.6; L/W = 3.1) (Berraf-Tebbal et al. 2014), *N. batangarum* (av. 15.5 × 5.5; L/W = 2.9) (Begoude et al. 2010), *N. cordaticola* (av. 23.3 × 5.3; L/W = 4.3) (Pavlic et al. 2009b), *N. kwambonambiense* (av. 22.3 × 6.3; L/W = 3.6) (Pavlic et al. 2009b), *N. occulatum* (av. 18.3 × 5.2; L/W = 3.5) (Sakalidis et al. 2011), *N. parvum* (av. 17.1 × 5.5; L/W = 3.2) (Phillips et al. 2013), *N. ribis* (av. 20.8 × 5.5; L/W = 3.8) (Slippers et al. 2004a), *N. sinense* (av. 18.7 × 7.7; L/W = 2.4) (Zhang et al. 2017), *N. sinoeucalypti* (av. 17.7 × 5.2; L/W = 3.4) (this study) and *N. umdonicola* (av. 19.4 × 5.5; L/W = 3.5) (Pavlic et al. 2009b). The conidial size of *N. brasiliense* remains unknown (Marques et al. 2013) (Table 4).

Neofusicoccum microconidium G.Q. Li & S.F. Chen, *sp. nov.* — MycoBank MB822326; Fig. 9

Etymology. Named for the small conidia of this fungus.

Sexual morph unknown. *Conidiomata* pycnidial, produced on pine needles on WA within 2–4 wk, solitary, globose to ovoid, dark brown to black, up to 895 µm wide, 1729 µm high, embedded in needle tissue, semi-immersed to superficial, unilocular, with a central ostiole, exuding conidia in a white mucoid mass. *Conidiophores* reduced to *conidiogenous cells*. *Conidiogenous cells* holoblastic, discrete, hyaline, cylindrical, phialidic with periclinal thickening, (10.5–)12.5–18(–20.5) × (2–)2.5–3(–3.5) µm. *Paraphyses* not seen. *Conidia* hyaline, thin-walled, smooth with granular contents, unicellular, aseptate narrowly fusiform, base subtruncate to bluntly rounded, (10–)11.5–13(–14.5) × (4–)4.5–5.5(–6) µm (av. = 12.3 × 5 µm, n = 100; L/W = 2.5) (Table 4).

