



Cryphonectriaceae on Mytales in China: phylogeny, host range, and pathogenicity

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Key words

Eucalyptus
fungal pathogen
host jump
Myrtaceae
new taxa
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Abstract Plantation-grown *Eucalyptus* (Myrtaceae) and other trees residing in the *Mytales* have been widely planted in southern China. These fungal pathogens include species of *Cryphonectriaceae* that are well-known to cause stem and branch canker disease on *Mytales* trees. During recent disease surveys in southern China, sporocarps with typical characteristics of *Cryphonectriaceae* were observed on the surfaces of cankers on the stems and branches of *Mytales* trees. In this study, a total of 164 *Cryphonectriaceae* isolates were identified based on comparisons of DNA sequences of the partial conserved nuclear large subunit (LSU) ribosomal DNA, internal transcribed spacer (ITS) regions including the 5.8S gene of the ribosomal DNA operon, two regions of the β-tubulin (*tub2/tub1*) gene, and the translation elongation factor 1-alpha (*tef1*) gene region, as well as their morphological characteristics. The results showed that eight species reside in four genera of *Cryphonectriaceae* occurring on the genera *Eucalyptus*, *Melastoma* (*Melastomataceae*), *Psidium* (Myrtaceae), *Syzygium* (Myrtaceae), and *Terminalia* (*Combretaceae*) in *Mytales*. These fungal species include *Chrysoporthe deuterocubensis*, *Celoporthe syzygii*, *Cel. eucalypti*, *Cel. guangdongensis*, *Cel. cerciana*, a new genus and two new species, as well as one new species of *Aurifilum*. These new taxa are hereby described as *Parvomorbus* gen. nov., *Par. eucalypti* sp. nov., *Par. guangdongensis* sp. nov., and *Aurifilum terminali* sp. nov. Pathogenicity tests showed that the eight species of *Cryphonectriaceae* are pathogenic to two *Eucalyptus* hybrid seedlings, *Melastoma sanguineum* branches, and *Psidium guajava* and *Syzygium jambos* seedlings. The overall data showed that *Chr. deuterocubensis* is the most aggressive, followed by *Par. eucalypti*. Significant differences in tolerance were observed between the two tested *Eucalyptus* hybrid genotypes, suggesting that disease-tolerant genotypes can be selected for disease management in the *Eucalyptus* industry.

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INTRODUCTION

The *Cryphonectriaceae* accommodates fungi previously classified in the *Cryphonectria-Endothia* complex (Castlebury et al. 2002, Gryzenhout et al. 2006c), which was established to include *Cryphonectria*, *Endothia* and three other genera, namely *Amphilogia*, *Chrysoporthe*, and *Rostraureum* (Gryzenhout et al. 2006c). Currently, 25 genera have been identified and described in the *Cryphonectriaceae* (Cheewangkoon et al. 2009, Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Crous et al. 2012a, b, 2015, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Ferreira et al. 2019). With the exception of *Chrysocrypta*, *Chrysófolia*, and *Foliocryphia*, which were isolated from leaf spots of eucalypts (Myrtaceae, Mytales) (Cheewangkoon et al. 2009, Crous et al. 2012a, b, 2015, 2019) and healthy leaves of *Barringtonia acutangula* (Lecythidaceae, Ericales) (Suwannarach et al. 2016), the other genera were isolated from trees associated with blight, die-back or canker (Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Ferreira et al. 2019, Jiang et al. 2019). The *Cryphonectriaceae* includes a group of fungi that present many of the world's most important pathogens of trees (Gryzenhout et al. 2006c, 2009), the best known of which is the chestnut blight pathogen, *Cryphonectria parasitica*, in Europe and North

America (Anagnostakis 1987, 1992). Other tree pathogens in the family include the *Eucalyptus* (Myrtaceae, Mytales) pathogens *Chrysoporthe austroafricana* in Africa (Wingfield et al. 1989), *Chr. cubensis* in South America (Hodges et al. 1976), and *Chr. deuterocubensis* in south-eastern Asia (Old et al. 2003), the pin oak (*Quercus palustris*) (Fagaceae, Fagales) pathogen *Endothia gyroza* in North America (Stipes & Phipps 1971) and an aggressive pathogen of native *Rapanea melanophloeos* (Myrsinaceae, Ericales), and *Immersiporthe knoxdaviesiana*, in South Africa (Chen et al. 2013a).

Host plants of the *Cryphonectriaceae* include more than 100 tree species in over 26 families of 16 orders, particularly in the families Fagaceae, Melastomataceae, and Myrtaceae (Mytales) (Cheewangkoon et al. 2009, Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Ferreira et al. 2019). In China, seven *Cryphonectriaceae* genera, *Aurantiosacculus*, *Cryphonectria*, *Chrysoporthe*, *Celoporthe*, *Corticimorbus*, *Chrysomorbus* and *Endothia* have been identified from diseased trees. *Aurantiosacculus castaneae* has been isolated from branches and twigs of Chinese chestnut (*Castanea mollissima*) (Fagaceae) (Jiang et al. 2019). Species of *Cryphonectria* were isolated from trees of Fagaceae, *Cryphonectria parasitica* has been isolated from *C. mollissima* on which it causes canker and die-back (Fairchild 1913, Shear & Stevens 1913, Jiang et al. 2018, 2019), *Cry. japonica* is known from cankers on *Quercus* (Teng 1934, Myburg et al. 2004a, Gryzenhout et al. 2009, Jiang et al. 2019), *Cry. quercicola* and *Cry. quercus* from diseased stems of *Quercus wutaishansea* and *Q. aliena* var. *acuteserrata*, respectively (Jiang et al. 2018), *Cry. neoparasitica* and *Endothia*

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chinensis from diseased branches of *C. mollissima* (Jiang et al. 2019). Species of *Chrysoporthe*, *Celoporthe*, *Corticimorbus* and *Chrysomorbus* isolated in China all originated from trees in *Myrtaceae* or *Melastomataceae*, and include *Chr. deutero-cubensis*, from multiple *Eucalyptus* hybrid genotypes, and *Syzygium cumini* (*Myrtaceae*) (Chen et al. 2010, Van der Merwe et al. 2010); *Celoporthe syzygii*, from *Eucalyptus grandis* hybrid, *S. cumini* and *Melastoma candidum* (*Melastomataceae*) (Chen et al. 2011, Wang et al. 2018); *Cel. cerciana*, *Cel. eucalypti*, and *Cel. guangdongensis*, from species of *Eucalyptus* (Chen et al. 2011, Wang et al. 2018); *Corticimorbus sinomyrti*, from *Rhodomyrtus tomentosa* (*Myrtaceae*) (Chen et al. 2016) and *Chrysomorbus lagerstroemiae* from *Lagerstroemia speciosa* (*Lythraceae*, *Mytales*) (Chen et al. 2018). Inoculation tests have shown that all of the species of *Cryphonectriaceae* from *Myrtaceae*, *Melastomataceae*, and *Lythraceae* are pathogenic to their original hosts and to *Eucalyptus* (Chen et al. 2010, 2011, 2016, 2018, Wang et al. 2018).

Mytales plants are widely distributed particularly in tropical and sub-tropical regions in the world, and seven of the nine families of *Mytales* are distributed in China, including *Alzateaceae*, *Combretaceae*, *Crypteroniaceae*, *Lythraceae*, *Melastomataceae*, *Myrtaceae*, and *Onagraceae* (Editorial Committee of Flora of China 1988, Angiosperm Phylogeny Group 2009). Species of *Melastomataceae* and *Myrtaceae* are distributed in tropical and sub-tropical regions in southern China and include more than 160 species distributed across 25 genera of *Melastomataceae*, and more than 120 species distributed across 16 genera of *Myrtaceae* (Editorial Committee of Flora of China 1988). Some species are native to China, such as species of *Acmena*, *Baeckea*, *Cleistocalyx*, *Decaspermum*, *Psidium*, *Pyrenocarpa*, *Rhodamnia*, *Rhodomyrtus*, and *Syzygium* which belong to the family *Myrtaceae* (Editorial Committee of Flora of China 1988). Myrtle trees are important in the wood industry, fruit industry, and landscape greening in southern China (Zhan & Lan 2012, Huang & Zhu 2014, Xie et al. 2017).

Based on previous research results, it is evident that many new taxa remain to be discovered from *Mytales* trees in China (Chen et al. 2010, 2011, 2016, 2018, Wang et al. 2018). Previous research results further indicated that various species of *Cryphonectriaceae* are regarded as high-risk pathogens because they cause severe diseases and have undergone host shifts between native and cultivated trees, particularly native *Mytales* trees to commercially propagated *Eucalyptus* (Slippers et al. 2005, Gryzenhout et al. 2009, Van der Merwe et al. 2010, 2013, Wingfield et al. 2015). In order to better understand the species diversity and pathogenicity of *Cryphonectriaceae* on *Eucalyptus* and other *Mytales* species in southern China, intensive disease surveys were conducted in *Eucalyptus* plantations and other *Mytales* trees in the proximity of *Eucalyptus* plantations. The aims of this study were to:

1. identify these fungi based on phylogenetic analyses and morphological comparisons;
2. understand the host diversity of these *Cryphonectriaceae* fungi; and
3. test their pathogenicity on *Eucalyptus* and the other *Mytales* trees from which these fungi were originally isolated.

MATERIALS AND METHODS

Disease symptoms, samples, and fungal isolations

Disease surveys on *Mytales* trees were conducted in GuangDong, GuangXi and HaiNan Provinces, as well as in the Hong Kong Region during October 2013 and August 2016. The main specific areas surveyed included a number of sites in the ZhanJiang Regions in GuangDong Province, where *Eucalyptus*

plantations are widely planted, and other *Mytales* trees are commonly distributed (Table 1). The surveyed trees include different *Eucalyptus* hybrid genotypes in plantations (Fig. 1a–c), *Melastoma* shrubs in *Eucalyptus* plantations (Fig. 2a, g), *Psidium guajava* (*Myrtaceae*) (Fig. S1a), *Syzygium* species (Fig. S2a, e), and *Terminalia neotaliala* (*Combretaceae*) (Fig. S3a) planted in nurseries and parks. Other *Mytales* and areas surveyed included plantation *Eucalyptus* in GuiGang Region in GuangXi Province, *Syzygium samarangense* trees in WaiNing Region in HaiNan Province, and *Melastoma* shrubs in the Hong Kong Region. The disease symptoms on the *Mytales* trees included cankers on the branches, stems, and bases (Fig. 1a–c, f, 2b, S1d, S2b, S3a–b, d), lesions and cracks in the bark (Fig. 1e, h, S1b, e, S2d, S3c), stem sections proximal to the cankers that were largely dying (Fig. 2d, S1c), stems that break readily in the wind (Fig. 1d, S2a), tree/shrub death due to canker girdling of stems (Fig. 2h, S1a), and die-back also observed on species of *Melastoma* and *Syzygium* (Fig. 2c, S2e). Yellow, orange, or black sporocarps were present on the surface of the infected bark (Fig. 1g, 2e–f, i, S1f, S2c, f, S3e–f) and roots (Fig. 2j), which display the typical morphological characteristics of *Cryphonectriaceae* (Gryzenhout et al. 2009, Chen et al. 2010, 2016, 2018, Wang et al. 2018). Where these were observed, pieces of infected bark, or sections of infected branches and roots bearing sporocarps were removed from the trees/shrubs and taken to the laboratory for morphological examination and further assessment, with two to five bark pieces collected from each of the sampled trees/shrubs.

For the *Cryphonectriaceae* isolations, the stromata were exposed using a sterile sharp scalpel blade under a dissecting microscope to cut open the sporocarps, and the spore masses were transferred to 2 % malt extract agar (MEA) (20 g malt extract, 20 g agar per L water) and incubated at room temperature until colonies developed. To obtain pure cultures, single hyphal tips from the colonies were transferred to 2 % MEA. Two isolates were isolated from each piece of bark collected from the diseased trees/shrubs. The cultures were deposited in the Culture Collection from Southern Forests (CSF), located at the China Eucalypt Research Centre, Chinese Academy of Forestry, ZhanJiang, GuangDong Province, China, and representative cultures of novel species were deposited at the China General Microbiological Culture Collection Center (CGMCC), Beijing, China. Isolates linked to the type specimens, original bark, and branch specimens bearing sporocarps connected to representative isolates were deposited in the Collection of the Central South Forestry Fungi of China (CSFF), GuangDong Province, China, and the mycological fungarium of the Institute of Microbiology, Chinese Academy of Sciences (HMAS), Beijing, China.

DNA extraction, PCR amplification and sequencing

Cryphonectriaceae isolates obtained from each of all sampled *Mytales* trees were selected for DNA sequence analyses. Prior to DNA extraction, the selected isolates were grown on 2 % MEA at 25 ± 2 °C for 10 d. The actively growing mycelia of each isolate were directly scraped from the surface of the MEA medium with a sterile scalpel and transferred into 2 mL Eppendorf tubes. Total genomic DNA was extracted using the 'Method 5: grinding and CTAB' protocol described by Van Burik et al. (1998). The extracted DNA was dissolved in 30 µL TE buffer (1 M Tris-HCl and 0.5 M EDTA, pH 8.0) and then treated with 2.5 µL RNase (1 mg/mL) for 1 hour at 37 °C to degrade any existing RNA. The resulting DNA concentrations were evaluated using a NanoDrop 2000 spectrometer (Thermo Fisher Scientific Inc., Waltham, MA, USA).

Five gene regions were amplified using the polymerase chain reaction. These included the partial conserved nuclear large

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

Species	Isolate No.	Geno-type No. ¹	Geno-type No. ²	Host	Location	GPS information			GenBank accession No.		
						Collector	ITS	tub2	tub1	tef1	LSU
<i>Chrysopeltis deuterocarbis</i>	CSF3003	1	AAA-	<i>Melastoma candidum</i>	Lantau, Lido, Hong Kong, China	N/A ³	M.J. Wingfield & S.F. Chen	MK955908	MN263601	MN263635	N/A
	CSF5004	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MK955909	MN263602	MN263636	N/A
	CSF5005	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MK955910	MN263603	MN263637	N/A
	CSF5006	1	A-A-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MK955905	MN263604	MN263638	N/A
	CSF5013	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263506	MN263604	MN263639	N/A
	CSF5014	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263507	MN263605	MN263700	N/A
	CSF5019	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263508	MN263606	MN263701	N/A
	CSF5020	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263509	MN263607	MN263702	N/A
	CSF5021	1	AAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263510	MN263608	MN263703	N/A
	CSF5025	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263511	MN263609	MN263704	N/A
	CSF5026	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263512	MN263610	MN263705	N/A
	CSF5027	1	A-A-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263513	N/A	MN263706	N/A
	CSF5028	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263514	MN263611	MN263707	N/A
	CSF5031 ^a	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263515	MN263612	MN263708	N/A
	CSF5040	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263516	MN263613	MN263709	N/A
	CSF5087 ^b	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263517	MN263614	MN263710	N/A
	CSF5088	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263518	MN263615	MN263711	N/A
	CSF5089	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263519	MN263616	MN263712	N/A
	CSF5090 ^c	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263520	MN263617	MN263713	N/A
	CSF5091	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263521	MN263618	MN263714	N/A
	CSF5092	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263522	MN263619	MN263715	N/A
	CSF5095	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263523	MN263620	MN263716	N/A
	CSF5097	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263524	MN263621	MN263717	N/A
	CSF5099	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263525	MN263622	MN263718	N/A
	CSF5100	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263526	MN263623	MN263719	N/A
	CSF5104	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263527	MN263624	MN263720	N/A
	CSF5105	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263528	MN263625	MN263721	N/A
	CSF5108	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263529	MN263626	MN263722	N/A
	CSF5109	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263530	MN263627	MN263723	N/A
	CSF5113	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263531	MN263628	MN263724	N/A
	CSF5122	1	AAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263532	MN263629	MN263725	N/A
	CSF5123 ^d	1	AAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN263533	MN263630	MN263732	N/A
	CSF5146 ^{e,f}	1	AAA-A	<i>M. sanguineum</i>	LingBei, SuiXi, ZhanLiang, GuangDong, China	N21°16'0" 96.0" E110°05'32".690"	S.F. Chen & W. Wang	MN263534	MN263631	MN263737	N/A
	CSF5045 ^f	1	AAA-	<i>M. sanguineum</i>	LingBei, SuiXi, ZhanLiang, GuangDong, China	N21°16'0" 96.0" E110°05'32".690"	S.F. Chen & W. Wang	MN263535	MN263632	MN263738	N/A
	CSF5048 ^{e,g}	1	AAA-	<i>M. sanguineum</i>	LingBei, SuiXi, ZhanLiang, GuangDong, China	N21°16'0" 96.0" E110°05'32".690"	S.F. Chen & W. Wang	MN263536	MN263633	MN263739	N/A
	CSF766 ^e	1	AAA-	<i>M. sanguineum</i>	QuanZhaung, XiaShan, ZhanLiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263537	MN263634	MN263740	N/A
	CSF8768	1	AAA-	<i>M. sanguineum</i>	QuanZhaung, XiaShan, ZhanLiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263538	MN263635	MN263741	N/A
	CSF8769	1	AAA-	<i>M. sanguineum</i>	QuanZhaung, XiaShan, ZhanLiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263548	MN263645	MN263742	N/A
	CSF8771 ^e	1	AAA-	<i>M. sanguineum</i>	QuanZhaung, XiaShan, ZhanLiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263540	MN263637	MN263733	N/A
	CSF10560 ^{e,g}	1	AAA-	<i>Pstdium guajava</i>	QuanZhaung, XiaShan, ZhanLiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263541	MN263638	MN263734	N/A
	CSF10561 ^e	1	AAA-	<i>Syzgium guajava</i>	QuanZhaung, XiaShan, ZhanLiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263542	MN263639	MN263735	N/A
	CSF87788 ^{e,g}	1	AAA-	<i>S. samaranigense</i>	ChangFeng, WanNing, Hainan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263544	MN263641	MN263737	N/A
	CSF87790	1	AAA-	<i>S. samaranigense</i>	ChangFeng, WanNing, Hainan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263545	MN263642	MN263738	N/A
	CSF87791	1	AAA-	<i>S. samaranigense</i>	ChangFeng, WanNing, Hainan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263546	MN263643	MN263739	N/A
	CSF87792	1	AAA-	<i>S. samaranigense</i>	ChangFeng, WanNing, Hainan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263547	MN263644	MN263740	N/A
	CSF87793 ^e	1	AAA-	<i>S. samaranigense</i>	ChangFeng, WanNing, Hainan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263548	MN263645	MN263741	N/A
	CSF8029 ^{e,g}	2	AAB-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263549	MN263646	MN263742	N/A
	CSF5030 ^e	2	AAB-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263550	MN263647	MN263743	N/A
	CSF5041 ^{e,g}	3	ABA-A	<i>M. sanguineum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263551	MN263648	MN263744	N/A
	CSF5042 ^e	3	ABA-A	<i>M. sanguineum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263552	MN263649	MN263745	N/A

Table 1 (cont.)

Species	Isolate No.	Geno-type No. ¹	Host	Location	GPS information		Collector	GenBank accession No.		
					ITS	tub2		tub1	tef1	LSU
<i>Chrysopeltis deuterocambensis</i> (cont.)	CSF10786 ^a	4	BAA-A	<i>S. jambos</i>	XiHu, Leizhou, Zhanjiang, GuangDong, China	N20°54'50.200" E110°5'15.300"	S.F. Chen & W. Wang	MN2633553	MN2633650	MN2633746
	CSF10787 ^a	4	BAA-	<i>S. jambos</i>	XiHu, Leizhou, Zhanjiang, GuangDong, China	N20°54'50.200" E110°5'15.300"	S.F. Chen & W. Wang	MN2633554	MN2633651	MN2633747
	CSF10564 ^{a,5,9}	5	BAB-A	<i>P. guajava</i>	QuanZaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°25'54.457"	S.F. Chen & G.Q. Li	MN2633555	MN2633652	MN2633748
	CSF10744 ^a	6	BBA-	<i>M. sanguineum</i>	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang	MN2633556	MN2633653	MN2633749
	CSF10745 ^{a,5,9}	6	BBA-A	<i>M. sanguineum</i>	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang	MN2633557	MN2633654	MN2633750
	CSF10565 ^{a,5,9}	7	CAB-A	<i>P. guajava</i>	QuanZaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°25'54.457"	S.F. Chen & G.Q. Li	MN2633558	MN2633655	MN2633751
	CSF10555	7	CAB-A	<i>P. guajava</i>	QuanZaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°25'54.457"	S.F. Chen & G.Q. Li	MN2633559	MN2633656	MN2633752
	CSF10556 ^a	7	CAB-.	<i>P. guajava</i>	QuanZaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°25'54.457"	S.F. Chen & G.Q. Li	MN2633560	MN2633657	MN2633753
	CSF10557	7	CAB-.	<i>Eucalyptus urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.0" E110°24'13.0"	S.F. Chen	MN2633561	MN2633658	MN2633754
	CSF3813 ^{5,9}	8	DAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633563	MN2633660	MN2633756
	CSF9007 ^b	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633564	MN2633661	MN2633757
	CSF9008 ^b	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633565	MN2633662	MN2633758
	CSF9009	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633566	MN2633663	MN2633759
	CSF9010	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633567	MN2633664	MN2633760
	CSF9015	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633568	MN2633665	MN2633761
	CSF5016	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633569	MN2633666	MN2633762
	CSF5093	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633571	MN2633667	MN2633763
	CSF5094	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633572	MN2633668	MN2633764
	CSF5106	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633573	MN2633670	MN2633765
	CSF5107	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633574	MN2633671	MN2633767
	CSF5116	8	DAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633575	MN2633672	MN2633768
	CSF5117 ^{4,5}	8	DAA-A	<i>M. sanguineum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633576	MN2633673	MN2633769
	CSF5043	8	DAA--	<i>M. sanguineum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633577	MN2633674	MN2633770
	CSF5044	8	DAA--	<i>M. sanguineum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633578	MN2633675	MN2633771
	CSF5126 ^b	8	DAA-A	<i>M. sanguineum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633579	MN2633676	MN2633772
	CSF5127	8	DAA--	<i>M. sanguineum</i>	Lantau, Lido, Hong Kong, China	N/A	S.F. Chen	MN2633580	MN2633677	MN2633773
	CSF5128 ^b	8	DAA--	Unknown species of Myrtaceae	HaIBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN2633581	MN2633678	MN2633774
	CSF5761 ^b	8	DA--A	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000" E110°24'13.000"	S.F. Chen	MN2633582	MN2633679	MN2633775
	CSF5814 ^{4,5,9}	9	EEAA	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000" E110°24'13.000"	S.F. Chen	MN2633583	MN2633680	MN2633776
	CSF5815	9	EAA--	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000" E110°24'13.000"	S.F. Chen	MN2633584	MN2633681	MN2633777
	CSF3816	9	EAA--	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000" E110°24'13.000"	S.F. Chen	MN2633585	MN2633682	MN2633778
	CSF5817	9	EAA--	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000" E110°24'13.000"	S.F. Chen	MN2633586	MN2633683	MN2633779
	CSF5818	9	EAA--	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000" E110°24'13.000"	S.F. Chen	MN2633587	MN2633684	MN2633780
	CSF5819 ^b	9	EAA--	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000" E110°24'13.000"	S.F. Chen	MN2633588	MN2633685	MN2633781
	CSF5011	10	F----	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633587	N/A	N/A
	CSF5012 ^{4,5,9}	10	FAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633588	MN2633684	MN2633789
	CSF5110	10	F----	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633589	N/A	N/A
	CSF5111 ^{5,9}	10	FAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633590	N/A	MN2633810
	CSF5022 ^{4,5,9}	11	GAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633591	MN2633686	MN2633811
	CSF5023	11	GAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633592	MN2633687	MN2633812
	CSF5024 ⁵	11	GAA--	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN2633593	MN2633688	N/A
	CSF5765 ^{5,9}	11	GAA-A	Unknown species of Myrtaceae	HaIBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN2633594	MN2633689	MN2633812
	CSF5759 ^c	11	GAA--	Unknown species of Myrtaceae	HaIBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN2633595	MN2633690	N/A

Table 1 (cont.)

