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Cryphonectriaceae on *Myrtales* in China: phylogeny, host range, and pathogenicity

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Key words

Eucalyptus
fungal pathogen
host jump
Myrtaceae
new taxa
plantation forestry

Abstract Plantation-grown *Eucalyptus* (*Myrtaceae*) and other trees residing in the *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales*. 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 *Parvosmorbus* 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*, *Chrysofolia*, and *Foliocryphia*, which were isolated from leaf spots of eucalypts (*Myrtaceae*, *Myrtales*) (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*, *Myrtales*) 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 gyrosa* 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* (*Myrtales*) (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. deuterocubensis*, 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*, *Myrtales*) (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).

Myrtales plants are widely distributed particularly in tropical and sub-tropical regions in the world, and seven of the nine families of *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* species in southern China, intensive disease surveys were conducted in *Eucalyptus* plantations and other *Myrtales* 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 *Myrtales* trees from which these fungi were originally isolated.

MATERIALS AND METHODS

Disease symptoms, samples, and fungal isolations

Disease surveys on *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* 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[2]	Host	Location	GPS information	Collector	GenBank accession No.				
								ITS	*tub2*	*tub1*	*tef1*	LSU
Chrysoporthe deuterocunbensis	CSF3003	1	AAA--	*Melastoma candidum*	Lantau, Lidao, Hong Kong, China	N/A[3]	M.J. Wingfield & S.F. Chen	MK955908	MN263601	MN263695	N/A	N/A
	CSF3004	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MK955909	MN263602	MN263696	N/A	N/A
	CSF3005	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MK955910	MN263603	MN263697	N/A	N/A
	CSF3006	1	A-A--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263505	N/A	MN263698	N/A	N/A
	CSF3013	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263506	MN263604	MN263699	N/A	N/A
	CSF3014	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263507	MN263605	MN263700	N/A	N/A
	CSF3019	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263508	MN263606	MN263701	N/A	N/A
	CSF3020	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263509	MN263607	MN263702	N/A	N/A
	CSF3021	1	AAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263510	MN263608	MN263703	N/A	MN263791
	CSF3025	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263511	MN263609	MN263704	N/A	N/A
	CSF3026	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263512	MN263610	MN263705	N/A	N/A
	CSF3027	1	A-A--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263513	N/A	MN263706	N/A	N/A
	CSF3028	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263514	MN263611	MN263707	N/A	N/A
	CSF3031[5]	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263515	MN263612	MN263708	N/A	N/A
	CSF3040	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263516	MN263613	MN263709	N/A	N/A
	CSF3087[9]	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263517	MN263614	MN263710	N/A	N/A
	CSF3088	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263518	MN263615	MN263711	N/A	N/A
	CSF3089	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263519	MN263616	MN263712	N/A	N/A
	CSF3090[9]	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263520	MN263617	MN263713	N/A	N/A
	CSF3091	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263521	MN263618	MN263714	N/A	N/A
	CSF3092	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263522	MN263619	MN263715	N/A	N/A
	CSF3095	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263523	MN263620	MN263716	N/A	N/A
	CSF3097	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263524	MN263621	MN263717	N/A	N/A
	CSF3099	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263525	MN263622	MN263718	N/A	N/A
	CSF3100	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263526	MN263623	MN263719	N/A	N/A
	CSF3104	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263527	MN263624	MN263720	N/A	N/A
	CSF3105	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263528	MN263625	MN263721	N/A	N/A
	CSF3108	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263529	MN263626	MN263722	N/A	N/A
	CSF3109	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263530	MN263627	MN263723	N/A	N/A
	CSF3113	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263531	MN263628	MN263724	N/A	N/A
	CSF3122	1	AAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263532	MN263629	MN263725	N/A	N/A
	CSF3123[5,9]	1	AAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263533	MN263630	MN263726	N/A	MN263792
	CSF10456[4,5]	1	AAA-A	*M. sanguineum*	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN263534	MN263631	MN263727	N/A	MN263793
	CSF10457	1	AAA--	*M. sanguineum*	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN263535	MN263632	MN263728	N/A	N/A
	CSF10458[5,9]	1	AAA--	*M. sanguineum*	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN263536	MN263633	MN263729	N/A	N/A
	CSF8766[5]	1	AAA--	*M. sanguineum*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263537	MN263634	MN263730	N/A	N/A
	CSF8768	1	AAA--	*M. sanguineum*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263538	MN263635	MN263731	N/A	N/A
	CSF8769	1	AAA--	*M. sanguineum*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263539	MN263636	MN263732	N/A	N/A
	CSF8771[5,9]	1	AAA--	*M. sanguineum*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	J. Roux & S.F. Chen	MN263540	MN263637	MN263733	N/A	N/A
	CSF10560[5,9]	1	AAA--	*Psidium guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263541	MN263638	MN263734	N/A	N/A
	CSF10561[5]	1	AAA--	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263542	MN263639	MN263735	N/A	N/A
	CSF8788[5,9]	1	AAA--	*Syzygium samarangense*	ChangFeng, WanNing, HaiNan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263543	MN263640	MN263736	N/A	N/A
	CSF8789	1	AAA--	*S. samarangense*	ChangFeng, WanNing, HaiNan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263544	MN263641	MN263737	N/A	N/A
	CSF8790	1	AAA--	*S. samarangense*	ChangFeng, WanNing, HaiNan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263545	MN263642	MN263738	N/A	N/A
	CSF8791	1	AAA--	*S. samarangense*	ChangFeng, WanNing, HaiNan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263546	MN263643	MN263739	N/A	N/A
	CSF8792	1	AAA--	*S. samarangense*	ChangFeng, WanNing, HaiNan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263547	MN263644	MN263740	N/A	N/A
	CSF8793[5]	1	AAA--	*S. samarangense*	ChangFeng, WanNing, HaiNan, China	N18°46'53.571" E110°14'38.055"	J. Roux & S.F. Chen	MN263548	MN263645	MN263741	N/A	N/A
	CSF3029[4,5,9]	2	AAB-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263549	MN263646	MN263742	N/A	MN263794
	CSF3030[5]	2	AAB-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263550	MN263647	MN263743	N/A	MN263795
	CSF3041[4,5,9]	3	ABA-A	*M. sanguineum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263551	MN263648	MN263744	N/A	MN263796
	CSF3042[5]	3	ABA-A	*M. sanguineum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263552	MN263649	MN263745	N/A	MN263797

Table 1 (cont.)

Species	Isolate No.	Genotype No.[1]	Genotype[2]	Host	Location	GPS information	Collector	GenBank accession No.				
								ITS	*tub2*	*tub1*	*tef1*	LSU
Chrysoporthe deuterocunbensis (cont.)	CSF10786[4,5]	4	BAA-A	*S. jambos*	XiHu, LeiZhou, ZhanJiang, GuangDong, China	N20°54'50.200" E110°5'15.300"	S.F. Chen & W. Wang	MN263553	MN263650	MN263746	N/A	MN263798
	CSF10787[5,9]	4	BAA--	*S. jambos*	XiHu, LeiZhou, ZhanJiang, GuangDong, China	N20°54'50.200" E110°5'15.300"	S.F. Chen & W. Wang	MN263554	MN263651	MN263747	N/A	N/A
	CSF10564[4,5,9]	5	BAB-A	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263555	MN263652	MN263748	N/A	MN263799
	CSF10744[5]	6	BBA--	*M. sanguineum*	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang	MN263556	MN263653	MN263749	N/A	N/A
	CSF10745[4,5,9]	6	BBA-A	*M. sanguineum*	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang	MN263557	MN263654	MN263750	N/A	MN263800
	CSF10554[4,5,9]	7	CAB-A	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263558	MN263655	MN263751	N/A	MN263801
	CSF10555	7	CAB-A	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263559	MN263656	MN263752	N/A	MN263802
	CSF10556[5]	7	CAB-A	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263560	MN263657	MN263753	N/A	MN263803
	CSF10557	7	CAB--	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen & G.Q. Li	MN263561	MN263658	MN263754	N/A	N/A
	CSF3813[5,9]	8	DAA-A	*Eucalyptus urophylla* × *E. grandis* hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.0" E110°24'13.0"	S.F. Chen	MN263562	MN263659	MN263755	N/A	MN263804
	CSF3007[5]	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263563	MN263660	MN263756	N/A	N/A
	CSF3008[9]	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263564	MN263661	MN263757	N/A	N/A
	CSF3009	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263565	MN263662	MN263758	N/A	N/A
	CSF3010	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263566	MN263663	MN263759	N/A	N/A
	CSF3015	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263567	MN263664	MN263760	N/A	N/A
	CSF3016	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263568	MN263665	MN263761	N/A	N/A
	CSF3093	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263569	MN263666	MN263762	N/A	N/A
	CSF3094	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263570	MN263667	MN263763	N/A	N/A
	CSF3106	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263571	MN263668	MN263764	N/A	N/A
	CSF3107	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263572	MN263669	MN263765	N/A	N/A
	CSF3116	8	DAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263573	MN263670	MN263766	N/A	N/A
	CSF3117[4,5]	8	DAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263574	MN263671	MN263767	N/A	MN263805
	CSF3043	8	DAA--	*M. sanguineum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263575	MN263672	MN263768	N/A	N/A
	CSF3044	8	DAA--	*M. sanguineum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263576	MN263673	MN263769	N/A	N/A
	CSF3126[5]	8	DAA-A	*M. sanguineum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263577	MN263674	MN263770	N/A	MN263806
	CSF3127	8	DAA--	*M. sanguineum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263578	MN263675	MN263771	N/A	N/A
	CSF3128[5]	8	DAA--	*M. sanguineum*	Lantau, Lidao, Hong Kong, China	N/A	S.F. Chen	MN263579	MN263676	MN263772	N/A	N/A
	CSF8761[5]	8	DA--A	Unknown species of *Myrtaceae*	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263580	MN263677	N/A	N/A	MN263807
	CSF3814[4,5,9]	9	EAA-A	*E. urophylla* × *E. grandis* hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000", E110°24'13.000"	S.F. Chen	MN263581	MN263678	MN263773	N/A	MN263808
	CSF3815	9	EAA--	*E. urophylla* × *E. grandis* hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000", E110°24'13.000"	S.F. Chen	MN263582	MN263679	MN263774	N/A	N/A
	CSF3816	9	EAA--	*E. urophylla* × *E. grandis* hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000", E110°24'13.000"	S.F. Chen	MN263583	MN263680	MN263775	N/A	N/A
	CSF3817	9	EAA--	*E. urophylla* × *E. grandis* hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000", E110°24'13.000"	S.F. Chen	MN263584	MN263681	MN263776	N/A	N/A
	CSF3818	9	EAA--	*E. urophylla* × *E. grandis* hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000", E110°24'13.000"	S.F. Chen	MN263585	MN263682	MN263777	N/A	N/A
	CSF3819[5]	9	EAA--	*E. urophylla* × *E. grandis* hybrid clone	DaXin, PingNan, GuiGang, GuangXi, China	N23°17'29.000", E110°24'13.000"	S.F. Chen	MN263586	MN263683	MN263778	N/A	N/A
	CSF3011	10	F---	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263587	N/A	N/A	N/A	N/A
	CSF3012[4,5,9]	10	FAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263588	MN263684	MN263779	N/A	MN263809
	CSF3110	10	F---	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263589	N/A	N/A	N/A	N/A
	CSF3111[5]	10	FAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263590	MN263685	MN263780	N/A	MN263810
	CSF3022[4,5,9]	11	GAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263591	MN263686	MN263781	N/A	MN263811
	CSF3023	11	GAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263592	MN263687	MN263782	N/A	N/A
	CSF3024[5]	11	GAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263593	MN263688	MN263783	N/A	N/A
	CSF8758[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	MN263594	MN263689	MN263784	N/A	MN263812
	CSF8759[5]	11	GAA--	Unknown species of *Myrtaceae*	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263595	MN263690	MN263785	N/A	N/A

Table 1 (cont.)