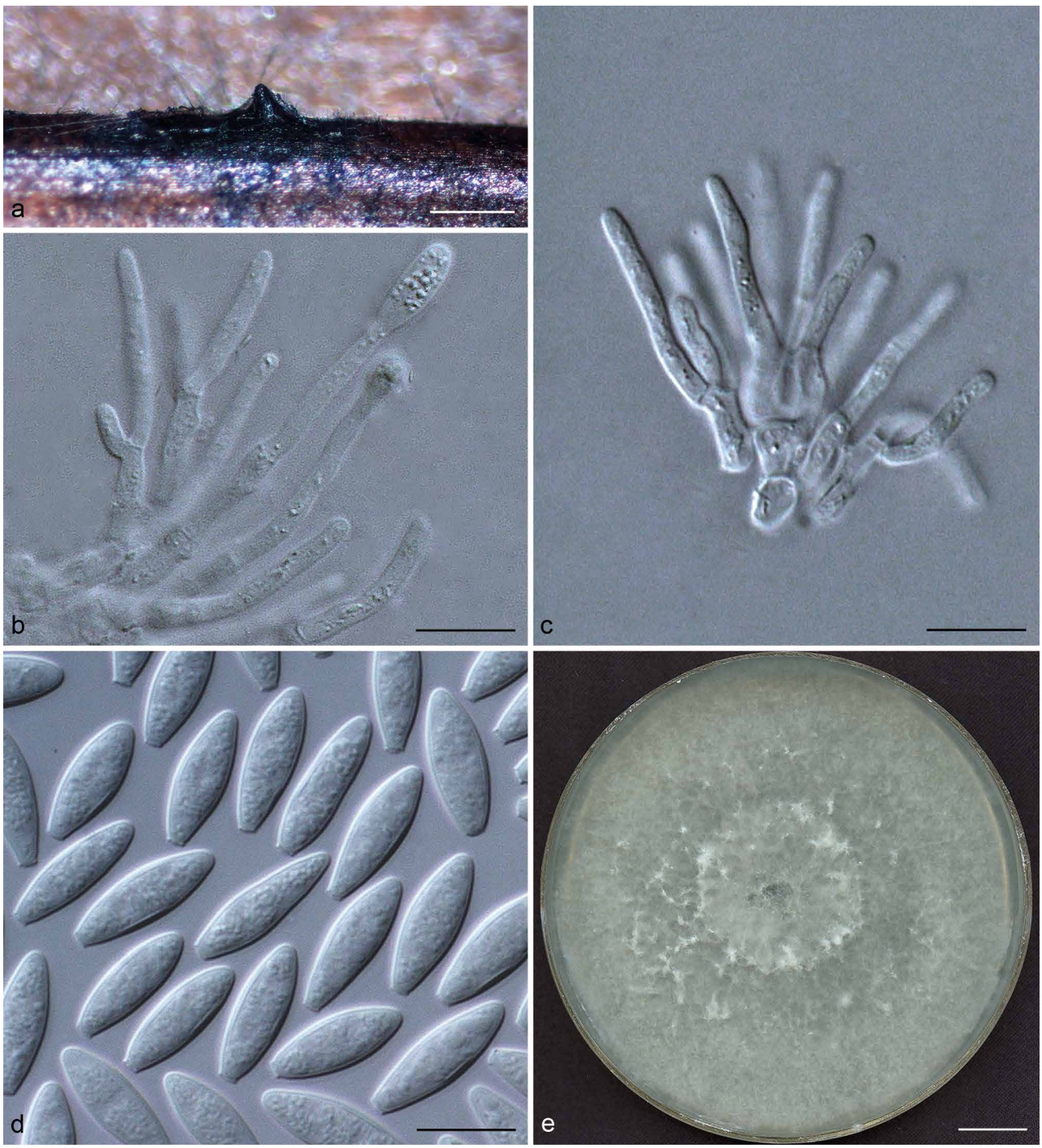


Fig. 8 *Neofusicoccum hongkongense*. a. Conidiomata formed on pine needle culture; b. conidiogenous cells and developing conidia; c. conidiogenous cells; d. conidia; e. living culture after 10 d on 2 % MEA (front). — Scale bars: a = 500 µm; b–d = 10 µm; e = 1 cm.

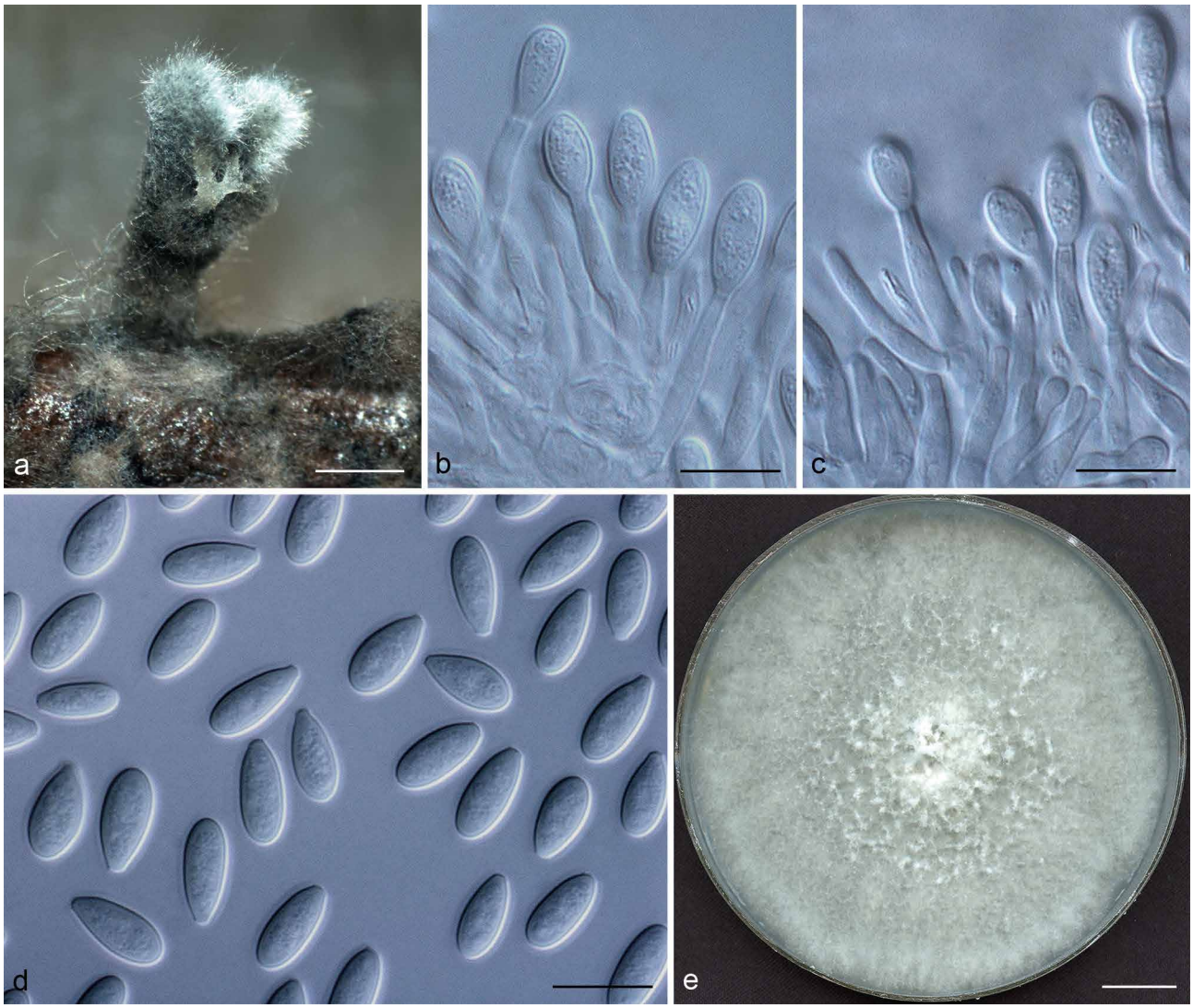


Fig. 9 *Neofusicoccum microconidium*. a. Conidiomata formed on pine needle culture; b–c. conidiogenous cells and developing conidia; d. conidia; e. living culture after 10 d on 2 % MEA (front). — Scale bars: a = 500 µm; b–d = 10 µm; e = 1 cm.

Culture characteristics — Colonies on MEA have fluffy mycelia with an uneven margin and a few cottony aerial mycelia reaching to the lid of the Petri plate, with an appressed mycelial mat that is sparse to moderately dense. Colony mycelia initially white, becoming pale mouse grey (15’’’’d) to olivaceous grey (21’’’’i) at the surface and olivaceous grey (21’’’’i) to iron grey (23’’’’k) at the reverse within 10–14 d. Optimal growth temperature is 30 °C, reaching the edge of the 90 mm plates after 5 d. No growth at 5 °C. After 5 d, colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C, 35 °C and 40 °C reach 24 mm, 34 mm, 66 mm, 74 mm, 86 mm, 36 mm and 8 mm, respectively.