Species	Isolate No.	Geno-type No. ¹	Geno-type No. ²	Host	Location	GPS information	Collector	GenBank accession No.				
								ITS	tub2	tub1	tef1	LSU
<i>Chrysopeltis deuterocarpos</i> (cont.)	CSF035 ^{5,9}	12	HAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263596	MN263691	MN263786	N/A	MN263813
	CSF036	12	HAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263597	N/A	MN263787	N/A	MN263814
	CSF037	12	HAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263598	MN263692	MN263788	N/A	N/A
	CSF038	12	HAA-	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263599	MN263693	MN263789	N/A	N/A
	CSF114 ⁵	12	HAA-A	<i>M. candidum</i>	Lantau, Lido, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263600	MN263694	MN263790	N/A	MN263815
<i>Celaporthe syzygii</i>	CSF748 ^{4,5}	1	AAAAA	<i>E. urophylla</i> hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'30"E 110°51'40"	J. Roux & S.F. Chen	MN263299	MN263345	MN263391	MN263437	MN263483
	CSF749 ^{5,9}	1	AAAA-	<i>E. urophylla</i> hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'30"E 110°51'40"	J. Roux & S.F. Chen	MN263300	MN263346	MN263392	MN263438	N/A
	CSF1036 ^{5,9}	2	ABBB	<i>P. guajava</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.60"E 110°23'33.000"	S.F. Chen	MN263301	MN263347	MN263393	MN263439	MN263484
	CSF1063 ⁷	2	ABBB-	<i>P. guajava</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.60"E 110°23'33.000"	S.F. Chen	MN263302	MN263348	MN263394	MN263440	N/A
	CSF1064 ⁵	2	ABBB-	<i>P. guajava</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.60"E 110°23'33.000"	S.F. Chen	MN263303	MN263349	MN263395	MN263441	N/A
	CSF113 ^{4,5}	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263304	MN263350	MN263396	MN263442	MN263485
	CSF9114	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263305	MN263351	MN263397	MN263443	N/A
	CSF9115	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263306	MN263352	MN263398	MN263444	N/A
	CSF9116	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263307	MN263353	MN263399	MN263445	N/A
	CSF9117	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263308	MN263354	MN263400	MN263446	N/A
	CSF9118	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263309	MN263355	MN263401	MN263447	N/A
	CSF9119	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263310	MN263356	MN263402	MN263448	N/A
	CSF9120	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263311	MN263357	MN263403	MN263449	N/A
	CSF9121	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263312	MN263358	MN263404	MN263450	N/A
	CSF9122	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263313	MN263359	MN263405	MN263451	N/A
	CSF9123	2	ABBB-	<i>S. hancei</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263314	MN263360	MN263406	MN263452	N/A
	CSF124 ^{5,9}	2	ABBB-	<i>E. urophylla</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356"E 110°23'54.457"	S.F. Chen	MN263315	MN263361	MN263407	MN263453	N/A
	CSF10695 ^{5,9}	3	ACBB-	<i>E. urophylla</i> hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924"E 110°05'11.600"	S.F. Chen & W. Wang	MN263316	MN263362	MN263408	MN263454	MN263486
	CSF10695 ⁶	3	ACBB-	<i>E. urophylla</i> hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924"E 110°05'11.600"	S.F. Chen & W. Wang	MN263317	MN263363	MN263409	MN263455	N/A
	CSF10657 ⁵	4	BACB-	<i>E. urophylla</i>	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924"E 110°05'11.600"	S.F. Chen & W. Wang	MN263318	MN263364	MN263410	MN263456	N/A
	CSF10658	4	BACB-	<i>E. urophylla</i> hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924"E 110°05'11.600"	S.F. Chen & W. Wang	MN263319	MN263365	MN263411	MN263457	N/A
	CSF10659 ^{5,9}	4	BACB-	<i>E. urophylla</i> hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924"E 110°05'11.600"	S.F. Chen & W. Wang	MN263320	MN263366	MN263412	MN263458	MN263487
	CSF10619 ^{4,5,9}	5	BBBB-	<i>S. samaranigrae</i>	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800"E 110°14'07.500"	S.F. Chen & G.Q. Li	MN263321	MN263367	MN263413	MN263459	MN263488
	CSF10794 ^{5,9}	6	BBCB-	<i>S. jambos</i>	ChengNan, LianJiang, ZhanJiang, GuangDong, China	N21°35'23.240"E 110°15'51.770"	S.F. Chen & W. Wang	MN263322	MN263368	MN263414	MN263460	MN263489
	CSF10642 ⁹	6	BBBC-	<i>S. samaranigrae</i>	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800"E 110°14'07.500"	S.F. Chen & G.Q. Li	MN263323	MN263369	MN263415	MN263461	N/A
	CSF10605 ⁹	6	BBBC-	<i>S. samaranigrae</i>	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800"E 110°14'07.500"	S.F. Chen & G.Q. Li	MN263324	MN263370	MN263416	MN263462	N/A
	CSF10616 ⁵	6	BBCC-	<i>S. samaranigrae</i>	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800"E 110°14'07.500"	S.F. Chen & G.Q. Li	MN263325	MN263371	MN263417	MN263463	N/A
	CSF10647 ^{5,9}	7	BBCCA-	<i>P. guajava</i>	QuanZhuang, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.600"E 110°23'33.000"	S.F. Chen	MN263326	MN263372	MN263418	MN263464	MN263490
	CSF752 ^{4,5,9}	8	BBDBA	<i>Szygium</i> like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263327	MN263373	MN263419	MN263465	MN263491
	CSF753	8	BBDB-	<i>Szygium</i> like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263328	MN263374	MN263420	MN263466	N/A
	CSF754	8	BBDB-	<i>Szygium</i> like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263329	MN263375	MN263421	MN263467	N/A
	CSF755 ⁶	8	BBDB-	<i>Szygium</i> like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263330	MN263376	MN263422	MN263468	N/A
	CSF10597 ^{4,5,9}	9	BDDBA	<i>S. samaranigrae</i> Unknown species	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800"E 110°14'07.500"	S.F. Chen & G.Q. Li	MN263331	MN263377	MN263423	MN263469	MN263492
	CSF762 ^{4,5,9}	10	BDDBA	<i>Myrtaceae</i> Unknown species	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263332	MN263378	MN263424	MN263470	MN263493
	CSF8763	10	BDDBA	<i>Myrtaceae</i> Unknown species	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263333	MN263379	MN263425	MN263471	MN263494
	CSF8764	10	BDDBA	<i>Myrtaceae</i> Unknown species	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263334	MN263380	MN263426	MN263472	MN263495
	CSF8765 ⁵	10	BDDBA	<i>Myrtaceae</i>	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930"E 110°24'26.977"	S.F. Chen	MN263335	MN263381	MN263427	MN263473	MN263496

Table 1 (cont.)

Species	Isolate No.	Geno-type No. ¹	Host	Location	GPS information	Collector	GenBank accession No.					
							ITS	tub2	tub1	tef1	LSU	
<i>Celopeltis syzigi</i> (cont.)	CSF10627 ^a :5.9	11	CEDCA	S. samaranagense	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263336	MN263382	MN263428	MN263474	
	CSF10628 ^b	11	CEDCA	S. samaranagense	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263337	MN263383	MN263429	MN263498	
<i>Cel. eucalypti</i>	CSF10618 ^a :5.9	12	CFBBA	S. samaranagense	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263338	MN263384	MN263430	MN263499	
	CSF10768 ^a :5.9	13	CGEDA	S. jambos	ChengBei, XuMen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263339	MN263385	MN263431	MN263477	
<i>Cel. guangdongensis</i>	CSF10770 ^a :5.9	13	DHFE-	S. jambos	ChengBei, XuMen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263340	MN263386	MN263432	MN263501	
	CSF10774 ^a :5.9	14	DHFEA	S. jambos	ChengBei, XuMen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263341	MN263387	MN263433	NIA	
	CSF10775 ^a :5.9	14	DHFEA	S. jambos	ChengBei, XuMen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263342	MN263388	MN263434	MN263502	
	CSF10778 ^b	14	DHFEA	E. grandis	LingBei, SuiXi, ZhanJiang, GuangDong, China	N20°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang	MN263343	MN263389	MN263435	MN263503	
	CSF10731 ^a :5.9	15	EBGBA	hybrid clone	Terminalia neotaliala	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199834	MN258767	MN258772	MN258782
<i>Aurifilum terminali</i>	CSF10748 ^a :5.8.9	1	AAAAAA	T. neotaliala	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199835	MN258768	MN258773	MN258783	
	CSF10754 ^a :5.5	1	AAAAAA	T. neotaliala	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199836	MN258769	MN258774	MN258784	
	CSF10755 ^a :5.7.8	1	AAAAAA	T. neotaliala	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199837	MN258770	MN258775	MN258785	
	CSF10757 ^a :5.8.7.8.9	1	AAAAAA	T. neotaliala	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199838	MN258771	MN258776	MN258786	
	CSF10762 ^a :5.5	1	AAAAAA	E. urophylla	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258877	MN258891	MN258895	MN258893	
	CSF20604 ^a :8.9	1	AAAAAA	E. grandis hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258788	MN258802	MN258816	MN258844	
	CSF20614 ^a :5.6.7	1	AAAAAA	E. urophylla	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258789	MN258803	MN258817	MN258831	
	CSF20624 ^b	1	AAAAAA	E. urophylla	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258790	MN258804	MN258818	MN258832	
<i>Panosporotus eucalypti</i>	CSF20614 ^a :5.6.7	1	AAAAAA	E. grandis hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258791	MN258805	MN258819	MN258833	
	CSF20634 ^b	1	AAAAAA	E. urophylla	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258792	MN258806	MN258820	MN258834	
	CSF20644 ^b	1	AAAAAA	E. grandis hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258793	MN258807	MN258821	MN258835	
	CSF20654 ^b	1	AAAAAA	E. urophylla	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°19'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258794	MN258808	MN258822	MN258836	
	CSF8776 ^a :5.7.8.9	1	AAAAAA	E. grandis hybrid clone	YaTang, LianJiang, ZhanJiang, GuangDong, China	N21°33'43.000" E110°15'57.700"	J. Roux & S.F. Chen	MN258795	MN258809	MN258823	MN258837	
	CSF8777 ^a :5.7.8	1	AAAAAA	E. urophylla	YaTang, LianJiang, ZhanJiang, GuangDong, China	N21°33'43.000" E110°15'57.700"	J. Roux & S.F. Chen	MN258796	MN258810	MN258824	MN258838	
<i>Par. guangdongensis</i>	CSF10437 ^a :5.5	2	BBBAA	E. urophylla	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258797	MN258811	MN258825	MN258833	
	CSF10440 ^a :5	2	BBBAA	E. urophylla	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258798	MN258812	MN258826	MN258840	
	CSF10459 ^a :5	2	BBBAA	E. urophylla	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258799	MN258813	MN258827	MN258841	
	CSF10460 ^a :5.6.7.8.9	2	BBBAA	E. urophylla	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258800	MN258814	MN258828	MN258842	
	CSF10738 ^a :5.7.8.9	2	BBBAA	E. grandis	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang					

¹ Genotype number within genera of Chrysopeltite, Celopeltite, Aurifilum and Parvomorbus.² Genotype within each genus, determined by sequences of ITS, tub2, tub2, tef1 and LSU five regions; '-' means not available.³ N/A = not available.⁴ Isolates used for phylogenetic analyses of 'Genetic placements in Cyphanectriaceae' and 'Species identification in Cyphanectriaceae'.⁵ Isolates used for phylogenetic analyses of Chrysopeltite and 'Phylogenetic analyses of Celopeltite'.⁶ Isolates ex-type.⁷ Isolates used to produce sporocarps.⁸ Isolates used for culture growth.⁹ Isolates used in pathogenicity tests.



Fig. 1 Disease symptoms on *Eucalyptus* trees associated with infection by *Cryphonectriaceae*. a–c. Cankers caused on the main stems of infected trees by (a) *Chrysoporthe deuterocubensis*, (b) *Celoporthe cerciana*, and (c) *Parvosporbus eucalypti*; d. stems infected by *Chr. deuterocubensis* readily break in the wind; e. lesion developing on the stem infected by *Chr. deuterocubensis*; f. canker caused by *Chr. deuterocubensis* on the base; g. sporocarps of *Chr. deuterocubensis* on bark; h. young canker caused by *Par. eucalypti* on the stem.

subunit (LSU) ribosomal DNA, internal transcribed spacer (ITS) regions including the 5.8S gene of the ribosomal DNA operon, two regions of the β -tubulin (*tub2/tub1*) gene, and the translation elongation factor 1-alpha (*tef1*) gene region. The LSU, ITS, *tub2*, *tub1*, and *tef1* regions were amplified using the primers and method presented by Chen et al. (2011) previously. The PCR products were sequenced following the method described by Chen et al. (2011). Nucleotide sequences were edited with MEGA4 (Tamura et al. 2007).

The regions of ITS, *tub2*, and *tub1* genes were sequenced for all isolates used in this study. The genotype for each isolate was determined by the sequences of ITS, *tub2*, and *tub1* genes, and one to two isolates of each genotype (ITS/ *tub2/tub1*) were sequenced for the LSU region, depending on the isolate number in each genotype. The *tef1* gene region was sequenced for the isolates in the genera for which this region was used for species identification (Chen et al. 2011, Vermeulen et al. 2013).



Fig. 2 Disease symptoms on *Melastoma* species associated with infection by *Cryphonectriaceae*. a. *Melastoma sanguineum* growing in a *Eucalyptus* plantation; b–c. stem canker (b) and die-back (c) on *M. sanguineum* caused by *Chrysoporthe deuterocubensis*; d. stem necrosis after infecting by *Chr. deuterocubensis*; e–f. arrows show the sporocarps of *Chr. deuterocubensis* on the bark of (e) the main stem and (f) branch; g. *Melastoma candidum* growing in the proximity of *Eucalyptus* plantations; h. dying *M. candidum* after infection with *Chr. deuterocubensis*; i–j. sporocarps of *Chr. deuterocubensis* on (i) the main stem and (j) roots (arrows) of *M. candidum*.

Phylogenetic analyses

The preliminary identities of the isolates sequenced in this study were obtained by conducting a standard nucleotide BLAST search using the ITS, *tub2*, and *tub1* sequences. The BLAST results showed that the isolates collected in this study were mainly grouped in the genera *Chrysoporthe* and *Celoporthe*; a few isolates were grouped in *Aurifilum*; and a few isolates appear to present a novel genus of *Cryphonectriaceae*. Phylogenetic analyses for *Cryphonectriaceae* identification in the current study were conducted for both genetic and species identification.

Generic placement in *Cryphonectriaceae*

The datasets of the sequences of the LSU gene region, as well as a combination of the sequences of 5.8S rDNA and the exon regions of the *tub* (*tub2* and *tub1*) gene regions (including partial exon 4, exon 5, partial exon 6 and partial exon 7), were used successfully to clarify the genera of *Cryphonectriaceae* (Gryzenhout et al. 2009, Chen et al. 2011, 2013a, b, 2016, 2018, Ali et al. 2018, Ferreira et al. 2019). To determine the generic placement of the isolates collected from *Myrtales* in this study, LSU and 5.8S rRNA/exons of *tub* (*tub2* and *tub1*) gene sequences from ex-type strains of the described species/genera in *Cryphonectriaceae* were compared with sequences generated in the current study (Table 2). The datasets of the LSU and 5.8S rRNA/exons of *tub* (*tub2* and *tub1*) gene sequences were not combined for further analyses, since the sequences of some *Cryphonectriaceae* isolates were not available for both datasets. For analyses of the LSU, the datasets of Chen et al. (2018) were used as templates, and the recently published LSU sequences of *Capillaureum caryovora* and *Myrtonectria myrtacearum* (*Cryphonectriaceae*) were included (Ali et al. 2018, Ferreira et al. 2019). *Togninia minima* (CBS 6580) (*Togniniaceae*, *Togniniales*), *Tog. fraxinopensylvanica* (ATCC 26664), and *Phaeoacremonium minimum* (A207) (*Togniniaceae*) were used as outgroups (Gryzenhout et al. 2009, Gramaje et al. 2015, Chen et al. 2018).

For analyses of the sequences of 5.8S rRNA and exons of *tub* (*tub2* and *tub1*) genes, the datasets of Chen et al. (2018) were used as templates, and the recently published ITS, *tub2*, and *tub1* sequences of *Cap. caryovora*, *Cel. borbonica*, *Cel. cerciana*, *Cel. tibouchineae*, *Cry. quercicola*, *Cry. quercus* and *Myr. myrtacearum* (*Cryphonectriaceae*) were combined (Ali et al. 2018, Jiang et al. 2018, Ferreira et al. 2019). Two isolates of *Diaporthe ambigua* (CMW5288 and CMW5587) (*Diaporthaceae*, *Diaporthales*) were used as outgroups for analyses of the sequences of the 5.8S rRNA and exons of the *tub* (*tub2* and *tub1*) gene regions (Gryzenhout et al. 2009, Chen et al. 2018). The partition homogeneity test (PHT), as implemented in PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford 2003), was used to determine if conflict existed between the datasets for the 5.8S rRNA gene and exons of the *tub* (*tub2* and *tub1*) gene prior to performing combined analyses in PAUP (Farris et al. 1995, Huelsenbeck et al. 1996).

Species identification in *Cryphonectriaceae*

To determine the species identities and phylogenetic relationships between the isolates from China and previously described species of *Cryphonectriaceae*, sequences of the ITS and *tub* (*tub2* and *tub1*) gene regions were analysed separately and in combination. The sequences of ITS and *tub* (*tub2* and *tub1*) of the isolates used in the 5.8S rRNA and exons of *tub* (*tub2* and *tub1*) gene analyses for genetic placement were used for species identification. Two isolates of *Diaporthe ambigua* (CMW5288 and CMW5587) were used as outgroups. PHT was used to determine if conflict existed among the ITS and

tub (*tub2* and *tub1*) datasets (Farris et al. 1995, Huelsenbeck et al. 1996) and was determined in PAUP v. 4.0b10.

Phylogenetic analyses of *Chrysoporthe*

For isolates grouping in the genus *Chrysoporthe* by the standard nucleotide BLAST search using the ITS, *tub2*, and *tub1* sequences, sequences of the ITS and *tub* (*tub2* and *tub1*) gene regions were analysed separately and in combination to determine the phylogenetic relationships between the isolates from China and previously described species of *Chrysoporthe*. Two isolates of *Holocryphia capensis* (CMW37329 and CMW37887) were used as outgroups. PHT was used to determine if conflict existed among the ITS and *tub* datasets (Farris et al. 1995, Huelsenbeck et al. 1996).

Phylogenetic analyses of *Celoporthe*

For isolates that grouped in *Celoporthe* via the standard nucleotide BLAST search using the ITS, *tub2*, and *tub1* sequences, sequences of the ITS, *tub* (*tub2* and *tub1*) and *tef1* gene region were analysed separately and in combination to determine the phylogenetic relationships between the isolates from China and previously described species of *Celoporthe*. Two isolates of *Hol. capensis* (CMW37329 and CMW37887) were used as outgroups. PHT was used to determine if conflict existed among the ITS, *tub* and *tef1* datasets (Farris et al. 1995, Huelsenbeck et al. 1996).

The sequences of each of the single gene datasets, as well as for a combined dataset consisting of two to three regions, were aligned using MAFFT online v. 7 (<http://mafft.cbrc.jp/alignment/server/>) (Katoh & Standley 2013) using the iterative refinement method (FFT-NS-i setting). The alignments were edited manually with MEGA4 (Tamura et al. 2007). Alignments were deposited in TreeBASE (<http://treebase.org>). Maximum parsimony (MP) and maximum likelihood (ML) were used to assess branch support in the phylogenetic analyses.

PAUP v. 4.0 b10 (Swofford 2003) was used for MP analyses, with gaps treated as the fifth character. Uninformative characters were excluded, and informative characters were unordered and of equal weight with 1000 random addition replicates. The most parsimonious trees were obtained using the heuristic search function with stepwise addition, tree bisection, and reconstruction branch swapping. Maxtrees were set to 5000 and zero-length branches were collapsed. A bootstrap analysis (50 % majority rule, 1000 replicates) was done to determine statistical support for the internal nodes in the trees. Tree length (TL), consistency index (CI), retention index (RI), and homoplasy index (HI) were used to assess the trees (Hillis & Huelsenbeck 1992).

PhyML v. 3.1 was used for the ML analyses for each dataset (Guindon & Gascuel 2003). The software package jModeltest v. 1.2.5 was used to determine the best nucleotide substitution model for each dataset (Posada 2008). In PhyML, the maximum number of retained trees was set to 1000, and nodal support was determined by non-parametric bootstrapping with 1000 replicates. The phylogenetic trees were viewed in MEGA4 for both the MP and ML analyses.

Morphology

The *Cryphonectriaceae* fungi collected in this study were compared with previously published *Cryphonectriaceae* (Cheewangkoon et al. 2009, Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Crous et al. 2012a, b, 2015, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Ferreira et al. 2019). To describe the morphological characteristics of the potential new fungal species, thin branches of a *E. urophylla* × *E. grandis*

Table 2 Isolates from previous studies used in the phylogenetic analyses in the current study.