Species	Isolate No.	Geno-type No.[1]	Geno-type[2]	Host	Location	GPS information	Collector	GenBank accession No.				
								ITS	*tub2*	*tub1*	*tef1*	LSU
Chrysoporthe deuterocunbensis (cont.)	CSF3035[4,5,9]	12	HAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263596	MN263691	MN263786	N/A	MN263813
	CSF3036	12	H-A-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263597	N/A	MN263787	N/A	MN263814
	CSF3037	12	HAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263598	MN263692	MN263788	N/A	N/A
	CSF3038	12	HAA--	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263599	MN263693	MN263789	N/A	N/A
	CSF3114[5]	12	HAA-A	*M. candidum*	Lantau, Lidao, Hong Kong, China	N/A	M.J. Wingfield & S.F. Chen	MN263600	MN263694	MN263790	N/A	MN263815
Celoporthe syzygii	CSF8748[4,5]	1	AAAAA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'300" E110°5'140"	J. Roux & S.F. Chen	MN263299	MN263345	MN263391	MN263437	MN263483
	CSF8749[5,9]	1	AAAA-	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'300" E110°5'140"	J. Roux & S.F. Chen	MN263300	MN263346	MN263392	MN263438	N/A
	CSF10636[5,9]	2	ABBBA	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.600" E110°23'33.000"	S.F. Chen	MN263301	MN263347	MN263393	MN263439	MN263484
	CSF10637	2	ABBB-	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.600" E110°23'33.000"	S.F. Chen	MN263302	MN263348	MN263394	MN263440	N/A
	CSF10644[5]	2	ABBB-	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.600" E110°23'33.000"	S.F. Chen	MN263303	MN263349	MN263395	MN263441	N/A
	CSF9113[4,5]	2	ABBBA	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263304	MN263350	MN263396	MN263442	MN263485
	CSF9114	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263305	MN263351	MN263397	MN263443	N/A
	CSF9115	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263306	MN263352	MN263398	MN263444	N/A
	CSF9116	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263307	MN263353	MN263399	MN263445	N/A
	CSF9117	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263308	MN263354	MN263400	MN263446	N/A
	CSF9118	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263309	MN263355	MN263401	MN263447	N/A
	CSF9119	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263310	MN263356	MN263402	MN263448	N/A
	CSF9120	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263311	MN263357	MN263403	MN263449	N/A
	CSF9121	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263312	MN263358	MN263404	MN263450	N/A
	CSF9122	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263313	MN263359	MN263405	MN263451	N/A
	CSF9123	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263314	MN263360	MN263406	MN263452	N/A
	CSF9124[5,9]	2	ABBB-	*S. hancei*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'29.356" E110°23'54.457"	S.F. Chen	MN263315	MN263361	MN263407	MN263453	N/A
	CSF10695[4,5,9]	3	ACBBA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924" E110°05'11.600"	S.F. Chen & W. Wang	MN263316	MN263362	MN263408	MN263454	MN263486
	CSF10699[5]	3	ACBB-	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924" E110°05'11.600"	S.F. Chen & W. Wang	MN263317	MN263363	MN263409	MN263455	N/A
	CSF10657[5]	4	BACB-	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924" E110°05'11.600"	S.F. Chen & W. Wang	MN263318	MN263364	MN263410	MN263456	N/A
	CSF10658	4	BACB-	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924" E110°05'11.600"	S.F. Chen & W. Wang	MN263319	MN263365	MN263411	MN263457	N/A
	CSF10659[4,5,9]	4	BACBA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.924" E110°05'11.600"	S.F. Chen & W. Wang	MN263320	MN263366	MN263412	MN263458	MN263487
	CSF10619[4,5,9]	5	BBBBA	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263321	MN263367	MN263413	MN263459	MN263488
	CSF10794[4,5,9]	6	BBCBA	*S. jambos*	ChengNan, LianJiang, ZhanJiang, GuangDong, China	N21°35'23.240" E110°15'51.770"	S.F. Chen & W. Wang	MN263322	MN263368	MN263414	MN263460	MN263489
	CSF10604[5,9]	6	BBCB-	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263323	MN263369	MN263415	MN263461	N/A
	CSF10605[9]	6	BBCB-	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263324	MN263370	MN263416	MN263462	N/A
	CSF10616[5]	6	BBCB-	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263325	MN263371	MN263417	MN263463	N/A
	CSF10647[4,5,9]	7	BBCCA	*P. guajava*	QuanZhaung, XiaShan, ZhanJiang, GuangDong, China	N21°13'39.600" E110°23'33.000"	S.F. Chen	MN263326	MN263372	MN263418	MN263464	MN263490
	CSF8752[4,5,9]	8	BBDBA	*Syzygium* like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263327	MN263373	MN263419	MN263465	MN263491
	CSF8753	8	BBDB-	*Syzygium* like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263328	MN263374	MN263420	MN263466	N/A
	CSF8754	8	BBDB-	*Syzygium* like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263329	MN263375	MN263421	MN263467	N/A
	CSF8755[5]	8	BBDB-	*Syzygium* like	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263330	MN263376	MN263422	MN263468	N/A
	CSF10597[4,5,9]	9	BDBBA	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263331	MN263377	MN263423	MN263469	MN263492
	CSF8762[4,5,9]	10	BDDBA	Unknown species of *Myrtaceae*	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263332	MN263378	MN263424	MN263470	MN263493
	CSF8763	10	BDDBA	Unknown species of *Myrtaceae*	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263333	MN263379	MN263425	MN263471	MN263494
	CSF8764	10	BDDBA	Unknown species of *Myrtaceae*	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263334	MN263380	MN263426	MN263472	MN263495
	CSF8765[5]	10	BDDBA	Unknown species of *Myrtaceae*	HaiBin, ChiKan, ZhanJiang, GuangDong, China	N21°14'42.930" E110°24'26.977"	S.F. Chen	MN263335	MN263381	MN263427	MN263473	MN263496

Table 1 (cont.)

Species	Isolate No.	Genotype No.[1]	Genotype[2]	Host	Location	GPS information	Collector	GenBank accession No.				
								ITS	*tub2*	*tub1*	*tef1*	LSU
Celoporthe syzygii (cont.)	CSF10627[4,5,9]	11	CEDCA	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263336	MN263382	MN263428	MN263474	MN263497
	CSF10628[5]	11	CEDCA	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263337	MN263383	MN263429	MN263475	MN263498
	CSF10618[4,5,9]	12	CFBBA	*S. samarangense*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°15'04.800" E110°14'07.500"	S.F. Chen & G.Q. Li	MN263338	MN263384	MN263430	MN263476	MN263499
Cel. eucalypti	CSF10768[4,5,9]	13	CGEDA	*S. jambos*	ChengBei, XuWen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263339	MN263385	MN263431	MN263477	MN263500
	CSF10770[5,9]	13	CGEDA	*S. jambos*	ChengBei, XuWen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263340	MN263386	MN263432	MN263478	MN263501
Cel. guangdongensis	CSF10774[9]	14	DHFE-	*S. jambos*	ChengBei, XuWen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263341	MN263387	MN263433	MN263479	N/A
	CSF10775[4,5,9]	14	DHFEA	*S. jambos*	ChengBei, XuWen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263342	MN263388	MN263434	MN263480	MN263502
	CSF10778[5]	14	DHFEA	*S. jambos*	ChengBei, XuWen, ZhanJiang, GuangDong, China	N20°20'8.480" E110°10'47.190"	S.F. Chen & W. Wang	MN263343	MN263389	MN263435	MN263481	MN263503
Cel. cerciana	CSF10731[4,5,9]	15	EBGBA	*E. grandis* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang	MN263344	MN263390	MN263436	MN263482	MN263504
Aurifilum terminali	CSF10748[4,5,7,8,9]	1	AAAAA	*Terminalia neotaliala*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199834	MN258767	MN258772	MN258777	MN258782
	CSF10754[4,5]	1	AAAAA	*T. neotaliala*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199835	MN258768	MN258773	MN258778	MN258783
	CSF10755[4,5,7,8]	1	AAAAA	*T. neotaliala*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199836	MN258769	MN258774	MN258779	MN258784
	CSF10757[4,5,6,7,8,9]	1	AAAAA	*T. neotaliala*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199837	MN258770	MN258775	MN258780	MN258785
	CSF10762[4,5]	1	AAAAA	*T. neotaliala*	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°13'27.630" E110°17'19.320"	S.F. Chen & W. Wang	MN199838	MN258771	MN258776	MN258781	MN258786
Parvosmorbus eucalypti	CSF2060[4,5,8,9]	1	AAAAA	*E. urophylla* × *E. grandis* hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°9'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258787	MN258801	MN258815	MN258829	MN258843
	CSF2061[4,5,6,7]	1	AAAAA	*E. urophylla* × *E. grandis* hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°9'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258788	MN258802	MN258816	MN258830	MN258844
	CSF2062[4,5]	1	AAAAA	*E. urophylla* × *E. grandis* hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°9'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258789	MN258803	MN258817	MN258831	MN258845
	CSF2063[4,5]	1	AAAAA	*E. urophylla* × *E. grandis* hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°9'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258790	MN258804	MN258818	MN258832	MN258846
	CSF2064[4,5]	1	AAAAA	*E. urophylla* × *E. grandis* hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°9'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258791	MN258805	MN258819	MN258833	MN258847
	CSF2065[4,5]	1	AAAAA	*E. urophylla* × *E. grandis* hybrid clone	HuGuang, MaZhang, ZhanJiang, GuangDong, China	N21°9'45.020" E110°17'19.430"	S.F. Chen & G.Q. Li	MN258792	MN258806	MN258820	MN258834	MN258848
	CSF8776[4,5,7,8,9]	1	AAAAA	*E. urophylla* hybrid clone	YaTang, LianJiang, ZhanJiang, GuangDong, China	N21°33'43.000" E110°1'55.700"	J. Roux & S.F. Chen	MN258793	MN258807	MN258821	MN258835	MN258849
	CSF8777[4,5,7,8]	1	AAAAA	*E. urophylla* hybrid clone	YaTang, LianJiang, ZhanJiang, GuangDong, China	N21°33'43.000" E110°1'55.700"	J. Roux & S.F. Chen	MN258794	MN258808	MN258822	MN258836	MN258850
Par. guangdongensis	CSF10437[4,5]	2	BBBAA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258795	MN258809	MN258823	MN258837	MN258851
	CSF10438[4,5,7,8]	2	BBBAA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258796	MN258810	MN258824	MN258838	MN258852
	CSF10440[4,5]	2	BBBAA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258797	MN258811	MN258825	MN258839	MN258853
	CSF10459[4,5]	2	BBBAA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258798	MN258812	MN258826	MN258840	MN258854
	CSF10460[4,5,6,7,8,9]	2	BBBAA	*E. urophylla* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'00.960" E110°05'32.690"	S.F. Chen & W. Wang	MN258799	MN258813	MN258827	MN258841	MN258855
	CSF10738[4,5,7,8,9]	2	BBBAA	*E. grandis* hybrid clone	LingBei, SuiXi, ZhanJiang, GuangDong, China	N21°16'02.972" E110°05'15.802"	S.F. Chen & W. Wang	MN258800	MN258814	MN258828	MN258842	MN258856