Specimens examined. China, GuangDong, from twigs of *E. urophylla* × *E. grandis*, fruiting structures induced on needles of *Pinus* sp. on water agar, 22 July 2014, *S.F. Chen & G.Q. Li* (holotype CSFF2032, culture ex-type CERC3497 = CGMCC3.18750); GuangDong, from twigs of *E. urophylla* × *E. grandis*, 22 July 2014, *S.F. Chen & G.Q. Li* (CSFF2033, culture CERC3498 = CGMCC3.18751).

Notes — *Neofusicoccum microconidium* is phylogenetically closely related to *N. mangiferae*. The two species can be distinguished from each other based on conidial morphology. Conidia of *N. microconidium* (av. 12.3 × 5; L/W = 2.5) are smaller than those of *N. mangiferae* (av. 13.6 × 5.4; L/W = 2–2.5) (Slippers et al. 2005) (Table 4).

Neofusicoccum sinoeucalypti G.Q. Li & S.F. Chen, *sp. nov.* — MycoBank MB822327; Fig. 10

Etymology. Named after the host genus *Eucalyptus* from which it was isolated for the first time.

Sexual morph solitary, globose to ovoid, dark brown to black, up to 1 007 µm wide, 685 µm high, embedded in needle tissue, semi-immersed to superficial, unilocular, with a central ostiole. *Conidiophores* absent. *Conidiogenous cells* holoblastic, discrete, hyaline, cylindrical to lageniform, phialidic with periclinal thickening, (10–)10.5–11 × 2–3 µm. *Paraphyses* not seen. *Conidia* hyaline, thin-walled, smooth with granular contents, unicellular, aseptate, narrowly fusiform, base subtruncate to bluntly rounded, (13–)15–20.5(–25.5) × (4–)5–5.5(–6.5) µm (av. = 17.7 × 5.2 µm, n = 100; L/W = 3.4). *Spermatophores* hyaline, smooth, cylindrical to subcylindrical. *Spermatogenous cells* discrete or integrated, hyaline, smooth, cylindrical, producing spermatia on their tips, holoblastic or proliferating via phialides with periclinal thickenings, 8.5–15.5 × 1.5–2 µm. *Spermatia* unicellular, aseptate, hyaline, thin-walled, allantoid to rod-shaped, 2.5–4.5 × 1.5 µm, L/W = 2.1.

Culture characteristics — Colonies on MEA have fluffy mycelia with an uneven margin and a few cottony aerial mycelia that reach to the lid of the Petri plate, with an appressed mycelial mat that is sparse to moderately dense. Colony mycelia are initially