Identity	Isolate no. ^{1,2}	Host	Location	Collector	GenBank accession no.			References	
					LSU	ITS	BT2	BT1	
<i>Amphilophia g/urosa</i>	CMW10469 ^T	<i>Elaeocarpus dentatus</i>	New Zealand	G.J. Samuels	AY194107	AF525714	AF525707	N/A ³	Gryzenhout et al. (2005a, 2006c)
	CMW10470	<i>Elaeocarpus dentatus</i>	New Zealand	G.J. Samuels	AY194108	AF525712	AF525708	N/A	Gryzenhout et al. (2005a, 2006c)
<i>Aurantioporthia corni</i>	ATCC266334	<i>Cornus alternifolia</i>	USA	N/A	AF277133	N/A	N/A	N/A	Zhang & Blackwell (2001)
	CMW10526	<i>Cor. alternifolia</i>	USA	S. Redlin	AF408343	DQ120762	DQ120769	N/A	Gryzenhout et al. (2006c)
	MES-1001		USA	W. Cullina	N/A	KF495039	N/A	N/A	Beier et al. (2015)
	CTS1001		USA	K. Kitka	N/A	KF495033	N/A	N/A	Beier et al. (2015)
<i>Aurantiosacculus acutulus</i>	CMW13218 ^T	<i>Euc. viminalis</i>	Australia	B.A. Summerell & P. Summerell	JQ6885520	JQ6885514	N/A	N/A	Crous et al. (2012a)
<i>Aurantiosacculus eucalyptorum</i>	CBS13026 ^T	<i>Eucalyptus globulus</i>	Australia	C. Mohammed & M. Glen	JQ6885515	JQ6885515	N/A	N/A	Crous et al. (2012a)
<i>Aurapex penicillata</i>	CMW10300 ^T	<i>Miconia thaezeans</i>	Colombia	C.A. Rodas	AY194103	AY214311	AY214275	N/A	Gryzenhout et al. (2006b, 2009)
	CMW11295	<i>Mic. thaezeans</i>	Colombia	C.A. Rodas	AY194089	N/A	N/A	N/A	Gryzenhout et al. (2009)
	CMW10035	<i>Mic. thaezeans</i>	Colombia	C.A. Rodas	N/A	AY214313	AY214277	N/A	Gryzenhout et al. (2006b, 2009)
<i>Aurifilium marmelostoma</i>	CMW28285 ^T	<i>Terminalia mantaly</i>	Cameroon	D. Begoude & J. Roux	FJ828255	FJ828255	FJ800585	N/A	Begoude et al. (2010), Vermeulen et al. (2011)
	CMW28288	<i>Ter. mantaly</i>	Cameroon	D. Begoude & J. Roux	FJ828256	FJ8005891	FJ800586	N/A	Begoude et al. (2010), Vermeulen et al. (2011)
<i>Capillaureum capayovora</i>	CBL02 ^T	<i>Caryocar brasiliense</i>	Brazil	Soares de Oliveira & Ferreira	MG192104	MG192094	MG211808	N/A	Ferreira et al. (2019)
	CBL06	<i>Caryocar brasiliense</i>	Brazil	Soares de Oliveira & Ferreira	MG192106	MG192096	MG211810	N/A	Ferreira et al. (2019)
<i>Celoporthis bordonica</i>	CMW44128 ^T	<i>Tibouchina grandiflora</i>	La Réunion	M. J. Wingfield	N/A	MG585741	N/A	N/A	Ali et al. (2018)
	CMW44139	<i>Tib. grandiflora</i>	La Réunion	M. J. Wingfield	N/A	MG585742	N/A	N/A	Ali et al. (2018)
<i>Celoporthis cerciana</i>	CERC9128 ^T	<i>Eucalyptus hybrid tree 4</i>	GuangDong, China	S. F. Chen	N/A	MH084412	MH084412	N/A	Wang et al. (2018)
	CERC9125	<i>Eucalyptus hybrid tree 1</i>	GuangDong, China	S. F. Chen	N/A	MH084409	MH084409	N/A	Wang et al. (2018)
<i>Celoporthis dispersa</i>	CMW9976 ^T	<i>Syzygium cordatum</i>	South Africa	M. Gryzenhout	HQ730853	DQ267130	DQ267142	N/A	Nakabonge et al. (2006), Chen et al. (2011)
	CMW9978	<i>S. cordatum</i>	South Africa	M. Gryzenhout	HQ730854	AY214316	DQ267141	N/A	Nakabonge et al. (2006), Chen et al. (2011)
<i>Celoporthis eucalypti</i>	CMW28900	<i>Eucalyptus clone EC48</i>	China	X.D. Zhou & S.F. Chen	HQ730862	HQ730836	HQ730826	N/A	Chen et al. (2011)
	CMW28908 ^T	<i>Eucalyptus clone EC48</i>	China	X.D. Zhou & S.F. Chen	HQ730863	HQ730837	HQ730827	N/A	Chen et al. (2011)
<i>Celoporthis fontana</i>	CMW29375	<i>S. guineense</i>	Zambia	M. Vermeulen & J. Roux	N/A	GU726952	GU726952	N/A	Vermeulen et al. (2013)
	CMW29376 ^T	<i>S. guineense</i>	Zambia	M. Vermeulen & J. Roux	N/A	GU726941	GU726953	N/A	Vermeulen et al. (2013)
<i>Celoporthis guangdongensis</i>	CMW12750 ^T	<i>Eucalyptus sp.</i>	China	T.I. Burgess	HQ730856	HQ730830	HQ730820	N/A	Chen et al. (2011)
	CMW10781 ^T	<i>Eucalyptus aromaticum</i>	Indonesia	M. J. Wingfield	HQ730855	AY084009	AY084021	N/A	Myburg et al. (2003), Chen et al. (2011)
<i>Celoporthis syzygii</i>	CMW34023 ^T	<i>S. curminii</i>	China	S. F. Chen	HQ730857	HQ730831	HQ730817	N/A	Chen et al. (2011)
	CMW34912	<i>S. curminii</i>	China	M. J. Wingfield & X.D. Zhou	HQ730859	HQ730833	HQ730827	N/A	Chen et al. (2011)
<i>Celoporthis tibouchinæae</i>	CMW44126 ^T	<i>Tib. grandiflora</i>	La Réunion	M. J. Wingfield	N/A	MG585747	N/A	N/A	Ali et al. (2018)
	CMW44127	<i>Tib. grandiflora</i>	La Réunion	M. J. Wingfield	N/A	MG585748	N/A	N/A	Ali et al. (2018)
<i>Celoporthis woodiana</i>	CMW13936 ^T	<i>Tib. granulosa</i>	South Africa	M. Gryzenhout	N/A	DQ267131	DQ267143	N/A	Vermuelen et al. (2013)
	CMW13937	<i>Tib. granulosa</i>	South Africa	M. Gryzenhout	N/A	DQ267132	DQ267144	N/A	Vermuelen et al. (2013)
<i>Chrysopothis austroaficana</i>	CMW13228 ^T	<i>Corymbia sp.</i>	Australia	P.W. Crous & B.A. Summerell	JX0638867	N/A	N/A	N/A	Crous et al. (2012b)
	CBS13909 ^T	<i>Euc. urophylla × Euc. grandis</i>	Colombia	M. J. Wingfield	KR476771	KR476738	N/A	N/A	Crous et al. (2015)
<i>Chrysopothis legerstromiaeae</i>	CERC85810 ^T	<i>Lagerstroemia speciosa</i>	China	J. Roux & S.F. Chen	KY929330	KY929340	KY929350	N/A	Chen et al. (2018)
	CMW62	<i>L. speciosa</i>	China	S.F. Chen	KY929328	KY929338	KY929348	N/A	Chen et al. (2018)
<i>Chrysopothis colombiana</i>	CMW9327	<i>Euc. grandis</i>	South Africa	M. J. Wingfield	AY194097	AF292041	AF273458	N/A	Myburg et al. (2002b), Gryzenhout et al. (2006c)
	CMW21137 ^T	<i>Tib. granulosa</i>	South Africa	J. Roux	N/A	AF273473	AF273455	N/A	Myburg et al. (2002b), Gryzenhout et al. (2006c)
<i>Chrysopothis cubensis</i>	CBS10281	<i>Euc. grandis</i>	Cameroon	I.A.S. Gibson	AF408338	N/A	AF273462	N/A	Castlebury et al. (2002)
	CMW10453	<i>Euc. urophylla</i>	Democratic Republic of the Congo	N/A	AF408339	AY063476	AY063480	N/A	Gryzenhout et al. (2004)
<i>Chrysopothis saligna</i>	CMW8758	<i>Eucalyptus sp.</i>	Venezuela	M. J. Wingfield	AY194098	AF046988	AF273463	N/A	Castlebury et al. (2002), Gryzenhout et al. (2006c)
	CMW10669	<i>Eucalyptus sp.</i>	Republic of the Congo	J. Roux	N/A	AF5335122	AF5335126	N/A	Myburg et al. (2002b), Gryzenhout et al. (2006c)
<i>Chrysopothis semidecandra</i>	CMW10639	<i>Euc. grandis</i>	Colombia	C.A. Rodas	N/A	AY263421	AY263419	N/A	Castlebury et al. (2002)
	CMW10639	<i>Eucalyptus sp.</i>	Indonesia	M. J. Wingfield	N/A	AY214304	AY214268	N/A	Gryzenhout et al. (2004)
<i>Chrysopothis deuterocubensis</i>	CMW10450	<i>S. aromaticum</i>	Indonesia	N/A	AY084002	AY084014	AY084026	N/A	Myburg et al. (2003)
	CMW11287 ^T	<i>Euc. grandis</i>	Ecuador	M. J. Wingfield	N/A	AY214289	AY214253	N/A	Gryzenhout et al. (2005b)
<i>Chrysopothis hodgeana</i>	CMW10625	<i>Euc. grandis</i>	Ecuador	M. J. Wingfield	N/A	AY214290	AY214254	N/A	Gryzenhout et al. (2005b)
	CMW9955	<i>Mic. thaezeans</i>	Colombia	C.A. Rodas	N/A	AY9563670	AY9563679	N/A	Rodas et al. (2005)
<i>Chrysopothis semidecandra</i>	CMW10641 ^T =	<i>Tib. semidecandra</i>	Colombia	R. Athelaez	N/A	AY9563669	AY956378	N/A	Gryzenhout et al. (2004)
	CBS115854		Colombia	R. Athelaez	N/A	AY692322	AY692325	N/A	Gryzenhout et al. (2004)

Table 2 (cont.)

Identity	Isolate No. ^{1,2}	Host	Location	Collector	GenBank accession no.				References	
					LSU	ITS	BT2	BT1		
<i>Chrysopeltis inopina</i>	CMW12727 ^T	<i>Tib. lepidota</i>	Colombia	R. Arbelaez	N/A	DQ3688777	DQ3688807	DQ3688806	Gryzenhout et al. (2006d)	
	CMW12729	<i>Tib. lepidota</i>	Colombia	R. Arbelaez	N/A	DQ3688778	DQ3688809	DQ3688808	Gryzenhout et al. (2006d)	
	CMW29940 ^{T=}	<i>S. guineense</i>	Zambia	D. Chungu & J. Roux	N/A	FJ655005	FJ805236	FJ805230	Chungu et al. (2010)	
<i>Chrysopeltis zambiensis</i>	CBS124488	<i>S. guineense</i>	Zambia	D. Chungu & J. Roux	N/A	FJ655007	FJ805238	FJ805232	Chungu et al. (2010)	
	CMW29942 ⁼									
	CBS124490 ^{T=}	<i>Euc. grandis</i>	Zambia	D. Chungu & J. Roux	N/A	FJ655002	FJ805233	FJ805709	Chungu et al. (2010)	
	CMW29930 ⁼	<i>Euc. grandis</i>	Zambia	D. Chungu & J. Roux	N/A	FJ655004	FJ805235	FJ858711	Chungu et al. (2010)	
<i>Conticimborus sinomyrti</i>	CERC3629 ^T	<i>Rhodomyrtus tomentosa</i>	China	S.F. Chen & G.Q. Li	KT167179	KT167189	KT167189	KT167189	Chen et al. (2016)	
	CERC3631	<i>Rho. tomentosa</i>	China	S.F. Chen & G.Q. Li	KT167180	KT167170	KT167190	KT167190	Chen et al. (2016)	
<i>Cryphonectria decipiens</i>	CMW10436	<i>Quercus suber</i>	Portugal	B. d' Oliveira	JQ862750	AF4525710	AF4525703	N/A	Myburg et al. (2004b), Chen et al. (2013a)	
	CMW10438	<i>Castanea sativa</i>	Italy	A. Biraghi	N/A	AF368327	A3F368349	N/A	Venter et al. (2002), Myburg et al. (2004b)	
<i>Cryphonectria japonica</i>	CMW10527	<i>Q. mongolica</i>	Russia	L. Vasiljeva	AF408341	DQ120761	DQ120768	DQ120767	Castlebury et al. (2002), Gryzenhout et al. (2006c)	
	CMW10528	<i>Q. mongolica</i>	Russia	L. Vasiljeva	AF408340	DQ120760	DQ120766	DQ120765	Castlebury et al. (2002), Gryzenhout et al. (2006c)	
	CMW13742	<i>Q. grosseserrata</i>	Japan	T. Kobayashi	N/A	AY697936	AY6979362	AY6979361	Myburg et al. (2004a)	
	CMW13747	<i>Q. serrata</i>	Japan	T. Kobayashi	N/A	AY697937	AY6979364	AY6979363	Myburg et al. (2004a)	
<i>Cryphonectria macrospora</i>	CMW10463	<i>Cas. cuspidata</i>	Japan	T. Kobayashi	N/A	AF368331	A3F368350	AF368351	Gryzenhout et al. (2006c)	
	CMW10914	<i>Cas. cuspidata</i>	Japan	T. Kobayashi	N/A	JQ627249	AY6979342	AY6979734	Gryzenhout et al. (2006c), Chen et al. (2013a)	
<i>Cryphonectria parasitica</i>	N/A	<i>Castanea</i> sp.	USA	R.J. Stipes	AF277132	N/A	N/A	N/A	Zhang & Blackwell (2001)	
	CMW7048	<i>Q. virginiana</i>	USA	AY194100	AF368330	AF273470	AF273076	N/A	Venter et al. (2002), Gryzenhout et al. (2006c)	
	CMW13749	<i>Cas. mollisima</i>	Japan	N/A	AY697937	AY6979344	AY6979343	N/A	Myburg et al. (2004a)	
<i>Cryphonectria quercicola</i>	CFCC52140 ^T	<i>Q. wutaishansea</i>	ShaanXi, China	N. Jiang	N/A	MG866026	MG866013	MG866118	Jiang et al. (2018)	
	CFCC52141	<i>Q. wutaishansea</i>	ShaanXi, China	N. Jiang	N/A	MG866027	MG866114	MG866118	Jiang et al. (2018)	
<i>Cryphonectria quercus</i>	CFCC52138 ^T	<i>Q. aliena</i> var. <i>acuteserrata</i>	ShaanXi, China	N. Jiang	N/A	MG866024	MG866111	MG866115	Jiang et al. (2018)	
	CFCC52139	<i>Q. aliena</i> var. <i>acuteserrata</i>	ShaanXi, China	N. Jiang	N/A	MG866025	MG866112	MG866116	N/A	
<i>Cryphonectria radicalis</i>	CMW10455	<i>Q. suber</i>	Italy	A. Biraghi	AY194101	AF452113	AF525712	AF525705	Gryzenhout et al. (2006c)	
	CMW10477	<i>Q. suber</i>	Italy	A. Biraghi	AY194102	AF368328	AF368347	AF368347	Venter et al. (2002), Gryzenhout et al. (2006c)	
	CMW13754	<i>Fagus japonica</i>	Japan	T. Kobayashi	N/A	AY697932	AY697954	AY697953	Myburg et al. (2004a)	
<i>Cryptometrinia aestuescens</i>	CMW18790	<i>Euc. grandis</i>	Indonesia	M.J. Wingfield	HQ171211	GQ369458	GQ369455	GQ369455	Gryzenhout et al. (2010), Vermeulen et al. (2011)	
	CMW28535 ⁼	<i>Euc. grandis</i>	North Sumatra, Indonesia	M.J. Wingfield	N/A	GQ369457	GQ369454	GQ369454	N/A	
<i>Diversimorbus metrosiderotis</i>	CBS12409	<i>Metrosideros angustifolia</i>	South Africa	J. Roux	JQ862827	JQ862852	JQ862911	N/A	Chen et al. (2013b)	
	CMW37321	<i>Mét. angustifolia</i>	South Africa	J. Roux	JQ862828	JQ862871	JQ862953	JQ862912	Chen et al. (2013b)	
	CMW37322 ^T	<i>Mét. angustifolia</i>	USA	N/A	AF362555	N/A	N/A	N/A	Gryzenhout et al. (2009)	
<i>Endothia grossa</i>	NA	<i>Quercus</i> sp.	USA	R.J. Stipes	AY194114	AF568325	AF568336	N/A	Venter et al. (2002), Gryzenhout et al. (2006c)	
	CMW2091	<i>Q. palustris</i>	USA	R.J. Stipes	AY194115	AF568326	AF568338	N/A	Venter et al. (2002), Gryzenhout et al. (2006c)	
	CMW10442	<i>Euc. coccifera</i>	Australia	C. Mohammed	GQ303307	GQ303276	N/A	N/A	Cheewangkoon et al. (2009)	
	CMW124779 ^T	<i>Met. angustifolia</i>	South Africa	J. Roux, S.F. Chen & F. Roets	JQ862811	JQ862854	JQ862936	JQ863051	Chen et al. (2013b)	
	CMW37887 ^T	<i>Met. angustifolia</i>	South Africa	J. Roux, S.F. Chen & F. Roets	JQ862816	JQ862859	JQ862941	JQ862900	Chen et al. (2013b)	
<i>Foliocyphiphia capensis</i>	CMW37329	<i>Euc. grandis</i>	South Africa	M. Ventier	JQ862794	JQ862837	JQ862919	JQ862878	Chen et al. (2013b)	
	CMW7033 ^T	<i>Euc. saligna</i>	South Africa	M. Ventier	JQ862795	JQ862838	JQ862920	JQ862879	Chen et al. (2013b)	
	CMW37335	<i>Met. angustifolia</i>	South Africa	J. Roux & S.F. Chen	JQ862791	JQ862834	JQ862916	JQ862875	Chen et al. (2013b)	
	CMW37336	<i>Met. angustifolia</i>	South Africa	J. Roux & S.F. Chen	JQ862792	JQ862835	JQ862917	JQ862876	Chen et al. (2013b)	
	CMW37337 ^T	<i>Met. angustifolia</i>	South Africa	J. Roux & S.F. Chen	JQ862798	JQ862841	JQ862923	JQ862882	Chen et al. (2013b)	
	CMW37338	<i>Met. angustifolia</i>	South Africa	J. Roux & S.F. Chen	JQ862799	JQ862842	JQ862924	JQ862883	Chen et al. (2013b)	
	CMW6246	<i>Tib. granulosa</i>	Australia	M.J. Wingfield	JQ862892	JQ862845	JQ862927	JQ862886	Chen et al. (2013b)	
	CMW10015	<i>Euc. fastigata</i>	New Zealand	R.J. van Boven	JQ862806	JQ862849	JQ862931	JQ862890	Chen et al. (2013b)	
	CMW37314 ^T	<i>Rapanea melanophloeos</i>	South Africa	M.J. Wingfield & J. Roux	JQ862755	JQ862765	JQ862775	JQ862878	Chen et al. (2013a)	
	CMW37315	<i>Rap. melanophloeos</i>	South Africa	M.J. Wingfield & J. Roux	JQ862756	JQ862776	JQ862786	N/A	Chen et al. (2013a)	
	CMW28274	<i>Galpinia transvaalica</i>	Swaziland	J. Roux	HQ171213	GU726946	GU726958	GU726958	N/A	Vermulen et al. (2011)

Table 2 (cont.)

Identity	Isolate No. ^{1,2}	Host	Location	Collector	GenBank accession no.			References
					LSU	ITS	BT2	
<i>Latruncula auroriae</i> (cont.)	CMW28276 ^t	<i>G. transvaalica</i>	Swaziland	J. Roux	HQ730872	GU726947	GU726959	N/A
	CMW28275	<i>G. transvaalica</i>	Swaziland	J. Roux	HQ171214	HQ171207	HQ171207	N/A
<i>Luteocirrus shearii</i>	CBS130775	<i>Banksia baxteri</i>	Australia	C. Crane	KC197024	KC197009	KC197015	N/A
	CBS130776 ^t	<i>B. baxteri</i>	Australia	C. Crane	KC197019	KC197021	KC197006	N/A
<i>Microthia havanensis</i>	CMW11299	<i>Myrica faya</i>	Madeira	N/A	AY194087	N/A	N/A	Gryzenhout et al. (2009)
	CMW11300	<i>Myr. faya</i>	Madeira	N/A	AY194088	N/A	N/A	Gryzenhout et al. (2009)
	CMW11301	<i>Myr. faya</i>	Azores	C.S. Hodges & D.E. Gardner	AY214323	AY214287	AY214251	N/A
	CMW14550	<i>E. saligna</i>	Mexico	C.S. Hodges	N/A	DQ368735	DQ368742	DQ368741
<i>Myronectria myrtacearum</i>	CMW4633 ^t	<i>Heptopyxis natalensis</i>	South Africa	Ali & J. Roux	MG585750	MG585734	MG585720	N/A
	CMW46335	<i>S. cordatum</i>	South Africa	Ali & J. Roux	MG585751	MG585737	MG585721	N/A
<i>Rostraeum tropicale</i>	CMW9972	<i>Terminalia ivorensis</i>	Ecuador	M.J. Wingfield	AY194092	AY167436	AY167431	AY167426
	CMW10796 ^t	<i>Ter. ivorensis</i>	Ecuador	M.J. Wingfield	N/A	AY167438	AY167433	N/A
	CMW9971	<i>Ter. ivorensis</i>	Ecuador	M.J. Wingfield	N/A	AY167435	AY167430	N/A
	CMW18119 ^t	<i>Coccoloba uvifera</i>	USA	C.S. Hodges	EF392860	DQ368755	DQ368759	N/A
	CMW18115	<i>Coc. uvifera</i>	USA	C.S. Hodges	N/A	DQ368756	DQ368761	DQ368760
	CMW5587	<i>Malus domestica</i>	South Africa	W.A. Smit	N/A	AF543818	AF543822	N/A
	CMW5288	<i>M. domestica</i>	South Africa	W.A. Smit	N/A	AF543817	AF543821	Gryzenhout et al. (2006a)
								Gryzenhout et al. (2006a)

¹ Designation of isolates and culture collections: ATCC = American Type Culture Collection, Manassas, USA; CBL represent isolates in Ferreira et al. (2019); CBS = Westerdijk Fungal Biodiversity Institute, Utrecht, Netherlands; CERC = China Eucalypt Research Centre (CERC), Chinese Academy of Forestry (CAF), Zhanjiang, Guangdong, China; CFFCC = China Forestry Culture Collection Center, Beijing, China; CMW = Tree Protection Co-operative Program, Forestry and Agricultural Biotechnology Institute, University of Pretoria, South Africa; MES, CTS

² Following isolate number means isolates are ex-type or from samples that have been linked morphologically to type material of the species.

³ N/A = not available.

hybrid genotype (CEPT53), which is widely cultivated in plantations in southern China, were used to induce the production of sporocarps. This method has previously been effectively used in morphological studies for species of *Cryphonectriaceae* (Chen et al. 2011, 2016, Vermeulen et al. 2013, Wang et al. 2018).

The isolates identified as new species by DNA sequence analyses were grown on 2 % water agar (WA) (20 g agar per L water) plates, to which sterilised freshly cut branch sections (0.5–1 cm diam, 2–3 cm length) of the *Eucalyptus* hybrid genotype CEPT53 were added. These fungi with branch sections on 2 % WA were incubated at room temperature for 6–8 wk until sporocarps emerged.

The induced sporocarps were removed from the specimens under a dissecting microscope and then embedded in Leica Biosystems Tissue Freezing Medium (Leica Biosystems Nussloch GmbH, Nussloch, Germany) and sectioned (10 µm thick) using a Microtome Cryostat Microm HM550 (Microm International GmbH, Thermo Fisher Scientific, Walldorf, Germany) at –20 °C to observe stromata and stromatic tissue. Conidiophores, conidiogenous cells and conidia were measured after crushing the sporocarps on microscope slides in sterilized water. For the holotype specimens, 50 measurements were performed for each morphological feature, and 30 measurements per character were made for the remaining specimens.

Measurements were recorded using an Axio Imager A1 microscope (Carl Zeiss Ltd., Munchen, Germany) and an AxioCam ERc 5S digital camera with Zeiss Axio Vision Rel. 4.8 software (Carl Zeiss Ltd., Munchen, Germany). Characteristics of the new species in this study were compared with those published genera and species in *Cryphonectriaceae* (Table 2). The results are presented as (minimum–) (mean – standard deviation) – (mean + standard deviation) (–maximum).

Isolates identified as new species were selected for studying culture characteristics. After the isolates were grown for 7 d on 2 % MEA, a 5-mm plug was removed from each culture and transferred to the centres of 90-mm MEA Petri dishes. The cultures were incubated in the dark under temperatures ranging from 5 °C to 35 °C at 5 °C intervals. Five replicate plates for each isolate at each temperature condition were prepared. Two diameter measurements, perpendicular to each other, were taken daily for each colony until the fastest growing culture had covered the 90 mm Petri dishes. Averages of the diameter measurements at each of the seven temperatures were computed with Microsoft Excel 2013 (Microsoft Corporation, Albuquerque, NM, USA). Colony colours were determined by incubating the isolates on fresh 2 % MEA at 25 °C in the dark after 7 d. The colour descriptions of the sporocarps and colonies were according to the colour charts of Rayner (1970).

Pathogenicity tests

Inoculations were conducted to determine the pathogenicity of the identified *Cryphonectriaceae* species on different *Myrtales* from which the fungi were obtained. This was done to fulfil Koch's postulates and to understand the pathogenicity differences between *Cryphonectriaceae* species on different *Myrtales*. In the current study, all of the identified species of *Cryphonectriaceae* were inoculated on the *Myrtales* from which the isolates were primarily obtained, and these *Myrtales* included *Eucalyptus* hybrid genotypes, *Melastoma sanguineum*, *P. guajava*, and *Syzygium jambos*. The inoculated *Myrtales* included seedlings of two *Eucalyptus* hybrid genotypes, branches of *M. sanguineum*, seedlings of *P. guajava* and seedlings of *S. jambos*. Furthermore, the isolates representing one new species from *T. neotaliala* were inoculated on the branches of *T. neotaliala*.

Isolates from *Mytales* representing different species of *Cryphonectriaceae* identified by DNA sequence comparisons and morphological characteristics were selected for inoculation. The selected isolates were grown on 2 % MEA at 25 °C for 10 d prior to inoculation. Each of the selected isolates were inoculated on 10 seedlings or branches of each inoculated *Mytales*, and 10 additional seedlings or branches were inoculated with sterile MEA plugs to serve as negative controls. The inoculations on seedlings of two *Eucalyptus* hybrid genotypes, *P. guajava* and *S. jambos* were conducted in the glasshouse. The inoculations on branches of *M. sanguineum* and *T. neotaliala* were conducted in the field. Two widely planted *E. grandis* hybrid genotypes (CEPT46 and CEPT53) were used for inoculations, and the inoculated *Eucalyptus* seedlings were 1-yr-old, approximately 2 m tall, and 10 mm diam. The inoculated *P. guajava* seedlings were 18-mo-old, approximately 1 m tall, and 15 mm diam, and these seedlings were purchased from the same nursery. *Syzygium jambos* seedlings for the inoculations were 2-yr-old, approximately 1.5 m tall and 15 mm diam, and these seedlings were cultivated from the seeds of one single *S. jambos* tree. Ten *M. sanguineum* trees in one *Eucalyptus* plantation were selected for inoculations. The trees were 5–6-yr-old, and the main stems were 6–8 cm diam. Each of the selected isolates were inoculated on 10 branches from 10 trees, and the branches were 1-yr-old and 8–10 mm diam. Ten 10-yr-old *T. neotaliala* trees in a nursery were selected. The main stems were 15–20 cm diam, and each of the selected isolates were inoculated on 10 branches from 10 trees, and the branches were 1-yr-old, and 8–10 mm diam.

The inoculations on seedlings and branches were conducted using the same method described by Chen et al. (2010, 2013b). The inoculations were conducted in July 2018 and the results were evaluated after 6 wk by measuring the lengths (mm) of the lesions on the cambium. For re-isolations, small pieces of discoloured xylem from the edges of the resultant lesions were cut and placed on 2 % MEA at room temperature. Re-isolations of all seedlings/branches inoculated as negative controls and from four randomly selected trees per isolate were conducted. The identities of the re-isolated fungi were confirmed by morphological comparisons. The inoculation results were analysed using SPSS Statistics 20 software (IBM Corp., Armonk, NY, USA) by one-way analysis of variance (ANOVA).