[1] Genotype number within genera of *Chrysoporthe*, *Celoporthe*, *Aurifilum* and *Parvosmorbus*.
[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 *Cryphonectriaceae*' and 'Species identification in *Cryphonectriaceae*'.
[5] Isolates used for phylogenetic analyses of 'Phylogenetic analyses of *Chrysoporthe*' and 'Phylogenetic analyses of *Celoporthe*'.
[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) *Parvosmorbus 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. fraxinopennsylvanica* (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 1 000 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 5 000 and zero-length branches were collapsed. A bootstrap analysis (50 % majority rule, 1 000 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 1 000, and nodal support was determined by non-parametric bootstrapping with 1 000 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*	*TEF*	
Amphilogia gyrosa	CMW10469[T]	*Elaeocarpus dentatus*	New Zealand	G.J. Samuels	AY194107	AF452111	AF525714	AF525707	N/A[3]	Gryzenhout et al. (2005a, 2006c)
	CMW10470	*Ela. dentatus*	New Zealand	G.J. Samuels	AY194108	AF452112	AF525715	AF525708	N/A	Gryzenhout et al. (2005a, 2006c)
Aurantioporthe corni	ATCC66834	*Cornus alternifolia*	USA	N/A	AF277133	N/A	N/A	N/A	N/A	Zhang & Blackwell (2001)
	CMW10526	*Cor. alternifolia*	USA	S. Redlin	AF408343	DQ120762	DQ120770	DQ120769	N/A	Gryzenhout et al. (2006c)
	MES1001	N/A	USA	W. Cullina	N/A	KF495039	N/A	KF495069	N/A	Beier et al. (2015)
	CTS1001	N/A	USA	K. Kitka	N/A	KF495033	N/A	KF495063	N/A	Beier et al. (2015)
Aurantiosacculus acutatus	CBS132181[T]	*Euc. viminalis*	Australia	B.A. Summerell & P. Summerell	JQ685520	JQ685514	N/A	N/A	N/A	Crous et al. (2012a)
Aurantiosacculus eucalyptorum	CBS130826[T]	*Eucalyptus globulus*	Australia	C. Mohammed & M. Glen	JQ685521	JQ685515	N/A	N/A	N/A	Crous et al. (2012a)
Aurapex penicillata	CMW10030[T]	*Miconia theaezans*	Colombia	C.A. Rodas	AY194103	AY214311	AY214275	AY214239	N/A	Gryzenhout et al. (2006b, 2009)
	CMW11295	*Mic. theaezans*	Colombia	C.A. Rodas	AY194089	N/A	N/A	N/A	N/A	Gryzenhout et al. (2009)
	CMW10035	*Mic. theaezans*	Colombia	C.A. Rodas	N/A	AY214313	AY214277	AY214241	N/A	Gryzenhout et al. (2006b, 2009)
Aurifilum marmelostoma	CMW28285[T]	*Terminalia mantaly*	Cameroon	D. Begoude & J. Roux	HQ171215	FJ882855	FJ900590	FJ900585	N/A	Begoude et al. (2010), Vermeulen et al. (2011)
	CMW28288	*Ter. ivorensis*	Cameroon	D. Begoude & J. Roux	HQ171216	FJ882856	FJ900591	FJ900586	N/A	Begoude et al. (2010), Vermeulen et al. (2011)
Capillaureum caryovora	CBL02[T]	*Caryocar brasiliense*	Brazil	Soares de Oliveira & Ferreira	MG192104	MG192094	MG211808	MG211827	N/A	Ferreira et al. (2019)
	CBL06	*Caryocar brasiliense*	Brazil	Soares de Oliveira & Ferreira	MG192106	MG192096	MG211810	MG211829	N/A	Ferreira et al. (2019)
Celoporthe borbonica	CMW44128[T]	*Tibouchina grandiflora*	La Réunion	M. J. Wingfield	N/A	MG585741	N/A	MG585725	N/A	Ali et al. (2018)
	CMW44139	*Tib. grandiflora*	La Réunion	M. J. Wingfield	N/A	MG585742	N/A	MG585726	N/A	Ali et al. (2018)
Celoporthe cerciana	CERC9128[T]	*Eucalyptus* hybrid tree 4	GuangDong, China	S. F. Chen	N/A	MH084352	MH084412	MH084382	MH084442	Wang et al. (2018)
	CERC9125	*Eucalyptus* hybrid tree 1	GuangDong, China	S. F. Chen	N/A	MH084349	MH084409	MH084379	MH084439	Wang et al. (2018)
Celoporthe dispersa	CMW9976[T]	*Syzygium cordatum*	South Africa	M. Gryzenhout	HQ730853	DQ267130	DQ267142	DQ267136	HQ730840	Nakabonge et al. (2006), Chen et al. (2011)
	CMW9978	*S. cordatum*	South Africa	M. Gryzenhout	HQ730854	AY214316	DQ267141	DQ267135	HQ730841	Nakabonge et al. (2006), Chen et al. (2011)
Celoporthe eucalypti	CMW26900	*Eucalyptus* clone EC48	China	X.D. Zhou & S.F. Chen	HQ730862	HQ730836	HQ730826	HQ730816	HQ730849	Chen et al. (2011)
	CMW26908[T]	*Eucalyptus* clone EC48	China	X.D. Zhou & S.F. Chen	HQ730863	HQ730837	HQ730827	HQ730817	HQ730850	Chen et al. (2011)
Celoporthe fontana	CMW29375	*S. guineense*	Zambia	M. Vermeulen & J. Roux	N/A	GU726940	GU726952	GU726952	JQ824073	Vermeulen et al. (2013)
	CMW29376[T]	*S. guineense*	Zambia	M. Vermeulen & J Roux	N/A	GU726941	GU726953	GU726953	JQ824074	Vermeulen et al. (2013)
Celoporthe guangdongensis	CMW12750[T]	*Eucalyptus* sp.	China	T.I. Burgess	HQ730856	HQ730830	HQ730820	HQ730810	HQ730843	Chen et al. (2011)
Celoporthe indonesiensis	CMW10781[T]	*S. aromaticum*	Indonesia	M.J. Wingfield	HQ730855	AY084009	AY084021	AY084033	HQ730842	Myburg et al. (2003), Chen et al. (2011)
Celoporthe syzygii	CMW34023[T]	*S. cumini*	China	S.F. Chen	HQ730857	HQ730831	HQ730821	HQ730811	HQ730844	Chen et al. (2011)
	CMW24912	*S. cumini*	China	M.J. Wingfield & X.D. Zhou	HQ730859	HQ730833	HQ730823	HQ730813	HQ730846	Chen et al. (2011)
Celoporthe tibouchineae	CMW44126[T]	*Tib. grandiflora*	La Réunion	M. J. Wingfield	N/A	MG585747	N/A	MG585731	N/A	Ali et al. (2018)
	CMW44127	*Tib. grandiflora*	La Réunion	M. J. Wingfield	N/A	MG585748	N/A	MG585732	N/A	Ali et al. (2018)
Celoporthe woodiana	CMW13936[T]	*Tib. granulosa*	South Africa	M. Gryzenhout	N/A	DQ267131	DQ267143	DQ267137	JQ824071	Vermeulen et al. (2013)
	CMW13937	*Tib. granulosa*	South Africa	M. Gryzenhout	N/A	DQ267132	DQ267144	DQ267138	JQ824072	Vermeulen et al. (2013)
Chrysocrypta corymbiae	CBS132528[T]	*Corymbia* sp.	Australia	P.W. Crous & B.A. Summerell	JX069851	JX069867	N/A	N/A	N/A	Crous et al. (2012b)
Chrysofolia colombiana	CBS139909[T]	*Euc. urophylla* × *Euc. grandis*	Colombia	M.J. Wingfield	KR476771	KR476738	N/A	N/A	N/A	Crous et al. (2015)
Chrysomorbus lagerstroemiae	CERC8780	*Lagerstroemia speciosa*	China	J. Roux & S.F. Chen	KY929320	KY929330	KY929340	KY929350	N/A	Chen et al. (2018)
	CERC8810[T]	*L. speciosa*	China	S.F. Chen	KY929328	KY929338	KY929348	KY929358	N/A	Chen et al. (2018)
Chrysoporthe austroafricana	CMW62	*Euc. grandis*	South Africa	M.J. Wingfield	AY194097	AF292041	AF273458	AF273063	N/A	Myburg et al. (2002b), Gryzenhout et al. (2006c)
	CMW9327	*Tib. granulosa*	South Africa	J. Roux	N/A	AF273473	AF273455	AF273060	N/A	Myburg et al. (2002a)
	CMW2113[T]	*Euc. grandis*	South Africa	M.J. Wingfield	N/A	AF046892	AF273462	AF273067	N/A	Myburg et al. (1999, 2002b)
Chrysoporthe cubensis	CBS101281	*Euc. urophylla*	Cameroon	I.A.S. Gibson	AF408338	N/A	N/A	N/A	N/A	Castlebury et al. (2002)
	CMW10453	*Euc. saligna*	Democratic Republic of the Congo	N/A	AF408339	AY063476	AY063480	AY063478	N/A	Castlebury et al. (2002), Gryzenhout et al. (2005b)
	CMW8758	*Eucalyptus* sp.	Venezuela	M.J. Wingfield	AY194098	AF046898	AF273463	AF273068	N/A	Myburg et al. (2002b), Gryzenhout et al. (2006c)
	CMW10669	*Eucalyptus* sp.	Republic of the Congo	J. Roux	N/A	AF535122	AF535126	AF535124	N/A	Gryzenhout et al. (2004, 2005b)
	CMW10639	*Euc. grandis*	Colombia	C.A. Rodas	N/A	AY263421	AY263420	AY263419	N/A	Gryzenhout et al. (2004)
Chrysoporthe deuterocubensis	CMW11290	*Eucalyptus* sp.	Indonesia	M.J. Wingfield	N/A	AY214304	AY214268	AY214232	N/A	Gryzenhout et al. (2004)
	CMW8651	*S. aromaticum*	Indonesia	M.J. Wingfield	N/A	AY084002	AY084014	AY084026	N/A	Myburg et al. (2003)
Chrysoporthe doradensis	CMW11287[T]	*Euc. grandis*	Ecuador	M.J. Wingfield	N/A	AY214289	AY214253	AY214217	N/A	Gryzenhout et al. (2005b)
	CMW11286	*Euc. grandis*	Ecuador	M.J. Wingfield	N/A	AY214290	AY214254	AY214218	N/A	Gryzenhout et al. (2005b)
Chrysoporthe hodgesiana	CMW10625	*Mic. theaezans*	Colombia	C.A. Rodas	N/A	AY956970	AY956980	AY956979	N/A	Rodas et al. (2005)
	CMW9995	*Tib. semidecandra*	Colombia	R. Arbelaez	N/A	AY956969	AY956978	AY956977	N/A	Rodas et al. (2005)
	CMW10641[T]= CBS115854	*Tib. semidecandra*	Colombia	R. Arbelaez	N/A	AY692322	AY692325	AY692326	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*	*TEF*	
Chrysoporthe inopina	CMW12727[T]	*Tib. lepidota*	Colombia	R. Arbelaez	N/A	DQ368777	DQ368807	DQ368806	N/A	Gryzenhout et al. (2006d)
	CMW12729	*Tib. lepidota*	Colombia	R. Arbelaez	N/A	DQ368778	DQ368809	DQ368808	N/A	Gryzenhout et al. (2006d)
Chrysoporthe syzygiicola	CMW29940[T]= CBS124488	*S. guineense*	Zambia	D. Chungu & J. Roux	N/A	FJ655005	FJ805236	FJ805230	N/A	Chungu et al. (2010)
	CMW29942= CBS124490	*S. guineense*	Zambia	D. Chungu & J. Roux	N/A	FJ655007	FJ805238	FJ805232	N/A	Chungu et al. (2010)
Chrysoporthe zambiensis	CMW29928[T]= CBS124503	*Euc. grandis*	Zambia	D. Chungu & J. Roux	N/A	FJ655002	FJ805233	FJ858709	N/A	Chungu et al. (2010)
	CMW29930= CBS124502	*Euc. grandis*	Zambia	D. Chungu & J. Roux	N/A	FJ655004	FJ805235	FJ858711	N/A	Chungu et al. (2010)
Corticimorbus sinomyrti	CERC3629[T]	*Rhodomyrtus tomentosa*	China	S.F. Chen & G.Q. Li	KT167179	KT167169	KT167189	KT167189	N/A	Chen et al. (2016)
	CERC3631	*Rho. tomentosa*	China	S.F. Chen & G.Q. Li	KT167180	KT167170	KT167190	KT167190	N/A	Chen et al. (2016)
Cryphonectria decipiens	CMW10436	*Quercus suber*	Portugal	B. d'Oliviera	JQ862750	AF452117	AF525710	AF525703	N/A	Myburg et al. (2004b), Chen et al. (2013a)
	CMW10484	*Castanea sativa*	Italy	A. Biraghi	N/A	AF368327	AF368349	AF368349	N/A	Venter et al. (2002), Myburg et al. (2004b)
Cryphonectria japonica	CMW10527	*Q. mongolica*	Russia	L. Vasilyeva	AF408341	DQ120761	DQ120768	DQ120767	N/A	Castlebury et al. (2002), Gryzenhout et al. (2006c)
	CMW10528	*Q. mongolica*	Russia	L. Vasilyeva	AF408340	DQ120760	DQ120766	DQ120765	N/A	Castlebury et al. (2002), Gryzenhout et al. (2006c)
	CMW13742	*Q. grosseserrata*	Japan	T. Kobayashi	N/A	AY697936	AY697962	AY697961	N/A	Myburg et al. (2004a)
	CMW13747	*Q. serrata*	Japan	T. Kobayashi	N/A	AY697937	AY697964	AY697963	N/A	Myburg et al. (2004a)
Cryphonectria macrospora	CMW10463	*Cas. cuspidata*	Japan	T. Kobayashi	N/A	AF368331	AF368350	AF368351	N/A	Gryzenhout et al. (2006c)
	CMW10914	*Cas. cuspidata*	Japan	T. Kobayashi	JQ862749	AY697942	AY697974	AY697973	N/A	Gryzenhout et al. (2006c), Chen et al. (2013a)
Cryphonectria parasitica	N/A	*Castanea* sp.	N/A	N/A	AF277132	N/A	N/A	N/A	N/A	Zhang & Blackwell (2001)
	CMW7048	*Q. virginiana*	USA	R.J. Stipes	AY194100	AF368330	AF273470	AF273076	N/A	Venter et al. (2002), Gryzenhout et al. (2006c)
	CMW13749	*Cas. mollisima*	Japan	N/A	N/A	AY697927	AY697944	AY697943	N/A	Myburg et al. (2004a)
Cryphonectria quercicola	CFCC52140[T]	*Q. wutaishansea*	ShaanXi, China	N. Jiang	N/A	MG866026	MG896113	MG896117	N/A	Jiang et al. (2018)
	CFCC52141	*Q. wutaishansea*	ShaanXi, China	N. Jiang	N/A	MG866027	MG896114	MG896118	N/A	Jiang et al. (2018)
Cryphonectria quercus	CFCC52138[T]	*Q. aliena* var. *acuteserrata*	ShaanXi, China	N. Jiang	N/A	MG866024	MG896111	MG896115	N/A	Jiang et al. (2018)
	CFCC52139	*Q. aliena* var. *acuteserrata*	ShaanXi, China	N. Jiang	N/A	MG866025	MG896112	MG896116	N/A	Jiang et al. (2018)
Cryphonectria radicalis	CMW10455	*Q. suber*	Italy	A. Biraghi	AY194101	AF452113	AF525712	AF525705	N/A	Gryzenhout et al. (2006c)
	CMW10477	*Q. suber*	Italy	A. Biraghi	AY194102	AF368328	AF368347	AF368347	N/A	Venter et al. (2002), Gryzenhout et al. (2006c)
	CMW13754	*Fagus japonica*	Japan	T. Kobayashi	N/A	AY697932	AY697954	AY697953	N/A	Myburg et al. (2004a)
Cryptometrion aestuescens	CMW18790	*Euc. grandis*	Indonesia	M.J. Wingfield	HQ171211	GQ369458	GQ369455	GQ369455	N/A	Gryzenhout et al. (2010), Vermeulen et al. (2011)
	CMW18793	*Euc. grandis*	Indonesia	M.J. Wingfield	HQ171212	GQ369459	GQ369456	GQ369456	N/A	Gryzenhout et al. (2010), Vermeulen et al. (2011)
	CMW28535[T]= CBS124009	*Euc. grandis*	North Sumatra, Indonesia	M.J. Wingfield	N/A	GQ369457	GQ369454	GQ369454	N/A	Gryzenhout et al. (2010)
Diversimorbus metrosiderotis	CMW37321	*Metrosideros angustifolia*	South Africa	J. Roux	JQ862827	JQ862870	JQ862952	JQ862911	N/A	Chen et al. (2013b)
	CMW37322[T]	*Met. angustifolia*	South Africa	J. Roux	JQ862828	JQ862871	JQ862953	JQ862912	N/A	Chen et al. (2013b)
Endothia gyrosa	N/A	*Quercus* sp.	USA	N/A	AF362555	N/A	N/A	N/A	N/A	Gryzenhout et al. (2009)
	CMW2091	*Q. palustris*	USA	R.J. Stipes	AY194114	AF368325	AF368336	AF368337	N/A	Venter et al. (2002), Gryzenhout et al. (2006c)
	CMW10442	*Q. palustris*	USA	R.J. Stipes	AY194115	AF368326	AF368338	AF368339	N/A	Venter et al. (2002), Gryzenhout et al. (2006c)
Foliocryphia eucalypt	CBS124779[T]	*Euc. coccifera*	Australia	C. Mohammed	GQ303307	GQ303276	N/A	N/A	N/A	Cheewangkoon et al. (2009)
Holocryphia capensis	CMW37887[T]	*Met. angustifolia*	South Africa	J. Roux, S.F. Chen & F. Roets	JQ862811	JQ862854	JQ862936	JQ862895	JQ863051	Chen et al. (2013b)
	CMW37329	*Met. angustifolia*	South Africa	J. Roux & S.F. Chen	JQ862816	JQ862859	JQ862941	JQ862900	JQ863056	Chen et al. (2013b)
Holocryphia eucalypti	CMW7033[T]	*Euc. grandis*	South Africa	M. Venter	JQ862794	JQ862837	JQ862919	JQ862878	JQ863034	Chen et al. (2013b)
	CMW7035	*Euc. saligna*	South Africa	M. Venter	JQ862795	JQ862838	JQ862920	JQ862879	JQ863035	Chen et al. (2013b)
Holocryphia gleniana	CMW37334[T]	*Met. angustifolia*	South Africa	J. Roux & S.F. Chen	JQ862791	JQ862834	JQ862916	JQ862875	JQ863031	Chen et al. (2013b)
	CMW37335	*Met. angustifolia*	South Africa	J. Roux & S.F. Chen	JQ862792	JQ862835	JQ862917	JQ862876	JQ863032	Chen et al. (2013b)
Holocryphia mzansi	CMW37337[T]	*Met. angustifolia*	South Africa	J. Roux & S.F. Chen	JQ862798	JQ862841	JQ862923	JQ862882	JQ863038	Chen et al. (2013b)
	CMW37338	*Met. angustifolia*	South Africa	J. Roux & S.F. Chen	JQ862799	JQ862842	JQ862924	JQ862883	JQ863039	Chen et al. (2013b)
Holocryphia sp.	CMW6246	*Tib. granulosa*	Australia	M.J. Wingfield	JQ862802	JQ862845	JQ862927	JQ862886	JQ863042	Chen et al. (2013b)
Holocryphia sp.	CMW10015	*Euc. fastigata*	New Zealand	R.J. van Boven	JQ862806	JQ862849	JQ862931	JQ862890	JQ863046	Chen et al. (2013b)
Immersiporthe knoxdaviesiana	CMW37314[T]	*Rapanea melanophloeos*	South Africa	M.J. Wingfield & J. Roux	JQ862755	JQ862765	JQ862775	JQ862785	N/A	Chen et al. (2013a)
	CMW37315	*Rap. melanophloeos*	South Africa	M.J. Wingfield & J. Roux	JQ862756	JQ862766	JQ862776	JQ862786	N/A	Chen et al. (2013a)
Latruncella aurorae	CMW28274	*Galpinia transvaalica*	Swaziland	J. Roux	HQ171213	GU726946	GU726958	GU726958	N/A	Vermeulen et al. (2011)