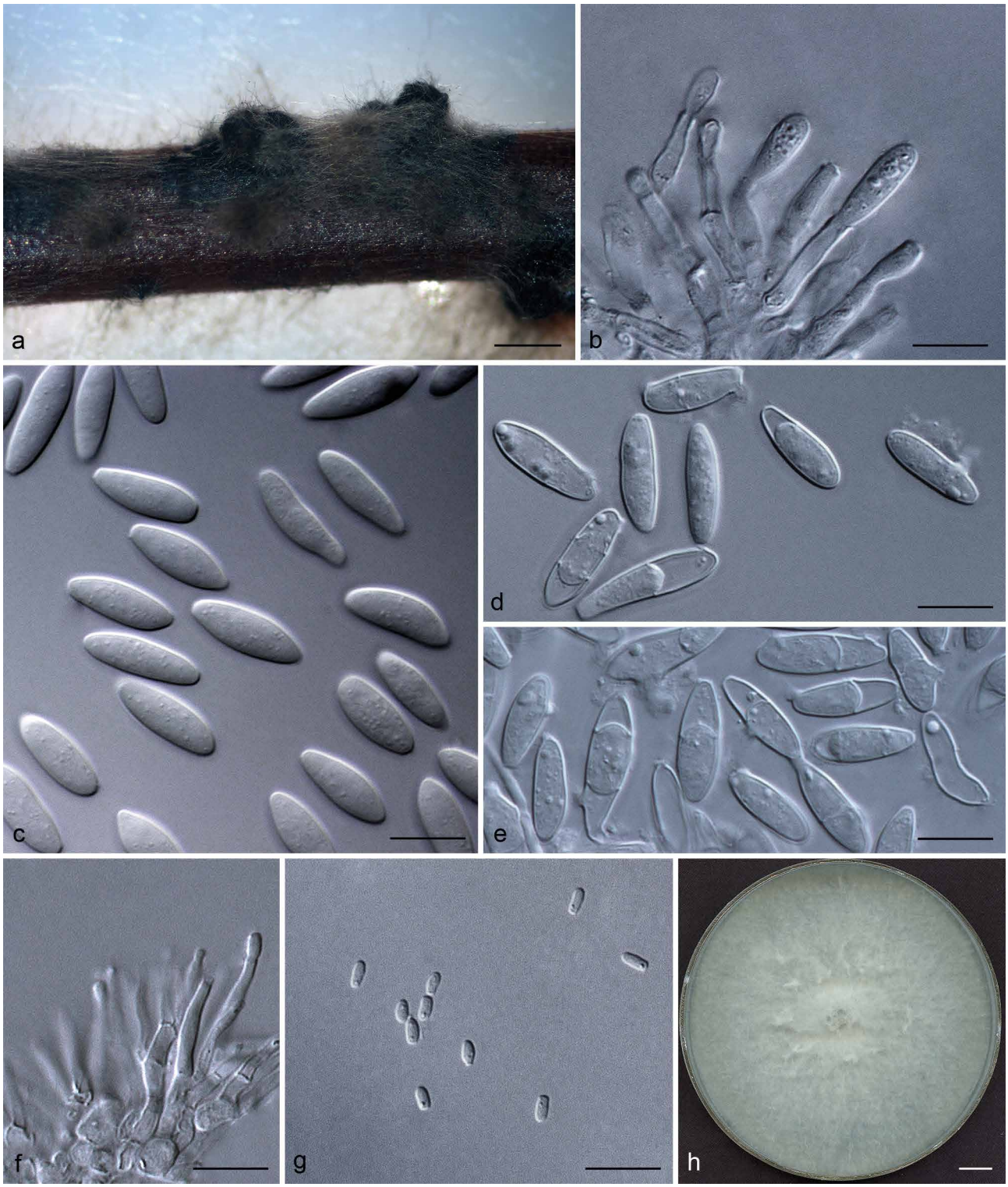


Fig. 10 *Neofusicoccum sinoeucalypti*. a. Conidiomata formed on pine needle culture; b. conidiogenous cells and developing conidia; c. immature conidia; d–e. mature conidia with 1–2 septa; f. spermatogenous cells; g. spermatia; h. living culture after 10 d on 2 % MEA (front). — Scale bars: a = 500 µm; b–g = 10 µm; h = 1 cm.

white, becoming pale mouse grey (15‴″d) to mouse grey (13‴″i) at the surface and olivaceous buff (21‴d) to iron grey (23‴″k) at the reverse within 10–14 d. Optimal growth temperature is 30 °C, reaching the edge of the 90 mm plates after 5 d. No growth at 5 °C or 40 °C. After 5 d, colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C and 35 °C reach 25 mm, 31 mm, 53 mm, 78 mm, 90 mm and 11 mm, respectively.

Specimens examined. China, GuangDong, from twigs of *E. urophylla* × *E. grandis*, fruiting structures induced on needles of *Pinus* sp. on water agar, 30 July 2013, *S.F. Chen & G.Q. Li* (holotype CSFF2036, culture ex-type CERC2005 = CGMCC3.18752); GuangXi, from twigs of *E. urophylla* × *E. grandis*, 25 Oct. 2013, *S.F. Chen & G.Q. Li* (CSFF2037, culture CERC2265 = CGMCC3.18753); GuangXi, from twigs of *Eucalyptus* hybrid, 22 May 2014, *S.F. Chen & G.Q. Li* (CSFF2038, culture CERC3416 = CGMCC3.18754).

Notes — *Neofusicoccum sinoeucalypti* clustered in the *N. parvum*/*N. ribis* species complex. Other species in this complex include *N. algeriense*, *N. batangarum*, *N. brasiliense*, *N. cordaticola*, *N. hongkongense* (this study), *N. kwambonambiense*, *N. occulatum*, *N. parvum*, *N. ribis* and *N. umdonicola*. For these species, except *N. brasiliense* (morphological data not available) (Marques et al. 2013), spermatia have been reported only in *N. sinoeucalypti* and are allantoid to rod-shaped. Conidia of

N. sinoeucalypti (av. 17.7 × 5.2; L/W = 3.4) are longer and wider than those of *N. hongkongense* (av. 14.1 × 4.7; L/W = 3), longer and narrower than those of *N. batangarum* (av. 15.5 × 5.5; L/W = 2.9) (Begoude et al. 2010) and *N. parvum* (av. 17.1 × 5.5; L/W = 3.2) (Phillips et al. 2013), shorter and narrower than those of *N. cordaticola* (av. 23.3 × 5.3; L/W = 4.3) (Pavlic et al. 2009b), *N. kwambonambiense* (av. 22.3 × 6.3; L/W = 3.6) (Pavlic et al. 2009b), *N. ribis* (av. 20.8 × 5.5; L/W = 3.8) (Slippers et al. 2004a), *N. sinense* (av. 18.7 × 7.7; L/W = 2.4) (Zhang et al. 2017) and *N. umdonicola* (av. 19.4 × 5.5; L/W = 3.5) (Pavlic et al. 2009b), shorter than those of *N. occulatum* (av. 18.3 × 5.2; L/W = 3.5) (Sakalidis et al. 2011), and narrower than those of *N. algeriense* (av. 17.6 × 5.6; L/W = 3.1) (Berraf-Tebbal et al. 2014). The optimal growth temperature of *N. sinoeucalypti* (30 °C) is different compared to *N. algeriense* (25 °C) (Berraf-Tebbal et al. 2014), *N. batangarum* (25 °C) (Begoude et al. 2010), *N. brasiliense* (27.7 °C) (Marques et al. 2013), *N. hongkongense* (25 °C) (this study), *N. occulatum* (25 °C) (Sakalidis et al. 2011) and *N. ribis* (25 °C) (Slippers et al. 2004a) (Table 4).