RESULTS

Fungal isolation

The isolates obtained in this study were isolated mainly from *Eucalyptus* hybrid genotypes, *M. sanguineum*, *P. guajava*, and *S. jambos*, and a relatively small number of isolates were from *M. candidum*, *S. hancei*, *S. samarangense*, and *T. neotaliala*. In total, 445 isolates with typical morphological characteristics of *Cryphonectriaceae* were isolated. One to two isolates from each tree were selected for further study, depending on the culture morphology among the isolates obtained from the same tree, and 164 isolates were ultimately selected for further analyses.

A total of 164 isolates were obtained from *Mytales* trees in GuangDong, GuangXi and HaiNan Provinces, as well as in the Hong Kong Region. The 86 isolates obtained from GuangDong Province were collected from ZhanJiang Region: these included two isolates from two trees in one *E. grandis* hybrid plantation, 14 isolates from seven trees in four *E. urophylla* hybrid plantations, and six isolates from three trees in one *E. urophylla* × *E. grandis* hybrid plantation. On *M. sanguineum*, five isolates were collected from three shrubs in two *E. urophylla* × *E. grandis* hybrid plantations, and four isolates were collected from two shrubs in a park. Eleven isolates were obtained from six

P. guajava trees in two parks. On trees of *Syzygium*, 12 isolates were from eight *S. hancei* trees in a park, eight isolates from four *S. jambos* trees in three parks, eight isolates from five *S. samarangense* trees in a park, and four isolates from two *Syzygium*-like trees in a park. Five isolates were obtained from three *T. neotaliala* trees in a park. Seven additional isolates were collected from four trees of one unknown species of *Myrtaceae* (Table 1). In GuangXi Province, seven isolates were obtained from four trees in one *E. urophylla* × *E. grandis* hybrid plantation. Six isolates from HaiNan Province were isolated from six *S. samarangense* trees (Table 1). In the Hong Kong Region, all 65 isolates were collected from *Melastoma* shrubs in one natural protection area, and these included 58 isolates from 30 *M. candidum* shrubs and seven isolates from four *M. sanguineum* shrubs (Table 1).

Phylogenetic analyses

For the 164 isolates selected for sequencing in this study, the PCR fragments were approximately 620, 490, 510, 310, and 1300 bp for the ITS, *tub2*, *tub1*, *tef1*, and LSU regions, respectively. All sequences obtained in this study were deposited in GenBank (Table 1). The genotype for each isolate was determined based on the ITS, *tub2*, *tub1*, *tef1*, and LSU sequences (Table 1). Since a relatively large number of isolates were sequenced in this study, one isolate of each genotype was selected and used for phylogenetic analyses of 'Generic placement in *Cryphonectriaceae*' and 'Species identification in *Cryphonectriaceae*' (Table 1). For 'Phylogenetic analyses of *Chrysoporthe*' and 'Phylogenetic analyses of *Celoporthe*', one to two isolates were selected from each host × location in each genotype, depending on the number of isolates of each host × location (Table 1). For the isolates representing new species/genus, all isolates were used in all phylogenetic analyses (Table 1). The alignments of each of the datasets were deposited in TreeBASE (<http://purl.org/phylo/treebase/phylows/study/TB2:S25021>). The number of taxa and characters in each of the datasets, and a summary of the most important parameters applied in the maximum parsimony (MP) and maximum likelihood (ML) analyses, are presented in Table 3.

Generic placement in *Cryphonectriaceae*

Although the inferred phylogenetic relationships among genera differed between MP and ML analyses, each genus in the *Cryphonectriaceae* formed a unique phylogenetic clade in both the MP and ML analyses based on LSU sequence, with the exception of *Cryphonectria* (Fig. 3). Isolates collected from *Mytales* in this study were clearly grouped in the family *Cryphonectriaceae*, forming four distinct Clusters (Clusters A–D) (Fig. 3). With the exception of isolates CSF2060–CSF2065, CSF8776, CSF8777, CSF10437, CSF10438, CSF10440, CSF10459, CSF10460, and CSF10738, which grouped in a distinct Cluster (Cluster D), the other isolates in Clusters A–C grouped within the genera *Chrysoporthe*, *Celoporthe*, and *Aurifilum*, respectively. The distinct Cluster D was separated from all other genera and was supported by high bootstrap values (ML/MP: 98 %/84 %) (Fig. 3). The isolates in Cluster D represent a novel genus in the family *Cryphonectriaceae* (Fig. 3).

The PHT for the datasets of 5.8S rRNA and exons of the *tub* (*tub2* and *tub1*) gene regions indicated that the two datasets were congruent ($P = 0.890$), and thus they were consequently combined for further analyses (Cunningham 1997). Phylogenetic analyses indicated that all of the *Cryphonectriaceae* genera formed independent phylogenetic clades with high bootstrap values (ML > 80 %, MP > 80 %) both in the ML and MP analyses, with the exception of *Cryphonectria* (Fig. 4). Though the positions of the genera relative to each other were different in the MP and ML analyses, the topology of the two analyses was

Table 3 Datasets used and the statistics resulting from the phylogenetic analyses.

Family/Genus	Dataset	No. of taxa	No. of bp ¹	PIC ²				Maximum parsimony			
				No. of trees	Tree length	C _i ³	RI ⁴	RC ⁵	HI ⁶		
<i>Cryphonectriaceae</i>	LSU	135	631	138	1000	350	0.500	0.845	0.500		
	5.8S+BT2+BT1	151	675	115	1000	288	0.524	0.916	0.476		
	ITS	156	615	299	1014	1479	0.430	0.909	0.570		
	BT2+BT1	151	927	486	1000	2261	0.446	0.908	0.554		
	ITS+BT2+BT1	156	1542	785	85	3829	0.431	0.905	0.569		
	ITS	59	488	79	1	81	0.975	0.988	0.025		
	BT2+BT1	59	822	169	6	188	0.941	0.976	0.910	0.059	
	ITS+BT2+BT1	59	1310	248	6	274	0.934	0.964	0.900	0.066	
<i>Chrysoporthe</i>	ITS	48	512	92	17	126	0.865	0.963	0.833	0.135	
	BT2+BT1	48	822	134	5000	182	0.885	0.955	0.844	0.115	
	TEF	44	280	73	3	90	0.933	0.973	0.908	0.067	
	ITS+BT2+BT1+TEF	48	1614	299	4	409	0.952	0.866	0.824	0.134	
Family/Genus	Dataset	Subst. model ⁷	NST ⁸	Rate matrix				Maximum likelihood			
				Subst. model ⁷	Ti/Tv ratio ⁹	p-inv	Gamma	Subst. model ⁷	Ti/Tv ratio ⁹	p-inv	Rates
<i>Cryphonectriaceae</i>	LSU	TIM2+I+G	6	2.278	7.181	2.278	1	18.36	–	0.51	0.484
	5.8S+BT2+BT1	TIM2+I+G	6	1	2.66	1	1	10.311	–	0.73	2.392
	ITS	TIM2+I+G	6	1.949	3.04	1.949	1	6.317	–	0.37	0.541
	BT2+BT1	HKY+++G	2	–	–	–	–	–	2.45	0.47	1.5
	ITS+BT2+BT1	TVM+I+G	6	1.261	4.477	1.261	1	4.477	–	0.445	0.956
	ITS	K80	2	–	–	–	–	–	1.155	0	–
	BT2+BT1	TIM1+G	6	1	1.818	0.289	0.289	3.54	–	0	0.28
	ITS+BT2+BT1	TIM1+G	6	1	2	0.442	0.442	3.563	–	0	0.182
<i>Chrysoporthe</i>	ITS	TPM2+G	2	–	–	–	–	–	–	0	0.411
	BT2+BT1	TIM3+G	6	3.621	7.552	1	3.621	15.109	–	0	0.024
	TEF	TPM2u+G	2	–	–	–	–	–	2.812	0	0.3
	ITS+BT2+BT1+TEF	TrN+G	6	1	2.823	1	1	4.258	–	0	0.166

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.

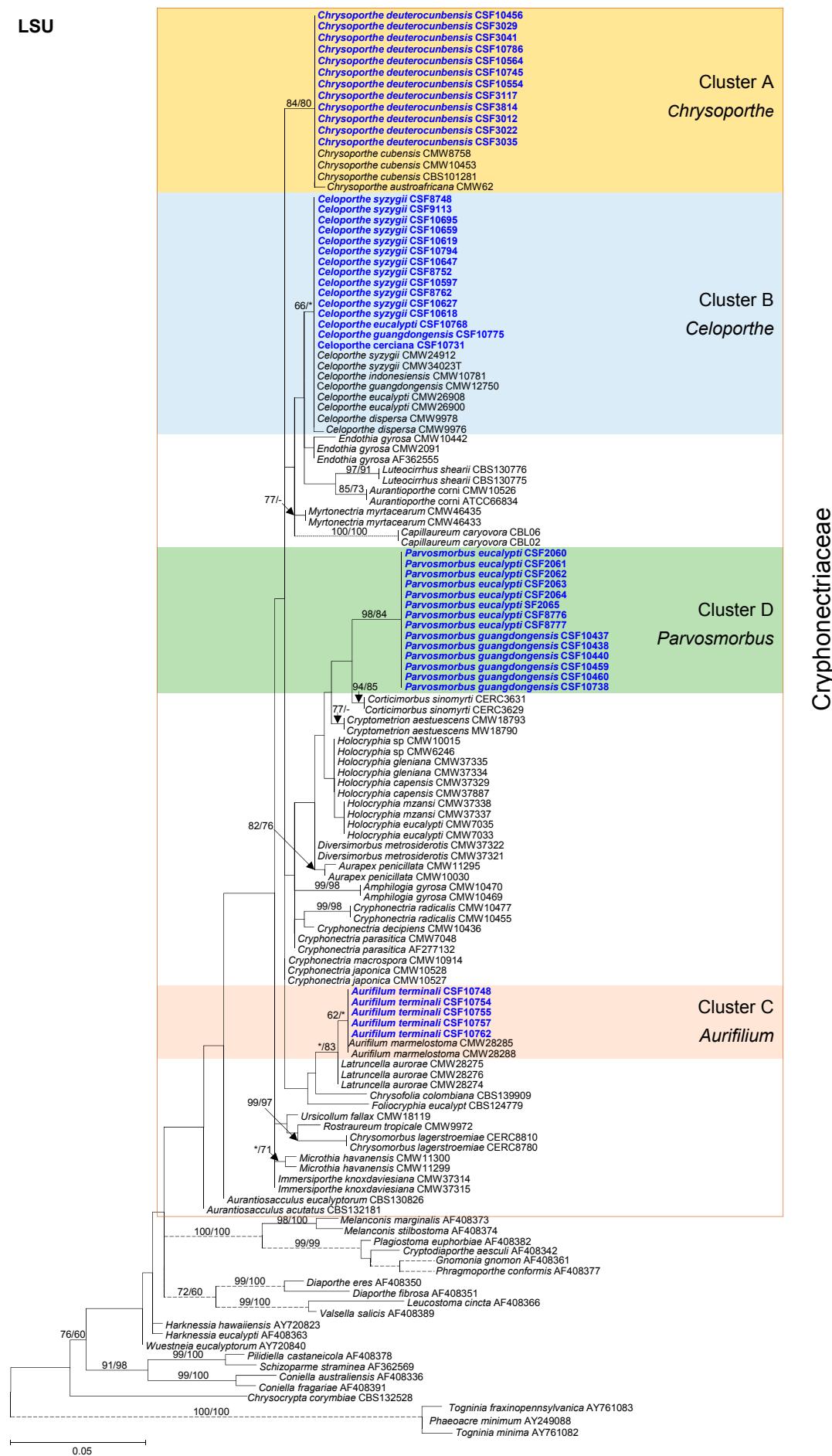


Fig. 3 Phylogenetic tree based on maximum likelihood (ML) analysis of LSU DNA sequences for various genera in Diaporthales. Bootstrap values $\geq 70\%$ for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70 % are marked with *, and absent analysis values are marked with -. Isolates collected in this study are in **bold** and blue. *Togninia minima* (CBS6580) (*Togniniaceae*), *Tog. fraxinopennsylvanica* (ATCC26664), and *Phaeoacremonium minimum* (A207) (*Togniniaceae*) were used as outgroup taxa.

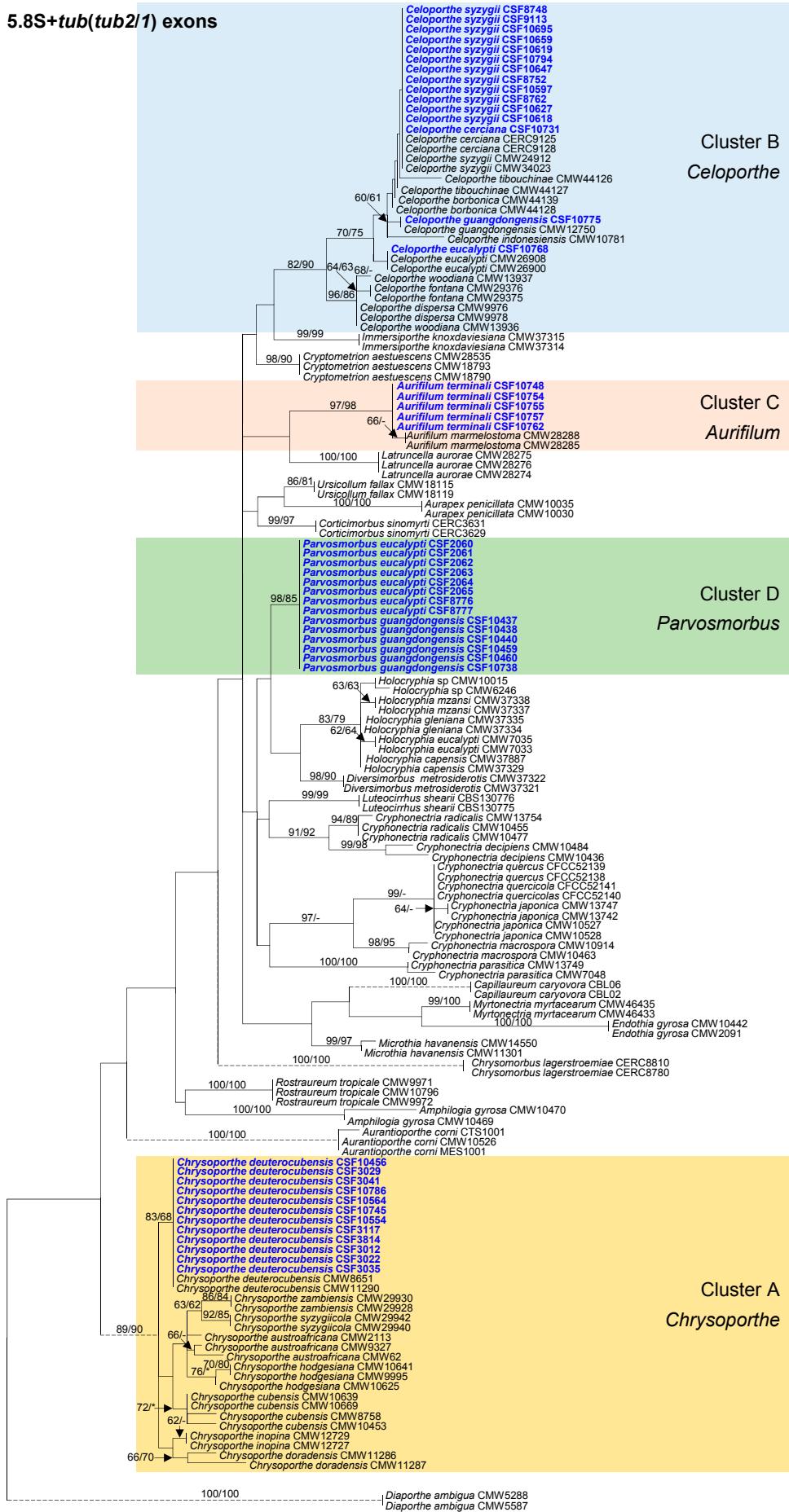


Fig. 4 Phylogenetic tree based on maximum likelihood (ML) analysis of a combined DNA sequence dataset of regions of the 5.8S rRNA gene, and partial exon 4, exon 5, partial exon 6 and partial exon 7 of the *tub* genes, for species in *Cyphonoctriaceae*. Bootstrap values $\geq 70\%$ for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70 % are marked with *, and absent analysis values are marked with -. Isolates collected in this study are in **bold** and blue. *Diaporthe ambigua* (CMW5287 and CMW5588) (*Diaporthaceae*) was used as outgroup taxon.

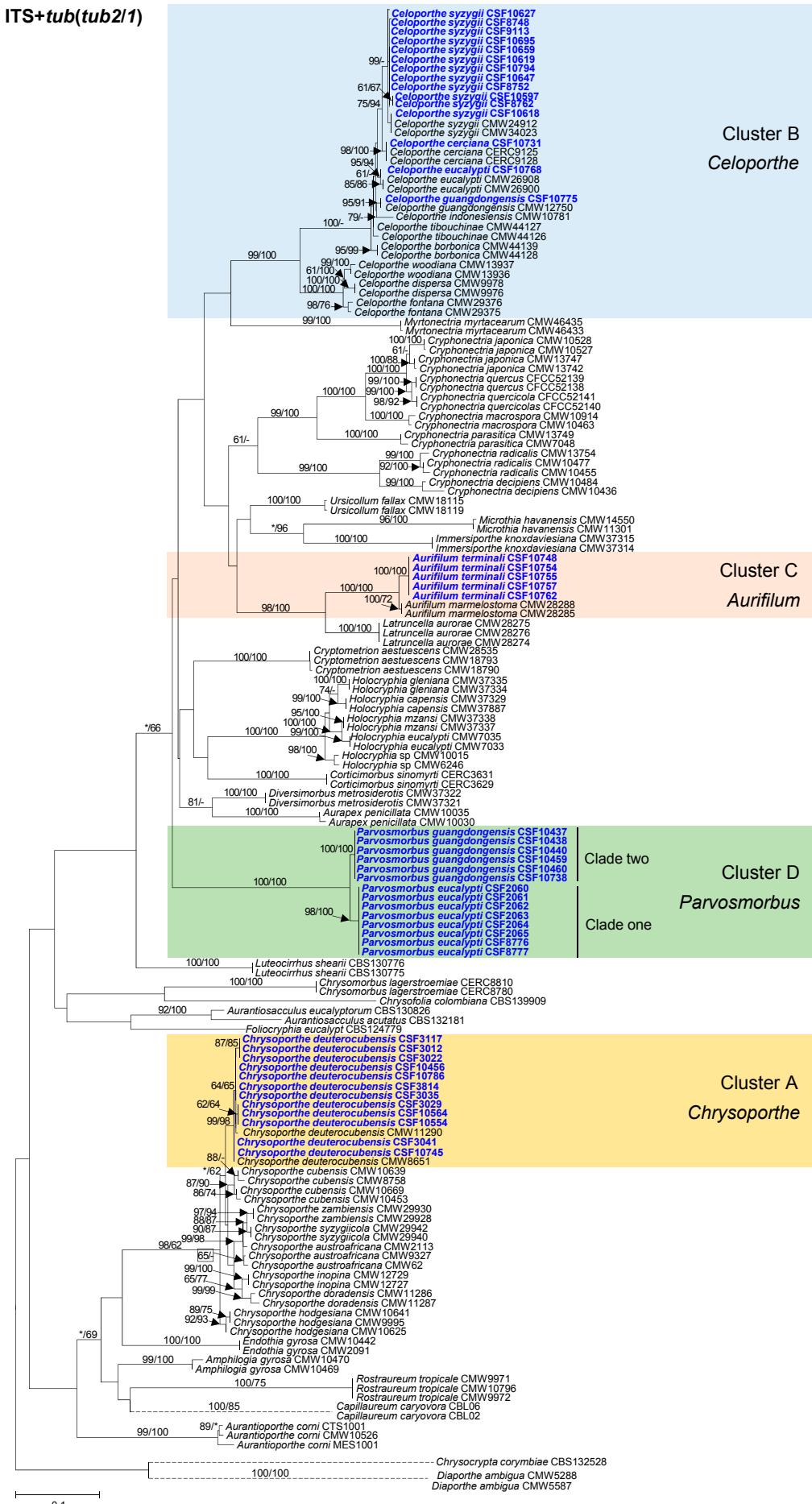


Fig. 5 Phylogenetic trees based on maximum likelihood (ML) analyses of a combined DNA sequence dataset of combination of ITS and *tub* (*tub2/tub1*) regions for various genera in the *Diaporthales*. Bootstrap values $\geq 70\%$ for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70 % are marked with *, and absent analysis values are marked with -. Isolates collected in this study are in **bold** and blue. *Diaporthambigua* (CMW5287 and CMW5588) (*Diaporthaceae*) was used as outgroup taxon.

similar for most genera. Based on the phylogenetic analyses of the combined sequences of the 5.8S gene and *tub* exons, the *Myrtaceae* isolates obtained in this study were distributed across four Clusters (Clusters A–D). The isolates in Clusters A and B were grouped within the genera *Chrysoporthe* and *Celoporthe*, respectively. The isolates obtained in this study in Cluster C were phylogenetically close to *Aurifilum marmelostoma*, but formed one independent clade (Fig. 4). Isolates in Cluster D were separated from all other genera and were supported by high bootstrap values (ML/MP: 98 %/85 %), thus representing a novel genus in the *Cryphonectriaceae* (Fig. 4).

Species identification in *Cryphonectriaceae*

For the datasets of the ITS and *tub* (*tub2* and *tub1*), the PHT generated a value of $P = 0.001$, and consequently, the sequence

data for ITS and *tub* regions were combined (Cunningham 1997). For each of the ITS, *tub* (*tub2* and *tub1*), and ITS+*tub* datasets, the ML and MP analyses generated trees with generally consistent topologies and phylogenetic relationships among taxa. Based on the phylogenetic analyses of the ITS, *tub* (*tub2* and *tub1*), and ITS+*tub* datasets, the isolates obtained in this study resided in four Clusters (Clusters A–D) (Fig. 5, S4, S5).

The isolates in Clusters A and B were grouped within the genera *Chrysoporthe* and *Celoporthe*, respectively (Fig. 5, S4, S5). All of the isolates in Cluster A were identified as *Chr. deuterocubensis* (Fig. 5, S4, S5). The isolates in Cluster B were distinguished into four species, including *Cel. syzygii*, *Cel. eucalypti*, *Cel. guangdongensis* and *Cel. cerciana* (Fig. 5, S4, S5). The species identification details of *Chrysoporthe* and *Celoporthe* are presented in the following sections ‘Phylogenetic

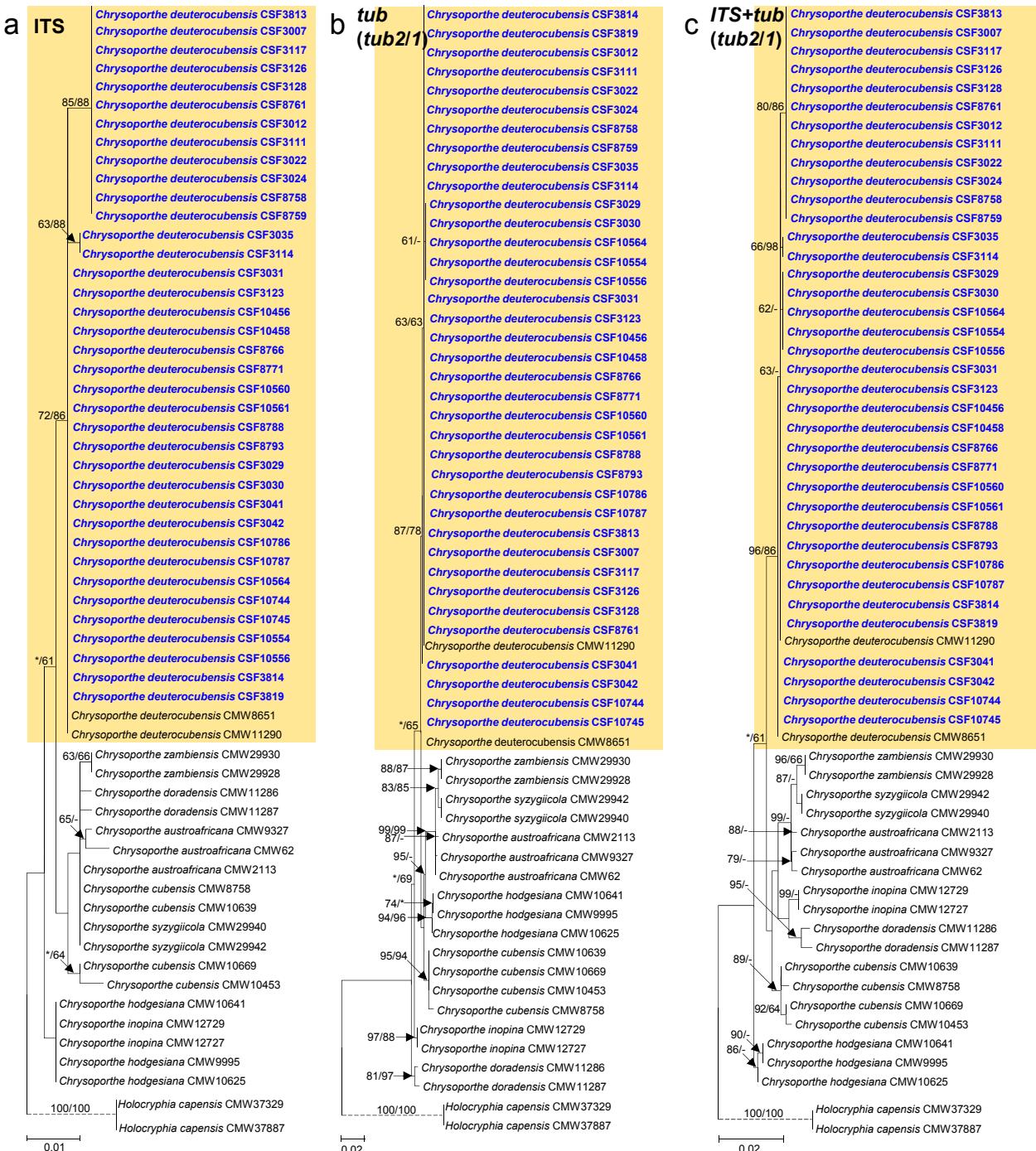


Fig. 6 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Chrysoporthe*. a. ITS region; b. two regions of *tub* (*tub2/tub1*); c. combination of ITS and *tub* (*tub2/tub1*). Bootstrap values $\geq 70\%$ for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70 % are marked with *, and absent analysis values are marked with -. Isolates collected in this study are in **bold** and blue. *Holcophypha capensis* (CMW37329 and CMW37887) was used as outgroup taxon.