Table 2 (cont.)

Identity	Isolate No.[1,2]	Host	Location	Collector	GenBank accession no.					References
					LSU	ITS	*BT2*	*BT1*	*TEF*	
Latruncella aurorae (cont.)	CMW28276[T]	*G. transvaalica*	Swaziland	J. Roux	HQ730872	GU726947	GU726959	GU726959	N/A	Vermeulen et al. (2011), Chen et al. (2011)
	CMW28275	*G. transvaalica*	Swaziland	J. Roux	HQ171214	HQ171209	HQ171207	HQ171207	N/A	Vermeulen et al. (2011)
Luteocirrhus shearii	CBS130775	*Banksia baxteri*	Australia	C. Crane	KC197018	KC197024	KC197009	KC197015	N/A	Crane & Burgess (2013)
	CBS130776[T]	*B. baxteri*	Australia	C. Crane	KC197019	KC197021	KC197006	KC197012	N/A	Crane & Burgess (2013)
Microthia havanensis	CMW11299	*Myrica faya*	Madeira	N/A	AY194087	N/A	N/A	N/A	N/A	Gryzenhout et al. (2009)
	CMW11300	*Myr. faya*	Madeira	N/A	AY194088	N/A	N/A	N/A	N/A	Gryzenhout et al. (2009)
	CMW11301	*Myr. faya*	Azores	C.S. Hodges & D.E. Gardner	N/A	AY214323	AY214287	AY214251	N/A	Gryzenhout et al. (2006a)
	CMW14550	*E. saligna*	Mexico	C.S. Hodges	N/A	DQ368735	DQ368742	DQ368741	N/A	Gryzenhout et al. (2006a)
Myrtonectria myrtacearum	CMW46433[T]	*Heteropyxis natalensis*	South Africa	Ali & J. Roux	MG585750	MG585736	MG585734	MG585720	N/A	Ali et al. (2018)
	CMW46435	*S. cordatum*	South Africa	Ali & J. Roux	MG585751	MG585737	MG585735	MG585721	N/A	Ali et al. (2018)
Rostraureum tropicale	CMW9972	*Terminalia ivorensis*	Ecuador	M.J. Wingfield	AY194092	AY167436	AY167431	AY167426	N/A	Gryzenhout et al. (2005c, 2006c)
	CMW10796[T]	*Ter. ivorensis*	Ecuador	M.J. Wingfield	N/A	AY167438	AY167433	AY167428	N/A	Gryzenhout et al. (2005c)
	CMW9971	*Ter. ivorensis*	Ecuador	M.J. Wingfield	N/A	AY167435	AY167430	AY167425	N/A	Gryzenhout et al. (2005c)
Ursicollum fallax	CMW18119[T]	*Coccoloba uvifera*	USA	C.S. Hodges	EF392860	DQ368755	DQ368759	DQ368758	N/A	Gryzenhout et al. (2006a, 2009)
	CMW18115	*Coc. uvifera*	USA	C.S. Hodges	N/A	DQ368756	DQ368761	DQ368760	N/A	Gryzenhout et al. (2006a)
Diaporthe ambigua	CMW5587	Malus domestica	South Africa	W.A. Smit	N/A	AF543818	AF543822	AF543820	N/A	Gryzenhout et al. (2006a)
	CMW5288	M. domestica	South Africa	W.A. Smit	N/A	AF543817	AF543821	AF543819	N/A	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; CFCC = 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 represent isolates in Beier et al. (2015).