Distribution of Botryosphaeriaceae

According to the phylogenetic and morphological analyses of the 105 isolates collected in this study, twelve species of *Botryosphaeriaceae* were identified from seven hosts in the FuJian, GuangDong, GuangXi, HaiNan and HeNan Provinces and the Hong Kong Region of China (Fig. 11). These species include *B. fusispora* (21 isolates: all from *Eucalyptus* hybrids), *B. pseudoramosa* (12 isolates: 8 from *Eucalyptus* hybrids, 4 from *M. sanguineum*), *B. qingyuanensis* (2 isolates: both from one *Eucalyptus* hybrid), *B. wangensis* (3 isolates: all from *C. deodara*), *C. atrovirens* (5 isolates: all from *D. longan*), *L. brasiliense* (1 isolate: from a *Eucalyptus* hybrid), *L. pseudotheobromae* (19 isolates: 17 from unknown *Eucalyptus* hybrids, two from *E. urophylla* × *E. grandis*), *L. theobromae* (20 isolates: six from unknown *Eucalyptus* hybrids, five from *E. urophylla* × *E. grandis*, 2 from *C. lanceolata*, 5 from *D. longan*, 2 from *P. hanceana*), *N. hongkongense* (3 isolates: all from *A. cunninghamii*), *N. microconidium* (2 isolates: both from *E. urophylla* × *E. grandis*), *N. parvum* (6 isolates: all from *E. urophylla* × *E. grandis*) and *N. sinoeucalypti* (11 isolates: nine from *E. urophylla* × *E. grandis*, two from *Eucalyptus* hybrids) (Table 1, Fig. 11). The 81 isolates collected from *Eucalyptus* trees include nine species (except for *B. wangensis*, *C. atrovirens* and *N. hongkongense*) of *Botryosphaeriaceae*. Of these nine species from *Eucalyptus*, *B. fusispora* (26 % of the isolates), *L. pseudotheobromae* (23 % of the isolates) and *L. theobromae* (14 % of the isolates) are dominant and are distributed throughout the surveyed Provinces of South China. Of the 12 species of *Botryosphaeriaceae*, *L. theobromae* (isolated from *C. lanceolata*, *D. longan*, a *Eucalyptus* hybrid and *P. hanceana*) and *B. pseudoramosa* (isolated from a *Eucalyptus* hybrid and *M. sanguineum*) were collected from more than one plant host (Fig. 11).