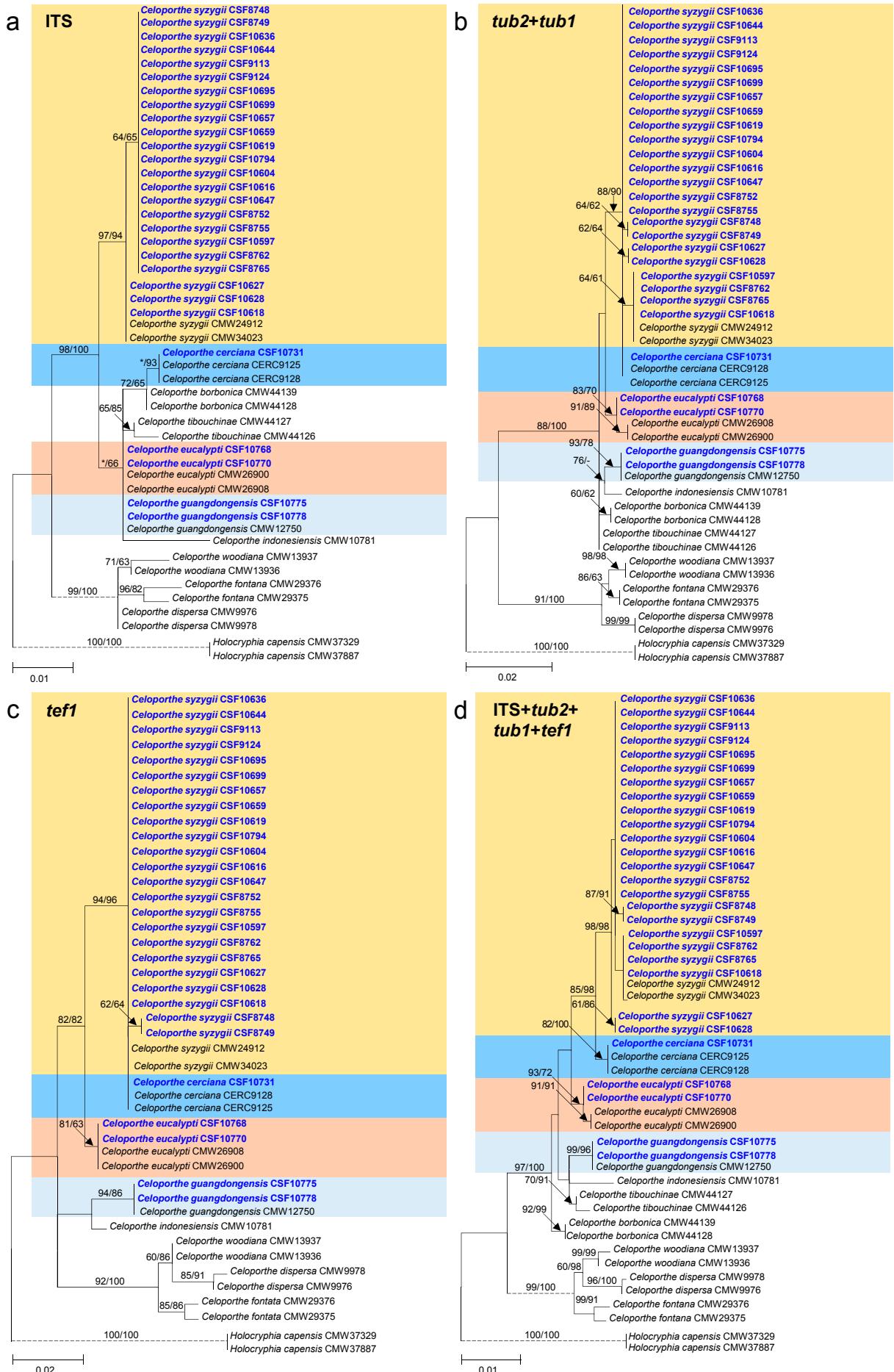


Fig. 7 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Celoporthes*. a: ITS region; b: two regions of *tub* (*tub2/tub1*); c: *tef1* gene region; d: combination of ITS, *tub2/tub1*, and *tef1* regions. Bootstrap values $\geq 70\%$ for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70 % are marked with *, and absent analysis values are marked with -. Isolates collected in this study are in **bold** and blue. *Holcryspha capensis* (CMW37329 and CMW37887) was used as outgroup taxon.

analyses of *Chrysoporthe*' and 'Phylogenetic analyses of *Celoporthe*', respectively. Further isolates from all host × location representing all of the genotypes based on sequences ITS, tub2, tub1, tef1, and LSU were used for the following analyses. The isolates obtained in this study in Cluster C that were phylogenetically close to *Aur. marmelostoma*, formed one independent clade that was supported by high bootstrap values (ITS, ML/MP: 96 %/100 %; tub, ML/MP: 100 %/100 %; ITS+tub, ML/MP: 100 %/100 %) (Fig. 5, S4, S5). These isolates represent a novel species of *Aurifilum*.

Isolates in Cluster D were separated from all other genera and were also supported by high bootstrap values (ITS, ML/MP: 100 %/100 %; tub, ML/MP: 100 %/100 %; ITS+tub, ML/MP: 100 %/100 %) (Fig. 5, S4, S5), representing a novel genus. Two clades formed within Cluster D and were also supported by high bootstrap values (Clade one, ITS, ML/MP: not available/not available; tub, ML/MP: 99 %/87 %; ITS+tub, ML/MP: 98 %/100 %; Clade two, ITS, ML/MP: 99 %/96 %; tub, ML/MP: 99 %/not available; ITS+tub, ML/MP: 100 %/100 %) (Fig. 5, S4, S5). The analyses indicated that the isolates in Cluster D represent two novel species, which resided in a novel genus of *Cryphonectriaceae*.

Phylogenetic analyses of Chrysoporthe

For the ITS and tub (tub2 and tub1) datasets of *Chrysoporthe*, the PHT generated a value of $P = 0.041$, and consequently, the sequence data for ITS and tub regions were combined (Cunningham 1997). Based on the phylogenetic analyses of the ITS, tub, and ITS+tub datasets, the isolates representing all of the genotypes from each host × location reside in the same Cluster, which were grouped with the species *Chr. deuterocubensis* (Fig. 6a–c). In this Cluster, isolates obtained in this study formed several subclades in each of the ITS and tub trees. However, the bootstrap values were not significant in the ITS and tub trees (Fig. 6a–b), which suggests that these differences reflect intraspecific rather than interspecific variations. The isolates obtained in this study that grouped with *Chrysoporthe* were identified as *Chr. deuterocubensis*.

Phylogenetic analyses of Celoporthe

For the ITS, tub (tub2 and tub1), and tef1 datasets of *Celoporthe*, the PHT generated a value of $P = 0.009$, and consequently, the sequence data for ITS, tub, and tef1 regions were combined (Cunningham 1997). Based on the phylogenetic analyses of the ITS, tub, tef1, and ITS+tub+tef1 datasets, isolate CSF10731 and the ex-type strain of *Cel. cerciana* (CERC9128) were grouped into the same monophyletic cluster, identified as *Cel. cerciana* (Fig. 7a–d); isolates CSF10775 and CSF10778 grouped in the same monophyletic cluster with the ex-type strain of *Cel. guangdongensis* (CMW12750) (Fig. 7a–d). Isolates CSF10768 and CSF10770 formed one independent clade that was close to the *Cel. eucalypti* clade in the tub2+tub1 tree (Fig. 7b), while the two isolates and the ex-type strain of *Cel. eucalypti* (CMW26908) grouped in the same monophyletic cluster in the ITS and tef1 trees (Fig. 7a, c), which suggests that the differences in tub sequences reflect intraspecific rather than interspecific variations, and thus the two isolates were identified as *Cel. eucalypti*. Among the ITS, tub, and tef1 trees, the remaining isolates obtained in this study were grouped into the same cluster with *Cel. syzygii* or formed single independent clades, but the bootstrap values within the *Cel. syzygii* clade were not significant (Fig. 7a–d), which suggests that these differences reflect intraspecific rather than interspecific variations, and thus these isolates were identified as *Cel. syzygii*.

Morphology

Consistent with the phylogenetic analyses, the morphology of the fungi from *Mytales* in this study shared typical characteristics of species within *Cryphonectriaceae* (Cheewangkoon et al. 2009, Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Crous et al. 2012a, b, 2015, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Ferreira et al. 2019). Isolates phylogenetically identified as species of *Chrysoporthe* and *Celoporthe* were morphologically similar to species of these two genera in terms of both sexual and asexual morphs (Gryzenhout et al. 2009, Chen et al. 2010, 2011, Chungu et al. 2010, Vermeulen et al. 2013, Ali et al. 2018).

Nine isolates that reside in phylogenetic Cluster C (CSF10748, CSF10755, and CSF10757) and Cluster D (Clade one: CSF2061, CSF8776 and CSF8777; Clade two: CSF10438, CSF10460, and 10738) (Fig. 2–4) were inoculated artificially under glasshouse conditions to produce sporocarps (Table 1). Asexual sporocarps of the nine isolates were produced on the incised *Eucalyptus* branches after 6 wk. Nine isolates identified as new species were selected for an assessment of culture characteristics (Table 1).

Isolates obtained in this study in Cluster C, which were phylogenetically close but separate from *Aur. marmelostoma*, had uniformly orange conidiomata that were broadly convex, with darkened tissue around the ostiolar openings. Stromatic tissue was prosenchymatous, and paraphyses or cylindrical sterile cells were present. These morphological characteristics are consistent with *Aurifilum* (Begoude et al. 2010). Some morphological differences were observed between the *Aurifilum* isolates included in this study and *Aur. marmelostoma*, such as the presence of conidiomatal necks, which are absent from *Aur. marmelostoma* (Begoude et al. 2010). Growth differences were also observed between the *Aurifilum* isolates in this study and *Aur. marmelostoma* (Begoude et al. 2010), suggesting that they represent a new species of *Aurifilum*.

Colonies of the proposed new genus present in Cluster D turned yellow in lactic acid and purple in 3 % KOH, which is similar to other genera of *Cryphonectriaceae* (Castlebury et al. 2002, Gryzenhout et al. 2009). These fungi possessed black conidiomata that were superficial to slightly immersed, conical to globose and without necks, stromatic tissue of *textura porrecta*, and lacked paraphyses. These characters distinguished these isolates from other genera in *Cryphonectriaceae* (Cheewangkoon et al. 2009, Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Crous et al. 2012a, b, 2015, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Ferreira et al. 2019, Jiang et al. 2019).

Based on phylogenetic analyses of species in *Cryphonectriaceae* (Clade one and Clade two) in Cluster D, morphological differences were also observed, particularly with regards to conidial size. Isolates that grouped in Cluster D represent a novel genus and two novel species of *Cryphonectriaceae*.

TAXONOMY

Based on the phylogenetic analyses and morphological characteristics, the isolates from *Mytales* in southern China represent four distinct genera in *Cryphonectriaceae*. Isolates present in phylogenetic Cluster A represent *Chrysoporthe*, and one single species, *Chr. deuterocubensis*, was identified (Fig. 3–6). Isolates in Cluster B represent *Celoporthe*, and *Cel. syzygii*, *Cel. eucalypti*, *Cel. guangdongensis*, and *Cel. cerciana* were identified (Fig. 3–5, 7). The isolates in Cluster C represent one novel species of *Aurifilum*, named here as *Aurifilum terminalis* sp. nov. (Fig. 3–5). Isolates residing in Cluster D represent a

previously undescribed genus, named here as *Parvosmorbus* gen. nov., and the two phylogenetic clades (Clade one and Clade two) (Fig. 3–5) represent two novel species, namely *Parvosmorbus eucalypti* sp. nov. and *Par. guangdongensis* sp. nov. The unknown genus and species are described as follows:

***Parvosmorbus* W. Wang & S.F. Chen, gen. nov.** — MycoBank MB832455

Etymology. Latin, *parvos*, small, *morbus*, disease, describing the fungus on the host bark and the fact that it causes disease.

Type species. *Parvosmorbus eucalypti* W. Wang & S.F. Chen.

Conidiomata as conidial locules, orange when young, becoming black when mature, conical to globose, superficial to slightly immersed, without necks, unilocular, seldom multilocular, stromatic tissue *textura porrecta*. **Conidiophores** aseptate, cylindrical, occasionally with separating septa and branching, hyaline. **Conidiogenous cells** cylindrical or flask-shaped with attenuated apices. **Paraphyses** absent. **Conidia** hyaline, fusoid to oval, aseptate.

Notes — *Parvosmorbus* is morphologically different from the other nine *Cryphonectriaceae* genera *Aurapex*, *Capillaureum*,

Celoporthe, *Chrysotilia*, *Chrysoporthe*, *Corticimorbus*, *Diversimorbus*, *Luteocirrus*, and *Myrtonectria* (Gryzenhout et al. 2004, 2006b, 2009, Nakabonge et al. 2006, Chen et al. 2011, 2013b, 2016, Crane & Burgess 2013, Vermeulen et al. 2013, Crous et al. 2015, Ali et al. 2018, Ferreira et al. 2019) in having conidiomata that lack necks and paraphyses, and having conidiomatal tissue of *textura porrecta*.

***Parvosmorbus eucalypti* W. Wang & S.F. Chen, sp. nov.** — MycoBank MB832456; Fig. 8

Etymology. Refers to *Eucalyptus*, the host genus from which this species was isolated.

Typus. CHINA, GuangDong Province, ZhanJiang Region, MaZhang District, HuGuang town (N21°9'45.020" E110°17'19.430"), from the stem bark of *E. urophylla* × *E. grandis* hybrid genotype, 2 Oct. 2013, S. Chen & G. Li, CSFF2047 (holotype HMAS290462, ex-type culture CSF2061 = CGMCC3.19512).

No ascostromata were observed on the *Eucalyptus* bark collected from the plantations or on the inoculated *Eucalyptus* branch tissue. **Conidiomata** pycnidial, superficial to slightly immersed, solitary, conical to globose, without necks, bright yellow when young, fuscous black when mature. **Conidiomatal**

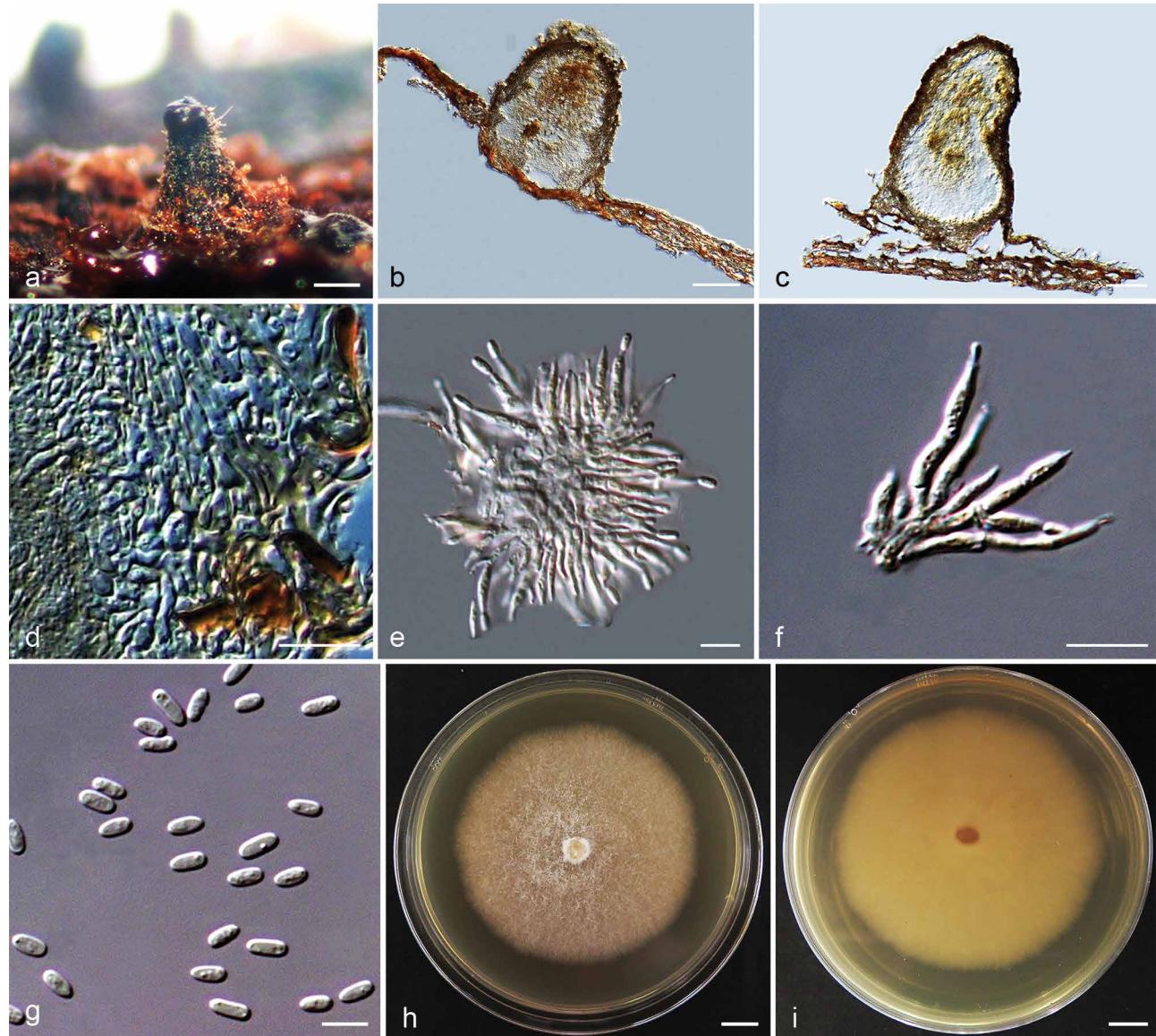


Fig. 8 Asexual sporocarps of *Parvosmorbus eucalypti*. a. Black conidiomata on the bark; b–c. longitudinal section through the conidioma showing unilocular stroma; d. *textura porrecta* stromatic tissue of the conidioma; e–f. aseptate, cylindrical conidiophores and cylindrical conidiogenous cells; g. fusoid to oval, aseptate conidia; h–i. living cultures after growing for 7 d on MEA at 25 °C, (h) front, (i) reverse. — Scale bars: a = 100 µm; b–c = 50 µm; d = 10 µm; e–g = 5 µm; h–i = 10 mm.

base 140–770 µm (av. 357 µm) high above the level of bark and 104–471 µm (av. 242 µm) wide. *Conidiomatal locules* unilocular, locules 59–276 µm (av. 174 µm) diam. *Stromatic tissue textura porrecta*. *Conidiophores* hyaline, branched irregularly at the base or above into cylindrical cells, with or without separating septa, (5.5–)11.5–12.5(–24.5) µm (av. 12 µm) long. *Conidiogenous cells* phialidic, cylindrical with or without attenuated apices, (1–)2(–2.5) µm (av. 1.8 µm) wide. *Paraphyses* or cylindrical sterile cells absent. *Conidia* hyaline, aseptate, fusoid, occasionally allantoid, exuded through opening at stromatal surface as brown to orange droplets, (3–)4(–4.5) × (1–)1.5(–2) µm (av. 3.9 × 1.4 µm).

Culture characteristics — Colonies on MEA fluffy with an uneven margin, white when young, turning yellowish white after 10 d. Colony reverse white to yellowish white. Optimal growth temperature 30 °C, no growth at 5 °C. After 7 d, the colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C, and 35 °C had reached 9.7, 12, 29, 44, 48, and 18 mm, respectively.

Substrate — Bark of *E. urophylla* × *E. grandis* hybrid genotype and *E. urophylla* hybrid genotype.

Distribution — GuangDong Province, China.

Additional materials examined. CHINA, GuangDong Province, LianJiang Region, YaTang Town (N21°33'43.0" E110°01'55.7"), from the branch bark of *E. urophylla* hybrid genotype, 1 Nov. 2015, J. Roux & S. Chen, CSFF2048, HMAS290463, culture CSF8776 = CGMCC3.19513; GuangDong Province, LianJiang Region, YaTang Town (N21°33'43.0" E110°01'55.7"), from the branch bark of *E. urophylla* hybrid genotype, 1 Nov. 2015, J. Roux & S. Chen, CSFF2049, culture CSF8777.

Notes — *Parvosporbus eucalypti* is morphologically most similar to *Corticimorbus sinomyrti*. These two species could be distinguished by growth characteristics in culture, with the optimal growth temperatures of *Par. eucalypti* and *Cor. sinomyrti* being 30 °C and 25 °C, respectively (Chen et al. 2016).

***Parvosporbus guangdongensis* W. Wang & S.F. Chen, sp. nov.** — MycoBank MB832457; Fig. 9

Etymology. Name reflects the GuangDong Province where this species was first collected.

Typus. CHINA, GuangDong Province, ZhanJiang Region, SuiXi county, LingBei Town (N21°16'00.960" E110°05'32.690"), from the stem bark of the *E. urophylla* hybrid genotype, 28 July 2016, S. Chen & W. Wang, CSFF2050 (holotype HMAS290464, ex-type culture CSF10460 = CGMCC3.19514).