[2] [T] 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 *Myrtales* 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 *Myrtales*, 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 (BM 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 *Myrtales* 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 *Myrtales* 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]	Maximum parsimony						
				PIC[2]	No. of trees	Tree length	CI[3]	RI[4]	RC[5]	HI[6]
Cryphonectriaceae	LSU	135	631	138	1000	350	0.500	0.845	0.845	0.500
	5.8S+BT2+BT1	151	675	115	1000	288	0.524	0.916	0.916	0.476
	ITS	156	615	299	1014	1479	0.430	0.909	0.909	0.570
	BT2+BT1	151	927	486	1000	2261	0.446	0.908	0.908	0.554
	ITS+BT2+BT1	156	1542	785	85	3829	0.431	0.905	0.905	0.569
Chrysoporthe	ITS	59	488	79	1	81	0.975	0.988	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
Celoporthe	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	0.866	0.952	0.824	0.134

Family / Genus	Dataset	Maximum likelihood									
		Subst. model[7]	NST[8]	Rate matrix				Ti/Tv ratio[9]	p-inv	Gamma	Rates
Cryphonectriaceae	LSU	TIM2+I+G	6	2.278	7.181	2.278	1	18.36	–	0.51	0.484	gamma
	5.8S+BT2+BT1	TIM2+I+G	6	1	2.66	1	1	10.311	–	0.73	2.392	gamma
	ITS	TIM2+I+G	6	1.949	3.04	1.949	1	6.317	–	0.37	0.541	gamma
	BT2+BT1	HKY+I+G	2	–	–	–	–	–	2.45	0.47	1.5	gamma
	ITS+BT2+BT1	TVM+I+G	6	1.261	4.477	1.261	1	4.477	–	0.445	0.956	gamma
Chrysoporthe	ITS	K80	2	–	–	–	–	–	1.155	0	–	equal
	BT2+BT1	TIM1+G	6	1	1.818	0.289	0.289	3.54	–	0	0.28	gamma
	ITS+BT2+BT1	TIM1+G	6	1	2	0.442	0.442	3.563	–	0	0.182	gamma
Celoporthe	ITS	TPM2+G	2	–	–	–	–	–	1.383	0	0.411	gamma
	BT2+BT1	TIM3+G	6	3.621	7.552	1	3.621	15.109	–	0	0.024	gamma
	TEF	TPM2uf+G	2	–	–	–	–	–	2.812	0	0.3	gamma
	ITS+BT2+BT1+TEF	TrN+G	6	1	2.823	1	1	4.258	–	0	0.166	gamma

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

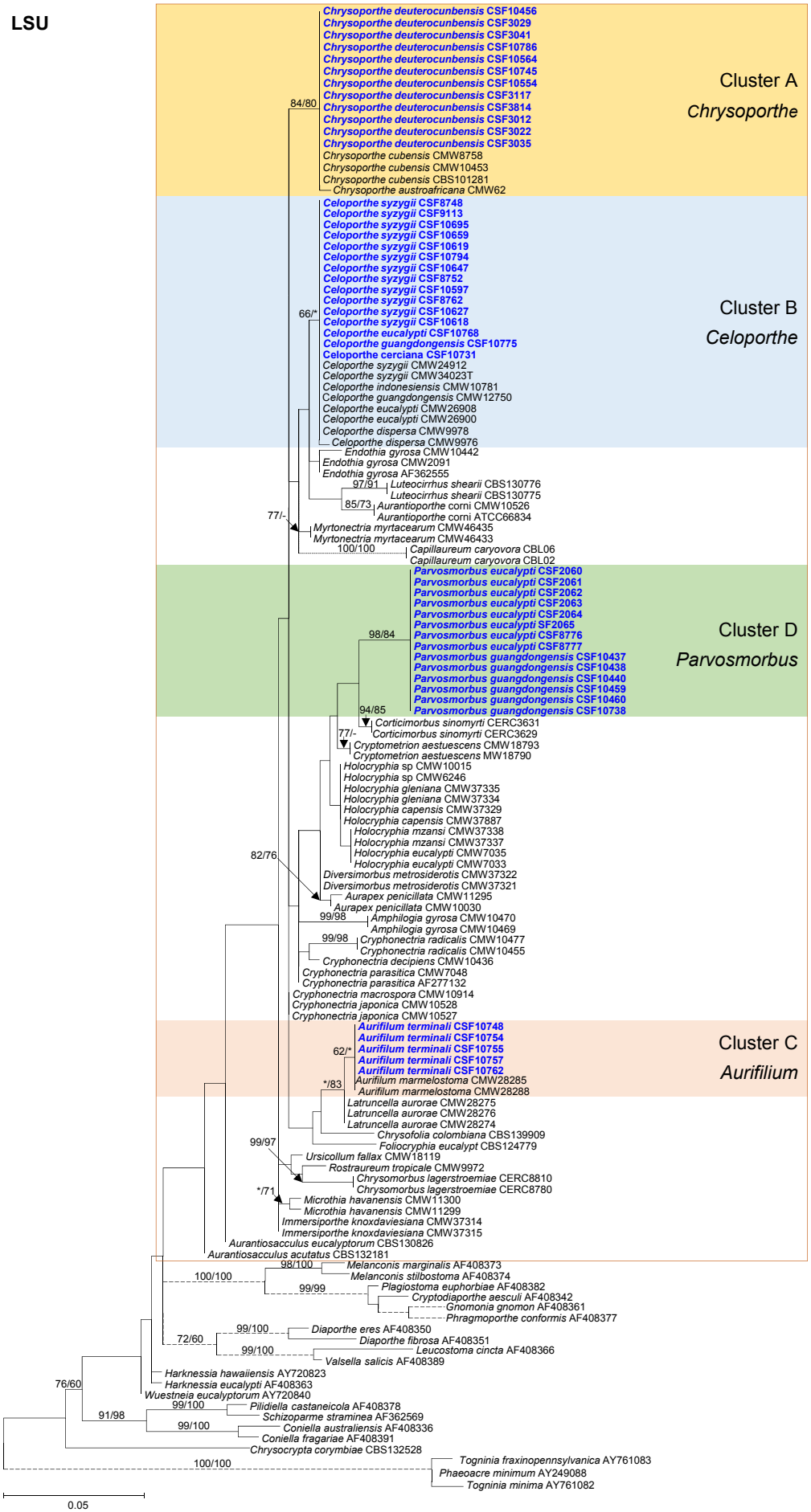

Fig. 3 Phylogenetic tree based on maximum likelihood (ML) analysis of LSU DNA sequences for various genera in *Diaporthales*. Bootstrap values ≥ 70 % for ML and MP (maximum parsimony) analyses are presented at branches as follows: ML/MP. Bootstrap values lower than 70 % are marked with *, and absent 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.

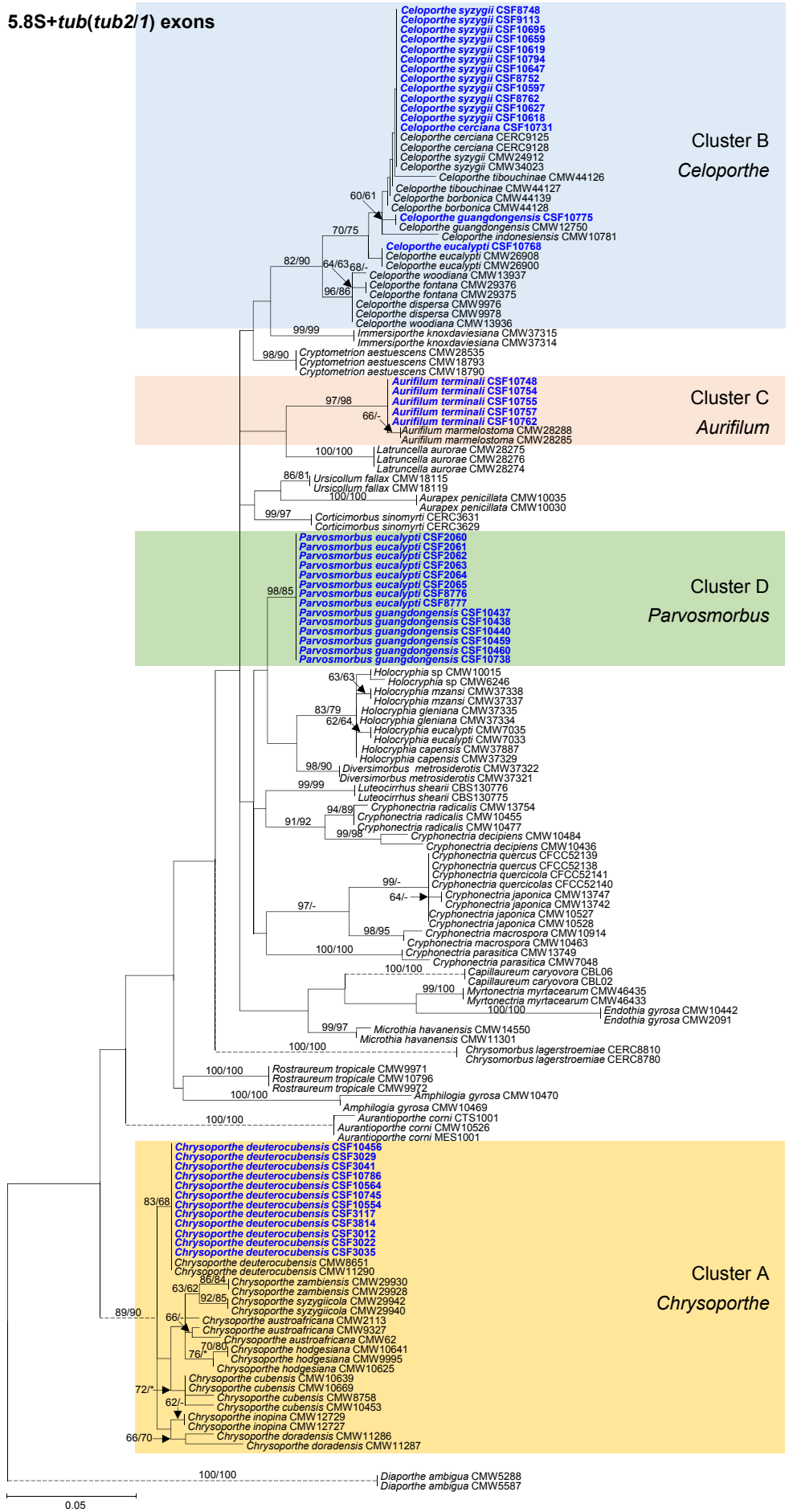

Fig. 4 Phylogenetic tree based on maximum likelihood (ML) analysis of a combined DNA sequence dataset of regions of the 5.8S rRNA gene, and partial exon 4, exon 5, partial exon 6 and partial exon 7 of the *tub* genes, for species in *Cryphonectriaceae*. Bootstrap values ≥ 70 % for ML and MP (maximum 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 ≥ 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.