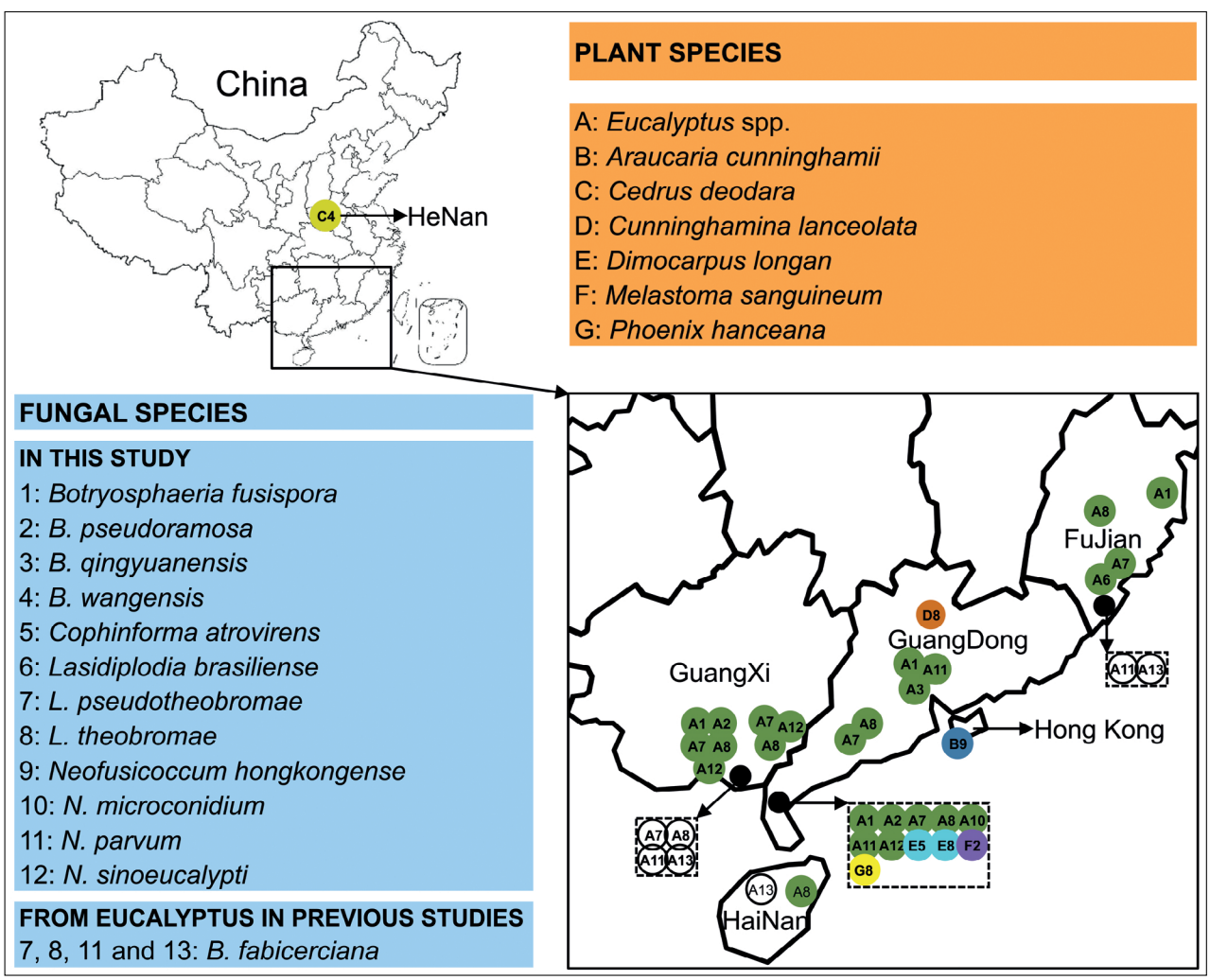


Fig. 11 Map showing the 12 species of *Botryosphaeriaceae* detected from different regions and plant hosts. The different *Botryosphaeriaceae* species are indicated as numbers 1 to 12; the plant hosts are shown as letters A to G. For example, A8 indicates *L. theobromae* (number 8 of fungal species) isolated from *Eucalyptus* spp. (letter A of plant species) in HaiNan Province. The pies in colours indicate *Botryosphaeriaceae* isolated from different plant hosts in this study, the pies without colour indicate *Botryosphaeriaceae* species reported from *Eucalyptus* in previous studies (Chen et al. 2011c, Li et al. 2015a).

Table 5 Average lesion length (mm) on seedlings of three *Eucalyptus* clones inoculated with *Botryosphaeriaceae*.

Species	Isolates	*Eucalyptus* clones		
		CEPT-11	CEPT-12	CEPT-13
Botryosphaeria fusispora	CERC1998	17.6 ± 1.8 m-p[1]	27.1 ± 9.3 k-p	10.6 ± 0.7 op
	CERC2274	10.3 ± 0.4 op	10.7 ± 0.4 op	9.2 ± 0.2 op
	CERC2930	12.3 ± 1.2 op	13.9 ± 2.4 m-p	14.5 ± 1.6 m-p
	CERC3446	12.0 ± 0.6 op	17.5 ± 4.5 m-p	15.5 ± 2.8 m-p
B. pseudoramosa	CERC2001	13.5 ± 0.8 n-p	15.5 ± 4.0 m-p	11.1 ± 0.5 op
	CERC3452	16.8 ± 2.0 m-p	26.9 ± 7.3 k-p	13.9 ± 1.9 m-p
B. qingyuanensis	CERC2946	10.4 ± 0.5 op	16.2 ± 5.6 m-p	11.1 ± 0.8 op
	CERC2947	11.0 ± 0.5 op	18.2 ± 5.2 l-p	10.4 ± 0.5 op
B. wangensis	CERC2298	10.6 ± 0.5 op	12.3 ± 0.8 op	10.0 ± 0.2 op
	CERC2299	9.3 ± 1.1 op	11.1 ± 0.3 op	9.8 ± 0.1 op
Cophinforma atrovirens	CERC3484	11.0 ± 1.5 op	10.0 ± 1.5 op	8.8 ± 1.1 op
	CERC3489	12.2 ± 0.7 op	9.2 ± 0.2 op	9.4 ± 0.3 op
Lasiodiplodia brasiliense	CERC2284	41.7 ± 5.6 j-m	139.7 ± 27.3 cd	95.8 ± 15.7 f
L. pseudotheobromae	CERC2286	90.7 ± 16.9 fg	84.5 ± 12.6 f-h	100.1 ± 21.8 ef
	CERC3417	78.4 ± 9.7 fg	121.0 ± 12.6 de	128.4 ± 12.2 d
	CERC3495	120.9 ± 11.5 de	138.1 ± 12.8 cd	85.9 ± 9.5 fg
L. theobromae	CERC3420	26.7 ± 2.3 k-p	46.6 ± 7.5 i-l	26.8 ± 5.6 k-p
	CERC3513	123.9 ± 16.0 d	150.7 ± 21.9 b	219.5 ± 19.8 a
	CERC3516	126.3 ± 13.1 d	142.0 ± 21.6 bc	173.5 ± 18.7 b
Neofusicoccum hongkongense	CERC2968	17.7 ± 1.2 m-p	12.9 ± 2.2 op	14.6 ± 1.2 m-p
	CERC2973	21.6 ± 1.2 k-p	31.8 ± 5.6 k-p	18.7 ± 1.3 m-p
N. microconidium	CERC3497	32.7 ± 2.2 k-p	47.7 ± 7.5 i-k	40.8 ± 6.8 j-n
	CERC3498	16.6 ± 1.2 m-p	17.2 ± 1.7 m-p	20.8 ± 4.3 l-p
N. parvum	CERC2951	10.3 ± 0.5 op	11.9 ± 0.9 op	10.3 ± 0.3 op
	CERC3504	17.3 ± 0.7 m-p	30.1 ± 5.2 k-p	22.1 ± 3.2 k-p
	CERC3509	16.0 ± 1.5 m-p	17.5 ± 4.0 k-p	15.3 ± 2.4 m-p
N. sinoeucalypti	CERC2005	27.5 ± 4.7 k-p	68.0 ± 9.0 g-i	62.3 ± 8.7 h-j
	CERC3463	30.9 ± 4.8 k-p	24.0 ± 4.3 k-p	39.3 ± 7.7 j-o
Control		10.5 ± 0.6 op	10.0 ± 0.2 op	9.4 ± 0.3 op

[1] Mean ± SE followed by different lowercase letters indicates treatments that are significantly different ($P < 0.05$); Mean = average lesion length; SE = standard error of mean.