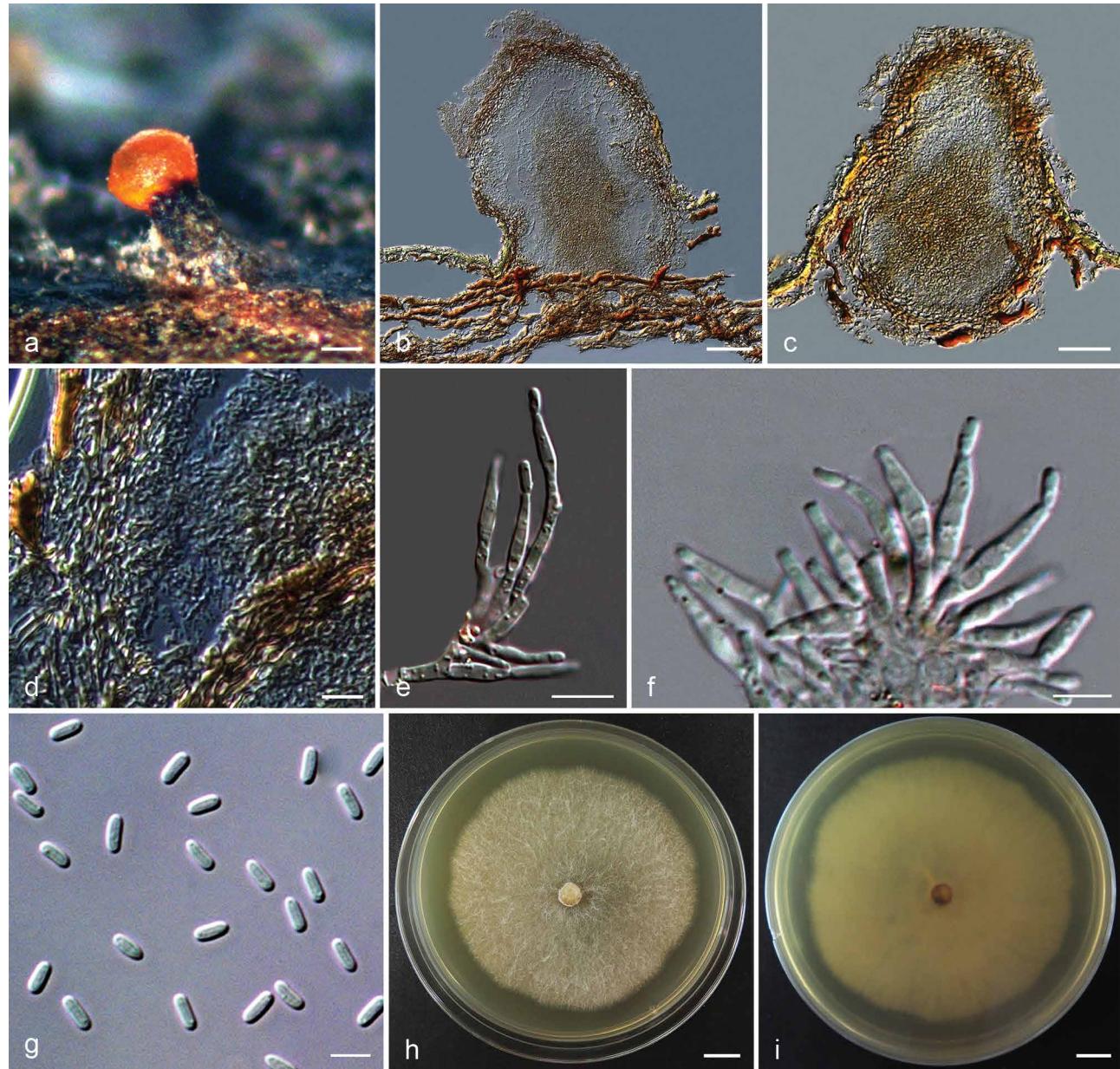


Fig. 9 Asexual sporocarps of *Parvosporbus guangdongensis*. a. Black conidiomata with an orange conidial spore mass; b–c. longitudinal section through conidioma showing unilocular stroma; d. *textura porrecta* stromatic tissue of the conidioma; e–f. aseptate, cylindrical conidiophores and cylindrical conidiogenous cells; g. fusoid to oval, aseptate conidia; h–i. living cultures after growing 7 d on MEA at 25 °C, (h) front, (i) reverse. — Scale bars: a = 100 µm; b–c = 50 µm; d = 10 µm; e–g = 5 µm; h–i = 10 mm.

No ascostromata were observed on the *Eucalyptus* bark collected from the plantations or on the inoculated *Eucalyptus* branch tissue. *Conidiomata* pycnidial, superficial to slightly immersed, solitary, conical to globose without necks, bright yellow when young, fuscous black when mature. *Conidiomatal base* 133–556 µm (av. 280 µm) high above the level of the bark and 66–420 µm (av. 150 µm) wide. *Conidiomatal locules* unilocular, locules 76–223 µm (av. 135 µm) diam. *Stromatic tissue textura porrecta*. *Conidiophores* hyaline, branched irregularly at the base or above into cylindrical cells, with or without separating septa, (5–)9–9.5(–31) µm (av. 9.2 µm) long. *Conidiogenous cells* phialidic, cylindrical with or without attenuated apices, (1–)2 µm (av. 1.8 µm) wide. *Paraphyses* or cylindrical sterile cells absent. *Conidia* hyaline, aseptate, oblong to fusoid, occasionally allantoid, exuded through an opening at the stromatal surface as orange droplets, (3–)3.5(–4.5) × (1–)1.5 µm (av. 3.6 × 1.4 µm).

Culture characteristics — Colonies on MEA fluffy with an uneven margin, white when young, turning yellowish white after 10 d. Colony reverse white to yellowish white. Optimal growth temperature 30 °C, no growth at 5 °C. After 7 d, the colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C, and 35 °C had reached 14, 15, 29, 46, 53, and 24 mm, respectively.

Substrate — Bark of *E. urophylla* hybrid genotype and *E. grandis* hybrid genotype.

Distribution — GuangDong Province, China.

Additional materials examined. CHINA, GuangDong Province, ZhanJiang Region, SuiXi County, LingBei Town (N21°16'02.972" E110°05'15.802"), from the stem bark of the *E. grandis* hybrid genotype, 28 July 2016, S. Chen & W. Wang, CSFF2051, HMAS290465, living culture CSF10738 = CGMCC3.19515; GuangDong Province, ZhanJiang Region, SuiXi County, LingBei Town (N21°16'00.960" E110°05'32.690"), from the stem bark of *E. urophylla* hybrid genotype, 28 July 2016, S. Chen & W. Wang, CSFF2052, living culture CSF10438.

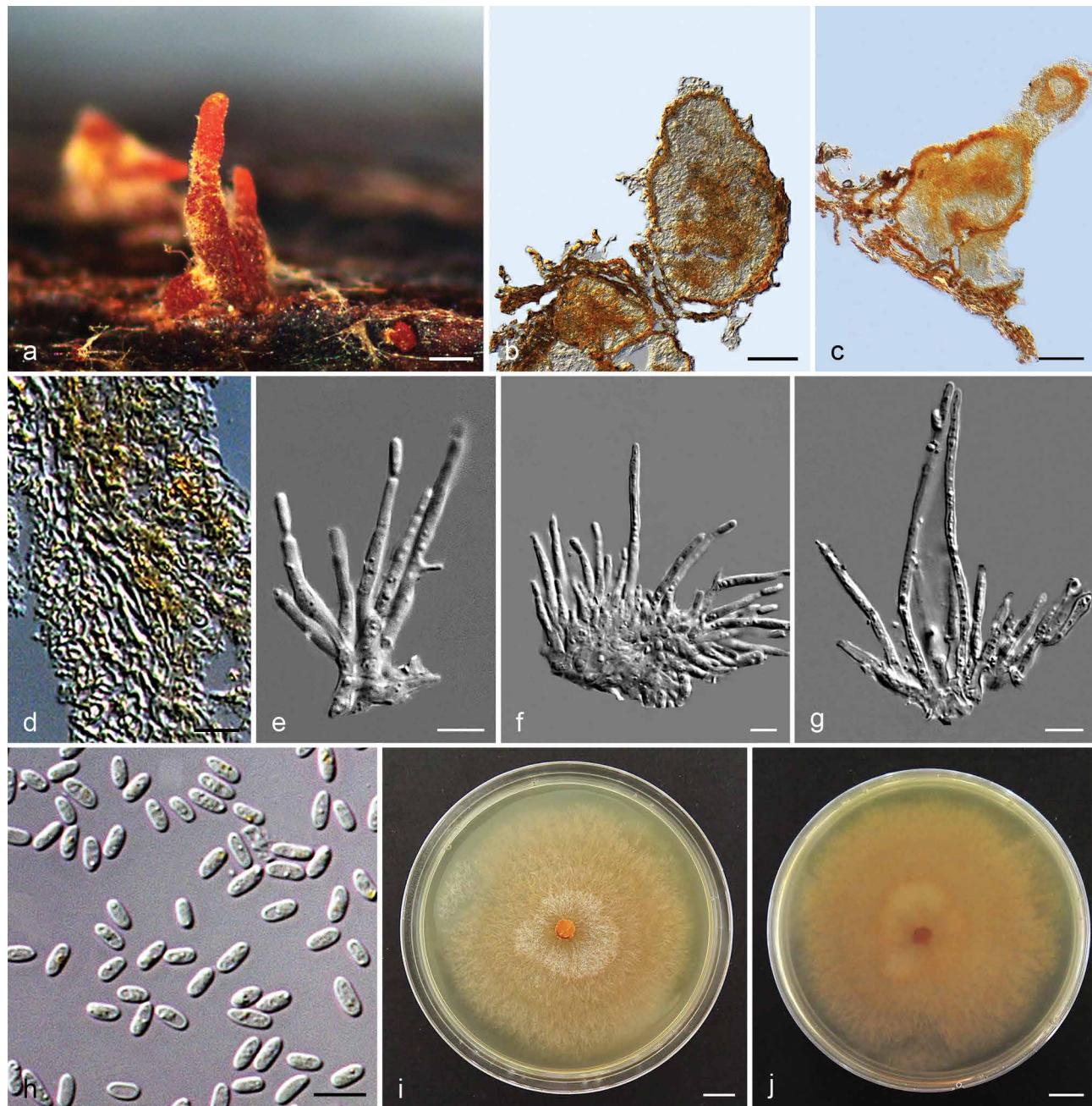


Fig. 10 Asexual sporocarps of *Aurilium terminali*. a. Orange conidiomata with orange necks; b–c. longitudinal section through the conidioma showing orange and unilocular stroma; d. prosenchymatous stromatic tissue of the conidioma; e–f. conidiophores and cylindrical conidiogenous cells; g. paraphyses; h. oblong to fusoid, aseptate conidia; i–j. living cultures after growing 7 d on MEA at 25 °C, (i) front, (j) reverse. — Scale bars: a = 100 µm; b–c = 50 µm; d = 10 µm; e–h = 5 µm; i–j = 10 mm.

Notes — *Parvomorbus guangdongensis* is morphologically similar to *Par. eucalypti*, but the conidia of *Par. eucalypti* (av. 3.9 × 1.4 µm) are slightly larger than those of *Par. guangdongensis* (av. 3.6 × 1.4 µm). *Parvomorbus guangdongensis* differs from *Par. eucalypti* by uniquely fixed DNA nucleotides in three nuclear loci, ITS (ITS1, 5.8S, ITS2) positions 124 (C), 279 (A), 280 (A), 281 (A), 282 (A), and 283 (A); *tub2* positions 145 (G) and 146 (G); *tub1* positions 139 (T), 140 (G), and 150 (T).

Aurifilum terminali W. Wang & S.F. Chen, sp. nov. — MycoBank MB832458; Fig. 10

Etymology. Refers to *Terminalia*, the host genus from which this fungus was isolated.

Type. CHINA, GuangDong Province, ZhanJiang Region, MaZhang District, HuGuang Town (N21°13'27.63" E110°17'19.32"), from twigs of one *Terminalia neotaliala* tree, 28 July 2016, S. Chen & W. Wang, CSFF2054 (holotype HMAS290466, ex-type culture CSF10757 = CGMCC3.19517).

No ascostromata were observed on the *Eucalyptus* bark collected from the plantations or on the inoculated *Eucalyptus* branch tissue. *Conidiomata* pycnidial, superficial to slightly immersed, yellow when young, bright orange when mature, solitary, constantly broadly convex, rostrate to conical, tissue around ostiolar openings darkened, necks appeared sporadically, constantly without necks. *Conidiomatal base* 213–924 µm (av. 524 µm) high above the level of bark and 100–665 µm (av. 263 µm) wide. *Conidiomatal locules* unilocular, locules 78–471 µm (av. 241 µm) diam. *Stromatic tissue* prosenchymatous. *Conidiophores* hyaline, branched irregularly at the base or above into cylindrical cells, with or without separating septa, (8–)13.5(–21.5) µm (av. 13.5 µm) long. *Conidiogenous cells* phialidic, cylindrical with or without attenuated apices, (1.5–)2(–2.5) µm (av. 1.8 µm) wide. *Paraphyses* or cylindrical sterile cells occurring among conidiophores, up to 63 µm (av. 35 µm). *Conidia* hyaline, aseptate, oblong to fusoid, occasionally allantoid, exuded through an opening at the stromatal surface as orange droplets, (3.5–)4(–4.5) × (1–)1.5(–2) µm (av. 3.9 × 1.6 µm).

Culture characteristics — Colonies on MEA fluffy with an uneven margin, white when young, turning orange after 10 d. Col-

ony reverse orange. Optimal growth temperature (25–)30 °C, no growth at 5 °C. After 7 d, the colonies at 10 °C, 15 °C, 20 °C, 25 °C, 30 °C, and 35 °C had reached 13, 16, 36, 64, 68, and 29 mm, respectively.

Substrate — Bark of *Terminalia neotaliala*.

Distribution — GuangDong Province, China.

Additional materials examined. CHINA, GuangDong Province, ZhanJiang Region, MaZhang District, HuGuang Town (N21°13'27.63" E110°17'19.32"), from twigs of one *T. neotaliala* tree, 28 July 2016, S. Chen & W. Wang, CSFF2053, HMAS290467, culture CSF10748 = CGMCC3.19516; GuangDong Province, ZhanJiang Region, MaZhang District, HuGuang Town (N21°13'27.63" E110°17'19.32"), from twigs of one *T. neotaliala* tree, 28 July 2016, S. Chen & W. Wang, CSFF2055, culture CSF10755.

Notes — Two species were described in the genus *Aurifilum*, including *Aur. marmelostoma* and *Aur. terminali*. *Aurifilum terminali* morphologically differs from *Aur. marmelostoma* by the presence of conidiomatal necks (Begoude et al. 2010). *Aurifilum terminali* could also be distinguished from *Aur. marmelostoma* by growth characteristics in culture. At 10 °C and 35 °C, *Aur. terminali* grows relatively slowly, while no growth was observed for *Aur. marmelostoma* (Begoude et al. 2010).

DIVERSITY AND DISTRIBUTION OF CRYPTONECTRIACEAE ON MYRTALES

According to the phylogenetic analyses and morphological comparisons of the 164 isolates obtained from five genera of *Myrtales*, eight species present in four genera (*Chrysoporthe*, *Celoporthe*, *Aurifilum*, and *Parvomorbus* gen. nov.) were identified. Of the 164 isolates, 99 isolates in the genus *Chrysoporthe* were all identified as *Chr. deuterocubensis*; the 46 *Celoporthe* isolates include 40 isolates of *Cel. syzygii*, two isolates of *Cel. eucalypti*, three isolates of *Cel. guangdongensis* and one isolate of *Cel. cerciana*; five isolates in genus *Aurifilum* were named as *Aur. terminali*. For the 14 isolates identified as the new genus *Parvomorbus*, eight isolates were named as *Par. eucalypti* and six as *Par. guangdongensis* (Table 1, 4).

Of the eight species of *Cryptonectriaceae* identified in this study, *Chr. deuterocubensis* (60 % of the isolates from *Myrtales*) is the dominant species, followed by *Cel. syzygii* (24 % of the

Table 4 Cryptonectriaceae isolated from *Myrtales* trees in China in the current study.

Species	Host	Location	Collector
<i>Chrysoporthe deuterocubensis</i>	<i>Eucalyptus urophylla</i> × <i>E. grandis</i> hybrid clone	PingNan, GuiGang, GuangXi, China	S.F. Chen
	<i>Melastoma candidum</i>	LiDao, Hong Kong, China	M.J. Wingfield & S.F. Chen
	<i>M. sanguineum</i>	SuiXi, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
	<i>M. sanguineum</i>	XiaShan, ZhanJiang, GuangDong, China	J. Roux & S.F. Chen
	<i>M. sanguineum</i>	LiDao, Hong Kong, China	M.J. Wingfield & S.F. Chen
	<i>Psidium guajava</i>	XiaShan, ZhanJiang, GuangDong, China	S.F. Chen & G.Q. Li
	<i>Syzygium jambos</i>	LeiZhou, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
	<i>S. samarangense</i>	WanNing, HaiNan, China	J. Roux & S.F. Chen
	Unknown species of <i>Myrtaceae</i>	ChiKan, ZhanJiang, GuangDong, China	S.F. Chen
	<i>E. urophylla</i> hybrid clone	SuiXi, ZhanJiang, GuangDong, China	J. Roux & S.F. Chen
<i>Celoporthe syzygii</i>	<i>P. guajava</i>	XiaShan, ZhanJiang, GuangDong, China	S.F. Chen
	<i>S. hancei</i>	XiaShan, ZhanJiang, GuangDong, China	S.F. Chen
	<i>S. jambos</i>	LianJiang, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
	<i>S. samarangense</i>	MaZhang, ZhanJiang, GuangDong, China	S.F. Chen & G.Q. Li
	Syzygium like	ChiKan, ZhanJiang, GuangDong, China	S.F. Chen
	Unknown species of <i>Myrtaceae</i>	ChiKan, ZhanJiang, GuangDong, China	S.F. Chen
<i>Cel. eucalypti</i>	<i>S. jambos</i>	XuWen, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
<i>Cel. guangdongensis</i>	<i>S. jambos</i>	XuWen, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
<i>Cel. cerciana</i> ¹	<i>E. grandis</i> hybrid clone	SuiXi, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
<i>Aurifilum terminali</i>	<i>Terminalia neotaliala</i>	MaZhang, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
<i>Parvomorbus eucalypti</i>	<i>E. urophylla</i> × <i>E. grandis</i> hybrid clone	MaZhang, ZhanJiang, GuangDong, China	S.F. Chen & G.Q. Li
	<i>E. urophylla</i> hybrid clone	LianJiang, ZhanJiang, GuangDong, China	J. Roux & S.F. Chen
<i>Par. guangdongensis</i>	<i>E. urophylla</i> hybrid clone	SuiXi, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang
	<i>E. grandis</i> hybrid clone	SuiXi, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang

¹Also reported in previous study (Wang et al. 2018).

isolates from *Mytales*). In the current study, *Chr. deuterocubensis* and *Cel. syzygii* were isolated from trees/shrubs of four and three sampled genera of *Mytales*, respectively. Each of the remaining six species of *Cryphonectriaceae* was only isolated from the trees of one *Mytales* genus (Table 4).

Based on the genotype for each isolate determined by the ITS, *tub2*, *tub1*, *tef1*, and LSU sequences, 12 genotypes were generated for the isolates obtained from *Chr. deuterocubensis* and *Cel. syzygii*, respectively (Table 1, 4). Six and five genotypes exist on *M. candidum* and *S. samarangense* for *Chr. deuterocubensis* and *Cel. syzygii*, respectively. No more than three genotypes exist on the remaining species of *Mytales*, both for *Chr. deuterocubensis* and *Cel. syzygii* (Table 1, 4). With the exception of *Chr. deuterocubensis* or *Cel. syzygii*, only one genotype was generated for the isolates obtained from each of the remaining six *Cryphonectriaceae* species (Table 1, 4).

Species of *Cryphonectriaceae* were also isolated from *Mytales* in previous studies (Table 5). With the exception of *Cel. cerciana*, which was reported from the same genotype of *E. grandis* previously, the *Cryphonectriaceae* isolates from related *Mytales* species in the current study constitute new reports (Table 4, 5).

Pathogenicity tests

Forty-six isolates representing the eight species of *Cryphonectriaceae* identified in this study were used for inoculations on seedlings of two *Eucalyptus* hybrid genotypes, the branches of *M. sanguineum*, and the seedlings of *P. guajava* and *S. jambos*. These include 20 isolates of *Chr. deuterocubensis*, 15 isolates of *Cel. syzygii*, one isolate of *Cel. cerciana*, and each of two isolates of *Cel. eucalypti*, *Cel. guangdongensis*, *Aur. terminali*, *Par. eucalypti*, and *Par. guangdongensis* (Table 1, 6). Two isolates of *Aur. terminali* (CSF10748 and CSF10757) were also inoculated on the branches of *T. neotaliala* (Table 1, 6).

All of the inoculated isolates produced lesions on the tested seedling stems or tree branches, whereas only wounds but no lesions were produced in the control inoculations (Fig. S6). Isolates of each species caused death to branches of *M. sanguineum* and seedlings of *P. guajava* (Table 6), and relatively large numbers of *P. guajava* were killed by the inoculated isolates (Fig. S7).

For the inoculations on the seedlings of two *Eucalyptus* hybrid genotypes, overall, the isolates of *Chr. deuterocubensis* generally produced relatively longer lesions than of the other seven species of *Cryphonectriaceae* (Table 6, Fig. 11). For the tested *Eucalyptus* genotype CEPT53, the lesions produced by the *Chr. deuterocubensis* isolates were all significantly longer than the wounds caused by the negative controls, except for isolates CSF3087, CSF3090, CSF8771, CSF8758, and CSF3035 ($P < 0.05$) (Table 6). For isolates in the other seven species of *Cryphonectriaceae*, isolates CSF8749, CSF10605, CSF8752, CSF10618 (*Cel. syzygii*), CSF10775 (*Cel. guangdongensis*), and CSF8776 (*Par. eucalypti*) also produced significantly longer lesions on the *Eucalyptus* genotype CEPT53 ($P < 0.05$) (Table 6). Analysis of variance indicated that there were significant differences in the susceptibility of the two *Eucalyptus* genotypes to some of the isolates/species we tested. For example, the lesions produced by isolates CSF10458, CSF10560, CSF8788, CSF3041, CSF10787, CSF10564, CSF10754, CSF3813, CSF3008, CSF3814, CSF3012 (*Chr. deuterocubensis*), CSF10605, CSF8752, CSF10618 (*Cel. syzygii*), and CSF8776 (*Par. eucalypti*) on *Eucalyptus* genotype CEPT53 were significantly longer than that of the *Eucalyptus* genotype CEPT46 ($P < 0.05$) (Table 6). Overall, the lesions caused by the eight species on the *Eucalyptus* genotype CEPT46 were shorter than genotype CEPT53, which indicates that genotype CEPT46 is more tolerant than CEPT53 (Fig. 11).

For inoculation on *M. sanguineum* branches, the overall data revealed that the lesions produced by *Chr. deuterocubensis* were significantly longer than that of the other seven *Cryphonectriaceae* species (Fig. 12). Excluding isolates CSF8771, CSF10787 and CSF8758, the lesions produced by all of the other 17 isolates of *Chr. deuterocubensis* were all significantly longer than the wounds caused by the negative controls ($P < 0.05$) (Table 6). For the other genera, isolates CSF8752 (*Cel. syzygii*) and CSF8776 (*Par. eucalypti*) produced significantly longer lesions (Table 6).

The lesions produced by the *Cryphonectriaceae* isolates on the *P. guajava* seedlings developed rapidly following inoculation. *Chrysoporthe deuterocubensis* is an aggressive pathogen of *P. guajava* seedlings, and 19 of the 20 inoculated isolates possessed the ability to kill the inoculated stems within 6 wk (Table 6, Fig. S7). Isolates of *Cel. syzygii*, *Cel. guangdongensis*,

Table 5 *Cryphonectriaceae* isolated from *Mytales* trees in China in previous studies.

Species	Host	Location	Collector	References
<i>Chrysoporthe deuterocubensis</i>	<i>Eucalyptus camaldulensis</i>	LeDong, HaiNan, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2010)
	<i>E. grandis</i>	GuangDong, China	M.J. Wingfield	Chen et al. (2010)
	<i>E. urophylla × E. grandis</i>	HePu, BeiHai, GuangXi, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2010)
	<i>Eucalyptus</i> EC48 clone	LeiZhou, ZhanJiang, GuangDong, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2010)
	<i>Eucalyptus</i> U6 clone	ChengMai, HaiNan, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2010)
	<i>Eucalyptus</i> U6 clone	LeiZhou, ZhanJiang, GuangDong, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2010)
	<i>Eucalyptus</i> W5 clone	LeiZhou, ZhanJiang, GuangDong, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2010)
	<i>Eucalyptus</i> sp.	GuangDong, China	T.I. Burgess	Chen et al. (2010)
	<i>Eucalyptus</i> sp.	Hong Kong, China	N/A ¹	Hodges et al. (1976), Myburg et al. (1999)
	<i>Syzygium cumini</i>	XiaShan, ZhanJiang, GuangDong, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2010)
	<i>S. samarangense</i>	PingTung, TaiWan, China	N/A	Fan et al. (2013)
<i>Celoporthe syzygii</i>	<i>E. grandis</i> hybrid clone	SuiXi, ZhanJiang, GuangDong, China	S.F. Chen & W. Wang	Wang et al. (2018)
<i>Cel. syzygii</i>	<i>S. cumini</i>	XiaShan, ZhanJiang, GuangDong, China	M.J. Wingfield & X.D. Zhou	Chen et al. (2011)
<i>Cel. eucalypti</i>	<i>Eucalyptus</i> EC48 clone	SuiXi, ZhanJiang, GuangDong, China	X.D. Zhou & S.F. Chen	Chen et al. (2011)
<i>Cel. guangdongensis</i>	<i>Eucalyptus</i> sp.	GuangDong, China	T.I. Burgess	Chen et al. (2011)
<i>Cel. cerciana</i>	<i>E. grandis</i> hybrid clone	SuiXi, ZhanJiang, GuangDong, China	S.F. Chen	Wang et al. (2018)
<i>Chrysomorus lagerstroemiae</i>	<i>Lagerstroemia speciosa</i>	ChiKan, ZhanJiang, GuangDong, China	S.F. Chen	Chen et al. (2018)
<i>Chr. lagerstroemiae</i>	<i>L. speciosa</i>	HaiKou, HaiNan, China	J.Roux & S.F. Chen	Chen et al. (2018)
<i>Corticimorus sinomyrti</i>	<i>Rhodomyrtus tomentosa</i>	LiDiao, Hong Kong, China	M.J. Wingfield & S.F. Chen	Chen et al. (2016)
<i>Cor. sinomyrti</i>	<i>R. tomentosa</i>	HePu, BeiHai, GuangXi, China	S.F. Chen & G.Q. Li	Chen et al. (2016)

¹N/A = not available.