similar for most genera. Based on the phylogenetic analyses of the combined sequences of the 5.8S gene and *tub* exons, the *Myrtales* 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

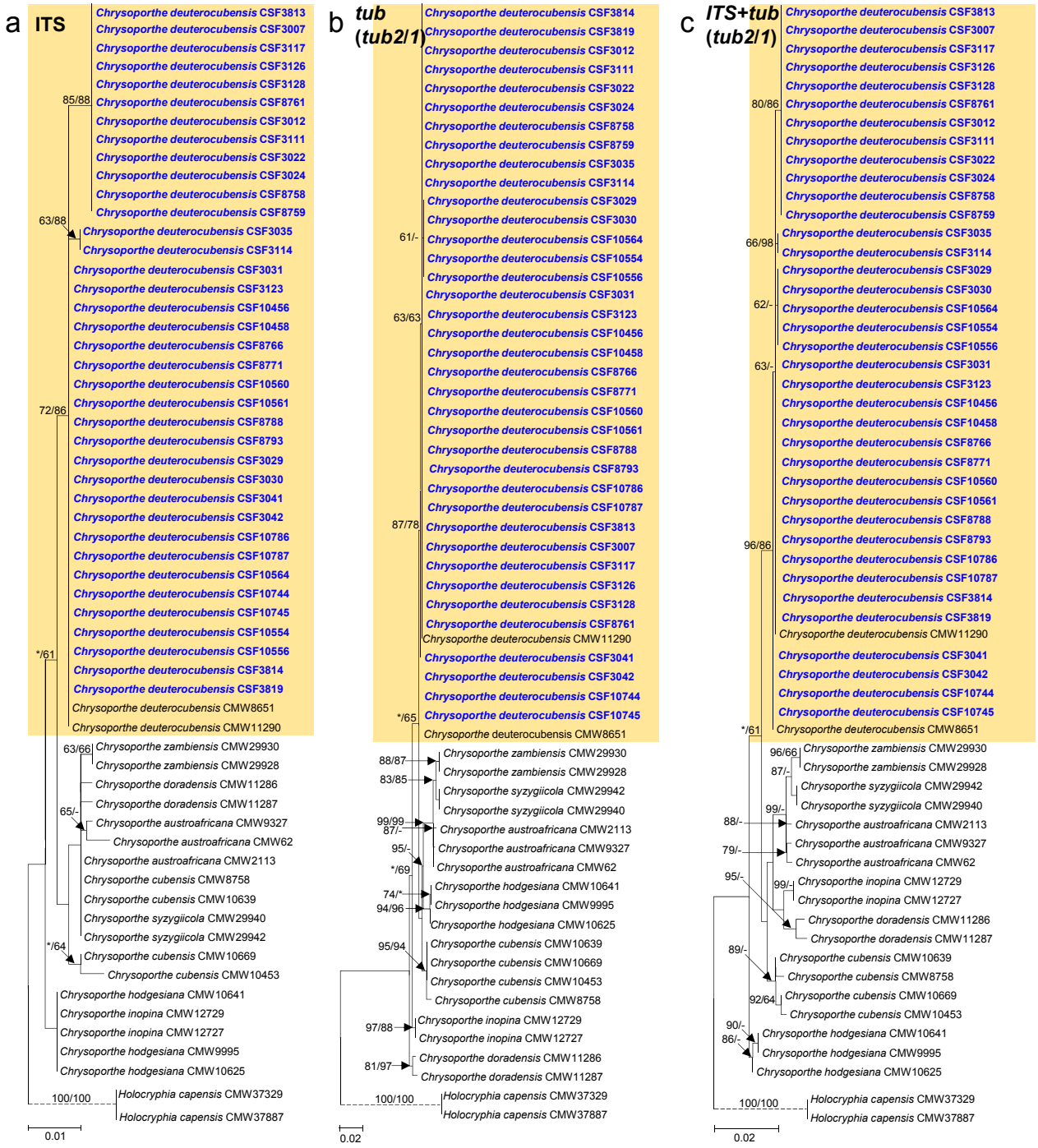

Fig. 6 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Chrysoporthe*. a. ITS region; b. two regions of *tub* (*tub2*/*tub1*); c. combination of ITS and *tub* (*tub2*/*tub1*) regions. Bootstrap values ≥ 70 % for ML and MP (maximum parsimony) analyses are presented at branches 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. *Holocryphia capensis* (CMW37329 and CMW37887) was used as outgroup taxon.

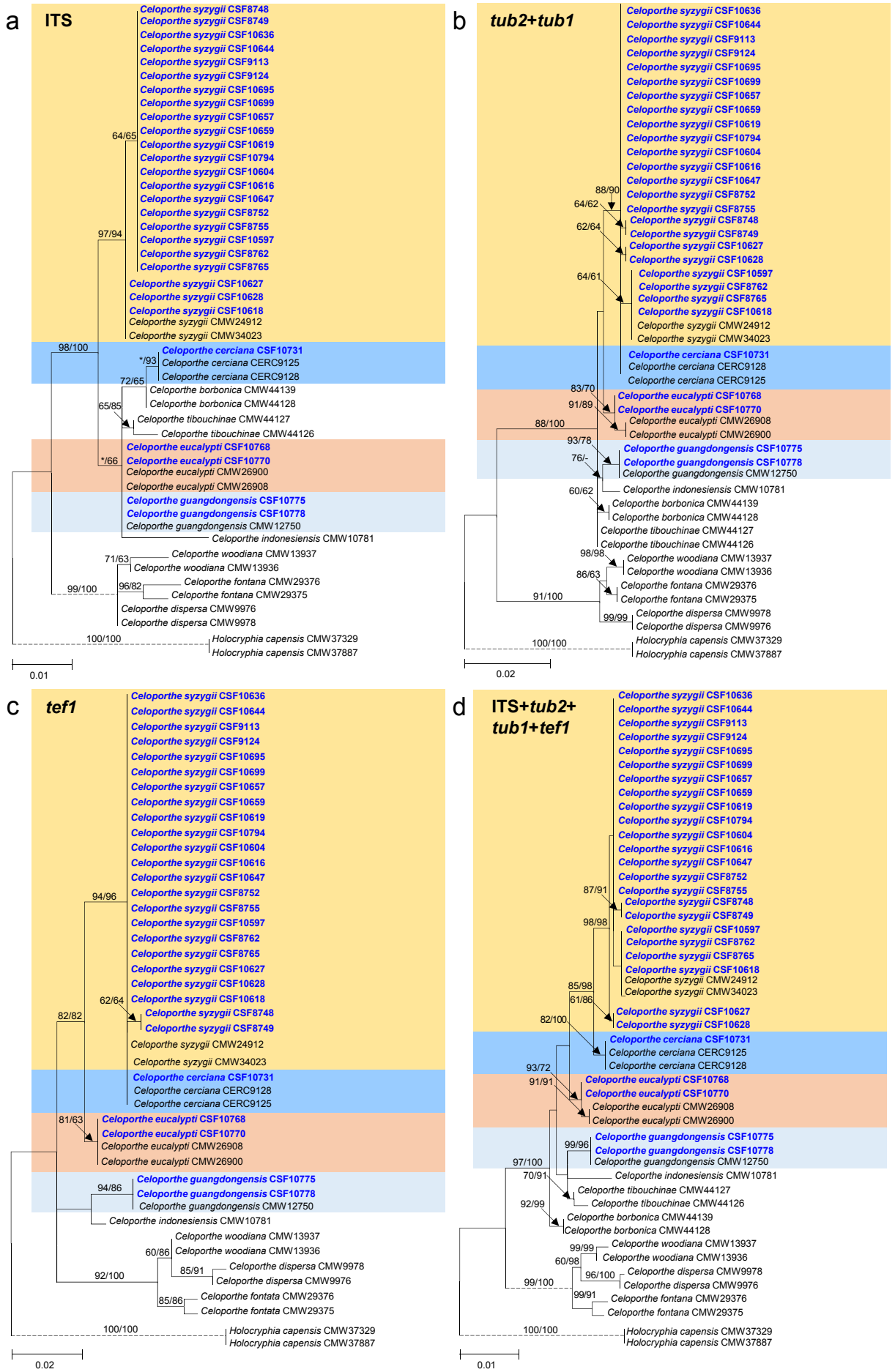

Fig. 7 Phylogenetic trees based on maximum likelihood (ML) analyses for species in *Celoporthe*. a. ITS region; b. two regions of *tub* (*tub2*/*tub1*); c. *tef1* gene region; d. combination of ITS, *tub2*/*tub1*, and *tef1* regions. Bootstrap values ≥ 70 % for ML and MP (maximum parsimony) analyses 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. *Holocryphia 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 *Myrtales* 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 *Myrtales* 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*, *Chrysofolia*, *Chrysoporthe*, *Corticimorbus*, *Diversimorbus*, *Luteocirrhus*, 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*