Pathogenicity tests

Twenty-eight isolates representing the 12 species of *Botryosphaeriaceae* identified in this study were used for inoculations on three different *Eucalyptus* clones (different parents) (Table 1, 5). Pathogenicity tests indicate that all of the *Botryosphaeriaceae* isolates tested produce lesions on stems of the three *Eucalyptus* clones, while MEA unclonised plugs produced only wounds. Overall, isolates in species of *Lasiodiplodia* produce relatively longer lesions than that of *Botryosphaeria*, *Cophinforma* and *Neofusicoccum*. For all three tested *Eucalyptus* clones, the lesions produced by *Lasiodiplodia* isolates are all significantly longer than the wounds caused by negative controls, except isolate CERC3420 (*L. theobromae*) on CEPT-11 and CEPT-13 ($P < 0.05$) (Table 5). For isolates in the genera of *Botryosphaeria*, *Cophinforma* and *Neofusicoccum*, isolates CERC3497 (*N. microconidium*) and CERC2005 (*N. sinoeucalypti*) also produce significantly longer lesions on CEPT-11 and CEPT-13 ($P < 0.05$) (Table 5). Analysis of variance shows significant differences in the susceptibility of the three *Eucalyptus* clones to some of the isolates we tested. For example, the lesions produced by isolate CERC2284 (*L. brasiliense*) on three *Eucalyptus* clones are significantly different from each other ($P < 0.05$) (Table 5). Analysis of results also show that not all the isolates of the same species of *Botryosphaeriaceae* react in the same manner to the *Eucalyptus* clones. For example, lesions produced by isolate CERC3420 (*L. theobromae*) on clone CEPT-12 are significantly longer than those on CEPT-13, whereas lesions produced by isolate CERC3513 (*L. theobromae*) on CEPT-12 are significantly shorter than those on CEPT-13 ($P < 0.05$) (Table 5). In addition, based on the lesions caused by all *Botryosphaeriaceae* isolates in this study, CEPT-11 (average lesion length: 33.0 ± 2.4 mm) is more tolerant than CEPT-12 (average lesion length: 44.2 ± 3.2 mm) and CEPT-13 (average lesion length: 42.0 ± 3.4 mm). All 12 species of *Botryosphaeriaceae* were re-isolated successfully from the lesions, and no *Botryosphaeriaceae* were isolated from the negative controls, thus fulfilling Koch's postulates.

DISCUSSION

In this study, disease samples from symptomatic trees with stem cankers, shoot and twig blight were collected mainly from *Eucalyptus* and six other plant hosts in China. *Botryosphaeriaceae* was isolated from these diseased samples. Based on phylogenetic analyses and morphological characteristics, 12 species of *Botryosphaeriaceae* were isolated from these samples and the genera *Botryosphaeria*, *Cophinforma*, *Lasiodiplodia* and *Neofusicoccum* were identified from among a relatively large collection of isolates. These species include *Botryosphaeria fusispora*, *Cophinforma atrovirens*, *Lasiodiplodia brasilience*, *L. pseudotheobromae*, *L. theobromae*, *Neofusicoccum parvum* and each of three previously undescribed species of *Botryosphaeria* and *Neofusicoccum*, namely *B. pseudoramosa* sp. nov., *B. qingyuanensis* sp. nov., *B. wangensis* sp. nov., *N. hongkongense* sp. nov., *N. microconidium* sp. nov. and *N. sinoeucalypti* sp. nov.

In this study, ITS, *tef1*, *tub*, *rpb2*, *cmdA*, LSU and SSU sequences were generated to distinguish and describe new species of *Botryosphaeria*, *Cophinforma*, *Lasiodiplodia* and *Neofusicoccum*. For the six to seven regions used for analyses of *Botryosphaeria*, *Lasiodiplodia* and *Neofusicoccum*, phylogenetic analyses based on sequence comparisons show that polymorphic nucleotides exist between some isolates collected in this study and other closely related species. Sequences of the ITS, *tef1* and *tub* regions are widely used to distinguish and describe new species of *Botryosphaeria*, *Lasiodiplodia* and *Neofusicoccum* of *Botryosphaeriaceae* (Phillips et al. 2013, Chen et al. 2015, Linaldeddu et al. 2015, Coutinho et al. 2017), except ITS, *tef1* and *tub*, *rpb2* genes are also used for the species identification of *Neofusicoccum* (Pavlic et al. 2009a,

Sakalidis et al. 2011, Osorio et al. 2017, Yang et al. 2017) and *rpb2* and *cmdA* are also used for *Lasiodiplodia* (Cruywagen et al. 2017, Dou et al. 2017a, b, Osorio et al. 2017). The phylogenetic analyses based on a combination of the three to five regions (*Botryosphaeria*: ITS, *tef1* and *tub*; *Lasiodiplodia*: ITS, *tef1*, *tub*, *rpb2* and *cmdA*; *Neofusicoccum*: ITS, *tef1*, *tub* and *rpb2*) indicated that these isolates form independent phylogenetic clades supported by high bootstrap values, which are identified and described as six new species. In the other Chinese isolates, the differences we did find occurred only in one of the two (*Cophinforma*), six (*Botryosphaeria* and *Neofusicoccum*) or seven (*Lasiodiplodia*) regions, these isolates reside in the same clade to previously identified species or form independent phylogenetic clades but not supported by high bootstrap values, and they were identified as *B. fusispora*, *C. atrovirens*, *L. brasiliense*, *L. pseudotheobromae*, *L. theobroma* and *N. parvum*.