Table 6 Average lesion length (mm) on the seedlings or branches of the two *Eucalyptus* clones, *Melastoma sanguineum*, and *Syzygium jambos* inoculated with *Cryphonectriaceae*.

Species	Isolate number	Lesion length (average ± standard error of means) (mm) ¹			
		<i>Eucalyptus</i> CEPT53	<i>Eucalyptus</i> CEPT46	<i>M. sanguineum</i>	<i>S. jambos</i>
<i>Chrysoporthe deuterocubensis</i>	CSF3087 ³	20.3±3.1 g-o	13.3±2.1 m-p	20.6±1.9 f-m	25.2±7.7 d-l
	CSF3090 ^{2,3}	21.9±4.6 e-o	9.0±0.7 op	28.3±2.5 c-g	28.7±3.1 c-k
	CSF3123 ^{2,3}	26.2±3.3 b-m	13.7±3.1 m-p	30.4±4.0 b-e	36.2±3.3 a-e
	CSF10458 ³	36.7±2.7 a-c	18.7±5.7 j-p	29.1±1.3 c-f	49.3±2.4 a
	CSF8771	22.6±4.7 d-o	10.7±0.5 n-p	12.6±0.6 k-n	12.8±1.1 kl
	CSF10560 ³	42.5±4.7 a	18.5±2.6 j-p	38.6±3.9 b	33.3±6.7 b-i
	CSF8788 ³	26.3±1.3 c-m	10.7±0.8 n-p	21.4±2.6 f-k	35.5±4.1 a-g
	CSF3029 ^{2,3}	27.9±2.8 b-l	17.0±6.3 j-p	23.7±3.6 e-j	23.7±2.2 d-l
	CSF3041 ^{2,3}	36.5±3.3 a-c	13.7±2.6 m-p	35.0±3.2 bc	34.0±4.6 a-h
	CSF10787 ^{2,3}	33.0±3.8 a-g	13.5±1.8 m-p	18.9±2.4 h-n	18.4±3.3 h-l
	CSF10564 ³	32.9±5.4 a-g	18.5±4.6 j-p	25.3±3.7 d-i	38.5±6.0 a-d
	CSF10745 ³	34.2±3.9 a-e	10.0±1.8 n-p	25.7±2.8 d-h	25.3±5.5 d-l
	CSF10554 ³	29.1±3.0 b-k	18.0±4.1 j-p	47.8±3.3 a	34.2±11.3 a-h
	CSF3813 ³	33.4±4.5 a-h	10.5±0.7 n-p	21.1±2.9 f-l	25.0±6.3 d-l
	CSF3008 ³	31.9±3.3 a-i	10.2±1.7 n-p	36.7±4.3 bc	45.7±7.0 ab
	CSF3814 ³	38.9±4.4 ab	10.0±0.9 n-p	32.2±3.8 b-e	29.4±3.8 c-k
	CSF3012 ³	34.5±3.5 a-g	14.8±4.6 l-p	28.8±1.7 c-g	22.2±4.5 e-l
	CSF3022 ³	30.0±3.4 a-j	26.2±7.6 b-m	33.0±2.7 b-d	35.8±7.1 a-f
	CSF8758 ^{2,3}	18.6±3.0 j-p	10.2±1.1 n-p	19.4±1.9 h-n	27.2±4.8 c-l
	CSF3035 ^{2,3}	20.7±2.8 f-o	10.5±1.6 n-p	50.6±9.6 a	29.3±2.8 c-k
<i>Celoporthe syzygii</i>	CSF8749	23.3±3.3 d-n	10.3±3.2 n-p	16.5±4.4 i-n	19.0±3.3 g-l
	CSF10636 ³	20.3±2.9 g-o	13.5±2.1 m-p	15.9±1.6 j-n	15.8±1.9 j-l
	CSF9124 ³	22.0±2.8 e-o	10.2±0.4 n-p	16.8±1.5 h-n	17.2±1.0 i-l
	CSF10695 ^{2,3}	21.9±2.2 e-o	12.8±2.5 m-p	18.4±2.8 h-n	20.0±2.0 e-l
	CSF10659	21.1±3.6 f-o	15.0±2.4 l-p	14.2±2.0 k-n	15.7±3.4 j-l
	CSF10619	19.0±2.3 h-p	13.7±0.8 m-p	15.3±2.0 j-n	16.9±1.7 i-l
	CSF10794 ³	19.0±2.0 i-p	13.0±1.6 m-p	17.4±1.9 h-n	21.5±2.1 e-l
	CSF10604 ^{2,3}	19.6±2.1 h-p	12.0±0.8 n-p	12.0±1.1 k-n	19.0±2.4 g-l
	CSF10605 ²	29.7±5.5 b-j	16.3±2.7 k-p	14.9±1.7 j-n	24.0±3.3 d-l
	CSF10647	18.0±4.1 j-p	12.8±1.4 m-p	11.7±0.6 l-n	18.2±3.8 h-l
	CSF8752 ^{2,3}	33.7±10.3 a-f	14.0±1.5 m-p	20.1±2.1 g-m	19.3±2.9 f-l
	CSF10597	16.1±1.5 k-p	12.8±0.6 m-p	17.1±1.5 h-n	21.3±4.1 e-l
	CSF8762 ^{2,3}	22.2±1.6 e-o	11.3±0.9 n-p	12.7±1.2 k-n	22.0±3.3 e-l
	CSF10627 ²	19.0±2.3 i-p	10.2±0.8 n-p	12.3±0.8 k-n	19.0±3.8 g-l
	CSF10618 ²	32.7±8.8 a-g	11.2±0.4 n-p	12.0±0.6 k-n	42.5±8.0 a-c
	CSF10768 ²	11.6±0.5 n-p	10.8±0.7 n-p	11.7±0.8 l-n	13.7±2.3 j-l
	CSF10770 ²	16.0±1.6 k-p	10.2±0.7 n-p	16.4±1.8 i-n	30.2±10.4 b-j
<i>Cel. guangdongensis</i>	CSF10774 ^{2,3}	21.3±2.0 e-o	15.7±1.6 l-p	16.4±1.1 i-n	21.8±2.7 e-l
	CSF10775 ²	23.0±1.4 d-n	12.8±1.5 m-p	13.0±1.0 k-n	26.0±3.2 d-l
<i>Cel. cerciana</i>	CSF10731 ²	18.5±2.0 j-p	12.2±1.3 n-p	11.9±0.6 l-n	16.5±5.1 j-l
<i>Aurifilum terminali</i>	CSF10748 ²	13.0±0.7 m-p	12.8±2.2 m-p	13.5±1.1 k-n	11.3±0.6 l
<i>Parvomorbus eucalypti</i>	CSF10757 ²	13.8±0.9 m-p	11.2±1.3 n-p	11.4±0.3 mn	13.8±1.7 j-l
	CSF2060	18.0±2.8 j-p	12.4±1.4 n-p	11.4±0.7 mn	23.8±9.1 d-l
<i>Par. guangdongensis</i>	CSF8776 ^{2,3}	35.1±4.1 a-d	21.5±3.7 e-o	20.7±2.6 f-m	21.2±2.7 e-l
	CSF10460 ²	18.2±2.1 j-p	9.7±0.3 n-p	12.0±1.1 k-n	15.7±3.7 j-l
Control	CSF10738 ^{2,3}	20.1±3.1 g-o	12.8±1.5 m-p	13.4±1.5 k-n	13.0±0.9 kl
		8.9±1.1 op	6.0±0.0 p	10.1±0.2 n	11.3±0.6 l

¹ Numbers followed by different letters indicate treatments that were significantly different ($P = 0.05$).² Indicates the relative fungal isolates with the ability to kill the *M. sanguineum* branches in 6 wk after inoculation.³ Indicates the relative fungal isolates with the ability to kill the *P. guava* seedlings in 6 wk after inoculation.

Par. eucalypti, and *Par. guangdongensis* also killed the stem in a relatively short time. The isolates that caused stem death are indicated in Table 6.

On the *S. jambos* seedlings, the overall data revealed that the lesions produced by *Chr. deuterocubensis* and *Cel. guangdongensis* were significantly longer than the wounds caused by the negative controls (Fig. 13). Twelve isolates of *Chr. deuterocubensis*, and one isolate of *Cel. syzygii* (CSF10618) and *Cel. eucalypti* (CSF10770), respectively, produced significantly longer lesions than the wounds caused by the negative controls (Table 6).

For the two *Aur. terminali* isolates inoculated on the branches of the *T. neotaliala* trees, lesions with abundant sporocarps were produced by the inoculated fungi in 4 wk (Fig. S6u). The lesions

produced by isolate CSF10748 were significantly longer than the wounds caused by the negative control (Fig. 14).

The overall results of the inoculations on the *Eucalyptus* hybrid genotypes, *M. sanguineum* and *S. jambos* consistently indicated that the genus *Chrysoporthe* is most aggressive, followed by *Parvomorbus* and *Celoporthe* (Fig. 11–13). Within 6 wk after inoculation, yellow, orange, or black sporocarps and cankers were produced on the bark of the inoculated seedlings or branches. These structures displayed similar morphological characteristics as the conidiomata on the *Myrtaceae* trees in the field, and the re-isolated fungi from lesions shared the same culture morphology with the *Cryphonectriaceae* isolates originating from *Myrtaceae* trees. All of the species of *Cryphonectriaceae* were re-isolated from the lesions successfully, and no

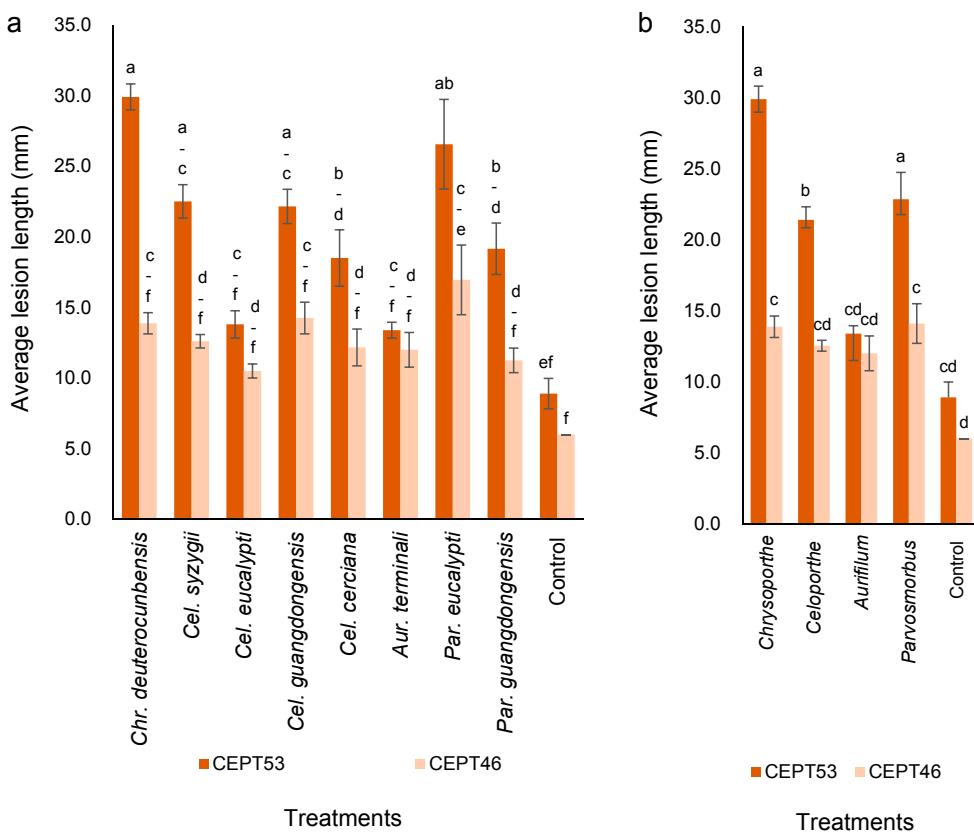


Fig. 11 a. Column chart indicating the average lesion length (in mm) produced by each species of *Cryphonectriaceae* on the seedlings of two *Eucalyptus* hybrid genotypes. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$); b. column chart indicating the average lesion length (in mm) produced by each genus of *Cryphonectriaceae* on two *Eucalyptus* hybrids. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$).

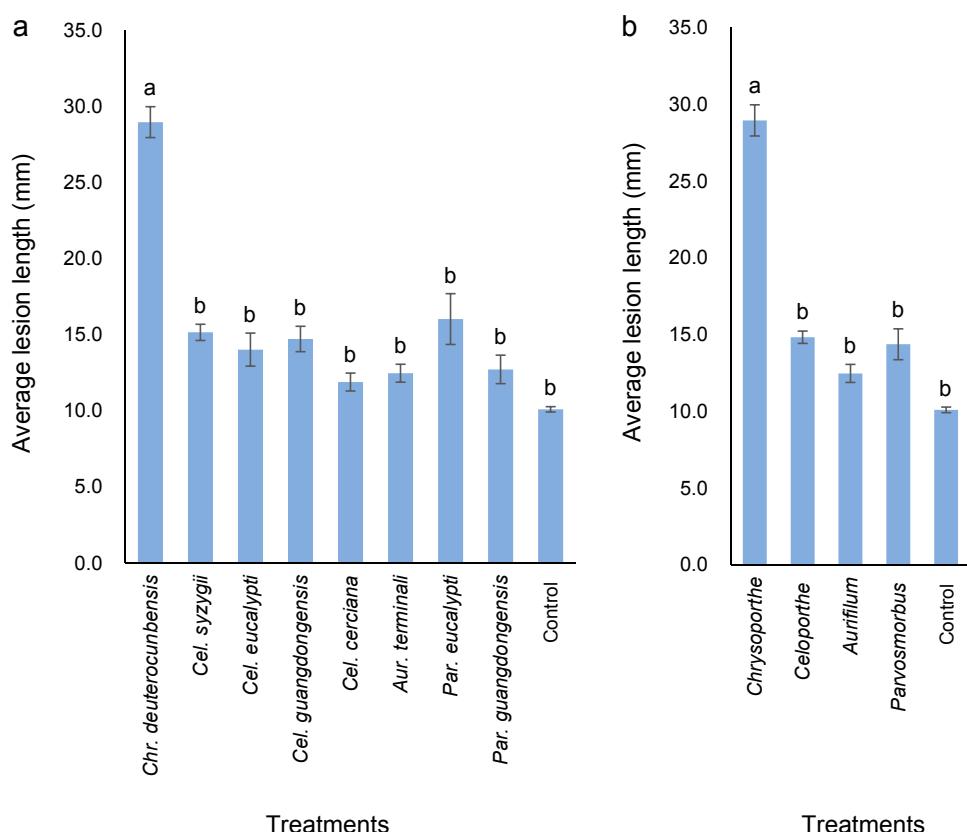


Fig. 12 a. Column chart indicating the average lesion length (in mm) produced by each species of *Cryphonectriaceae* on the branches of *Melastoma sanguineum*. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$); b. column chart indicating the average lesion length (in mm) produced by each genus of *Cryphonectriaceae* on the branches of *M. sanguineum*. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$).

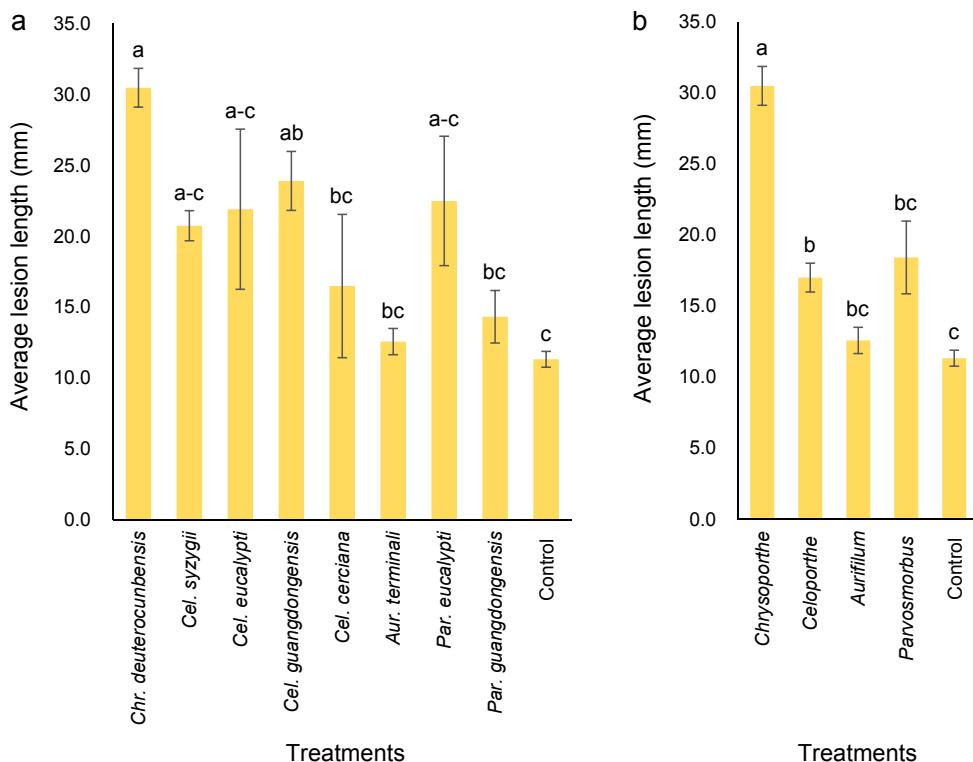


Fig. 13 a. Column chart indicating the average lesion length (in mm) produced by each species of *Cryphonectriaceae* on the branches of *Syzygium jambos*. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$); b. column chart indicating the average lesion length (in mm) produced by each genus of *Cryphonectriaceae* on the branches of *S. jambos*. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$).

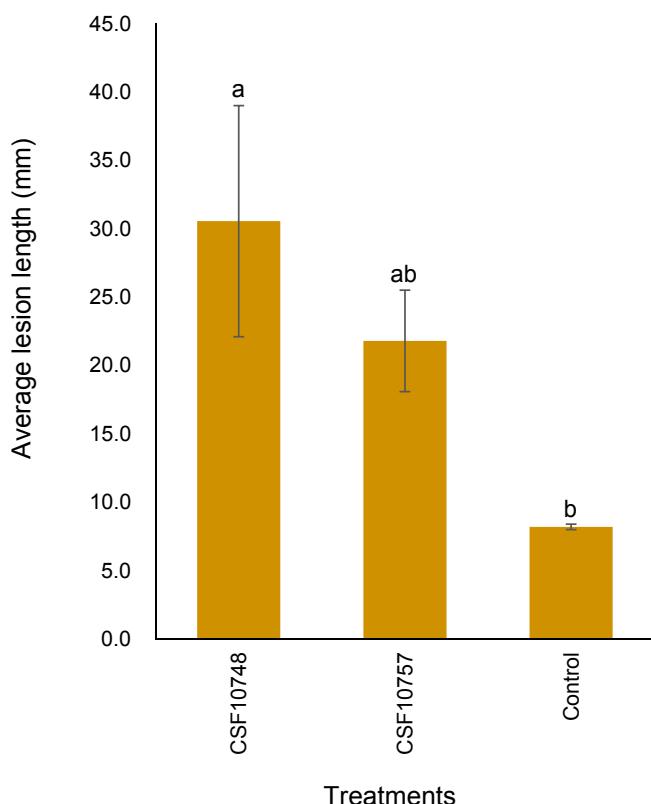


Fig. 14 Column chart indicating the average lesion length (in mm) produced by two isolates of *Aurifilum terminali* on the branches of *Terminalia neotaliala*. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$).

Cryphonectriaceae species were isolated from the negative controls, indicating the Koch's postulates had been fulfilled.

DISCUSSION

In this study, a large number of *Cryphonectriaceae* isolates were obtained from diseased *Eucalyptus* and other *Myrtales* trees in southern China, and eight species belonging to four genera of *Cryphonectriaceae* were identified from the five genera of *Myrtales*. The fungi isolated from the diseased tissues were identified based on phylogenetic analyses and morphological characteristics. *Chrysoporthe deuterocubensis*, *Cel. syzygii*, *Cel. eucalypti*, *Cel. guangdongensis*, and *Cel. cerciana*, representing a new genus and two species, as well as one new species of *Aurifilum* were identified and described. These new taxa were designated as *Parvomorbus* gen. nov., *Parvomorbus eucalypti* sp. nov., *Par. guangdongensis* sp. nov., and *Aurifilum terminali* sp. nov. Inoculation tests showed that the eight *Cryphonectriaceae* species identified and described in this study are pathogenic to the two tested *E. grandis* hybrid genotypes, *M. sanguineum*, *P. guajava*, and *S. jambos*.

Our results indicated that the *Cryphonectriaceae* are widely distributed on *Myrtales* in southern China. These included the notorious pathogen *Chr. deuterocubensis* identified from one *E. urophylla* × *E. grandis* hybrid genotype, *M. candidum*, *M. sanguineum*, *P. guajava*, *S. jambos*, and *S. samarangense*. *Celoporthe syzygii* from a *E. urophylla* hybrid genotype, *P. guajava*, *S. hancei*, *S. jambos*, and *S. samarangense*; *Cel. eucalypti* from *S. jambos*; *Cel. guangdongensis* from *S. jambos*; and *Cel. cerciana* from a *E. grandis* hybrid genotype. *Aurifilum terminali* sp. nov. was isolated from *T. neotaliala*. *Parvomorbus eucalypti* sp. nov. and *Par. guangdongensis* sp. nov. were identified from *Eucalyptus* hybrid genotypes. These all constitute new reports of *Cryphonectriaceae* on related *Myrtales* trees, with the exception of *Cel. cerciana*, which was reported from the same *E. grandis* genotype in a previous study (Wang et al. 2018).

For the *Cryphonectriaceae* fungi obtained in this study, isolates of *Chr. deuterocubensis* were dominant. *Chrysoporthe deuterocubensis* is a notorious pathogen that has been identified in China, Southeast Asia, Australia, Hawaii, and Tanzania from *Mytales*, especially *Eucalyptus* trees (Gryzenhout et al. 2004, 2009, Chen et al. 2010). In combination with the results from a previous study, this species has been isolated from a number of widely planted *Eucalyptus* hybrid genotypes in southern China (Chen et al. 2010). The inoculations consistently showed that it is pathogenic to all tested *Eucalyptus* genotypes, and different *Eucalyptus* genotypes exhibit different levels of tolerance. The inoculation results in the current study indicated that *Chr. deuterocubensis* is the most aggressive species among the eight *Cryphonectriaceae* species identified. These results suggested that *Chr. deuterocubensis* should be monitored carefully, since it causes significant losses to the *Eucalyptus* industry in China and other regions in south-eastern Asia (Gryzenhout et al. 2009, Chen et al. 2010), and selections of disease-tolerant *Eucalyptus* could be a useful means of managing Chrysoporthe canker disease.

Celoporthe is the most diverse genus of *Cryphonectriaceae* obtained in this study. This is consistent with previous research that suggests that *Celoporthe* species possibly have high genetic diversity in *Mytales* trees in southern China (Chen et al. 2011, Wang et al. 2018). For the four *Celoporthe* species identified in this study, *Cel. syzygii* constitutes the dominant species and accounted for 86 % of all obtained *Celoporthe* isolates. *Celoporthe syzygii* is the only species that was isolated from multiple *Mytales* genera. The results of the current study support an earlier study that suggested that *Cel. syzygii* might have a wide geographic and host distribution (Wang et al. 2018). The current and previous studies conducted on *Celoporthe* species in China showed that *Celoporthe* species produced distinct cankers or lesions on *Eucalyptus*, *P. guajava* and *Syzygium* trees, both in the field and glasshouse, which indicate that *Celoporthe* species serve as important pathogens for some species of *Mytales* in China (Chen et al. 2011, Wang et al. 2018).

In the current study, a new species, *Aur. terminali* sp. nov. was isolated from non-native *T. neotaliala*. In the genus *Aurifilum*, *Aur. marmelostoma* was the first described species, which was isolated from the bark of native *T. ivorensis* and the dead branches of non-native *T. mantaly* in Cameroon (Begoude et al. 2010). Currently, only two species of *Aurifilum* have been identified, both of which were isolated from *Terminalia* trees, and were pathogenic to inoculated *Terminalia* (Begoude et al. 2010). *Terminalia neotaliala* is a horticultural plant that is widely planted in parks and highway sides in southern China (Chen & Wang 2010). During our disease surveys, sporocarps of *Cryphonectriaceae* with different morphological characteristics were frequently observed on *T. neotaliala*, and we hypothesised that additional species of *Aurifilum* or other genera of *Cryphonectriaceae* also exist on these trees in southern China.