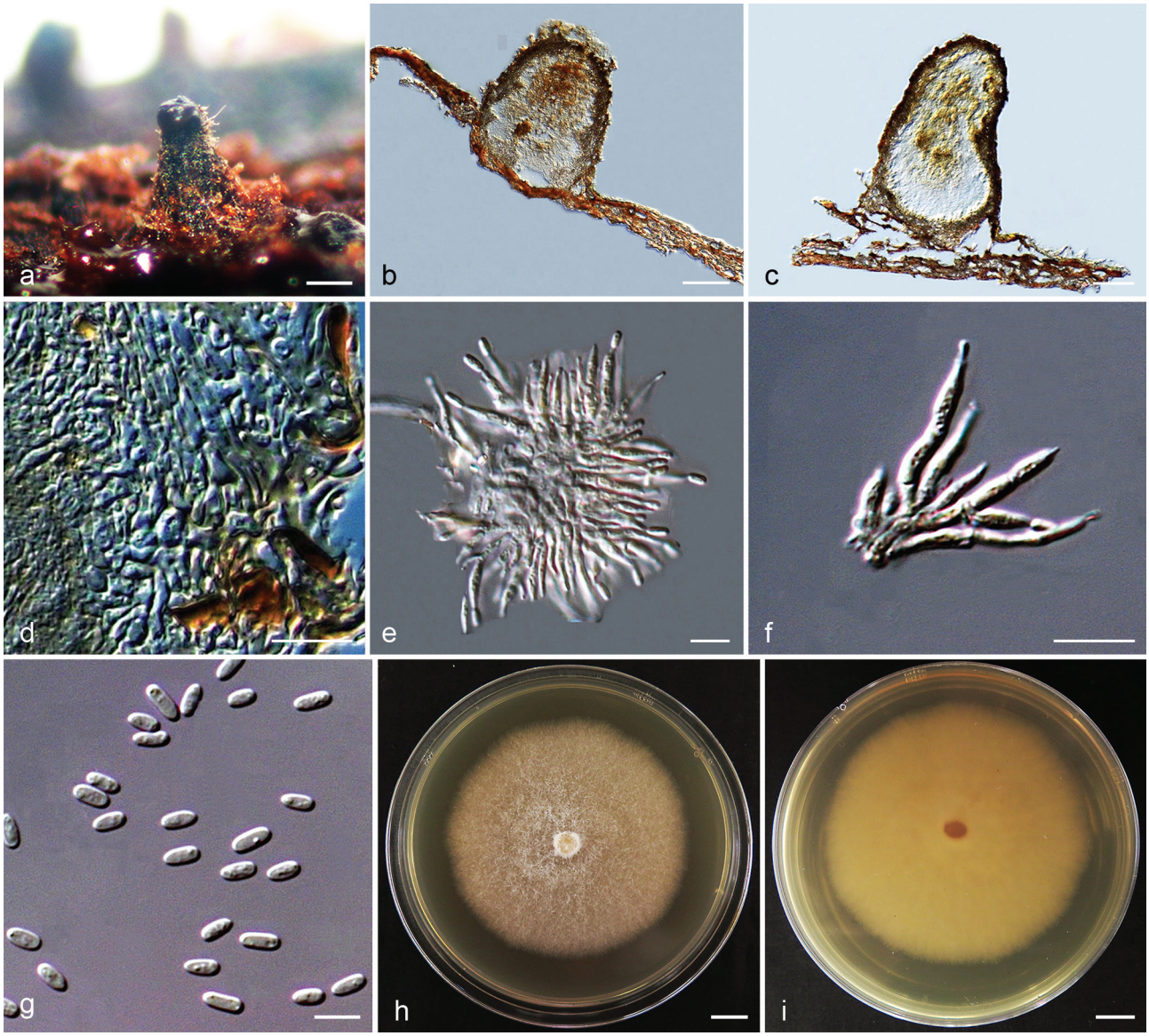

Fig. 8 Asexual sporocarps of *Parvosmorbus eucalypti*. a. Black conidiomata on the bark; b–c. longitudinal section through the conidioma showing unilocular stroma; d. *textura porrecta* stromatic tissue of the conidioma; e–f. aseptate, cylindrical conidiophores and cylindrical conidiogenous cells; g. 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 — *Parvosmorbus 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).

Parvosmorbus 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).

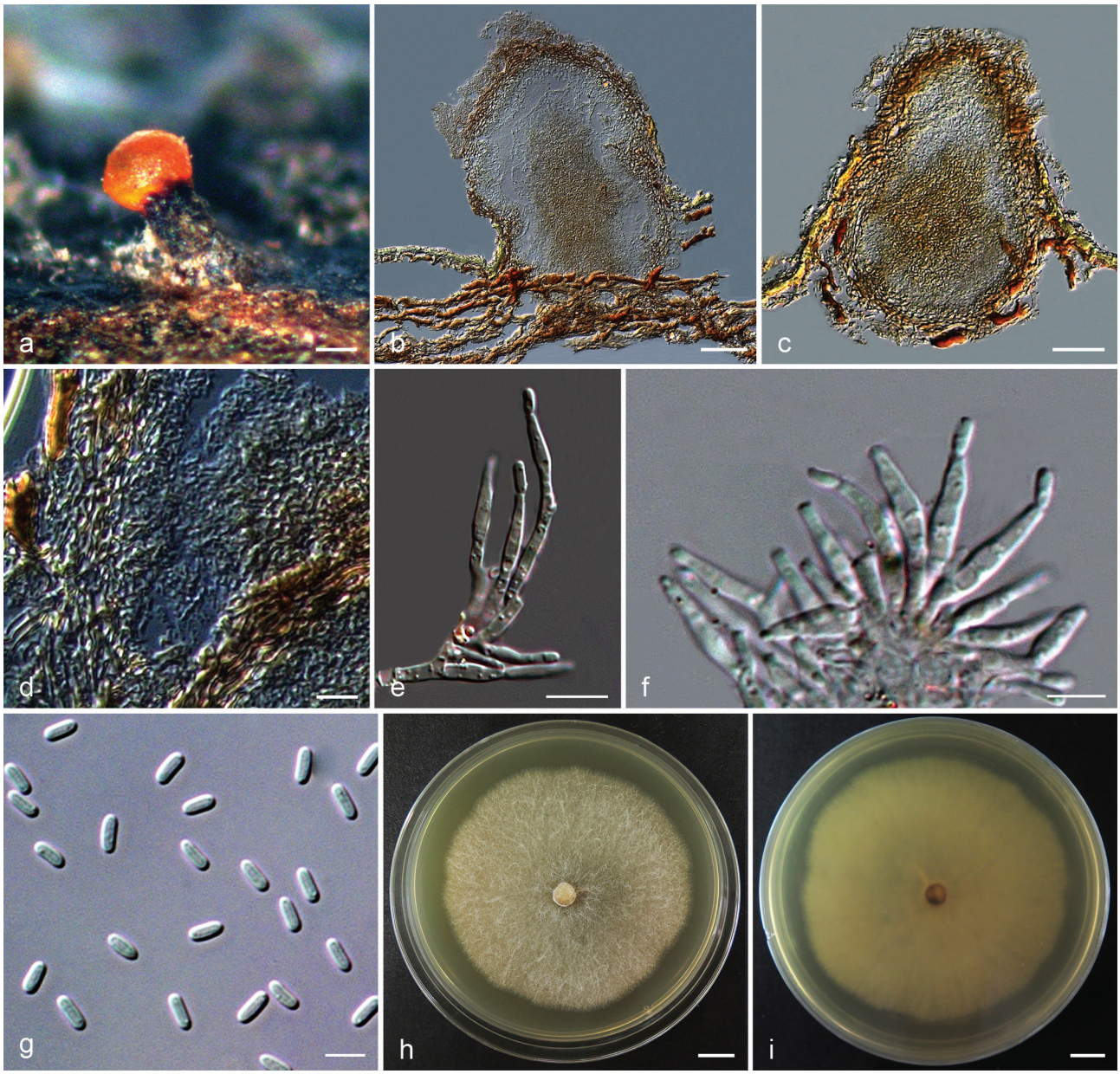

Fig. 9 Asexual sporocarps of *Parvosmorbus guangdongensis*. a. Black conidiomata with an orange conidial spore mass; b–c. longitudinal section through conidioma showing unilocular stroma; d. *textura porrecta* stromatic tissue of the conidioma; e–f. aseptate, cylindrical conidiophores and cylindrical 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.

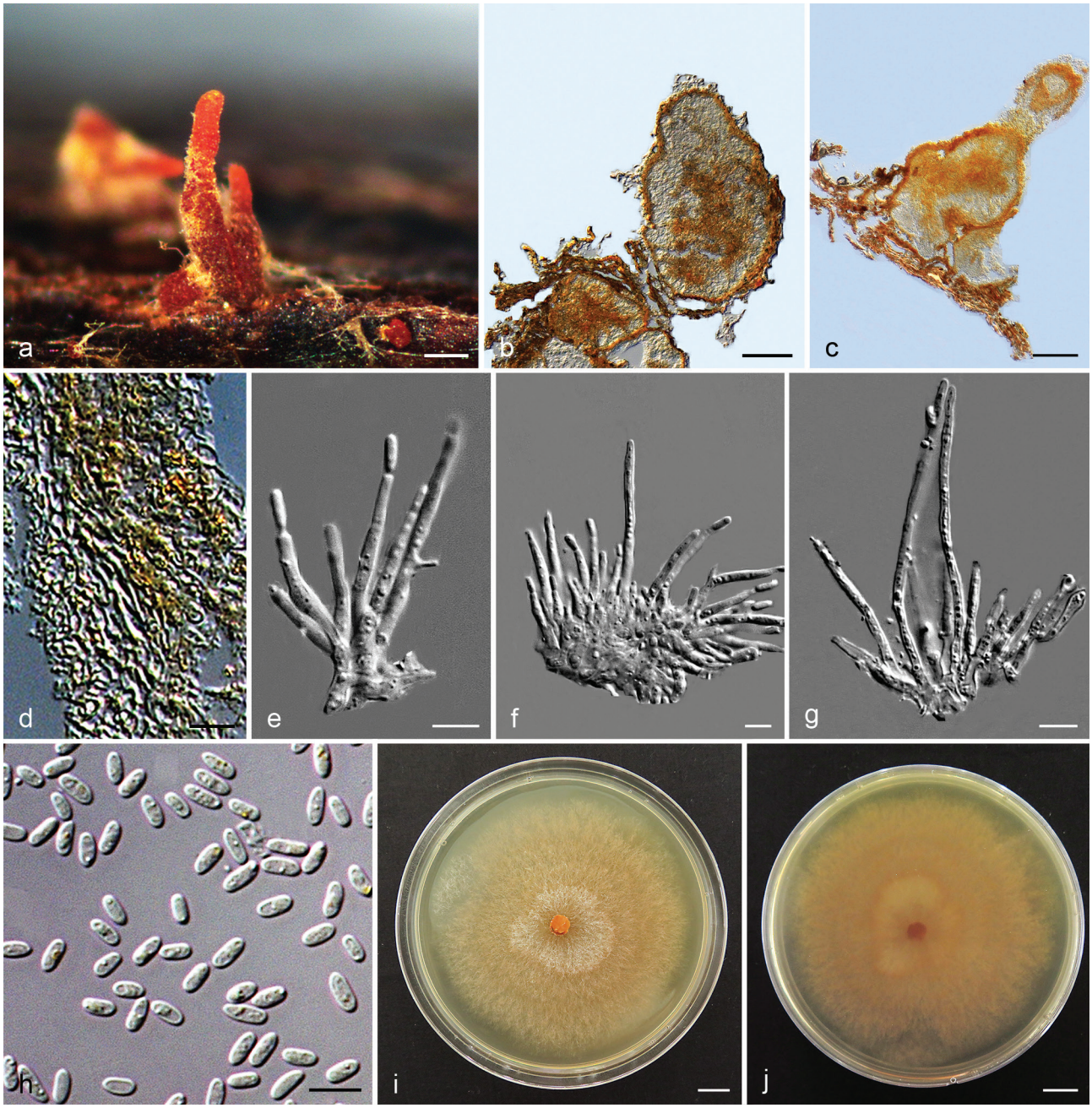

Fig. 10 Asexual sporocarps of *Aurifilum terminali*. a. Orange conidiomata with orange necks; b–c. longitudinal section through the conidioma showing orange and unilocular stroma; d. prosenchymatous stromatic tissue of the conidioma; e–f. conidiophores and cylindrical conidiogenous cells; g. paraphyses; 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 — *Parvosmorbus 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). *Parvosmorbus 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.

Typus. 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. Colony 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 CRYPHONECTRIACEAE ON MYRTALES

According 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 *Parvosmorbus* 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 *Parvosmorbus*, eight isolates were named as *Par. eucalypti* and six as *Par. guangdongensis* (Table 1, 4).

Of the eight species of *Cryphonectriaceae* 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 *Cryphonectriaceae* isolated from *Myrtales* trees in China in the current study.

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

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

isolates from *Myrtales*). In the current study, *Chr. deuterocubensis* and *Cel. syzygii* were isolated from trees/shrubs of four and three sampled genera of *Myrtales*, respectively. Each of the remaining six species of *Cryphonectriaceae* was only isolated from the trees of one *Myrtales* 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 *Myrtales*, 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* trees in China in previous studies.