The identification of 12 *Botryosphaeriaceae* species is also supported by morphological and/or biological characteristics. For each of the six species that have been described previously, their culture morphology and conidial characteristics are very similar to that of the type specimens. For the six newly described species in this study, morphological differences exist among them and other phylogenetically closely related species, especially in terms of the size and shape of conidia, as well as conidium septum characteristics. We also observed biological differences, for example optimal growth temperatures, among some of the species. For the six new species, *B. pseudoramosa*, *B. wangensis*, *N. hongkongense* and *N. microconidium* are easily distinguished from other phylogenetically close species based on conidial morphology. Although some overlap in conidial shape and size is observed among some species, such as *B. fabicerciana*, *B. kuwatsukai* and *B. qingyuanensis*, these species can be distinguished from each other by the presence of a conidial septum (older conidia) and microconidia, as well as the optimal growth temperature. The newly described species *N. sinoeucalypti* can be distinguished from other species with similar conidia in the *N. parvum*/*N. ribis* complex by conidial morphology and the optimal growth temperature.

Except for *B. wangensis*, *C. atrovirens* and *N. hongkongense*, the other nine species were isolated from *Eucalyptus* trees in South China. Of the *Botryosphaeriaceae* species isolated from *Eucalyptus*, *B. fusispora*, *L. pseudotheobromae* and *L. theobromae* are dominant and distributed in the GuangDong, GuangXi and HaiNan Provinces; *L. pseudotheobromae* and *L. theobromae* have also been found in previous studies (Chen et al. 2011c, Li et al. 2015a), suggesting that they may be widely distributed on *Eucalyptus* trees in other areas in South China. Four new species, *B. pseudoramosa*, *B. qingyuanensis*, *N. microconidium* and *N. sinoeucalypti*, were isolated from *Eucalyptus* in China. This study also presents the first report of *L. brasiliense* on *Eucalyptus* in the world. Species of *Botryosphaeriaceae* are distributed in all the areas surveyed where *Eucalyptus* is planted. The results of our study suggest that the species diversity of *Botryosphaeriaceae* on *Eucalyptus* in China may be higher than what was previously expected (Chen et al. 2011c).

In addition to *Botryosphaeriaceae* species identified on *Eucalyptus*, we also identified *B. pseudoramosa* from *Melastoma sanguineum*, *B. wangensis* from *C. deodara*, *C. atrovirens* from *D. longan*, *L. theobromae* from *C. lanceolata*, *D. longan* and *P. hanceana*, and *N. hongkongense* from *A. cunninghamii*. Aside from *L. theobromae* from *P. hanceana* (Lu et al. 2000), which has been reported previously, these *Botryosphaeriaceae* species are reported from their respective plant hosts for the first time. Disease materials were collected randomly from limited areas, including the areas which were adjacent to *Eucalyptus* plantations, and further work is needed to better understand the biodiversity and distribution of *Botryosphaeriaceae* on their hosts.

Based on sequence comparisons of the seven gene regions, the same genotype of *L. theobromae* was shared by species of *Eucalyptus* in all the surveyed provinces in South China, and *C. lanceolata*, *D. longan* and *P. hanceana* planted in GuangDong Province (Table 1). We isolated the newly described species *B. pseudoramosa* from both *Eucalyptus* trees and *M. sanguineum*, and isolates from different hosts in geographically close areas do share the same genotype (Table 1). These results provide confirmation for the wide host range of *L. theobromae* and *B. pseudoramosa* on different plants. Previous studies used genetic diversity and geographic distribution comparisons to show the wide host range of *N. mediterraneum* on different crop trees in California (Chen et al. 2014a, b). The results of our current study further show that some *Botryosphaeriaceae* have wide geographic and host ranges.

Inoculation experiments revealed that all species of *Botryosphaeriaceae* identified in this study are pathogenic to the tested *Eucalyptus* clones, which is consistent with previous work showing that *Botryosphaeriaceae* species include important pathogens of *Eucalyptus* (Pavlic et al. 2007, Mohali et al. 2009, Rodas et al. 2009, Chen et al. 2011c). Pathogenicity tests in this study showed that species of *Lasiodiplodia* are more aggressive than *Botryosphaeria* and *Neofusicoccum* on three *Eucalyptus* clones, including one clone of *E. urophylla* × *E. grandis*, which is consistent with results in previous studies (Chen et al. 2011c). Results in Mohali et al. (2009) showed that some species of *Neofusicoccum* were more aggressive than *Lasiodiplodia* on clones of *E. urophylla* × *E. grandis*, which indicated that resistance of different genotypes of *E. urophylla* × *E. grandis* can be significantly different. Therefore, the identification of commercially available *Eucalyptus* genotypes resistant to *Botryosphaeriaceae* will promote the selection of resistant materials for wide-scale planting.

Of the fungal species we found, *L. theobromae* and *L. pseudotheobromae* are the most aggressive and are also widely distributed on *Eucalyptus* trees in different regions; it is essential that these pathogens be monitored carefully to help make decisions regarding disease management. Except for species of *Lasiodiplodia*, other fungi of the genera *Botryosphaeria*, *Cophinforma* and *Neofusicoccum* also produce lesions on inoculated seedlings; although these species are not highly virulent to *Eucalyptus* and are not widespread, these fungi still need to be monitored carefully because some of them may be highly aggressive to their original hosts or may spread and act as important pathogens in a suitable environment.

Our results in this study indicate that some species of *Botryosphaeriaceae* are widely distributed in different geographic regions on different hosts. These fungal species have significant potential to cause diseases of *Eucalyptus*. Management of the diseases on *Eucalyptus* reported in this study will need to rely on sound breeding programs to select *Eucalyptus* genotypes to match climatic and edaphic factors and silvicultural practices (spacing and thinning) as part of an integrated management strategy (Old et al. 2003). Further study is needed to better understand the genetic diversity of the species at the population level and to understand the biological and epidemiological characteristics of these species to help with long-term disease management.

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