Parvosmisorbus represents the ninth genus in *Cryphonectriaceae* to be discovered in China and is the 26th genus to be added to this family, which includes many important tree pathogens (Cheewangkoon et al. 2009, Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Crous et al. 2012a, b, 2015, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Jiang et al. 2018, 2019, Wang et al. 2018, Ferreira et al. 2019). *Parvosmisorbus* can be distinguished from all other genera in the family based on morphology and DNA sequence data. *Parvosmisorbus* is the third genus of *Cryphonectriaceae* to be discovered on *Eucalyptus* trees in China. As observed in species of *Chrysoporthe* and *Celoporthe* in previous studies (Chen et al. 2010, 2011, Wang et al. 2018), *Par. eucalypti* and *Par. guangdongensis* were also isolated from

different *Eucalyptus* genotypes at different sites in southern China. Further *Parvomisorbus* species may exist on *Eucalyptus* plantations as observed with *Celoporthe* (Chen et al. 2011, Wang et al. 2018). Inoculations in the current study indicated that species of *Parvomisorbus* are pathogenic to *Eucalyptus* genotypes and other *Mytales*. At the sites where *Par. eucalypti* and *Par. guangdongensis* were isolated, *Chr. deuterocubensis*, *Cel. syzygii*, *Cel. eucalypti*, and *Cel. cerciana* were also isolated from the same *Eucalyptus* hybrid genotype. These results suggest that the disease on *Eucalyptus* at these sites might have resulted from the interaction of species in different genera of *Cryphonectriaceae*.

Based on the ITS, *tub2*, *tub1*, *tef1*, and LSU sequence data, the genotype of each isolate was determined in the present study. The results indicated that the genotypic diversity of *Chr. deuterocubensis* and *Cel. syzygii* is much higher than the other six *Cryphonectriaceae* species, and these genotypes were found on different *Mytales* trees, including the native tree species. For example, for *Chr. deuterocubensis*, six genotypes exist on native *M. candidum* trees, and no more than three genotypes were found on other *Mytales* species. *Melastoma candidum* is widely distributed in natural forests and *Eucalyptus* plantations in southern China. Evidence suggests that *Chr. cubensis*, the sister species of *Chr. deuterocubensis*, is probably capable of switching between non-native plantation *Eucalyptus* and native *Miconia rubiginosa* (*Melastomataceae*) trees in Colombia (Van der Merwe et al. 2013). Whether this also occurred for *Chr. deuterocubensis* between non-native *Eucalyptus* trees and native *Mytales* in southern China still requires further study. In the *Cryphonectriaceae*, only one or two species were identified on each of most genera, with the exception of *Celoporthe*, *Chrysoporthe*, *Cryphonectria*, and *Holocryphia* (Cheewangkoon et al. 2009, Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Crous et al. 2012a, b, 2015, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Beier et al. 2015, Ali et al. 2018, Jiang et al. 2018, 2019, Wang et al. 2018, Ferreira et al. 2019). A limited number of species were identified for most genera of *Cryphonectriaceae*. One potential reason is that limited *Cryphonectriaceae* surveys were conducted in the past. It is possible that more species in each genus of *Cryphonectriaceae* will be isolated and described after more surveys have been conducted on diseases caused by *Cryphonectriaceae*. For example, since the genus *Celoporthe* was established based on *Celoporthe dispersa* in 2006 (Nakabonge et al. 2006), multiple species of *Celoporthe* were identified and described after more intensive surveys were conducted on *Mytales* plants (Chen et al. 2011, Vermeulen et al. 2013, Ali et al. 2018, Wang et al. 2018).

Research results in previous and current studies showed that many species of *Cryphonectriaceae* inhabit *Fagaceae* and *Mytales* hosts (Gryzenhout et al. 2009, 2010, Begoude et al. 2010, Vermeulen et al. 2011, 2013, Crous et al. 2012a, b, 2015, Chen et al. 2013a, b, 2016, 2018, Crane & Burgess 2013, Ali et al. 2018, Jiang et al. 2018, 2019, Wang et al. 2018, Ferreira et al. 2019). One reason is extensive investigations were conducted on plants of these three families *Fagaceae*, *Melastomataceae*, and *Myrtaceae*, and some fungi of *Cryphonectriaceae* may specifically infect these plants. Furthermore, evidence for host shifting exists for *Cryphonectriaceae* within *Mytales* (Wingfield et al. 2001, Rodas et al. 2005, Van der Merwe et al. 2013), which appears to be a mechanism for species of *Cryphonectriaceae* to expand their host range.

Cryphonectriaceae includes many of the world's most important pathogens of trees, especially in the families *Fagaceae*, *Melastomataceae*, and *Myrtaceae* (Gryzenhout et al. 2009, Chen et al. 2010, Van der Merwe et al. 2010). *Mytales* trees are widely planted in southern China to meet the economic

and ecological needs of the country (Editorial Committee of Flora of China 1988, Zhan & Lan 2012, Huang & Zhu 2014, Xie et al. 2017). Previous and current research results have indicated that some species of *Cryphonectriaceae* represent important pathogens to *Mytales* trees, and these fungi induce distinct lesions or rapidly kill the branches/seedlings (Chen et al. 2010, 2011, 2016, 2018, Wang et al. 2018). Many new taxa remain to be discovered and it is likely that some of these will be important pathogens of *Mytales* trees in southern China. The findings of this study expand our knowledge of the genetic diversity, host and geographic range, and pathogenicity differences of *Cryphonectriaceae* on *Mytales*, which are crucially important for the disease management of *Cryphonectriaceae* on *Mytales* in southern China.

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REFERENCES

- Ali DB, Marincowitz S, Wingfield MJ, et al. 2018. Novel *Cryphonectriaceae* from La Réunion and South Africa, and their pathogenicity on Eucalyptus. *Mycological Progress* 17: 953–966.
- Anagnostakis SL. 1987. Chestnut blight: the classical problem of an introduced pathogen. *Mycologia* 79: 23–37.
- Anagnostakis SL. 1992. Chestnuts and the introduction of chestnut blight. *Annual Report of the Northern Nut Growers Association* 83: 39–42.
- Angiosperm Phylogeny Group. 2009. An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG III. *Botanical Journal of the Linnean Society* 161: 105–121.
- Begoude BAD, Gryzenhout M, Wingfield MJ, et al. 2010. Aurifilum, a new fungal genus in the *Cryphonectriaceae* from Terminalia species in Cameroon. *Antonie van Leeuwenhoek* 98: 263–278.
- Beier GL, Hokanson SC, Bates ST, et al. 2015. Aurantioporthe corni gen. et comb. nov., an endophyte and pathogen of *Cornus alternifolia*. *Mycologia* 107: 66–79.
- Castlebury LA, Rossman AY, Jaklitsch WJ, et al. 2002. A preliminary overview of the Diaporthales based on large subunit nuclear ribosomal DNA sequences. *Mycologia* 94: 1017–1031.
- Cheewangkoon R, Groenewald JZ, Summerell BA, et al. 2009. Myrtaceae, a cache of fungal biodiversity. *Persoonia* 23: 55–85.
- Chen SF, Gryzenhout M, Roux J, et al. 2010. Identification and pathogenicity of Chrysoporthe cubensis on Eucalyptus and Syzygium spp. in South China. *Plant Disease* 94: 1143–1150.
- Chen SF, Gryzenhout M, Roux J, et al. 2011. Novel species of Celoporthe from Eucalyptus and Syzygium trees in China and Indonesia. *Mycologia* 103: 1384–1410.
- Chen SF, Liu QL, Li GQ, et al. 2018. A new genus of *Cryphonectriaceae* causes stem canker on *Lagerstroemia speciosa* in South China. *Plant Pathology* 67: 107–123.
- Chen SF, Wingfield MJ, Li GQ, et al. 2016. Corticimorbus sinomyrti gen. et sp. nov. (*Cryphonectriaceae*) pathogenic to native *Rhodomyrtus tomentosa* (Myrtaceae) in South China. *Plant Pathology* 65: 1254–1266.
- Chen SF, Wingfield MJ, Roets F, et al. 2013a. A serious canker caused by Immersiporthe knoxdaviesiana gen. et sp. nov. (*Cryphonectriaceae*) on native *Rapanea melanophloeos* in South Africa. *Plant Pathology* 62: 667–678.
- Chen SF, Wingfield MJ, Roux J. 2013b. Diversimorbus metrosiderotis gen. et sp. nov. and three new species of Holocryphia (*Cryphonectriaceae*) associated with cankers on native *Metrosideros angustifolia* trees in South Africa. *Fungal Biology* 117: 289–310.
- Chen X, Wang HJ. 2010. Elegant ornamental tree, *Terminalia neotaliala*. *South China Agriculture* 2: 68–69. [In Chinese.]
- Chungu D, Gryzenhout M, Muimba-Kankolongo A, et al. 2010. Taxonomy and pathogenicity of two novel Chrysoporthe species from *Eucalyptus grandis* and *Syzygium guineense* in Zambia. *Mycological Progress* 9: 379–393.
- Crane C, Burgess TI. 2013. Luteocirrus shearii gen. sp. nov. (*Diaporthales, Cryphonectriaceae*) pathogenic to Proteaceae in the South Western Australian Floristic Region. *IMA Fungus* 4: 111–122.
- Crous PW, Summerell BA, Alfenas AC, et al. 2012a. Genera of diaporthalean coelomycetes associated with leaf spots of tree hosts. *Persoonia* 28: 66–75.
- Crous PW, Summerell BA, Shivas RG, et al. 2012b. Fungal Planet description sheets: 107–127. *Persoonia* 28: 138–182.
- Crous PW, Wingfield MJ, Cheewangkoon R, et al. 2019. Foliar pathogens of eucalypts. *Studies in Mycology* 94: 125–298.
- Crous PW, Wingfield MJ, Guarro J, et al. 2015. Fungal Planet description sheets: 320–370. *Persoonia* 34: 167–266.
- Cunningham CW. 1997. Can three incongruence tests predict when data should be combined. *Molecular Biology and Evolution* 14: 733–740.
- Editorial Committee of Flora of China. 1988. *Flora of China*. Volume 53(1–2). Beijing, Science Press.
- Fairchild D. 1913. The discovery of the chestnut bark disease in China. *Science* 38: 297–299.
- Fan MC, Huang CC, Huang JS, et al. 2013. First report of Chrysoporthe deuterocubensis causing canker on *Syzygium samarangense* in Taiwan. *Plant Disease* 97: 1508–1508.
- Farris JS, Källersjö M, Kluge AG, et al. 1995. Testing significance of incongruence. *Cladistics* 10: 315–319.
- Ferreira MA, Soares de Oliveira ME, Silva GA, et al. 2019. Capillaureum caryovora gen. sp. nov. (*Cryphonectriaceae*) pathogenic to pequi (*Caryocar brasiliense*) in Brazil. *Mycological Progress* 18: 385–403.
- Gramaje D, Mostert L, Groenewald JZ, et al. 2015. Phaeoacremonium: From esca disease to phaeohyphomycosis. *Fungal Biology* 119: 759–783.
- Gryzenhout M, Glen HF, Wingfield BD, et al. 2005a. Amphilogia gen. nov. for *Cryphonectria*-like fungi from *Elaeocarpus* spp. in New Zealand and Sri Lanka. *Taxon* 54: 1009–1021.
- Gryzenhout M, Myburg H, Hodges CS, et al. 2006a. Microthia, Holocryphia and Ursicollum, three new genera on *Eucalyptus* and *Coccoloba* for fungi previously known as *Cryphonectria*. *Studies in Mycology* 55: 35–52.
- Gryzenhout M, Myburg H, Rodas CA, et al. 2006b. Aurapex penicillata gen. sp. nov. from native *Miconia theaezans* and *Tibouchina* spp. in Colombia. *Mycologia* 98: 105–115.
- Gryzenhout M, Myburg H, Van der Merwe NA, et al. 2004. Chrysoporthe, a new genus to accommodate *Cryphonectria cubensis*. *Studies in Mycology* 50: 119–142.
- Gryzenhout M, Myburg H, Wingfield BD, et al. 2005b. Chrysoporthe doradensis sp. nov. pathogenic to *Eucalyptus* in Ecuador. *Fungal Diversity* 20: 39–57.
- Gryzenhout M, Myburg H, Wingfield BD, et al. 2005c. Rostraureum tropicale gen. sp. nov. (*Diaporthales*) associated with dying *Terminalia ivorensis* in Ecuador. *Mycological Research* 109: 1029–1044.
- Gryzenhout M, Myburg H, Wingfield BD, et al. 2006c. *Cryphonectriaceae* (*Diaporthales*), a new family including *Cryphonectria*, *Chrysoporthe*, *Endothia* and allied genera. *Mycologia* 98: 239–249.
- Gryzenhout M, Rodas CA, Menas Portales J, et al. 2006d. Novel hosts of the *Eucalyptus* canker pathogen *Chrysoporthe cubensis* and a new *Chrysoporthe* species from Colombia. *Mycological Research* 110: 833–845.
- Gryzenhout M, Tarigan M, Clegg PA, et al. 2010. Cryptometrion aestuescens gen. sp. nov. (*Cryphonectriaceae*) pathogenic to *Eucalyptus* in Indonesia. *Australasian Plant Pathology* 39: 161–169.
- Gryzenhout M, Wingfield BD, Wingfield MJ. 2009. Taxonomy, phylogeny, and ecology of bark-inhabiting and tree pathogenic fungi in the *Cryphonectriaceae*. APS Press, St Paul, MN, USA.
- Guindon S, Gascuel O. 2003. A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Systematic Biology* 52: 696–704.
- Hillis DM, Huelsenbeck JP. 1992. Signal, noise, and reliability in molecular phylogenetic analyses. *Journal of Heredity* 83: 189–195.
- Hodges CS, Reis MS, Ferreira FA, et al. 1976. O cancro do eucalipto causado por *Diaporthe cubensis* Bruner. *Fitopatologia Brasileira* 1: 129–169.
- Huang D, Zhu GF. 2014. Utilization status of ornamental plant resources of Melastomataceae in Guangdong Province. *South China Agriculture* 8: 1–7. [In Chinese.]
- Huelsenbeck JP, Bull JJ, Cunningham CW. 1996. Combining data in phylogenetic analysis. *Trends in Ecology & Evolution* 11: 152–158.
- Jiang N, Fan XL, Tian CM. 2019. Identification and pathogenicity of *Cryphonectriaceae* species associated with chestnut canker in China. *Plant Pathology* 68: 1132–1145. doi: <https://doi.org/10.1111/ppa.13033>.
- Jiang N, Fan XL, Yang Q, et al. 2018. Two novel species of *Cryphonectria* from *Quercus* in China. *Phytotaxa* 347: 243–250.
- Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution* 30: 772–780.

- Myburg H, Gryzenhout M, Heath R, et al. 2002a. Cryphonectria canker on Tibouchina in South Africa. *Mycological Research* 106: 1299–1306.
- Myburg H, Gryzenhout M, Wingfield BD, et al. 2002b. β -tubulin and histone H3 gene sequences distinguish *Cryphonectria cubensis* from South Africa, Asia and South America. *Canadian Journal of Botany* 80: 590–596.
- Myburg H, Gryzenhout M, Wingfield BD, et al. 2003. Conspecificity of *Endothia eugeniae* and *Cryphonectria cubensis*: A re-evaluation based on morphology and DNA sequence data. *Mycoscience* 44: 187–196.
- Myburg H, Gryzenhout M, Wingfield BD, et al. 2004a. DNA sequence data and morphology define *Cryphonectria* species in Europe, China, and Japan. *Canadian Journal of Botany* 82: 1730–1743.
- Myburg H, Gryzenhout M, Wingfield BD, et al. 2004b. Phylogenetic relationships of *Cryphonectria* and *Endothia* species, based on DNA sequence data and morphology. *Mycologia* 96: 990–1001.
- Myburg H, Wingfield BD, Wingfield MJ. 1999. Phylogeny of *Cryphonectria cubensis* and allied species inferred from DNA analysis. *Mycologia* 91: 243–250.
- Nakabonge G, Gryzenhout M, Roux J, et al. 2006. *Celoporthe dispersa* gen. et sp. nov. from native Myrtaceae in South Africa. *Studies in Mycology* 55: 255–267.
- Old KM, Wingfield MJ, Yuan ZQ. 2003. A manual of diseases of eucalypts in South-East Asia. Centre for International Forestry Research, Jakarta, Indonesia.
- Posada D. 2008. jModelTest: phylogenetic model averaging. *Molecular Biology and Evolution* 25: 1253–1256.
- Rayner RW. 1970. A mycological colour chart. Kew, UK, Commonwealth Mycological Institute and British Mycological Society.
- Rodas CA, Gryzenhout M, Myburg H, et al. 2005. Discovery of the Eucalyptus canker pathogen *Chrysoporthe cubensis* on native *Miconia* (Melastomataceae) in Colombia. *Plant Pathology* 54: 460–470.
- Shear CL, Stevens NE. 1913. The chestnut blight parasite (*Endothia parasitica*) from China. *Science* 38: 295–297.
- Slippers B, Stenlid J, Wingfield MJ. 2005. Emerging pathogens: fungal host jumps following anthropogenic introduction. *Trends in Ecology & Evolution* 20: 420–421.
- Stipes RJ, Phipps PM. 1971. A species of *Endothia* associated with a canker disease of pin oak (*Quercus palustris*) in Virginia. *Plant Disease Reporter* 55: 467–469.
- Suwannarach N, Kumla J, Sri-Ngernyuang K, et al. 2016. A new endophytic fungus, *Chrysosporia barringtoniae* sp. nov., from Thailand. *Mycoscience* 57: 361–365.
- Swofford DL. 2003. PAUP*. Phylogenetic Analysis Using Parsimony (*and other methods). Version 4.0b10. Sinauer Associates, Sunderland, MA, USA.
- Tamura K, Dudley J, Nei M, et al. 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biological and Evolution* 24: 1596–1599.
- Teng SC. 1934. Notes on Sphaeriales from China. *Sinensis* 4: 359–433.
- Van Burik JAH, Schreckhise RW, White TC, et al. 1998. Comparison of six extraction techniques for isolation of DNA from filamentous fungi. *Medical Mycology* 36: 299–303.
- Van der Merwe NA, Gryzenhout M, Steenkamp ET, et al. 2010. Multigene phylogenetic and population differentiation data confirm the existence of a cryptic species within *Chrysoporthe cubensis*. *Fungal Biology* 114: 966–979.
- Van der Merwe NA, Steenkamp ET, Rodas C, et al. 2013. Host switching between native and non-native trees in a population of the canker pathogen *Chrysoporthe cubensis* from Colombia. *Plant Pathology* 62: 642–648.
- Venter M, Myburg H, Wingfield BD, et al. 2002. A new species of *Cryphonectria* from South Africa and Australia, pathogenic on Eucalyptus. *Sydowia* 54: 98–117.
- Vermeulen M, Gryzenhout M, Wingfield MJ, et al. 2011. New records of *Cryphonectriaceae* from southern Africa including *Latruncellus aurorae* gen. sp. nov. *Mycologia* 103: 554–569.
- Vermeulen M, Gryzenhout M, Wingfield MJ, et al. 2013. Species delineation in the tree pathogen genus *Celoporthe* (*Cryphonectriaceae*) in southern Africa. *Mycologia* 105: 297–311.
- Wang W, Liu QL, Li GQ, et al. 2018. Phylogeny and pathogenicity of *Celoporthe* species from plantation Eucalyptus in Southern China. *Plant Disease* 102: 1915–1927.
- Wingfield MJ, Brockerhoff EG, Wingfield BD, et al. 2015. Planted forest health: the need for a global strategy. *Science* 349: 832–836.
- Wingfield MJ, Rodas C, Myburg H, et al. 2001. *Cryphonectria* canker on Tibouchina in Colombia. *Forest Pathology* 31: 297–306.
- Wingfield MJ, Swart WJ, Abear B. 1989. First record of *Cryphonectria* canker of *Eucalyptus* in South Africa. *Phytophylactica* 21: 311–313.
- Xie YJ, Arnold RJ, Wu ZH, et al. 2017. Advances in eucalypt research in China. *Frontiers of Agricultural Science and Engineering* 4: 380–390.
- Zhan HL, Lan WG. 2012. Development and application of Myrtaceae in southern China. *Journal of Anhui Agricultural Sciences* 40: 6573–6575. [In Chinese.]
- Zhang N, Blackwell M. 2001. Molecular phylogeny of dogwood anthracnose fungus (*Discula destructiva*) and the Diaporthales. *Mycologia* 93: 355–365.

Supplementary materials

Fig. S1 Disease symptoms on *Psidium guajava* associated with infection by *Cryphonectriaceae*. a. Dead *P. guajava* tree caused by *Chrysoporthe deuterocubensis*; b. cracking of the bark on *P. guajava* associated with canker by *Chr. deuterocubensis*; c. the arrows show necrosis after infection by *Chr. deuterocubensis*; d. cracking of bark on *P. guajava* base caused by *Chr. deuterocubensis*; e–f. sporocarps of *Celoporthe syzygii* on the stem of *P. guajava*.

Fig. S2 Disease symptoms on *Syzygium* species associated with infection by *Cryphonectriaceae*. a. Stems of *Syzygium jambos* damaged by species of *Celoporthe* and the formation of epicormic shoots after stem breakage; b. the arrows indicate canker on the stem of *S. jambos* after infection by *Celoporthe* species; c. sporocarps of *Celoporthe* on the stem of *S. jambos*; d. cracking of the bark on *S. jambos* caused by *Chrysoporthe deuterocubensis*; e. die-back of *Syzygium hancei* caused by *Celoporthe syzygii*; f. sporocarps of *Cel. syzygii* on the branch of *S. hancei*.

Fig. S3 Disease symptoms on *Terminalia neotaliala* associated with infection by *Aurifilum* species. a. Arrow indicates the dead branches of *T. neotaliala* caused by *Aurifilum* species; b. lesion developing on the branch (yellow arrows) and dead branch (red arrows); c. enlargement of the lesion developing on the branch (arrows); d. canker caused by *Aurifilum* species on the main stem and branches; e–f. sporocarps of *Aurifilum* species on the stem (e) and branch (f) of *T. neotaliala*.

Fig. S4 Phylogenetic trees based on maximum likelihood (ML) analyses of DNA sequence dataset of ITS region for various genera in the *Diaporthales*. Bootstrap values $\geq 70\%$ for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70% are marked with *, and absent analysis values are marked with -. Isolates collected in this study are in **bold** and blue. *Diaporthe ambigua* (CMW5287 and CMW5588) (*Diaporthaceae*) was used as outgroup taxon.

Fig. S5 Phylogenetic trees based on maximum likelihood (ML) analyses of DNA sequence dataset of two regions of the *tub* (*tub2/tub1*) for various genera in the *Diaporthales*. Bootstrap values $\geq 70\%$ for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70% are marked with *, and absent analysis values are marked with -. Isolates collected in this study are in **bold** and blue. *Diaporthe ambigua* (CMW5287 and CMW5588) (*Diaporthaceae*) was used as outgroup taxon.

Fig. S6 Lesions and wounds resulting from the inoculation of *Cryphonectriaceae* and negative control onto *Eucalyptus* seedlings (a–f), *Melastoma sanguineum* branches (g–l), *Syzygium jambos* seedlings (m–r) and *Terminalia neotaliala* branches (s–x). a–b. Lesion on *Eucalyptus* genotype CEPT46 produced by isolates (a) CSF3012 and (b) CSF10564 (*Chrysoporthe deuterocubensis*); c–d. lesions on *Eucalyptus* genotype CEPT53 produced by isolate (c) CSF10775 (*Celoporthe guangdongensis*) and (d) CSF8776 (*Parvomorbus eucalypti*); e–f. negative controls showing the absence of lesion development on *Eucalyptus* genotypes CEPT46 (e) and CEPT53 (f); g–k. lesions on *M. sanguineum* produced by isolate (g) CSF10619 (*Cel. syzygii*), (h) CSF10770 (*Cel. eucalypti*), (i) CSF10775 (*Cel. guangdongensis*), (j) CSF10748 (*Aurifilum terminali*), and (k) CSF8776 (*Par. eucalypti*); l. negative controls showing the absence of lesion development on *M. sanguineum*; m–q. lesions on *S. jambos* produced by isolate (m) CSF10554 and (n) CSF10458 (*Chr. deuterocubensis*), (o) CSF10618 and (p) CSF10794 (*Cel. syzygii*), (q) CSF10774 (*Cel. guangdongensis*); r. negative controls showing absence of lesion development on *S. jambos*; s–v. lesions on *T. neotaliala* produced by isolate (s–u) CSF10747 and (v) CSF10757 (*Aur. terminali*); w–x. negative controls showing the absence of lesion development on *T. neotaliala*.

Fig. S7 Symptoms associated with infection by various isolates (species) of *Cryphonectriaceae* on *Psidium guajava*. a. Living branch inoculated by isolate CSF8771 (*Chrysoporthe deuterocubensis*); b–d. dying branches caused by isolates (b) CSF10554 (*Chr. deuterocubensis*), (c) CSF10636 (*Celoporthe syzygii*), and (d) CSF8776 (*Parvomorbus eucalypti*).