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

[1] N/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]			
		Eucalyptus CEPT53	*Eucalyptus* CEPT46	*M. sanguineum*	*S. jambos*
Chrysoporthe deuterocunbensis	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
Celoporthe syzygii	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
Cel. guangdongensis	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
Cel. cerciana	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
Aurifilum terminali	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
	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
Parvosmorbus eucalypti	CSF2060	18.0±2.8 j-p	12.4±1.4 n-p	11.4±0.7 mn	23.8±9.1 d-l
	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
Par. guangdongensis	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
	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
Control		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. guajava* 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 *Parvosmorbus* 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 *Myrtales* trees in the field, and the re-isolated fungi from lesions shared the same culture morphology with the *Cryphonectriaceae* isolates originating from *Myrtales* trees. All of the species of *Cryphonectriaceae* were re-isolated from the lesions successfully, and no

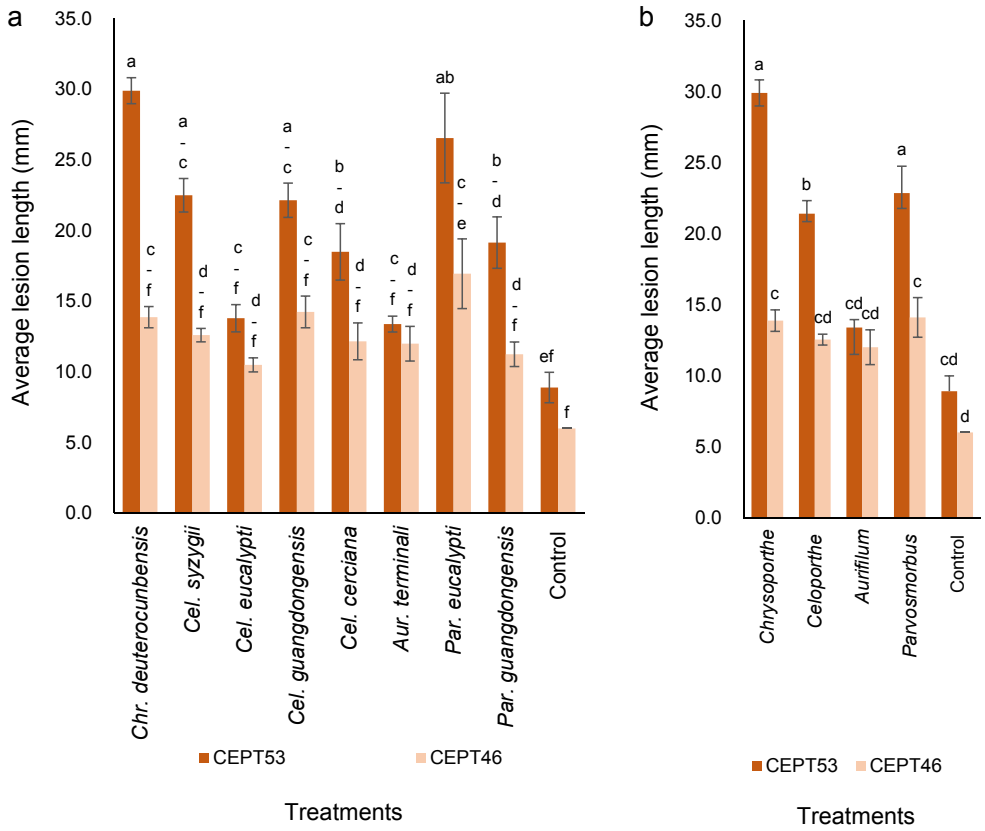

Fig. 11 a. Column chart indicating the average lesion length (in mm) produced by each species of *Cryphonectriaceae* on the seedlings of two *Eucalyptus* hybrid genotypes. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$); b. column chart indicating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

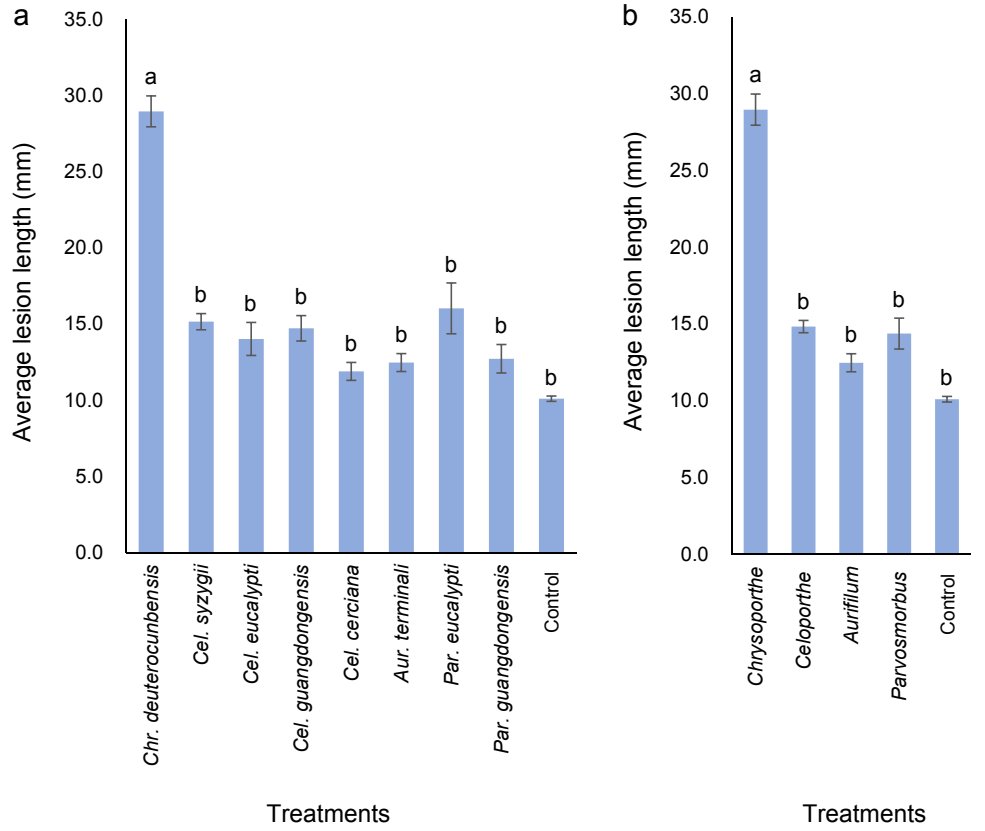

Fig. 12 a. Column chart indicating the average lesion length (in mm) produced by each species of *Cryphonectriaceae* on the branches of *Melastoma sanguineum*. Bars topped with different letters indicate treatment means that are significantly different ($P = 0.05$); b. column chart indicating the average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

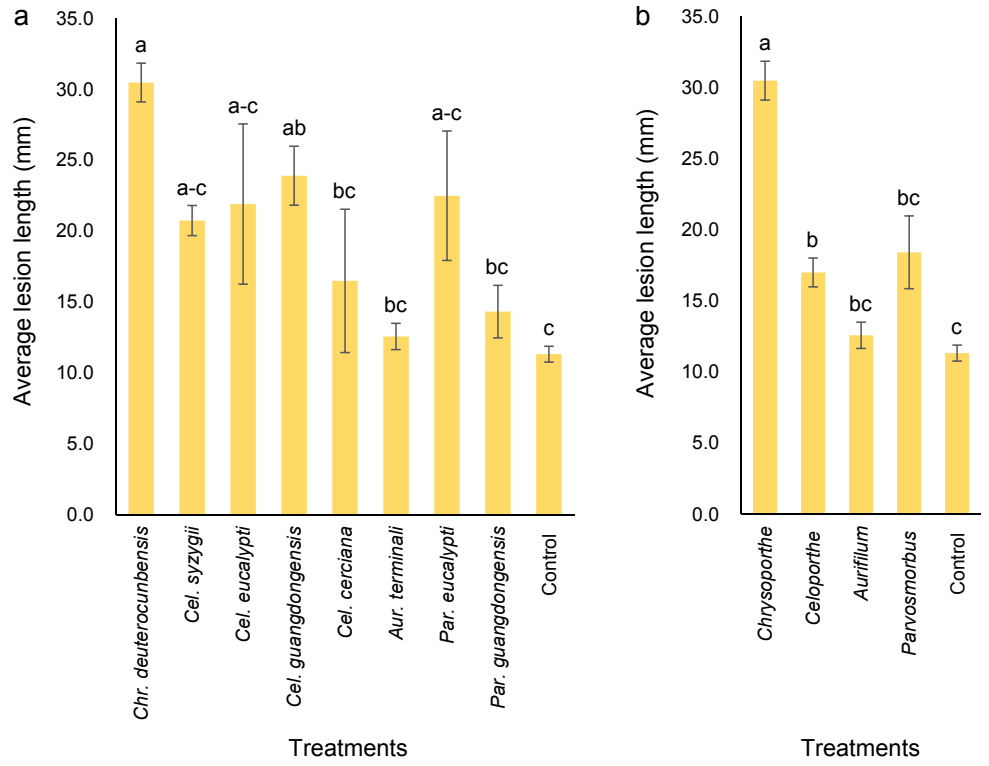

Fig. 13 a. Column chart indicating the average lesion length (in mm) produced by each species of *Cryphonectriaceae* on the branches of *Syzygium jambos*. Bars topped with different letters indicate treatment means that are significantly different (P = 0.05); b. column chart indicating the average lesion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

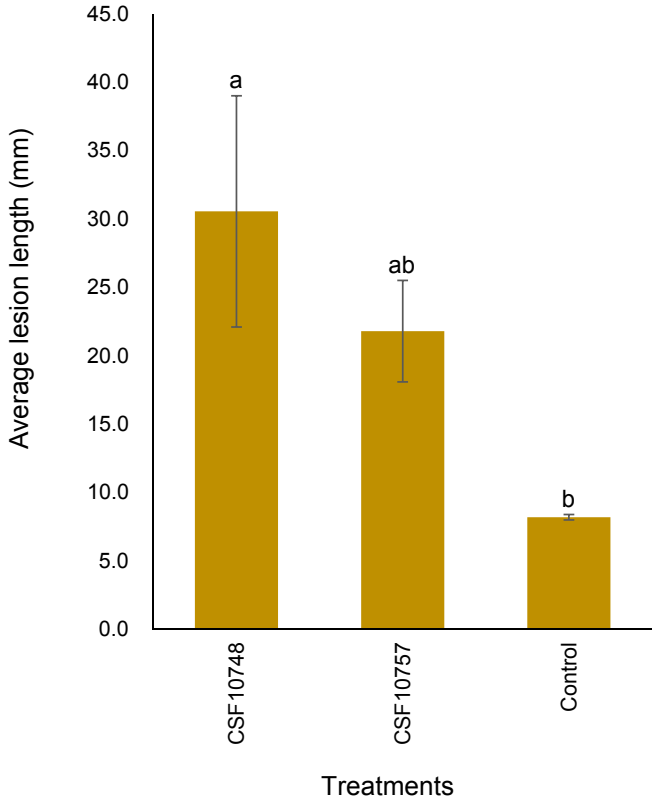

Fig. 14 Column chart indicating the average lesion length (in mm) produced by two isolates of *Aurifilum terminali* on the branches of *Terminalia neotaliala*. Bars topped with different letters indicate treatment means that are significantly different (P = 0.05).

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 *Parvosmorbus* gen. nov., *Parvosmorbus 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*. *Parvosmorbus 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 *Myrtales*, 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* 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.

Parvosmorbus 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, Ferreira et al. 2019). *Parvosmorbus* can be distinguished from all other genera in the family based on morphology and DNA sequence data. *Parvosmorbus* 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 *Parvosmorbus* 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 *Parvosmorbus* are pathogenic to *Eucalyptus* genotypes and other *Myrtales*. 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales* (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 expanded 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). *Myrtales* 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 *Myrtales* 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 *Myrtales* 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 *Myrtales*, which are crucially important for the disease management of *Cryphonectriaceae* on *Myrtales* in southern China.

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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 ≥ 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 ≥ 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 (*Parvosmorbus 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 (*Parvosmorbus eucalypti*).